UNIVERSITEIT GENT

FACULTY OF SCIENCES

TAXONOMY AND BIOGEOGRAPHY OF THE MYSIDA (PERACARIDA, CRUSTACEA):

A GLOBAL APPROACH THROUGH THE BIOLOGICAL INFORMATION SYSTEM NEMYS

Taxonomie en biogeografie van de Mysida:
Een globale aanpak via het Biologisch Informatiesysteem NeMys

Tim Deprez

Promotor: Prof. Dr. Magda Vincx
Co-promotor: Prof. Dr. Jan Mees

Academic year 2005 – 2006

Rector: Prof. Dr. Paul Van Cauwenberge
Dean: Prof. Dr. Herwig Dejonghe

Thesis submitted in partial fulfillment of the requirements for the degree of
Doctor in Science (Biology)

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SUMMARY

The Mysida (opossum shrimps) are a globally occurring order of Crustacea with 1086 species described. They are registered from all Oceans from the coasts until the deep sea. A biogeographical study covering this group on a global scale has never been done. Some global occurring genera (e.g. *Siriella* and *Anchialina*) cause systematic problems for many researchers. In order to study the global biogeographical patterns and to review these two genera, the digital biological information system NeMys was created.

NeMys is a generic online Biological Information System, which is developed as a research tool able to store any kind of biological relevant information. The two backbones of the system are systematic information and literature. As literature is one of the key components in taxonomic research, published information (data sources) is used throughout the whole system. Any data record in the database is linked with its data source, being in most cases a publication. All data are linked to taxa, and hence the systematic hierarchy and its history are a second crucial part.

Next to these two sets of data a number of linked data modules are available:

(1) geographic data: the exact location on which taxa have been recorded, based upon published literature, collection specimen information or field observations.

(2) morphological data: the morphological features of species can be entered making use of characters and character states, measurements, or text based descriptions. Morphological data can be reused in identification keys.

(3) media data: any kind of multimedia file may be linked to taxa (pictures, movies, drawings, …).

(4) molecular data: molecular data derived from GenBank is listed up.

(5) collection data: detailed information on specimens in natural history collections. Specimens can be documented with pictures and morphological data.

(6) any other kind of biological relevant information: through a generic component any kind of data can be added. For each dataset an unlimited number of data fields can be defined.

The generical construction of the database, meaning the system can be used for any group of organisms and any kind of data, and the online availability, may be considered as the key features of this application.

NeMys is accessible through an online interface. All data consultation, data entry, and data management is done through web forms. Depending of the security settings, any registered user in the system can enter data. A number of extra tools ('NeMys toolkit') allow to explore the data from different point of views. Geographical data can be displayed through an online graphical GIS system, some basic biogeographical statistics can be done, extra documentation can be added through a glossary and methodology section, and morphological data can be used in an online identification system (NeMysKey). NeMysKey is an online polytomous key, which can be updated and compared with original descriptions at any time. As such it is a dynamic environment allowing to keep keys updated with the most current state of art in taxonomy. Different keys automatically link up with each other. A key to genus level will for instance link to a key to species level of a particular genus in the first key. A tool still under construction offers the possibility to add unpublished data in restricted private section. All features of the system can hence be used on new data and facilitate the scientific interpretation of it.

NeMys is connected to a number of international biodiversity portals (GBIF – http://www.gbif.org, OBIS – http://www.iobis.org, EurOBIS – http://www.marbef.org/data/eurobis.php, ERMS – http://www.marbef.org/data/erms.php). Data in NeMys can as such be consulted through these data portals and also through a mirror site hosted at VLIZ (http://www.vliz.be/vmdcdata/nemys/).

NeMys is used as the tool to examine the biogeography of the Mysida in general. About 10000 geographical records derived from about 700 publications were added for the Mysida. The North Atlantic European region was found to be the most documented area. Although the research effort in different areas did differ a lot, making use of biogeographical area models and some sampling effort independent statistical techniques, it was possible to find the following patterns in the distribution of Mysida:

(1) distributions of Mysida do reflect the history of the oceanic basins. As such some 'older genera' can be distinguished occurring in different oceanic basins and some 'younger taxa' limited to one ocean and thus came into existence after the formation of the oceanic basins.

(2) three large global regions of high or distinct diversity are recognised, and as such may also evolutionary play an important role: East Indies, Caribbean Area, Antarctica.

(3) many small areas with a distinct diversity (on species level) are found. They are, mainly due to the lack of a sufficient amount of data, sometimes dubious: Red Sea, Agulhus current area, Mediterranean Sea, Californian Coast, W-Australia, North West Pacific.

(4) temperature is a limiting factor for the distribution of many genera/species.

(5) Eastern and Western coastal faunas of oceans do not have much taxa in common. Mysids do not disperse (except for oceanic taxa) making use of oceanic currents.

(6) The Darwin-Wallace paradigm interpreted from a long tectonical history perspective is the main explaining process for the observed distributions.

The setup of the current dataset does not allow to analyze biogeographical processes on a small scale. An analysis of the European fauna did only show that the fauna of enclosed areas (Mediterranean Sea, Black Sea and Scandinavian-Baltic Sea) does differ a lot with the fauna of the Atlantic Ocean related areas. Many

more data with many more environmental metadata is needed for a small scale biogeographical study of Mysida.

The genus *Anchialina* with 16 species was the first globally occurring genus which was studied in more detail. For each species, a detailed morphological description (based on literature and specimen observations) and a biogeographical overview is given. These new observations on specimens complete some limited original species descriptions and as solve the taxonomic problematic issues in this genus. The morphological and geographical data was used in a phylogenetic analysis. Two groups earlier described in the literature, the '*typica*'-group and the '*grossa*'-group are found to be well defined and stable. Adding the distributional data to a second analysis did not cause changes in the phylogenetic trees, meaning the distribution reflects the evolutionary history of this genus. Only one species (*Anchialina typica*) has a global oceanic distribution while others have a limited range and are restricted to coastal areas. Two dichotomous (the first one on the sexually dimorphic third male pleopod, the second one on a mixing of somatic and sexually dimorphic characters) keys and one polytomous digital identification key are presented.

A second taxonomic study focuses on the species rich genus *Siriella* (66 species). The six groups of species defined by Ii (1964) are tested using morphology based phylogenetic analysis. All groups except the '*Anomala*' and '*Aequiremis*' group were found to be well-defined in the phylogenetic analysis. *Siriella anomala* is as such placed in the '*Aequiremis*' group. A biogeographical study was carried out and compared with the phylogenetic results. The distribution of this genus fits with the biogeographical model presented by Briggs (1974). Comparing the distributional patterns with the phylogenetic results lead to the conclusion that the evolution of the genus knows a long history probably driven by tectonic processes and vicariant speciation. Variations in morphology were reported for *S. pacifica*, *S. roosevelti, S. panamensis* and *S. thomposoni*. Additions to the original description of *S. paulsoni* were made. The morphological variability of *S. jaltensis* is discussed.

Biological Information Systems like NeMys have some advantages when used as tools for taxonomic and biogeographical research. Data management can be done very efficiently. Data analysis on a large number of records derived from different sources is possible. New morphological findings can be compared with the existing

descriptions and can phylogenetically be analyzed together with earlier described taxa. The creation of identification keys (formerly an intensive time-consuming task) is facilitated using the online polytomous version. Data can be shared efficiently with a high number of other users.

Although Biological Information Systems may be of great use in taxonomic research, they are only useful when a large enough amount of data is available. The creation of genuine scientific datasets on many more groups of taxa, still lacking global digital catalogues should be encouraged. When setting up a Biological Information System for a group of organisms, the research questions that need to be answered, should be kept in mind. The more detailed and broadly documented the dataset, the more possible answers it may give.

SAMENVATTING

Mysida (aasgarnalen) zijn een wereldwijd voorkomende ordo Crustacea waarvan tot op heden 1086 soorten beschreven zijn. Deze organismen worden gevonden in alle grote oceanen, zowel in de diepzee als in kustgebonden habitats. Tot op heden werd nog geen biogeografische studie van de Mysida op wereldschaal uitgevoerd. Enkele wereldwijd voorkomende genera (e.g. *Siriella* en *Anchialina*) veroorzaken voor veel onderzoekers nogal wat systematische problemen. Om deze groep biogeografisch te bestuderen en om beide genera morfologisch in detail te analyseren werd het digitaal biologisch informatiesysteem NeMys ontwikkeld.

NeMys is een generisch online biologisch informatiesysteem, dat in de eerste plaats ontwikkeld werd als onderzoeksinstrument. NeMys maakt het mogelijk eender welk type biologische informatie op te slaan. Systematische gegevens en literatuurgegevens vormen de ruggengraat van het hele concept. Literatuur is één van de belangrijkste gegevensbronnen bij taxonomisch onderzoek. Literatuur, waar mogelijk in digitaal formaat, wordt in de hele databank gebruikt als gegevensbron. Elk gegeven in de databank vereist een terugkoppeling zijn bron. Elk gegeven is naast literatuur gekoppeld aan een welbepaald taxon. Zodoende is de systematische informatie (en de daaraan gerelateerde geschiedenis) een tweede belangrijke component in het systeem.

Naast systematische informatie en literatuur zijn nog een aantal gekoppelde gegevens modules aanwezig:

(1) Geografische gegevens: de exacte plaats waar een bepaalde soort gerapporteerd werd, wordt opgeslagen. Deze informatie wordt afgeleid van literatuur, specimens uit collecties of veld observaties.

(2) Morfologische gegevens: de morfologische eigenschappen van een soort kunnen op een drietal manieren opgeslagen worden in de databank. Ofwel worden kenmerken en kenmerkentoestanden gebruikt, ofwel worden

metingen opgeslagen, ofwel wordt een tekstuele beschrijving van het organisme gegeven.

(3) Multimedia gegevens: soorten kunnen geïllustreerd worden met verschillende digitale multimedia gegevens (foto's, tekeningen, film, geluid, …)

(4) Moleculaire gegevens: op basis van de gegevens in GenBank worden voor elk taxon alle beschikbare moleculaire sequenties getoond.

(5) Collecties: het bestuderen van specimens uit erkende natuurhistorische collecties is een belangrijk onderdeel van taxonomisch onderzoek. Voor elke soort kunnen enerzijds algemene gegevens rond specimens opgeslagen worden. Anderzijds kan een gebruiker van het systeem specimens documenteren met morfologische observaties en digitale foto's.

(6) Andere types biologische informatie: aan de hand van de generische gegevens-component kan eender welk type biologische gegevens toegevoegd worden. Voor elke dataset kunnen een onbeperkt aantal velden aangemaakt worden.

De generische structuur van de databank, kan samen met de online beschikbaarheid, gezien worden als het belangrijkste onderscheidend kenmerk van NeMys. De generische structuur werd toegepast op verschillende facetten: de dataset kan gebruikt worden voor elke groep organismen, en eender welk type gegevens kan opgeslagen worden in het systeem.

NeMys is een web-gebaseerd systeem. Het invoeren en wijzigen van informatie en zelfs het beheer van de dataset gebeurt via on-line formulieren. Elke geregistreerde gebruiker kan op basis van zijn rechten, gegevens toevoegen aan het systeem. Naast de standaard invoer en consultatie formulieren werden een aantal extra hulpmiddelen ontwikkeld, die het mogelijk maken gegevens in NeMys op een andere manier weer te geven. De 'NeMys toolkit' maakt het mogelijk om op een visuele manier geografische gegevens weer te geven op kaartjes. Daarnaast kunnen gegevens gedocumenteerd worden met een trefwoordenlijst en een methodologisch documentarium. Een aantal biogeografische statistische analyses

kunnen uitgevoerd worden en morfologische gegevens kunnen aangewend worden in de polytome sleutels (NeMysKey). NeMysKey is een web-gebaseerd identificatiesysteem. Het is een dynamische omgeving die het toelaat om in de eerste plaats sleutels te maken, maar deze daarenboven ook actueel te houden met nieuwe taxonomische bevindingen. Sleutels in het systeem worden automatisch gekoppeld aan elkaar. Een sleutel waarmee het mogelijk is genera te onderscheiden zal bijvoorbeeld gekoppeld worden aan een sleutel waarmee soorten binnen een specifiek genus kunnen gedetermineerd worden. Een laatste onderdeel van de 'NeMys toolkit' maakt het mogelijk om in een beveiligde strikt persoonlijke werkomgeving, niet gepubliceerde onderzoeksgegevens toe te voegen. Dit onderdeel dat nog in volle ontwikkeling is, maakt het mogelijk nieuwe bevindingen te vergelijken met reeds gepubliceerde gegevens.

NeMys staat in verbinding met en levert gegevens aan een aantal internationale biodiversiteits portaal sites (GBIF – http://www.gbif.org, OBIS – http://www.iobis.org, EurOBIS – http://www.marbef.org/data/eurobis.php, ERMS – http://www.marbef.org/data/erms.php). Gegevens kunnen enerzijds via deze portaal systemen geconsulteerd worden, maar zijn anderzijds ook toegankelijk via een beperkte NeMys website die gehost wordt op het VLIZ (Vlaams Instituut voor de Zee - http://www.vliz.be/vmdcdata/nemys/).

NeMys werd gebruikt als hulpmiddel om de biogeografie van Mysida te onderzoeken. Ongeveer 10000 rapporteringen van soorten uit ongeveer 700 publicaties werden samengebracht in het systeem. Europese wateren bleken voor Mysida de best onderzochte regio te zijn. Hoewel de hoeveelheid onderzoek tussen verschillende gebieden sterk verschilde, konden door gebruik te maken van enerzijds 'gebieds'-modellen en anderzijds recente statistische methodes, toch een aantal algemene trends in de verspreiding van Mysida waargenomen worden:

(1) De verspreiding van aasgarnalen weerspiegelt de geschiedenis van de oceanen. Hierdoor kunnen enerzijds 'oudere genera' onderscheiden worden, die in verschillende oceanen voorkomen. Anderzijds kunnen 'jongere genera' aangeduid worden, die zich waarschijnlijk na het ontstaan van het oceanisch bassin hebben ontwikkeld, en zodoende in hun huidige verspreiding beperkt zijn tot slechts één oceaan.

(2) Drie regio's kunnen afgebakend worden die ofwel een hoge diversiteit vertonen en/of duidelijk verschillend zijn ten opzichte van andere regio's inzake taxonomische samenstelling: Oost-Indische Oceaan, het Caraïbisch gebied en Antarctica. Deze regio's hebben waarschijnlijk ook evolutionair een belangrijke rol gespeeld in het bepalen van dehuidige diversiteit van de Mysida.

(3) Er kunnen heel wat kleinere gebieden afgebakend worden met hoge of karakteristieke soortendiversiteit. Het aflijnen van deze gebieden kan echter soms twijfelachtig zijn, hoofdzakelijk doordat voor sommige gebieden momenteel slechts weinig gegevens ter beschikking zijn. Enkele gebieden met een specifieke Mysida-fauna zijn: de Rode Zee, de kustzone van Zuid-Afrika (Algulhas stroming), de Middellandse zee, de Californische kusten, West Australië en de Noord Westelijke Stille Oceaan.

(4) Temperatuur blijkt voor veel soorten en genera een limiterende factor te zijn in hun verspreiding.

(5) Fauna's van Westelijke en Oostelijke kusten van eenzelfde oceaan hebben weinig gemeenschappelijke soorten. De meeste Mysida blijken dus niet aan dispersie te doen via de grote oceanische stromingen.

(6) Het Darwin-Wallace paradigma, gezien in een tektonische context, blijkt het belangrijkste verklarend proces te zijn voor de huidige verspreiding.

De huidige dataset liet niet toe om ook biogeografische patronen op kleine schaal te bestuderen. Zo kon bij een analyse van de Europese gegevens enkel aangetoond worden dat de fauna van enkele (half-)afgesloten mariene gebieden (Middellandse Zee, Zwarte Zee en Baltische Zee) duidelijk verschillend is van deze van de kusten die verbonden zijn met de Atlantische Oceaan.

Het genus *Anchialina* dat een wereldwijde verspreiding kent, werd morfologisch in detail bestudeerd. Tot op vandaag werden 16 soorten voor dit genus beschreven. Voor elke soort werd een gedetailleerde beschrijving opgesteld op basis van literatuur gegevens en observaties op specimens. Deze beschrijvingen vormen voor een aantal soorten een aanvulling op de eerder beperkte gepubliceerde

beschrijvingen en helpen de taxonomische probleemgevallen oplossen. De morfologische gegevens werden ook gebruikt in een fylogenetische analyse. Twee eerder beschreven groepen, de '*typica* groep' en de '*grossa* groep' bleken goed ondersteund op basis van deze analyse. Wanneer in een tweede analyse distributie gegevens toegevoegd werden aan de morfologische dataset bleken de resultaten dezelfde te zijn. Dit impliceert dat de huidige fylogenie goed ondersteund wordt door de distributiepatronen. Twee dichotome sleutels (één op basis van de karakteristieken van de derde mannelijke pleopode en één gebruik makend van somatische en sexueel dimorfe kenmerken) en één digitale polytome sleutel werden opgesteld.

Naast *Anchialina* werd ook het meest soortenrijke genus *Siriella* (66 soorten) in detail bestudeerd. De zes groepen, die oorspronkelijk door Ii (1964) bescheven zijn, werden getest met behulp van een fylogenetische analyse op basis van morfologie. Alle groepen behalve de '*Anomala'* en *'Aequiremis'* groep werden goed ondersteund door deze analyse. De distributiepatronen van elke soort werden vergeleken met de fylogenetische resultaten. Op basis van deze vergelijking kon geconcludeerd worden dat het genus reeds een lange geschiedenis kent die door tektonische processen enerzijds en vicariante speciatie anderzijds bepaald werd. Morfologische variaties werden gerapporteerd voor *S. pacifica*, *S. roosevelti, S. panamensis* en *S. thomposoni*. De originele beschrijving van *S. paulsoni* werd aangevuld met extra observaties en gedetailleerde tekeningen. Daarenboven werd de hoge morfologische variabiliteit van *S. jaltensis* ter discussie gesteld.

Biologische informatiesystemen zoals NeMys kunnen dus een aantal voordelen bieden bij taxonomisch en biogeografisch onderzoek. Ten eerste kunnen gegevens op een efficiënte manier beheerd worden. Ten tweede zijn analyses mogelijk op een groot aantal gegevens van verschillende origine. Ten derde kunnen nieuwe bevindingen vergeleken worden met de reeds gekende informatie van eerder beschreven soorten. En kunnen nieuwe soorten ook fylogenetisch beter geplaatst worden. Het maken van identificatie sleutels wordt sterk vereenvoudigd via het online polytoom systeem. Gegevens kunnen bovendien heel eenvoudig en efficiënt uitgewisseld worden met andere gebruikers.

Hoewel Biologische Informatiesystemen een goed hulpmiddel kunnen zijn voor taxonomisch onderzoek, is de mate van het effectieve gebruik sterk afhankelijk van de hoeveelheid gegevens die erin aanwezig zijn. Het opzetten van dergelijke datasets voor een taxon waarvoor digitale overzichten nog niet bestaan zou sterk aangemoedigd moeten worden. Bij het opzetten van een Biologisch Informatiesysteem dienen echter altijd de initiële onderzoeksnoden in rekening gebracht te worden. Hoe gedetailleerder en hoe meer gedocumenteerd, hoe bruikbaarder een dataset wordt voor echt wetenschappelijk onderzoek.

OUTLINE OF THE THESIS

The order Mysida is considered by many authors as an important component of the hyperbenthic fauna worldwide (Mees *et al.*, 1997; Mauchline, 1980). Although this order is well studied (see large number of publications – chapter 3), consulting and retrieving species information is, due to a number of reasons, problematic. The presented type of work (taxonomy and biogeography) is impossible without having access to previously published information. The setup of a literature based archive is as such seen as the starting point for a study on a global scale of the biogeography of the Mysida, and the taxonomic status of two selected genera.

In the framework of the presented thesis published knowledge had to be brought together. In order to make this job preserve its value for the future, it was chosen to archive all data in a digital way. Reaching a broad audience who could gain profit from this archive is currently best achieved through an internet based system. At the time of the start of this Ph.D. project no software tools were available which fully filled the needs (see chapter 1) for this research. A new tool, NeMys, was developed and tested. Simultaneously with the investigations on the Mysida, there was a need in the research group for a similar archive approach for the free-living marine Nematoda. The developed biological information system had to be applicable for both Mysida and Nematoda. As a consequence, NeMys had to be generic in its architecture, meaning also other datasets of any kind of taxa could be added to the system.

In Chapter 1 'Facilitating biological research through a web based biological information system' the tool NeMys is presented as it runs in its current state. The constraints faced during the development, all available tools and the place of the system among other existing species information systems is discussed. NeMys was developed as a tool answering a number of research needs in terms of digital data storage: (1) it must be able to store systematic data in a historical context, (2) data sources have to be linked to the data digitally, (3) any kind of information must fit in the system, (4) representation, analysis and consultation tools for scientific data

consultation are needed, (5) all data management has to be applicable for multiple users at different locations, (6) the system has to be generic.

During the setup of the Mysida dataset much attention was given to morphological and geographical data. Making the morphological data applicable for a broader public than taxonomists was achieved by developing an identification tool fitting in the phylosophy of NeMys.

Chapter 2 'NeMysKey: a concept for documented polytomous digital identification keys' describes in detail the technical details behind the functioning of this generic web based identification key. Keys created with NeMysKey are embedded in the taxonomic background information available in NeMys. As a consequence this type of keys are much more a taxonomic evolving research tool than a finished standalone publication.

By using all characteristics of NeMys and NeMysKey a dataset was built documenting the Mysida at a global scale. In Chapter 3 'Encyclopedia Mysida: a global digital catalogue on the order Mysida' the characteristics of this dataset are listed. All available types of data (literature, systematics, morphology, geography, collections, pictures and molecules) are reported. Items requiring more attention in the future or with a problematic status are discussed. The Mysida dataset gives an overview about the information used to explore the biogeographical and taxonomical research questions described in the three following chapters.

Chapter 4 'Mysida biogeography patterns' focuses on the biogeographical patterns for the order. By using the about 10000 distribution records extracted from NeMys, it is tried to see whether or not it is possible to distinguish patterns in these distributions. To whole chapter tries to prove whether Mysida distributions are similar to patterns observed for other marine taxa. The biogeographical area models published by Briggs (1974), Mauchline (1980), Longhurst (1998), and a number of ecoregion models (Large Marine Ecosystems (Sherman *et al*., 1996), and the WWF marine ecoregions) were tested with some advanced statistical techniques and GIS tools. On a European level additional data obtained through the EurOBIS (http://www.marbef.org/data/) biodiversity data portal is taken into account. This

chapter illustrates the analysis possibilities on biogeography data extracted from published literature.

Both chapter 5 'A review of the genus *Anchialina*' and chapter 6 'A review of the genus *Siriella*' give a detailed morphology based study of two complete genera. Reviewing both genera was achieved by studying each species through the published literature available in NeMys and by observing the morphological features on specimens. Based on both the literature data and own observations on specimens, a dataset containing an extensive overview of morphological characters was made. This dataset was used for two aims. (1) By a phylogenetic analysis the evolutionary relationships between species were displayed and discussed. Where possible it was tried to link these results with the available distribution data. (2) For both genera relevant morphological features were embedded in a digital polytomous identification key making use of NeMysKey.

The final chapter 7 'Biological information systems as tools for taxonomic and biogeographic research' evaluates the used, somehow controversial, methodology in this thesis. The question whether taxonomic research should step on the digital highway is discussed extensively. Some thoughts on future developments and expectations in the field of biodiversity informatics form the endpoint of the thesis.

To conclude: This thesis may be considered as an illustration of giving answers to a number of research questions on the natural history of the Mysida, by making use of digital techniques facilitating retrieving answers fitting in a philosophy of free access to data and knowledge on the living world.

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CHAPTER 1 - FACILITATING BIOLOGICAL RESEARCH THROUGH A WEB BASED BIOLOGICAL INFORMATION SYSTEM

1. Introduction and state of the art

The Mysida (Peracarida, Eumalacostraca, Malacostraca, Crustacea) are a relative small group of organisms (1086 species) occurring in many marine environments worldwide. In order to analyze the geographical and morphological patterns of this order, the problem of scattered literature was encountered. Mysida are rather well documented for European waters (e.g. Tattersall & Tattersall, 1951; Macquart-Moulin & Maycas, 1995; van der Land, J. & Brattegard, T., 2001) and a few world lists exist as well (Gordon, 1957; Mauchline & Murano, 1977; Muller, 1993). Reviewing biogeographical patterns and morphology however is only possible when looking in detail at species descriptions and distribution data. These data are reported in the literature but are not centralized in one library.

The above mentioned problems are not typical for Mysida but are widely applicable to the taxonomy of organisms. Taxonomists describe new species, give a name to biological specimens, and write revisions on particular groups of organisms. To achieve all this, taxonomists relay on the knowledge of their ancestors. This knowledge is mostly only accessible through published papers.

Some of the tasks listed above, are not only of interest of taxonomists. Many ecologists, molecular biologists, even biochemists, conservationists … are in their research and activities faced with taxa or groups of biological organisms. These studies in many cases do only make sense if they are assigned the correct name. For the identification of specimens keys (if available), or critical reviews on certain taxa, are used.

The access to taxonomic, published information is crucial for many types of biological research. The problem with many literature sources is that these are often not centralized in one institute or library, and as such are not easily accessible.

Another problem linked with revisions of species-rich groups, is the amount of data that must be interpreted at once. Databases able to handle large amounts of data in a structured way could be the solution.

About ten years ago, the first biodiversity database systems have been created and some of these are nowadays well settled (Linnaeus© ETI (Schalk, 2005), DELTA (Dalwitz, 1993), LUCID (http://www.lucidcentral.org, 2005)). Although all of these database systems still play a major role in the field of biodiversity informatics, ten years ago, at the start of this project, none of the existing systems answered the needs for the proposed research, which require a detailed overview and archive of literature sources. Therefore, a new system, NeMys, was developed.

Two former biological database attempts were used as data test-cases for this new database: NeMaslan (Vincx *et al.*, 1999), a database on free living marine Nematodes and Mysidlan, a database on the Mysida of the Western Indian Ocean (Deprez *et al.*, 2001).

A 'quiet revolution' has been going on during the last few years in the field of biodiversity informatics. A large number of biodiversity information systems have been created (Bisby, 2000). These systems are now gradually moving together and a raising coherence and organization in architecture of all systems is observed. Global biodiversity initiatives, like GBIF, OBIS or Species2000, play an important role in bringing biodiversity information systems together, by enhancing the interoperability between different systems through common standards (Edwards *et al.* 2000). Gradually an 'encyclopaedia of life' as described by Wilson (2003) will arise.

In general five main groups of biodiversity information systems can be distinguished: (1) biodiversity software, (2) species databases, (3) taxonomic databases, (4) nomenclature databases, and (3) biodiversity portals.

- **Biodiversity software:** Software designed to digitally document biodiversity. The focus of the available packages differs a lot. Only a few systems are shortly illustrated below.

    - **Linnaeus II © :** This software package developed by ETI (Expert Center for Taxonomic Identification – http://www.eti.uva.nl) is designed as a data management tool for biodiversity data. Databases created with it can be published on the internet, although main focus

lays still on the creation of digital monographs on CD or DVD. The software allows documentation of taxa with text-based information, distribution patterns, identification keys, literature references and multimedia files. Currently no possibilities for online updating of datasets with multiple users created with the package are included. The package is platform independent and does not require powerful computers to run on (Schalk, 2005).

- **Specify :** This collection management package is designed as a tool for documentation of collection specimens (http://www.specifysoftware.org). The system links specimens with all kinds of relevant information. The package runs on local networks although recently export modules to a web-interface have been added. It includes even an automated setup of a digir-provider, enabling to link the database with biodiversity portals. Although it is a power-full system, it requires powerful MS Windows © server machines to be run on.

- **Lucid professional**: This package has been designed for creation of digital identification keys (http://www.lucidcentral.com). Keys are created with the 'Lucid professional package' and can be exported to a webbased version, or a cd-rom version. Taxa can be illustrated with text and figures.

- **Delta:** (http://delta-intkey.com/) Descriptive Language for Taxonomy is a format for storing taxonomic descriptions. The Delta System is an integrated set of programs based on the Delta-format. The package allows creation of conventional and polytomic keys. Data in the Delta-format can easily be exchanged with phylogenetic formats. (Dalwitz, 1980; Dalwitz *et al*, 1993). Many Delta related software packages, running on multiple platforms, have been designed.

- **Biotica © :** The Biótica information System has been designed to handle curatorial, nomenclatural, geographical, bibliographical and ecological data

(http://www.conabio.gob.mx/informacion/biotica_ingles/doctos/acerca_biotica.html). It is a desktop system, without possibilities of creating keys. The main language of the tool is Spanish, and due to this some parts are rather confusing in use. An ESRI © based mapping tool is included in the latest version. The package runs MS Windows © based systems.

- **Taxis:** This software tool is designed as a desktop information management system. Taxis (http://www.bio-tools.net) allows to store systematic, morphological, geographical, ecological and collection data. It has a lot of advanced features, such as a GIS tool, an identification key, and a report genereator. The package runs on MS Windows © systems.

- **3I:** The 3I package has been designed primarily for the creation of online accessible identification keys. The package is distributed as a desktop database and a couple of web-pages programmed in ASP allowing to make a key functioning through the internet. The database itself included many more features than these needed for creation of keys and can as such be used as a species documentation tool. (http://ctap.inhs.uiuc.edu/dmitriev/3i.asp).

- **Species databases:** Species databases are databases combining information on species level for a particular group. This information may include morphology, distributions, multimedia, descriptions … The focus for these systems lays much more on the data layer and much less on the architecture and tools. Only the most important web-accessible marine species databases will be listed here.

  - **Fishbase:** FishBase (http://www.fishbase.org) is a large information system with key information for all fishes of the world: summaries, photos, and maps plus detailed standardized data on population dynamics, reproduction, trophic ecology, morphology, physiology genetics and other topics (Froese & Pauly, 2005).

- **Algaebase:** AlgaeBase (http://www.algaebase.org) is a database with information on taxonomy, nomenclature, distribution and common names of algae. Currently, it mainly includes information regarding seaweeds (19,000 names, 8,000 species) (Guiry & Dhonncha, 2001; Guiry *et al.*, 2006).

- **Cephbase:** The purpose of CephBase (http://www.cephbase.utmb.edu/) is to provide taxonomic data, life history, distribution, images, videos, references and scientific contact information on all living species of cephalopods in an easy to access, user-friendly manner (Wood *et al.*, 2000).

- **Taxonomic databases:** Taxonomic databases are very similar to species databases but are limited to taxonomic information. Classification data, synonymies and literature are their main data components. Some extra sources like basic geographical records may also fit in this type of datasets.

  - **Biogeoinformatics of Hexacorallia:** The Hexacorals Database (http://www.kgs.ku.edu/Hexacoral/) is a compilation of publications concerning taxonomy, nomenclature, and geographic distribution of extant hexacorallians. Hexacorallia also provides tools for interfacing geospatial, taxonomic, and environmental data for a group of marine invertebrates.

  - **Faunaeuropaea:** This data portal brings together names of all European land and freshwater animals. It gives mainly taxonomic, bibliographic and distributional data for each species. Data in the database is provided by experts in taxonomy (http://www.faunaeur.org).

  - **ERMS:** The European Register of Marine Species (ERMS) (http://www.marbef.org/data) is a taxonomic list of species occurring in the European marine environment. Taxa in ERMS are illustrated with a number of additional data and links to relevant websites.

- **The Zoological Record:** The Zoological Record Online®, currently published by Thomson Scientific, and jointly by BIOSIS and the Zoological Society of London until 2003, is a comprehensive index to zoological and animal science literature. Data from this huge dataset is not freely accessible. The main focus of the dataset resides with taxonomic information and literature references (http://scientific.thomson.com/products/zr/).

- **uBio:** The Universal Biological Indexer and Organizer (uBio) project acts as a thesaurus of names of organisms. By combining a 'NameBank' (currently holding over 8 million names) and a 'ClassificationBank' it stores names in an intelligent historical context. Beside a taxonomical database this project offers a number of intelligent webservices based on taxonomic names: 'LinkIt' which locates scientific names in webpages and uses these to link to the NemaBank, 'FindIt' which locates names in uploaded files (based on the TaxonGrab functionality, Koning *et al.* 2005), and a number of others, some of them still under construction ('ParseIt', 'CrawlIt', …) (http://www.ubio.org).

- **Nomenclature databases:** These databases are in most cases checklists of taxonomic names. These can be regional or global.

  - **Species2000:** Species 2000 (http://www.species2000.org) is a group of database organisations. The goal of the project is to create a validated checklist of the world's species (plants, animals, fungi and microbes). This is being achieved by bringing together an array of global species databases covering each of the major groups of organisms. Each database covers all known species in the group, using a consistent taxonomic system.

  - **ITIS:** The Integrated Taxonomic Information System (ITIS) is an authoritative checklist of organisms of mainly North America. For a number of taxa also global checklists are presented (http://www.itis.usda.gov/).

- **Index Kewensis:** Index Kewensis (http://www.ipni.org) is an index of plant names dating back to 1885. This list currently contains over 400000 names and their linked accepted classification.

- **Biodiversity portals:** Biodiversity portals can be considered as access points to biodiversity data. The portals listed below do not create data themselves but offer a facility to join the data of a wide range of databases through one common interface. Many of these portals aim to provide global scale data although others are focused on a limited region. Data portals are a relative recent evolution, made possible by the development of advanced cross-internet data sharing techniques.

  - **GBIF:** The Global Biodiversity Information Facility (GBIF) (http://www.gbif.org) is an international organisation providing free universal access to biodiversity data. The project has a distributed organization, meaning that it consists of a number of regional nodes (national, institutional) all digitally linked to eachother. Currently two types of data are being shared through the network: Taxonomic names and specimens and observations (species distribution records). In total data on about 1 million taxonomic names and 40 million distribution records are available (Edwards *et al.*, 2000; Edwards, 2004; Hobern, 2003; Hobern, 2004).

  - **OBIS:** The Ocean Biogeographic Information System (OBIS) (http://www.iobis.org) is a biodiversity information facility for marine taxa established by the Census of Marine Life (CoML). The aim of this facility is to bring global data on marine life together with the use of internet and computer technology (Decker & O'Dor, 2003). OBIS is a web-based provider of global geo-referenced information on marine species. The OBIS Portal accesses data content, information infrastructure, and informatics tools - maps, visualizations, and models – to provide a dynamic, global facility in four dimensions (the three dimensions of space plus time). Since 2001 OBIS is the marine associate component of GBIF (see above). The future aims of this facility are to provide online data through a network of distributed

databases combining new data and historical data on marine taxa related to temporal, physical, and chemical parameters of the environment (Grassle, 2000; Zhang & Grassle 2002).

- **Zipcode Zoo:** This project aims to be a global 'field guide' to the worlds fauna and flora. All data available on this website is retrieved from database all over the world. This rather isolated project is online since 2005 and proves that through extraction of data from other sources an extensive amount of biodiversity data can be gathered. (http://www.zipcodezoo.com).

NeMys fits best in the 'biodiversity software' section, but datasets (like the Mysida dataset together with 6 others, see page 67) running in NeMys can also be placed in the 'species database' section.

Although the above listed software is well established and widely used, NeMys differs from them on a number of characteristics: the combination of a purely web-based architecture, the fully generic architecture and the compulsary links with data-sources are so far an unique combination in the field of biological information systems. Efforts were put into the development of NeMys because, from the beginning of the project, we were convinced of the added value in linking species information with their original data sources (which are a crucial part of information for taxonomists). The generic structure of NeMys is a result of the contempory request in the Marine Biology Section (UGent) research group of developing an information system for Nematodes and for Mysida (both taxa belong to the specialism of the research group). Moreover, the integration of NeMys in well established biodiversity portals (for example GBIF, OBIS, EurObis) gains much attention as well.

This chapter aims to illustrate the characteristics of NeMys in a broad and open context for a biological and an informatics oriented audience. The choice has been made to combine technical comments and, where needed, illustrative examples and low-level background information in one text.

2. Needs and Aims

The basic concept of NeMys was defined a few years ago and has during the development time of this biological information system never changed. Priority was given to the compulsory links with data sources in order to offer the possibilities to for example taxonomists, to verify the data sources used to enter specific data. NeMys was developed for scientific users, the main target group of the system, and offers a scientific database tool, able to store species-level information in a fully digital way.

The needs and aims can be summarized as follows:

- **Need 1:** Systematic data and its history have to be stored.
    - The first aim is to create a system that can store all systematic data and its related systematic history.
- **Need 2:** All data sources used should be linked digitally
    - The data-system must hold a digital library-system, if possible searchable at any level and linkable to any kind of data.
- **Need 3:** All kinds of biological data must be storable in the system
    - The third aim is to create a system, which in the first place stores morphological and biogeographical data, but which may be enlarged to store other information types.
- **Need 4:** Tools are needed for representation, analysis and consultation of the data.
    - A crucial aim is to create a system that cannot only **store data** but also **present data** in a clear way. A user interface breathing simplicity and easy to use is favourable.

- **Need 5:** Consultation and management of all the data must be done in a multi-user environment.

    - The system should be accessible by multiple users, if possible independent of the platform (e.g. MS Windows ©, Linux ©) used. Consequently the best option is to build a system running through a web browser.

- **Need 6:** The whole system needs to be generic – all developed technology must be applicable for all taxa.

    - The final aim is to create a system, not only working for Mysida but also for Nematoda, and for all kinds of taxa. This generic design must be applied to the database and to the user interfaces.

3. Structure of NeMys

The NeMys system consists of two main parts: a 'data'-layer and a 'user-interface'-layer. The 'data'-layer is hosted on a database-server (SQL-server), the user-interface-layer on a web-server (IIS[i]). These two layers are kept physically separated mainly for security and maintenance reasons. The 'data'-layer is stored on a machine not connected to the internet. As such, the data feeding the application is hidden and secured, and is independent from the 'user-interface'-layer. A third piece of technology included, ensures data-exchange to biodiversity portals (Digir-provider). This part also runs on the machine hosting the 'user-interface'-layer, as these exchange services need to be accessible from the internet.

The technical details on software and database architecture are listed in appendix 2.

The database behind NeMys was initially based on the NemasLan, MysidLan, (Deprez *et al*., 2001; Vincx *et al*., 1999) architecture. Each dataset had its own database, with its own possibilities and restrictions. This architecture implied maintenance on 'data'-layer and 'user-interface'-layer for each separate dataset. This important drawback led to the redesign of the different databases into one overall 'data'-layer with one overall 'user-interface'-layer.

In general in both the 'data'-layer as the 'user-interface'-layer the following data-modules can be recognised: (1) systematic data, (2) literature data, (3) morphological and morphometric data, (4) geographic data, (5) multimedia data, (6) molecular data, (7) collections data, and (8) generic data.

Next to these eight main units also other data can be entered (for example: internet links, notes, people-information, …). All data-modules can be accessed through the web-interface. Data-entry and data-management use web-based forms. Some crucial items in NeMys are only very recently activated and grouped in the 'NeMys toolkit': (1) Online identification keys, (2) generic data structure based upon the concept of parametric relations, (3) a geographic mapping-module, (4) a private workbench enabling the addition of unpublished data in a restricted personal environment, and (5) biogeographic data analysis tools.

3.1. DATABASE STRUCTURE

Initially the database structure was relational in the conventional way (making use of well-defined data tables, linked together with 'one-to-many'[ii] and 'many-to-many'[iii] relationships). In a later stage some types of data needed a more generic way of storing data. This was done by adding parametric relations (see Parametric relationships) to the database, meaning that relations between subsets of data are depending on parameters stored together with the data. This facilitates the use of one user-interface for multiple purposes.

NeMys is currently implemented for Mysida, Nematoda, Peperomia, European Reptilia and Amphibia, European ladybirds (Coccinellidae), Turbellaria and phytoplankton of the North Sea. Some parts of NeMys are rather specific for one dataset. These parts will be mentioned in this chapter when relevant.

3.1.1. Database relation scheme

In figure 1 a generalized scheme of the NeMys database is presented. A detailed version showing all tables and relationships is available in the online appendix at http://intramar.ugent.be/nemys/phd/ and in appendix 3 (see page 102).

The eight data units and the five metadata units are shown in figure 1. The data units represented in light gray consist of one table or a set of closely linked tables. All data units are linked with each other (displayed by the arrows). Metadata units are sets of database tables not storing taxon-related data. They hold all kinds of data, mainly facilitating the correct functioning of the user-interface. Data and metadata can be treated separately and exist without each other. In many cases, metadata is crucial for correct interpretation of the data. All data and metadata units will be explained briefly below.

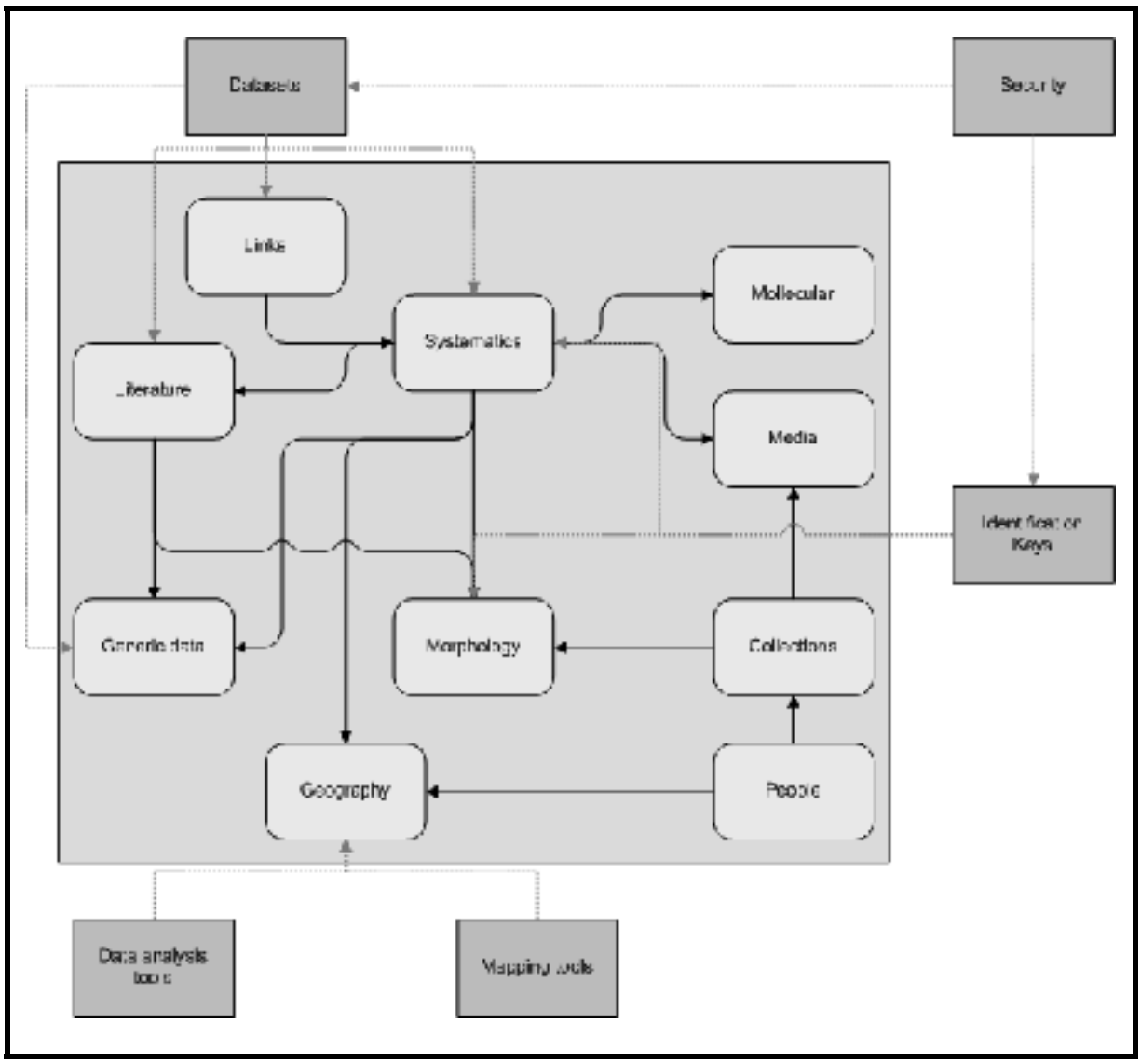


Figure 1. Generalized scheme of the NeMys database

- **3.1.2. Overview of true DATA units**

Data units only store data related with taxa in NeMys. They consist of series of distinct linked tables. The species *Mesopodopsis slabberi* (Van Beneden, 1861) is used to illustrate what kind of data is stored in the eight data units. On places where no relevant example for this species can be found, an example from another dataset is taken.

3.1.2.1. 'Systematics' data unit

This 'Systematics' data unit holds one main table ('tu') which stores all systematic records. A second smaller table ('tblranks') is a list of all possible taxonomic levels (Phylum, Classis, Ordo, Familia, Genus, Species, ...). The 'tu'-table is constructed according to the hierarchical data concept as explained in the section 'focus points'. Common names are saved in another linked table ('tbl_vernecular'). Each common name has a language flag and a link to the data source. The 'tu' table architecture was taken from 'APHIA'- database hosted at VLIZ (http://www.vliz.be/vmdcdata/aphia/) and slightly changed according to specific needs in NeMys.

The species '*Mesopodopsis slabberi*' belongs to the genus '*Mesopodopsis',* which belongs to tribe 'Heteromysini', belonging to the subfamily 'Mysinae'.

The systematic names 'slabberi', 'Mesopodopsis', 'Heteromysini', 'Mysini' are saved in the 'tu' table. The assigned ranks (species, genus, tribe, subfamily) are taken from the table 'tblranks'.

Also the authority '(Van Beneden, 1861)' and eventual synonyms (*Macropsis slabberi, Mysis slabberi*) are saved in the 'tu' table.

The species receives an unique number (6756) which is used to link the species to other data units.

3.1.2.2. 'Literature' data unit

The literature component is of major importance for the system. A key principle in NeMys is the link between data and data source. This data source is mostly (90 %) published literature. The unit consists of one main table ‘tbldocuments’ holding all the references. Some references have a link to a digital version. References can be directly linked to taxa through the table ‘tbldoclink’. Other links to data are possible, although only when the reference has been used as the data source for geographic, morphological, ... data records.

> *M. slabberi* is reported from 88 literature sources. An example reference ‘Tattersall, W.M. & O. Tattersall (1951). The British Mysidacea. Ray Soc., London, 460pp.’ will as such be entered in the table ‘tbldocuments’ and receive the unique number ‘2996’.
>
> A link between the species and the reference is generated in ‘tbldoclink’ by linking ‘2996’ to ‘6756’ (the identifying number of the species).

3.1.2.3. 'Morphology' data unit

The ‘morphology’ data unit is designed according to the architecture of most morphological data systems (e.g. Delta (Dalwitz, 1993)). Characters ('tbl_characteristic') are morphological descriptive or morphometric. Descriptive characters are linked with character states ('tbl_state'). The combination of characters and character states, and morphometric characters and the measurements, facilitates the morphological diagnosis of a taxon. Morphological records can be based upon literature sources or observations on specimens (stored in the ‘collection’ data unit). The morphological descriptive data is also used in the identification keys.

> Tattersall & Tattersall (1951) describe *M. slabberi* with a long and narrow antennal scale, setose all around. Eyes are stalked. Females are between 11 and 13 mm. ‘Shape of the antennal scale’, ‘Shape of the eyes’ and ‘Female length’ are entered in the table ‘tblcharacteristic’ respectively as descriptive, and morphometric characteristics. The linked states ‘long and narrow’ and ‘setose all around’ are linked to ‘shape of the antennal scale, ‘stalked eyes’ are linked to ‘shape of the eyes’ in the table ‘tblstate’. The table ‘tblmorfo’ links characteristic, the state, the species and the source together through their unique identifiers. Values ‘11’ and ‘13’ are stored in the table ‘tblmeasurement’ together with the taxon number (6756) and the datasource number (2996).

3.1.2.4. 'Geography' data unit

Two types of geographical data are available: (1) data source related records and (2) observations.

The first group of records is always linked with a checkable data source (a literature source ('literature' data unit) or a specimen ('collections' data unit)). The most important table in this first group is the locations table ('tbl_location'). It is a nested hierarchical structure, meaning locations can be part of parental locations (for example: 'Ostend Harbour' is a part of the 'Belgian coast'). Locations are exact places, larger regions, or politically defined regions. 'Exact locations' are sampling stations defined by the exact geographical coordinates of the sampling point. 'Larger regions' describe a small geographic unit larger than a point but still are specified by one set of coordinates. In many cases these 'larger regions' are locations derived from literature sources where no exact sampling stations are listed. 'Politically defined regions' are larger geographic regions and are represented by a polygon (as external 'shape' file – see also the footnote on page **Error! Bookmark not defined.**). When displayed on maps, these regions are shown as polygons and not as points.

Links between locations and taxa are made through the table 'tblgeography'. Additional data such as catch date, depth, … are also stored in this table.

> *M. slabberi* is described by Tattersall and Tattersall (1951) from 'Firth of Forth', a small harbour along the North East coast of the United Kingdom.
>
> The station 'Firth of Forth' is entered in 'tbl_location' with the exact coordinates 56° 6' North, 3° 1' West as a 'larger region'. This station gets the unique number '39'.
>
> In the table 'tblgeography' all data is linked together as '6756','2996','39', respectively the taxon number, data source number and the location number.

The second group of geographic data (observations) are never linked with a consultable data source, but reflect the observations of taxa by people at a certain place and time. Places can be linked with predefined geographic units (e.g. Cities, UTM km squares, addresses ...). This type of geographic data is used in

observation based datasets (e.g. Eurocox – observation data of European ladybirds – see page 67).

3.1.2.5. 'Collections' data unit

Data on specimens (from herbaria, botanical gardens, museum collections, private collections) are stored in this unit. Each specimen is assigned to a collection. Together with a specimen collection data, identification data, morphological observations, pictures and/or movies can be saved.

> Two specimens of *M. slabberi* are available in the 'UGent Marine Biology Section' collection. Both are identified by Jan Mees in 1994. Specimens were caught in the Westerschelde.
>
> The collection 'UGent Marine Biology Section' is added to the collection table 'tblcollection'. Specimens are stored in the table 'tblspecimen', while identifications on specimens are stored in the table 'tblidentification' with a link to the species (6756) and the identifier (Jan Mees) (see 'People data unit'). A link to the location 'Westerschelde' (see 'geography' data unit) is also stored in 'tblspecimen'.

This data unit was designed in close collaboration with the data centre of VLIZ.

3.1.2.6. 'People' data unit

This entity is widely used throughout the system. It groups information on registered users on the system, contributors to the system, security rights (see also 'security' metadata unit) of people concerning data management.

> Jan Mees identified specimens of the species, Tim Deprez entered data on the species, … Both persons are stored in the 'people' data unit. 'Tim Deprez' receives extra editing rights as he is the responsible person for the Mysida dataset. Details stored for each person are their address, email address …

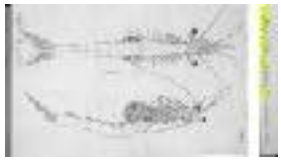
Currently data on people is still stored in three tables ('tbluser', 'tblpeople', 'contributors'). In the near future these three tables will be combined.

3.1.2.7. 'Media' data unit

External files are linked to items in the database with the 'Media' data unit. Items in the database are taxonomic units, collection specimens or even illustrations of

morphological character states. Currently images, movies and sounds, all in commonly used formats (images: JPG, GIF, TIFF[iv], PDF; Movies and Sounds: WMV, MP3 or MPEG[v]) are linked to the system. Two tables are of importance: 'tbl_media' which stores the media-files and their attributes (author, description, technical details), and 'tbl_medialinks' creating the links between media-files and items in the database.

For *M. slabberi* several pictures are available scanned from the personal notes of H. Nouvel (†). All scanned pictures are saved in the picture folder and file names and attributes are saved in the table 'tbl_media'. In the table 'tbl_medialinks' the link is made between the species (6756) and the media-file record. Each media file can as such be linked to several database items (species, specimen …)



3.1.2.8. 'Molecular' data unit

Data mainly extracted from Genbank (http://www.ncbi.nlm.nih.gov/) is presented in the 'Molecular' data unit. Other unpublished molecular data can be added to the system as well.

In Genbank the sequence of the 'cytochrome oxidase subunit I (COI) gene' is published for *M. slabberi*. Data is extracted from Genbank and pasted in FASTA[vi] format in the table 'tblmolecular' and linked with the species.

3.1.2.9. 'Generic data' unit

This part of the database makes it possible to store any kind of data in the database. It uses 'parametric relationships'. The technical details of this technique are explained below in more detail. All data is stored in different fields depending on the data-type of the field. Data-fields can easily be added. Fields can be grouped and can next to a taxon and a data source, also be linked with a geographical record. Text-based entries can semi-automatically be made interactive. This is done by adding predefined tags to words in the text. These tags are characterised by a 'tagtype' flag and the 'id' (unique number) of the item to link with (e.g. T=1&id=27334 means a link will be created to item 27334 of type 1, being a taxonomic unit). This technique of linking is based upon the WIKI technology (http://www.wiki.org).

Mauchline (1980) writes that *M. slabberi* feeds on detritus and other crustaceans. As no fields are available yet in the database which are able to save information on the diet of species, a new section on feeding is created in this unit named 'feeding'. One field 'feeding type' is added to this section. And the text based data is entered ('detritus' and 'crustaceans') in the field which stores text-based information.

3.1.2.10. 'Links' data unit

Four types of links stored in four different tables exist in the 'links' data unit.

(1) **Taxon specific links**: single links assigned to a specific taxon.

(2) **Dataset specific links**: links which are assigned to each member of a dataset. These links can be characterized by a parent taxon indicator, meaning a link is only active when a taxon is a child or sub-child of the selected taxon.

(3) **Overall links in NeMys**: links which appear on each taxon page in NeMys (for example: links to Gbif, Google ...).

(4) **Links to specific datasets**: The unique identifiers of taxa in other web based biological databases have been received. Taxa in NeMys also present in these other datasets receive a link to these sites (e.g. Fauna Europaea - http://www.faunaeur.org/ , Aphia - http://www.vliz.be/vmdcdata/aphia/index.htm , ERMS – http://www.marbef.org/data/erms.php)

There is species information available for *M. slabberi* on many websites. The name is available in the 'Species 2000' register of names. A link to Species 2000 taxon pages is provided automatically for each page by adding the speciesname in a specific URL. This first link is thus considered as an 'overall link in NeMys'. A link to the 'Fauna Europaea' portal is available. A list of numbers used in Fauna Europaea was entered in NeMys and as such a link to this portal is created for every species in NeMys available in 'Fauna Europaea' ('links to specific datasets'). Thirdly a website was found offering information of the role of *M. slabberi* in the functioning of tidal marshes along the Westerschelde. This link is added as a 'taxon specific' link.

- **3.1.3. Overview of METADATA units**

Metadata units do not store information on taxa, but help function the program properly. Data available in these sections determines the layout of the user-interface. The settings of the 'Mysida' dataset will be used to illustrate where needed each metadata unit.

3.1.3.1. 'Datasets' metadata unit

NeMys was originally a set of separated databases (see above). All databases were combined in one generic structure. This was done mainly for maintenance reasons. This combined structure implied settings for each dataset needed to be saved in the database. The 'datasets' metadata unit stores all variables related with each dataset: dataset interface settings and users.

The introduction text of the Mysida dataset is saved in the table 'tbltaxongroup', together with the dataset administrator, the file name of the picture on the start page, … Also the units to be active are set in this table. For the Mysida dataset 'the literature data unit', the 'geographical data unit', and 'keys' are among others activated.

Information about registered users is also stored in this section in the table 'tbluser'. Users registering to the system are choosing a dataset of first interest and are linked with the dataset.

Contributors are saved in the 'contributors' table. The role of their contribution and an eventual link to the users table is provided. Currently about 25 people are listed up as contributors to the Mysida dataset. For example Jan Haspeslagh provided literature through the Library of VLIZ (http://www.vliz.be), Bea Merckx played an important role in the data input on the genus Siriella, Jan Mees provided literature and support through the VLIZ.

3.1.3.2. 'Security' metadata unit

Online maintenance of a database with different users requires a security unit. Each user of the database has to request a login if he/she wants to use some more special features (mapping, identification, full-size images). Additionally to the basic rights, editing rights can be assigned to each user for each dataset. In total twelve security units were created. Each user can have specific rights to each of these twelve sections: (1) no rights at all – the user can do nothing with this set of data, even not seeing the data, (2) view rights – the user can view the data, (3) adding

rights – the user can add new data, and edit the data he added himself, (4) admin rights – the user can add, change and even delete any data.

The twelve security units were defined based on the database design: (1) **Taxonomy** (taxonomy related data security, such as taxon names, synonyms, and common names), (2) **Documents** (library-related security), (3) **Doc-linking** (rights concerning making links between taxa and references), (4) **Geography** (geographic data security), (5) **Morphology** (morphological data security, including the making of keys), (6) **Links** (rights for management of weblinks), (7) **Molecular** (molecular data security), (8) **Media** (linked media files security – images, movies, sounds), (9) **Generic data** (generic data module security), (10) **Collections** (collection management security), (11) **Research** (defines whether users can add private data making use of the 'private workbench' – see below), (12) **Manager** (Dataset responsibility rights. If set to admin, the user is able to do all maintenance tasks for the dataset: dataset settings administration (front text), user management (security), data control …)

3.1.3.3. 'Identification keys' metadata unit

The technical details of the identification keys are explained in chapter 2. The properties of the polytomous identification keys are stored in this unit: the layout of the key, the taxa belonging to a key, the characteristics used in a key. The data used for the functioning of the key is saved in both the 'Systematics' data unit and the 'morphology' data unit. Two tables are involved: the table 'idkey' stores a short description, the parent taxon, the author, … The table 'morf_concat' holds the members of the key and the links for each member to the assigned morphological data.

3.1.3.4. 'Mapping Tools' metadata unit

The mapping tools metadata unit saves the parameters used in NeMys mapping tools (see below): map layers ('tbl_map') and their properties, available symbols ('tbl_map_symbols') and their properties and settings for maps made by registered users ('user_map','user_map_layer','user_map_tax').

3.1.3.5. 'Data analysis Tools' metadata unit

Data analysis tools in NeMys let users perform online analysis of data. Analysis results can be saved in the database. Storing analysis data in the database prevents rerunning the analysis (this mostly takes a lot of work capacity). The technique is used for the creation of grid-based geographical and cross-table outputs. Results of the analysis can be downloaded and used in statistical packages. More details on this module are explained below in the 'NeMys toolkit' section.

- **3.1.4. Advanced database techniques used in NeMys**

3.1.4.1. Hierarchical data

Saving biological data is complex due to the variability in design of many datasets. Storing data in hierarchical structures[vii] often offers an opportunity to unravel this complexity. Hierarchical data structures are used in three cases in NeMys: classification data, geographic data, and in the general data structure used in combination with the parametric data concept (see page 20).

Nested self-referring structures are widely used for storing hierarchical data (Atiboul *et al*., 1987). Each record in a nested self-referring data table links to a parent record in the same table. When applying this to systematic data, all classification levels can be stored in one table. Each record refers to the parent systematic level, and has some additional parameters explaining the systematic rank, authority details and synonymy. Synonymy data is again self-referring but in most cases not hierarchical. When a taxon name links to itself, it means the taxon name is accepted. When it refers to another taxon, it is considered as a synonym of the linked taxon. An extract of the systematic self-referring table is shown in table 1. Nested self-referring systems are recognised more or less as the standard method in systematic data storage. The ‘tu’ table has a similar architecture as the tables used for classification data storage in other biodiversity databases such as ITIS (http://www.itis.usda.gov), ERMS (http://www.marbef.org/data), Aphia (http://www.vliz.be/vmdcdata/aphia/), …

Geographic data in NeMys is also stored in a self-referring data unit. A sampling station can be part of a small locality, which again can be part of a larger region (see page 18).

Taxon_id	Taxon_name	Taxon_level	Taxon_parent	Taxon_acc
1134	Mysida	100	1090	1134
1204	Mysidae	120	1134	1204
2818	Mysinae	140	1204	2818
2822	Heteromysini	160	2818	2822
6755	Mesopodopsis	180	2822	6755
6756	slabberi	220	6756	6756
15267	Podopsis	180	2822	6755
16235	slabberi	220	15267	6756

Table 1. extract of a self-referring table used for storage of systematic data

The table above shows an extract taken from the table 'tu'. Only the relevant fields and a few relevant records are shown. *Mesopodopsis* is a child of Heteromysini: the field 'taxon_parent' points to the number of the record 'Heteromysini' (2822). Similarly Heteromysini is a child of Mysinae. Two records are a child of Heteromysini: *Mesopodopsis* and *Podopsis* both have the number 2822 as 'Taxon_parent'. '*Podopopsis'* is not an accepted name: the field 'Taxon_acc' is pointing to the number 6755, being the unique number of '*Mesopodopsis'*. As such '*Posopsis'* is a synonym of '*Mesopodopsis'*. '*Mesopodopsis*' which is an accepted name is in the field 'Taxon_acc' referring to itself.

The field 'Taxon_level' is used to indicate the systematic level of the taxon name: 220 is a species, 180 is a genus.

3.1.4.2. Parametric relationships

Normal relational databases have a set of data tables with predefined relations between each of the tables (one-to-many and many-to-many relations: see footnote ii). An aim in the development of NeMys was to make the data system as generic as possible; the option of creating for each new subset of data new tables and fields was rejected. A rather abstract set of tables was made. This unit has a parametric architecture, and has the ability to store any kind of data. 'Parametric' means in this case that depending on parameters set in records in one table, relationships with and between other tables may change.

In general, data fields are defined in a first field-table. Each field gets a field-type (integer, decimal, text, choice-list, memo, true/false). Data for each field is depending on the field-type stored in different fields in a second data-table. This data-table has different fields according to the field-types listed before. Some field-types can be saved in one field in the data-table : integer, choice-list and true/false fields are all saved in the integer data-field.

The figure below gives a practical example of how a parametric system works:

'Box 1' shows the classical solution for adding new sets of data to a database. For each set of data a new table is made. 'Box 2' uses the same data but illustrates that only three tables can store an unlimited number of data subsets. A first table 'data categories' stores the name of the set of data. The second table 'fields' defines the fields for each set of data defined in 'data categories'. Finally the data is saved in the table 'records'. The values for a field are saved in the column matching the data-type of the field.

A detailed overview of the implementation of the 'parametric concept' used in NeMys is given below (figure 3):

A first table defines the data-categories (tbl_group_datatyp). Depending on the value entered in the field 'fix' a data-category is available for all datasets (value 1) or only for one dataset (value 0 - field 'gr'). The 'geo' field in this table defines whether a relationship is created with the geographical distribution table (tblgeography), and whether the data entered is linked to one specific recording of the species. An extra field 'parent' provides the possibility to define nested relationships and order data-categories hierarchically.

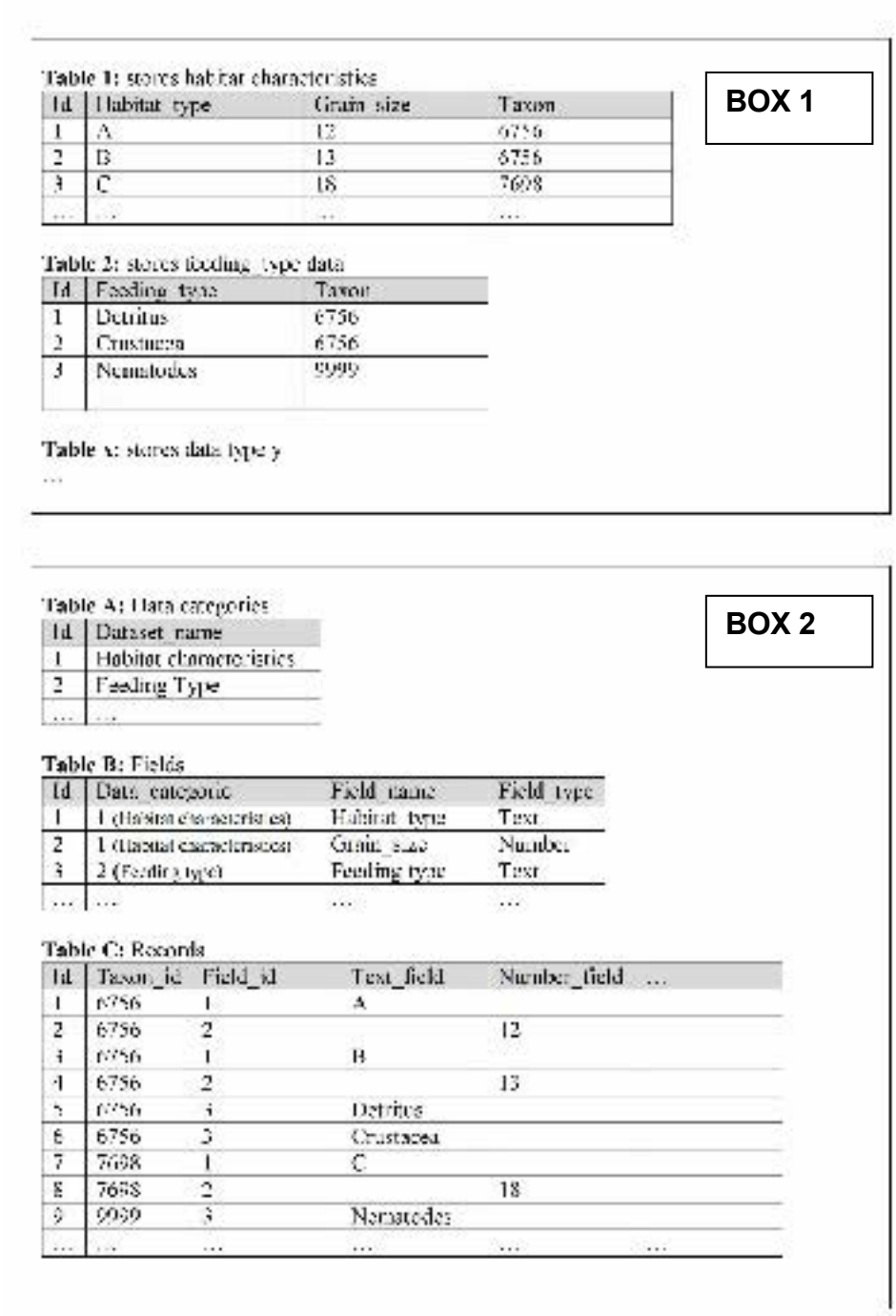


Table 1: stores habitat characteristics

Id	Habitat_type	Grain_size	Taxon
1	A	12	6756
2	B	13	6756
3	C	18	7698
…	…	…	…

BOX 1

Table 2: stores feeding_type data

Id	Feeding_type	Taxon
1	Detritus	6756
2	Crustacea	6756
3	Nematodes	9999

Table x: stores data type y

…

Table A: Data categories

Id	Dataset_name
1	Habitat characteristics
2	Feeding Type
…	…

BOX 2

Table B: Fields

Id	Data_categorie	Field_name	Field_type
1	1 (Habitat characteristics)	Habitat_type	Text
2	1 (Habitat characteristics)	Grain_size	Number
3	2 (Feeding type)	Feeding type	Text
…	…	…	…

Table C: Records

Id	Taxon_id	Field_id	Text_field	Number_field	…
1	6756	1	A		
2	6756	2		12	
3	6756	1	B		
4	6756	2		13	
5	6756	3	Detritus		
6	6756	3	Crustacea		
7	7698	1	C		
8	7698	2		18	
9	9999	3	Nematodes		
…	…	…	…	…	…

Figure 2. Example of implementation of a 'parametric' data concept

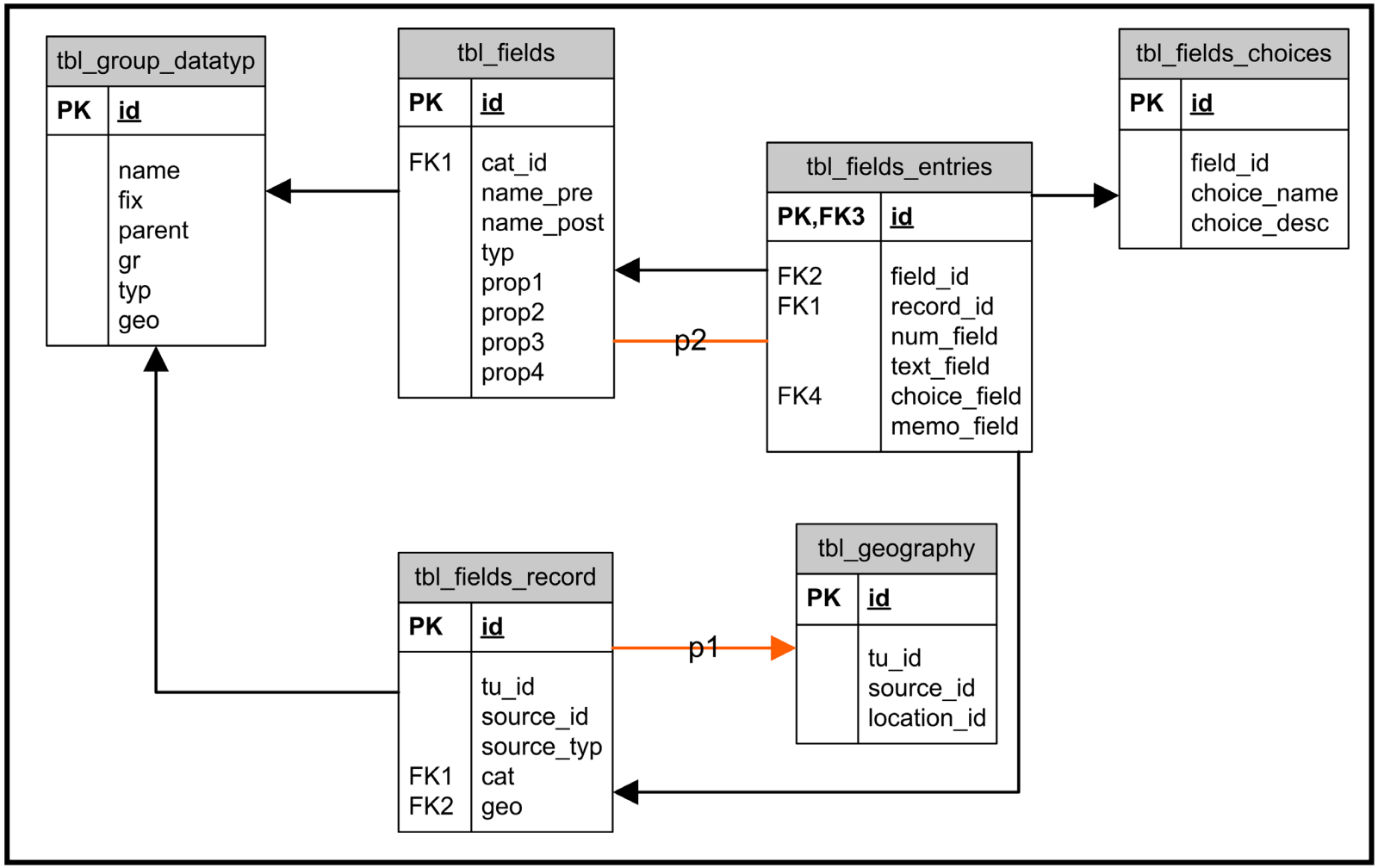


Figure 3. Database relationship scheme of the 'generic' data unit. Normal arrows are fixed relations, while arrows indicated with a 'p' sign are 'parametric' meaning the relation depends on a value entered in a record

A second table describes the data-fields for each data-category (tbl_fields). Data-types, field name, and field-properties are described in this table. The data-type field ('typ') indicates what a field looks like but sets also how and between which tables a relationship is virtually created. The next two tables are used to store the actual data. The table 'tbl_fields_record' connects a taxon ('tu_id') to a data-source ('source_id'). The field 'source_typ' defines whether the source is a literature source (1), a personal observation (2), an external dataset (3), or a website (4). This defines which table is linked to the data-source field. (case 1: relation with the references table 'tbldocuments').

The last table 'tbl_fields_entries' stores the actual data for the different fields defined in the fields table 'tbl_fields'. Depending on the data-type of a field, the data is stored in a different field (num_field – decimal numbers, choice_field – integer number, text_field – flat text 255 characters maximum, memo-field – rich text format fields). With these fields all possible kinds of data can be stored in an easy way. If the data-typ of a field is set to '3' being a choice list, an additional relationship is created with the table 'tbl_fields_choices' in which all possible choice entries are held. All of the tables described above have some management fields used to track 'who entered or edited what data when'.

A further optimization of this parametric concept can be achieved by splitting up the data-table ('tbl_fields_entries') in different tables. Each data-type gets its table: one table for integer values, one table for text values, ... Another option for optimization is combining all field types in one text field. Although this is a promising technique, text fields can be no longer than a certain number of characters (255 in Ms Access©).

Both optimizations are a much more efficient in terms of database file size as no empty fields are saved in the database. Programmatically the design in the first optimization technique becomes far more complex. When querying the dataset many more joins between tables must be made, which slows down the process of data querying.

An important advantage of the used design is that just one interface is needed for data consultation and data management.

▪ 3.2. USER-INTERFACE

The web-based user-interface is programmed in the visual basic based, ASP (Active Server Pages) web scripting language. The number of interfaces is kept low to enhance workability.

A scheme of the user-interface is presented in figure 4.

Four main units of user-interfaces can be distinguished: (1) a **portal** interface, (2) a **dataset** interface, (3) a **taxon** interface and a series of (4) **data-management** interfaces. Next to these four, two smaller interfaces, one on literature and one on geographic locations, are closely integrated with the first three. Figure 4 also shows that some programmatic features are reused all over the system. The Tree component ('Tree Comp') facilitates the graphical display of a taxonomic hierarchical tree, the mapping component ('Mapping comp') visualizes geographic data on maps and the media component ('Media comp') does all image manipulation tasks (generation of thumbnails, pdf creation, watermarking [viii]).

In addition to these basic interfaces a series of extra tools was developed and bundled in the **'NeMys toolkit'**. These tools are applications which use data in NeMys for different purposes than those available in the basic interfaces. Six tools are currently available for NeMys users: NeMysKey (identification keys), Data analysis tools, the NeMys-mapping tool, a glossary, a methodology unit, and a Private Workbench.

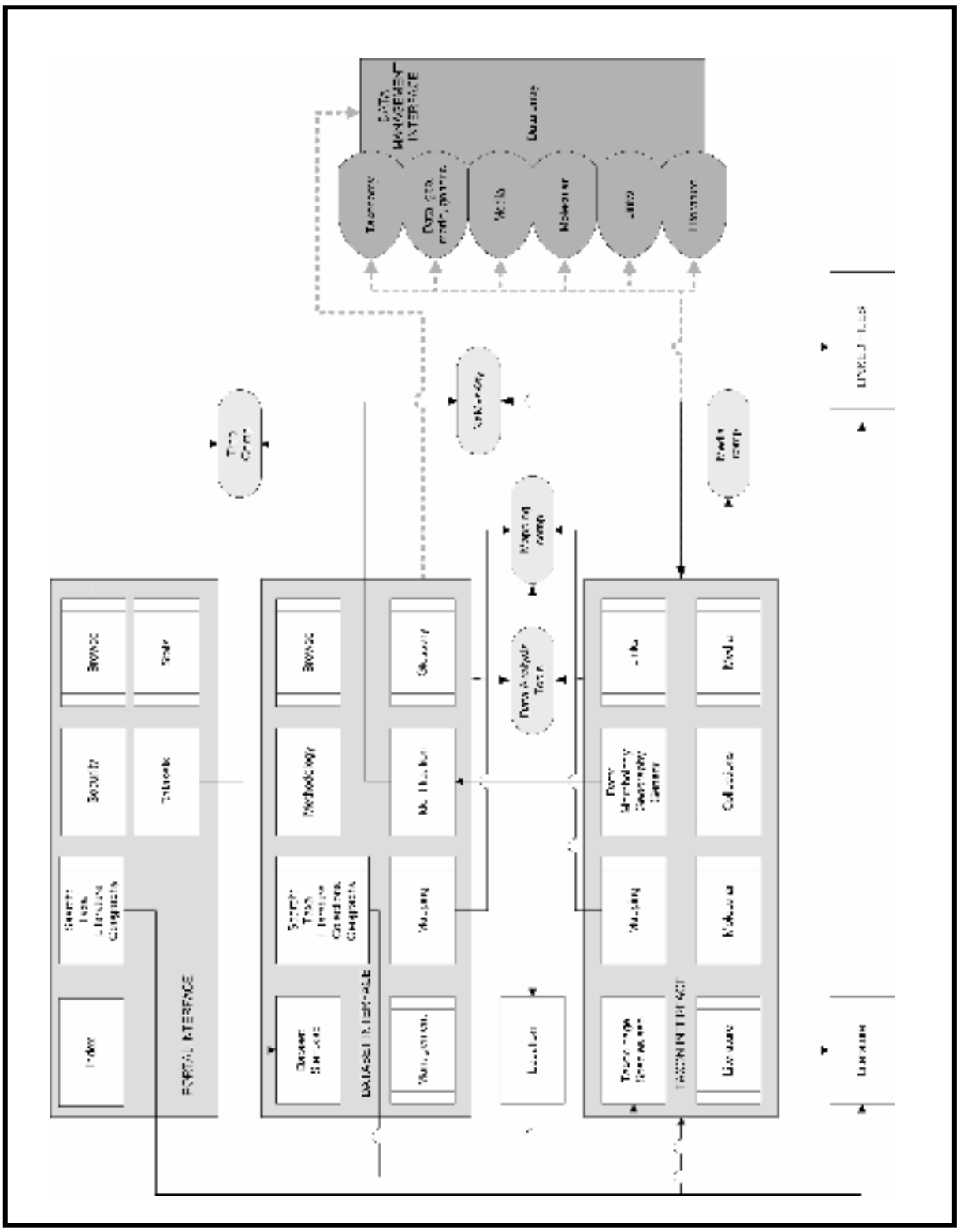


Figure 4. Scheme of the NeMys web-based user-interface

- **3.2.1. Portal interface**

The portal interface (figure 5) is the first screen seen when entering NeMys. On a first screen ('Introduction') some basic information on the system is given, new features are announced, some data policy related messages are shown (citation of data) and the language of the interface can be set.

The second page ('datasets') lists up all public datasets. This dataset page is the gateway to each separate dataset.

The 'browse' page uses the 'Tree component' and facilitates browsing through the systematic hierarchy of all datasets. Each item in the tree is linking to the taxon page of the particular taxon.

Figure 5. Four screens typical for the 'Portal' interface (left-top: start page, left-bottom: browse page, right-top:dataset page, right-bottom: systematic search interface)

The ‘search’ interface makes it possible to search for taxonomic entries, literature and geographic records in all datasets at once.

Three additional pages offer extra information on the background of NeMys. The 'publications' page lists up all publications and presentations on NeMys, the 'about' page gives an overview of basic structure of the system, main datasets, and responsibilities. The 'contact page' gives all necessary coordinates to contact the people behind NeMys.

The login pages lets registered users login to NeMys. Depending on their assigned rights, users get access to copyrighted material or can even add or edit data in the database. New users can also register to the system through this page.

- **3.2.2. Dataset interface**

The dataset interface is together with the taxon interface the most used page of the whole system. Many users are just interested in one dataset and arrive at NeMys through this page. The dataset interface consists of a number of sections accessible by the menu at the top of the page.

3.2.2.1. Introduction page

General information: A brief description of the contents and background of the dataset is given here. The responsible persons are listed up and some basic statistics are shown. These statistics give an overview of the data that changed since the last time a user visited the website. Through these a user is much better informed on changes and evolutions in the database. This option is obviously only available for registered users. A random list of 40 species is shown. This list allows users to jump to a species page without having to know species names.

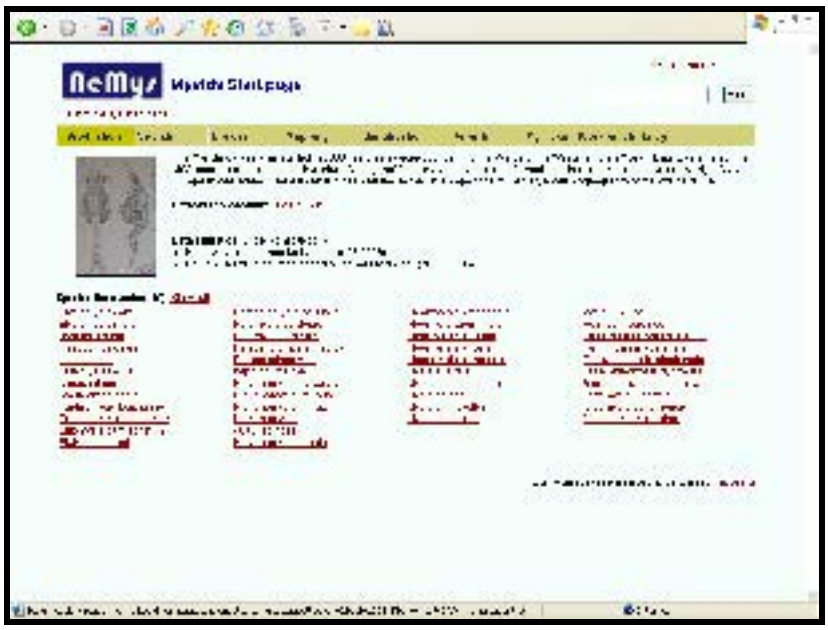


Figure 6. Illustration of a NeMys dataset introduction interface

Glossary: The glossary of the dataset is opened through this page. Glossary entries are ordered alphabetically. The explaining information (text and/or images) behind a glossary term is shown when the glossary term is selected. Glossary explanations may have links to other glossary terms.

Methodology: This section can be used to access methodological issues related to the dataset. The Nematoda dataset for example assembles commonly used techniques to prepare microscopic slides or techniques to create video-observations. Links to references can be added.

Contributors: All people collaborating in the setup of a dataset are listed, eventually with contact details and their specific role.

3.2.2.2. Search pages

Currently five methods for searching the database are included. The availability of these methods depends on the settings of the dataset. All five search methods allow the use of Boolean operators.

Taxonomy: Taxon names can be searched through this interface. A user can define whether to search for scientific names, common names or both. A search can be performed on species level, genus level or on all systematic levels. The results of a search action are displayed in a list, directing to the taxon page of each displayed taxon. Each taxon can be added to a basket. This basket can be used for the generation of reports on several taxa at once. When images are available for a taxon, this is indicated by a 'camera' icon.

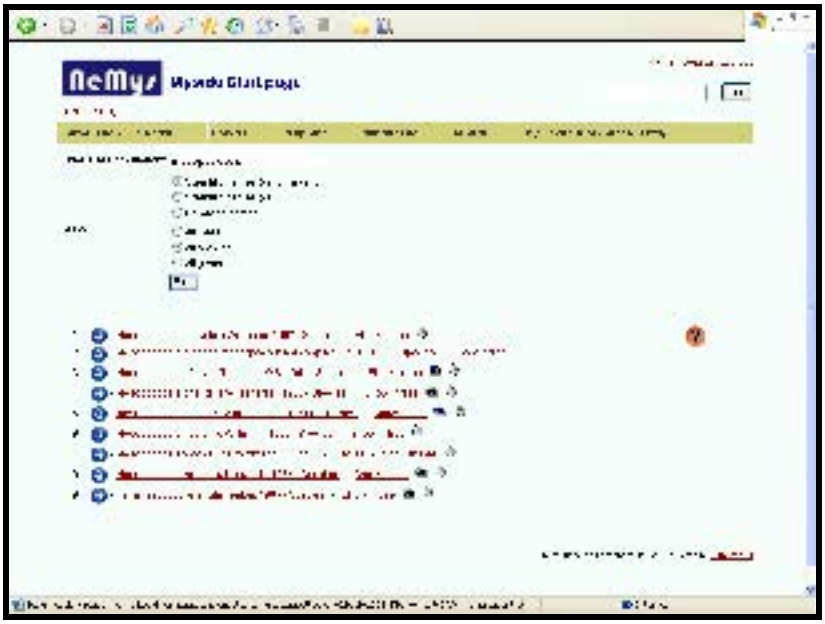


Figure 7. Illustration of the NeMys dataset taxonomic search interface

Literature: This page makes a search through the bibliographic dataset possible. Searching can be done on author names, year of publication, title of the publication, the full bibliographic reference, and library-number. This last criterion is mainly of use for the data manager to easily find a reference when using the database as a research tool. The results are again displayed in a list. An icon indicates whether a digital pdf-version of the reference is available. By clicking the 'paper-clip' icon the

reference is added to a reference list. Selecting a particular reference displays the data behind the reference through the 'literature page'. On this 'literature' page all taxa linked to the reference are listed and an overview of the data (morphological, geographical, …) is shown. Registered users have access to the pdf-version of the article, if available.

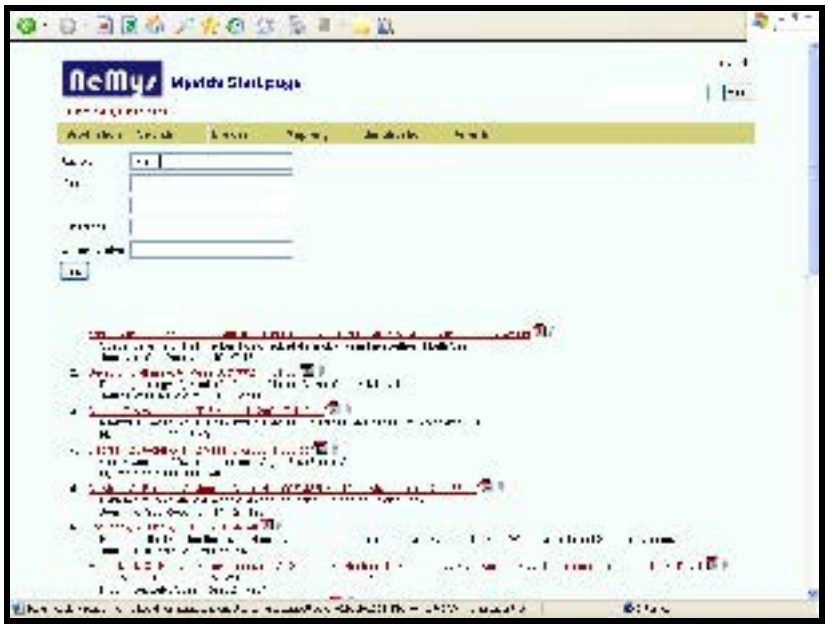


Figure 8. Illustration of the NeMys dataset library search interface

Collections: This option allows searching for museum specimen data. The results are displayed as a table with 8 fields: name of the collection, accession number of the specimen, taxon name, type status, date of collection, place of collection, collector and status. The full information behind a specimen is shown on the taxon interface.

This option is currently mainly used by collection managers organizing their data with NeMys. As an example, the Peperomia dataset has in NeMys a complete overview of the living specimen collection of the Ghent University Biology department.

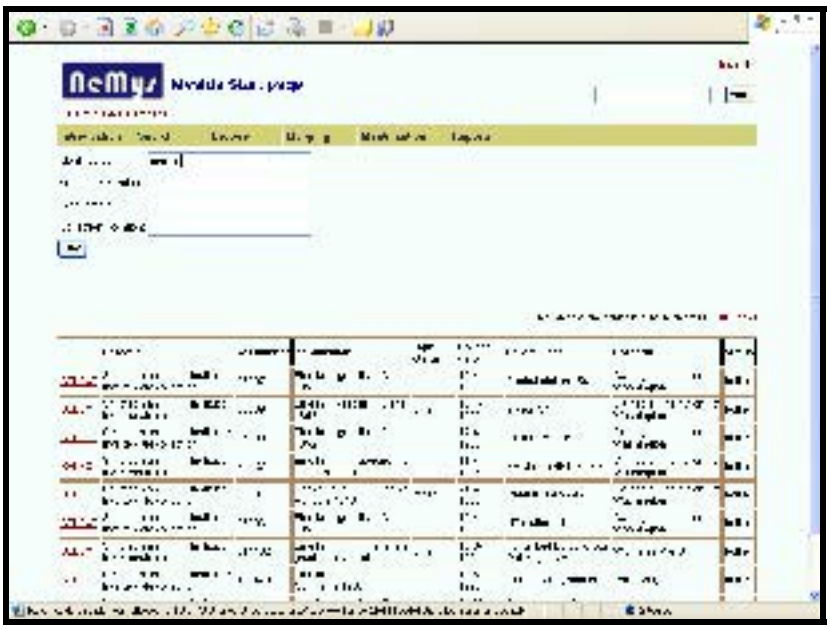


Figure 9. Illustration of the NeMys dataset collection search interface

Geography: The geographical search interface is both visual and textual. The visual part is a world map on which the area of interest can be selected. This tool is very useful, although it requires an SVG-viewer[ix] installed. The technology (SVG and javascript) behind this tool was developed at the VLIZ (Flanders Marine Institute – http://www.vliz.be). Text based search is possible by typing the name of a sampling station or by typing a latitudinal and longitudinal range. Two types of results are shown: (1) an overview of all locations matching the query, (2) an overview of all species occurring at the locations matching the query.

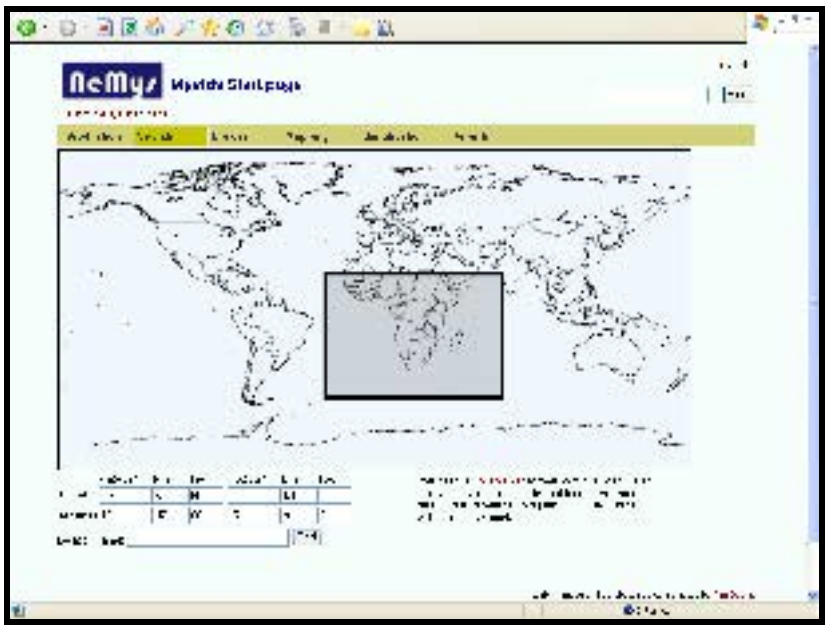


Figure 10. Illustration of the NeMys dataset geographic search interface

Full text pdf: This option allows searching the bibliographic dataset through the full text index of available digital versions of references (meaning searching on words occurring in the text). Only references are searched that have a pdf-version linked. Publications that do not have the searched criterion in the bibliographic data are with this tool traced.

3.2.2.3. Browse page

This page has exactly the same functionality as the browse page on the portal interface page (see above). Only the classification data related to the dataset is displayed.

3.2.2.4. Mapping page

The first option on the mapping page shows an overview map of all locations for which species data is available in the dataset. The map points displayed are clickable. Displaying the map is done with the NeMys mapping tools (see further – NeMys toolkit). A second option 'personal saved maps' (available for registered users) gives access to maps which were formerly made and saved by the user. Such maps are made using the basket-system (see page 48).

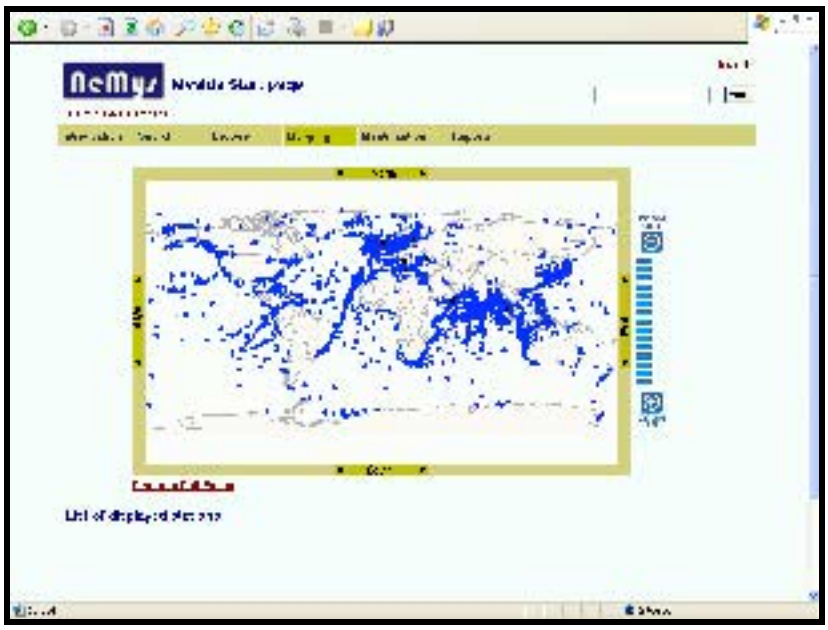


Figure 11. Illustration of the NeMys dataset full location map interface

3.2.2.5. Identification page

This page lists all the available keys in the dataset and allows users to access them making use of the NeMysKey tool(see chapter 2).

Figure 12. Illustration of the NeMys dataset identification key start interface

3.2.2.6. Reports page

Two types of reports are available: ‘Taxon lists’, and the ‘most popular taxa’. Taxon lists have a certain systematic level and display all taxa below a user-defined systematic level. (For example: all genera within a family are shown, all valid species within an order are shown, …)

3.2.2.7. Data entry pages

These pages are only accessible for users having administrative rights. The data entry pages at the dataset interface allow dataset-related data management:

(1) defining the rights of particular users

(2) checking the activities of users: data entry, data manipulation

(3) setting the dataset: news items, introduction text, module activation (for example: whether or not the collections module is used)

(4) data tree settings: definition of the generic data-module. This includes definition of new forms, fields, field-choices …

3.2.2.8. My Taxon Workbench

Users with a minimum of editing rights are allowed to create a private section. In this section a user can check his personal activity on NeMys, add and manage personal notes, add taxa which are not (yet) public available. Personal taxa can be completely documented with data, but are only visible by the user himself. Other users may get permission to view the data behind these hidden taxa. This section will be exploited much more in the near future.

- **3.2.3. Taxon interface**

The Taxon interface is the most important set of pages of the whole system. Users not entering through the portal or dataset interface jump in directly through the taxon interface. Most of these users enter the system after a search on an internet search engine (for example: Google – http://www.google.com).

3.2.3.1. Info page

The 'Info' page gives mainly systematic information. The full classification is shown, synonyms are displayed and when the taxon is not a species (lowest systematic level) all 'children' of the taxon are listed (being all systematic entries one step below the taxon of interest). The authority is given (author and year of description) and the data source used to enter the taxon name. If available, common names in different languages are listed. Some basic statistics of the page are given and links to other internet-related items are provided (for example links to portal pages as OBIS, or taxon specific links to a specific website).

Figure 13. Illustration of the NeMys species systematic info interface

3.2.3.2. Literature page

This page shows a list of all references linked with the taxon. Extra documentation can be provided by a link type indicator and a remark. Currently references are split up in pure NeMys references and references extracted from the Biology department reference library (http://www.biology.ugent.be).

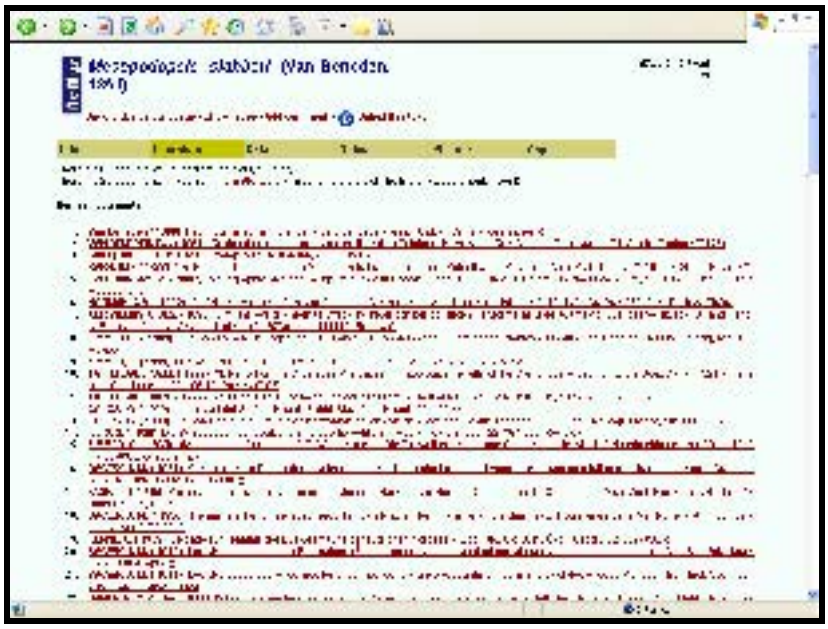


Figure 14. Illustration of the NeMys species bibliographic interface

3.2.3.3. Data page

In general the data page holds all other data then literature, images, systematics, collections and molecular data. Three main sections can be distinguished: (1) geographical data, (2) morphological data, and (3) generic data. All data is accessible through one interface. At the left, a data tree is shown, displaying all possible groups of data in a hierarchical ordering. Clicking an item in this tree displays the related data records. The number of records is highlighted for each subset of data.

Geographical data: Two types of records can be distinguished: (1) literature based records and (2) observation based records. The second type however is currently only used for the Coccinelidae dataset (see page 67), which is mainly build upon

large numbers of field observations. The literature based records are displayed in a table (location name, coordinates and the data-source). A link to more detailed information for the location, record and literature source is provided for each record. A link to the NeMys map and to the Google Earth desktop application is also provided (see page 54).

Morphological data: morphological and morphometric records are displayed in a table. The characteristics, their according state or measured value and the used data-source are shown.

Generic data: All other data is displayed in a similar way. For each record the data source and all values of all fields are shown. A link to a geographical record is possible (meaning the data entered was recorded at a specific location).

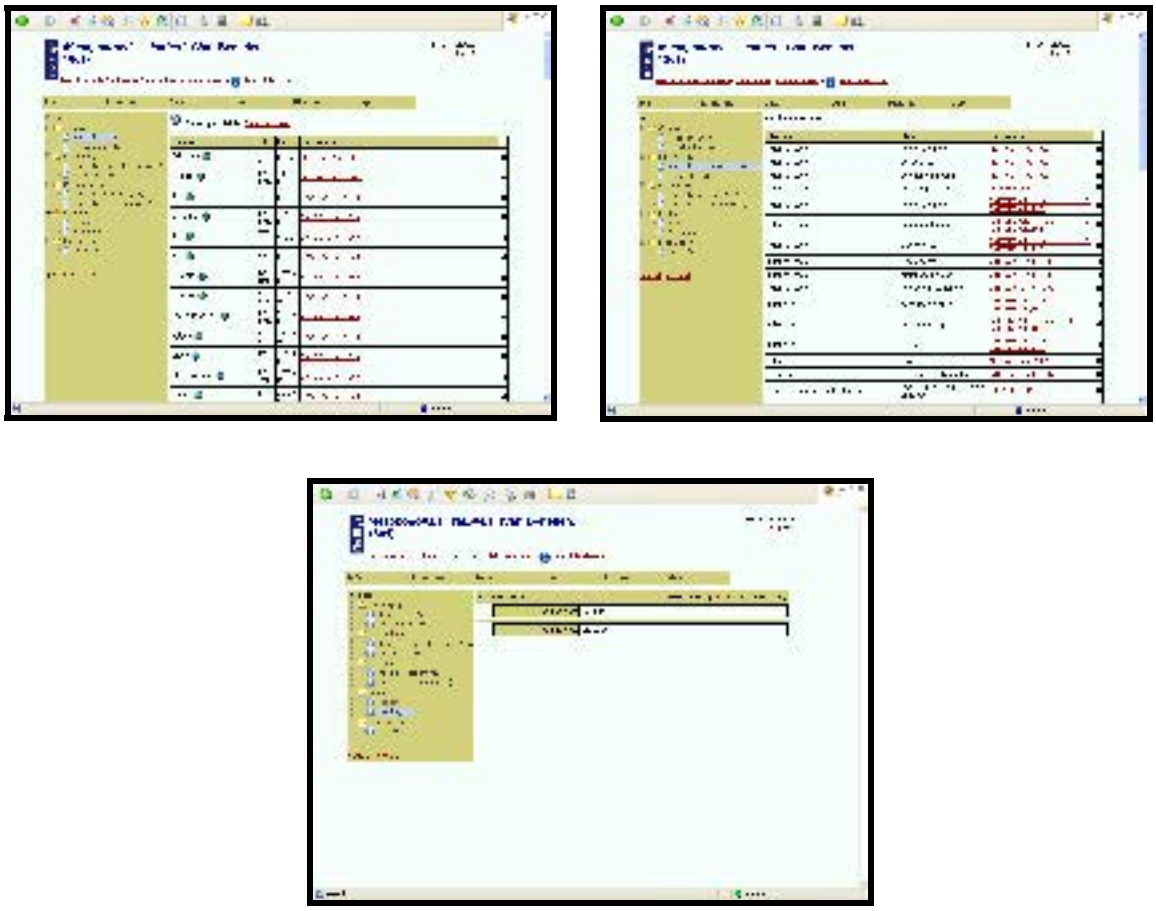


Figure 15. Illustration of three NeMys species data interfaces: (top-left) geographic records, (top-right) morphological records, (bottom) ecological records

3.2.3.4. Notes page

Although notes can be embedded in the 'generic data module' they are still displayed separately. Notes are considered as text based data. These can be morphological descriptions, ecological knowledge … The data source for a note can be a literature record or a person.

3.2.3.5. Pictures page

The multimedia section is currently named 'pictures', although many more types of multimedia files are allowed: movies, pdf-files, audio-files. The majority of the multimedia files are currently pictures. Pictures can be displayed as thumbnails, as a list, as a slideshow or can be exported to a pdf-document. Thumbnails are available for all users, full-size pictures and pdf-files are only available for registered users. All pictures have the copyright data embedded as a watermark.

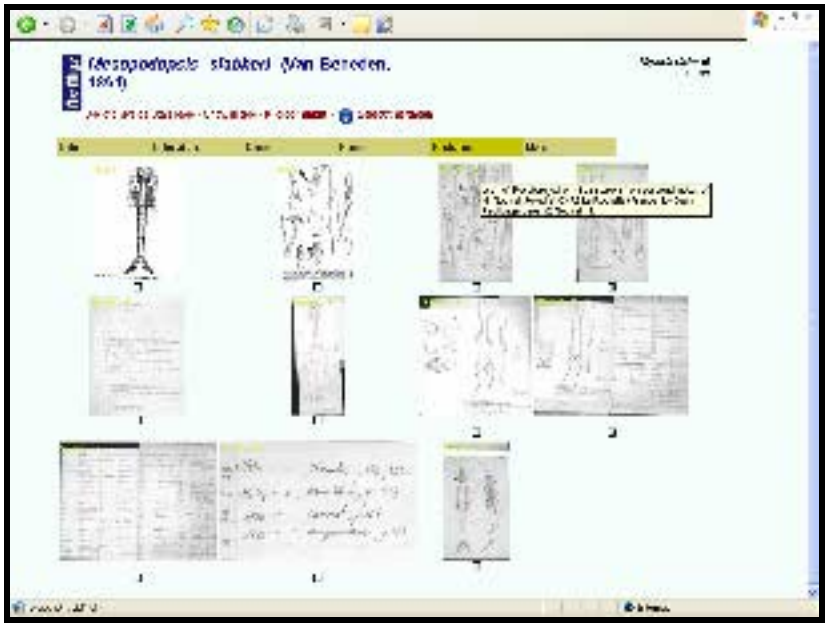


Figure 16. Illustration of the NeMys species multimedia interface

3.2.3.6. Map page

The map pages display all geographic records of a taxon. The NeMys mapping tool is used for this. Higher taxonomic levels will display the geographic records of all child taxa (for example: the map page of a genus will plot all records of all species belonging to this genus.)

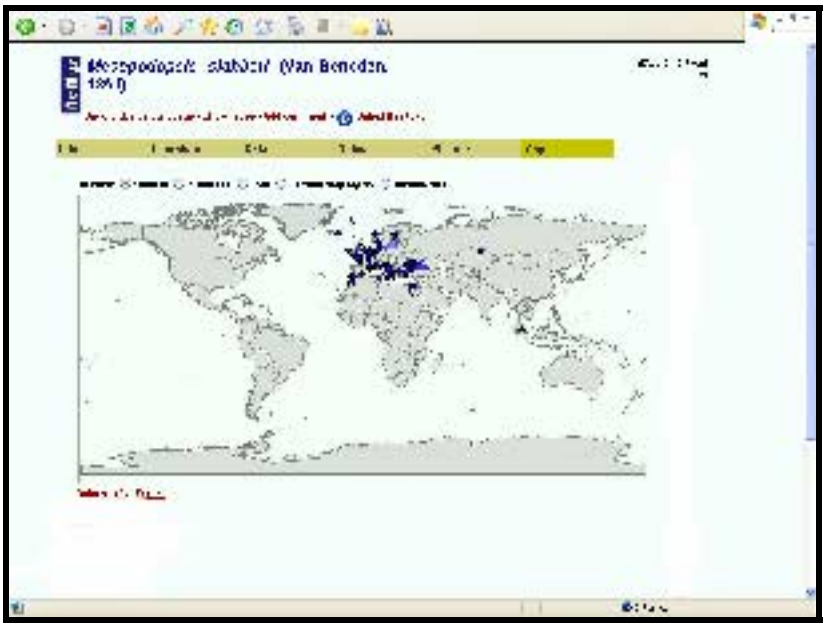


Figure 17. Illustration of the NeMys species distribution map interface

3.2.3.7. Collections page

In this section all collection items of the taxon (mostly species) are shown. Each collection item can additionally be documented with morphological data, pictures and notes. These entries are not literature linked but are based upon observations by a person on the specimen.

3.2.3.8. Molecular page

All molecular records available in genbank (http://www.ncbi.nlm.nih.gov) are displayed here.

3.2.3.9. Data entry pages

The data entry section is only available for users having additional rights for entering and editing data. From a species page, all species-related data entry can be done.

- **3.2.4. Data management pages**

Data entry is, as already mentioned, done online. Consequently the setup of the data entry pages is of high importance regarding the quality of the data in the dataset. Three basic rules are employed for all data-entry related pages:

1. before one can start entering data, a data source must be selected
2. data is not written to the database as long as not all steps of a data entry action are completed. All data entry interfaces are developed as step-wise procedures guiding a user in the process of data entry (for example: first select your data source, then select the taxon, then select a location, then add additional recording data, finally approve the data entry)
3. each piece of data added is documented with metadata: time of entry or change, the user (who entered the data).

Describing all of the possible data-entry pages is not done yet. More details on these pages will be available in the NeMys manual (summer 2006).

- **3.2.5. Advanced user-interface programming techniques**

3.2.5.1. Language module

The main language of the interface of NeMys is English. However, the language of the system is not fixed and can thus be changed. Switching languages is achieved by taking all hard-coded text out of the program code and by replacing it by currently about 300 variables. Where possible, variables are reused. For each language, a file was made, containing the values of these variables in the particular language. The example below shows the variable settings for the main menu on the NeMys start page:

English interface:	French interface:	Spanish interface:
Mi01 = "Introduction"	mi01 = "Introduction"	mi01 = "Introducción"
mi02 = "Datasets"	mi02 = "Ensembles de données"	mi02 = "Set de datos"
mi03 = "Browse"	mi03 = "Diagramme en arbre"	mi03 = "Arbol Taxonómico"
mi04 = "Search"	mi04 = "Cherchez"	mi04 = "Busque"
mi05 = "Publications"	mi05 = "Publications"	mi05 = "Publicaciones"
mi06 = "About"	mi06 = "À propos de"	mi06 = "Acerca de"
mi07 = "Contact"	mi07 = "Contact"	mi07 = "Contacto"
mi08 = "Login"	mi08 = "Connectez-vous"	mi08 = "Conexión"

Table 2. Example of interface variables facilitating the multiple languages of the interrface.

Currently, six language interfaces are included (English, French, Dutch, Spanish, Portuguese and Russian). More will be added soon (Slovenian, German, Polish).

Eighty percent of the interfaces have been made multilingual.

3.2.5.2. List generators – Taxon baskets & reference lists

NeMys allows registered users to create lists of taxa and references throughout the dataset. These lists are used to create overview reports of the selected items: maps of all selected taxa, reference list of all selected references.

These 'list generators' are made possible making use of cookies (text-based pieces of information which are stored temporarily at the users side). Items are added to the list by adding their value to the former value and separating it from the other values by a delimiter.

Example: cookievalue1 = "18-19-45-67-90-" , meaning item 18, 19, 45, 67 and 90 have been selected by the user.

This method can be explored much more by adding more reports or by using it on many more types of data (locations, data records, images, …).

An alternative for the use of cookies which are not allowed by every browser is the use of session-related variables, which are saved on the server. First tests have been carried out recently.

3.2.5.3. NeMys Toolkit

The 'NeMys Toolkit' has currently six tools giving some extra 'spirit' to the data in NeMys. Two types of tools exist: (1) 'documentation tools' and (2) 'data exploration tools'.

'Documentation tools' give extra documentation on data-set related issues, while 'data exploration tools' present the available data from an alternative point of view. The 'Glossary' and 'Methodology' tool are considered as 'documentation tools' while all others are 'data exploration tools'.

IDENTIFICATION KEYS

The identification tool (NeMysKey) offers the possibility to create online polytomous keys (see chapter 2). Morphological records linked to taxa are with this tool combined over several taxa, and re-used in an identification environment.

GLOSSARY

The glossary is added to facilitate the documentation of data in NeMys. Currently the majority of datasets hosted on NeMys are rather specialized. As a consequence there was a need to illustrate the data with taxon-specific vocabulary. Terms of the glossary can be documented with text, images, sounds and movies. This was achieved making use of an online rich text editor (WySiWyG^{x}). Terms are ordered alphabetically.

On a scheduled base (once a week) the glossary is linked with data in NeMys. Currently morphological terms (used in the identification keys) and notes are linked with the glossary. When a word from the glossary is present in the focused text, tags are added before and after the word of interest. These tags are interpreted in the user interface as links to glossary records. Glossary descriptions are also indexed, meaning the description of a glossary entry may contain a link to another glossary entry.

Figure 18. Illustration of the NeMys glossary interface

METHODOLOGY

The methodology tool is a second documentation tool, aiming to store methodological issues about taxa in the database. Currently mainly techniques used to get to data available in the database are described here.

> Nematode identification is based on the analysis of detailed morphological features only visible when preparing the specimens correctly. The making of microscopic slides is documented in the 'methodology' tool. The method can be illuminated with pictures or movies, and useful links to relevant literature may be added.
>
> A good example of the methodology tool can be seen in the Nematoda dataset: http://intramar.ugent.be/nemys/start.asp?group=2&c=37 .

PRIVATE WORKBENCH

The 'Private Workbench' enables registered users with data-entry rights to add data in a private hidden section. Taxa, sources or even small sets of data can be added without being visible to other users. These private taxa will be shown in the classification tree but are not accessible by other users. An option is offered to allow also other users to consult data from this 'private workbench'. The main aim of this

tool is to create a virtual environment facilitating the input of unpublished research data or the addition of data on species not officially described yet.

Currently the tool is still under development. In the near future a private workspace will be applicable for any type of data in NeMys. Technically implementing this tool is done by an extra level of security on the data-record level. Each record is flagged private or public. Authorized users are listed in an extra text field.

> *Siriella* species1, is an un-described species for which already ecological important data is known. As long as I did not describe the species and gave it a name, data on the species (morphology, pictures, …) can already be entered in the system through the 'Private Workbench'. The species is added in the table 'tu' and is flagged as '1' private, meaning that only I am allowed access the data on the species.
>
> If a colleague is interested in this species, I may give him authorisation to view the data on the species. The number of the NeMys-account of this person is added in an extra field setting the exceptions on private data.
>
> Private data can easily be made public by setting the flag to '0', meaning the data may be consulted by anybody.

BIOGEOGRAPHIC DATA ANALYSIS TOOLS

Biogeographic analysis tools in NeMys offer some basic biodiversity analysis possibilities. Currently three types of analysis are available: (1) Species richness plots, (2) Taxonomic diversity plots, (3) Ordination exports.

All three analyses are using taxon related geographic records. Analysis is not done on the raw data (stations), but on squares in an overlaying grid. Analysis can be done on a global scale or on a limited region. The precision of the grid (size of the squares) are set by the user.

Analyses always start from a parent taxon, meaning the tool is initiated from a certain taxon and data of all child taxa of this taxon is used (for example: when the genus '*Mesopodopsis*' is selected, analysis will be carried out on all *Mesopodopsis* species; when the order Mysida is selected, all data on all mysid species is taken into account).

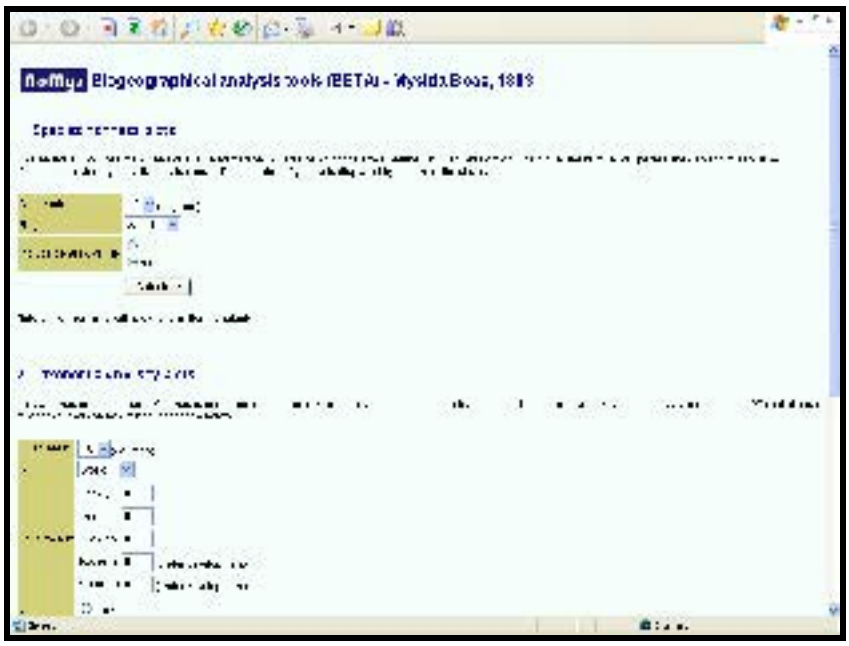


Figure 19. Illustration of the NeMys biogeographic analysis tool

The 'Species richness plot' calculates the number of species per grid-square. The more species present in a square the darker the circle visualizing the richness. The number of genera can be visualized by the size of these circles.

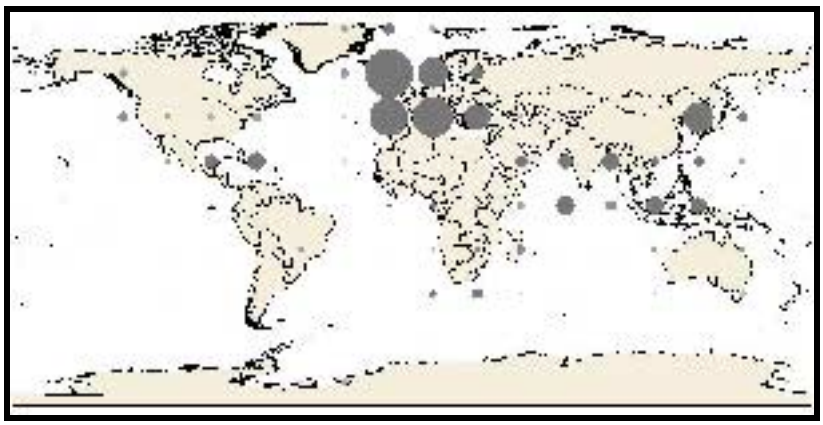


Figure 20. Illustration of species/genus richness map generated by the biogeographic analysis tool

The second tool ('taxonomy diversity plots') calculates a taxonomic diversity value for each square. Families, genera, and species can be assigned a different weight in the calculation. Currently only linear calculations are available:

DIVNEM = xfam*numfam + xgen*numgen + xspec*numspec

where ‘xfam’ is the weight assigned to a family and ‘numfam’ the number of families in a square; ‘xgen’ is the weight assigned to a genus and ‘numgen’ the number of genera; ‘xspec’ is the weight assigned to a species and ‘numspec’ the number of species.

To include the effect of sampling a correction, using based number of records or the number of sources used, can be taken into account. The weight of the correction factors can be set.

DIVNEM = DIVNEM/(xrec*numrec)+(xdoc*numdoc)+1

where ‘xrec’ is the weight assigned to a record and ‘numrec’ the number of records in a square; and ‘xdoc’ is the weight assigned to a literature source and ‘numdoc’ the number of sources used in a square;

Results of this test can be displayed in a map or as a table.

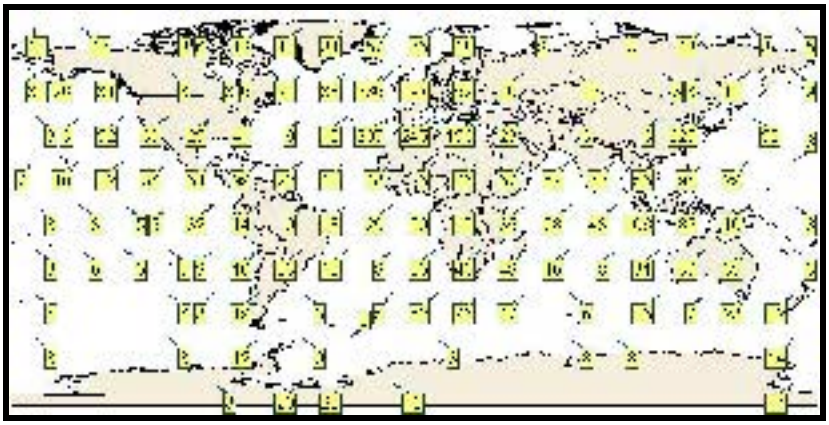


Figure 21. Illustration of a taxonomic diversity map generated by the biogeographic analysis tool

The third tool (‘Ordination exports’) exports parts of the dataset to a table. This table is designed to allow easy import in statistical packages. It generates a list with squares representing cells of a grid. For each square the represented species or genera are listed.

NeMys mapping tools

Biogeographic data is a significant component in NeMys. Clear access to this set of data requires a set of GIS-based analysis tools. Three types of geographic visualisation tools are developed: (1) Google map interface, (2) Google Earth export, (3) NeMys mapping tools.

1. Google map interface

A first visualization method displays the available information for each single location. A small map making use of the free javascript [xi] based Google-map api component (http://maps.google.com), visualizes the exact position of the location. Zooming and panning is possible. Users can switch between a boundary map and a satellite image map. Together with the map, all metadata on a location, other species recorded at the location and eventual other environmental information is shown.

Technically implementing this component is done by registering the web address at the Google Map website. A registration key facilitates the connection with to the Google map server. Plotting locations on a map is done by a few lines of javascript code:

```
var point = new Gpoint(X coordinate , Y coordinate);

var marker = new Gmarker(point,icon);

map.addOverlay(marker);
```

This mapping tool has some limitations: (1) All map-activity is client-sided, meaning speed and performance of the maps depends on the capacities of the machine and internet connectivity of the users. As a consequence, the more points plotted, the slower the map loads. (2) Display of the map depends on the availability of the Google map servers.

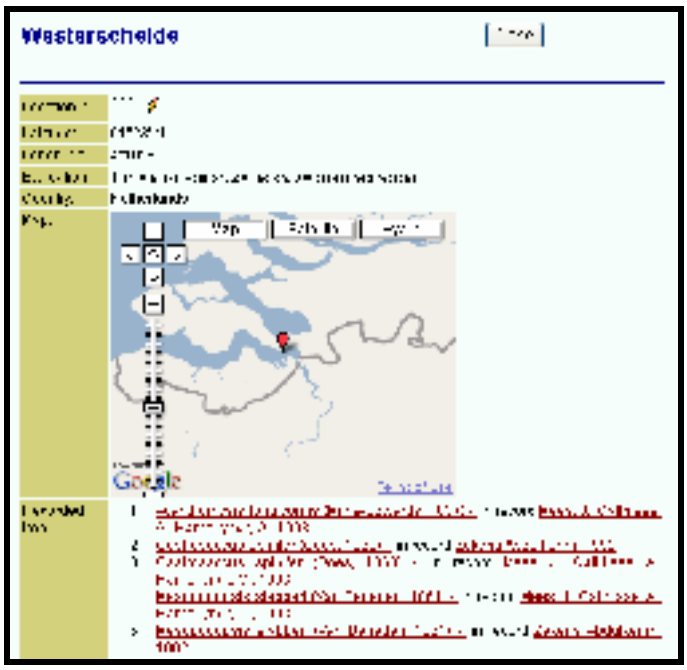


Figure 22. Illustration of map generated with Google Map©

2. Google earth export

A second mapping tool exports distribution records to the Google Earth desktop mapping tool (http://earth.google.com). This method obliges users to have the Google Earth application installed on their local computer. Data transfer between NeMys and Google Earth is done through KML files (an XML-based file format) generated on the server.

An example of a KML file is displayed in appendix 4.

Some advantages of using Google Earth are: (1) attractive maps with lots of interactivity, (2) data-layers like species distributions can be saved locally; (3) extra layers can be added.

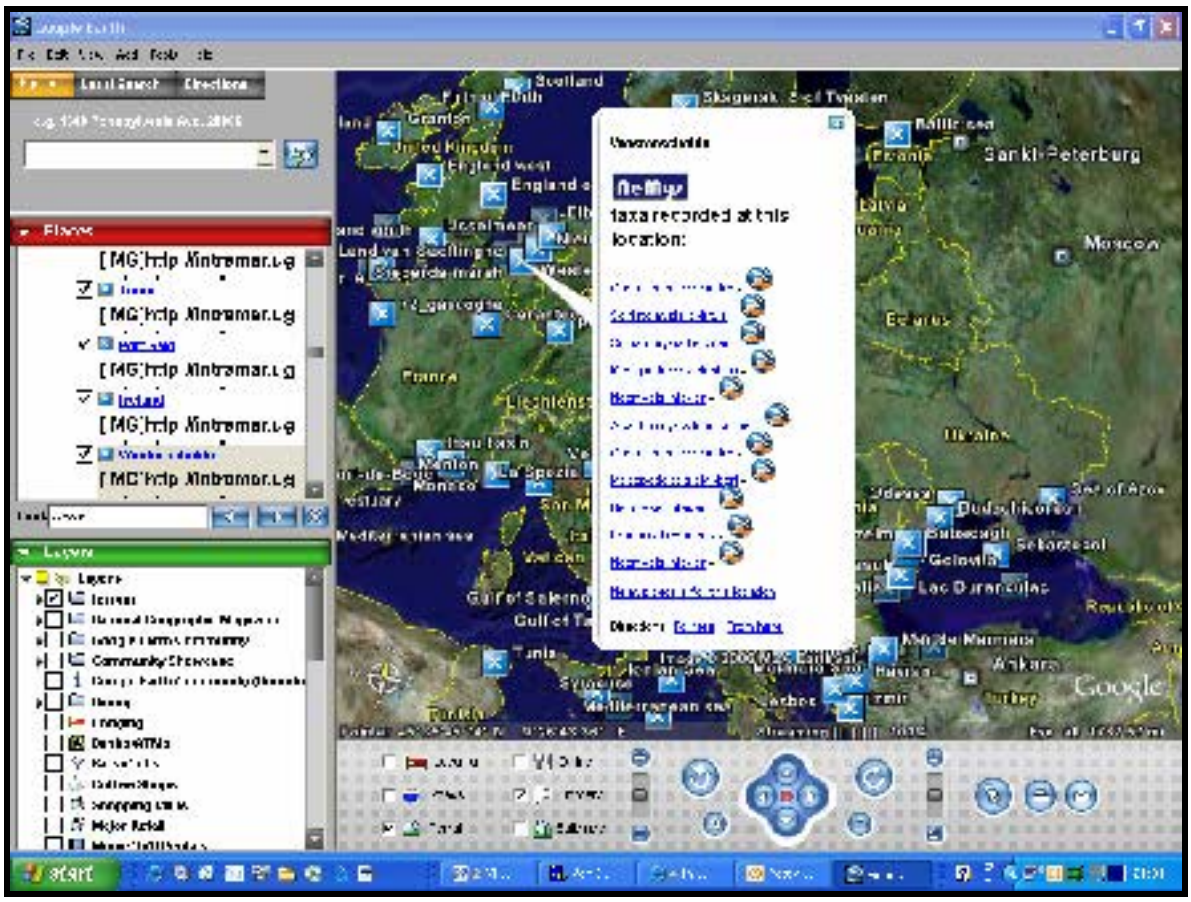


Figure 23. Illustration of Google Earth© application with imported NeMys distribution records

Although the Google-related mapping tools are very flashy and easy to use, for pure scientific data visualisation and analysis both are not the best option. They require a high speed internet connection for reasonable functioning. For scientific use, global or regional detailed maps, and scientific meaningful map layers are needed.

3. NeMys mapping tool

The first attempt in creating an online mapping tool was done with SVG (Scalable Vector Graphics), a XML vector based language. Visualization of points on a background map is relatively easy. More advanced applications (extra layers, switching projections, ...) need more programming, but also make the tool slower. Each time the map is loaded, the SVG-file is sent to the user. The more layers and points, ... the bigger the file and the slower maps are loading. Visualization of the SVG-files in the browser is only possible with a svg-viewer. Although these viewers

are freely available (http://www.adobe.com/svg/), the popular web browser Firefox© (http://www.mozilla.com/firefox) does not yet support this open standard.

Currently a server-side [xii] component, generating image-based maps, is used. The component AspMap© (http://www.vdstech.com/aspmap.htm) was found to be the most suitable for developing a scientific online mapping tool. With this component the 'NeMys mapping tool' was built. Distributions of taxa can be displayed on different backgrounds, in different geographical projections, with different attributes. Resulting maps are embedded as an image in the webpage. Panning, zooming and interactive identification of map-layer features is possible.

Through the basket-system (see page 48), the distributions of several taxa can be be plotted on a map. All map layers can be configured (colors, lines, symbols, labels) and additional background layers can be added. Currently 25 background layers are present, ranging from a global scale (for example: large marine ecosystems, global bathymetry) to a very detailed regional scale (for example: woods of Belgium). High-resolution images of a map can be downloaded for printing purposes.

Technical details:

The server-sided component AspMap© translates a set of GIS-layers to an image, which is send to the browser of the client. Independent of the number of layers the file-size of the image remains equal. Three layer types are used:

(1) **Shapefiles**: The ESRI Shapefile is a data-type used in many Geographic Information Systems software products. It was developed by ESRI (http://www.esri.com) primarily for use with their product ArcView.

(2) **Databases**: Data from databases is plotted as a map layer. At least an X-coordinate and Y-coordinate are needed. Additional informative data can be shown as labels or can be used as a parameter when visualising the point (for example point-size).

(3) **Points**: Separate points can be added through a point layer. Point attributes (coordinates, symbol, size, color, label, ...) can be hard-coded, derived from databases, or calculated from other variables.

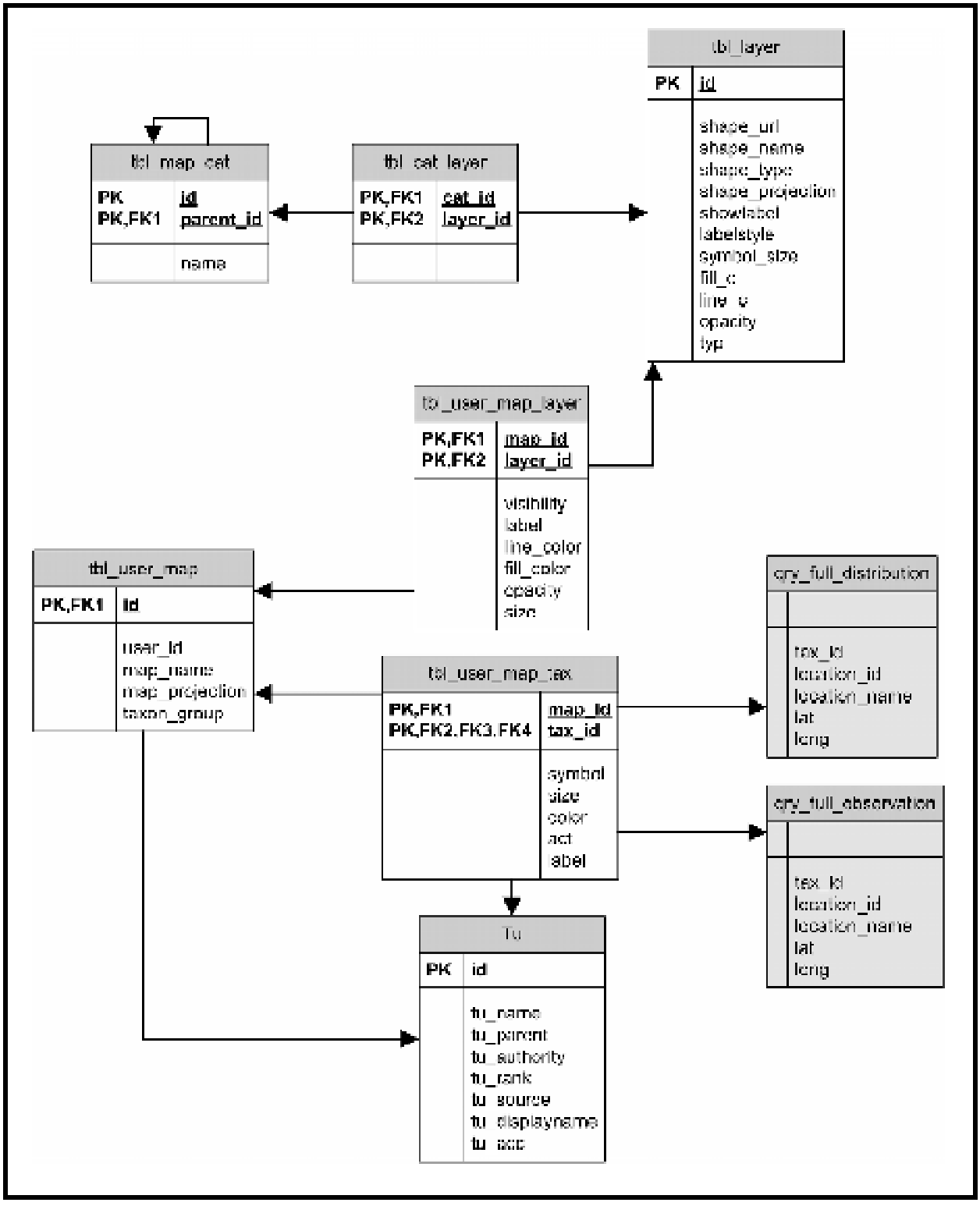
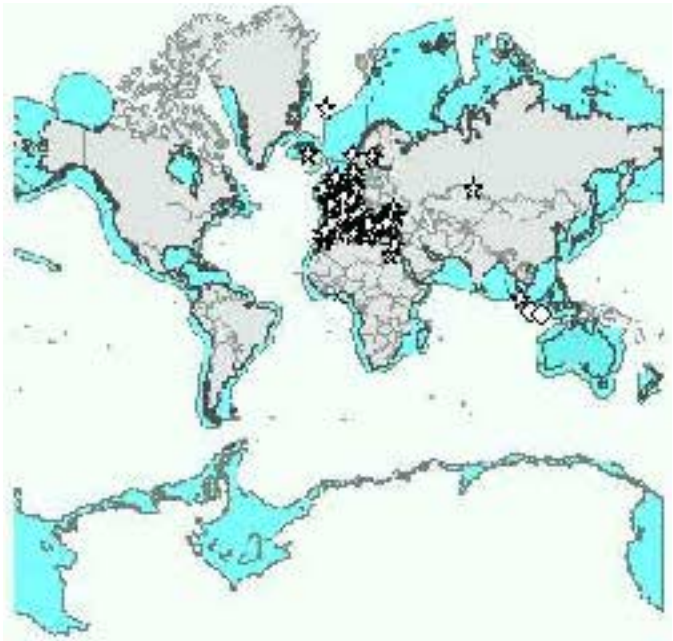


Figure 24. NeMys mapping tool data scheme

The data-scheme (figure 24) illustrates how data used for the mapping tool is organized in the database. For each user maps are saved in the table 'tbl_user_map'. Layers can be dynamically added through the layer-library ('tbl_map_cat', 'tbl_cat_layer', 'tbl_layer'). All map layers have a set of default settings (saved in 'tbl_layer') which can later be changed by the users (saved in 'tbl_user_map_layer'). The list of taxa displayed on a map is saved in the table 'tbl_user_map_tax'. Each taxon is plotted in a separate layer. For each layer options can be set (symbol, size, color, labels).

A distribution map is made for '*Mesopodopsis slabberi'* and '*Mesopodopsis orientalis'*. The map is saved as 'Mesopodopsis map' in the table 'tbl_user_map. This map gets number '718'. The distributions of both taxa are added to the map. In 'tbl_user_map_tax' the link between the map (718) and the taxa '15891' and '6756' are created. Additionally the in this table it is set that *M. orientalis* is displayed by circles and *M. slabberi* by stars. As background layers 'the world' and 'the large marine ecosystems' layer are selected and saved in 'tbl_user_map_layer' with some eventual properties. The projection of the map is set to 'plate carree' this is saved in the table 'tbl_user_map'. All this results in the following map:



▪ 3.3. DATA EXCHANGE PROTOCOLS

The NeMys database is currently shared in two ways: (1) through a mirror website hosted at VLIZ (Flanders Marine Institute – http://www.vliz.be), and (2) through a DIGIR provider on international biodiversity portal websites.

- **A. Mirror at VLIZ**

Since 2003, a mirror website of NeMys is hosted at VLIZ. Only a selection of the data is displayed through this mirror site. Only marine taxa with focus on systematic data, literature data and geography data can be accessed on the website (Deprez, 2006).

VLIZ is the data centre for many other marine biodiversity projects (Marbef – http://www.marbef.org, ERMS, Eurobis – http://www.marbef.org/data/). As a consequence marine records from the NeMys database are used and linked with these other projects hosted at VLIZ.

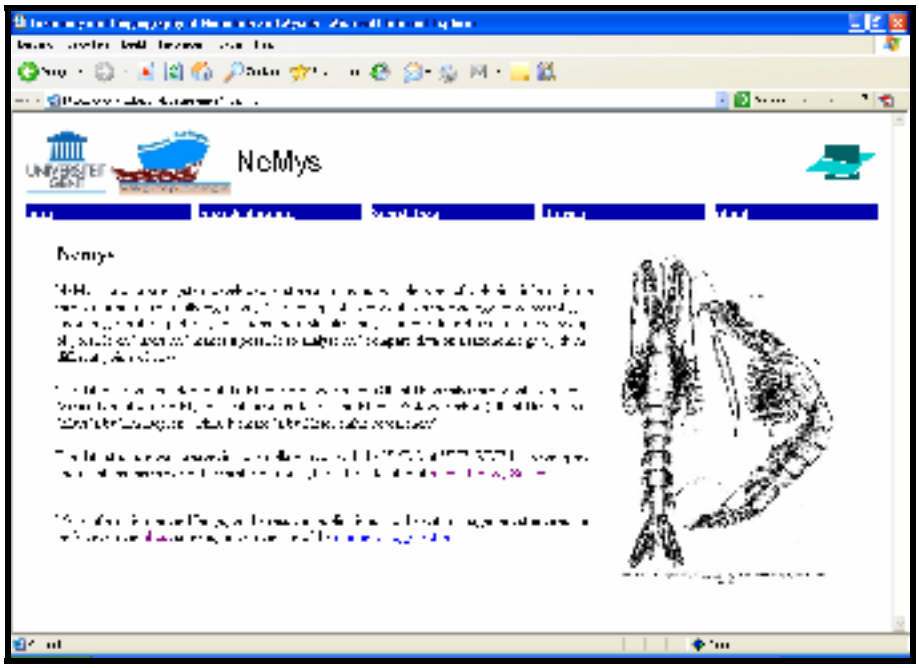


Figure 25. Illustration of the interface of the NeMys mirror website at VLIZ (http://www.vliz.be)

The mirror website at VLIZ has the advantage that data is accessible at any time. Moreover a mirror is a safe method of having a running backup of the data in a remote place.

The mirror website is accessible through: http://www.vliz.be/vmdcdata/nemys/

- **B. International biodiversity portals**

Since a few years technologies have been developed for sharing biodiversity data between databases in online environment (Graham *et al.* 2004). This is achieved making use of distributed data networks (Öszu & Valduriez, 1999). With these technologies, databases hosted on different physical and geographical locations can, if connected to the internet, communicate with each other. Since XML[xiii] became a widely accepted standard, technologies based upon this language make it possible to share data between online applications. The sharing of the data of NeMys with biodiversity portals is made possible by a DIGIR (Distributed Generic Information Retrieval – http://digir.net) provider. This PHP[xiv]-based program is able to receive an html-based request and sends back an answer to the requesting instance. The uniqueness of the system is that requests and answers can be packed in XML, according to predefined standard (scheme). The development of these standards has been the key for making this whole network of databases work properly (Heidoorn, 2001; Hobern, 2002; Hobern, 2004). A schematic view of the functioning of this technology is shown in figure 26.

Each provider is documented with a metadata definition (also in XML) which feeds the provider registry with data. This registry keeps track of all providers on the web and how and what data is served by it. An example of a metadata definition is shown in appendix 1 . The scheme used to exchange data is the Darwin Core V2 (http://digir.net/schema/conceptual/darwin/2003/1.0/darwin2.xsd). This scheme defines a series of fields that are used to exchange data. Some of the important fields used for NeMys are: ‘institutioncode’, ‘Collectioncode’, ‘Catalogue number’, ‘scientific name’, ‘kingdom’, ‘class’, …, ‘species’, ‘yearidentified’, ‘identiied by’, ‘collector’, …, ‘location’, ‘country’, ‘latitude’, ‘longitude’, …

Each provider can chose how many and which fields he fills with data from his dataset. Not all fields are applicable for each dataset. Detailed information on all fields and definitions can be found at http://digir.net/schema/conceptual/darwin/Core_andExtensions.html.

Data from NeMys is now shared with several portals:

(1) Eurobis: European node of the ocean biodiversity information system (Vanhoorne *et al.* 2004). Url: http://www.marbef.org/data

(2) GBIF: Global Biodiversity Information Facility - is an international organisation which focusses on the availability of data on biodiversity in general. It is like OBIS a provider of global geo-referenced distribution data of species for both marine and terrestrial environments (Edwards *et al.* 2000). Url: http://www.gbif.org

(3) OBIS: The 'Ocean Biogeographic Information System' is the information component of the Census of Marine Life (CoML). OBIS is a web-based provider of global geo-referenced information on marine species (Zhang & Grassle 2002). Url: http://www.iobis.org

(4) Scar-Marbin: This portal aims to bring together Antarctic marine biodiversity data. Data from this portal is shared with other biodiversity initiatives like OBIS and GBIF. Two datasets in NeMys are involved: the Nematoda dataset through the BIANZO project (http://www.bianzo.be) and the Mysida. Url: http://www.scarmarbin.be

(5) Zipcode Zoo: an online portal aiming to bring all kinds of online available species information together. Url: http://www.zipcodezoo.com

All listed portals display classification data and geographic records. For more detailed information users are sent to the NeMys pages.

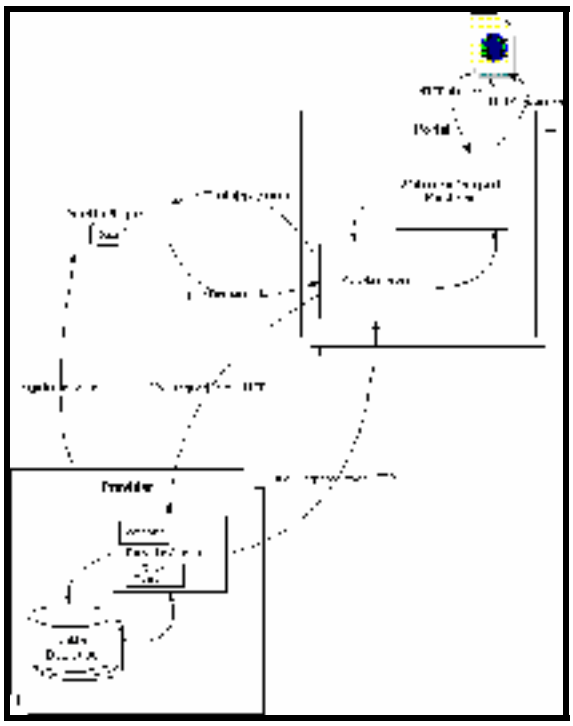


Figure 26. Scheme explaining the functioning of a digir provider (after http://digir.net)

4. NeMys Data policy

An important characteristic of NeMys is that data should be freely available to a wide range of users. However, recent developments like the 'private workbench', allow also data not freely consultable by anyone.

A general data policy is proposed. The data policies of other open systems were used as a model: the Marbef data policy at http://www.marbef.org/data/datapolicy.php and the GBIF data policy at http://www.gbif.org/DataProviders/Agreements/. More restrictive or open policies may be made for separate datasets in the system. The current policy may be revised with changing requirements.

4.1. NEMYS DATA POLICY PROPOSAL

The first guiding principle within the NeMys data system is the principle of free and open access to data on biodiversity (Arzberger *et al.* 2004; Froese *et al.* 2004). This is in line with the principles of the 'Clearing-House mechanism' statements of the Convention on Biological Diversity (CBD – http://www.biodiv.org/chm) and data policies of other major organisations like the Intergovernmental Oceanographic Commission (IOC), with the Conference statement of the Ocean Biodiversity Informatics conference held in Hamburg, 2004-11-29 till 2004-12-1.

The data policy of the originator of the data will take precedence over the data policy of NeMys. NeMys does not claim ownership of the data. The person responsible for a dataset may decide to withdraw his/her data from the NeMys system.

All the sources of data in the NeMys datasets will be acknowledged, on the level of the individual record in the database.

Data available in NeMys may only be used for personal, educational and scientific professional use. Commercial use of data is strictly forbidden. When using images from the NeMys website, authorisation for usage must be received from the copyright owners of each image.

A statement of 'proper use' for data available through the NeMys website is posted; visitors registering to the website are requested to confirm that they have read and agree with the proper use statement before they are given access to the data.

The proper use statement requires original data sources to be cited in papers that make use of data harvested from the NeMys website, and to cite the individual datasets, in case these individual datasets form an essential part of the data used in the publication.

By downloading or consulting data from this website, the visitor acknowledges that he/she agrees with the NeMys data policy, and agrees to the following:

If data are extracted from the NeMys website for secondary analysis resulting in a publication, the NeMys website should be cited.

> Deprez, T. ; Speybroeck, J. ; Steyaert, M. ; Vanreusel, A.; Vincx, M. 2005. NeMys. World Wide Web electronic publication. www.nemys.ugent.be, version ([month of consultation]/[year of consultation]).

Separate datasets should be cited as follows:

> [Name(s) of the person responsible for the dataset] ([year of consultation]). [Name of the dataset] hosted on NeMys. Available online at http://www.nemys.ugent.be . Consulted on [date of consultation].
>
> Example for the Mysida dataset:
>
> Deprez, T. (2006). Mysida dataset hosted on NeMys. Available online at http://www.nemys.ugent.be. Consulted on 2006-06-16.

Keys created with the NeMysKey tool should also be cited according to the citation appearing when opening a key.

If any individual dataset in NeMys constitutes a substantial proportion of the records used in the secondary analysis (i.e. more than 25% of the data are derived from this

source, or the data are essential to arrive at the conclusion of the analysis), the person responsible for the dataset should be contacted.

Use of the system for consultation of data is free. Access to copyrighted material requires registration. Using NeMys as a research tool, to set up a new database, is possible after contacting the Marine Biology Section, Ghent University (Tim Deprez or Magda Vincx).

5. NeMys in numbers

NeMys has throughout its existence gradually shown that it is applicable for a wide range of objectives. The amount and type of data, and statistics on the use of this data illustrate this. An overview of the data, and the user community is given below.

▪ 5.1. DATASETS IN NEMYS

Currently seven datasets are hosted on the NeMys platform. Some datasets are under constant revision while others are currently 'closed', meaning no changes have been made to the data during the last six months.

(1) The '**Mysida**' dataset focusses on the global biogeography and taxonomy of the order Mysida (Peracarida, Crustacea). This dataset will be explored in much more detail in the following chapters. It contains information about 1700 taxa. The dataset is maintained by Tim Deprez, working at the Marine Biology Section, Biology Department, Ghent University.

(2) The '**Nematoda**' dataset is the world reference dataset concerning free living marine Nematoda. It holds information on about 7000 taxa. Most of these are documented with illustrations, literature and for some regions also with distributional information. The dataset is maintained by the Marine Biology Section, Biology Department, Ghent University.

(3) The '**Turbellaria of the Belgian Continental Shelf**' is a small closed dataset with information on the 113 species ever reported from the Belgian marine waters. Most species are documented with references and distributional records. This dataset is maintained by the Marine Biology Section, Biology Department, Ghent University.

(4) The **'Phytoplankton**' database of the Belgian waters is a closed dataset, built as a Master thesis project. Fifty eight common phytoplankton species are documented with literature records, a short text-based species diagnosis

and pictures. The dataset is maintained by the 'Protistology and aquatic ecology research group', Biology Department, Ghent University.

(5) The '**Peperomia**' dataset covers the genus *Peperomia* (Piperacea) worldwide. This dataset is used in a cooperative project on the phylogeny and evolution of the giant genus *Peperomia*. Information on 2031 species, all documented with literature, morphological records, collection specimens and pictures, make it the world most complete dataset on this plant genus. The dataset is maintained by 'Research Group Spermatophytes', Biology Department, Ghent University and 'Technische Universität Dresden – Germany, Plant Phylogenetics & Phylogenomics Group'.

(6) The '**Euroherp**' dataset holds information on all European Amphibians and Reptiles. In total 456 taxa are represented in this dataset. Pictures, geographical records, literature, morphology and text based descriptions form the largest contribution in this dataset. Euroherp aims to be a knowledge centre for European amphibians and reptiles and is maintained by Jeroen Speybroeck (jeroen.speybroeck@ugent.be).

(7) The final public dataset is the '**Eurocox**' dataset. It groups all kinds of information on European ladybirds (Coccinellidae). Although just 261 species are present in the dataset, it contains a huge amount of observation records from currently mainly Belgian areas. The dataset is maintained by Tim Adriaens (tim.adriaens@inbo.be), INBO (http://www.inbo.be)

▪ 5.2. DATA IN NEMYS

The table below gives a brief overview of all public available data in NeMys. Only datasets which are still alive (still changing) are described in more detail. Three large dataset (Nematoda, Mysida and *Peperomia*) and two smaller ones (Euroherp and Eurocox) can be distinguished.

Number of taxa	**12562**	
	Nematoda	6926
	Peperomia	3216
	Mysida	1675
	Euroherp	456
	Eurocox	289
Number of references	**12083**	
	Mysida	3998
	Nematoda	3080
	Euroherp	1102
	Peperomia	871
	Eurocox	830
Number of scanned references	**8000**	
	Nematoda	2673
	Mysida	1523
	Euroherp	964
	Eurocox	137
Media files	**24000**	
	Nematoda	12732
	Mysida	7424
	Peperomia	2230
	Euroherp	585
	Eurocox	337
Number of geographic records	**17976**	
Number of morphologic records	**24369**	
Number of collection specimens	**1255**	
Number of links between literature and taxa	**50131**	

Table 3. Overview of types of data in NeMys

▪ 5.3. NEMYS USER COMMUNITY

Most of the data is freely available in NeMys. However consultation of copyrighted material and the use of some special tools (like the 'NeMys Toolkit') require a user to register to the system. Analysing the traffic on the website gives an idea on who is using the system for which purpose.

• 5.3.1. Registered users

In total 854 users have registered to the system (situation January 2006). Most people register to the Euroherp, Nematoda or Mysida dataset. Registered users represent currently 64 countries. Belgium, United Kingdom, Italy, Spain, United States, The Netherlands, France, Romania and Portugal have the largest contribution in number of users. Half of the registered users are from academic origin while others register as a private person. In the list of countries also a number of developing countries are represented: El Salvador, Cuba, Kenya, The Philippines. All continents are represented.

• 5.3.2. All users

The total number of users is much higher than the number of registered users. This means a lot of users are not using copyrighted material (such as PDF files or images) and are able to extract the needed information from the public available pages.

Actually the site is visited by an average of 500 visitors a day. One third of these visits are search robots (not human). The most popular pages are the species information pages with currently about 250000 page loads each month. The dataset start pages are loaded approximately 20000 times a month. The NeMys start page 7000 times a month. Most users enter the site through search engines of which Google© is the most popular one. The criteria searched for are next to obvious words like 'NeMys' or 'Euroherp' mostly species names.

5.3.2.1. Geography

Users come from are originating from 139 countries of which the Belgium, United states, Germany, United Kingdom, Netherlands, Spain, France, Italy, Canada and Poland are the most represented (Situation January 2006).

An analysis of the languages spoken by users of the system shows the following picture:

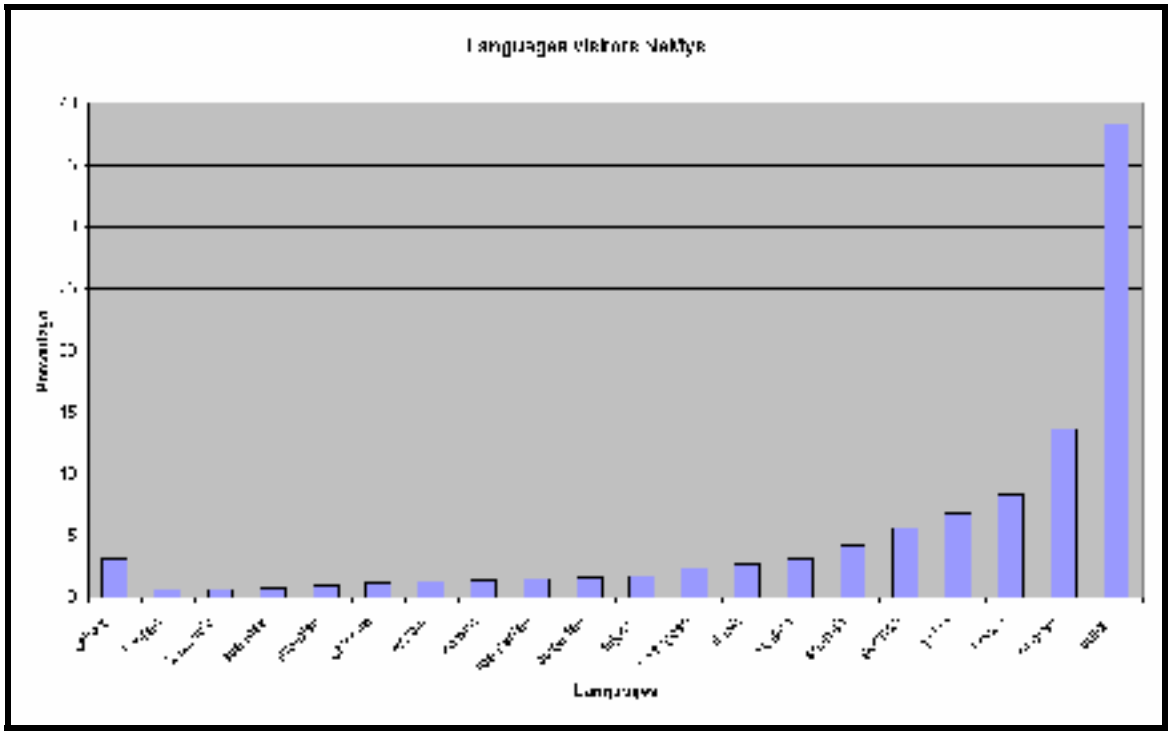


Figure 27. Languages spoken by registered users of NeMys

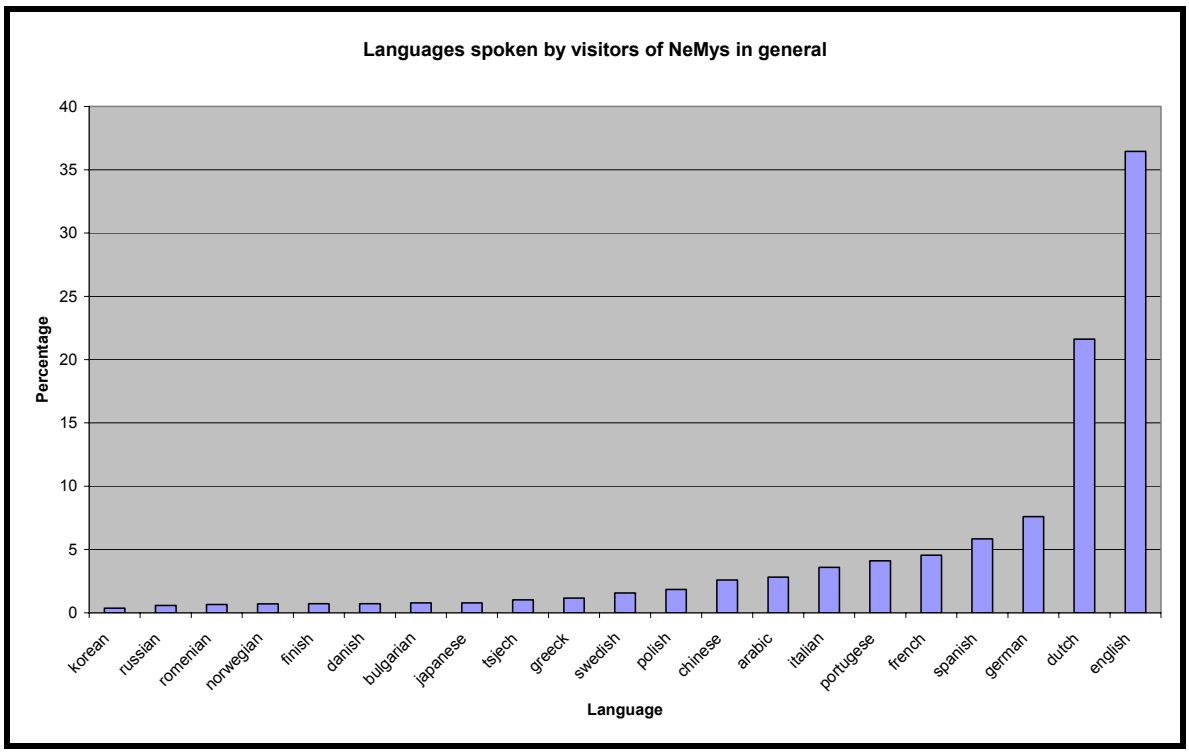


Figure 28. Languages spoken by all users of NeMys (registered and regular)

English, Dutch, German, Spanish and French are currently the most spoken languages of both registered and unregistered users of NeMys.

6. Discussion

The use of databases in biological research is recently common. Within taxonomy oriented research, the advantages of digital data management systems are not recognised well enough yet (Godfray, 2002). Few digital information sources are delivering data which is usable for taxonomic research. As taxonomy requires a large number of information types, a system able to manage this is required. NeMys may offer a solution as it allows data management for many types of data. The web based architecture acts as a platform to combine widespread published information together with new findings. NeMys can be seen as a living taxonomic archive: historical published data is protected and can be constantly updated.

Although the system is designed as a taxonomic research tool, it attracts a wide range of users. This demonstrates that taxonomic data becomes much more attractive and useful when managed in a digital open system.

Some specific characteristics (advantages and disadvantages) of NeMys are discussed below. Also some possible future developments will be highlighted.

▪ 6.1. GENERECITY

A question often asked when introducing people to NeMys is: “in what ways does NeMys differ from the other well-known biological database systems?”. An answer to this question may be that NeMys is a true **generic** system. It is taxon-independent and data-type independent.

Almost all well-established species-information systems have limitations on this point:

(1) **Taxon-related**: many systems focus on one taxon: for example Algaebase (Guiry *et al*, 2006) gives information on algae, Fishbase (Froese & Pauly, 2005) on fishes, Cephbase (Wood *et al*, 2000). Most of these databases have evolved from the speciality of the database managers or originators. Constructing a generic structure does not necessarily rise the complexity of the database structure. A few

additional tables and variables are enough to make a bio-information system work for any group of organisms. In general, indicating to which dataset a data record belongs makes a system generic.

(2) **Limitations in data-types**: An argument often used is that each taxon has its own requirements concerning data fields. By introducing the parametric data system it is now possible to add as many fields to a dataset as needed. Leaving the classical relational data model adds a lot of flexibility to the system and is far more efficient. No additional programming efforts are required, and no actions from the database managers are demanded when new sets of data are added. The generic parametric data structure has been implemented during the last year. Many data-fields still stored in 'old' classical tables in NeMys can fit in this generic structure. Except for geographic, literature, systematic, morphological and pictorial data all other data, groups can be merged into this system. This will allow the development of tools applicable for any kind of data (search interfaces, automated keyword linking, data export tools) and a common set of interfaces enhancing the user-friendliness.

(3) **Limited data playground**: Once data is in a bio-information system, it is necessary to get it out again. Presentation of the data in a digital bio-information system must be as generic as possible, in order to answer different research questions. As an example geographic data can be used. A generic presentation of the data requires a wide range of possibilities: lists, maps and exports to downloadable files. When developing playground tools it is of main importance to find out the user needs. The more users using the system, the more needs will arise.

A web based tool with a generic architecture like NeMys offers a number of advantages: (1) new projects making use of a generic package will be a lot easier to integrate with each other, (2) the creation of new tools is much more time and money efficient, (3) a blank “plug-and-play” system may encourage others to setup a species-information system (Wood *et al*, 2000).

▪ 6.2. DATABASE STRUCTURE & SCALABILITY

Currently all data and metadata in NeMys is maintained in one database. Due to the gradual development of the system, some parts of the database need some revision. Data on persons is stored in three different tables. The generic data unit is at this point in time not used efficiently enough. Web links, free text notes, molecular data can easily fit in this unit (see also paragraph above). Reorganising those two parts of data would eliminate up to seven tables in the database and make the whole structure much more transparent. A revision of the data structure is a job which needs prior attention in the near future.

Whether or not there is a future for NeMys will depend on how the application acts when more data comes available in it. For many parts of the database tests have been carried out on how the system acts with more data in it. The taxonomical unit has for this reason been filled up with all taxa (more than 400000) available in the Species 2000 database (version 2004) (http://www.species2000.org). The high number of taxa did not affect the functionality of the application. A similar test was done with geographic data. Random locations were added and plotted to the different mapping tools. SVG maps did not function properly anymore with high numbers of locations (> 1000). The javascript based Google Map©'s function well with the number of locations lower than 2000. The NeMys mapping tool allows plotting of 4000 points relatively easy. Map generation takes for all mapping tools more time with increase of data points. Similar tests have been done for morphological data and bibliographical data.

More crucial in terms of scalability of the system is the number of users being active simultaneously on the system. Analysis of the traffic reports learned that a number of tools do slow down if used by several users together: searches on the full-text index of literature sources, and mapping distribution data. However, all these may easily be solved in the future when upgrading the work power of the server hosting NeMys.

6.3. GEOGRAPHICAL DATA DISPLAY

Leading GIS [xv] applications such as Arcview (Arcview GIS 3.1 (1998); ESRI, Redlands, CA, USA) are by many researchers recognized as rather difficult software. On top of this the use of this software is not free and thus many researchers are excluded from geographic visualization tools. Free tools do exist but are often not developed from a biological user perspective (see http://www.freegis.org).

The GIS-tool in NeMys ('NeMys mapping tool', see page 54) is setup from a relatively unskilled users point of view. Through a series of easy interfaces an big series of maps can be quickly made. The tool does not require any software being installed.

During the setup of NeMys vector-based XML (SVG – Scalable Vector Graphics) was used for mapping purposes. This open-source technology is an interesting option for basic mapping of points, line and polygon-based maps. A client-side plugin is required. Some browsers still do not support well this W3C-approved standard (for example Firefox ©).

Notwithstanding the fact that the AspMap© component is not free, developmental cost is much lower and development time is much shorter. Many complex functions are included.

In the future it may be considered to use an open-source tool for mapping purposes. These freely available packages offer currently a valuable alternative for many commercial packages (some examples are: MapServer - http://mapserver.gis.umn.edu/, Cartoweb – http://www.cartoweb.org). An open-source tool for GIS would also fit much better in the philosophy of open and free access to data (see Open Gis Consortium – http://www.opengis.org).

▪ 6.4. DATA EXCHANGE – DISTRIBUTED SYSTEMS

NeMys is since a few years (since 2004) a data-provider for a number of biodiversity information portals through a digir-provider running on the system. Although this data-sharing fits in the philosophy of 'free access to data on natural history' (Berlin Declaration, 2003), for many providers it feels still as an act of charity. Data providers are not rewarded for the act of sharing their data. Users consulting the data through a portal will in most cases not acknowledge the original data providers but much more the data portals.

When looking at the website traffic statistics, almost no users enter the website through these portal websites. They are however mostly considered as an access point to biodiversity information (Bisby *et al.*, 2002). A few small technologically easy achievements on the side of the data portals would make a large difference:

(1) **Automatic data usage messaging**: data providers get a message when data is used (downloaded). These messages can be send or at the time of the request, or at a scheduled basis.

(2) **Automatic pinging**: scientific products are judged on numbers. Publications need to be cited, journals need to have high impact factors, websites need to have large visitor numbers. When data is retrieved from a portal, the number of visitors on the portal raises. The number of visitors on the data provider website does not change. An automatic visit to the originating website of the data provider, could help to solve this problem. A possible easy way of visiting the data-provider is using a small bitmap (for example a logo) stored at the data-providers web server. For most web scripting languages free tools are available to perform an automatic visit to a remote website (for example: ASP – DynuPing (http://www.dynu.com), PHP – ThePinger (http://www.hotscripts.com/Detailed/54254.html)).

(3) **Clear links:** when data is shown from different data-providers a good-visible link to the originator of the data should be included. Links should always go back to the original data-providers. In many cases, data-portals are data-

providers themselves for other data-portals. This implies mostly that the first data-portal is indicated as data-provider.

Data portals should provide some extra features making the delivery of data useful. A few possibilities are listed up:

(1) Many portals do have capacities to build tools which are technically complex. **A tool-portal** would as such be of great value for many data-providers delivering data to the portals. A tool-portal should be seen as a set of biological tools enabling users to work with these tools on specific sets of data. Two groups of tools may be distinguished: (1) webbased tools offering web-services to data-providers, (2) desktop tools for regular users of the data. A practical example of a webbased tool would be a mapping tool (see above): when geographical records for a taxon are available in NeMys, the external mapping tool can be used to display at first instance only the data from NeMys, but may offer the possibility to plot also the data from other data-providers. Next to advanced mapping tools, statistical tools, phylogenetic tools, error-checking tools, may be useful. The second series of tools is already offered a number of portals. EurObis offers possibilities to do online interactive mapping of taxa (http://www.marbef.org/data) (Vanhoorne *et al*., 2004). OBIS offers at its website a number of tools for modeling, mapping and prediction (http://www.iobis.org). GBIF offers tools for data cleaning, data hosting and data providing (http://www.gbif.org).

(2) **Error checking:** Many data on portal sites contains errors (e.g. many records do not have coordinates, marine taxa occur on the land, …). When providing data to a portal site, data should not be automatically integrated but first been approved by automated or man-driven error-checking. Automated checking is done in a limited amount of cases. An argument for not doing it, is that this data-quality control is too expensive. Data-providers however are since many years asking for peer-reviewed database publishing (see for example OBI conference statement, 2004 – http://www.vliz.be/obi/). A possible strategy in raising the quality of the data hosted on data portals may be a process of peer-review before publication.

Although data-exchange through the DIGIR technology is rather easy, it has some major constraints concerning biological databases; the nowadays used schemes (ABCD scheme or Darwin core – Hobern, 2003) do only permit the exchange of a limited set of data (taxon info, location info, …). A series of new schemes for other aspects of biological information should be developed. Recently the Taxonomic Databases Working Group (TDWG - http://www.nhm.ac.uk/hosted_sites/tdwg/) published a number of new standards similar to the ABCD scheme or the Darwin core for exchange of taxonomic descriptive data: for example SDD (Structure of Descriptive Data) (see http://wiki.tdwg.org/twiki/bin/view/SDD/Version1dot1) and Darwin Core 2 (see http://darwincore.calacademy.org/).

▪ 6.5. LANGUAGES

The user-interface of NeMys can be displayed in any possible language (see page 47). The graphs shown on page 71 show languages are important. For a scientific user community, English as interface language does not give any problems. Nevertheless, when looking at the language of the Google© search engine through which many users enter NeMys, most users do use the interface in their native language (for example: the Dutch, Italian, Spanish, French, German, Canadian and Polish Google© interface are used often to enter NeMys). Translating the interface in a range of languages may have a number of advantages: (1) a wider range of users will find its way to biological information systems, (2) people do feel more comfortable and as such will likely spend more time on the website. In the commercial IT environment, since many years the aspect of multilingual/multicultural websites is a hot topic. Many examples have shown that multilingual websites reach a much bigger public (Sun, 2001).

Currently only the interface is available in different languages. Data is still in English. It is questionable whether or not and what data should be available in multiple languages.

▪ 6.6. COPYRIGHTED MATERIAL

One of the most discussed problems concerning online scientific information systems is what to do with copyrighted material (Harnad, 1999; Lagoze & Van de Sompel, 2001; Kansa *et al.*, 2006). Recently many publishers are making journals partly or fully freely accessible on their websites. Papers can thus be consulted for free, but may still not be republished on other websites. This republishing is for incorporation in biological information systems critical. It is the only method to bring topic related (for example literature on a taxa) literature together and to benefit from full-text indexing tools (Koning *et al.*, 2005).

Republishing copyrighted material on the internet is currently forbidden by law. The federal Belgian laws of 30 june 1994, 31 august 1998 and 22 may 2005, state that normal copyrights only disappear 70 years after the death of the author of the work, and that publication of copyrighted publications is forbidden, unless authorization is obtained from the author or the holder of the copyright. This means in terms of biological literature only few mainly taxonomy oriented literature sources may be published on the web. However, a number of exceptions are embedded in these laws: the sharing of copyrighted data is allowed for strictly closed academic environments for research purposes. Similarly, reproduction of parts of publications is allowed for educational purposes. Currently copyrighted material is still archived in NeMys. The registration required to receive access to this data is a simple method for protecting this material, although legally forbidden. Communications on this matter with the juridical services of the Ghent University may hopefully lead to a solution on this matter.

Whether users need an original publication or not depends strongly requirements of a user. Only a limited number of users (for example taxonomists) do need the original publications for research purposes. This is reflected in the large number of users who do not register to NeMys and as such retrieve all needed information in the public open sections. A possible workaround for sharing copyrighted material may be achieved through **virtual community workbench**: a restricted area in a offering users to share data (for example literature) with other community members (see also ‘NeMys communities’). The main difference with the current registration

procedure is an added level of security. Only approved users are allowed to a community and every member of a community knows who else is a member of it. It is crucial that search engines like Google© do not have access to these closed environments.

Recently a number of initiatives have been established aiming to create open archives of literature (http://www.openarchives.org; Sante Fe Convention – Van de Sompel & Lagoze, 2000; OMA – Open Marien Archief : http://www.vliz.be/NL/Zeebibliotheek/Bib_OMA). These open archives may be the ultimate solution to the problem of republishing copyrighted material. The current problem of open archives is that many scientist need to be convinced to archive new publications in an open archive (Suber, 2002).

▪ 6.7. NEMYS COMMUNITIES

NeMys communities can be defined as: a group of users of NeMys who are able to share data in a virtual secured environment. One advantage is that sharing copyrighted material (see above) can be seen as juridical safer (although still not allowed). These communities may act as a meeting point for community members through online discussion boards and messaging systems.

▪ 6.8. EXTENSIONS OF THE NEMYS TOOLBOX

NeMys is not only a data presentation system. Much more it is a research tool through which data can be entered, edited and consulted in one overall online system and a data storage tool. Future developments of the system will focus on new on-line/off-line data-manipulation tools. Some of these tools were already developed and grouped in the 'NeMys toolkit' (see page 49).

- **6.8.1. Online statistical analysis tools**

Online statistical analysis of data in NeMys may be a valuable research tool. The freeware command-line based statistical package R (http://www.r-project.org/) offers possibilities to perform server-sided statistical analysis. The package is installed on a server, analysis requests are initiated from the website, results are depending on the amount of time an analysis takes sent to the browser or by email to the user.

- **6.8.2. Online phylogenetic analysis tools**

Phylogenetic analysis based on morphological data entered in the system would be an aid for many taxonomists. Morphological data could as such be used to facilitate identification keys, to create descriptions and to analyse relationships with sister taxa available in the tree. When describing new species, this tool would allow immediate analysis of the relation of the new species with others already described and available in the database. How this could technologically be achieved has not been studied yet.

- **6.8.3. Educational tools**

Since 2005 NeMys is used for **educational purposes** (for example: Nematology Course Ghent University, Second Year Bachelor Biology, Ghent University – course Biodiversity of Invertebrates). It is currently mainly used as a documentation tool and allows the student to explore the available identification system. In the near future a new educational module will be added. The possibility will be included to load slideshows used in courses or presented on conferences of meetings. A link to taxon names in these slide shows, will be created automatically. An opposite link will also be available, meaning that slides from slideshows will appear at the particular taxon page. This functionality would help students to get background information on taxa mentioned in a course. Technologically the software developed in the Ghent University 'C+ project' will be used (E-learning project developed by the 'Laboratory of Aquaculture' Ghent University, on http://zephyr.ugent.be). This Javascript based software creates thumbnails of all slides and extracts keywords and contents from them. All this information is stored in a xml-file. This xml-file, is together with the

original Powerpoint file and the thumbnails loaded to the web application, where necessary information is extracted and stored in the database.

- **6.8.4. Test environment**

A **NeMys-test environment** will be a useful tool as well. This would allow users to setup test dataset in which all possible features of the application can be tried. These test databases should not publicly be available, but may in a later phase, when setting up a real new dataset, be imported in the public section of the system.

▪ 6.9. PARALLEL CLASSIFICATIONS

A problem not yet tackled in NeMys is: how to manage different classifications. At this moment it is only possible to present one classification, with named nodes. Phylogenetic research however shows that for many taxa also alternative classifications can be found. Different authors in the field of classical taxonomy may also suggest a different classification for certain taxa. As long as a classification of a particular taxon is not agreed, different views on the classification exist and should be stored in the system (Raguenaud *et al.*, 2000). A problem with phylogenetic classifications is that not all nodes are necessarily named. The currently used classification data structure is not able to handle these tree-like structures. As phylogeny becomes more and more important for taxonomic research the possibility of adding phylogenetic data to the system may be of critical future importance. Treebase (http://www.treebase.org) offers already a platform linking published phylogenetic analysis (Piel *et al.*, 2000). In a first step direct linking to 'Treebase' may be an option to check for phylogenetic analysis on a specific taxon. In a second stage immediate visualization of phylogenetic relationships next to the classical systematic overview shall be developed. From a technical point of view storing the trees may be a problem. TreeBase solved the unnamed nodes issue by automatically adding names to the unnamed nodes. Phylogenetic trees mostly are stored as strings of the form 'a,(b,(d,c))'. The solution of TreeBase would allow these trees to fit in the hierarchical structure as used now.

6.10. LINKING TAXA

In NeMys there is no direct way of linking taxa to each other across different datasets. Indirectly, taxa are linked when they are described from the same data source, although this link does not say in what way and if taxa have a true biological meaningful link. Linking taxa could be interesting when defining biological relations between taxa. Simple examples could be: (1) 'taxon A' eats 'taxon B', (2) 'taxon C' is found together with 'Taxon D', (3) 'Taxon E' is a parasite of 'Taxon F'. Adding this option will enable users to create biological relationship schemes throughout the different datasets.

6.11. TOWARDS A DISTRIBUTED NEMYS ARCHITECTURE

The most promising future development may be the setup of a distributed NeMys architecture. Nowadays the whole system is hosted on one server in one location. For the current running datasets, this ‘shared hosting’ is the most efficient solution. New users may have good arguments to host their dataset on their own server (for example: data policy of institutes). A problem rising with a distributed architecture is augmented maintenance of the database and the web-structure. An outline of a possible scenario to construct a distributed NeMys application is given below. A distributed system may have a series of implications concerning maintenance costs, scalability, man power …, which are not well studied and consequently not documented yet.

The current existing structure should not really change. The ‘portal pages’ and ‘dataset pages’ can remain unchanged. However two types of datasets will be possible: (1) central datasets hosted at the main (current) NeMys server, (2) distributed datasets hosted at other servers. In order to keep the portal page updated a scheduled update of a central taxon list and reference list is favourable.

More technical problems will popup in designing an install package of a distributed dataset. Two possibilities can be explored: (1) a full all-in installation at the client-server (including all tools), (2) a ‘lite’ installation (all special tools – such as mapping tools - are used from a central NeMys toolkit).

This second 'lite' installation is currently favourable. Licences for the current used components (see appendix 2) would not be bought. Maintenance of the user interfaces at each distributed site would be much easier. However, if open-source technologies for mapping (see 6.3) and image manipulation would be considered, the problem of additional licences would disappear.

The user-interface is currently programmed in ASP. Although this is a MS Windows© oriented scripting language, the basic parts of the interface also run well on Sun Java System Active Server Pages 4.0, (see http://www.sun.com/software/chilisoft/), which is usable on other platforms than MS Windows©.

Before setting up a distributed system, the database would need some revision, and the current interfaces have to be checked thoroughly.

Currently the data-layer is hosted on a MS SQL Server. The format of the database is independent of the interface layer. It should thus be relatively easy to run NeMys with other database formats such as Oracle (http://www.oracle.com), MS Access, or MySQL (http://www.mysql.com).

A further development would even be a **desktop version** of the application. This would not necessarily cause a lot of technical problems! Making use of a package enabling running ASP - pages without having a server installed would facilitate this process. Packages as ALP (http://www.activelocalpages.com) offer this possibility.

▪ 6.12. NEMYS VERSUS OTHER BIOLOGICAL INFORMATION SYSTEMS

The introduction of this chapter provides a brief overview of some key players in the field of biodiversity information tools. A good understanding of NeMys requires a critical evaluation of this tool in comparison with other available systems. Comparing NeMys with the other available packages is not an easy task due to large differences in documentation of the different systems. Most system do provide a clear overview of their basic functionality and tools. However technical details are in many cases not discussed.

NeMys differs from most other systems on its philosophy of documentation. This work tries together with earlier produced documents (for example Deprez *et al.* 2004) to be open on its architecture, functionality and technical implementations. Many well established systems (Linnaeus©, Taxis© or Specify) do not provide many information on the functionality of the back layer. Delta forms an exception on this. Their used data formats and even basic functionality is extensively documented on their website (Dalwitz, 1980; Dalwitz, 1993 onwards; Dalwitz *et al.*, 1993 onwards).

	DATA Layer								Technology				INTERFACE Layer			
	Classification	Synonymy	Literature	Collection data	Geographic data	Morphological data	Multimedia data	Ecological data	Backup	Webbased	Platform	Multi-user	Mapping Tool	Identification Key	Collection management	Library management
Biolica	+	+	+	+	–	+	–		–		W				+	+
Delta	-	-	-	-		I		I;-		I	V	-	-	I	-	-
Linnaeus	+	+	+	+/-	–	+	–	+/-	–	+/-	V	-	+	+	-	+
Intkey	-	-	-	-	-	I		-		-	V	-	-	I	-	-
NeMys	+	+	+	+	–	+	–	+	-	+	W/V	+	+	+	+	+
Specify	I	-	I	I		-		-		-	W	I	-	-	I	-
Taxis	+	+	+	+	–	+	–	+/-	–	-	W	-	+	+	+	+
EI	+		+		-/	+		+/	–	+/	W			+		+

Table 4. Comparision of characteristics of software tools

- **6.12.1. Taxonomic and classification data**

Classification data can in most existing systems be stored. Lucid and Delta, both having identification keys as prior interest, do not pay much attention to this part of the data. NeMys, Taxis, Biotica, and Linnaeus are able to store documented taxonomic classifications. All portals, taxonomic databases and nomenclator databases (see page 3) are also able to save this data. The techniques used for saving classifications however differ. Most taxonomic databases (ERMS, ITIS) store their classification hierarchies similarly to NeMys (see page 24) with a self-referring table. This technique has no limitations concerning the number of classification levels involved. Although this technique is well documented and relatively easy to implement, some databases (mainly nomenclator databases) still use a flat table (with duplication data and limited number of taxonomic levels) (for example Species2000 and Index Kewensis). A drawback of storing hierarchies with self-referring systems is that listing the hierarchy of a particular species requires different database connections. Preventing this is achieved by using a calculated intermediate table or string, enumerating all parent levels of a taxon. ITIS has developed a compromise between a flat table and a self-referring hierarchy by storing genus and species data in a flat table. As such the binominal strings can easily be retrieved with only one data connection.

- **6.12.2. Literature**

All listed software tools (Linnaeus, Taxis, …) can save literature data. However, for all of them, except for NeMys, links between literature and data can only be made on the level of taxonomy (for example species bibliographies). NeMys goes one step further by requiring a link between the literature and kind of data entered. Linnaeus© is currently mostly used for creating monographs and keys on particular taxa. Although literature used for these monographs is shown, a link between each bit of data in these monographs and the literature sources is not required. All species databases and taxonomic databases do have bibliographic data on taxa.

The currently available biodiversity data portals do not focus on bibliographic data although this may be very valuable. The newly developed standards on data exchange by TDWG may encounter this problem.

- **6.12.3. Morphology and Identification keys**

Morphological data seems to be, next to distribution data, a key component in all software tools. Morphological data and identification keys mostly are strongly related. All tools make use of the concept of storing morphological data through characters and character states. By flagging the matching character states for each taxon in a key, morphological data is entered. Most tools do not store morphological data in a relational structure (through list) but use a matrix (flat table). This matrix facilitates the functioning of the identification key. NeMys stores the data in a relational structure, and uses pre-calculated values to make the key function. Most identification keys are polytomic (no fixed pathways) and illustrated. Lucid© also provides software tools for generation of dichotomic digital keys. Most keys are desktop based, although some (Linnaeus© and Delta) offer extra software to publish keys on the web.

NeMys differs on some points from other systems using morphology: data is stored in a relational structure, morphological data is linked with the datasource, the key is embedded in a much broader information system, and the whole identification key is web based. NeMys is currently the only system which offers a fully online identification system: development, management and consultation of keys is done online.

- **6.12.4. Geographic data and visualization tools**

Most software tools except Delta and Lucid (both designed as identification tools) offer possibilities to store and/or visualize geographic data. The number of properties for visualization differs a lot for each tool. Linnaeus© does not work with exact geo-referenced point locations but uses grids. Taxis offers a tool very similar to Esri Arcview©. NeMys is due to the web-based architecture more limited in extra properties. However, recent technologies raised the functionality of online mapping tools a lot.

- **6.12.6. Layout**

Much effort when developing tools goes to the front-layer, the interface. Many of the currently available tools are desktop based, while NeMys is web-based. Developing a web-based tool implies a number of limitations. The browser software, the bandwidth and security issues have to be taken into account when developing for a web-based environment. However, recent developments in web technologies allow the development of clear, professional looking systems. Comparing the interfaces of all available packages at a regular basis during the last years shows that currently the front-layer is at least as important as the data back-layer whereas earlier the data back-layer was much more importance. The attractiveness of the layout of a tool is in many cases more important than the data available, in order to attract new users.

- **6.12.7. Platforms and technologies**

Biological information systems have been developed for all platforms. Currently a few are purely MS Windows© based (Specify, Biotica, Taxis, and 3I) while all others are available for multiple platforms.

Web-based systems as NeMys have the advantage that the user-interface is not linked with a particular platform. Any web browser can access them. However, comparing all available web-based databases (species databases, taxonomic databases and portals) learns that most are built using open source software tools. A drawback of NeMys is that all interfaces and databases use MS Windows© based technologies (ASP, SQL Server) and thus require licenses for this software. Also a number of paying tools (gis tools, image manipulation tools) are used to offer extra functionalities. Although this does not have any implication for the users of the system, the eventual setup of a distributed NeMys database may require a revision of this philosophy.

For many systems (such as Linnaeus©, Lucid and Taxis) the database structure is not publicly documented. Although a relational database for storage of complex datasets may be considered as the best option, still some tools use a text based, non-relational data layer. An example of this are the basic Delta tools (for example

Intkey) although also relational structures exporting to the Delta-format were developed.

- **6.12.8. Target users**

The target users of a software package determine many characteristics of the package. Linnaeus© is developed as a tool for researchers although some products produced with it attract a broad audience. Tools designed for a broad audience have many more features than tools developed for specialists. Biotica and Specify were designed primarily as collection management packages, while Lucid, 3I, and Delta focus on morphological descriptions and identification keys. NeMys is designed for scientific research purposes, although due to some datasets (Euroherp & Eurocox) it does also attract a broader audience.

NeMys, Linnaeus© and Taxis are three packages developed with a similar scope, but still differ on many aspects. The web-based architecture, the used data-concept (link between data and source), and research tool design (datasets are never finished but constantly evolving) are the three distinguishing characteristics on which NeMys differs from Linnaeus© and Taxis.

▪ 6.13. NEMYS AS A RESEARCH TOOL … DOES IS WORK?

At the beginning of this chapter, it was mentioned NeMys was developed as a research tool for this PhD project. The next chapters will show how NeMys was used for a study on taxonomical, morphological and biogeographical data of Mysida.

Taxonomical research gains a lot of efficiency when storing the data in a proper way. Beside the scientific results that can be obtained, a digital online archive is created for future research. Although a number of tools in the system do facilitate biological research, this archiving function may be the most important reason for promoting the use of Biological Information Systems as research tools (Gewin, 2002).

A digital archiving platform for taxonomic and more general biological research data, gives a ‘second life’ to the work many taxonomists. As shown, a biological information system can be used by a wide range of users and as a consequence improve the consideration for the work of taxonomists (Godfray, 2002).

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8. Appendices

APPENDIX 1: NEMYS DIGIR METADATA SCHEME


```
<?xml version="1.0" encoding="utf-8" ?>
- <response xmlns="http://digir.net/schema/protocol/2003/1.0">
- <header>
<version>$Revision: 1.14 $</version>
<sendTime>2006-03-28T19:39:34+0200</sendTime>
<source>http://intramar.ugent.be:80/digir/DiGIR.php</source>
<destination>81.242.207.147</destination>
<type>metadata</type>
</header>
- <content>
- <metadata>
- <provider>
<name>intramar Provider</name>
<accessPoint>http://intramar.ugent.be:80/digir/DiGIR.php</accessPoint>
<implementation>$Revision: 1.14 $</implementation>
- <host>
<name>intramar Provider</name>
<code>Marbiol Ugent</code>
<relatedInformation>http://intramar:8080</relatedInformation>
- <contact type="administrative">
<name>Deprez Tim</name>
<title>Drs.</title>
<emailAddress>tim.deprez@ugent.be</emailAddress>
<phone>+32 9 264 85 27</phone>
</contact>
- <contact type="technical">
<name>Tim Deprez</name>
<title>Drs.</title>
<emailAddress>tim.deprez@ugent.be</emailAddress>
<phone>+32 9 264 85 27</phone>
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</host>
- <resource>
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<code>nemys</code>
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- <contact type="administrative">
<name>Tim Deprez</name>
<title>Manager VMDC</title>
<emailAddress>tim.deprez@ugent.be</emailAddress>
<phone>+32 9 2648527</phone>
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- <contact type="technical">
<name>Tim Deprez</name>
<title>Manager VMDC</title>
```

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</contact>
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<conceptualSchema schemaLocation="**http://digir.sourceforge.net/schema/conceptual/darwin/2003/1.0/darwin2.xsd**">**http://digir.net/schema/conceptual/darwin/2003/1.0**</conceptualSchema>
<recordIdentifier>**NeMys**</recordIdentifier>
<recordBasis>**observation**</recordBasis>
<numberOfRecords>**14728**</numberOfRecords>
<dateLastUpdated>**2004-06-29 12:00:00**</dateLastUpdated>
<minQueryTermLength>**0**</minQueryTermLength>
<maxSearchResponseRecords>**1000**</maxSearchResponseRecords>
<maxInventoryResponseRecords>**10000**</maxInventoryResponseRecords>
</resource>
</provider>
</metadata>
</content>
- <diagnostics>
<diagnostic code="**STATUS_INTERVAL**" severity="**info**">**600**</diagnostic>
<diagnostic code="**STATUS_DATA**" severity="**info**">**3,0,0**</diagnostic>
</diagnostics>
</response>

▪ APPENDIX 2: OVERVIEW OF TECHNICAL DETAILS

The database of the system is running on a database server running separately from the webserver hosting the user-interface. The server is MS SQL Server (version 2000), running on a MS Windows © 2003 server. Database maintenance is done through the MS SQL server Management console.

The webserver used is IIS (Internet Information Service) and runs on MS Windows © 2003 server.

The interfaces for adding and managing the data are programmed in ASP (Active Server Pages). A few additional commercial components were installed in order to achieve programmatically complex functionality:

1. Image manipulation: AspJpeg (http://www.aspjpeg.com) is used for on the fly resizing and manipulation of images. This component was developed by Persits Software, Inc., 90 Broad St., Suite 1703; New York, NY 10004

2. Pdf creation: AspPDF (http://www.asppdf.com) enables the dynamic creation of pdf-files. This software was also developed by 'Persits Software'.

3. Gis Mapping: Aspmap (http://www.vdstech.com/aspmap.htm) is a package allowing the dynamic creation of interactive maps based on different layer types. This package was developed by 'VDS technologies', 1050 S. State St. Dover, DE 19901 USA.

Indexing of the pdf-documents was achieved through the MS Windows © Indexing Server. Indexes on separate datasets are interrogated similarly to databases.

Backups of both the database and linked files are made automatically each two days. Backups are stored on another computer on the Network. Weekly a backup is copied to a central backup space hosted at the IT section of Ghent University.

Tracking the user activity on the NeMys website is done through the package WhosOn (version 4) (http://www.whoson.com). This package allows real-time monitoring of the use of the website. A vast number of reports can be created with it.

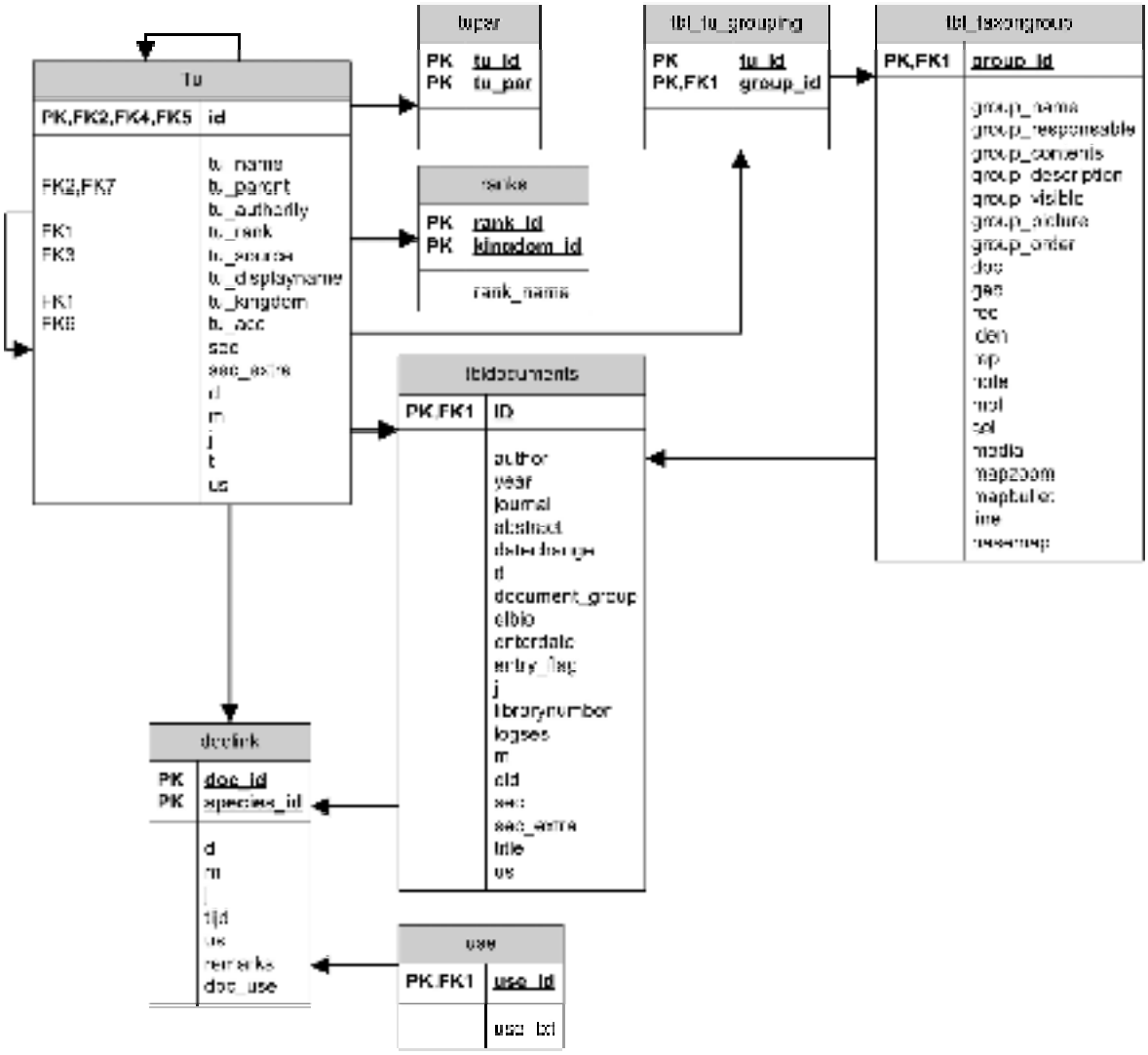
Data user-activity is stored in an SQL server database, and is as such easily consultable without the package.

The webserver hosting the website also has PHP installed. On this server a digir provider is installed. The provider is accessible through: http://intramar.ugent.be/digir/. Data extracted from the Nematoda and the Mysida dataset is accessible. Data is formatted according to the OBIS scheme (http://www.iobis.org/obis/obis.xsd) which is based upon the Darwin Core (http://digir.net/schema/conceptual/darwin/2003/1.0).

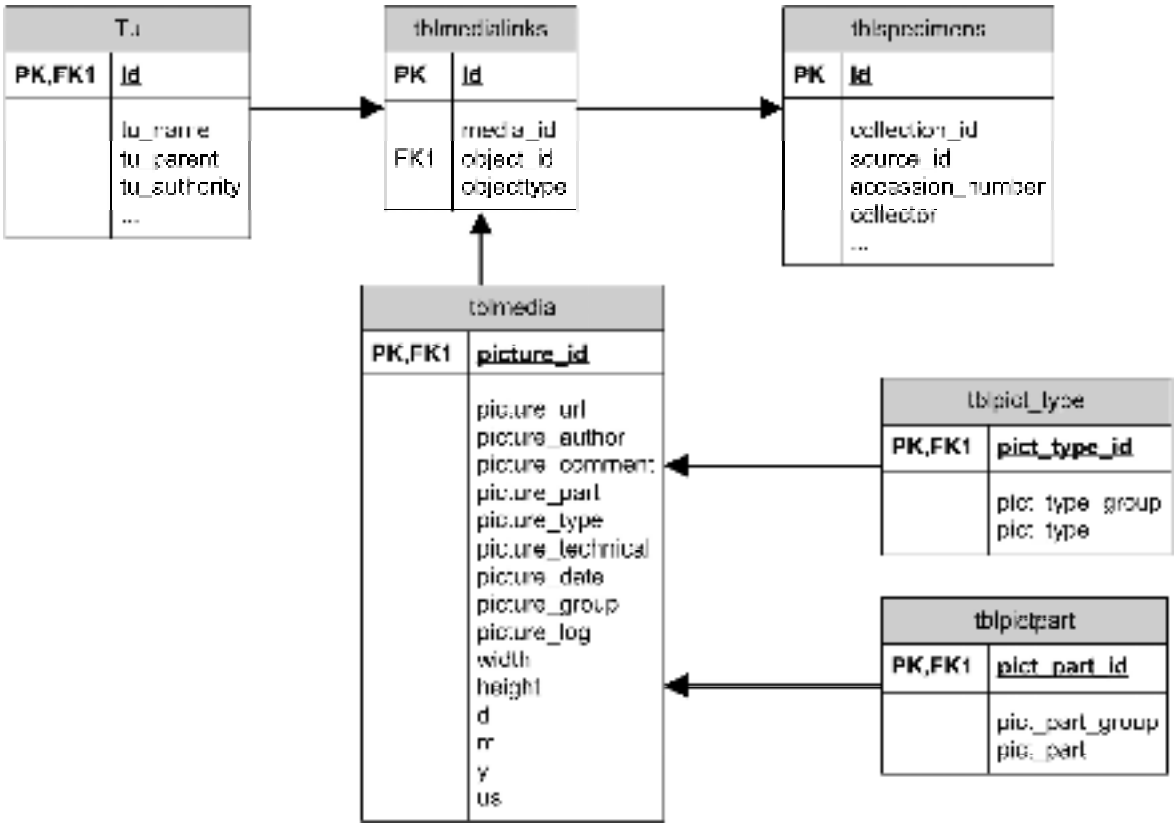
▪ APPENDIX 3: NEMYS DATABASE RELATIONAL SCHEMES

The structure of the database behind NeMys is illustrated through a number of relational schemes, each showing all tables related with the data units and metadata units as described on page 14.

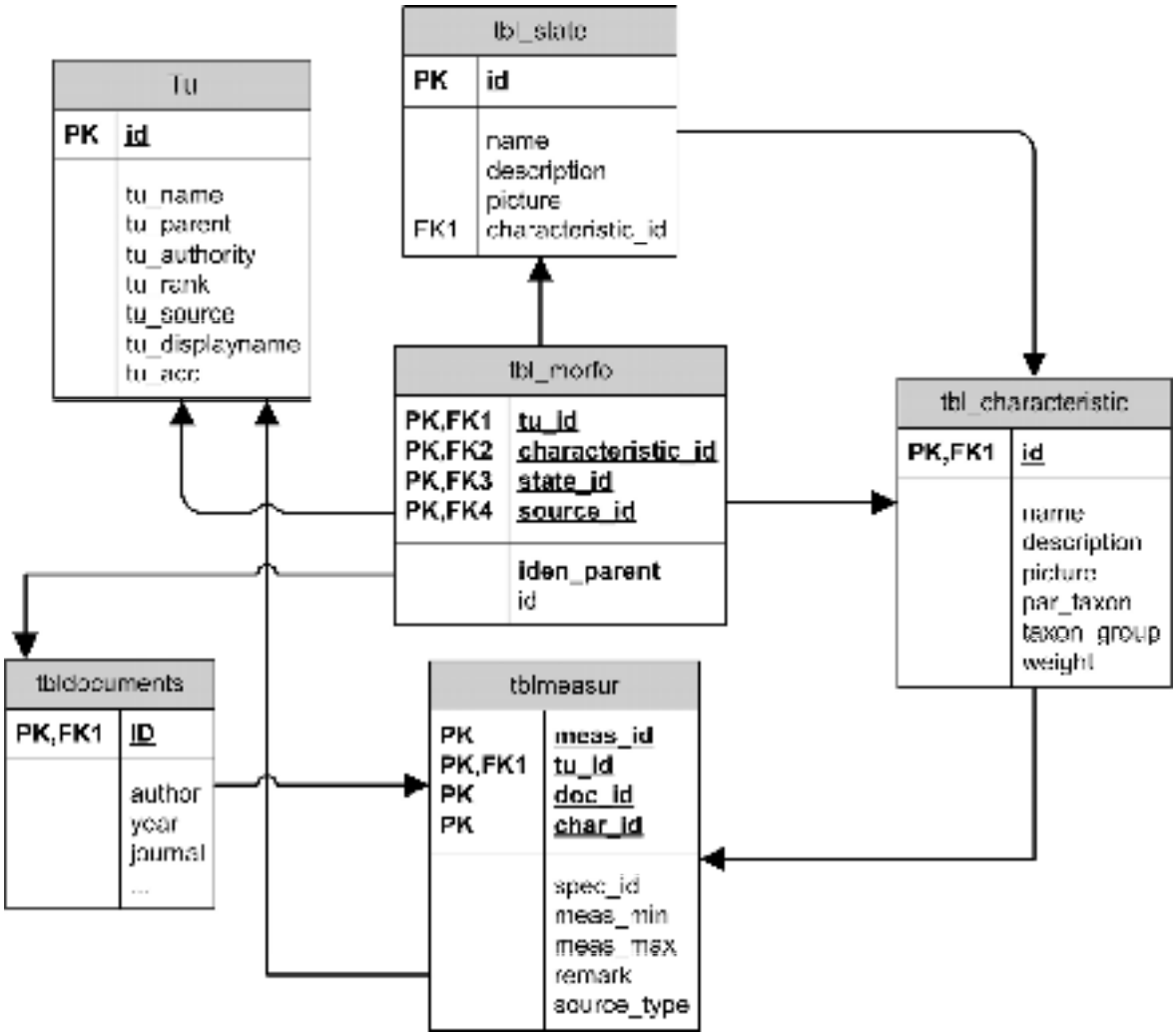
- **Scheme 1: Systematics & Literature**



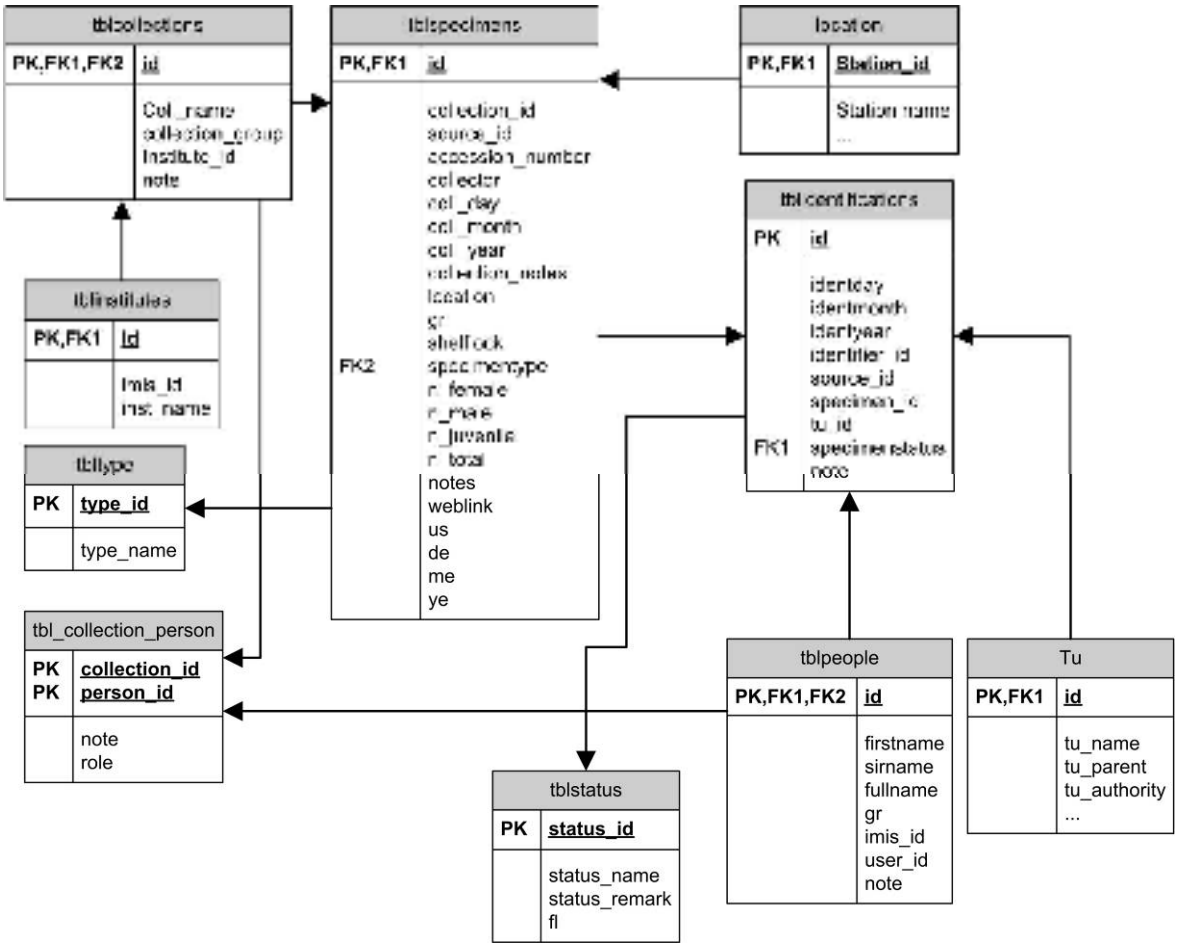
- **Scheme 2: Media**



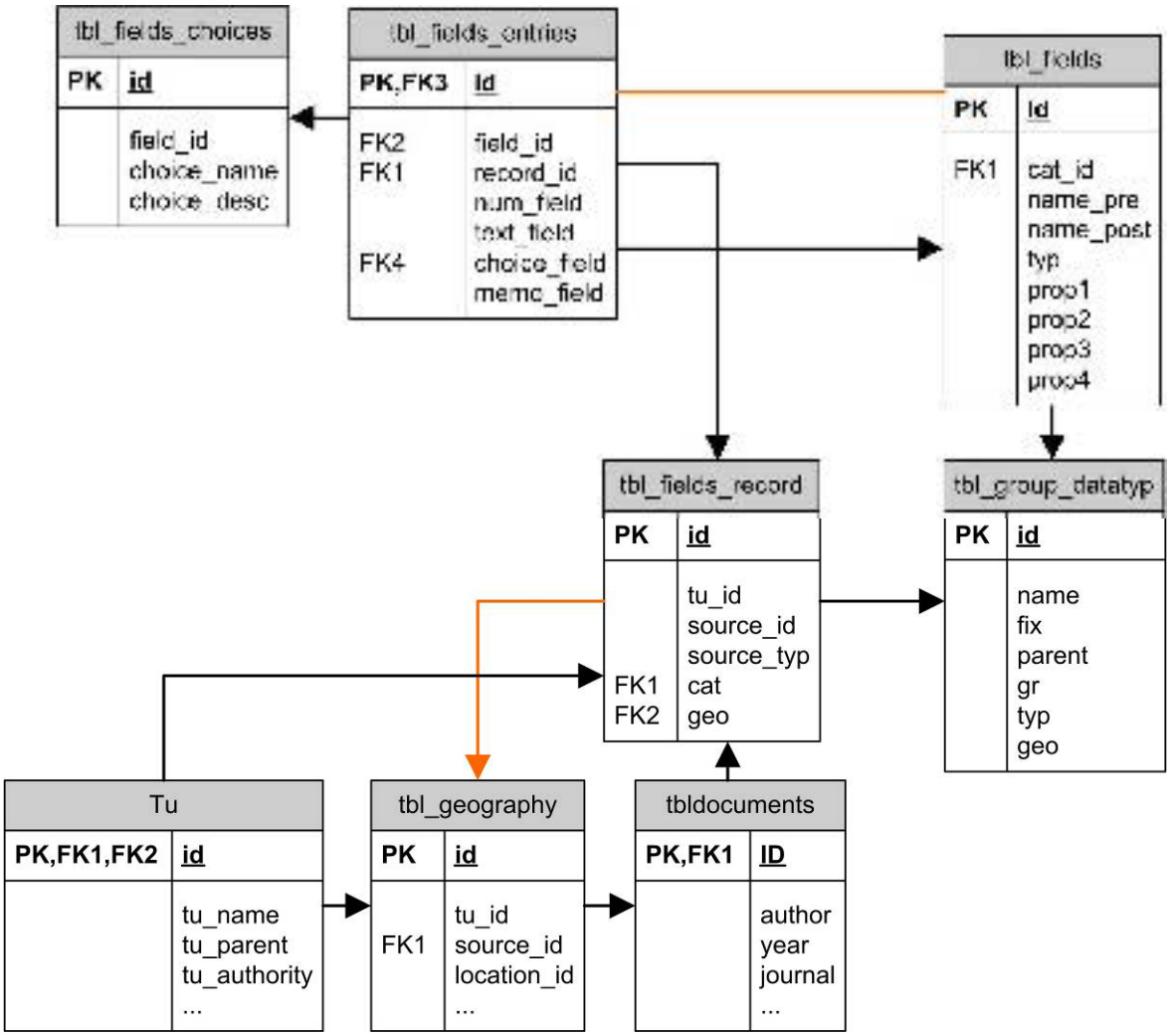
- **Scheme 3: Morphology**



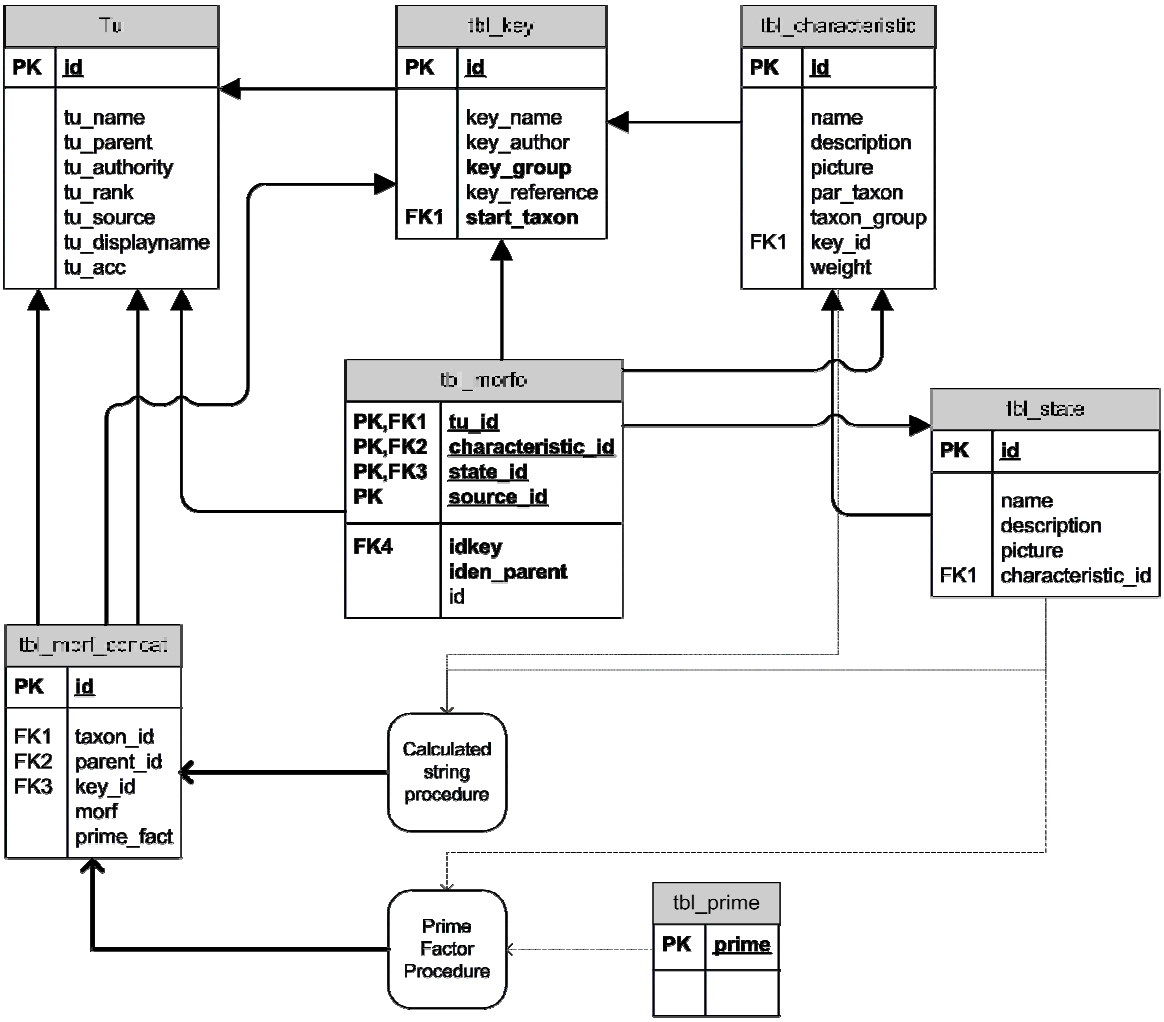
- **Scheme 4: Collections**



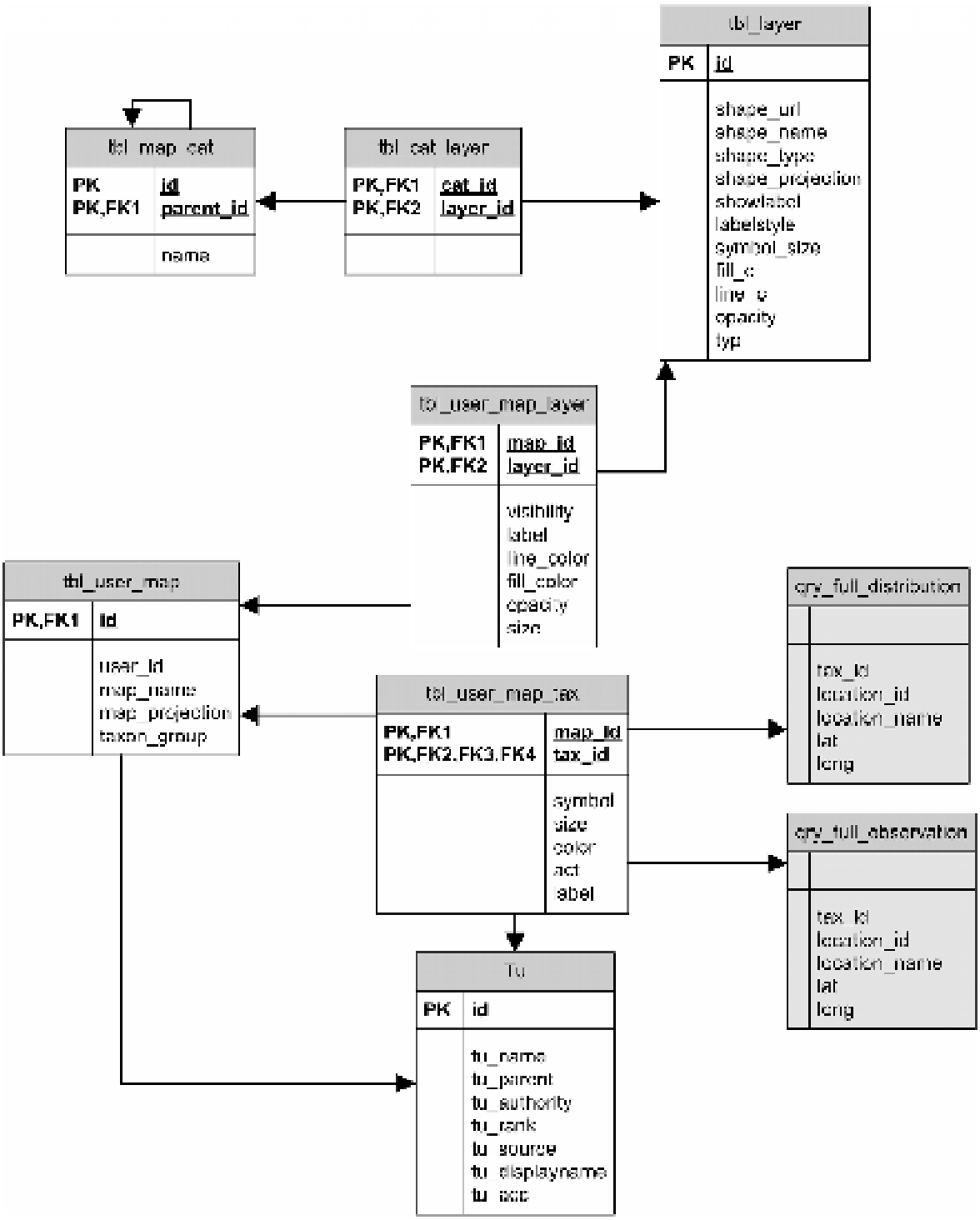
- **Scheme 5: Generic data**



- **Scheme 6: Identification keys**



- **Scheme 7: Mapping tools**



- **APPENDIX 4: EXAMPLE OF KML FILE – EXPORT TO GOOGLE EARTH**

```
<Placemark>
 <name>Westerschelde</name>
 <description><![CDATA[Westerschelde – Mesopodopsis slabberi]]></description>
 <LookAt>
  <longitude>3,55</longitude>
  <latitude>51,36</latitude>
  <range>300</range>
  <tilt>30</tilt>
  <heading>50</heading>
 </LookAt>
 <Style>
  <IconStyle>
   <Icon>
    <href>Icon</href>
    <x>224</x>
    <y>64</y>
    <w>16</w>
    <h>16</h>
   </Icon>
  </IconStyle>
 </Style>
 <Point>
  <extrude>1</extrude>
  <altitudeMode>relativeToGround</altitudeMode>
  <coordinates>Coordinates x,y</coordinates>
 </Point>
</Placemark>
```

[i] IIS stands for Internet Information Services. This software is the web-server package running on the Windows platform. It allows to make website available to the internet.

[ii] 'one-to-many' relationship: In a one-to-many relationship, a record in Table A can have many matching records in Table B, but a record in Table B has only onematching record in Table A.

[iii] 'many-to-many' relationship: In a many-to-many relationship, a record in Table A can have many matching records in Table B, and a record in Table B can have many matching records in Table A. This type of relationship is only possibleby defining a third table (called a junction table) whose primary key consists of two fields: the primary keys from both Tables A and B. A many-to-many relationship is really 2 one-to-many relationships with a third table

[iv] JPEG stands for 'Joint Photographic Experts Group' and is the most commonly used standard method of lossy compression for photographic images. The file format which employs this compression is commonly also called JPEG.

GIF stands for 'Graphics Interchange Format' and is of widespread usage in mainly webpages. A GIF file employs lossless data compression so that the file size of an image may be reduced without degrading the visual quality, provided the image fits into 256 colours.

TIFF stands for 'Tagged Image File Format'. It is a file format for mainly storing images, including photographs and line art.

[v] WMV is a generic name for the set of proprietary streaming video technologies developed by Microsoft. It is part of the Windows Media framework. WMV files are played by players such as MPlayer or Windows Media Player.

The 'Moving Picture Experts Group' or MPEG is a working group of ISO/IEC charged with the development of video and audio encoding standards. MPEG (pronounced EM-peg) has standardized the following compression formats and ancillary standards: MPEG (1,2, …) , MP3.

[vi] FASTA is a file format used to exchange information between genetic sequence databases. It is also the name of a DNA and Protein sequence alignment software package first described (as FASTP) by David J. Lipman and William R. Pearson in 1985. It is software running on each platform which is freely available for academic purposes. The format used for FASTA software is in genbank called FASTA.

[vii] Hierarchical structures are of the form: A belongs to B, B belongs to C, C belongs to D, … Consequently D is a direct parent of C and an indirect parent of B and A. A biological example can be: 'slabberi' belongs to 'Mesopodopsis', 'Mesopodopsis' belongs to 'Mysini', …

[viii] A thumbnail is a resized version of the original image. A thumbnail is much smaller in file-size and as such the web page loads much faster. Thumbnails in NeMys are generated on the fly though a server side image manipulation component.

A watermark on an image allows to put information in the picture itself. Mostly a watermark is an image or a piece of text overlayed with the original picture. Watermarks are mostly used to prevent misusage of images.

[ix] SVG: Scalable Vector Graphics. This is an XML-based protocol allowing the display of vector-based images. To be able to view SVG-graphics a (freely available) viewer must be installed. More information can be found at http://www.w3.org/Graphics/SVG/

[x] WYSIWYG is an acronym for 'What You See Is What You Get'. It is used in computing to describe a system in which content during editing appears very similar to the final product. It is a technology mainly developed for use in web-based environments allowing entering data to web-based systems without having to know 'html' (hyper text markup language), the common standard used to transport information over the internet.

[xi] Javscript is a client-side (program code is executed by the web-browser) scripting language. It is mainly used to add some interactivity to websites. These are mostly graphical and layout-related actions. Nevertheless also more advanced tasks can be done through javascript program: for example error checking on data input.

[xii] Server-side: is the opposite of client-side and means program code is ran on the web-server and pure html is sent to the browser of the user.

[xiii] XML stands for 'Extensible Markup Language' and is a W3C-recommended standard. (World Wide Web Consortium). XML provides a text-based language to describe and apply a tree-based structure to information. Each piece of data in an XML file is surrounded by tags describing the data type. Data can be structured hierarchically by putting tags in between other tags.

[xiv] PHP is a scripted programming language that can be used to create websites. It stands for 'PHP: Hypertext Preprocessor'. Similar to ASP, PHP runs on a web server and all code is ran on the server. The output is sent to the client browser.

[xv] GIS: A 'geographic information system' is a system for creating and managing spatial data and associated attributes. In the strictest sense, it is a computer system capable of integrating, storing, editing, analyzing, and displaying geographically-referenced information.

CHAPTER 2 - NEMYSKEY: A CONCEPT FOR DOCUMENTED, POLYTOMOUS DIGITAL IDENTIFICATION KEYS

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1. Abstract

Identifying organisms remains an intriguing question for anyone interested in the natural environment. NeMysKey is an open system, based on a comprehensive digital catalogue of taxa (NeMys), which may facilitate the identification process. A polytomous online system with a link to taxonomic literature, illustrated with pictures and linked to explaining glossaries encourages users to identify specimens in a genuine scientific way.

Keys of the format can, according to new insights, easily be updated online and thus are up to date at any time. NeMysKey is a platform encouraging collaboration between scientists: different keys can be made by different authors and can be fluently linked with each other. As the taxonomic basic work is connected to each taxon, the often underestimated work of taxonomists becomes visible for a much broader user community.

The two presented methods ('calculated strings' and 'prime number paradigm') may help the construction of other online similar identification keys. The more similar online keys become in construction, the easier they will link up with each other.

NeMys (http://www.nemys.ugent.be) and NeMysKey (http://www.nemys.ugent.be/nemyskey/) offer a scientific working tool combining identification tools, taxonomic documentation tools and mapping tools.

2. Introduction

Biological identification is an applied field of systematics dealing with the theory and practice of the diagnostic key construction. As new developments are arising from the Global Biodiversity Information Facility (http://www.gbif.org), Species 2000 (http://www.species2000.org) and other initiatives for creating on-line taxonomic databases, computer-based identification keys will have several, increasingly important roles to play. Although the purpose for assigning a name to a specimen may be very diverse, the naming itself remains for many taxa a challenging task. The three main reasons for this are: (1) the lack of keys for many groups, (2) the highly specialized nature of many keys and (3) the absence of traceable additional data (original description, pictures). For many potential users of taxonomic information - such as ecologists, conservation managers, students, and others - computer-based identification keys are likely to be the only effective portals by which they will be able to access the wealth of taxonomic data that is rapidly becoming available on the Internet.

Since the 1980's many desktop identification tools have been created. Most of these are based on matrices: Lucid – http://www.lucidcentral.org, Delta – http://delta-intkey.com (Dalwitz,1974; Dalwitz,1993), Linnaeus II © – http://www.eti.uva.nl (Schalk, 2005). The introduction of more accessible web-technologies facilitated the translation of these keys into web-based versions (for example: some keys are available in the ETI World Biodiversity Database http://ip30.eti.uva.nl/bis/index.php).

Although many of these systems are well established and frequently used, few of them offer the possibility to link to the original description of a species or provide possibilities for easy updating with new taxonomical findings.

The online biological information system NeMys (Deprez *et al*. 2004; 2005) offers a platform (NeMysKey - http://www.nemys.ugent.be/nemyskey) to make online polytomous identification keys that are simple in use and have the possibility to link to authentic and additional scientific species information.

3. Concept

The generic biological information system NeMys (Deprez *et al*. 2004) offers the possibility to store any kind of biological data on species or higher taxa digitally and in a web-based environment (see chapter 1). As an integrated component of it, a web-based, polytomous identification system is presented in this paper (NeMysKey). A multi-states key has the advantage that at any time in the identification process an overview of all possible characters and character-states is available. The presented key can easily be updated when new information becomes available. No character weighting is included in the key yet. By default characters are listed alphabetically, thought an arbitrary ordering of characters is possible.

Multi-entrance polytomous keys, with an unlimited number of characters, character states, and taxa are developed. The polytomous design offers users to start the identification process with those characters that are easily detected. Based upon the choices that have been made, the set of characters is narrowed down to those being relevant for further elimination of the remaining taxa. A limited error-tolerance is included, as taxa without data for certain characteristics are not eliminated from the remaining list of taxa.

All characters and their related states can be precisely defined with a text-based definition and/or are illustrated with pictures. In addition, terms in definitions can be linked interactively to a comprehensive glossary.

All taxa in the keys are linked with the taxon information page in the NeMys database. These pages display a digital archive of pictures, notes, literature, …

4. Methodology

4.1. STORING MORPHOLOGICAL DATA

All data in NeMys are stored into a relational database. Morphological characters with their according states are linked to a particular dataset and to a particular identification key. Meaningful characters can be shared between keys of one dataset. All characters are stored in a 'character' table, each accompanied with a parameter indicating the dataset and the key in which they are used. Character states are stored in a 'state' table, each linked to a character.

Morphological data is entered through an online data entry module. Before data can be added to the system, a published data source, from which the data are taken (*i.e.* a taxonomic description), has to be selected. Different sources can be selected if several are used during the construction of the key. Storing the data source together with the data facilitates to check the accuracy of the key.

Data is stored in a list, in which each row represents the link between a taxon, a data source, a morphological characteristic and its related state. The advantage of storing the data in a list, above storing it in a matrix, is that data can be added without limitation (an unlimited number of characters and states can be used for each key).

The data model used for storing morphological data, key data and metadata is shown in figure 1.

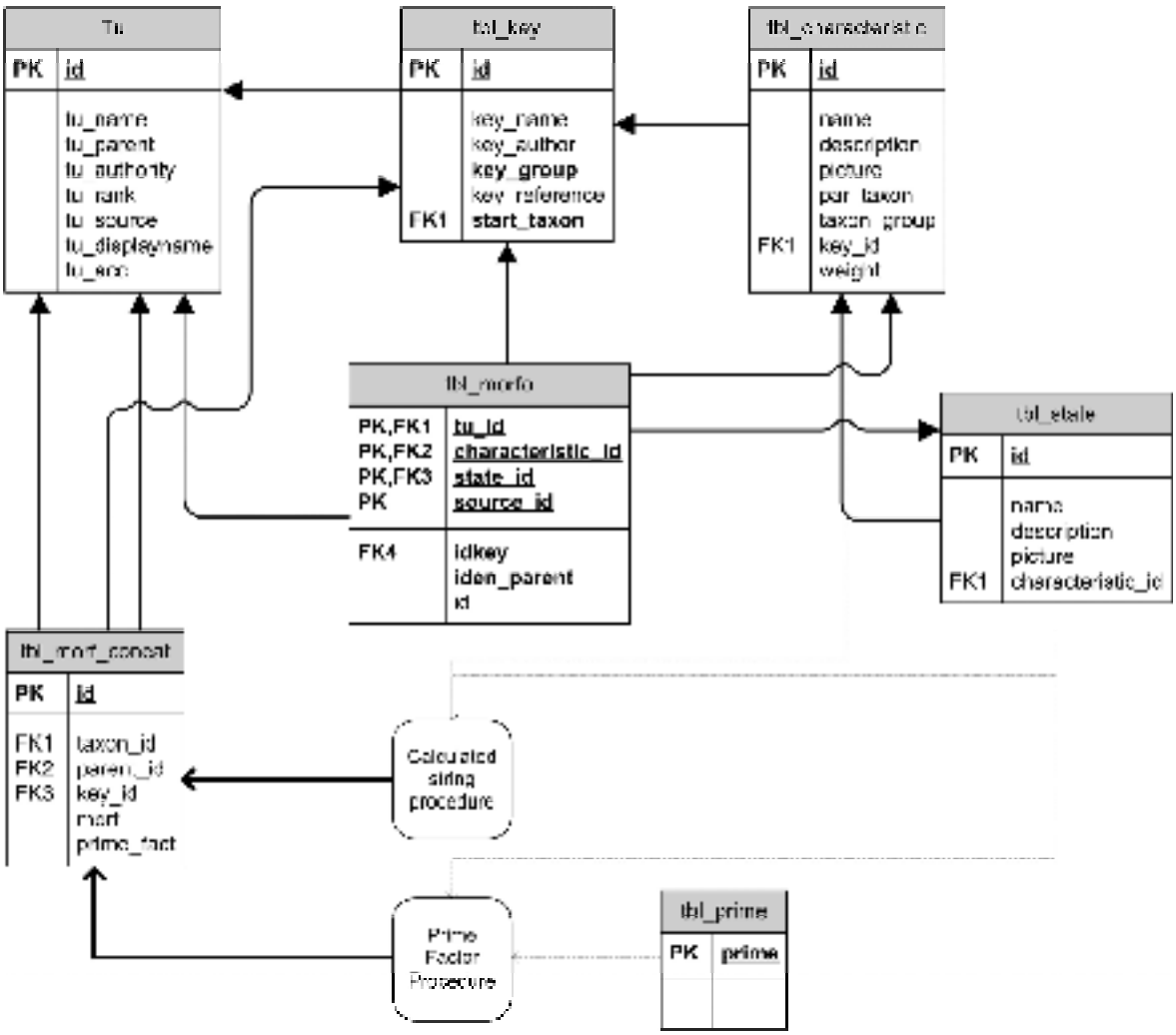

Figure 1. Identification key data model

▪ 4.2. DEFINING KEY MEMBERS

Although almost all data in NeMys is linked to a systematic backbone, the identification keys developed within NeMys do not necessarily reflect this classification. For many taxa, the accepted classification does not always concur with morphological similarities. These morphological characters are the most important data during the identification of a species or a taxon. Consequently the grouping of sister taxa (taxa belonging to a same parental group) is not always the best option in a key. As an example: Lorenzen (1981) assigned the Nematoda genus *Molgolaimus* to the family Desmodoridae. This genus has, like all Desmodoridae, reflexed ovaries. Nevertheless classifying it in the family Microlaimidae makes more sense for identification purpose. It shares all other morphological characters with this family except the ovaries and a conico-cylindrical tail (See 'Key to the free-living Nematoda', (Steyaert *et al*. 2005) in NeMysKey).

When building an identification key, it is not necessary to use the systematic levels as provided in the classification tree. With the NeMysKey-system, it is possible to group different taxa within 'pseudotaxa'. This may be especially useful to create groupings of look-alikes if this facilitates the identification process. For instance, it might be useful to group three genera into one 'pseudotaxon', and to create a separate key for all species of these three genera. A reason to do this may be the lack of clear morphological features allowing identification at genus level.

Each key is characterized by a starter or 'parent' taxon. This 'parent' taxon is a taxonomic unit that groups all members of a key. In this way a hierarchy is created that can be used to link separate keys to each other.

Table 1 gives an example of how keys can be linked. Key 'number 1' represents a key to the families of the order Mysida. Key 'number 2' will be linked to key 'number 1' through the family Gastrosaccinae. The Gastrosaccinae is selected as the 'parent taxon' for this second 'genus key'. This second key illustrates the concept of 'pseudo-taxa'. The marked 'Genus *Anchialina* + *Pseudanchialina*' is a pseudotaxon grouping two genera. Both are hard to distinguish after rapid investigation. The third key on with this pseudo-taxon as a 'parent' identifies species from the two genera.

Assigning taxa to keys is not an irreversible process. Taxa can easily be added, moved or removed.

Key number	Taxon	Parent taxon
1	Family Gastrosaccinae	Order Mysida
1	Family Siriellinae	Order Mysida
1	Family Mysinae	Order Mysida
1	Family Erythropinae	Order Mysida
2	Genus *Anchialina* + *Pseudanchialina*	Family Gastrosaccinae
2	Genus *Gastrosaccus*	Family Gastrosaccinae
2	Genus *Bowmaniella*	Family Gastrosaccinae
2	Genus *Iiella*	Family Gastrosaccinae
3	Species *Anchialina* 1	Genus *Anchialina* + *Pseudanchialina*
3	Species *Anchialina* 2	Genus *Anchialina* + *Pseudanchialina*
3	Species *Anchialina* 3	Genus *Anchialina* + *Pseudanchialina*
3	Species *Pseudanchialina* 1	Genus *Anchialina* + *Pseudanchialina*
3	Species *Pseudanchialina* 2	Genus *Anchialina* + *Pseudanchialina*

Table 1 Hierarchy in identification keys (part of tbl_morf_concat in figure 1)

▪ 4.3. CONCEPTS OF IDENTIFICATION (CALCULATED STRINGS – PRIMENUMBER PARADIGM)

A major issue in the development of an online identification key is 'speed'. A server-based solution has to be considered as the best option. It does not require high-performance computers from the client side. Reducing the number of needed data connections is of main importance for speeding database-driven web-applications. The most straightforward design for a web-based identification key would imply for each taken step (nested query) a cumulative number of table joins in the database connection. The higher the number of joins between tables, the slower the result is generated. The use of pre-calculated values that are stored with the key, makes it possible to keep the number of data connections (table joins) equal, irrespective of the number of taken steps.

Two methods using pre-calculated values are presented: a first one makes use of **'calculated strings'**, a second one uses '**prime numbers'**.

Table 2 shows an extract taken from 'tblmorfo' (see figure 1). This table stores the morphological data for each keys. Three hypothetical taxa (A,B and C) are represented with their according characters and character states (column 'charac' and 'state'). Each character and character state is allocated a unique number referring to the 'state' and 'character' tables ('tblstate' and 'tblcharacteristic' – see figure 1). The 'prime' column saves a unique prime number for each state. This prime number is used in the 'prime number paradigm method' (see further).

• 4.3.1. Calculated strings

The first technique uses 'calculated strings' to allow the online key to function properly. Calculating a string for each member of the key makes it possible to reduce the time needed to retrieve the result of a complex query (nested query). Although this method is a denormalization of a relational database, it is a simple method to reduce the number of table joins needed. The calculated string is created by concatenating all available characters with their states, separated by a delimiter (*e.g.* characters are preceded by '$', character states by 'µ').

Based upon the example shown in table 2 ‘taxon A’ is assigned the string $10µ5$11µ7$11µ9. No data is available for characteristic 12. This would mean that ‘taxon A’ is dropped out of the result if a state linked to characteristic 12 is selected. To bypass this, the value $12µ0 is added to the string to indicate the lack of data for this characteristic. The resulting string is saved in the table ‘morf_concat’. A snapshot from this table is shown in Table 2.

Each time morphological data for a key is added or removed; all calculated strings have to be recalculated.

Taxonname	charac	State	Prime number (PS)
Taxon A	10	5	2
Taxon A	11	7	3
Taxon A	11	9	5
Taxon B	10	6	7
Taxon B	11	7	3
Taxon B	12	18	11
Taxon C	10	5	2
Taxon C	10	8	13
Taxon C	11	9	5
Taxon C	12	19	17

Table 2 snapshot taken from tbl_morfo

Taxonname	Calculated String	Prime_factor PS-factor
Taxon A	$10µ5$11µ7$11µ9$12µ0	5610
Taxon B	$10µ6$11µ7$12µ18	231
Taxon C	$10µ5$10µ8$11µ9$12µ19	2210

Table 3. snapshot taken from morf_concat

During an identification, calculation of the result (defining which taxa are matching the selected variables) is relatively easy. For each taken step, the selected choices have to be remembered. This is achieved by a client-side cookie or a server-side session variable (http://www.w3schools.com/asp/asp_cookies.asp). The temporarily stored value is a concatenation of all character states chosen, separated by a delimiter. A practical example is shown in ‘box 1’. Based upon this value a query is formed retrieving the remaining taxa in each step:

“Select taxonname from concat_table where ([calculated string] like ‘%µstate1%’ or [calculated string] like ‘%$charac1µ0%’)”

With: ‘state1’ = character state chosen in the first step, ‘charac1’ = character chosen in the first step

For each additional step during identification, the following part is added to this query:

“and ([calculated string] like ‘%µstateX%’ or [calculated string] like ‘%$characXµ0%’)”

With: ‘stateX’ = character state chosen in step X, ‘characX’ = character chosen in step X.

A similar additive selection query is used to calculate the remaining choice options for each characteristic. If the remaining number of states in a characteristic is 1 or 0, it is left out of the possible choices. Only one connection (with the ‘concat_table’) is needed when retrieving the matching taxa.

The ‘calculated string’ method is a fast method for running online polytomous key. However it has some limitations. The calculated string may not exceed a certain number of characters. The calculated string must be stored in a text-field (‘like’ operator only functions well on text fields). For MS Access© the maximum length is 256 characters, for an MS SQL Server© database 4000 characters.

BOX 1: Example of identification procedure using the 'calculated string' method

1. start of the identification:
    a. three taxa are displayed (Taxon A, Taxon B and Taxon C)
    b. all characters with their states are shown
        i. Charac 10: state 5, state 6, state 8
        ii. Charac 11: state 7, state 9
        iii. Charac 12: state 18, state 19
2. 'character 12', 'state 18' is chosen in the first step
    a. A user-cookie 'ident_steps' is created: $12µ18
    b. The query giving the matching taxa is made: "Select taxonname from concat_table where ([calculated string] like '%µ18%' or [calculated string] like '%$12µ0%')"
3. Taxon B and Taxon A are displayed as matching taxa for the first step. Taxon A is kept in the result set although no data for characteristic 12 was filled in.
4. A new list of characters and states to chose from is formed
        i. Charac 10: state 5, state 6 ('state 8' is dropped out as it does not have a identifying value anymore)
        ii. Charac 11: state 7, state 9
        iii. Charac 12 is dropped out as only 1 state (18) is left when taking only Taxon A and Taxon B into account.
5. 'character 11', 'state 9' is chosen in a second step
    a. The cookie 'ident_steps' is changed into: $12µ18$11µ9
    b. The query interrogating the database looks as: "Select taxonname from concat_table where ([calculated string] like '%µ18%' or [calculated string] like '%$12µ0%') and ([calculated string] like '%µ9%' or [calculated string] like '%$11µ0%')"
6. Taxon A is shown as the only resulting taxon.

Note: undoing made choices is done by removing the data for this choice from the cookie 'ident_steps'

- **4.3.2. Prime number paradigm method**

A second method was developed aiming to be able to analyse the quality of a key (*i.e.* to check whether a sufficient number of characters and states has been added to the different taxa in the key in order to separate all taxa). The presented 'prime number paradigm method' may however also be used for both the basic functioning of the key and the analysis of the quality of a key.

A unique prime number is assigned to each morphological character state used in a key. Multiplication of all prime numbers (prime-product) assigned to the character states relative to a taxon leads to an integer number summarising the morphological definition of a taxon. In order to keep a taxon in the remaining list of taxa during identification (even if no data for a chosen characteristic has been added for the taxon) the 'prime-product' is multiplied with all prime-numbers assigned to character states coupled to lacking characteristics.

An example of these unique prime numbers is shown in table 2 (column 'prime').

The 'prime-product' for 'taxon A' is (2*3*5) = 30. As no data is available for characteristic 12, this result is multiplied by the prime numbers states for characteristic 12 (11 and 17). As a consequence, the result for 'taxon A' is (2*3*5) * (11*17) = 5610. The result for Taxon B is (7*3*11) = 231. Taxon 'prime-products' are saved in table 'morf_concat' in the field 'prime_factor' as shown in table 3.

Similarly to the former method ('Calculated strings'), the 'prime-products' need to be recalculated each time data in the key is added to or/and removed from the key. Ordering of the states during prime number assignment is very important to ensure that a certain prime number is always assigned to the same morphological character state.

Calculating the resulting remaining taxa after each identification step can be accomplished by checking whether the prime product is divisible by the multiplication of the prime numbers belonging to the chosen character states (PS).

If 'characteristic 11 – state 7' (prime number '3') and 'characteristic 10 – state 6' (prime number '7') have been selected, the PS-product would be (3 * 7) = 21.

Checking the query for divisible pairs of numbers is done by taking the integer value of the ‘prime product’ divided by the ‘PS-product’. If the multiplication of this integer with the ‘PS-product’ equals the original ‘prime product’, both are divisible. If two numbers are not divisible, the quotient will be a decimal number. The integer value of this decimal number multiplied by the ‘PS-product’ will always be lower than the original ‘prime product’.

E.g. divisible numbers: 21 / 7 = 3; integer(3) = 3 ; 3 * 7 = 21) (e.g. indivisible numbers: 21 / 5 = 4.2; integer(4,2) = 4 ; 4 * 5 = 20

When translating this into a query taking the results from the database, this will result in:

“select taxonname from concat_table where int(prime_factor/PS)*PS = prime_factor”

Instead of saving each state selected in a temporarily stored value only the ‘PS-product’ needs to be stored. After each step this product is multiplied by the prime number of the chosen character state

Removing selected states is achieved by dividing the stored ‘PS-product’ by the prime-number of the removed state.

Although the ‘prime number paradigma’ method looks at first sight more complex than the ‘calculated string’ method, it has the advantage that it can also be used to check whether taxa being separated from each other in a key. If the ‘prime products’ of two taxa are divisible, it implies two taxa can be regarded as morphologically undistinguishable by the key. A profound analysis of an identification key can be executed by checking whether ‘prime products’ of each possible pair of taxa are divisible. The results of this analysis can be visualised through a cross-diagram. The taxa used in a key are selected as row and column-headers. If two taxa are divisible the crossing-point of a row and a column is marked with an ‘E’ (Equal). If not, the crossing-point is marked with a ‘D’ (Different). A key for which all taxa can be distinguished from each other only displays ‘E’- marks on the diagonal of the cross-diagram. Two possible outputs of an analysis are shown in Figure 2. The first

diagram shows the output of an accurate, functional key with no undistinguishable taxa. In the second diagram it is impossible to distinguish taxon *G. olivae* from *G. gordonae*. The quotient of their 'prime products' (54419209043 / 54419209043) equals 1, meaning both species have exactly the same character states chosen. *G. dunckeri* cannot be distinguished from *G. namibensis.* The quotient equals an integer number (15906625574/1060441705 = 15). Oppositely *G. namimensis* can be distinguished from *G. dunckeri*. Additional morphological information is available for *G. namibensis*.

To prevent data overflow (depending on the database-engine used: all data fields have a maximum value), 'prime products' must be kept relatively low. This is achieved by always working with the first prime numbers.

M. aegyptica	E	D	D	D	D	D	D	17218306987
M. africana	D	E	D	D	D	D	D	1.27418232448601E+17
M. orientalis	D	D	E	D	D	D	D	6.11855131918329E+17
M. slabberi	D	D	D	E	D	D	D	3.03309459979734E+17
M. tropicalis	D	D	D	D	E	D	D	2098831
M. wooldridgei	D	D	D	D	D	E	D	212268889
M. zeylanica	D	D	D	D	D	D	E	5.22695064316706E+15

M. aegyptica
M. africana
M. orientalis
M. slabberi
M. tropicalis
M. wooldridgei
M. zeylanica

G. wittmanni	E	D	D	D	D	D	D	D	D	21289259494
G. bispinosa	D	E	D	D	D	D	D	D	D	368703024495
G. dunckeri	D	D	E	D	D	D	D	D	D	1060441705
G. brevifissura	D	D	D	E	D	D	D	D	D	294586906299
G. gordonae	D	D	D	D	E	D	D	E	D	54419209043
G. longifissura	D	D	D	D	D	E	D	D	D	1874138746
G. namibensis	D	D	E	D	D	D	E	D	D	15906625574
G. olivae	D	D	D	D	E	D	D	E	D	54419209043
G. psammodytes	D	D	D	D	D	D	D	D	E	175279

G. wittmanni
G. bispinosa
G. dunckeri
G. brevifissura
G. gordonae
G. longifissura
G. namibensis
G. olivae
G. psammodytes

Figure 2. Illustration of key-testing through 'the prime number paradigm'

5. User interface

The user interface for NeMysKey is programmed in the server-side scripting language ASP (Active Server Pages - http://www.asp.net) and uses some small piece of javascript code to enable the display of characters and character states in a hierarchical tree.

Characters and their related states are displayed at the left of the screen. Remaining taxa appear in a list at the right. Each time a character state is chosen, the remaining taxa are calculated (as described above) and only relevant characters are recalculated.

Chosen characters and character states are displayed at the bottom of the page. If needed, these can be unselected as explained above.

An arrow in a yellow box next to a remaining taxon indicates another key is available for possible further identification. The methodology behind this was explained in detail in the item ‘Defining key members’.

If character states have linked illustrations, these can be displayed through a pictorial selection board. Selecting an image selects the desired according character state.

For all taxa used in a key, a link to the taxon information page (in NeMys http://www.nemys.ugent.be) is provided. This facilitates verification of the identification by for example the original description of the species.

A help section ‘how to use the key’ gives a definition of all icons used, and a movie showing a demo of a working key can be downloaded.

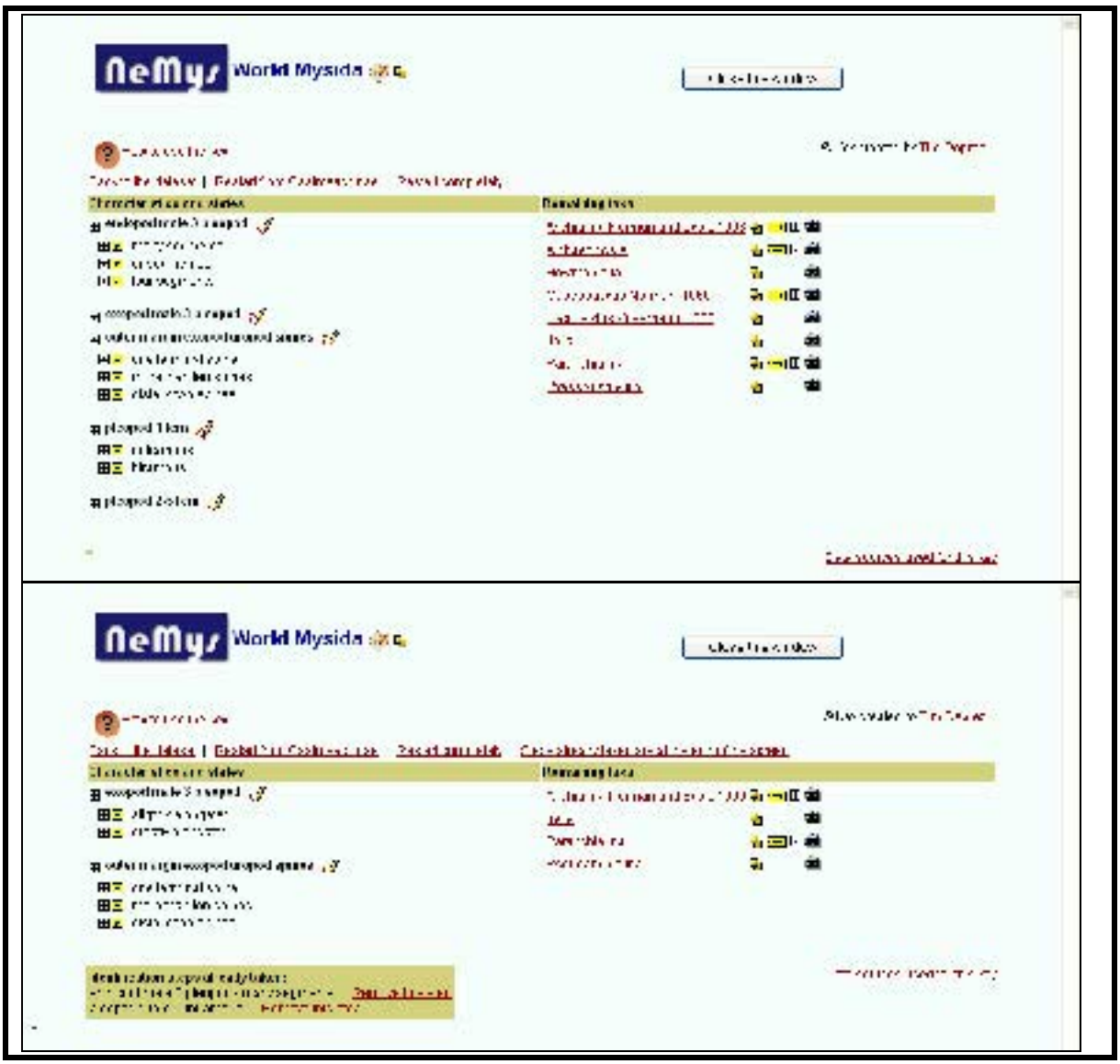

Figure 3 illustration of the NeMysKey user interface

6. Example keys

From march 2005 onwards, keys for several taxa were created with NeMysKey. Some examples demonstrating the diverse applicability are listed below.

1. World Mysida key (made by Deprez, T.). Identification key for the genera of the order Mysida. Many characters are illustrated. Some family keys are still preliminary or under construction. The World Mysida Key requires basic knowledge on mysid morphology.

2. Key to the genus *Mesopodopsis* (made by Deprez, T.) This key is based on three publications on this genus, all presenting dichotomous regional keys. By combining these keys and adding additional morphological descriptors, a digital polytomous key for all members of the genus was made. This example shows that it is relatively easy to translate dichotomous keys into polytomous digital versions. If new species are described for this genus, they can easily be added to this existing key.

3. Key to the free-living marine Nematoda (Steyaert, M. *et al*., 2005). This key was the collaborate work of a number of nematologists of the Marine Biology Section (Ghent University), each of them creating different parts of the key. This proves that different keys, made in a multi-user community can fluently link to each other. Nearly all characters and states are illustrated with images and linked to a clarifying glossary. This collection of keys is still an evolving product. Different parts of this huge puzzle (5000 species) are being filled in gradually.

4. Key to adult European amphibians and reptiles (made by Speybroeck, J.) This is a user-friendly species key to all known European amphibians and reptiles. It makes use of 'pseudotaxa' (see above) (e.g. 'lizards with legs') to guide users through the complex classification of these groups. It uses non-morphological characters (habitat, geographic range) as well. Identifications can be checked with photographs of all species. Several complex morphological characteristics are illustrated with pictures.

At this moment a number of other keys (e.g. Key to the European ladybird species by Adriaens, T., Key to the species of the genus Peperomia by Samain, M. & Vanderschaeve, L., etc.) are under construction and will be available soon.

7. Discussion

Is there a need for yet another digital identification key? An investigation of the existing digital identification systems learns that almost no intelligent online keys (identification systems which guide the user by adjusting the key according to choices made and by displaying only choices which are relevant for further identification) exist at this moment (except for some Linnaeus II © keys (Schalk,

2005 and keys made with the '3I' package (http://ctap.inhs.uiuc.edu/dmitriev/3i.asp)). A valuable comment on this would be that many biologists do not want an online system or do not have access to online resources. The key presented here, is a recent development and has been developed for online. Future developments however may focus on an offline usable version as well. In this context first tests have been carried out with offline use of ASP (active server pages) through the software ALP (Active Local Pages http://www.activelocalpages.com/). The final aim is to make all keys downloadable and usable in an offline environment. If a user is online an automatic check whether new updates are available would be done. If so, this new version of the data used for a key could be downloaded. This technology makes is possible to use the same programmatic code for both offline and online keys.

Some major advantages inherent to the web based architecture (which will remain the main focus of NeMysKey) are (1) the multi-user environment in which keys can grow, (2) the connectivity possibilities of related keys, and (3) the possibilities to keep keys up-to-date with the systematic state of the art.

A drawback of hard copy and also many electronic keys is that they are the result of a snapshot of the taxonomic knowledge at a certain point in time. Keys become superseded when taxonomic changes in the focussed group occur. Although for many taxa, the taxonomy is considered as stable, for many more taxa this is clearly not the case. Online keys have the advantage to be easily updated with new taxonomic findings.

The presented identification key is part of a much broader biological information system. Identification can as such be done in a taxonomy oriented way. Keys embedded in a broader information platform may be considered as helping tools in the identification process. Ending up with one single result is not necessary and sometimes not possible. In the case of multiple final taxa, users are forced to go back to the original descriptions and other background information in order to verify what species name is corresponding with the investigated specimen. Species with incomplete descriptions or dubious status may as such be incorporated in keys. Nematodes for example, do not have a stable or straightforward definition for many species. Consequently the development of identification keys for nematodes has

always been a laborious task. Classical keys don't offer the possibility to check all available other taxonomic knowledge on a species. Nematode keys in the NeMysKey architecture may be feasible as they do not always end up with a single taxon, meaning that different taxa may be hard to distinguish. By checking the original descriptions, it is often yet possible to correctly identify a specimen.

Ending up with different results may be regarded as a step backward, although from the scientific point of view it is a much more accurate way of working. Identifiers are forced to use taxonomic literature and a certain skill is required to come up with a good identification. The importance of the work of taxonomists is consequently obvious. Due to this literature linked methodology of identification, taxonomists are encouraged to make their taxonomic work understandable by non-taxonomists as well.

In the current setup multiple keys (family keys, genus keys, species keys) can be made by multiple users. All keys are offered together in one workspace and can fluently be linked to one another. An ideal situation would be that keys can also link up with keys made in a non-NeMys environment. A possibility for achieving this is the use of a standard exchange format through biodiversity portals. The Taxonomic Databases Working Group (TDWG) is currently finishing a standard allowing the exchange morphological data between applications (http://www.nhm.ac.uk/hosted_sites/tdwg/). The SDD scheme (Structure of Descriptive Data) (see http://wiki.tdwg.org/twiki/bin/view/SDD/Version1dot1) and Darwin Core 2 (see http://darwincore.calacademy.org/) may help to achieve the exchange of morphological data necessary in keys.

Although these XML-based techniques offer possibilities to exchange morphological data on species, this does not necessarily imply an exchange of keys. When making keys available through biodiversity portals, a number of additional data is needed, such as the members of a key, the parent of a key, and a series of metadata on a key. An exchange standard for keys may be an amalgation of the TDWG SDD standard and a number of key specific data units.

An exchange format for identification key data between different file formats may be favourable. It would allow users to use their favorite interface to work with the

different keys. The Marbef (http://www.marbef.org) responsive mode project Prope-Taxon (http://www.medobis.org/prope/index.php) aims to create facilities to link up keys on marine taxa of Europe. Nevertheless, a XML-based exchange standard, when developed in this project may also be usable for non-marine taxa.

In order to make NeMysKey fit in the philosophy of exchange between different identification systems, some preliminary tests have been carried out on exporting keys made with this tool to other formats. An export facility to the Delta format (http://delta-intkey.com) (Dalwitz, 1980; Dalwitz, 1993) for use with IntKey© has been designed and will be finalized and implemented soon.

The German philosopher Leibniz (1646-1716) presented a method to classify concepts based upon their characteristics (Couturat, 1903; Ross, 1984). In this method he experimented with a mathematical notation for each concept. Each characteristic of a concept is assigned two unique prime numbers (one positive ad one negative). Each concept could as such be described with a combination of these all prime numbers of all characteristic: being the sum of the product of all positive prime numbers and the product of all negative prime numbers. The presented 'prime number paradigm' can be considered as a modification of this method. Although the use of prime numbers was theoretically already well known many years ago, practically implementing it was not possible due to complex calculations. The current computer aided calculation power allows using prime numbers as helpful tools.

The use of prime numbers is a intriguing method which may also be promising in ecological modelling.

Keys seem to be the link between taxonomists and different end-users of taxonomy. Digital polytomous keys with the NeMys philosophy (link to background data) are forcing biologists to identify specimens with an amount of scientific criticism. In a first stage identifiers can make use of a user-friendly key. In the second phase of the identification process, users are invited to check whether the identification really matches the taxon, by looking at the available data in the linked bio-information system.

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CHAPTER 3 – ENCYCLOPEDIA MYSIDA: A GLOBAL DIGITAL CATALOGUE ON THE ORDER MYSIDA

1. Introduction

The study of the biogeography and taxonomy of the Mysida, an order belonging to the Crustacea, requires an extensive archive of published data on this group. For the setup of this archive and extracted information the biological information system NeMys was used.

Mysida are shrimp-like Crustacea occurring in large numbers in most coastal areas of the world. Systematically they belong to the superordo Peracarida, together with the Amphipoda, Tanaidacea, Isopoda, Lophogastrida, Cumacea, Mictacea, Thermosbaenacea and Spelaeogriphacea. The most unique features of this order are the presence of a statocyst in the endopod of the uropod and a marsupium in the female. This marsupium is a brood chamber in which the first larval stages are passed through; it is an enclosed sac formed by extensions of the female thoracopods.

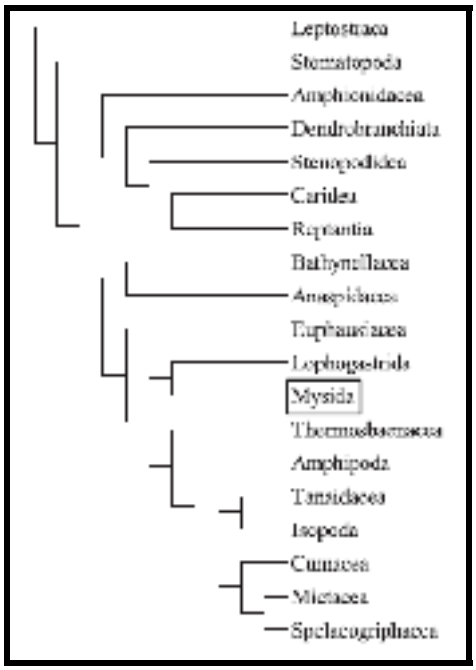

Figure 1. Phylogenetic place of the order Mysida in relation to 18 other important monophyletic groups of Crustacea (After Richter, 2001)

The Mysida, earlier known as a subordo of the ordo Mysidacea, have since 2001 been upgraded to the order level. They have a long history (200 years) of scientific research. The first species (*Praunus flexuosus*) was described in 1776. The most

recent species list consists of 1086 species. The group is considered as one of the 19 monophyletic groups of the Crustacea. The closest relatives are the Lophogastrida, formerly also a subordo of the ordo Mysidacea (Richter, 2001). Figure 1 illustrates the phylogenetic relationships between these 19 monophyletic groups.

Ecologically, members of this order are recognized as an important group of the hyperbenthos (Mees *et al.,* 1997). They are found for many fish species as the most important food resource (Mauchline, 1980).

Taxonomical research is, from a historical point of view, the most important type of research carried out. The most important mysid taxonomists (number of species and number of genera described) are listed in table 1. The most relevant taxonomic essay on higher systematic level was published by Hansen (1910). It encompasses the description of three subfamilies and four tribes.

Ecologically, mysids are used in a wide range of studies: foodwebs (for example Hostens & Mees, 1999; Aneer, 1980), community structures (e.g. Darnell, 1961; Dexter, 1992), species-related environmental ecology (e.g. Hakala, 1980; Holmquist, 1973) and ecotoxicology (Verslycke *et al.*, 2002; Verslycke *et al.*, 2004).

Recently the first publications on molecular phylogeny were published by Remerie et al. (2004) and Meland (2004). The analysis of morphological phylogenetic data started earlier (Kobusch, 1998; Meland, 2004).

This chapter describes how the dataset has been setup, what data is available in it and gives an overview of the limitations in the current data state of art. Future progress and key focus points are proposed.

Taxonomist	*Period*	*Number of species described*	*Number of genera described*	*Number of publications*
Walter Tattersall	1882 - 1942	111	23	77
Georg Ossian Sars	1837 - 1927	105	14	33
M. Murano		103	19	78
Mihai Bacescu	1908-1999	97	12	74
Ii		76	7	63
Olive Tattersall	1890 -1978	61	2	18
Hans Hansen	1855 - 1936	59	8	17
Henri Nouvel	1905 - 1974	42	6	46
Pillai	1920 - 1985	23	0	24
Thomas Bowman	1918 - 1995	14	1	17

Table 1. Ten most important taxonomists ordered by number of newly described species for the order Mysida with indication of the number of species and genera described and the number of Mysida related publications. (after http://www.nemys.ugent.be, http://tidepool.st.usm.edu/mysids/; Tattersall & Tattersall, 1952; Holthuis & Holthuis, 1975; Gordon, 1980; Kemp, 1980)

2. Origin of the dataset

The basis of the presented dataset was the database which has been created in the framework of the author's licentiate thesis. During the year 1999 it was constructed focusing on the Mysida fauna of the coastal areas of the Western Indian Ocean. This resulted, after eight months of extensive work, in the first public version of a database published as MysidLan (Deprez, 2001). Although the Mysidlan database concept did fill the needs for the Western Indian Ocean dataset, a global database setup needed a much more complex database design regarding the:

(1) Geographic data: the Mysidlan database was specifically constructed for a limited list of geographic areas. In a global approach, exact geographic records with exact coordinates, facilitating precise distribution analysis, were favorable.

(2) Morphological data: the Mysidlan database was designed for storage of only a limited number (30) of morphological characters. Detailed morphological studies on species from different genera (see Deprez, 2000; Deprez 2001), demonstrated that one set of characters applicable to all species of the ordo was an untenable way of working. When describing the morphological features of all species in detail, an architecture allowing the assignment of morphological characters to different systematic levels is needed.

(3) Systematic data: Mysidlan was able to retain a systematic hierarchy. The documentation of the historical aspect of this classification was not feasible and consequently not performed in the Mysidlan database. The new global dataset had to take the current systematic situation as well as past ideas on taxonomy in consideration.

(4) Other data types: creating an encyclopedia-like digital work on the global Mysida required a vast set of data types to be connected to the dataset (for example: pictures, ecological data, molecular data, specimen data, …). With Mysidlan only a limited number of data types could be encountered.

The first aim for the dataset was to present a systematic correct overview of the worlds known Mysida. Earlier, similar global systematic overviews were published through the classical paper circuit (Muller, 1993; Mauchline, 1980; Mauchline & Murano, 1977; Gordon, 1957). These publications give a good snapshot of the systematical state of art at a particular point in history. Additional information on geography, morphology or any other biological relevant information is, in these paper based publications, hard to implement. Moreover, updating with new findings is impossible.

3. Database setup and data overview

▪ 3.1. LITERATURE DATA

The main idea behind MysidLan, i.e. the link between data and a published data source, is kept as the keystone during the setup of the current database. As a consequence an extensive reference list of about 4000 references had to be compiled. For this dataset first attention was paid to literature published in peer-reviewed journals. Grey literature (for example: research reports, master thesis or PhD works) was not emphasized yet. In total more than 1500 literature sources were collected and made available in a digital format (pdf). The total amount of literature in a digital format is about 25000 pages. This first set of sources was used to enter the data currently available in the system. For each reference, data on systematics, geography, and where possible morphology was extracted and entered. Literature sources were obtained by several collection holders and libraries:

(1) a first series of documents was gathered through the different reprint libraries available at the **Ghent University** (Belgium). An ongoing digitization of the reprint collections helped to retrieve less relevant non-taxonomic literature.

(2) Several visits at the **Royal Belgian Institute of Natural Sciences** (Belgium), helped to retrieve various papers.

(3) Two visits to the **Natural History Museum in London** (UK) made it possible to perform research on the literature collections of Walter Tattersall and Olive Tattersall, two scientists of major importance for Mysida taxonomy, both active during mainly the first 50 years of the 20th century. Although many more publications are available in this collection it was only possible to digitize a limited number, mainly due to juridical and financial restrictions.

(4) A large number of reprint copies were obtained from **J.P. Lagardère** (France), who is managing the scientific heritage of Henri Nouvel (see further).

(5) Thanks to the **library of VLIZ** (Flanders Marine Institute) (Belgium), it was possible to retrieve very specific literature sources. This helped for instance to collect all published literature about the genus Siriella.

(6) Many reprints were obtained by contacting several researchers: T.H. Wooldridge, A. Connell, K. Wittmann, W. Price, V. Petriashov, M. Daneliya, R. Modlin, M. Murano, T. Iliffe, A. Brandt, K. Meland, T. Brattegard, E. Escobar-Briones.

▪ 3.2. SYSTEMATIC DATA

Another important step in the setup of the Mysida dataset was the compilation of a systematic list. Existing global checklists (Gordon, 1957; Mauchline, 1980; Muller, 1993) and a few regional checklists (Tattersall, 1952; Pillai 1965) were used. More detailed information on synonymy and new taxa were added gradually. A few online resources provided useful additional information. An example is "http://tidepool.st.usm.edu/mysids/", an online Mysida species list (Anderson *et al.*, 2005).

Family	Subfamily	Tribe	Number of genera	number of species
Lepidomysidae			1	9
Mysidae	Boreomysinae		1	39
	Gastrosaccinae		9	102
	Mysidellinae		1	16
	Mysinae	Aberomysini	1	1
		Calyptommini	2	3
		Erythropini	49	212
		Heteromysini	12	111
		Leptomysini	30	160
		Mancomysini	1	4
		Mysini	54	302
	Rhopalophthalminae		1	18
	Siriellinae		3	70
Stygiomysidae			1	6
Petalophthalmidae			6	33

Table 2. Overview of the number of genera and species of all Mysida families, subfamilies and tribes

The current dataset counts 173 genera and 1086 valid species. In total 270 synonyms are added. The order is divided in 4 families: Lepidomysidae, Mysidae,

Stygiomysidae, and Petalophthalmidae. The far most species rich family is the Mysidae consisting of 1038 species. Table 2 shows the higher taxonomy of the Mysida with for each lowest level higher than the genus level the number of genera and the number of species.

▪ 3.3. LITERATURE – SYSTEMATICS

Between the available literature and taxa in total about 10000 links were created. These links indicate data on a particular taxon is available in the publication. Of all species, 98 percent have currently at least one link to a literature sources. Most of these links have additional context information: (1) the type of data associated with the taxon (e.g. original description, review, biogeographical, feeding, ecology ....); (2) a text based remark (e.g. referring to the page in the document where the information is situated). The European species *Neomysis integer* has most linked references (178). The majority of links were formed manually while reading the publications. However, about one third of the existing links were assigned semi-automatically making use of full text indexes made of all pdf-files. Such semi-automatically linking is only feasible for publications which can be transformed in OCR-ed pdf-files.

Pdf-indexing is a technique that has been exploited while exploring the added value of full-text indexes of electronic documents. All electronic documents are stored on a server equipped with an indexing system being able to index documents in pdf-format. Such full-text index allows fast searching for specific words in the documents. An application built on this full-text index is the semi-automatic linking of species to these electronic documents. An automated procedure scans each electronic document and checks for occurrences of species names. In order to prevent a large number of errors, only matches for full species names (genus name + species name) are allowed. The result of this technique is list of suggested taxa that are available in the document. In a next step, an authorized user checks whether there is indeed data available for the suggested taxa. The technique is in the first place a help tool for data entry and as a consequence speeds up this process significantly! Less relevant literature sources are with this technique also easily retrieved.

▪ 3.4. GEOGRAPHIC DATA

Geographic data was entered by linking species with locations. All locations were entered with exact coordinates, extracted from the publication or indirectly retrieved, by using gazetteers (Microsoft Encarta 2005 ©, Geonet Names Server at http://earth-info.nga.mil/, Geographic Names Information System (United states, Antarctica) at http://geonames.usgs.gov/pls/gnispublic). All coordinates were entered using the WGS84 standard (http://www.wgs84.com). Each record was documented with some additional information, if available in the publication: (1) catch date, (2) minimum and maximum catch depth, (3) text-based remarks. The database contains currently 9185 distribution records for 726 species. A world map displaying all available distribution records is shown in figure 2.

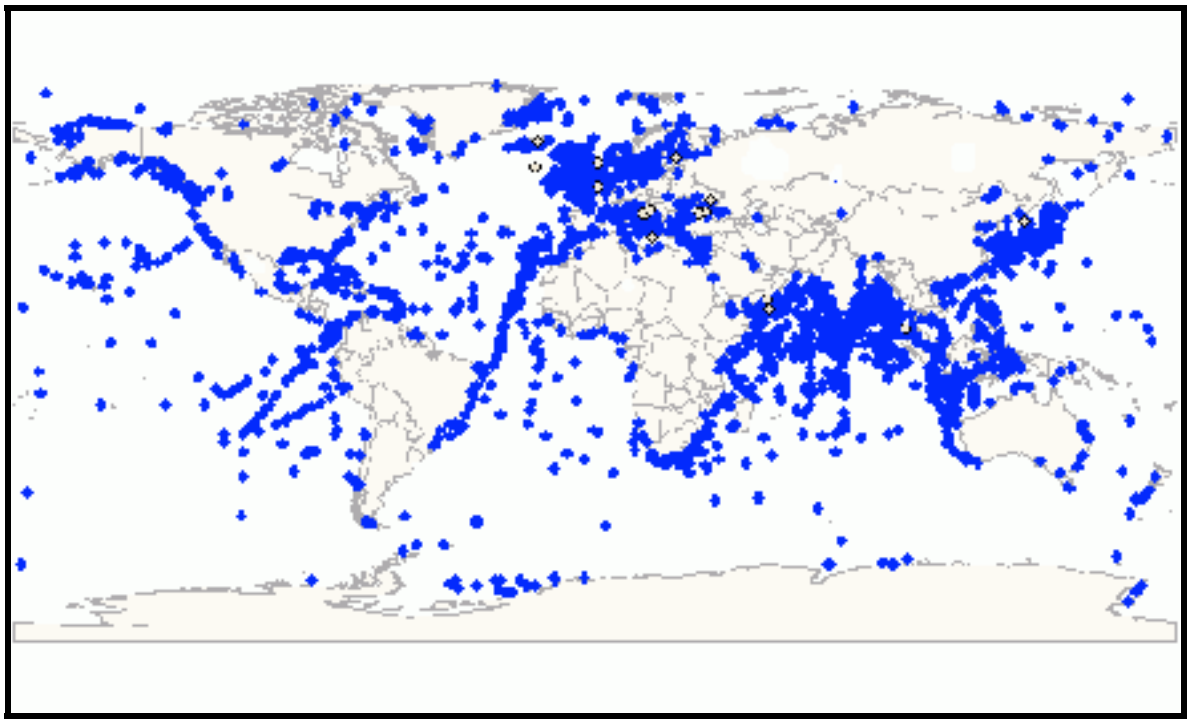

Figure 2. Global overview of geographic records of Mysida in NeMys

▪ 3.5. MORPHOLOGICAL DATA

Initially, forty common characters and related character states were used for all taxa. Later on, more detailed research on smaller groups of taxa revealed that more specific morphological features for a limited group of taxa are needed to correctly

describe the morphology of a species. Most of these taxon-specific morphological characters were entered by creating identification keys (through NeMysKey), for selected groups of taxa. The basic set of forty morphological and morphometrical characters is entered for at least all European and Western Indian Ocean species. This data has not much been exploited yet due to the current lack of efficient search mechanisms.

The total number of characters, of which 34 are morphometric, used is 254.

Morphological records were added for 71 genera (all species inherit the genus specific data) and detailed information on species level was entered for 237 species (in total 9052 records). Data on measurements is available for 129 species (464 records).Many species still lack detailed morphological information. However, almost all species have at least an illustration or the original description linked.

- **3.9.1. Species descriptions**

Most of the above listed data sections have been used to describe two new species belonging to the order Mysida. *Gastrosaccus wittmanni* was described from Algoa Bay (South Africa) (see appendix 2). Analysis of the morphological features of this species helped to define the general and genus specific morphological characters. A second species described, *Idiomysis mozambicus* (see appendix 3), emphasized the need for genus related morphological characters.

- **3.9.2. Identification keys**

Six keys where developed through NeMysKey: an overall key to family or genus level and several genus keys to species level (*Anchialina*, *Gastrosaccus*, *Mesopodopsis*, *Siriella*, *Archaeomysis*, *Paranchialina*). The key for the genus Siriella illustrates how a polytomous key can facilitate the identification of a species-rich genus.

▪ 3.6. MEDIA DATA

A large number of images displaying the diagnostic features were added for almost all species (2350 linked to 734 species). Images were obtained through the following sources:

(1) about 1500 images were derived from the personal notes of Henri Nouvel (1905-1974). This famous French scientist worked at the University of Toulouse on different invertebrate taxa, one of them being the Mysida. He produced about 50 taxonomic publications on this group, describing 42 new species. For this work he gathered lots of notes and publications on Mysida. These were, after his death, well preserved by J.P. Lagardère (La Rochelle, France), a former student of H. Nouvel. These notes included mostly unpublished drawings, morphological comments, or other biological observations. With the help of J.P. Lagardère it was possible to preserve this collection for future use and release it for a broader audience by linking it in a digital format to the Mysida dataset in NeMys.

(2) A few hundred images (mostly photographs) were produced from personal observations on specimens.

(3) Digital photographs of specimens (in toto or dissected parts) sent by colleague mysid researchers were also linked to the database.

▪ 3.7. COLLECTION – SPECIMEN DATA

A taxonomical review still requires analysis of specimens. A start has been made to give an overview of mysid specimens available in collections worldwide.

By contacting a vast number of museum curators, it was possible to retrieve data for five specimen collections: (1) Smithsonian Institution Washington, US; (2) Museum Nacional De Ciencas Naturales, Madrid Spain; (3) Royal Belgian Institute of Natural Sciences, Brussels Belgium; (4) Research Collection of Baltic Mysids of Mikhail Daneliya, Russia; (5) Ugent Marine Biology Section Reference collection, Ghent Belgium. Several other collection managers agreed to collaborate in the near future

mostly after digitization of the collections (Danish Natural History Museum, Natural History Museum London – United Kingdom, South African Natural History Museum, Zoological Institute of St. Petersburg - Russia). Currently, data for about 700 specimens is available on 150 species.

All natural history collections found currently having Mysida specimens in their collections are listed in appendix 1.

▪ 3.8. MOLECULAR DATA

An important source of information is molecular data. Since early 2005, 276 molecular sequences have been extracted from NCBI GenBank (http://www.ncbi.nlm.nih.gov/) for 61 species. Currently extraction is still performed on a manual basis. A link to the Genbank record is provided. The number of molecular records is rising constantly during the last years. First records go back to 1999; a gradual increase of records published in Genbank is observed over years (Figure 3).

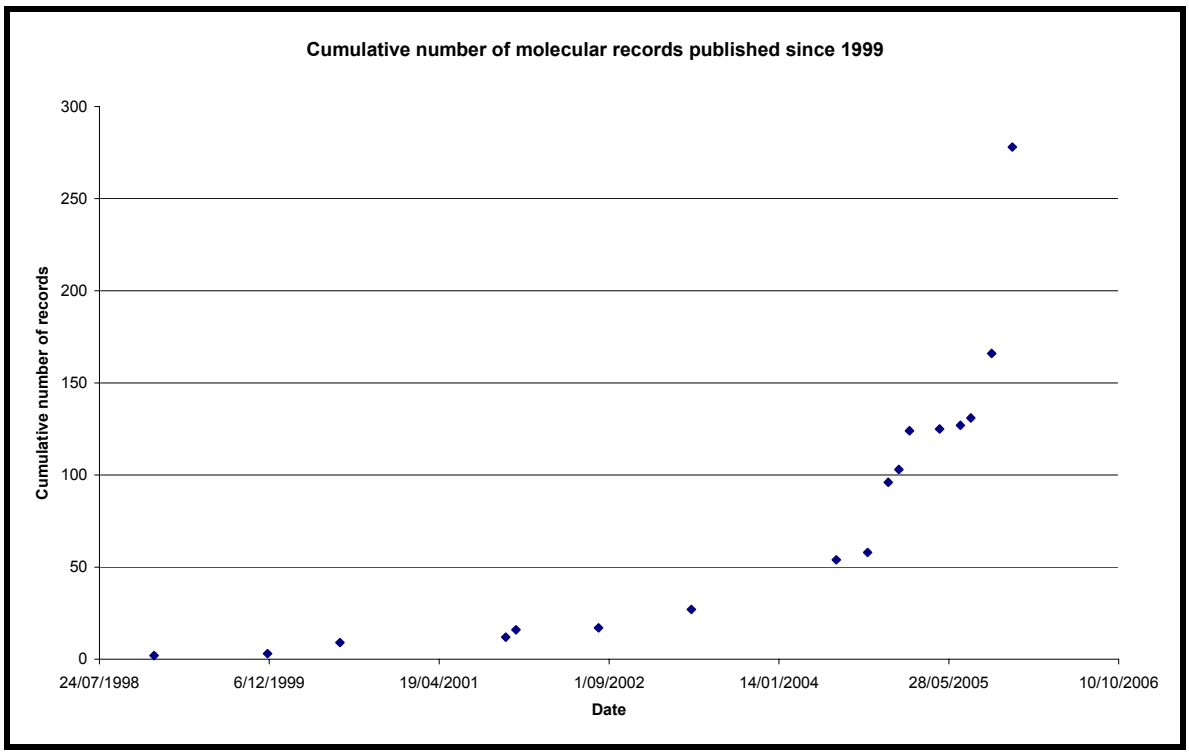

Figure 3. Cumulative number of molecular records on mysids published on GenBank

4. Discussion

Although the present dataset gives a well documented overview of the state of art of many aspects of the Mysida, many parts still need more emphasis in the future.

▪ 4.1. DATA COVERAGE

• 4.1.1. Literature data

Most of the references ever published on Mysida are brought together in this dataset. Just about one quarter is available in a digital format. Although legally there are a number of objections for creating digital collections of literature on a group of taxa, it has some major research related advantages. Semi-automated extraction techniques can be applied on digital literature collections (see pdf-indexing). This facilitates users to search through literature collections in a more profound and efficient way. The creation of a digital literature archive is an efficient way of preserving this data for the future. Data in digital format permit fast and efficient reference work during taxonomic research.

The prevailing literature list gives a good overview of the published literature. Nevertheless many more sources may be available in 'grey literature': for example PhD-thesis, publications in non-peer-reviewed journals, …. A quest for these may be interesting to get a better data cover for some selected parts of the database (for example geographical data).

• 4.1.2. Systematic data

All species currently described are available in the database. The historical context of many species (synonymies) still needs further attention. For several groups, e.g. Gastrosaccinae, Siriellinae the presented data may be considered as complete.

Although this part of the database is currently well covered, constant revision is needed based on the most recent publications.

- **4.1.3. Morphological data**

Concerning morphology and identification keys still an enormous amount of work has to be done. The general morphology up to genus level is relatively well documented. On species level, much more detailed descriptive data needs to be added. The best way to achieve this is by reviewing each genus in detail. Through the NeMysKey tool it is possible to keep an overview on the whole genus and gradually get into more detail for each species. For many small genera the complexity of this task is acceptable, while for larger species-rich genera (i.e. '*Mysidopsis*, *Acanthomysis*, *Heteromysis*, …') this is a time consuming difficult task.

- **4.1.4. Multimedia data**

More photographs, illustrating specific morphological features, would increase the employability and the attractiveness of the dataset. Photographs of complete specimens generally do not show enough morphological features in detail to be appropriate for research purposes. Photographs of the distinguishing features (in microscope slides) would be a great help for identification purposes. Such image collection can play a major role in the development of a virtual museum collection.

Digital specimen collections would require a standard set of photographs of all distinguishing features. An interesting procedure may be the production of small movies simulating focusing through a microscope. This method allows the visualization of the three-dimensional structures (Deley & Bert, 2002). Digital specimen collections will increase the efficiency of work of taxonomists. Less time and money (traveling to musea is not longer required) is needed to obtain and check the morphological details of specimens (Causey *et al*., 2004; Hong *et al*., 2000). Initiatives like Zoobank (http://www.afriherp.org/ZooBank/Zoobank.htm) (Polaszek *et al.*, 2005) may play an important role in this matter.

- **4.1.5. Distribution data**

The literature based geographical records give a relative good cover for Europe, the Indian Ocean and the Indo-Pacific coastal areas. Not many records were assembled for North American coastal waters. Many parts of this region however are well-documented in the literature. South American coastal waters are not well

investigated. Data, derived from museum collections or unpublished literature, may help to get a better cover for these areas.

The presented dataset shows displays clearly which regions should be of prior interest for new inventory research: The West African coastline and the South American coastlines may help to understand global patterns in the distribution of Mysida (see chapter 4). Many other regions, which are only poorly documented from old research projects, would likely also be reinvestigated.

- **4.1.6. Molecular data**

Currently all molecular records available in the GenBank database are present. An automated procedure for linking with GenBank would be favorable. The yearly yearly increase of new data on Mysida becoming available would as such not require an increase in data input effort. Techniques for extraction of data from GenBank are relatively well described for analysis purposes. Linking to species information systems however, still requires more investigation and documentation.

- **4.1.7. Specimen collections**

The number of specimens extracted from natural history collection record sets is rather low. The main reasons for this are that many, mainly smaller collections, are not digitized yet. The list of collections holding specimens in their collections (appendix 1) shows that far more specimens than now catalogued do exist. Currently no collection portals exist facilitating a cross search through all worldwide national history collections.

For many taxa only few type specimens can be traced. The revisions of the genera *Anchialina* and *Siriella* (see chapter 5 & 6) illustrate this problem very clear. In many cases the available material is in bad conservational state and distinguishing morphological features can not longer be observed. This is again an argument for the development of digital reference collections with large numbers of photographs of all morphological features.

- **4.1.8. Others**

The generic data module (see chapter 1) is just since mid 2005 active. As a consequence the possibilities of this module have not been used a lot for the Mysida datasets yet. Future research however, may utilize this tool intensively. It would allow to document ecological relevant data on Mysida species (for example: habitat type, salinity range, feeding strategy, clustering strategy, relations to other taxa). These ecological records may open the dataset for a broader ecologically interested public, and eventually play a role in other research: ecological foodwebs, modeling, host-guest relationship research ….

▪ 4.2. LESSONS LEARNED: HOW TO SET UP A BIODIVERSITY DATABASE

The presented dataset may be considered as a good test case for setting up a species information database. Some experiences from this case study may ease the setup of new similar datasets.

• 4.2.1. How to start?

Literature turns out to be the key component for a genuine scientific species database. Literature information should thus be the first point of emphasis. Try to set up a reference list on the focused group of taxa. Search engines like 'Web of science' or Google Scholar© may be useful for recent publications. However the analysis of bibliographies in publications still delivers the best results for older literature. Consult as many as possible media when tracing literature. Secondly try to collect as many as possible publications, preferably in a digital format. Through Natural History Libraries and by getting in contact with other researchers in the field many publications can be relatively easy obtained. Storing this data digitally opens a number of possibilities in terms of data extraction (see 4.1.1.). Digitization of hard copy publications used to be a very time consuming job. Evolutions in technology both hardware (scanners, copiers) and software (less errors in OCR [1]software) did speed up this task significantly.

A classification is a second essential piece of data needed. Extract it from species checklists, regional reviews or online species databases.

Depending on the emphasis of the database two possible pathways can be followed for data entry: (1) work taxon by taxon, (2) work publication by publication.

Well-delineated case studies on a small group of taxa also help to make the data entry job to be more attractive. It allows obtaining results in a relatively fast. Entering the data publication by publication is experienced to be very efficient, when only focusing on one type of data (for example distribution data). This method does not require being scientifically critical and in terms of costs, it can be carried out by less qualified people.

- **4.2.2. How to keep it alive?**

Behind each living dataset, an active person is needed. This means datasets will not survive when no-one is the driving power behind it. As long as decision makers believe encyclopedia-like datasets can be maintained by a group of people, assuming everyone will do a part of the job voluntarily, an acceptable level of completion will never be reached. Species information databases require a long-term vision and need a constant driving human force.

NeMys-like datasets are never finished. They are a constant evolving concept, trying to follow the state of the art of research.

[1] OCR: Optical Character Recognition: The technique used to translate an image of a text-based document into digital text. The shape of characters is recognised by the software and translated into the character.

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6. Appendices

▪ 6.1. APPENDIX 1: LIST OF NATURAL HISTORY COLLECTIONS HOLDING MYSIDA SPECIMENS

For each collection the status of the Mysida samples, contact details and the web address is given.

- Harvard College Invertebrate Collections (UK)
    - 56 samples with Mysida containing 26 different species
    - Url: http://collections.oeb.harvard.edu/
- The University of Georgia Museum of Natural History (US)
    - Mysida are available in the collections, collections have not been digitized yet.
    - Contact through Dr. Freeman B.J.
    - Url: http://naturalhistory.uga.edu/htmldocs/collections/invertebrates.asp
- Natural History Museum London (UK)
    - Recent invertebrate collections are not indexed yet, although about 300 samples are available for about 70 species. Conservation status of many (mainly older) samples is bad
    - Contact through Miranda Lowe
    - Url: http://www.nhm.ac.uk/info/email.html

- Smithsonian national museum of Natural history (US)
    - Samples
    - Contact through Cheril Bright
    - Url: http://goode.si.edu/webnew/pages/nmnh/iz/Query.php
- Santa Barbara Museum of Natural History (US)
    - Mysida are available in the collections, collections have not been digitized yet.
    - Contact through Patricia Sadeghian
    - Url: http://www.sbnature.org/collections/invert/index.htm
- The Australian Museum (Australia)
    - Small numbers of Mysida samples available.
    - Contact through Penny Berents
    - Url: http://www.amonline.net.au/invertebrates/cru/index.htm
- Yale Peabody Museum (US)
    - 98 lots of Mysida belonging to 34 species
    - Url: http://george.peabody.yale.edu/iz/
- Natural History Museum Madrid (Spain)
    - 160 lots of Mysida – currently being indexed and reviewed by Tim Deprez
    - Contact through Miguel Villena
    - Url: http://www.mncn.csic.es/home800.php

- Natuurmuseum Rotterdam (The Netherlands)
    - A few lots (30) with typical species from the Netherlands (e.g. *Gastrosaccus spinifer*, *Neomysis integer, Praunus flexuosus*)
    - Url: http://www.nmr.nl/
- The North Carolina Museum of Natural Sciences (US)
    - Mysida are available in the collections, collections have not been digitized yet
    - Contact through John Cooper
    - Url: http://www.naturalsciences.org/research/inverts/index.html
- University of Hamburg (Germany)
    - Many lots mainly from Arctic and Antarctic origin.
    - Contact through Angelica Brandt
    - Url: http://www.uni-hamburg.de/
- Zoological Institute – Saint Petersbourg (Russia)
    - About 1500 lots of Mysida mainly originating from Arctic and Antarctic areas.
    - Contact through Victor Petryashov
    - Url: http://www.zin.ru
- Muséum National d' Histoire Naturelle (France)
    - Contact through Jean Paul Lagardère
    - Url: http://www.mnhn.fr/museum/foffice/science/science/sommaire.xsp

- South African Museum - Cape town (South Africa)
    - Mainly samples of species occurring along the South African Coastline
    - Url: http://www.museums.org.za/sam
- Royal Belgian Institute of Natural Sciences (Belgium)
    - Contact through Frank Fiers
    - Url: http://www.natuurwetenschappen.be
- Zoology Museum Ugent (Belgium)
    - Contact through Dominique Verschelde
    - Url: http://www.zoologymuseum.ugent.be
- Zoological Museum Copenhagen (Denmark)
    - 112 lots containing 60 species
    - Url: http://www.zmuc.dk

▪ 6.2. APPENDIX 2: A NEW SPECIES OF *GASTROSACCUS* (CRUSTACEA, MYSIDACEA) FROM ALGOA BAY (SOUTH AFRICA)

Authors: Tim Deprez, Tris Wooldridge & Jan Mees

Published as: Deprez, T.; Wooldridge, T.; Mees, J. (2000). A new species of *Gastrosaccus* (Crustacea, Mysidacea) from Algoa Bay (South Africa). Hydrobiologia 441: 141-148.

Key words: Gastrosaccus wittmanni, mysid, surface water, South-Africa

• 6.2.1. Abstract

Gastrosaccus wittmanni sp.nov. was collected from surface-waters near Kings beach in Algoa bay (South Africa). Morphologically, it is characterised by having seven strong spines on each side of the telson. In between the strong spines spinules are present except between the first most proximal pair. The endopod of the first female pleopod bears one terminal plumose seta. Most of the setae on antennules, antennae, thoracopods, pleopods and uropods are jointed.

• 6.2.2. Introduction

A new species of *Gastrosaccus* (*G. wittmanni)* is described and illustrated from Algoa Bay, South Africa. The species was collected near Kings beach (figure 1) in relatively calm water where fairly extensive rocky reefs occur (depth ± 5m). The species was also caught in deeper water (18-20 m) (Wooldridge 1983).

Sampling was done with a large conical planktonnet (diameter 1.5 m, length 6.5 m and mesh aperture of 500 µm). Eleven series of samples were collected at intervals of about two months between series.

Density (number of individuals per m^3 of water) was relatively low and did not exceed 6. For a list of accompanying species see table 1.

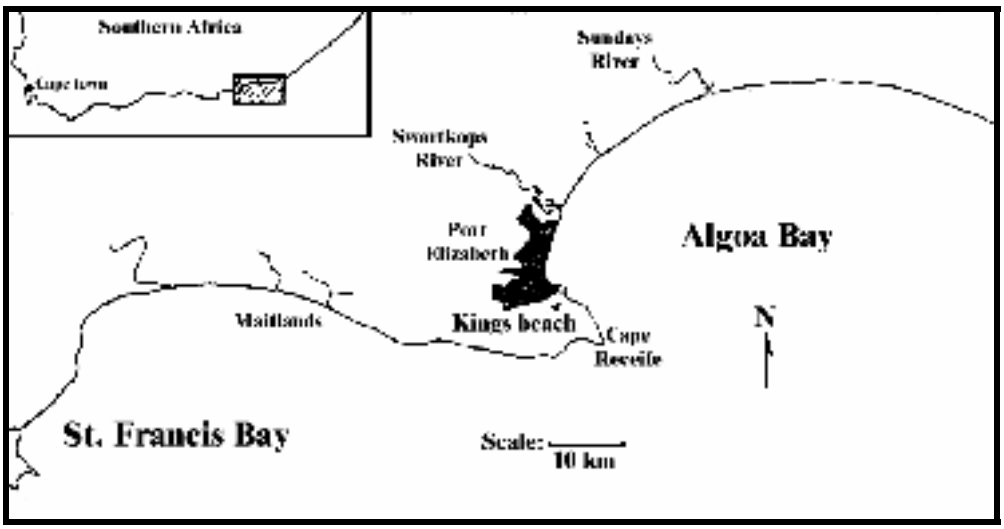

Figure 1. Algoa bay showing the location of the sampling site (Wooldridge 1983)

- **6.2.3. Material**

Holotype: SAM-A44230. Adult male lodged in the South African Museum, Cape Town. Collected in Algoa Bay, near Kings Beach, South Africa, 25 August 1981.

- **6.2.4. Derivatio nominis**

Dedicated to Carl Wittmann for his contribution to the knowledge of Mysidacea in the Indian Ocean.

Species	Abundance
Acanthomysis sp.	28
Doxomysis sp.	84
Gastrosaccus brevifissura	2
G. psammodytes	6
G. olivae	1
G. wittmanni	**6**
Mysidopsis bispinosa	1
M. major	277
M. schultzei	1
M. similes	1
Nouvelia natalensis	5
Rhopalophthalmus terranatalis	1
Siriella sp.	1

Table 1. Maximum abundance in m3 water of mysid species caught during a 2 year sampling programme. Data from Wooldridge (1983).

- **6.2.5. Description**

The morphological characteristics refer to both sexes, unless otherwise stated. Total length of adult females ranged between 6,0 mm and 10,0 mm; adult males between 5,8 mm and 6,4 mm. Range in length incorporates seasonal effects as temperature in summer (10-2-1981) and in winter (25-8-1981).

Carapace rather short, leaving the last thoracic somite exposed in dorsal view. Anterior carapace margin produced into a pointed rostrum, extending to the edge of the base of eyestalks (Figure 2A). Posterior dorsal margin of carapace deeply emarginate, each side of emargination split along the midlenght to form two lobes, one forwardly directed and the other backwardly directed. Lobes overlap each other.

Antennule (Figure 2B), first segment of peduncle almost twice as long as broad, equal in length to second and third combined. Three short setae on outer margin. Second segment short with three strong spines set obliquely along lateral margin distally. Third peduncular segment twice the length of the second, bearing a small hooklike process at the base of the outer flagellum. Outer flagellum swollen at the base and, in the male, fringed with a row of setae.

Antennal scale (Figure 2C) about three times as long as broad. Lateral margin straight, outer edge terminating in a strong spine that does not extend beyond the rounded apex. Inner margin with c. 19 jointed plumose setae. Setation on peduncle as shown (Figure 2C).

Mandible (Figure 2D) with three-segmented palp, proximal segment short, unarmed. Second and third segment bearing spinose plumose setae as illustrated, the third with a comb-like process at distal end.

Maxilla (Figure 2E) with large exopodite bearing thirteen plumose setae along outer border. Terminal segment of endopod similar in form to that of other members of the genus. Palp, coxal end basal endites heavily spinose as illustrated.

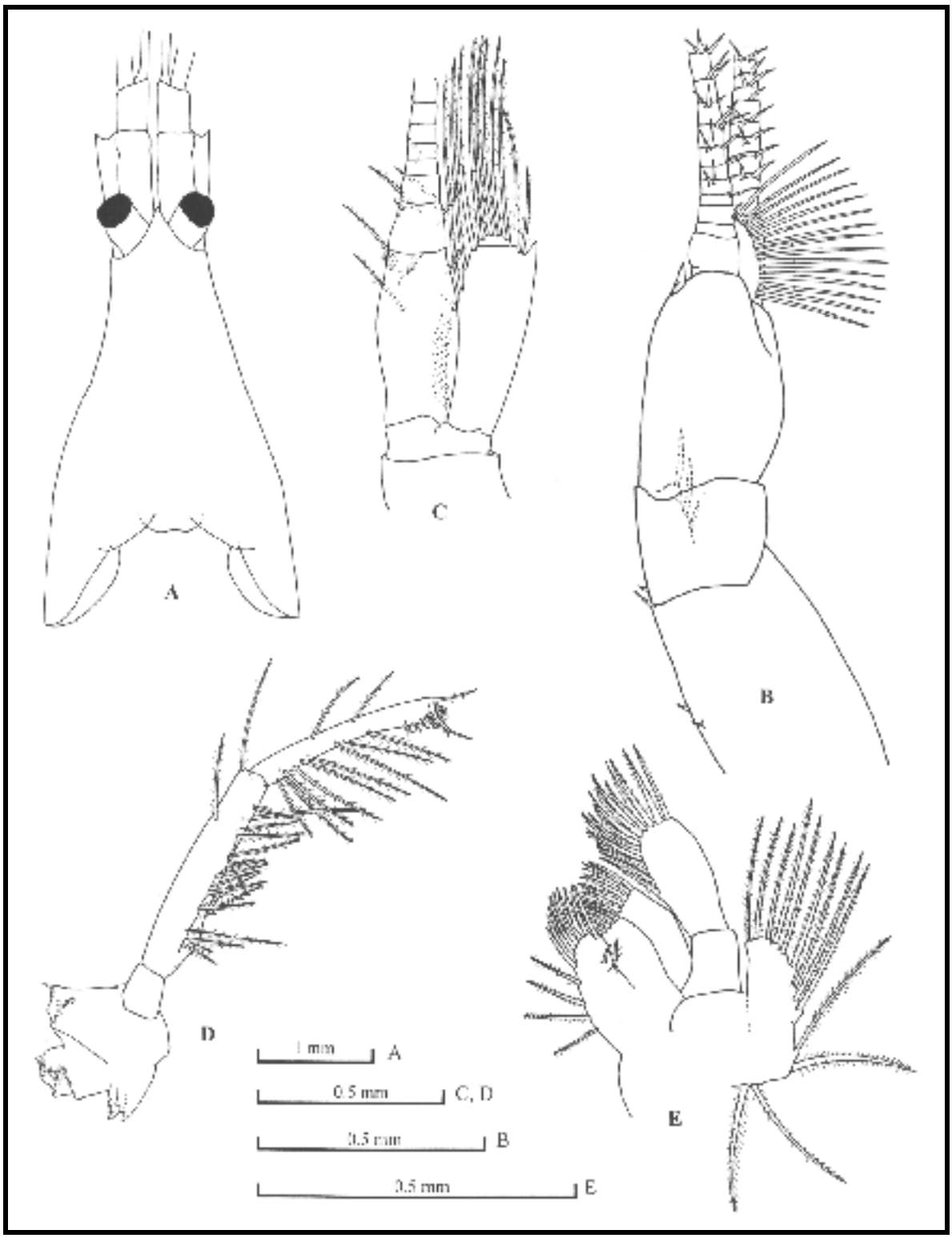

Figure 2. Gastrosaccus wittmanni sp. nov. A. Carapaces in dorsal view. B. Antennule. C. Antennal scale. D. Mandible. E. Maxilla.

Endopod of first thoracic limb (Figure 3A) short and densely setose, especially along inner lateral margin. Dactylus without claw. First exopod segment expanded, outer distal angle with a tooth (Figure 3B). Flagellum 12-segmented, each segment with two jointed long plumose setae.

Second thoracic limb similar in form to first. First exopod segment also with a small tooth on outer distal angle. Flagellum with 12 segments.

Third to eight (Figure 3C) thoracic limbs similar in form. Carpus and propodus fused and divided into 15 subsegments. First sub-segment small with one non-plumose seta. Second, third and fourth segments large with second and third equal in length and 2 to 3 times larger as fourth, bearing spines, plumose setae and small jointed setae as shown (Figure 3C). Each subsegment from the fifth to the fourteenth bears two long plumose setae, 1-2 spines and one small jointed seta with two setules.

First exopod segment on each limb expanded, armed with a small tooth on the outer distal angle. Exopod flagellum with c. 12 segments. Each segment with two long jointed plumose setae.

First female pleopod (Figure 3D) with long slender sympod armed with three proximal and three distal jointed long plumose setae. Exopod c. two times as long as broad bearing one terminal plumose seta with a joint. Endopod twice as long as wide, bluntly rounded at distal end and bearing 7 plumose setae, 2 of them with a joint and 5 non-plumose setae.

Second female pleopod (Figure 3E) in the form of an unjointed plate, nearly six times as long as the mid-with bearing 13 plumose setae. Ten of these setae are jointed and three of them unjointed and non-plumose. Remaining pleopods in female similar in form and size to second.

First male pleopod (Figure 4A) with swollen enlarged sympod; outer margin fringed with eleven jointed plumose setae. Endopod unsegmented, c. one-third length of exopod and three times as long as wide. Endopod armed with two terminal jointed plumose setae, two subterminal unjointed plumose setae and five non-plumose setae of which one is jointed. Exopod 7-segmented, each segment bearing two jointed plumose setae.

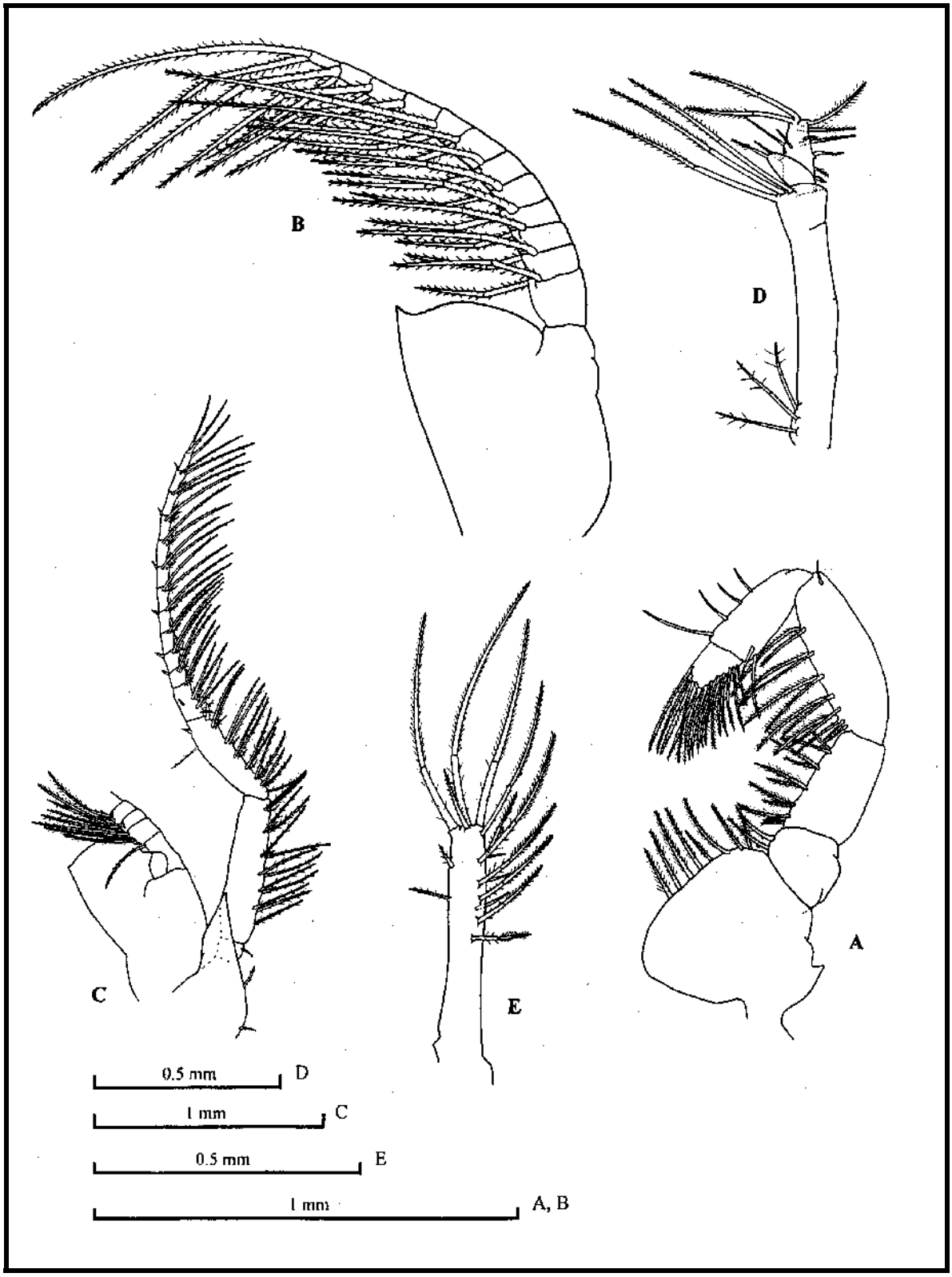

Figure 3. Gastrosaccus wittmanni sp. nov. A. Endopod of first thoracopod. B. Exopod of first thoracopod. C. Seventh thoracic limb. D. First pleopod of female. E. Second pleopod of female.

Second male pleopod (Figure 4B) with rectangular sympod. Endopod five-segmented and equal in length to sympod. A well developed lobe near base of first endopod-segment, armed with 3 small non-plumose setae and 3 long plumose setae. First segment armed with 3 small non-plumose setae and 3 longer plumose setae. Remaining endopod segments with two jointed plumose setae. Exopod of 8 segments and c. twice as long as endopod. On each exopod-segment two long plumose jointed setae.

Third male pleopod (Figure 4C) with 3-segmented endopod. First segment armed with 7 non-plumose setae and six plumose setae, of which two are jointed. Three of these setae on a lobe: one plumose and two non-plumose. Last endopod-segment with one long distally jointed plumose seta. Endopod two-thirds length of first segment of exopod. Exopod four-segmented, extending to proximal end of last abdominal segment. First three segments almost equal in length. Fourth segment half length of first. Fourth segment (Figure 4D) armed with one spine near distally end and distally two setae, one with a bifid apex and armed with two small spines on the inner margin.

Remaining pleopods in male similar in form. Endopod single-segmented. Exopod four-segmented in pleopods 4, 5 and 6.

Uropods (Figure 4E & 4F) extending beyond telson, exopod equal in length to endopod and bearing 16 strong regular spines along outer margin. These spines curved and finely plumose along the posterior margins. Endopod with 6 long spines spaced regularly among setae along inner margin. First spine located at posterior edge of statocyst. Two groups of plumose setae (3 & 4) near the base of the endopod as illustrated (Figure 4F). Outer margin of endopod with a row of plumose setae that increase in length posteriorly. A series of c. 11 fine plumose setae set among longer setae on outer endopod margin.

Telson (Figure 4G) c. three times longer than basal width. Lateral margins armed with seven strong spines. Six smaller spines interposed between large as illustrated. Apical spines c. twice length of the strong lateral spines. Cleft one-sixth length of telson and armed with c. 12 graduated spinules on either side.

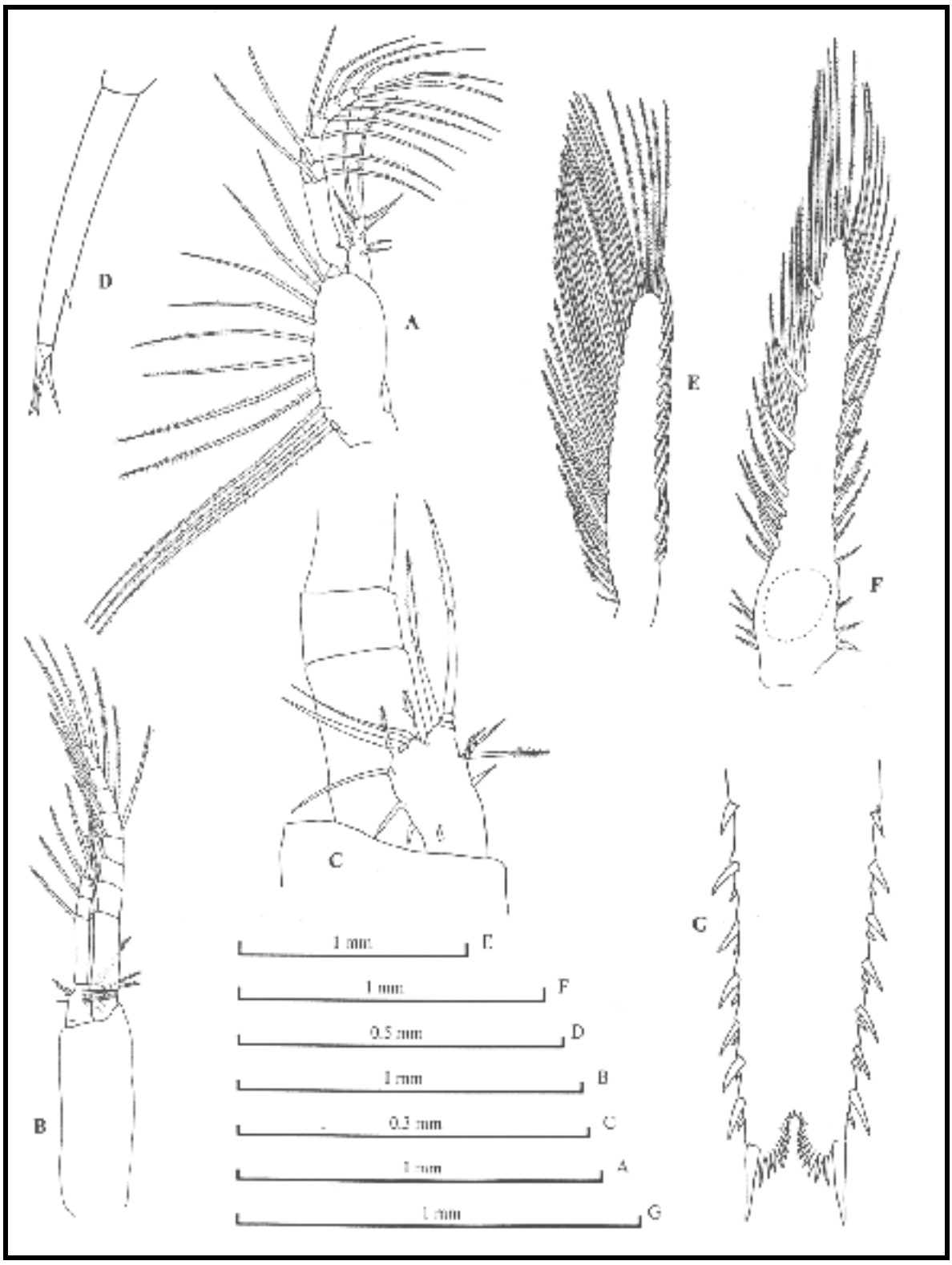

Figure 4. *Gastrosaccus wittmanni* sp. nov. A. First pleopod of male. B. Second pleopod of male. C. Third pleopod of male. D. Terminal exopod segment of third pleopod of male. E. Exopod of uropod. F. Endopod of uropod. G. Telson.

- **6.2.7. Remarks**

Gastrosaccus wittamanni, new species*,* is compared with other South African *Gastrosaccus* species in table 2.

Gastrosaccus wittmanni has closest affinities with *G. longifissura* Wooldridge, 1978 and *G. bispinosa* Wooldridge, 1978, both from the east coast of the African continent and *G. madagascariensis* Wooldridge, Mees and Webb 1997 from the coast of Madagscar. The number of lateral large spines on the telson of all four species is seven. There all also spinules in between the large spines (table 2).

A clear distinguishing character of *G. wittmanni* concerns the telson: the presence of small spinules between all large spines except the proximal pairs on each side. In the other species the spinules are mainly located between the distal spines.

Exopods of the thoracic limbs have small characteristic jointed setae in the present species as well as two small setules near the joint. In none of the other species the joint was described.

Another distinguishing features of *G. wittmanni* concerns the first female pleopod: the endopod bears just one terminal plumose setae. *G. madagascariensis* has a row of eight plumose setae, *G. longifissura* bears five plumose setae and *G. bispinosa* nine.

Species	G. wittmanni	G. bispinosa	G. dunckeri	G. brevifissura	G. gordonae	G. longifissura	G. olivae	G. psammodytes
Habitat	Subtidal	Subtidal	Coastal					
Carapace								
Length	Small	Large		Small			Short	Long
Rostrum	Blunt	Rounded, triangular	Short blunt	Short rounded	Sharp	Blunt	Short blunt	Long, round.	Blunt, short
Pleopod 1, male								
Exopod segments	7	10	9	5	0	5	10	6	___
Pleopod 2, male								
Exopod segments	6	11	9	5	0	7	10	6	
Endopod segments	6	6	7	7	8	5	10	6	___
Pleopod 3, male									
Length terminal spines	Equal	Equal	Subequal	subequal	Unequal	Unequal	Subequal	Subequal	___
Telson									
No. lateral spines	7	7	12-16	7	0	7	5-6	6	6
No. lateral denticles	6	7-8	2	1	30	5	7	6	0
Max. No. spinules between spines	1-2	5	7	1	6	4	2	6	0
Spines									
Terminal spines	Long, strong	Long, strong	Long	Long, strong	Long, robust	Long, robust	Long, strong	Long, strong	Long, strong
No. denticles	12-13	20-22	12?	3-5	25	23-26	24	16	22
Length/telson max.	0.17	0.25	0.14	0.1	0.35	0.21	0.18	0.17	0.5
Uropod									
Lateral exopod spines	16	14	15	12	14	16	14	14-15	16
Lateral endopod spines	6	7 + 2	17	5	10 + 2	7	5	7	8
Body length min:	5.8	11	9	11.5	9	8	9	9	14.2
Body length max:	10	17.5	9	12	9	10.5	11	6	14.3

Table 2. Key characteristics that distinguish Gastrosaccus wittmanni, G. bispinosa, G. dunckeri, G. brevifissura, G. gordonae, C. longifissura, G. namibensis, G. olivae and G. psammodytes. Data from Tattersall (1952), Tattersall (1958) Pillai (1964) Bacescu (1970), Wooldridge (1978) and Wooldridge & McLachlan (1987).

- **6.2.8. References**

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▪ 6.3. APPENDIX 3: *IDIOMYSIS MOZAMBICUS*, A NEW MYSID SPECIES (MYSIDACEA) FROM MOZAMBIQUE

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Published as: Deprez, T.; Wooldridge, T.; Mees, J. (2001). *Idiomysis mozambicus*, a new mysid species (Crustacea: Mysidacea) from Mozambique. Hydrobiologia 459(1-3): 47-49.

Key words: Idiomysis, mysid, Mozambique, nearshore

• 6.3.1. Abstract

Idiomysis mozambicus is described from coastal waters of Mozambique. The species can be distinguished from the other species of the genus by the one-segmented antennal scale, the two-segmented exopod of the fourth male pleopod, and the bluntly pointed rostrum.

• 6.3.2. Introduction

The genus *Idiomysis* (tribe Mysini) comprises three species to date. *I. inermis* Tattersal, 1922 was described from the Gulf of Manaar, India (Tattersall, 1922) and later also recorded and redescribed from Moreton Bay, Australia (Greenwood and Hadley, 1982). The other two *Idiomysis* species are *I. tsurnamali* Bacescu, 1973 from the Gulf of Elat, Red Sea, Israel and *I. japonica* Murano 1978 from the Nagasaki Prefecture, Japan.

Idiomysis mozambicus is the fourth species of the genus. Several specimens were collected from Nacala Bay, Mozambique in October 1997. Samples were taken after dark with a small hyperbenthic sled (50 x 30 cm) at a depth of approximately 4 metres. The bottom consisted of uneven rock and patches of sand.

• 6.3.3. Material

Holotype (SAM-A44966) lodged in the South African Museum, Cape Town. Adult female from Nacala Bay collected by T. Wooldridge October 1997.

Paratype material (23420) lodged in the Royal Belgian Institute of Natural Sciences. Two adult males and two adult females from Nacala Bay collected by T. Wooldridge, October 1997.

- **6.3.4. Description**

The morphological characteristics refer to both sexes, unless otherwise stated. Total length of adult females ranged between 2.6 and 2.9 mm (4 specimens); adult males measured 2.9 and 3.9 mm.

Carapace rather short, leaving the last thoracic somites exposed in dorsal view (Figure 1A). Anterior carapace margin produced into a bluntly rounded rostrum, extending in between the eyes up to two thirds of the length of the cornea (Figure 1B). Posterior dorsal margin of carapace deeply emarginate, distal lateral parts produced into wing-like extensions. Whether this is as a morphological characteristic or an artefact due to conservation in ethanol 70% is unclear (Figure 1A).

First segment of female antennular peduncle (Figure 1C) with a proximally extending lobe armed with two typical spines and one plumose seta. The segment also bears three other plumose setae. Second segment with a small lobe with two small non-plumose setae. Third segment twice as long as second and bearing eight setae, one of which is plumose; five of the non-plumose setae are located on the proximally extending lobe.

First segment of exopod wearing 5 long setae and 1 short seta. Antennular peduncle of male (figure 1D) with appendix masculina looking like hirsute lobe.

Antennal scale (Figure 1E) about two times as long as broad. Lateral margins curved, distal end rounded. Inner margin, distal end en distal third of outer margin armed with c. 21 plumose jointed setae.

Maxilla (Figure 1F) with small exopodite bearing seven short plumose setae along outer border. Terminal segment of endopod rectangular with nine plumose and two non-plumose setae. Global shape of maxilla and maxillule (lateral view) as illustrated.

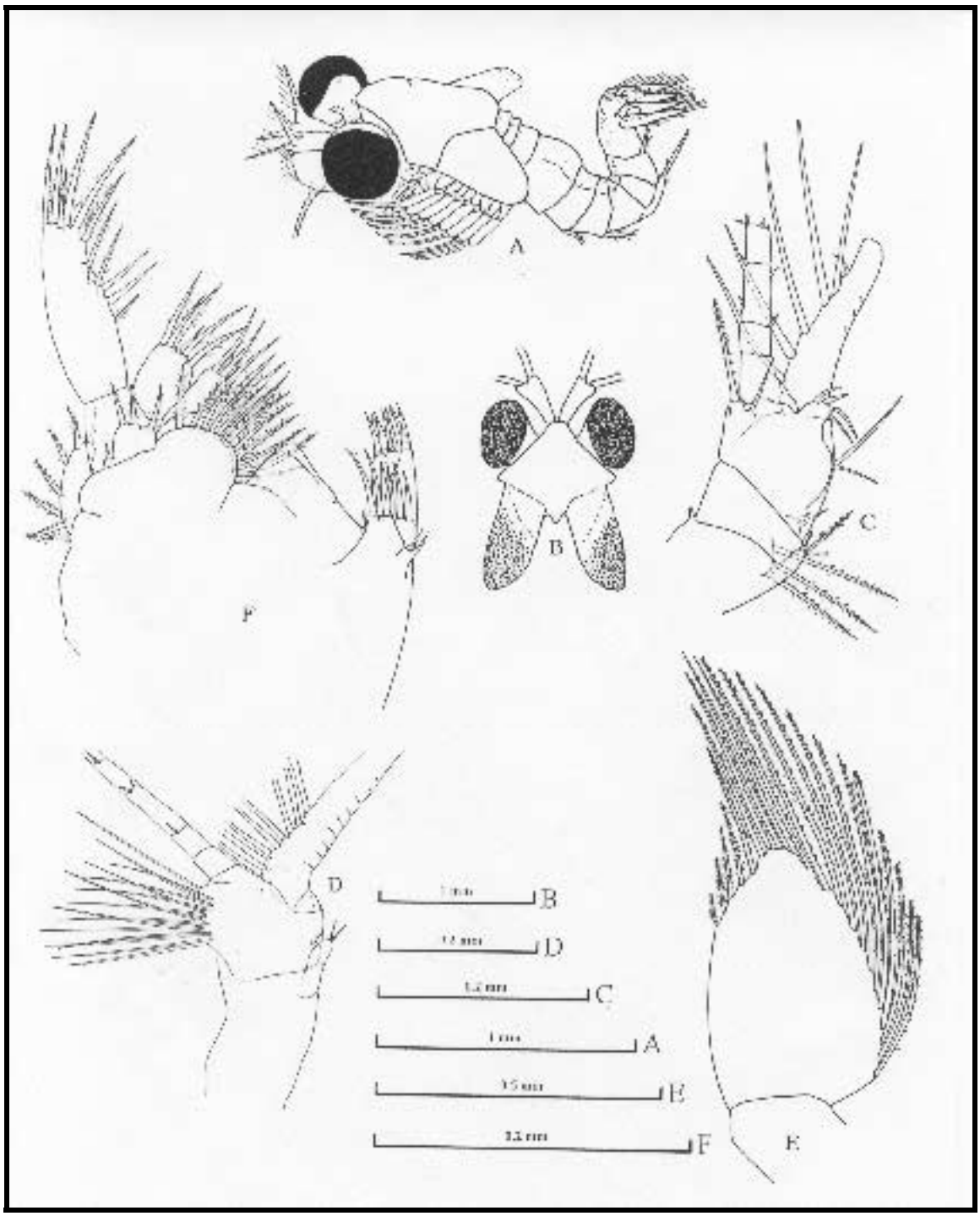

Figure 1. *Idiomysis mozambicus* sp. nov. A. Adult male in lateral view. B. Carapace in dorsal view. C. Antennular peduncle of female. D. Antennular peduncle of male. E. Antennal scale, F. Maxilla (with part of maxillule).

Endopod of first thoracic limb (Figure 2A) short and densely setose, especially along inner lateral margin. First segment of exopod expanded. Flagellum 7-segmented, first three segments non-setose, fourth segment bearing 1 plumose seta and last

three segments bearing two long plumose setae each. Second thoracic limb similar in form to first (not figured).

Third to eight thoracic limbs similar in form. First exopod is composed of eight segments, the others of nine segments. Proximal exopod segments armed with one long plumose seta, distal segments armed with two plumose setae (Figure 2B). Marsupium with two pairs of lamellae; lamella of eighth thoracic limb as illustrated in Figure 3A.

First, second, third and fifth pleopods in both sexes simple unjointed plates with 9 to 12 plumose setae (Figure 3B and Figure 3C). Fourth pleopod sexually dimorphic. Female fourth pleopod similar to other pleopods.

Male endopod small unsegmented plate with three terminal setae, one of which plumose, and a clear side lobe bearing four plumose setae. Male exopod consists of two segments: first segment bears one small non-plumose seta distally, second segment with small proximal setules and ending in a stout seta, approximately the same length as the segment (Figure 2C). When abdomen in normal bent posture, tip of exopod reaches to posterior borders of uropods.

Uropods (Figure 3D and Figure 3E) extending beyond telson. Exopod equal in length to endopod. Exopod setose all around, bearing c. 25 long plumose setae. Endopod also setose all around, with 18 long plumose setae. Endopod with four short plumose setae spaced regularly among the long plumose setae of the outer margin. Second group of three short plumose setae on the outer margin above statocyst.

Telson short, broad triangular plate, as broad as long, with bluntly rounded apex, smooth and unarmed, as in other members of the genus.

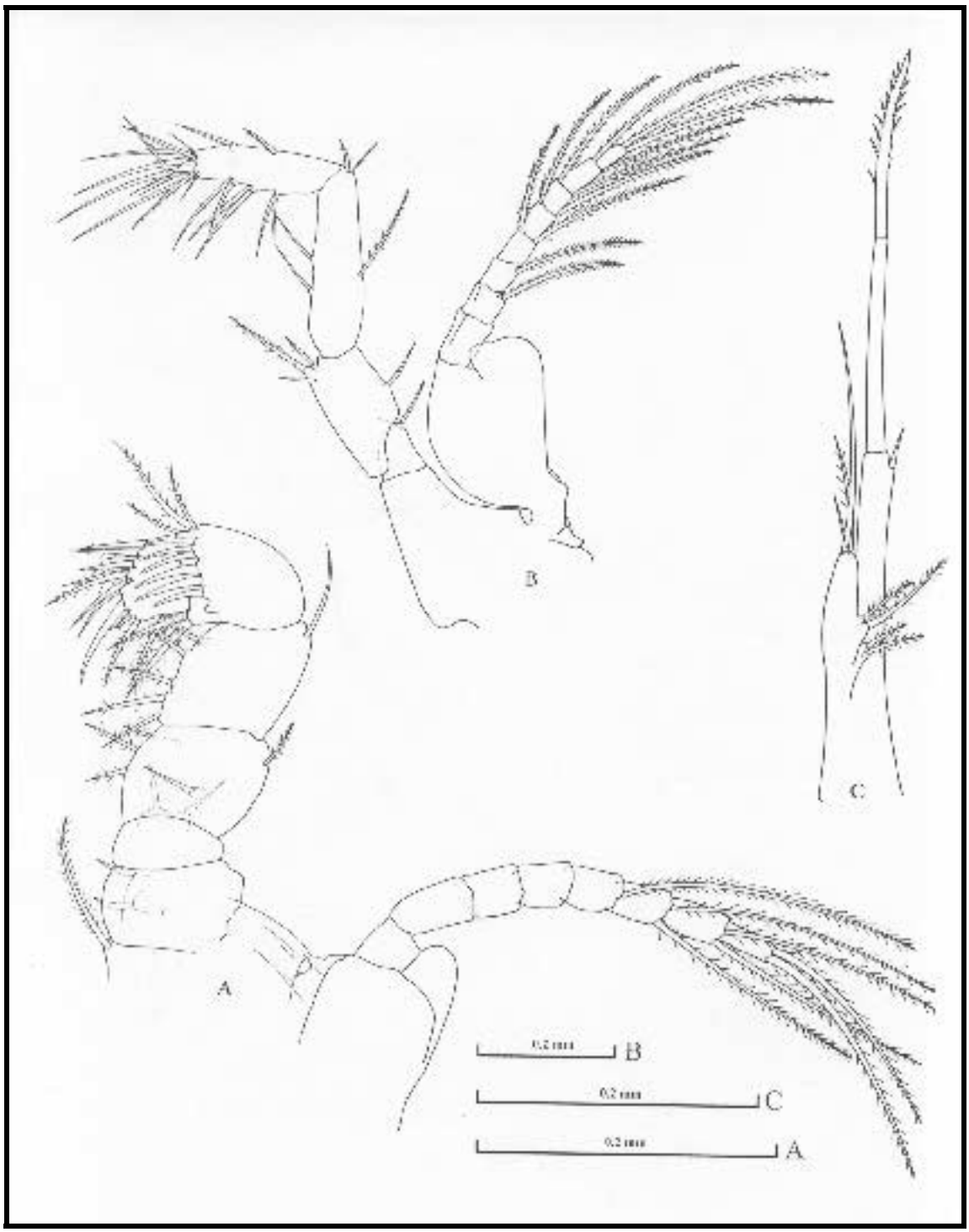

Figure 2. *Idiomysis mozambicus* sp. nov. A. First thoracopod. B. Sixth thoracopod. C. Fourth pleopod of male.

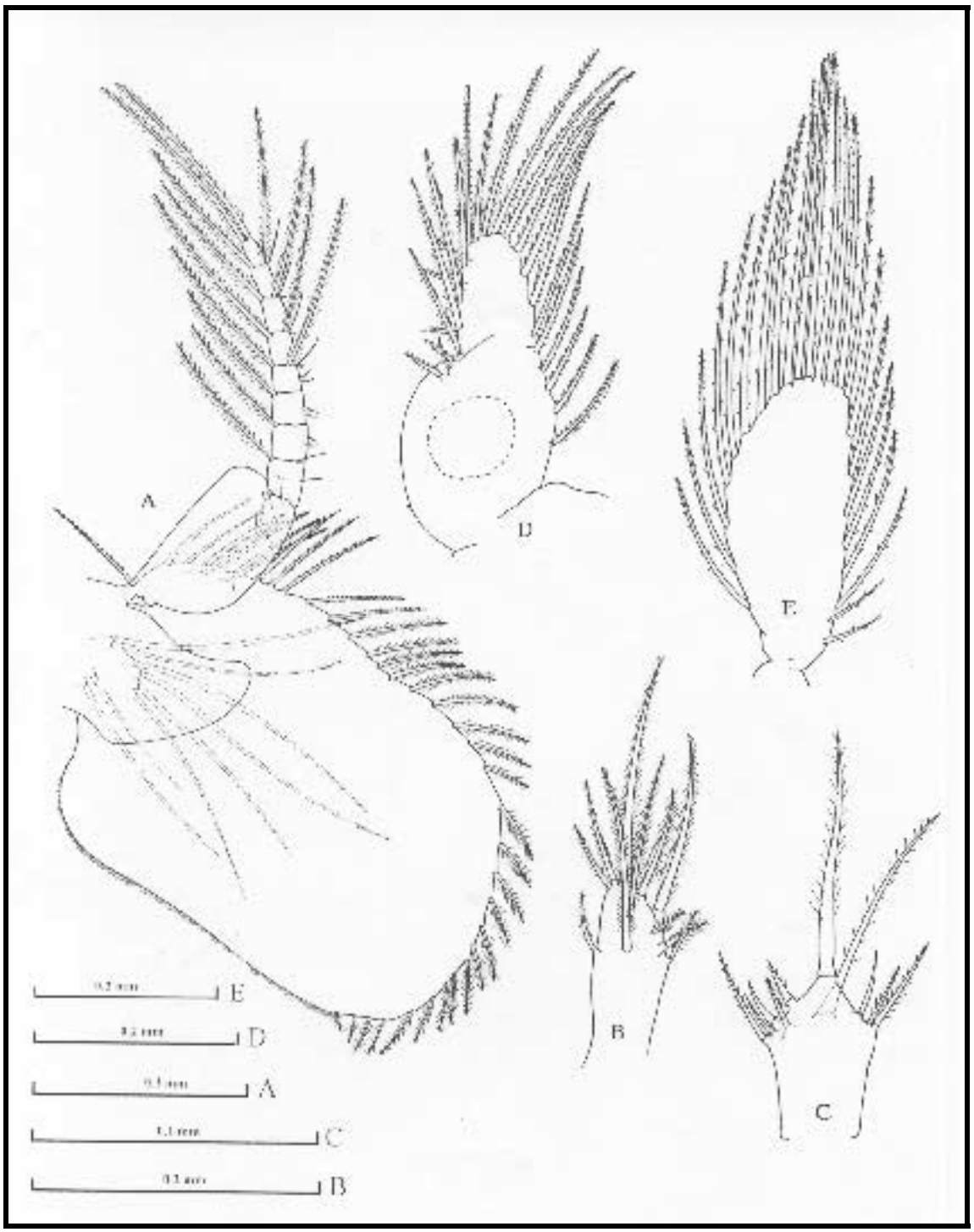

Figure 3. *Idiomysis mozambicus* sp. nov. A. Eight thoracopod in adult female with oostegite, B. Second pleopod in female. C. First pleopod in male. D. Endopod of uropod. E. Exopod of uropod.

- **6.3.5. Remarks**

The morphological characters that distinguish *Idiomysis mozambicus* from the other species of the genus mainly concern the antennal scale, the uropods, the fourth male pleopod and the rostrum.

The exopod of the fourth male pleopod consists of two segments in *I. mozambicus*, while in all other species of the genus there is only one. Another distinguishing characteristic is the female pleopod, which bears up to 11 plumose setae versus five to eight in other species.

I. mozambicus has closest affinities with *I. inermis*. The new species can easily be distinguished from *I. japonica* and *I. tsurnamali*: the antennal scale of *I. mozambicus* only consists of one segment, while there are two segments in *I. japonica*; in *I. mozambicus* the uropod rami are equal in length, while in *I. tsurnamali* the endopod of the uropod is distinctly shorter than the exopod. *I. mozambicus* can be distinguished from *I. inermis* by the shape of its rostrum: the rostrum of *I. mozambicus* is triangular and bluntly pointed, while in *I. inermis* it is clearly rounded.

- **6.3.6. Identification key for the species of the genus *Idiomysis***

1. - Antennal scale consists of two segments, endopod of uropod smaller in length than exopod → *Idiomysis japonica*

   - Antennal scale consists of one segment → 2

2. - Endopod of uropod equal in length than exopod → 3

   - Endopod of uropod smaller in lenghth than exopod → *I. tsurnamali*

3. - Rostrum triangular and bluntly pointed, exopod of fourth male pleopod 2-segmented → *I. mozambicus*

   - Rostrum clearly rounded, exopod of fourth male pleopod unsegmented → *I. Inermis*

- **6.3.7. References**

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CHAPTER 4 - MYSIDA BIOGEOGRAPHY PATTERNS

1. Abstract

The biogeography of Mysida has never been profoundly studied on a global scale. The Mysida database hosted on the NeMys biological information system brings a large amount of published distribution data together. This dataset is in this study used for testing the applicability of formerly published 'area models' and 'process models'. By using sample size independent statistical techniques and GIS analysis tools, the following observations can be made: there is a clear separation between Northern and Southern faunas, some genera have endemic distribution while few others have a global distribution (*Siriella*, *Gastrosaccus*, *Anchialina*, and *Boreomysis*), some regions have due to their physico-chemical characteristics or history typical distinct faunas, the 'Briggs' (1974) and 'Mauchline' (1980) area model fit well for Mysida distributions.

An additional analysis on the European area with additional data derived from the EurOBIS biodiversity data portal shows a clear North-South gradient in Mysida faunas. A few regions (e.g. Scandinavian seas, Black Sea and Mediterranean Sea) have a distinct taxonomic composition.

More data for both the global and the regional analysis would allow a much better understanding of the Mysida biogeography.

2. Introduction

Biogeography is the science attempting to document and understand spatial patterns of biodiversity. It studies present and past distributions of organisms (Brown & Lomolino, 1998). Studying the biogeography of a group, in this case the order Mysida, is trying to formulate answers to the following questions:

(1) Where do Mysida occur and why do they occur in this range?

(2) What makes Mysida live where they do and what prevents them from colonizing other areas?

(3) How did historical events play a role in the currently observed distributions?

(4) Why are there more species of Mysida in one area than another?

Biogeographical studies can be carried out on different levels (spatial range, taxonomic range). This depends on the aims of the study, the type of available data, the taxonomic level of the studied group … The current study aims to look at large scale patterns for the complete order over a long time.

Biogeography deals with patterns of distributions, and processes which lead to these patterns. The Darwin-Wallace dispersal paradigm, which assumes that taxa evolve from a point centre of origin and colonize a range matching their physicochemical optimal environment through a physical movement, is currently the most used theory explaining marine biogeography (Heads, 2005). Following this Darwin-Wallace paradigm, non-disjunctive distributions can easily be explained. The centre of origin may be found in the observed distribution range. However, disjunctive distributions are a topic of lively discussion. Non-disjunctive distribution ranges may be explained by for example historical tectonic events. The certainty that the observed distribution is the true realized distribution is a prerequisite. Moreover, sampling and research effort must be taken into account when interpreting taxon distributions.

The processes beneath biogeographical observed patterns can be classified in four groups:

- **Processes on a large spatial scale over a long period of time** (for example the earth's tectonic history). When using these processes, it is important to delineate a time frame. If the studied group appeared 20000 years ago, it is irrelevant to consider tectonic events of the last 10 million. Traditionally, the age of a group is estimated based on fossils (Donovan & Paul, 1998). A fossil-derived age should be considered as an indication of the minimum age (Rhodes, 1979). More recently, molecular clocks offer a valuable alternative for age determination of a species. Although regularly used, the correctness of the estimated age depends largely on the calibration of these molecular clocks (Palumbi, 1997). For the Mysida, fossil recordings are reported for 14 genera. Two of these genera currently still exist (*Siriella* and *Paramysis*). Most specimens date from the Callovian (between 160 and 165 million years ago). Events starting from the late Jurassic can be used to explain the Mysida distributions.

- **Processes on a large spatial scale actually occurring** (for example major oceanic currents). Most physico-chemical global processes are well described for the marine environment. They form the basis of currently widely used area models, such as the Large Marine Ecosystem concept (Sherman *et al*., 1992) and the biogeographic zones delineated by Briggs (1974). Variations in surface sea temperature and salinity, global oceanic currents, seasonal fluctuations in primary production, and several other processes were used to define the borders of a series of biogeographic provinces. These provinces are also reflected by typical faunal compositions. For Mysida, any of these models were tested yet.

- **Processes on a small geographic scale over a long period of time** (for example the forming of an isthmus, or sea level rises). The definition of a 'small geographic' scale depends strongly on the area or observed process. Typical processes fitting this group are the formation of an island, the forming of a sea, or the closing of an isthmus. Although the underlying reason for these processes may be a large scale tectonic event, just one geographical area with typical distinct characteristics is taken into account. These processes may explain high rates of endemism in semi-enclosed or formerly

enclosed marine areas. Two typical examples are the Red Sea (Longhurst, 1998) and the Mediterranean Sea (Pérés, 1967; Briggs, 1974), both recognised as areas with high levels of endemism.

- **Ongoing processes on a small geographic scale** (for example the influence of a river mouth). These processes can only be used to explain short term, regional patterns. They may explain the reasons for the presence or absence of a species in typical habitats. The presence of mangroves for example has a large impact on the species composition of an area. Duke (1995) states that the complexity of these habitats leads to higher species richness. Similar patterns are found for corals and sea grasses (McCoy & Heck, 1976). For this study, the available dataset does not contain enough short term observations. Habitat ranges of particular species or groups of species will not be studied.

Based on biogeographic observations of different groups of taxa, biogeographic models have been constructed. Two types of models are distinguished: 'area' models and 'process' models. **Area models** consider the partition of the earth's seas. Some frequently used models are: (1) Briggs coastal areas (1974), Longhurst's marine provinces (1998), Large Marine Ecosystems (Sherman *et al*., 1996), WWF marine ecoregions (http://www.worldwildlife.org). For Mysida, Mauchline and Murano (1977) defined another, consisting of 13 large regions. Similar to this last area model, taxon specific models have been constructed for a vast number of taxa (for example the Clupeidae marine provinces (Rosa & Laevastu, 1959)).

Process models try to explain distribution patterns, often visualized by an area model. A widely used model is the Island equilibrium theory (MacArthur & Wilson, 1967). This theory explains the faunal taxon richness variations in geographic disjunctive areas, often called 'islands'. Although this theory has strongly influenced the understanding of many distribution patterns, current research shows this model to be too simplistic and the need for a new better model (Lomolino, 2000).

Heads (2005) summarizes large scale process models at the one hand as traditional Darwin-Wallace dispersal models, and on the other as pangeographical

models. The first models assume a centre of origin and dispersal mechanisms. In this context, dispersal mechanisms should not be interpreted as the movements of individuals away from a certain point. Passive large scale movements, caused by physical changes such as tectonic events (see above), should however be taken into account. The second series of models (pangeography) explains the observed patterns, through vicariance or allopatry without a center of origin. The latter group of theories are currently most considered in marine biogeography. Vicariance may also have played a role, although most likely on a smaller geographic scale (Whittaker, 1998).

During the last decades, the analysis of distributions of taxa has become popular. However, the used methodologies differ a lot. Most studies start from occurrence data. These data may be extracted from literature or derived from research datasets. Global scale analysis mostly use published occurrence data. Occurrence data on taxa is progressively made available on a number of biodiversity portals, such as GBIF (http://www.gbif.org – Global Biodiversity Information Facility) or OBIS (http://www.iobis.org – Ocean Biodiversity Information System) (see also chapter 1). Global biogeographical analyses on these kind of data have been carried out already for a number of groups (Briggs, 2006; Proches & Marshall, 2001; Lambshead & Boucher, 2003; O'Hara & Gary 2000; Glasby & Alvarez, 1999; Proches, 2002). For the majority of groups, especially marine taxa, no studies emphasising on global biogeography have been published so far. The main reasons for this hiatus are relatively clear: few global geographical oriented data-sets do exist and analyses on a global scale were impossible, due to the lack of technology (databasing techniques, statistical analysis of large datasets, GIS-software).

The Mysida were never thoroughly analysed on a global scale from a biogeographical perspective. One attempt was provided by Mauchline (1980). In addition, global checklists, as published by Gordon (1957), Mauchline & Murano (1977), and Muller (1993), give some information on the biogeography of several species. Mauchline (1980) mentions in his chapter on geographical distribution that the incompleteness of data concerning geographical occurrences of taxa, makes mapping of taxa of limited value.

Mysida are a rather special group of Crustacea, as they lack larval planktonic phases. The larval development takes place in the marsupium and juveniles leave mostly when they are able to swim. This reproductive strategy limits the passive dispersal capacities and therefore such may limit the geographical range of a species. Although no true global studies are published yet, many studies have been published focussing on the fauna of small regions (British waters: Tattersall & Tattersall, 1952; Indian waters: Pillai, 1965; Japan: Ii, 1964). Most of these works give a detailed overview of the local fauna, although do not describe the underlying reasons for the observed distributions.

A global dataset, extracted from publications, will be used in this study. Both area and process models will be applied. Different area models will be tested, and some published process models will be used to explain the observed distributions. Due to the limitations of the dataset, no species- or genus- specific conclusions concerning their occupied niches or habitats will be drawn.

3. Materials and methods

An overview of the used data and methodologies are listed below.

▪ 3.1. AVAILABLE DATASET

The data used for this work was extracted from two sources: (1) the NeMys – Mysida dataset and the (2) EurOBIS biodiversity web portal (http://www.marbef.org/data). The NeMys dataset contains 9185 records for a total of 726 species belonging to 126 of the 162 described genera. All subfamilies are represented in this database.

The NeMys dataset uses data extracted from published literature sources. Data was extracted from a total of 420 literature sources, most of them with a taxonomical or biogeographical scope. The following regional reviews were included: Black Sea & Mediterranean Sea - Bacescu, (1954); North East Pacific Ocean - Banner (1948); the Caribbean area - Brattegard (1970) and Brattegard (1973); Indian Ocean – Hansen (1910), Pillai (1965) and Pillai (1973); open Atlantic Ocean – Hargreaves (1985); Japan – Ii (1964); South Africa – Tattersall (1952); North Sea and British coastal waters – Tattersall & Tattersall (1951a); Western Atlantic Ocean – Tattersall (1951b); Scandinavian area – Zimmer (1909). Only few literature sources on ecological topics are currently available in the dataset. 'Grey' literature (like Ph.D. theses or research reports) is not included yet.

The EurOBIS dataset was taken into account for analyses on the Mysida fauna of European waters. Although 5623 records were downloaded from the OBIS portal, only 986 were usable. Many records lacked details on lower identification levels (no genus name reported, no species name given) and could as such not be used. Other data in the EurOBIS dataset was extracted from the NeMys Mysida database and was consequently a duplication of the already available data. After taking out all duplicated values and incomplete records, data of 56 species belonging to 24 genera were retained.

For both datasets doubtful records (i.e. records with strange location parameters – for example records on land, latitudes higher than 90°, 0° longitudes and latitudes) were eliminated.

Common data-fields in both the NeMys and EurOBIS dataset are: Latitude – in decimal degrees, Longitude – in decimal degrees, Species data – split up in two fields: NeMys-species number and NeMys species name, Genus data – split up in two fields: NeMys-genus number and NeMys genus name.

The NeMys dataset contains some more additional data, which might be useful in understanding some of the presented results: (1) year of publication, (2) the literature source used, (3) unique number of the location.

▪ 3.2. GLOBAL DATA ANALYSIS

• 3.2.1. Latitudinal gradients:

The first global analysis investigates latitudinal gradients in two ways: (1) by analysing the number of species or/and number of genera in 10 degree latitudinal classes, (2) by examining the latitudinal range of genera separately. Additional information, in order to understand the impact of sampling effort, on the number of sources published and the number of locations is also presented.

The average taxonomic distinctness (Delta+) and the variation of average taxonomic distinctness (Lambda+) were calculated for each latitudinal range (Warwick & Clarke, 1995). Equal step lengths between each taxonomic level were assumed. The path length between two species connected only at the highest taxonomic level is set to 100 (Clarke & Warwick, 1999). Six taxonomic levels were used: Order, Family, Subfamily, Tribe, Genus and species. These diversity indexes allow having a sampling-effort independent view on the diversity of a certain area. Funnel plots displaying the 95% probabilities for different numbers of species are plotted together with the calculated values. If the 'Delta+' value of a region is higher than the 95% probability, this can be interpreted as the region to be taxonomically more diverse than was to be expected. If the value is lower, the region is less taxonomically diverse. Similar plots are made for the variation in taxonomic

distinctness (Lambda+). Regions with a high 'Lambda+' value have a large number of monospecific genera, or monogeneric families. Both diversity indices (Delta+ and Lambda+) offer a way to interpret diversity without taking into account the number of samples (strongly related with research effort)

- **3.2.2. Grid-based diversity and richness analysis:**

The freely available software package Diva-GIS (Hijmans, 2005 - http://diva.riu.cip.cgiar.org/) was used for these analyses. It allows the calculation of common biodiversity indices (see below), in a visual GIS based environment. The software was developed for terrestrial, botanical purposes. Some possibly interesting features (for example climate based area predictions) could not be used. The package basically allows adding map layers of different formats (Esri© shape files or MsAccess©-linked point files) and performs calculations on layers separately or sets of layers. Most analyses are done with user-defined overlaying grids. Results of these calculations are displayed by colour gradients. Calculated grids can be saved as new layers, and included in new analyses.

Calculations on taxon richness result in grids with numbers of taxa for each grid cell. The option 'circular neighbourhood' was used in all analyses, meaning calculations are not done on squares with arbitrary borders, but through circles with its centre in the centre point of each grid cell and with a specified radius (Bonham-Carter, 1994 and Cressie, 1991). This method produces smoother surfaces than analysis done with the 'simple' method (points on borders are assigned to one cell, the value of a point in a cell is assigned to only that cell irrespective the distance to neighbouring cells, results are related to the grid definition: slight changes in grid properties may result in clearly different results) (Heijmans *et al*., 2005).

Taxon diversity for each grid cell was expressed as the 'Shannon' diversity index (Shannon & Weaver, 1949; Magurran, 1988). The number of locations in each cell is used as the number of records for calculation of the index.

'Richness' and 'diversity' calculations were done on both genus and species level. A second circular neighbourhood analysis was carried out on the grid produced by the first analysis. The image based on this second neighbour joining abstraction, lowers

the importance of rich areas with surrounding poor areas and raises the value of areas with equal or richer surrounding areas. The granularity of the image is rougher at first sight. It however shows much clearer larger regions of high importance.

Additionally, richness analyses were carried out for the number of literature sources and the number of locations. A correlation was calculated between the number of literature sources (as a measure for research effort) and the number of observed species. The correlation was based on a 20 degree squares overlay. This correlation and richness plots for literature and locations may help to understand the by-effect of sampling and research effort.

By means of these analyses some areas of high richness and/or diversity were delineated. They were used in faunal similarity analyses.

▪ 3.3. TESTING GLOBAL BIODIVERSITY MODELS

A series of global biodiversity models were compared with Mysida distributions. Grids grouping the stations were treated as stations in which taxa occur. Regional taxonomic composition lists for each tested biodiversity model were made. The provinces described for each model are stored in Arcview shape files by separate polygons. With Arcview 3.2, an intersection is made of these polygon-shape files (each biogeographical area is represented by a polygon) with the distribution records imported as point-shape files. This results in lists of taxa for each province. These lists are used to analyse the taxonomic composition of each area.

A list of all taxa found in each region is made and checks on the uniqueness of the fauna for each region is being checked. This analysis is done on genus level by creating cross-tables (tables with regions as column heads, taxa as row heads and number of species as values) (see appendix 1-4). These derived cross-table datasets were used as inputs for a nonmetric multidimensional scaling analysis (nMDS) based on faunal similarities. The nearer areas are plotted in these analyses, the more similar is the faunal composition of the areas. When all areas are spread over the total plot, and similarities between the regions are low, this may be

interpreted as a fit of the model with the observed Mysida distributions. Cluster analysis plots were used as a second way to visualize similarities between areas.

The regions delineated in the diversity and richness analysis (see above) are tested similarly. A grid with the faunal composition of each grid cell is calculated (5°) and an indicator of the region in which the grid-cell is placed is added. A similarity based nMDS allows analysing the taxon composition similarity of all grid cells and gives an idea of the faunal composition of each area. Together with the similarity analysis an Analysis of Similarity (ANOSIM) is carried out. This analysis gives a numerical value of the similarity between regions.

All biogeographical models were also tested on their taxonomic compositions. Therefore the average taxonomic distinctness (Delta+) and variation of average taxonomic distinctness (Lambda+) were calculated for each region (Warwick & Clarke, 1995) (see above). All taxonomic diversity analyses and nonmetric multidimensional scaling analyses were done with PRIMER v5.2.9 (Clarke & Gorly, 2001).

For each biogeographical model a series of diversity and richness indices were calculated also by means of PRIMER v5.2.9:

(1) Number of species 'S' = 'species richness'

(2) Margalef's index of total species diversity (1958) as 'd'

$d=S-1/\ln N$, where N stands for the total number of species,

(3) Shannon's index of individual species diversity *H'*

$H'=-\Sigma (n_i/N)*\ln(n_i/N)$ (Shannon & Weaver, 1963),

(4) average taxonomic distinctness as 'delta+',

(5) variation in taxonomic distinctness as 'lambda+'.

The following area models were tested:

(1) Large Marine Ecosystems: Large Marine Ecosystems (LMEs) are regions of ocean space reaching from coastal areas (*e.g.* river basins and estuaries) to the seaward boundary of continental shelves and the seaward margins of coastal current systems. They are relatively large regions (> 200 000 km²) and characterized by bathymetry, hydrography, and productivity. The LME concept was launched after the 1992 Earth Summit (UNCED, Rio de Janeiro, 1992) as one of the ways to halt, and even reverse, the deterioration of coastal waters. In total 64 areas were delineated. Figure 1 shows all areas (after http://www.edc.uri.edu/lme/default.htm; Sherman *et al*., 1992).

(2) World Wildlife Fund Marine Ecoregions: This model represents 43 global marine ecoregions sharing a large majority of their species, dynamics, and environmental conditions. The data set contains the marine ecoregions of the 'Global 200' ecoregions. 'Global 200' ecoregions are a collection of the Earth's most biological diverse and rich terrestrial, freshwater, and marine habitats. World Wildlife Fund Marine Ecoregions provide a global view of marine ecoregions defined by the World Wildlife Fund Conservation Science Program 2001 (http://www.worldwildlife.org) (figure 2).

(3) Briggs biodiversity model: Briggs divided the global marine coastal waters in 37 distinct regions. Open water zones are treated separately. As Mysida are described in essence from coastal regions (Mauchline, 1980) only the coastal (continental shelve) zones were taken into account. The division is mainly based upon temperature and oceanic current patterns. For each area also zoological data is provided (figure 3).

(4) Mauchline Mysida Ecoregions: Mauchline & Murano (1977) published a world list of Mysida. In this work they present a division of the world seas in 13 large regions (figure 4). Mauchline (1980) retakes this division, although smaller sub-regions as the Red Sea and the Mediterranean are not considered as separate parts. In both publications, each region is documented with numbers of species, typical species, and immigrant species from surrounding areas.

The model of Longhurst (1998) was not tested. Except for the oceanic regions, it is almost equal to the model defined by Briggs (1974). The number of oceanic records is too low to give reliable results.

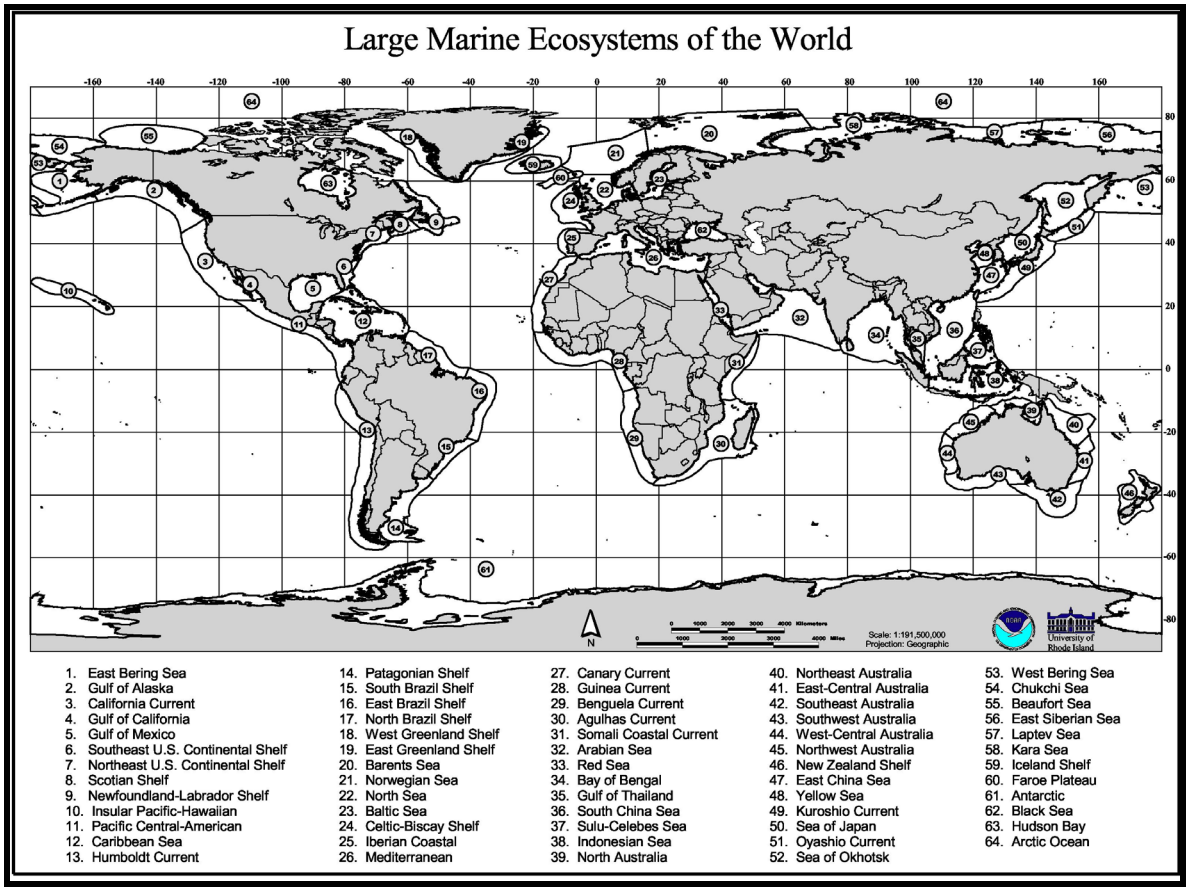
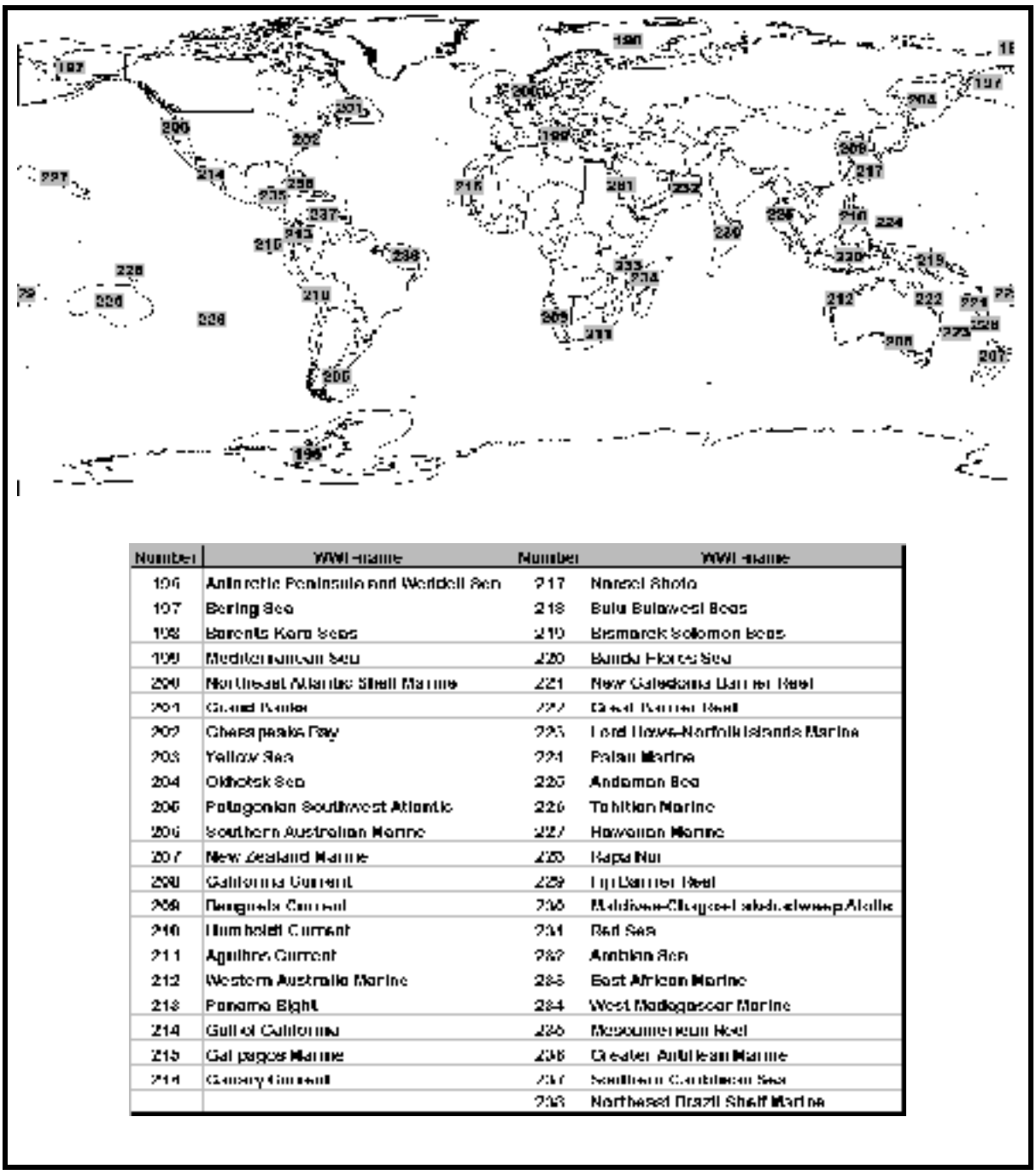


Figure 1. Large Marine Ecosystems of the world (after http://www.edc.uri.edu/lme/default.htm)



Number	WWF name	Number	WWF name
106	Antarctic Peninsula and Weddell Sea	217	Nansei Shoto
107	Bering Sea	218	Sulu Sulawesi Seas
108	Barents Kara Seas	219	Bismarck Solomon Seas
109	Mediterranean Sea	220	Banda Flores Sea
200	Northeast Atlantic Shelf Marine	221	New Caledonia Barrier Reef
201	Grand Banks	222	Great Barrier Reef
202	Chesapeake Bay	223	Lord Howe-Norfolk Islands Marine
203	Yellow Sea	224	Palau Marine
204	Okhotsk Sea	225	Andaman Sea
205	Patagonian Southwest Atlantic	226	Tahitian Marine
206	Southern Australian Marine	227	Hawaiian Marine
207	New Zealand Marine	228	Rapa Nui
208	California Current	229	Fiji Barrier Reef
209	Benguela Current	230	Maldives-Chagos Lakshadweep Atolls
210	Humboldt Current	231	Red Sea
211	Agulhas Current	232	Arabian Sea
212	Western Australia Marine	233	East African Marine
213	Panama Bight	234	West Madagascar Marine
214	Gulf of California	235	Mesoamerican Reef
215	Galapagos Marine	236	Greater Antillean Marine
216	Canary Current	237	Southern Caribbean Sea
		238	Northeast Brazil Shelf Marine

Figure 2. Marine WWF ecoregions

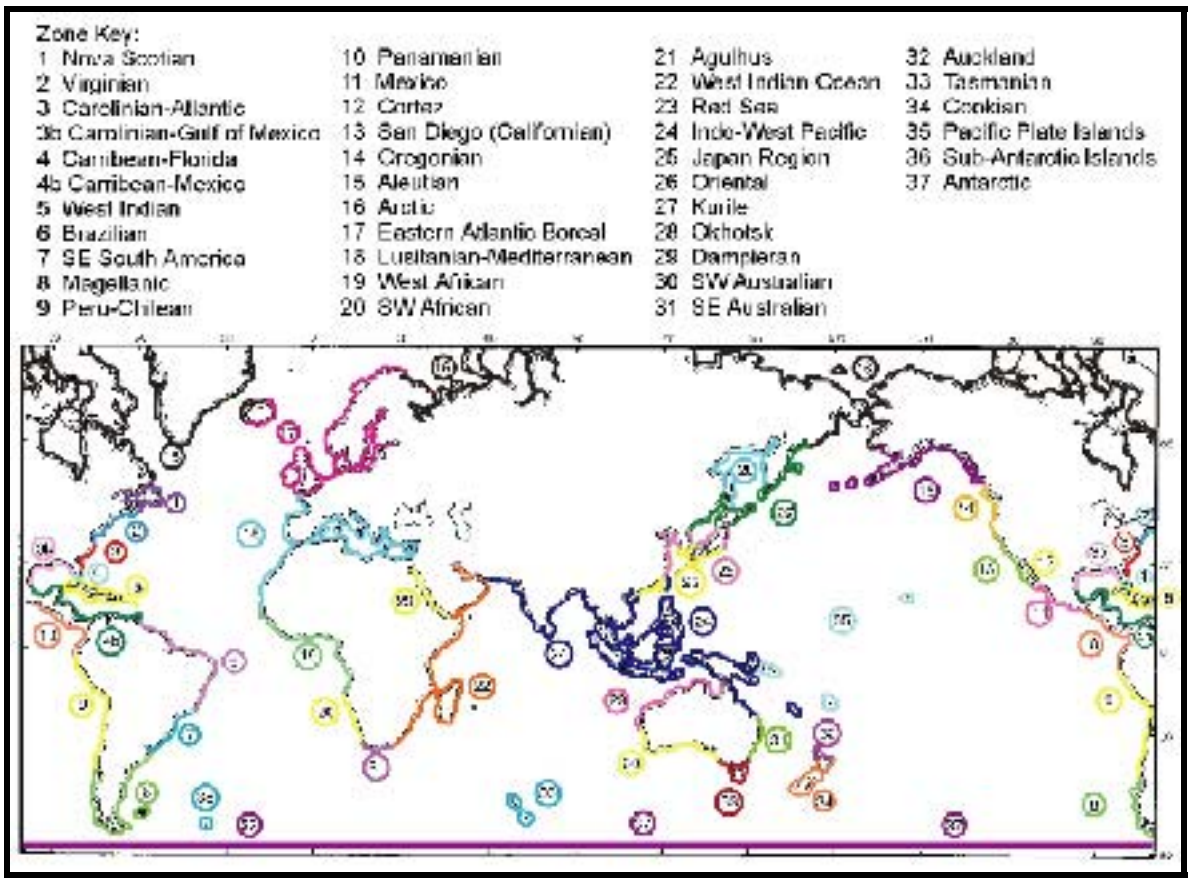


Figure 3. Biodiversity zones according to Briggs (1974)

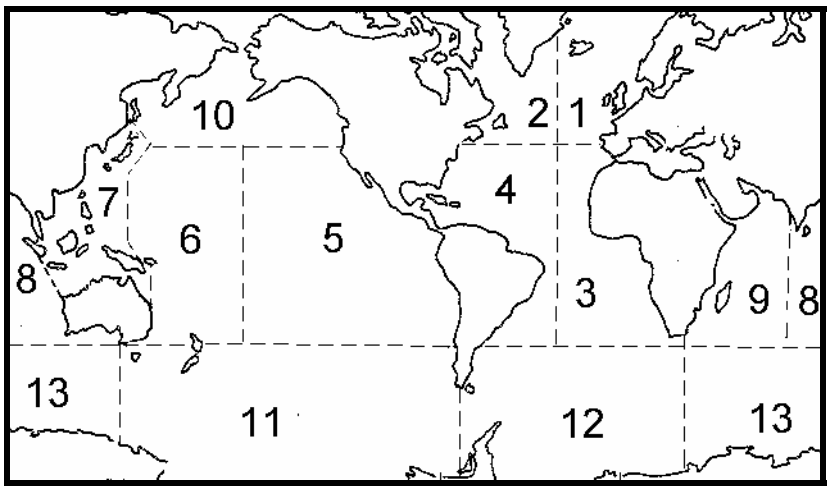


Figure 4. World map showing the areas as defined by Mauchline (1980) concept. (1: North East Atlantic, 2: North West Atlantic, 3: East Atlantic, 4: West Atlantic, 5: East Pacific, 6: West Pacific, 7: Australasian, 8: East Indian, 9: Western Indian, 10: North Pacific, 11: South Pacific, 12: South Atlantic, 13: South Indian) (adopted from Mauchline & Murano, 1977)

▪ 3.4. REGIONAL ANALYSIS – EUROPE

The European dataset was tested similarly as the global dataset. Species diversity and species richness was calculated for an overlaying grid of 2°. The European region is divided into 29 marine areas based upon the 'World seas' database. This database represents the boundaries for the major oceans and seas of the world. The source for the boundaries is the publication 'Limits of Oceans & Seas, Special Publication No. 23' published by the IHO in 1953. (http://ioc.unesco.org/oceanteacher/resourcekit/M3/Formats/Geography/OceansSeas.htm). The database was made available by VLIZ (http://www.vliz.be).

All marine areas in this area model were compared on faunal composition by calculation of diversity indices, by examining the similarities in faunal composition through nMDS and cluster analysis and by analysing the taxonomic composition (average taxonomic distinctness and variation of average taxonomic distinctness) (see above).

4. Results

▪ 4.1. GLOBAL ANALYSIS

• 4.1.1. Measuring the sampling effort

It is of major importance to have an idea of the influence of the research effort on the observed biogeographic patterns. Figure 5 plots the richness of locations for each 5 degrees cell, of which species data was entered, on a grid overlaying the world. The darkest cells represent up to 140 sample locations per cell. The sampling effort for each region can also be expressed as the number of publications published on a specific region. Figure 6 gives a 5 degree grid-plot of the number of publications for each grid cell. A similar pattern for number of locations and number of publications is observed.

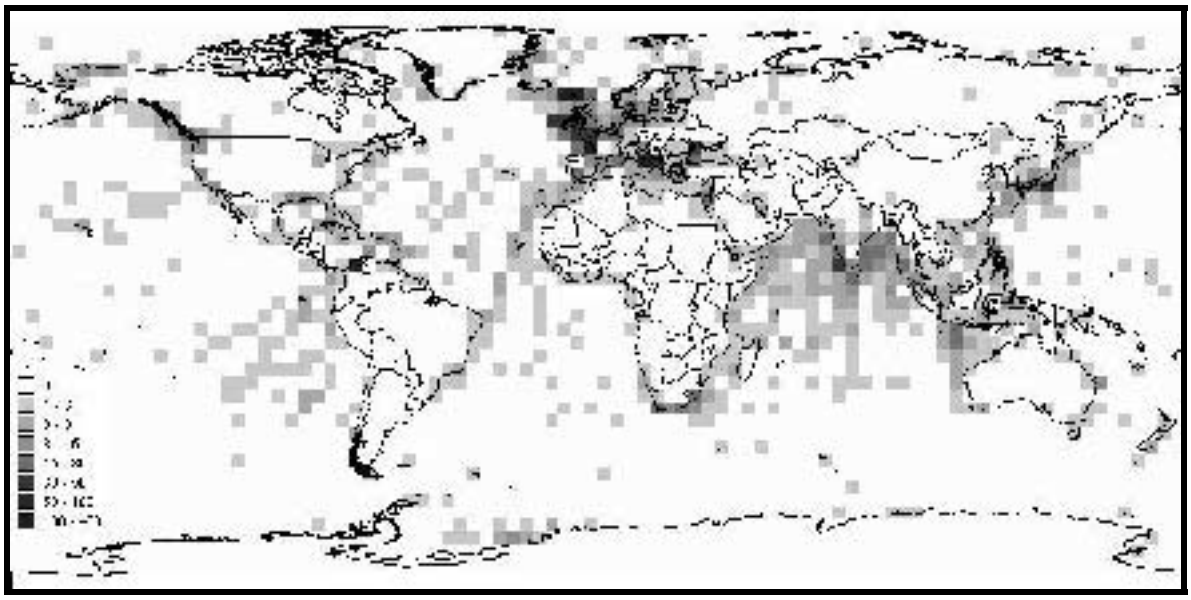


Figure 5. Global plot of richness of sample locations in a 5° grid

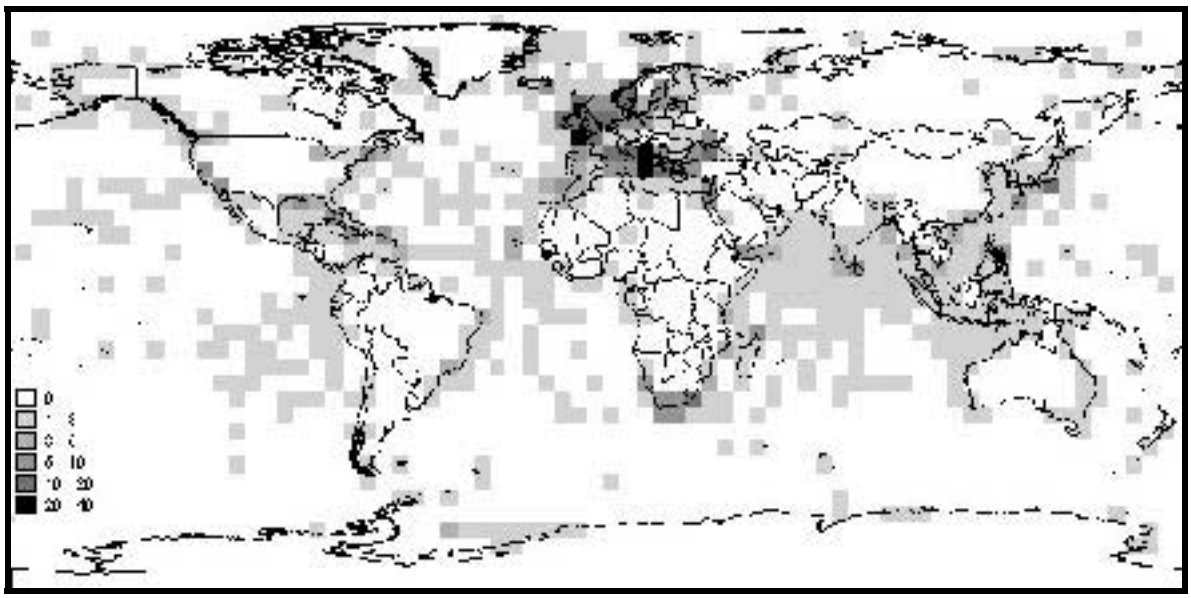


Figure 6. Richness plot of used sources representing the research effort in each area (5° grid)

A correlation was calculated between the number of literature sources for a region and the number of observed species (figure 7). The number of species and sources were extracted for each 10 degrees latitudinal zone. A linear correlation is found. Each species recorded corresponds with about two literature sources. An analysis taking into account the types of literature would possibly give a more nuanced picture.

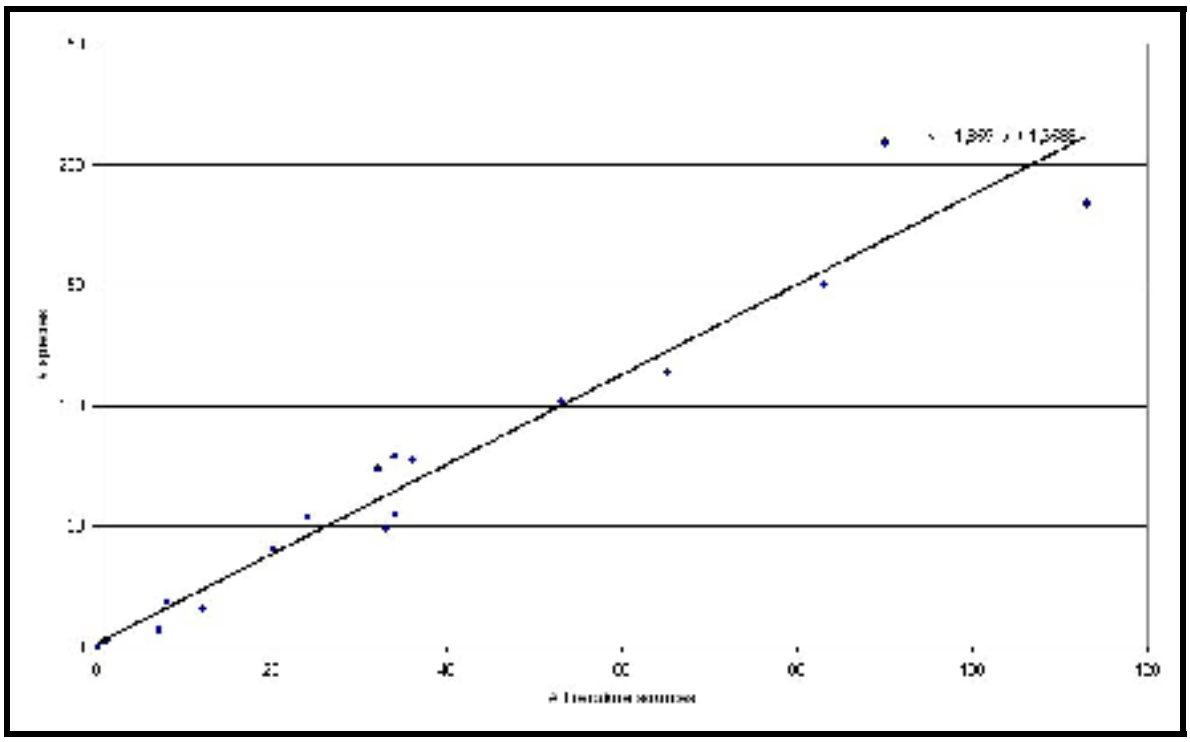


Figure 7. Correlation between the number of literature sources and the number of species, based on data for each 10 degree latitudinal zone

- **4.1.2. Latitudinal patterns**

The latitudinal ranges for genera and species are presented in figure 8 for each 10° latitudinal class. In the Southern hemisphere the number of taxa (genera and species) is much lower than in the Northern hemisphere.

The taxonomic research history of the Northern hemisphere, displayed as the cumulative number of species described during time, has reached a plateau phasis. However, similar analysis for seemingly less diverse areas shows that a plateau phasis is not reached yet (figure 9). For both the Indian and the Pacific Ocean many more species may still be expected. The research effort for all three regions, expressed as the number of publications, explains this effect. The dataset contains 96 publications with data on Pacific Ocean taxa, 71 publications on Indian Ocean taxa and 185 publications on European taxa.

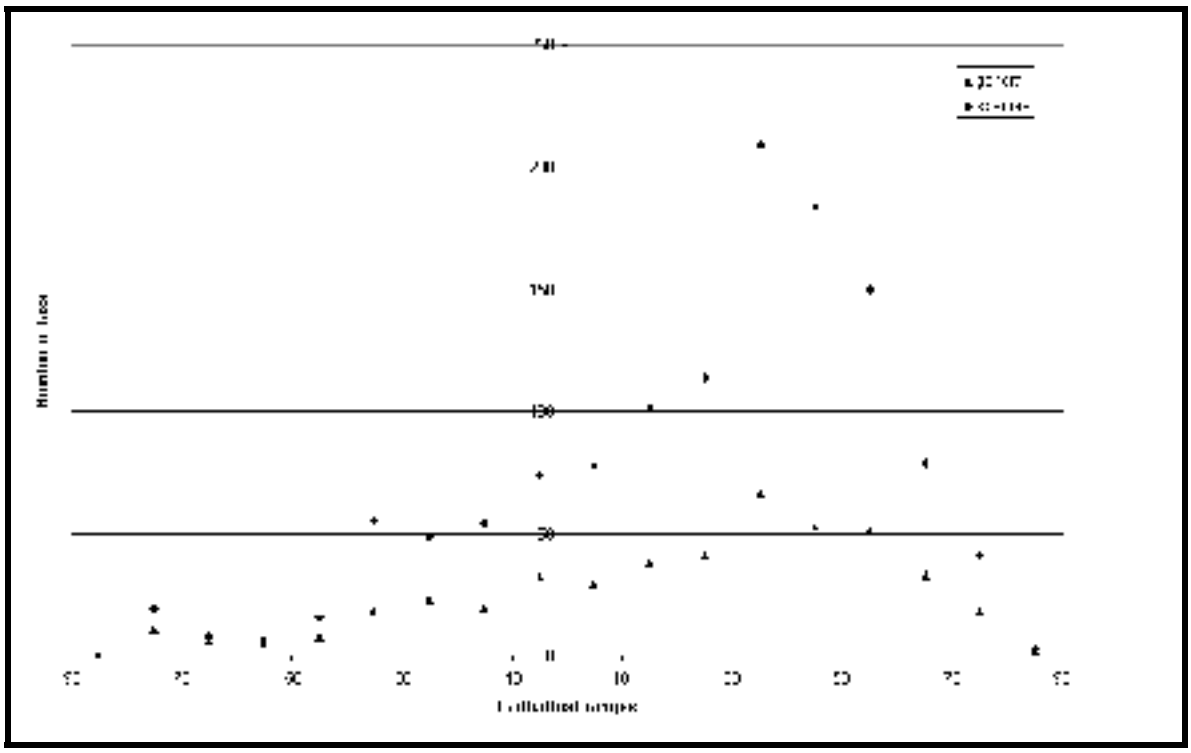


Figure 8. Number of genera and species for each 10° latitudinal class

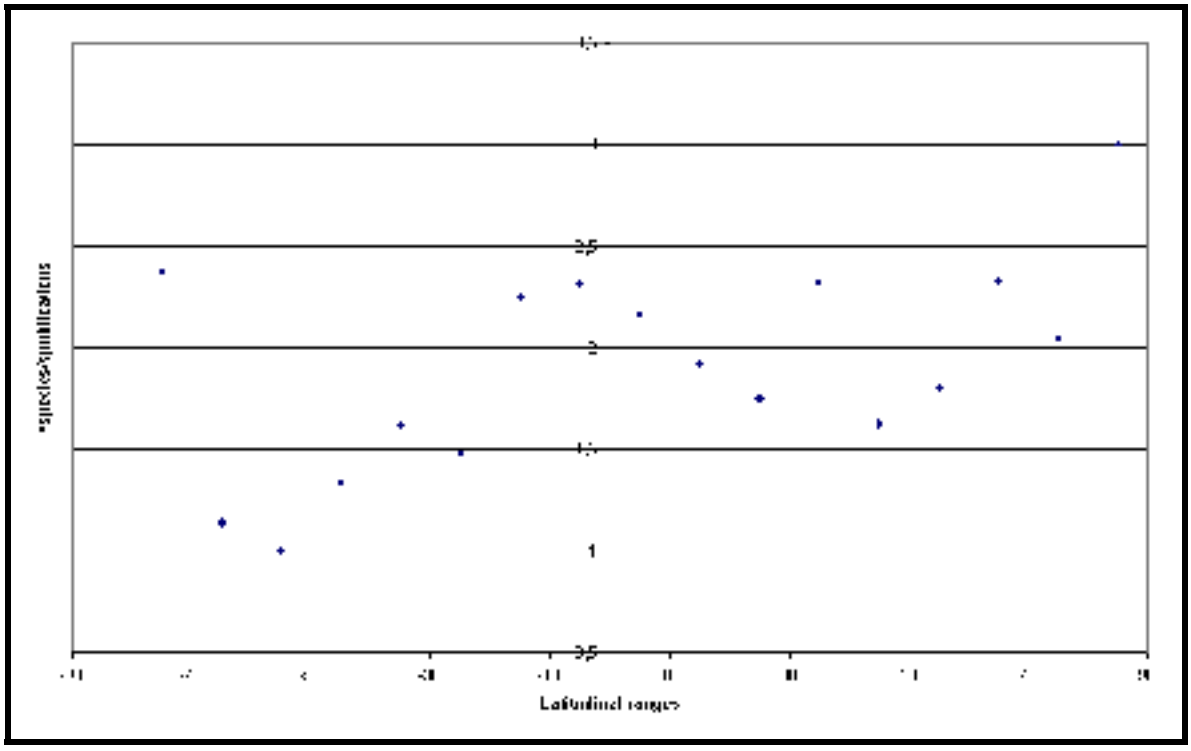


Figure 9. Number of genera and species for each 10° latitudinal class standardized towards sampling effort

Figure 9 takes the sampling effort into account, by dividing the number of taxa for each region by the research effort (expressed as the number of publications). High ratios are found in polar and equatorial regions. The large relative contribution of the Northern moderate regions corresponds strongly with the research effort in this region (figures 5, 6, and 7).

Although not clearly pronounced, the equatorial areas (for example -5, 15) show a higher taxonomic diversity (Delta+) (figure 11). The polar areas clearly have a lower diversity than is expected (dotted line). Most tropical and subtropical areas have a high variability in their taxonomic composition (Lambda+). Also the Antarctic appears as highly variable (meaning that a lot of genera are monospecific, a lot of tribes contain few genera). Nevertheless points plotted at the left side of the figures must be treated with caution, as they represent few species.

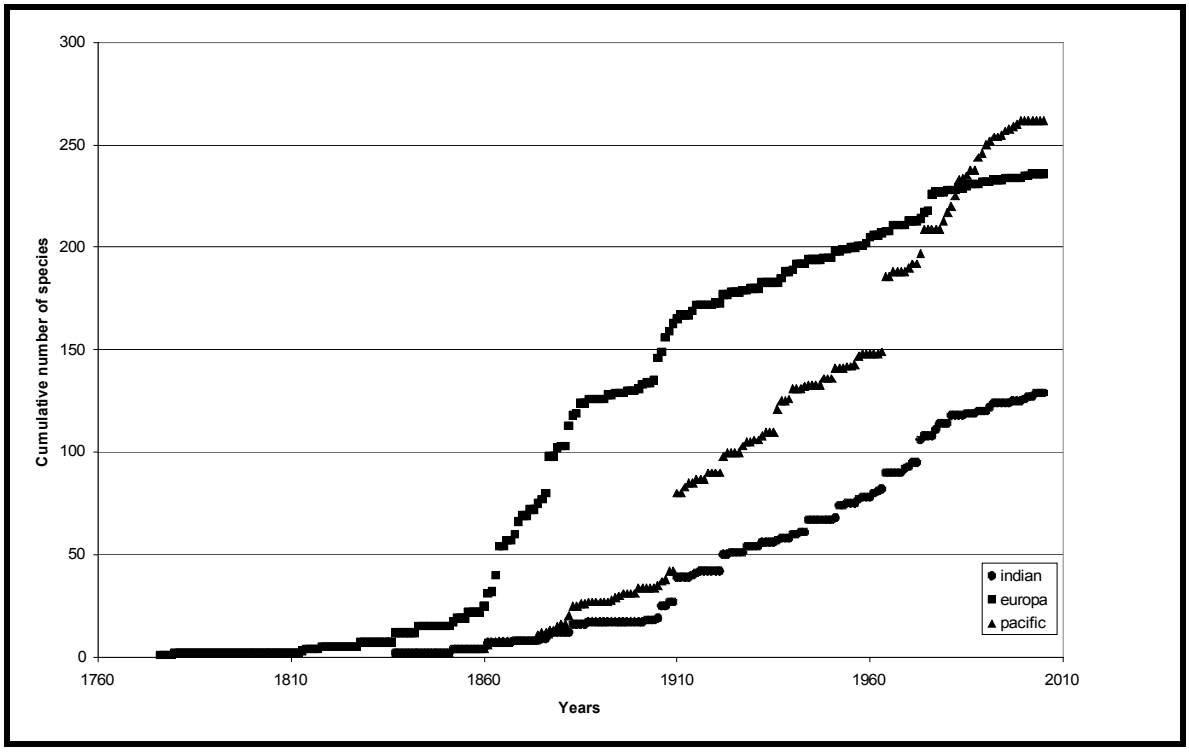


Figure 10. cumulative number of species described in three large global regions (North Atlantic European Waters, Indian Ocean and the Pacific Ocean)

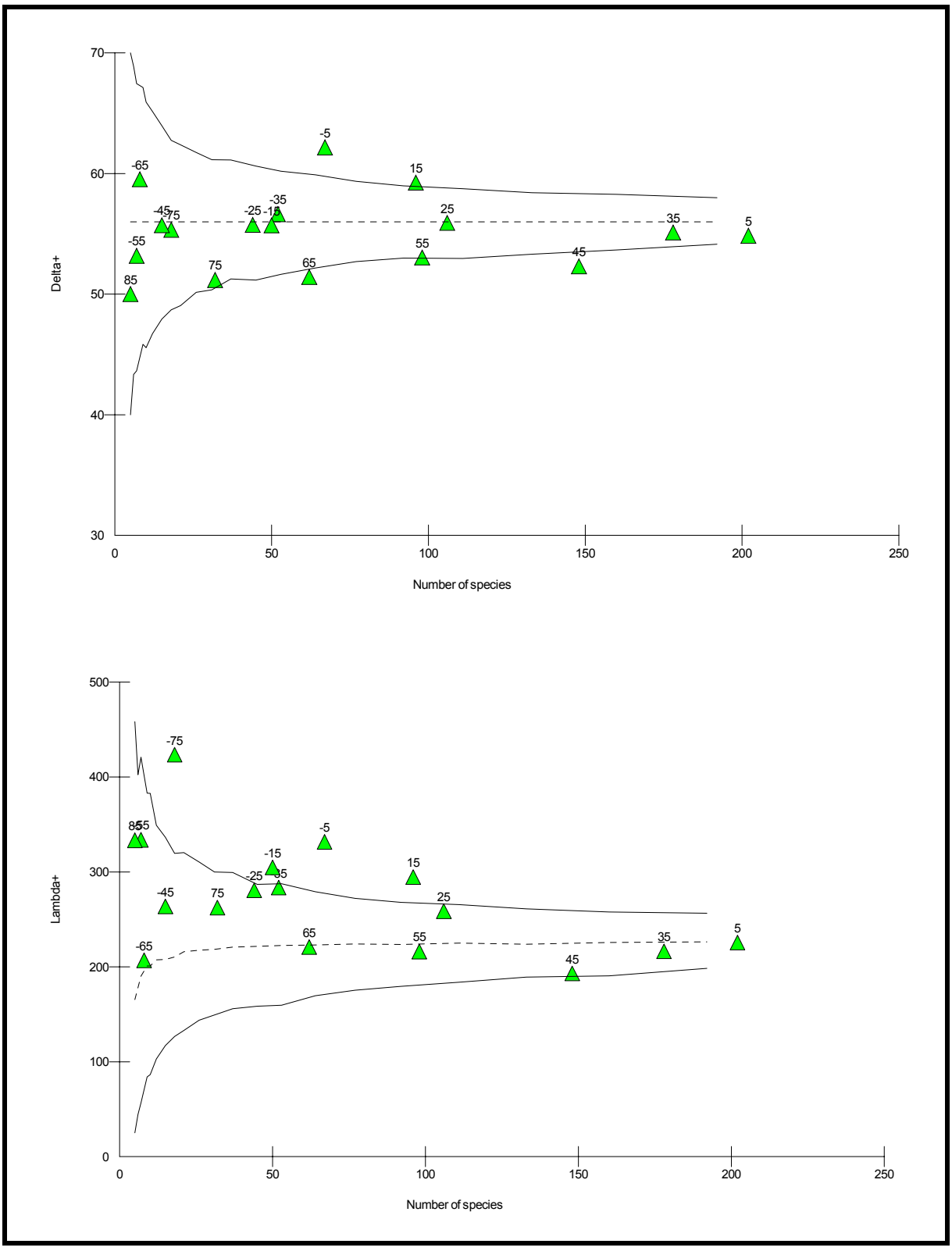
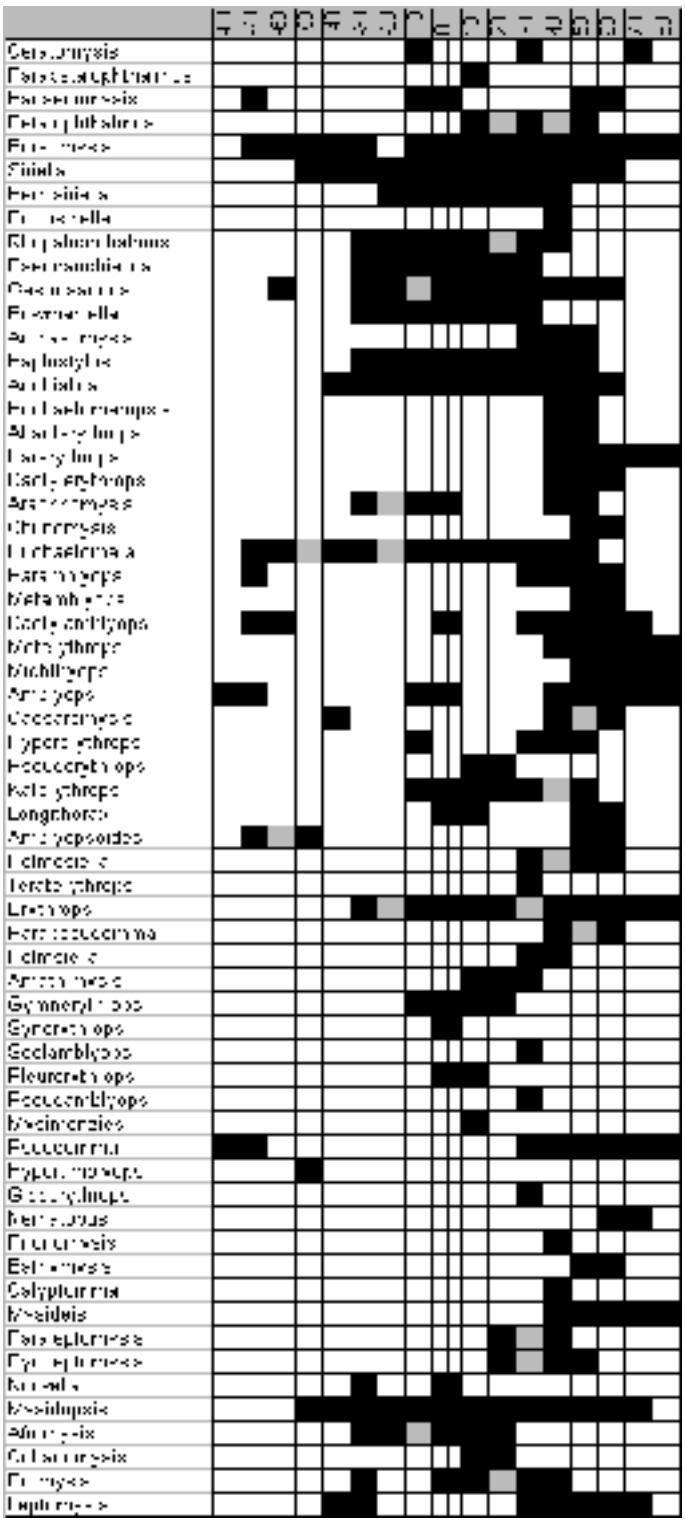


Figure 11. 95% probability funnels for Average Taxonomic Distinctness and Variation in Taxonomic distinctness plotted against the number of species for different mysida assemblages in 10° latitudinal classes. Dashed lines indicate the simulated Delta + and Lambda + from 1000 random selections from the master list of 1086 Species



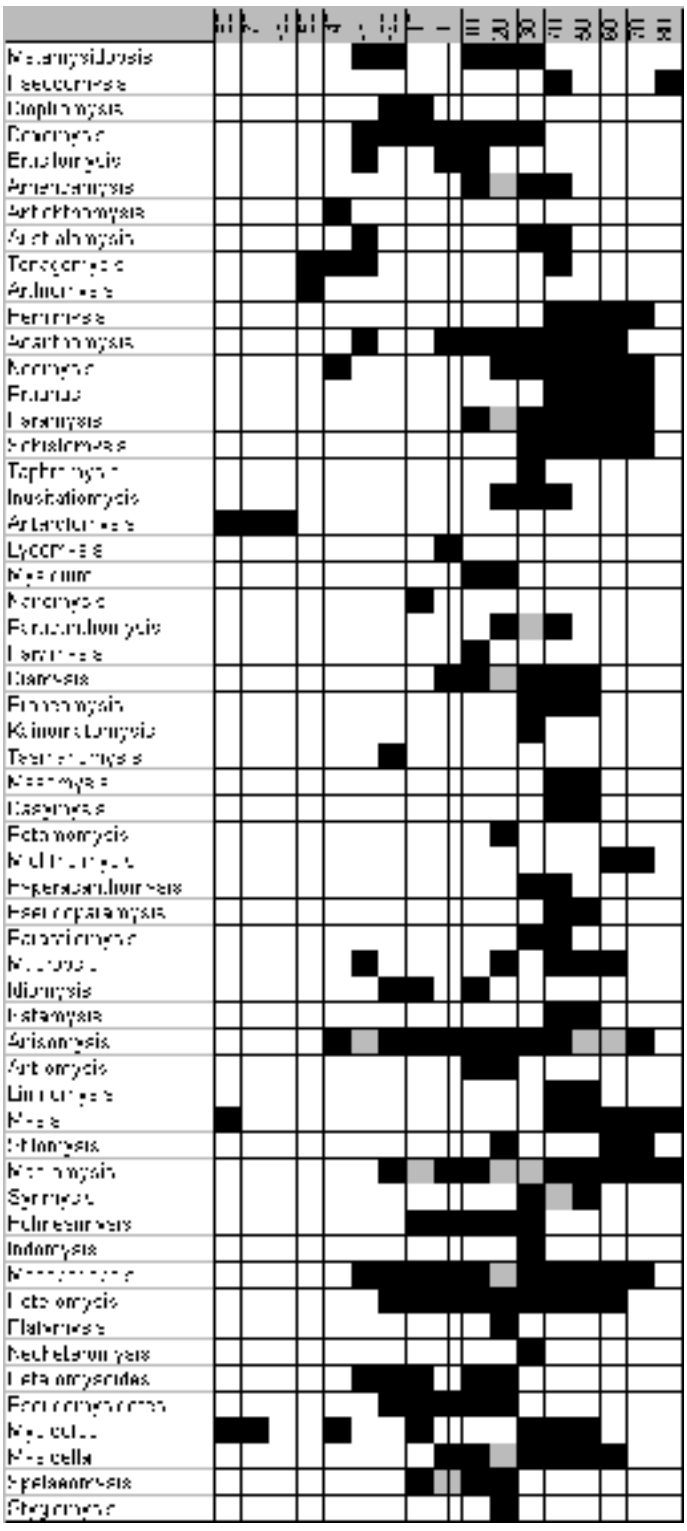


Table 1. Latitudinal ranges for all mysid genera (ordered systematically) available in the dataset. Latitudinal ranges with a distinct presence of a particular genus are shown in black, zones in grey to indicate possible latitudinal ranges. The grey filling was only applied when data for surrounding classes was available and where locations were close to the borders of this zone.

Latitudinal ranges for 120 genera are analyzed (table 1). Some genera have a broad latitudinal range (≥ 100 degrees): *Boreomysis, Siriella, Euchaetomera, Mysidopsis, Erythrops, Praunus, Anisomysis* and *Mesopodopsis*. Most genera have a northern occurrence border at 60-70 degrees. Only few genera have representatives reported from Polar regions: *Praunus, Mysis, Pseudomysis, Mysideis, Amblyops, Michthyops, Pseudomma, Meterythrops, Parerythrops, Boreomysis,* and *Erythrops*. *Boreomysis* is a typical oceanic species, regularly reported from Polar areas. Six genera belong to the tribe Erythropini (*Amblyops, Michthyops, Pseudomma, Meterythrops, Parerythrops, and Erythrops*). No representatives of the (sub) families Lepidomysidae, Petalophtaelmidae, Stygiomysidae, Mysidae (Siriellinae, Gastrosaccinae, Mysidellinae, Rhopalophthalminae) occur in cold areas. This indicates that temperature may be a limiting factor for the distribution of Mysida.

The large number of genera having a latitudinal distribution linked with warmer waters (40° S to 40° N) may also be an indication of temperature related distributions: *Hemisiriella, Rhopalophthalmus, Pseudanchialina, Bowmaniella, Haplostylus, Amathamysis, Gymnerythrops, Afromysis, Promysis, Cubanomysis, Metamysidopsis, Dioptromysis, Doxomysis, Brasilomysis, Americamysis, Australomysis, Lycomysis, Mysidium, Paracanthomysis, Antromysis,* and *Spelaeomysis*.

Many genera (32) are limited to small latitudinal ranges. They are restricted to either the Northern hemisphere, either the Southern hemisphere. The longitudinal ranges of these genera are also very small. These taxa may be considered as typical for certain areas (endemics).

- **4.1.3. Global richness and diversity analysis**

Five regions with high species richness (Shannon) can be defined: (1) Europe, (2) the South-African coastline, (3) Oceanic waters related to the Indian Plate, (4) the West Pacific border, and (5) the Caribbean area (figure 12).

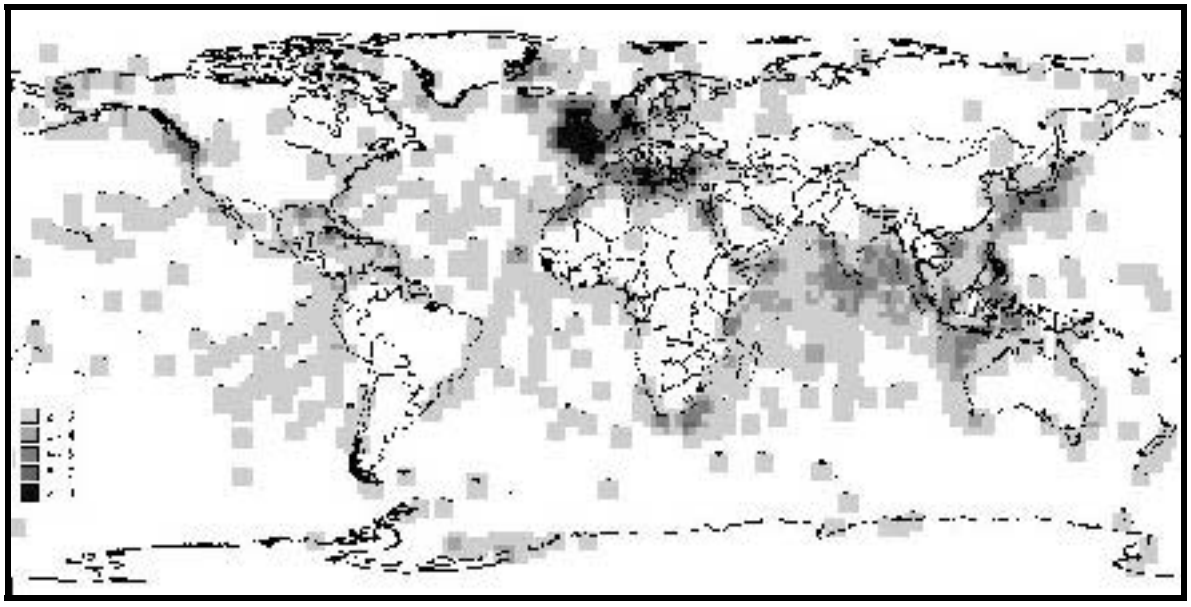


Figure 12. Species richness plot on a 2° grid after (3x3) neighbour joining on richness values. Values in the legend are a relative indication of richness.

The analysis of diversity gives similar results. The same regions can be defined, although the 'West Pacific region', indicated as one species rich region in the richness analysis splits up in two regions: a 'Japanese region' and an 'Indonesian region'. Two other regions are noticeable as highly diverse: the 'entrance of the Red Sea' and the 'Antarctic Ross Sea area'. (figure 13)

A combination of these results may lead to the conclusion that Mysida are not equally distributed. According to the present analysis, there are certain regions of high diversity. Eleven areas are selected. Whether they can be considered as faunal provinces (areas with a distinct taxonomic composition, due to biogeographical processes) will further be analyzed. (figure 14)

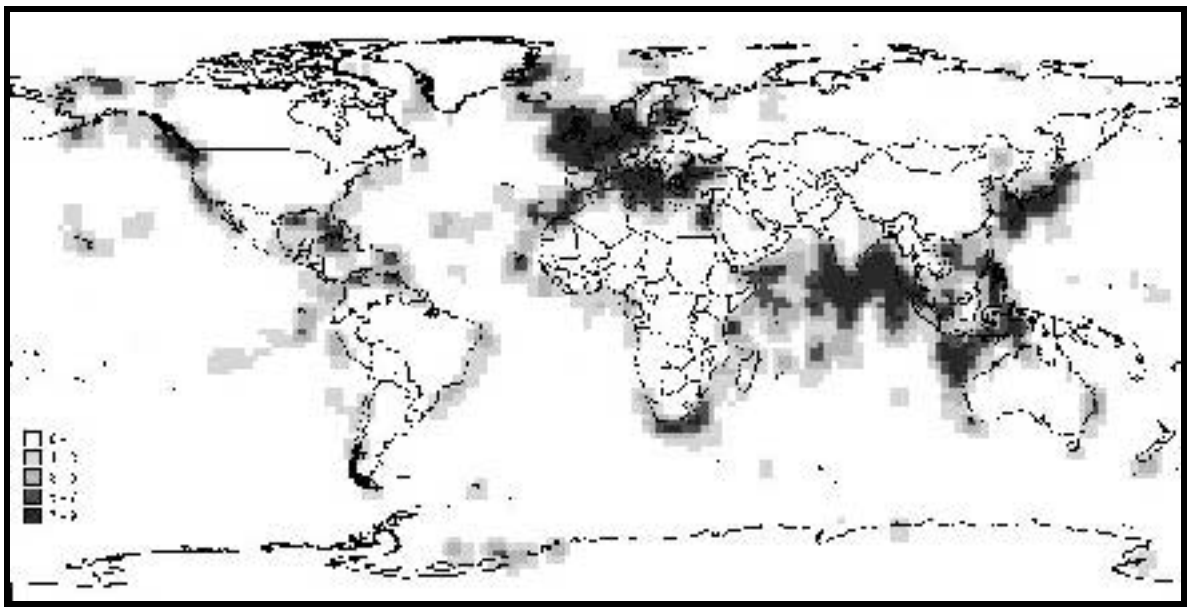


Figure 13. Species diversity plot on a 2° grid after (3x3) neighbour-joining based on Shannon. Values in the legend are a relative indication of diversity.

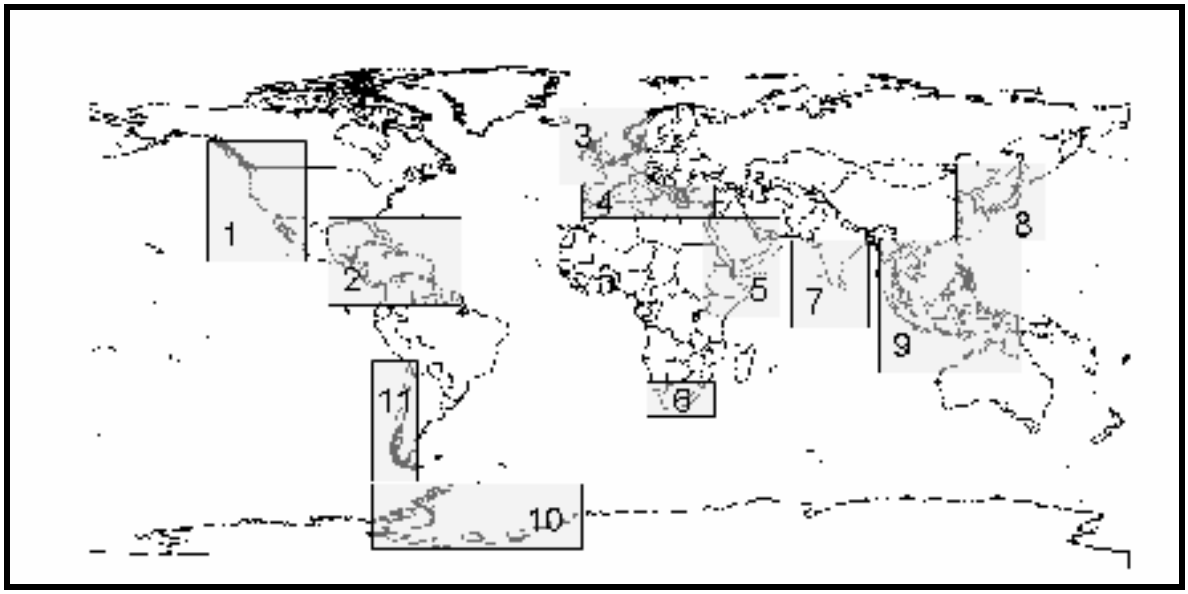


Figure 14. Map of the world with indication of preliminary areas with distinct diversity and/or richness (1. North East Pacific area, 2. Caribbean Area, 3. North East Atlantic Area, 4. Mediterranean Area, 5. Red Sea Area, 6. South African Area, 7. India Area, 8. Japan area, 9. West Pacific Indonesian Area, 10. Antarctic Ross Area, 11. South East Pacific

Examination of the faunal composition of the eleven selected areas is performed by nMDS analysis on a 5° cell grid grouping all locations and related taxa. A total of 307 grid cells contained 726 species. Each grid cell was assigned to the region number (see above), in order to distinguish and visualize the different regions. Only grid cells, belonging to a single region, were used in the analysis (147 cells). The resulting plot (based on Bray-Curtis taxon composition similarity) is displayed in figure 15. One cluster of closely related grid cells is formed. Four grid cells (Region 11 – South east pacific; Region 9 – West Pacific Indonesian; Region 10 – Antarctic Ross Sea; Region 2 – Caribbean Area) are plotted distinctly apart from this cluster. This means that the taxonomic composition of these grid cells is clearly different from the ones. The ANOSIM analysis (table 2) clearly indicates problems with certain areas. The relatively low 'R'-values can have their origin in: (1) the large areas, and/or (2) the under-sampling of some regions.

	1	2	3	4	5	6	7	8	9	10	11
2											
3											
4											
5											
6											
7											
8											
9											
10											
11											

1 > R > 0.7		Groups are clearly different from each other
0.7 > R > 0.5		Groups are clearly different although some stations are overlapping
0.5 > R > 0.4		Groups are overlapping but can still be distinguished from each other
0.4 > R > 0.2		Groups are overlapping and some stations can be distinguished
0.2 > R > 0		Groups cannot be distinguished from each other
0 > R		Samples between groups are more equal than samples within a group

Table 2. Anosim analysis showing the R values of the cross table

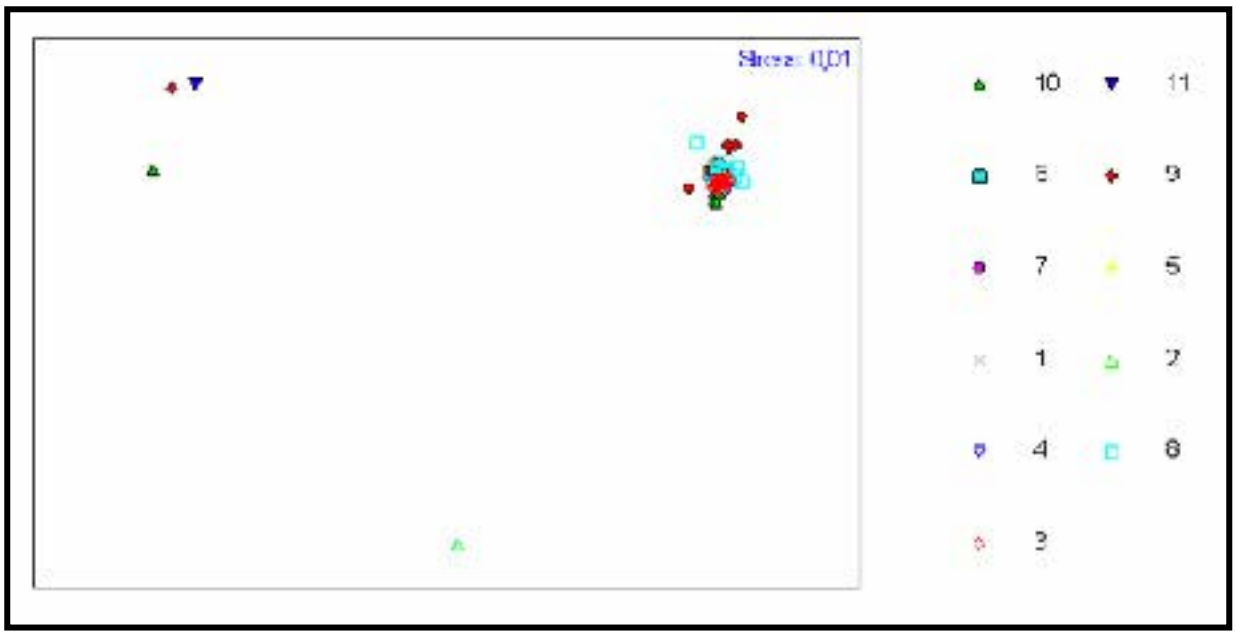


Figure 15. Output of nonmetric multidimensional scaling analysis of the similarity matrix based upon presence/abscence data of genera in each of the areas

Most cells cluster together in the nMDS analysis. No relations between cells in this cluster can be found yet. A second analysis is performed on a limited dataset and visualizes the (dis-)similarities in taxonomic composition in the cluster of regions (see first analysis). As most data are available from the Eastern part of the world, only these areas were selected (regions 3, 4, 6, 7, 8, 9). Region 10 is also left out, as it is already shown to be clearly different from the other regions. Region 5 is left out because it is not distinguishable from any other region (see table 2 – low 'R' values).

The second MDS analysis, only focusing on the areas 3, 4, 6, 7, 8, and 9, clearly shows the similarity in fauna between the different areas. Although the low 'R'-values in the pair wise ANOSIM analysis, more detailed conclusions can be formulated. (figure 16 & table 3).

The fauna of the Northern European area (North East Atlantic) clearly differs from the fauna of all other regions. The fauna of the Mediterranean is most similar to the North European fauna, although still distinguishable. The Mediterranean Mysida fauna distinctly differs from the South-African and Indian fauna. Nevertheless, a relatively high similarity is found with the West Pacific and Japanese fauna. The

main reason for this may be the relatively low number of samples in the Mediterranean region.

The plot nicely displays the close relation between all Indian Ocean related regions. The fauna of the West Pacific Indonesian area completely overlaps with the Indian fauna and is almost undistinguishable from the Japanese fauna. All this leads to the conclusion that no true faunal provinces can be found in the Indian Ocean. However, a shift in faunal composition is observed in this area. This implies all Indian Ocean areas having a common history related to speciation.

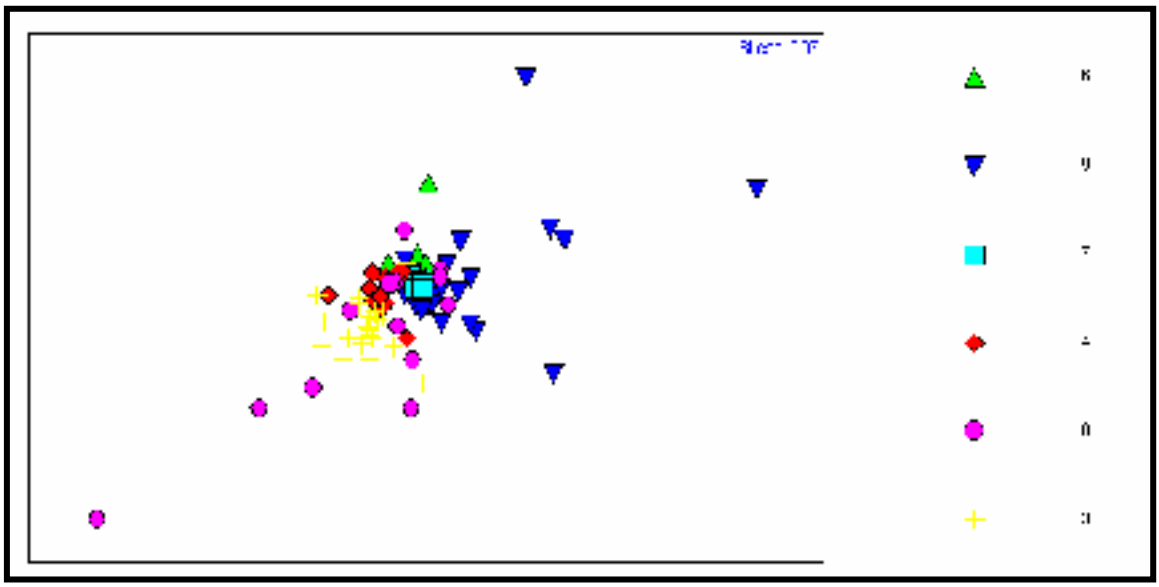


Figure 16. Output of nonmetric multidimensional scaling analysis of the similarity matrix based upon presence/abscence data of distinct genera in selected group of species-rich/species-diverse areas

	3	4	6	7	8
4					
6					
7					
8					
9					

Table 3. Anosim analysis results of the similarity matrix based upon presence/abscence data of distinct genera in selected group of species-rich/species-diverse areas (color legend see table 2)

- **4.1.4. Testing biogeography models**

4.1.4.1. LME concept

The genus compositions (with indication of the number of species), for all large Marine Ecosystem areas, are shown in appendix 1. Three genera (*Siriella, Anchialina* and *Boreomysis*) occur in more than 40 % of all areas. Thirty-six genera (more than 33%) only occur in 1 region. This means that they have a distribution bound to this region, or areas outside the large marine ecosystem provinces. Sixteen regions have mono-regional genera (endemic genera): Sulu-Celebes Sea (1), North West Australian Shelf (1), North Australian shelf (1), Iceland shelf (1), East China sea (1), Celtic Biskay shelf (1), Antarctica (1), Arabian Sea (2), California Current (2), Agulhas Current (3), Black Sea (4), Caribbean Sea (4), Indonesian Sea (4), Mediterranean Sea (4), Kuroshio current (5). The regions, with the highest proportion of endemics are, except for the Black Sea, all tropical or southern hemisphere regions (Southern Asian Shelf – 33%, North Australian shelf – 33%, Indonesian sea – 21%, Caribbean Sea – 22%, Black Sea – 27% and Agulhas Current – 22%).

The ten most genus and species rich areas are: Celtic-Biscay Shelf (45 gen., 114 sp.), Mediterranean Sea (38 gen., 98 sp.), North Sea (31 gen., 91 sp.), Kuroshio Current (26 gen., 83 sp.), Norwegian Sea (22 gen., 54 sp.), Arabian Sea (23 gen., 45 sp.), Agulhas Current (18 gen., 41 sp.), Caribbean Sea (18 gen., 38 sp.), South China Sea (13 gen., 37 sp.), and the Indonesian Sea (19 gen., 35 sp.).

A nMDS analysis was done on the similarity of the generic taxonomic composition (figure 17). The most abundant genera (> 40% of the areas) were left out of the analysis (*Siriella*, *Anchialina*, *Boreomysis*). Four areas are clearly different from the others: the 'New Zealand Shelf', the 'West Bering Sea', 'North Brazil Shelf' and the 'Gulf of California'. A cluster analysis (figure 18) on the same dataset shows the relations of similarity between all regions. Two pairs of areas have an equal generic composition: (1) 'East Siberian Sea', 'Newfoundland-Labrador Shelf' and (2) 'Chukchi Sea' and 'Beaufort Sea'. Both pairs consist of neighbor areas. Other similar regions are 'Kara Sea' and 'West Greenland Shelf'. They cluster relatively close

together with 'East Greenland Shelf', 'Iceland Shelf' and 'Faroe Plateau'. This group forms one branch including all Arctic and Northern Atlantic related areas.

In general geographical neighboring areas cluster relatively well together based on generic composition.

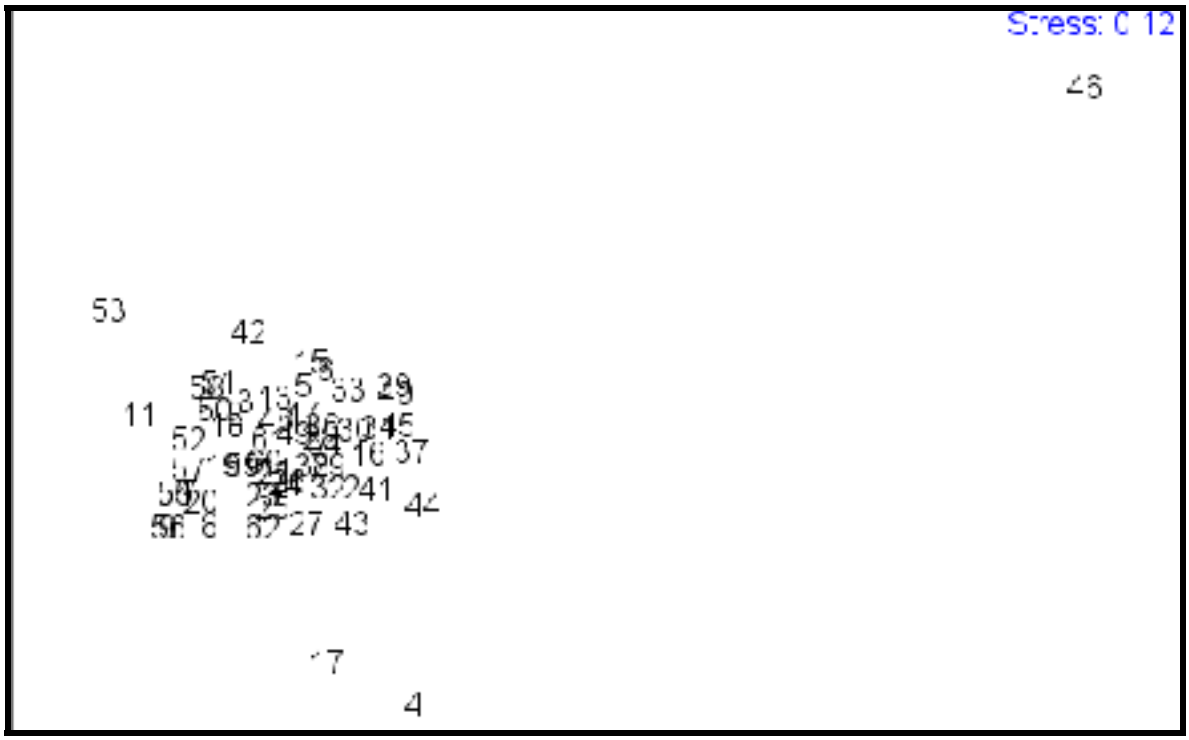


Figure 17. Output of Non-metric Multi-dimensional scalind (MDS) on genus presence/abscence data in Large Marine Ecosystem Areas (stress 0.12).

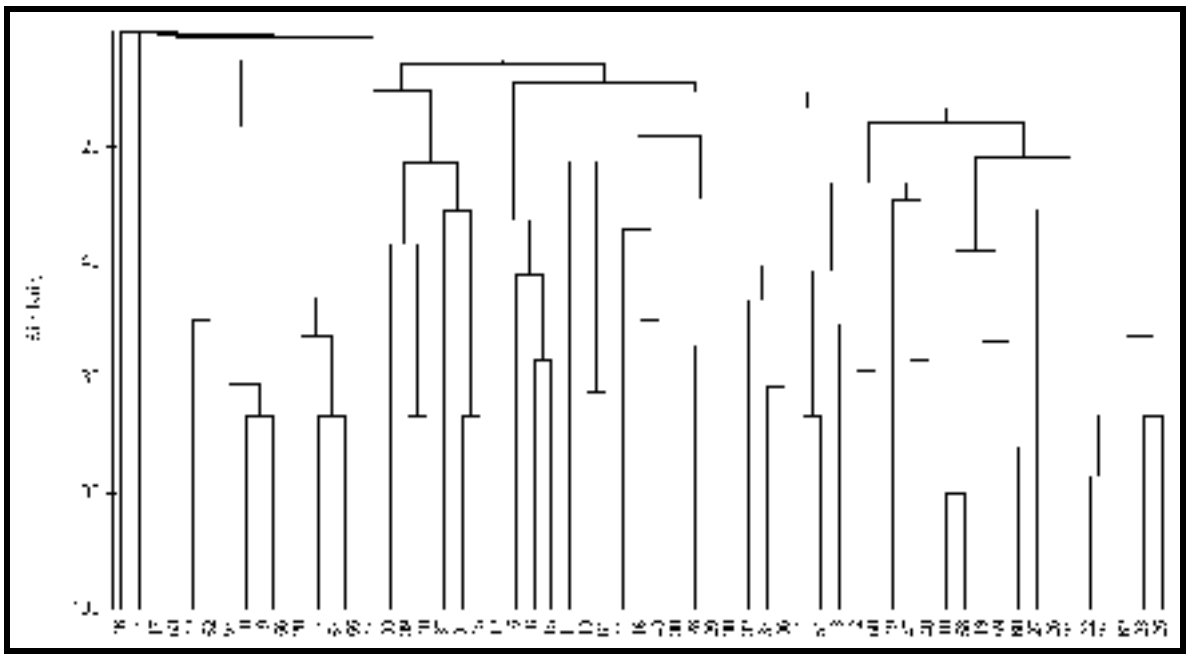


Figure 18. Cluster analysis output on genus presence/abscence data in LME areas

Only few regions can be selected upon their diversity (table 4). The 'Arabian sea' and the 'Indonesian Sea' combine a high average taxonomic distinctness (Delta+) value with relative high number of species (S) meaning both regions have a true taxonomic diverse composition with also a relative high number of 'rare' species (Lambda+) (figure 19). Although most of the regions fall within the expected taxonomic diversity ranges, many are plotted below the average expected values (dotted line). This is mainly due to the small number of species (table 4) and the limited research effort in these areas (see figure 5, 6, and 7). However, the regions stated above, and the 'Guinea Current' and 'Humboldt Current', can be selected as regions with distinct taxonomic compositions.

	S	D	H'(loge)	Delta+	Lambda+
Agulhas Current	38	10,17	3,63	56,49	254,94
Antarctica	16	5,41	2,77	55,00	368,51
Arabian Sea	40	10,57	3,68	58,37	358,61
Baltic Sea	17	5,64	2,83	48,16	178,40
Barents Sea	5	2,48	1,60	55,00	280,55
Bay of Bengal	32	8,94	3,46	57,35	267,86
Beaufort Sea	4	2,16	1,38	47,22	408,95
Benguela Current	19	6,11	2,94	55,16	381,04
Black Sea	25	7,45	3,21	43,00	301,00
California Current	13	4,67	2,56	50,42	185,01
Canary Current	14	4,92	2,63	57,69	294,91

Caribbean Sea	38	10,17	3,63	57,01	307,16
Celtic-Biscay Shelf	77	17,49	4,34	53,76	229,33
Chukchi Sea	4	2,16	1,38	27,77	61,72
East Bering Sea	11	4,17	2,39	45,45	337,92
East Brazil Shelf	3	1,82	1,09	55,55	246,91
East Central Australian Shelf	9	3,64	2,19	46,75	429,31
East China Sea	19	6,11	2,94	54,77	271,21
East Greenland Shelf	13	4,67	2,56	48,50	207,87
East Siberian Sea	2	1,44	0,69	66,66	0
Faroe Plateau	22	6,79	3,09	53,39	319,18
Guinea Current	14	4,92	2,63	58,24	209,85
Gulf of Alaska	17	5,64	2,83	50,98	240,05
Gulf of Mexico	11	4,17	2,39	55,75	234,52
Gulf of Thailand	2	1,44	0,69	16,66	0
Humboldt Current	14	4,92	2,63	66,11	430,10
Iberian Coastal	15	5,16	2,70	56,82	162,40
Iceland Shelf	12	4,42	2,48	54,29	280,39
Indonesian Sea	33	9,15	3,49	58,04	346,08
Insular Pacific-Hawaiian	2	1,44	0,69	16,66	0
Kara Sea	3	1,82	1,09	55,55	246,91
Kuroshio Current	80	18,02	4,38	54,66	288,60
Laptev Sea	4	2,16	1,38	47,22	408,95
Mediterranean Sea	69	16,06	4,23	54,99	176,22
New Zealand Shelf	3	1,82	1,09	16,66	0
Newfoundland-Labrador Shelf	1		0	0	0
North Australian Shelf	9	3,64	2,19	43,98	542,48
North Brazil Shelf	2	1,44	0,69	33,33	0
North Sea	57	13,85	4,04	54,26	218,20
Northeast Australian Shelf	5	2,48	1,60	51,66	525
Northeast U_S_ Continental Shelf	6	2,79	1,79	35,55	143,20
Northwest Australian Shelf	6	2,79	1,79	55,55	209,87
Norwegian Sea	42	10,96	3,73	53,65	234,71
Oyashio Current	4	2,16	1,38	63,88	38,58
Pacific Central-American Coastal	4	2,16	1,38	50	1111,11
Red Sea	10	3,90	2,30	56,29	336,89
Scotian Shelf	2	1,44	0,69	50	0
Sea of Japan	11	4,17	2,39	48,78	261,15
Sea of Okhotsk	4	2,16	1,38	52,77	408,95
Somali Coastal Current	9	3,64	2,19	56,94	237,26
South Brazil Shelf	3	1,82	1,09	55,55	246,91
South China Sea	35	9,56	3,55	54,76	349,87
Southeast Australian Shelf	3	1,82	1,09	61,11	61,72
Southeast U_S_ Continental Shelf	5	2,48	1,60	56,66	177,77
Southwest Australian Shelf	5	2,48	1,60	48,33	525,00
Sulu-Celebes Sea	20	6,34	2,99	49,56	588,98

West Bering Sea	1		0	0	0
West Central Australian Shelf	3	1,82	1,09	50	555,55
West Greenland Shelf	6	2,79	1,79	48,88	387,65
Yellow Sea	9	3,64	2,19	54,16	345,29

Table 4. Diversity indices for each LME region (S= number of species, d=Margalev species richness, H'= Shannon diversity, Delta+ = Taxonomic Diversity compared to the Mysida species master list, Lambda + = Taxonomic distinctness)

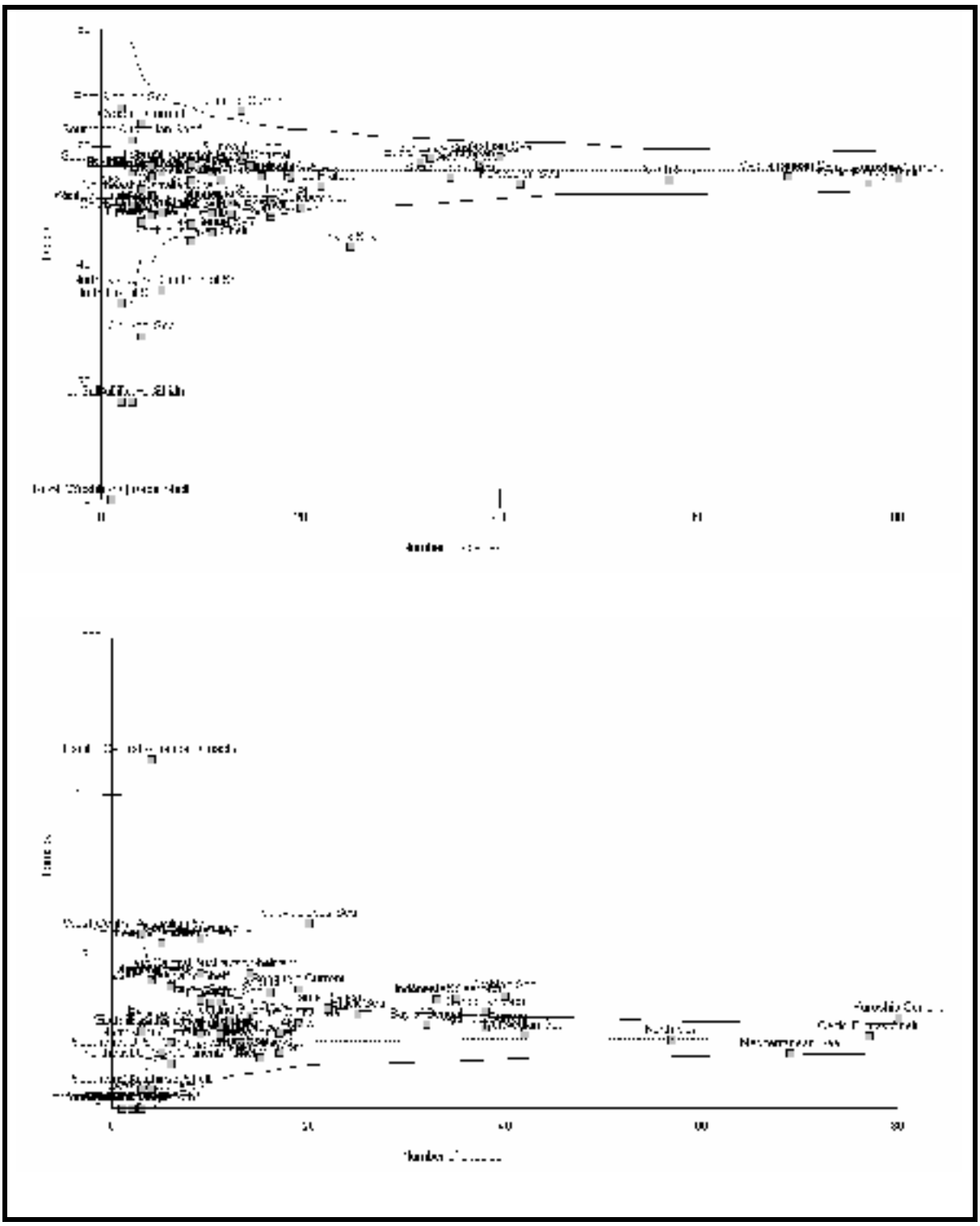


Figure 19. 95% probability funnels for Average Taxonomic Distinctness and Variation in Taxonomic distinctness plotted against the number of species for different Mysida assemblages in the Large Marine Ecosystem areas. Dashed lines indicate the simulated Delta + and Lambda + random 1000 selections from the master list of 1160 species.

Almost half (40%) of the genera are restricted to a single region (see appendix 2). Ten regions have records of only one genus (Bismarck-Solomon Seas, Chesapeake Bay, Galapagos Marine, Hawaiian Marine, Mesoamerican Reef, New Caledonia Barrier Reef, Palau Marine, Panama Bight, Patagonian Southwest Atlantic, Rapa Nui). This may be due to the small size of the areas (compared to areas in different biogeographic models).

Two genera are represented in more than 40 % of the regions: *Siriella*, and *Anchialina*. They will not be included in the genus based similarity analyses presented below. By eliminating both genera, nine regions were cancelled from the analysis, meaning these regions did only have records of *Anchialina* and *Siriella* (Bismarck-Solomon Seas, Galapagos Marine, Great Barrier Reef, Hawaiian Marine, Mesoamerican Reef, Palau Marine, Panama Bight, Rapa Nui, Tahitian Marine). Seven of these were listed earlier as regions with records limited to one genus.

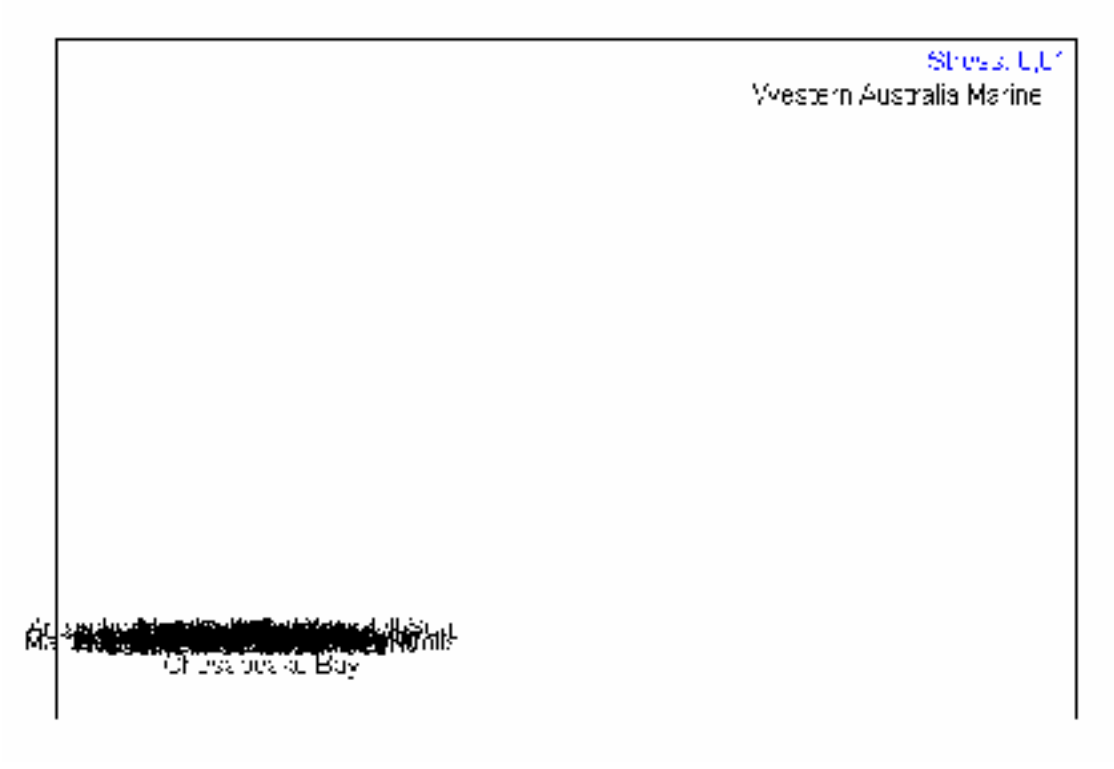


Figure 20. Output of nMDS analysis based on similarity of genus composition of the WWF – ecoregions. *Siriella* and *Anchialina* are taken out the dataset.

The first output of the similarity analysis indicates that the area 'Western Australia Marine' is very different from other regions (figure 20). This region only has records of *Tasmanomysis*, apart from of *Anchialina* and *Siriella* (both dropped out of the dataset). In order to understand the relationships between the other areas, the 'Western Australia Marine' area was cancelled from the dataset for a second analysis (figures 21 & 22). Certain geographic related regions have a similar taxonomic composition. Many geographic distinct regions however do also cluster well together. This is most likely due to the low number of generally occurring genera and the relatively small size of the regions. Six areas can be selected with both high species richness and high taxonomic diversity: (1) Humboldt current, (2) Greater Antillean Marine, (3) West Madagascar Marine, (4) Andaman Sea, (5) Yellow Sea, (6) East African Marine (table 5 and figure 23).

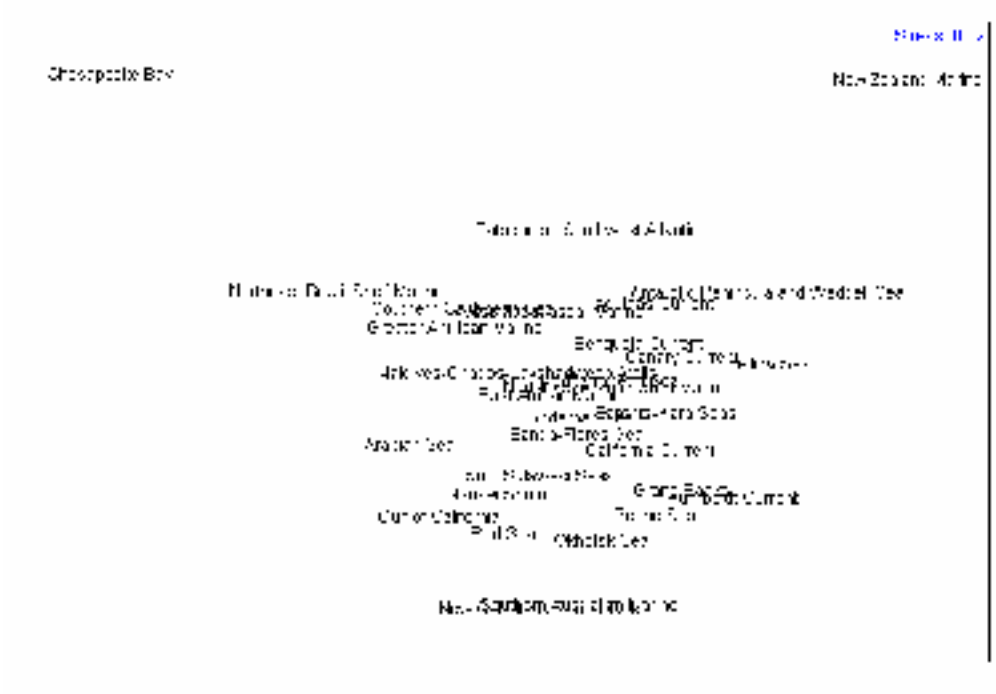


Figure 21 Output of nMDS analysis based on similarity of genus composition of the WWF – ecoregions. *Siriella* and *Anchialina* are taken out the dataset. (without Australia)

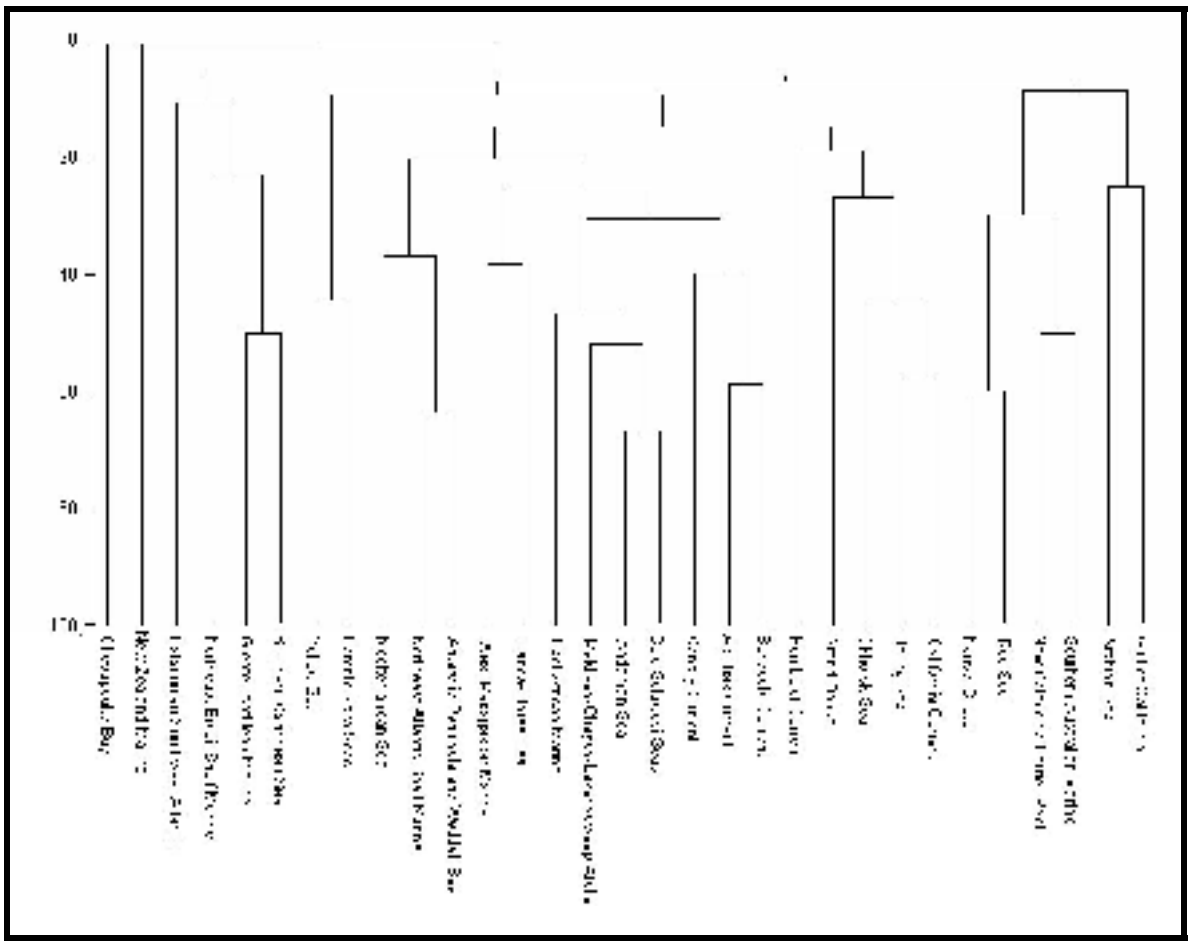


Figure 22. Output of cluster analysis based on similarity of genus composition of the WWF – ecoregions. *Siriella* and *Anchialina* are taken out the dataset.

Most regions have a taxonomic diversity within the expected range. However, some regions have a high average variation in taxonomic distinctness (Lambda+), meaning many genera are represented by only one to a few species. Three regions have high 'Lambda+' values and a relatively high number of species: (1) Sulu-Sulawesi Seas, (2) Nansei Shoto, (3) Banda-Flores Sea.

Another striking observation is the rather low taxonomic diversity of the 'North East Atlantic Shelf', primarily recognised as species rich and diverse.

	S	d	H'(loge)	Delta+	Lambda+
Agulhas Current	33	6,36	3,21	56,53	284,01
Andaman Sea	20	4,34	2,49	58,94	224,03
Antarctic Peninsula and Weddell Sea	3	1,44	1,03	61,11	61,72
Arabian Sea	15	3,36	1,65	54,60	579,33
Banda-Flores Sea	36	7,60	3,21	57,93	342,65
Barents-Kara Seas	22	5,95	2,96	51,58	250,00
Benguela Current	18	4,82	2,74	53,59	384,68
Bering Sea	15	3,18	1,90	46,19	329,40
Bismarck-Solomon Seas	1		0	0	0
California Current	24	5,07	2,44	49,81	206,28
Canary Current	17	4,04	2,40	57,96	265,38
Chesapeake Bay	1		0	0	0
East African Marine	22	6,05	2,76	58,00	204,01
Gal pagos Marine	2	0,62	0,50	16,66	0
Grand Banks	5	2,23	1,56	58,33	236,11
Great Barrier Reef	4	2,16	1,38	41,66	625
Greater Antillean Marine	15	3,65	2,16	61,58	333,98
Gulf of California	2	1,44	0,69	66,66	0
Hawaiian Marine	2	0,40	0,45	16,66	0
Humboldt Current	11	3,89	2,35	65,15	669,42
Maldives-Chagos-Lakshadweep Atolls	28	5,24	2,13	57,76	304,27
Mediterranean Sea	77	11,58	3,60	55,06	180,27
Mesoamerican Reef	2	0,72	0,69	16,66	0
Nansei Shoto	26	6,52	3,09	52,20	460,94
New Caledonia Barrier Reef	1		0	0	0
New Zealand Marine	4	1,67	1,32	41,66	625
Northeast Atlantic Shelf Marine	95	11,60	3,23	53,06	223,67
Northeast Brazil Shelf Marine	4	1,86	1,33	61,11	154,32
Okhotsk Sea	6	2,79	1,79	58,88	217,28
Palau Marine	1	0	0	0	0
Panama Bight	2	1,44	0,69	16,66	0
Patagonian Southwest Atlantic	1		0	0	0
Red Sea	10	2,87	2,08	56,29	336,89
Southern Australian Marine	6	2,56	1,74	55,55	395,06
Southern Caribbean Sea	32	5,52	2,93	51,00	235,31
Sulu-Sulawesi Seas	24	5,16	2,65	53,98	497,40
Tahitian Marine	1		0	0	0
West Madagascar Marine	14	4,33	2,45	60,62	332,82
Western Australia Marine	1		0	0	0
Yellow Sea	12	3,61	2,24	58,83	405,88

Table 5. Diversity indices for each WWF region (S= number of species, d=Margalev species richness, H'= Shannon diversity, Delta+ = Taxonomic Diversity compared to the Mysida species master list, Lambda + = Taxonomic distinctness)

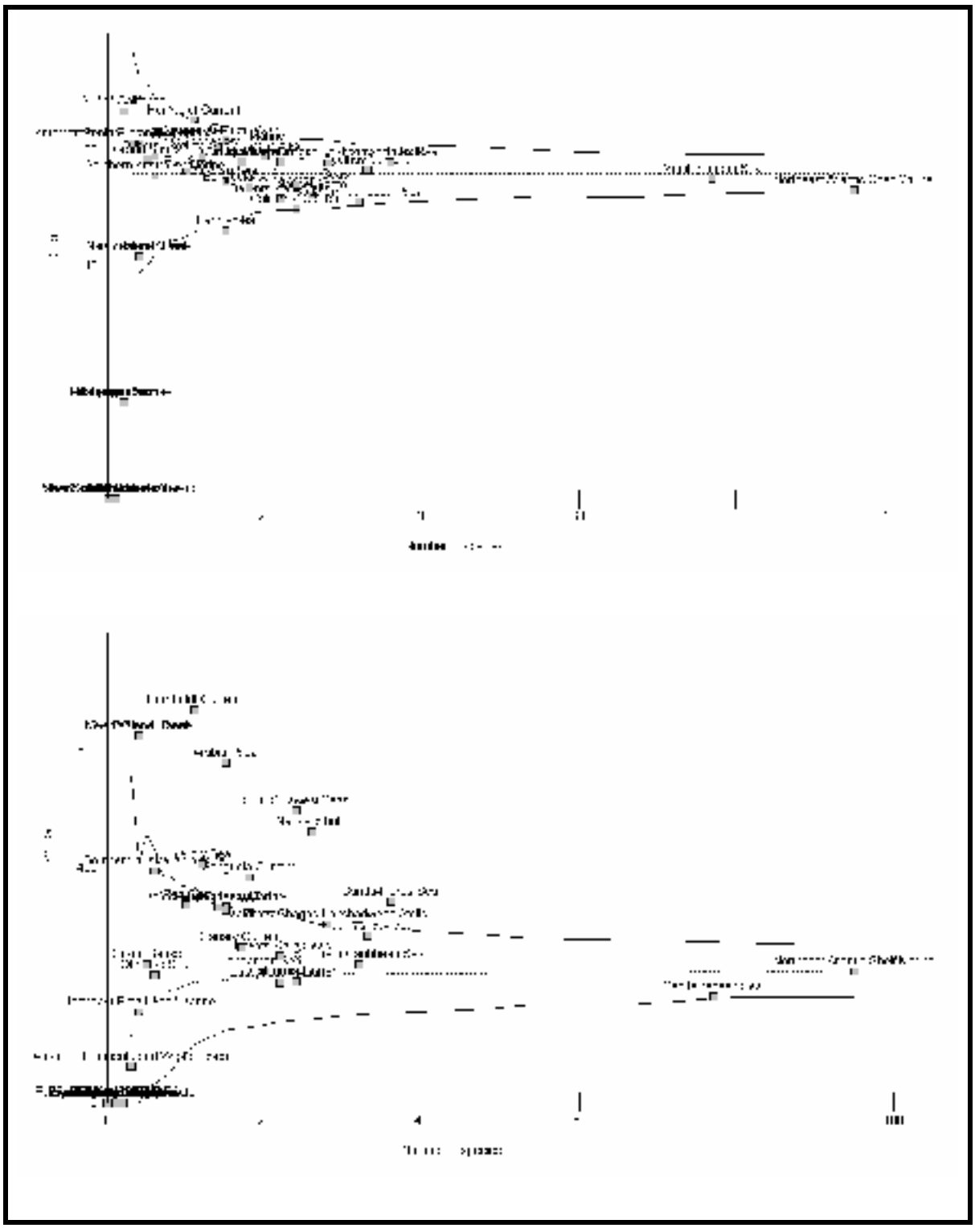


Figure 23. 95% probability funnels for Average Taxonomic Distinctness and Variation in Taxonomic distinctness plotted against the number of species for different Mysida assemblages in the WWF marine ecoregions. Dashed lines indicate the simulated Delta + and Lambda + from random 1000 selections from the master list of 1086 species

4.1.4.3. Mauchline concept

This concept uses the largest areas. The cluster and the nMDS output of the similarity analysis in genus diversity show some nice patterns (figure 24 & 25). The Indian Ocean - related areas cluster well together (Australasian, East Indian, West Indian). Also the 'East Atlantic' and 'North-East Atlantic' cluster together. This branch shows more similarities with the Indian Ocean branch than with the Western Atlantic Areas. All Antarctic regions form one branch with relatively high similarity values, the Pacific Ocean is clearly split in a Western ('West Pacific') and Eastern ('North Pacific' and 'East Pacific') region. The nMDS output (figure 25) illustrates the oceanic pattern even more clearly.

The Southern regions tend to be more taxonomic diverse than the Northern Regions (figure 26 and table 6).

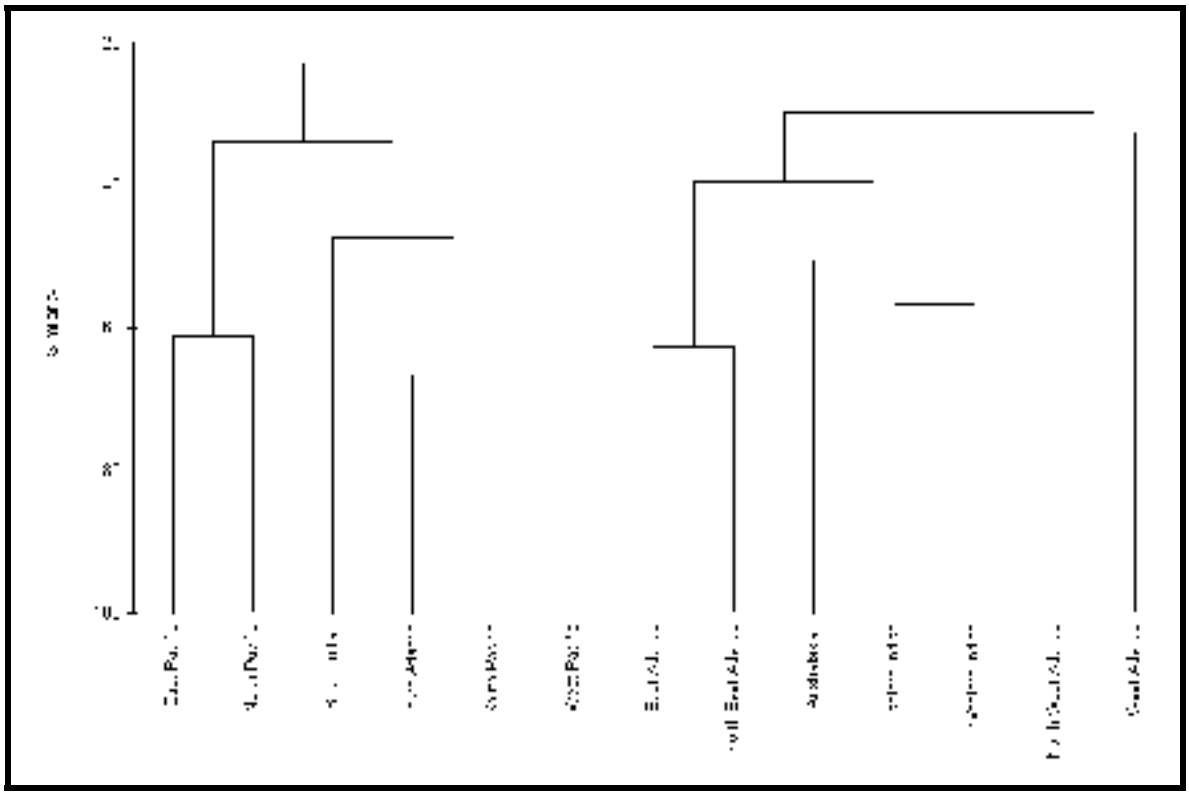


Figure 24. Cluster analysis output on genus presence/abscende data in the Mauchline Areas

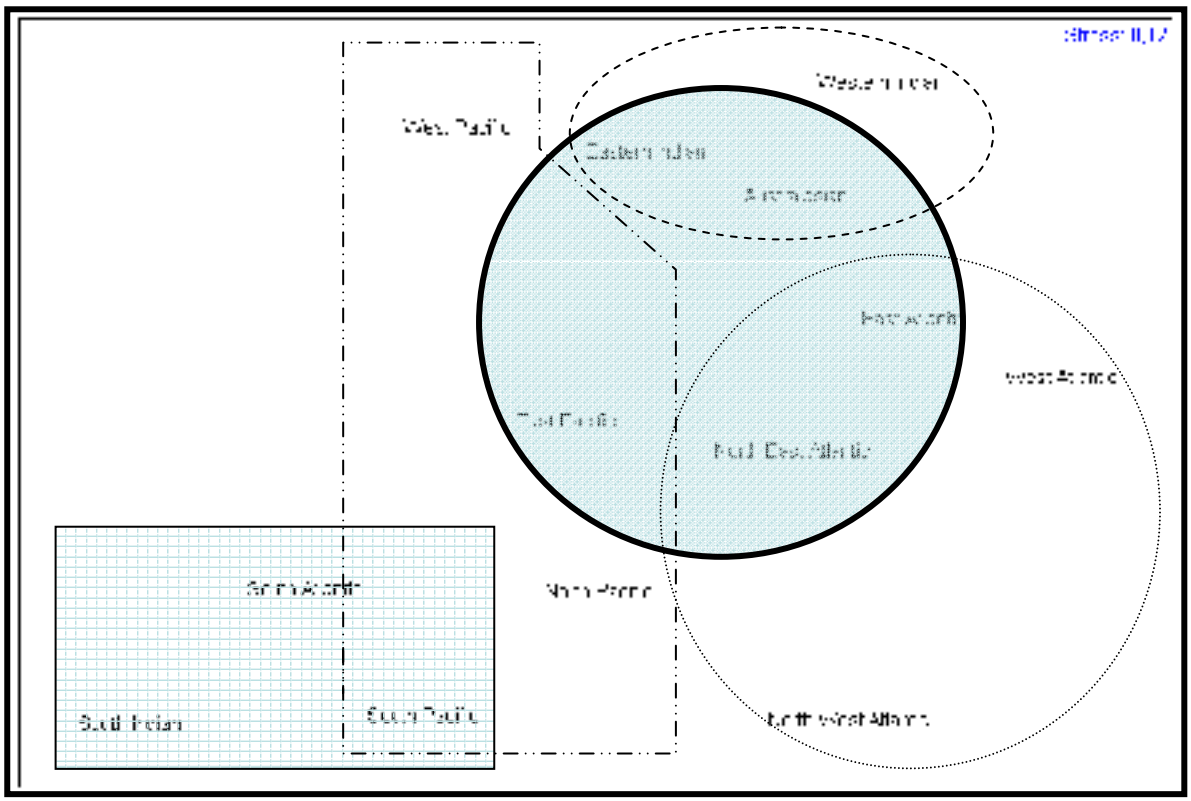


Figure 25. Output of Non-metric Multi-dimensional scalind (MDS) on genus presence/absence data in Large Marine Ecosystem Areas (stress 0.12)

	S	D	H'(loge)	Delta+	Lambda+
Australasian	193	36,48	5,26	55,96	234,46
East Atlantic	178	34,15	5,18	53,13	203,00
East Pacific	39	10,37	3,66	61,11	359,37
Eastern Indian	42	10,96	3,73	57,23	265,04
North East Atlantic	109	23,02	4,69	52,96	218,00
North Pacific	30	8,52	3,40	49,46	273,02
North West Atlantic	24	7,23	3,17	54,46	298,06
South Atlantic	19	6,11	2,94	56,23	298,97
South Indian	7	3,08	1,94	56,34	303,60
South Pacific	15	5,16	2,70	58,25	328,69
West Atlantic	73	16,78	4,29	55,24	249,53
West Pacific	23	7,01	3,13	54,08	393,94
Western Indian	105	22,34	4,65	59,72	280,47

Table 6. Diversity indices for each 'Mauchline' region (S= number of species, d=Margalev species richness, H'= Shannon diversity, Delta+ = Taxonomic Diversity compared to the Mysida species master list, Lambda + = Taxonomic distinctness)

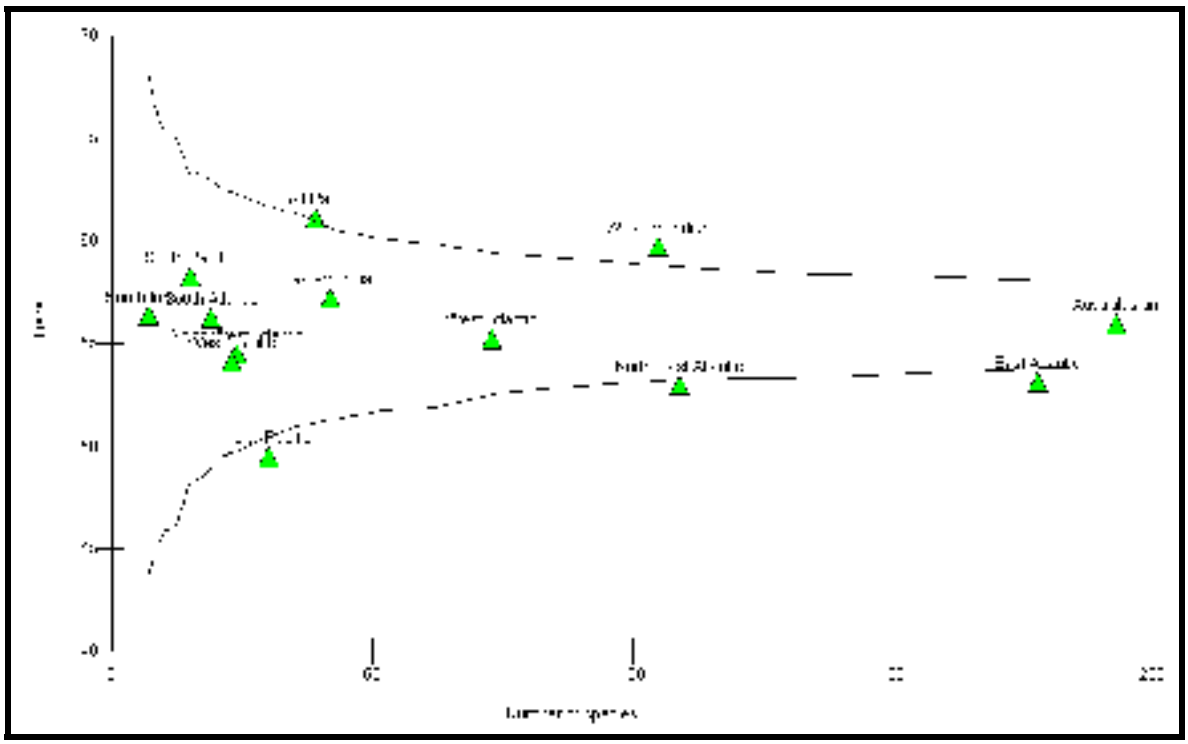


Figure 26. 95% probability funnels for Average Taxonomic Distinctness and Variation in Taxonomic distinctness plotted against the number of species for different Mysida assemblages in the Mauchline Biogeography areas. Dashed lines indicate the simulated Delta + and Lambda + from 1000 random selections from the master list of 1086 species

4.1.4.4. Briggs concept

The areas used in this model are rather small due to their restriction to mainly coastal areas. However, still 551 species belonging to 111 genera are retained in the database. About 2000 records were dropped, 8150 were kept.

The dominant genera were *Siriella* (present in 61% of all regions) and *Anchialina* (present in 43% of all regions).

The first analysis (figure 27), using genus presence/absence similarity, does not show distinctly overlapping regions. Certain regions cluster closely together, others clearly differ.

Some regions can be grouped based on the cluster and nMDS analysis (figures 27 & 28):

Group 1: Carribean, West Indian, Carolinian, SE-South American

Group 2: Agulhus and SW african

Group 3: Indo-West Pacific, West Indian Ocean and Japan region

Group 4: Okhotsk, Aleutian, Kurile

Group 5: SW Australian, SE Australia and the Red Sea

Three regions tend to be more taxonomic diverse: the West Indian Ocean, the Indo-West Pacific and the Peru-Chilian region. Concerning variation in taxonomic distinctness, again the Indo-West Pacific, Japan region, all Australian areas and again Peru-Chilian have clearly high values.

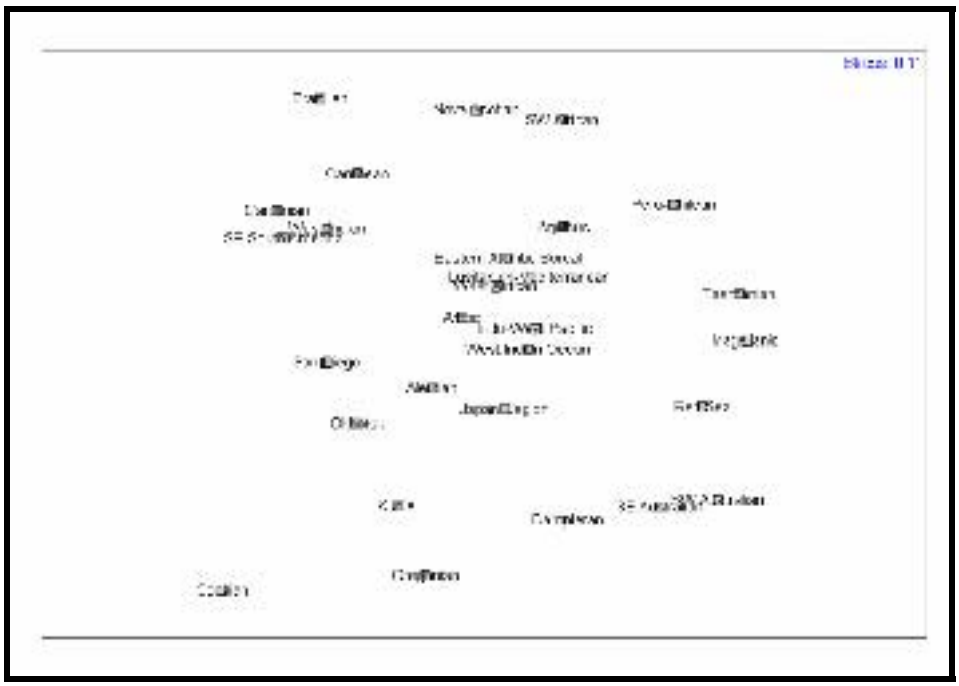


Figure 27. Output of Non-metric Multi-dimensional scalind (MDS) on genus presence/absence data in Briggs (1974) marine areas (stress 0.11). Dominant genera are not included in the analysis.

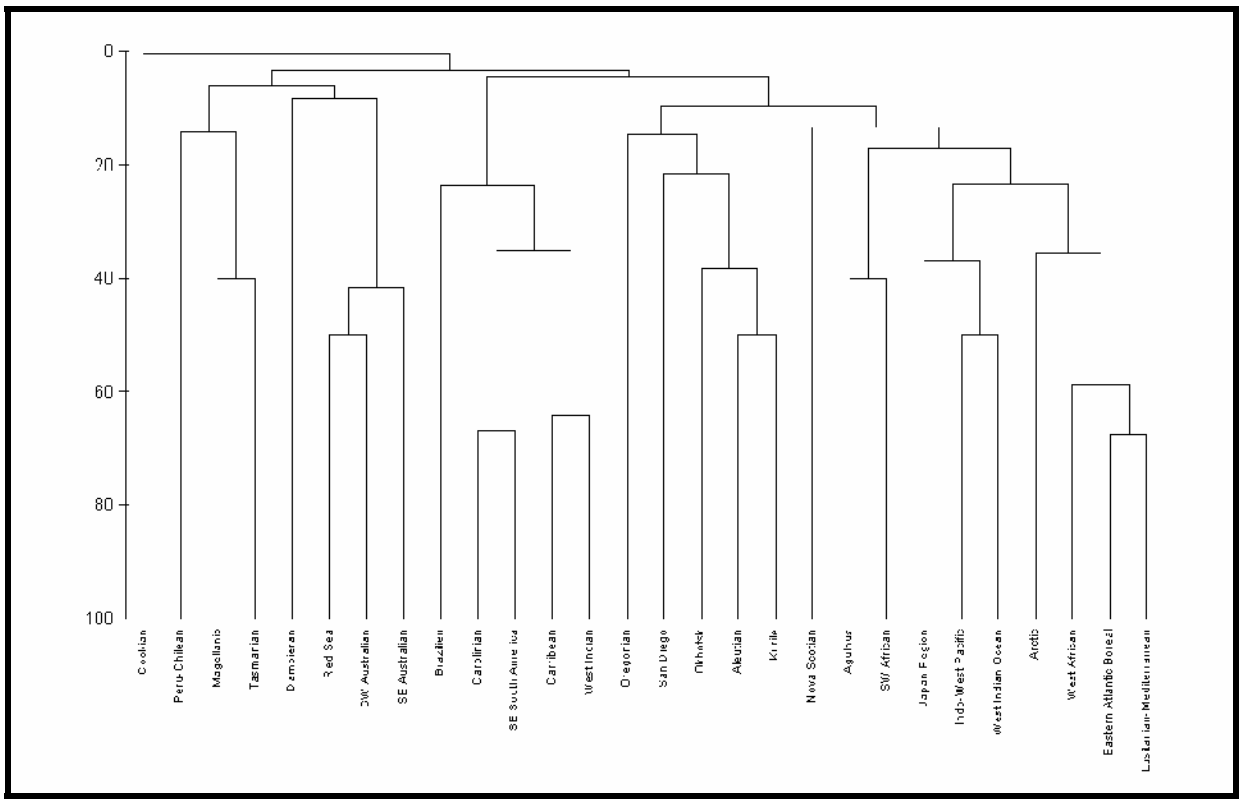


Figure 28. Cluster analysis output on genus presence/abscende data in the Briggs Marine Areas. Dominant genera are not included in the analysis

	S	D	H'(loge)	Delta+	Lambda+
Agulhus	27	7,88	3,29	57,50	261,85
Aleutian	18	5,88	2,89	50,43	243,09
Arctic	40	10,57	3,68	50,17	281,30
Brazilien	7	3,08	1,94	59,52	200,30
Carolinian	5	2,48	1,60	60	177,77
Carribean	34	9,35	3,52	51,81	232,90
Cookian	4	2,16	1,38	41,66	625,00
Dampieran	19	6,11	2,94	46,78	478,60
Eastern Atlantic Boreal	89	19,60	4,48	53,93	218,19
Indo-West Pacific	102	21,83	4,62	59,30	270,61
Japan Region	65	15,33	4,17	54,14	287,45
Kurile	12	4,42	2,48	56,81	336,50
Lusitanian-Mediterranean	120	24,85	4,78	53,37	200,27
Magellanic	6	2,79	1,79	52,22	180,24
Mexico	2	1,44	0,69	16,66	0
Nova Scotian	10	3,90	2,30	45,18	242,24
Okhotsk	9	3,64	2,19	53,70	372,08
Oregonian	5	2,48	1,60	50,00	277,77
Panamanian	3	1,82	1,09	16,66	0
Peru-Chilean	12	4,42	2,48	65,40	633,92
Red Sea	9	3,64	2,19	57,87	269,84
San Diego	13	4,67	2,56	46,79	164,22
SE Australian	13	4,67	2,56	50,21	416,62
SE South America	7	3,08	1,94	40,47	306,12
SW African	18	5,88	2,89	55,77	338,85
SW Australian	9	3,64	2,19	43,05	576,77
Tasmanian	3	1,82	1,09	61,11	61,72
West African	150	29,73	5,01	51,91	205,11
West Indian	35	9,56	3,55	57,59	272,44
West Indian Ocean	50	12,52	3,91	60,31	270,06

Table 7. Diversity indices for each 'Briggs' biodiversity regions (S= number of species, d=Margalev species richness, H'= Shannon diversity, Delta+ = Taxonomic Diversity compared to the Mysida species master list, Lambda + = Taxonomic distinctness)

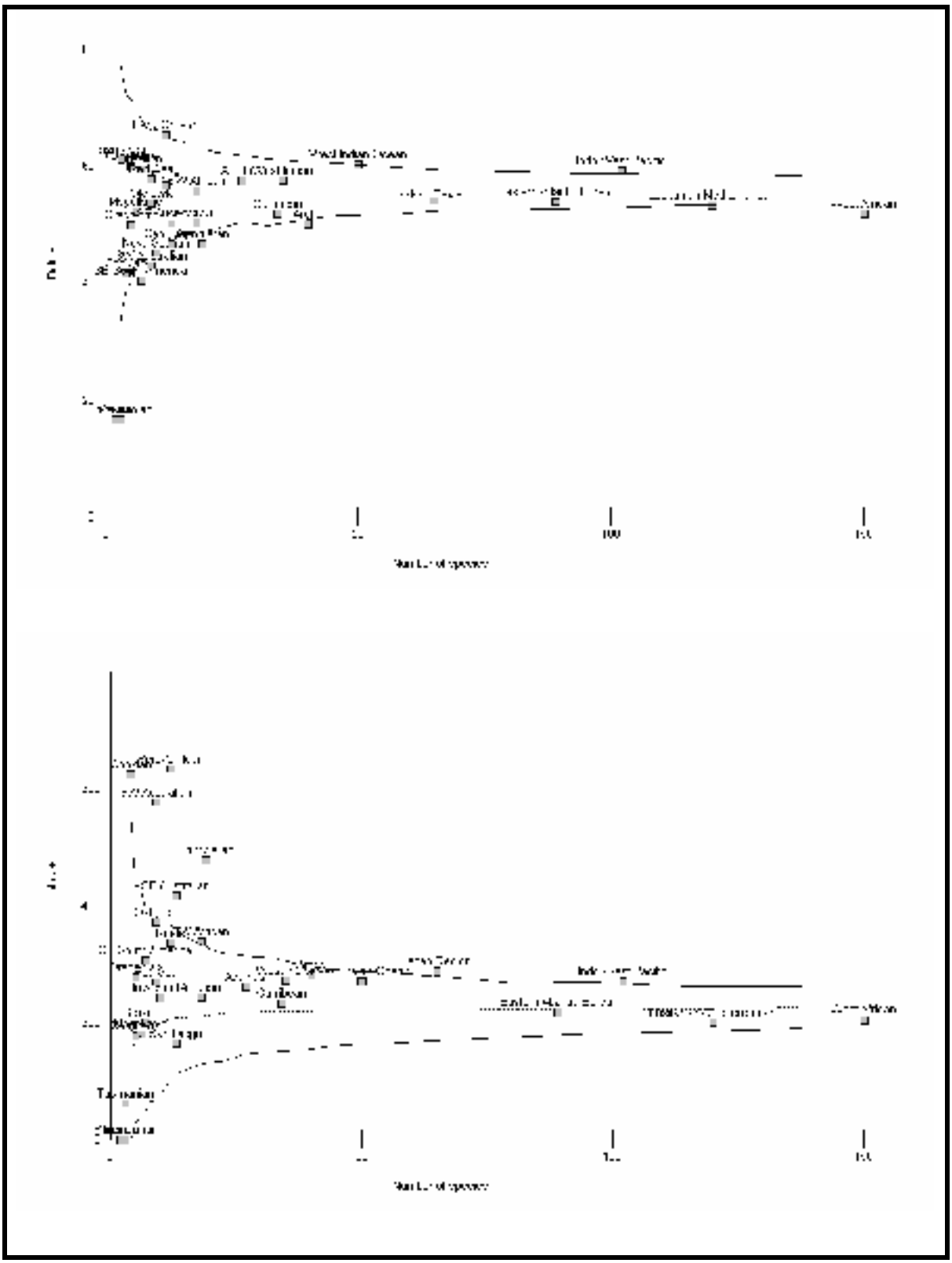


Figure 29. 95% probability funnels for Average Taxonomic Distinctness and Variation in Taxonomic distinctness plotted against the number of species for different Mysida assemblages in the Briggs Biogeography areas. Dashed lines indicate the simulated Delta + and Lambda + from 1000 random selections from the master list of 1086 Species

- **4.1.5. Summary of global results**

The major trends in all presented analyses are:

(1) The larger the analyzed areas, the clearer relations between the different areas are (see Mauchline model on page 221).

(2) North-South division: the latitudinal analysis of the genus distributions and the tests with biogeography models both show there is a clear difference in taxonomic composition between the Northern and Southern hemisphere. Although the Northern hemisphere is much more investigated, its taxonomic composition (including all taxonomic levels) is poorer than in the Southern.

(3) Certain genera seem to have an endemic distribution. They mostly occur in tropical areas and in the Southern hemisphere. The amount of endemism is clearly related to the size of the studied areas. A combined scan through both the latitudinal ranges and the different tested biogeography area models produces a list of true endemic genera: *Antarctomysis, Antichthomysis, Atlanterythrops, Brasilomysis, Calyptomma, Holmesimysis, Holmsiella, Nanomysis, Neoheteromysis, Pseudomysidetes, Synerythrops and Tasmanomysis*. (figure 30)

(4) Few genera have a wide geographic distribution, namely *Siriella, Gastrosaccus*, *Anchialina*, *Boreomysis*.

(5) A number of smaller regions contain a typical mysid fauna: (1) Red sea area, (2) Antarctica, (3) Caribbean area, (4) Western Australia, (5) Banda Flores Sea, (6) Southern Australian Area, (7) California Current Area, (8) Mediterranean Sea, (9) Yellow sea, (10) Maladives area.

(6) Certain areas show a high taxonomic variation in their fauna: (1) East Indies, (2) North-Western Indian Ocean, (3) Japan, (4) Carribean area.

(7) The ‘Mauchline’ area model and the ‘Briggs’ area model gave the clearest results (the distribution of Mysida fits most in these area models). All others had at least some regions with very high similarities. Furthermore, data had to be reduced by removing outliers, in order to get clear results.

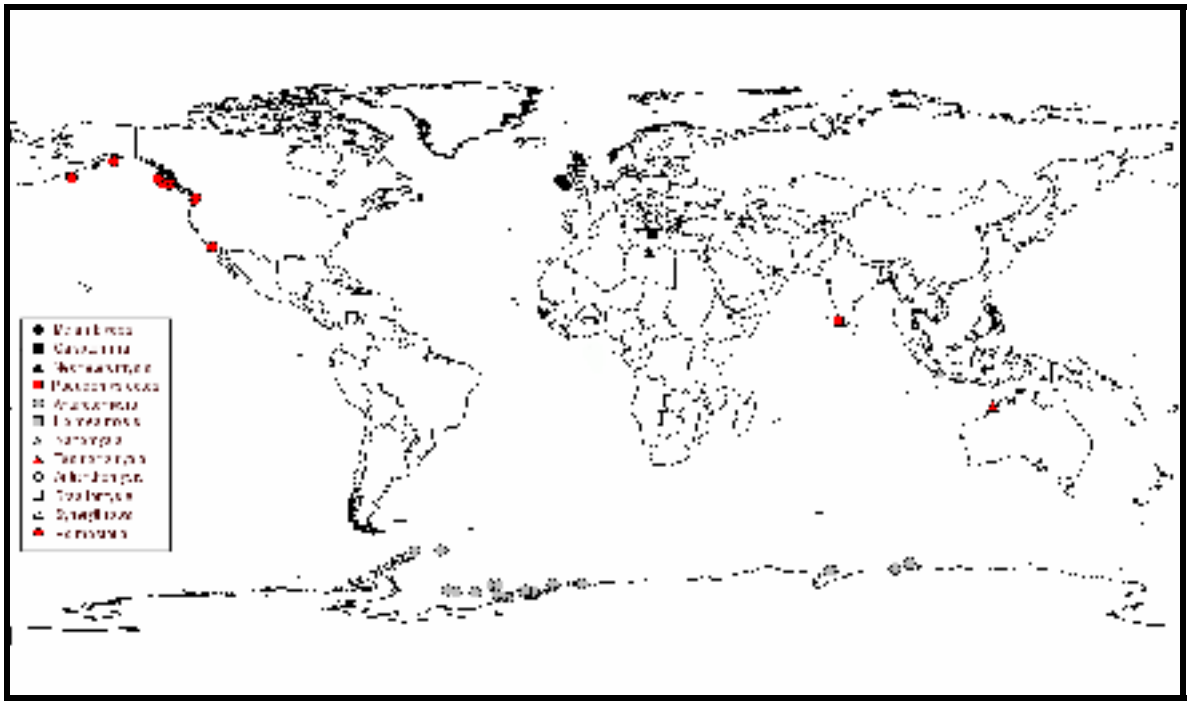


Figure 30. Distributions of genera with a limited geographical spreading

▪ 4.2. REGIONAL ANALYSIS (EUROPE)

The European area (between 30° and 90° North and between 30° West and 50° East) turns out to be the most frequently sampled area. The cumulative species description rate reached a plateau phase (figure 10), meaning the fauna of the region is well-described. Therefore, the European area is analyzed separately in greater detail.

• 4.2.1. Data overview

The total number of records used is 6219 (EurOBIS: 986, NeMys: 5233). Most records (92%) are coastal (figure 31). Although the locations are randomly well spread, some regions still lack a good cover: the Iberian area, and the Southern coasts of the Mediterranean Sea.

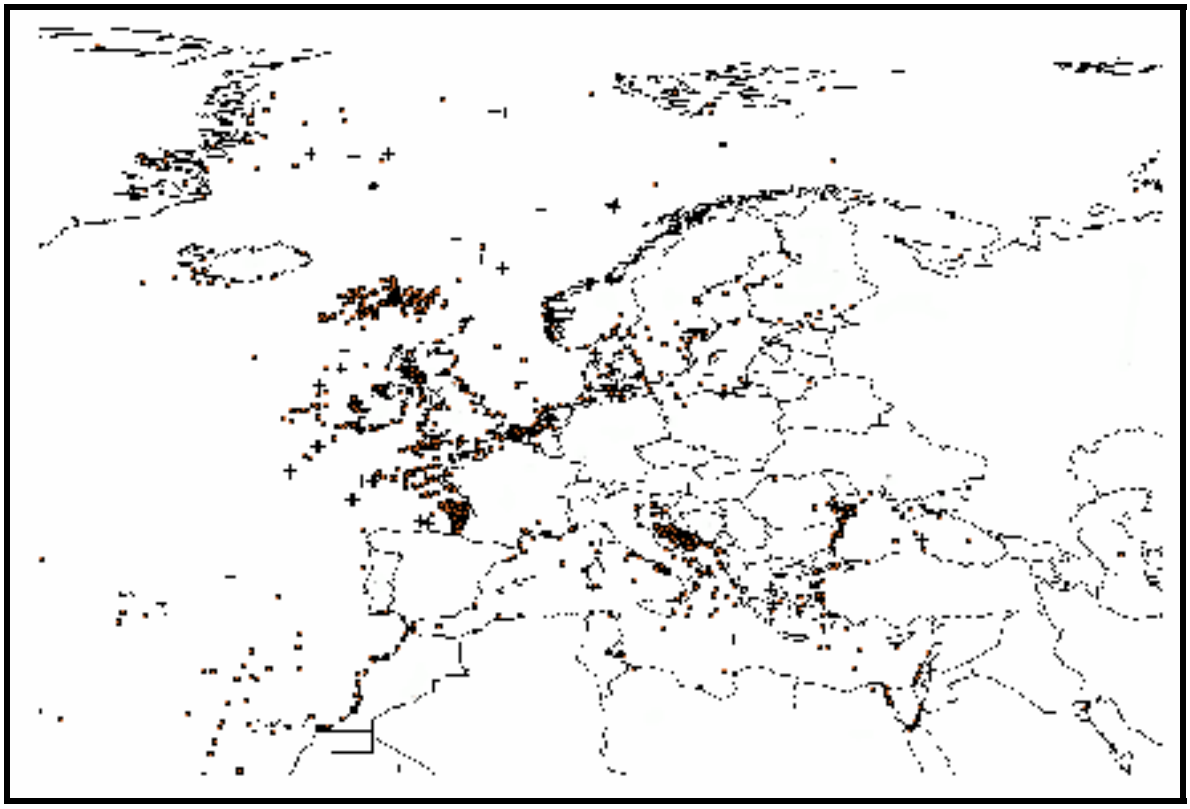


Figure 31. Distribution of European Mysida records (+ : EurOBIS records; □ : NeMys records)

- **4.2.2. Richness and diversity**

The coast of the UK, the Channel area, the Gulf of Biscay, the Adriatic sea and the Black Sea are found to be more species rich than other areas (figure 32). The same regions, combined with the Aegean Sea, show up in the species diversity analysis (figure 33).

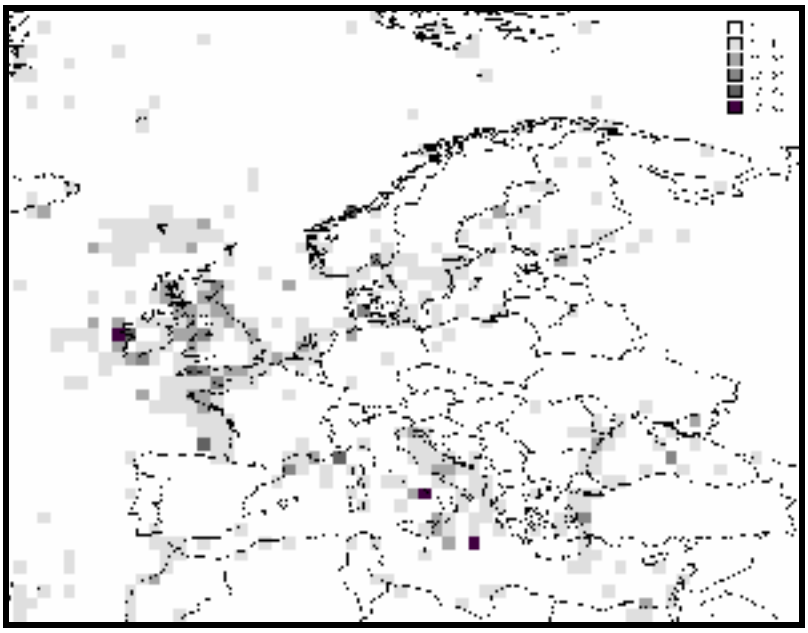


Figure 32. Species richness plot on a 2° overlay grid for the European Area

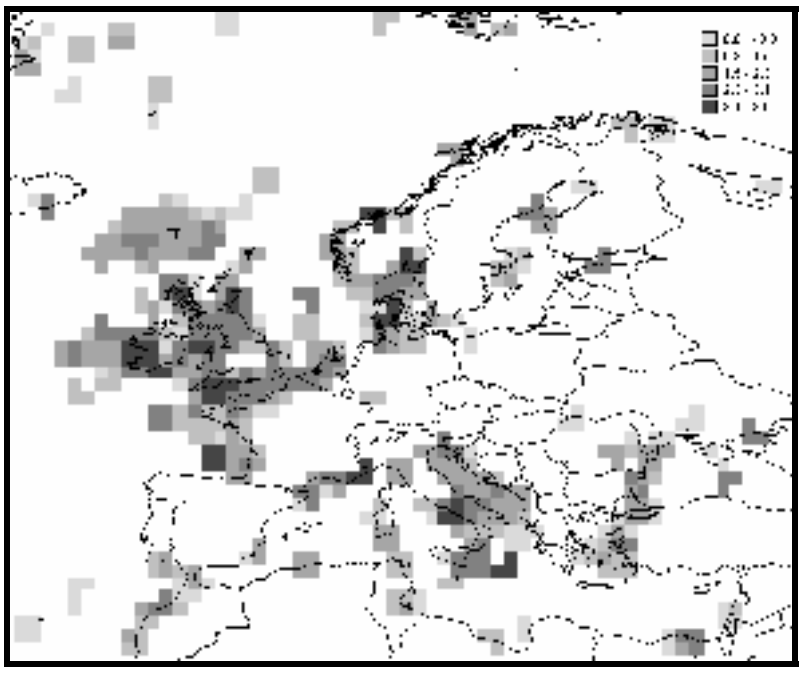


Figure 33. Species diversity plot on a 2° overlay grid for the European area (Shannon)

- **4.2.3. Regional analysis**

The European dataset is analyzed similar to the global analysis. The study area is divided in 29 areas (see page 230): Adriatic Sea, Aegean Sea, Alboran Sea, Baltic Sea, Barentsz Sea, Bay of Biscay, Black Sea, Bristol Channel, Celtic Sea, English Channel, Greenland Sea, Gulf of Bothnia, Gulf of Finland, Inner Seas off the West Coast of Scotland, Ionian Sea, Irish Sea and St. George's Channel, Kattegat, Ligurian Sea, Mediterranean Sea - Eastern Basin, Mediterranean Sea - Western Basin, North Atlantic Ocean, North Sea, Norwegian Sea, Sea of Azov, Sea of Marmara, Skaggerak, Strait of Gibraltar, Tyrrhenian Sea, White Sea. For each area the fauna was specified. In total 52 genera and 154 species were found.

	S	D	H'(loge)	Delta+	Lambda+
Adriatic Sea	26	7,67	3,25	55,79	221,97
Aegean Sea	23	7,01	3,13	57,11	215,08
Alboran Sea	1		0	0	0
Baltic Sea	7	3,08	1,94	45,23	268,32
Barentsz Sea	3	1,82	1,09	50,00	555,55
Bay of Biscay	42	10,96	3,73	55,01	209,41
Black Sea	27	7,88	3,29	42,07	297,20
Bristol Channel	3	1,82	1,09	50,00	555,55
Celtic Sea	34	9,35	3,52	52,13	201,40
English Channel	35	9,56	3,55	55,09	217,70
Greenland Sea	20	6,34	2,99	47,36	174,36
Gulf of Bothnia	13	4,67	2,56	46,79	157,10
Gulf of Finland	8	3,36	2,07	43,45	264,66
Inner Seas off the West Coast of Scotland	23	7,01	3,13	53,03	216,99
Ionian Sea	45	11,55	3,80	54,96	179,31
Irish Sea and St_ George's Channel	33	9,15	3,49	52,93	199,18
Kattegat	7	3,08	1,94	49,20	197,78
Ligurian Sea	7	3,08	1,94	57,14	226,75
Mediterranean Sea - Eastern Basin	9	3,64	2,19	59,72	175,54
Mediterranean Sea - Western Basin	39	10,37	3,66	55,39	183,03
North Atlantic Ocean	72	16,60	4,27	54,29	247,63
North Sea	40	10,57	3,68	56,43	222,52
Norwegian Sea	42	10,96	3,73	53,65	234,71
Sea of Azov	11	4,17	2,39	51,81	269,42
Sea of Marmara	5	2,48	1,60	65,00	25,00
Skaggerak	21	6,56	3,04	50,39	173,12
Tyrrhenian Sea	41	10,77	3,71	55,50	199,67
White Sea	1		0	0	0

Table 8. Diversity indices for each european marine area (S= number of species, d=Margalev species richness, H'= Shannon diversity, Delta+ = Taxonomic Diversity compared to the Mysida species master list, Lambda + = Taxonomic distinctness)

The White Sea and the Alboran sea were left out for further analysis. They have only one species reported and, as a consequence, no representative results can be derived. The cluster and nMDS outputs, based upon the species assemblages of all marine areas (figure 34 & 35), illustrate following patterns: (1) regions are arranged along a latitudinal gradient, (2) Scandinavian Seas cluster together, (3) most Mediterranean related areas also cluster together (except the eastern part of the Mediterranean Sea), (4) North Sea related areas also cluster well together.

Based on these analyses, 4 regional faunas can be distinguished in Europe with each region characterized by a number of typical species:

1. North-East Atlantic fauna: *Amblyops kempi, A. spinifera, A. tenuicauda, A. trisetosa, Amblyopsoides ohlinii, Atlanterythrops crassipes, Bathymysis helgae, Boreomysis inermis, B. tridens, B. vanhoeffeni, Chunomysis diadema, Dactylamblyops goniops, Dactylerythrops bidigitata, D. dactylops, D. dimorpha, Hansenomysis fyllae, Hypererythrops serriventer, Katerythrops oceanae, Metamblyops oculata, Meterythrops picta, Michthyops parva, Mysidella biscayensis, M. typhlops, Paramblyops bidigitata, Parapseudomma calloplura, Parerythrops bispinosa, Parerythrops paucispinosa, Petalophthalmus armiger, Pseudomma affine, P. jasi, P. nanum, P. truncatum, Schistomysis kervillei.*

2. Mediterranean fauna: *Boreomysis tregouboffi, Calyptomma puritani, Diamysis camassai, Erythrops neapolitana, E. peterdohrni, Euchaetomera glyphidophthalmica, Euchaetomeropsis merolepis, Gastrosaccus mediterraneus, G. roscoffensis, Haplostylus bacescui, H. lobatus, H. magnilobatus, Hemimysis speluncola, Heteromysis arianii, H. armoricana, H. eideri, H. lybiana, H. microps, Hypererythrops richardi, Leptomysis buergii, L. megalops, L. posidoniae, Mesopodopsis aegyptica, Neoheteromysis muelleri, Paraleptomysis apiops, P. banyulensis, Paramysis kosswigi, Parerythrops lobiancoi, Pseudomma chatoni, Pyroleptomysis rubra, Siriella castellabatensis.*

3. Black Sea Fauna: *Diamysis pengoi, Hemimysis anomala, H. serrata, Katamysis warpachowsky, Mesomysis intermedia, Mesomysis Kowalewskyi, Mesomysis kröyeri, Neomysis intermedia, Paramysis kessleri, P. kroyeri, P. lacustris, P. pontica, P. proconnesia, P. ullskyi.*

4. Scandinavian fauna: *Amblyops sarsii, Boreomysis artica, Meterythrops robusta, Michthyops theeli, Mysideis grandis, Mysis polaris, Pseudomma théeli, Pseudomysis abyssi.*

Five species are generalists. They occur in all European seas: *Hemimysis lamornae, Gastrosaccus spinifer, Erythrops erythropthalma, Schistomysis ornate* (absent in the Black Sea), *Schistomysis spiritus* (absent in the Black Sea).

The taxonomic composition of all European areas id confined to more or less the expected ranges (figure 36). The Black Sea variation in taxonomic distinctness is lower than expected. This may be due to a large number of 'endemic' species belonging to the genus *Paramysis*. Finally, all members of the region-typical fauna belong to the *Mysinae.* Therefore, the variation at higher taxonomic level is rather low.

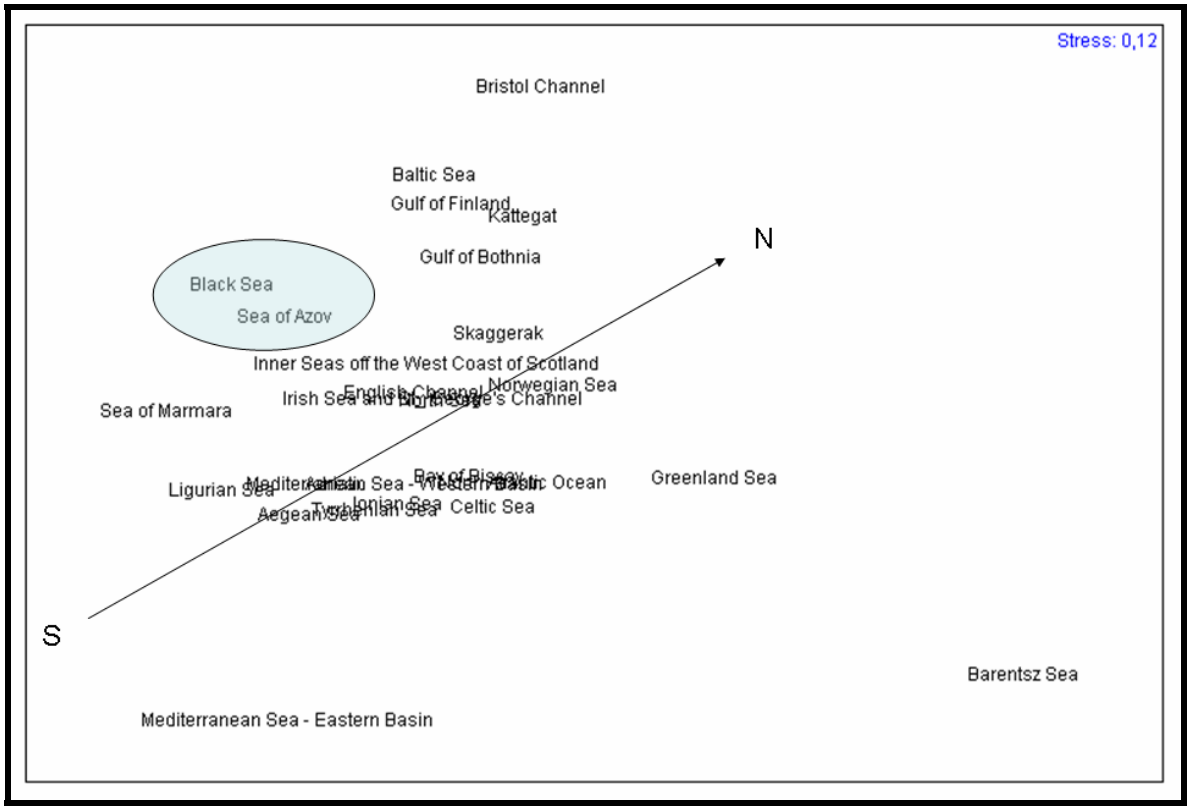


Figure 34. Output of Non-metric Multi-dimensional scalind (MDS) on species presence/absence data in European marine areas (stress 0.12)

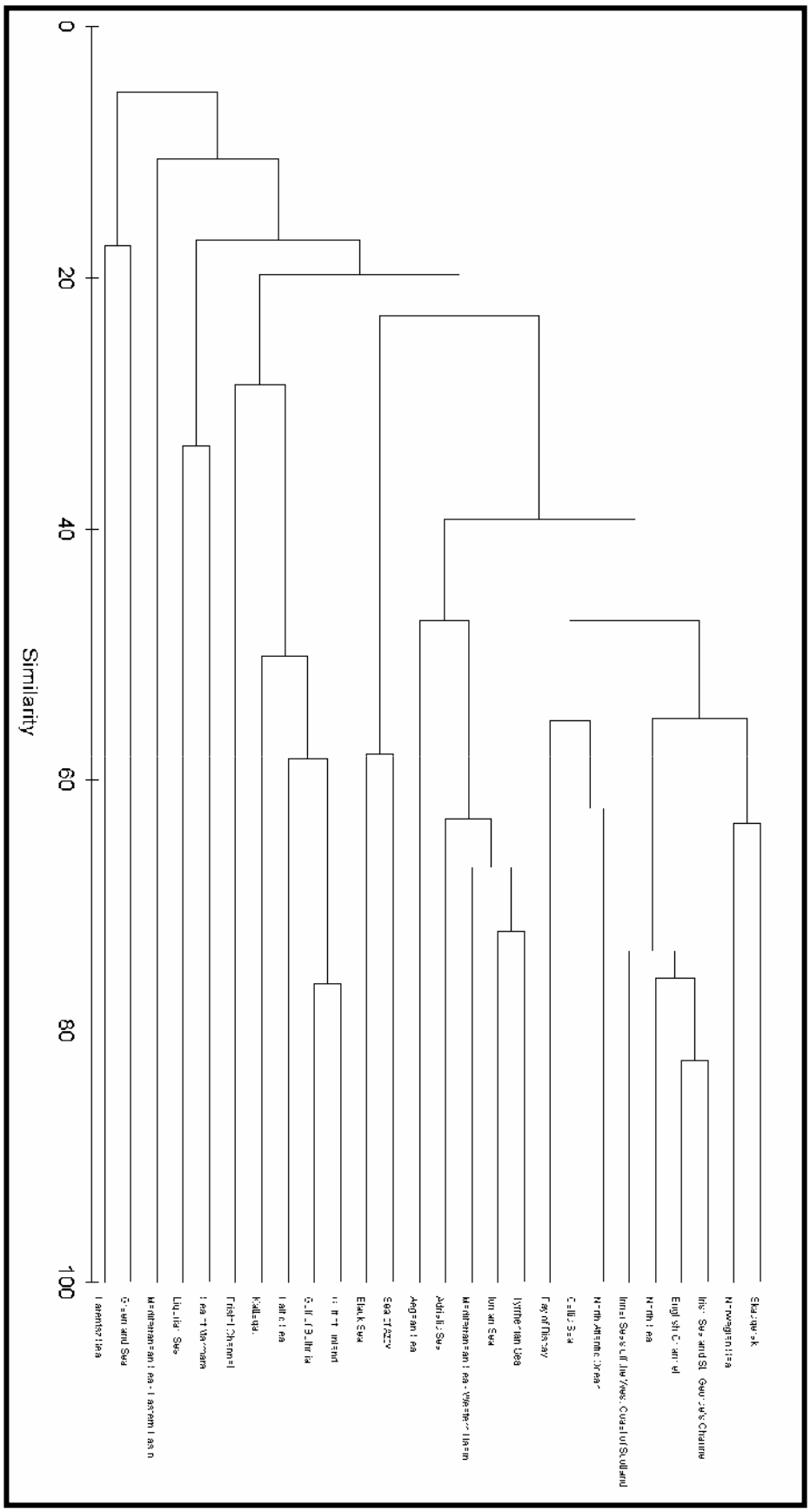


Figure 35. Cluster analysis based upon species presence/absence similarity data for 27 european marine areas

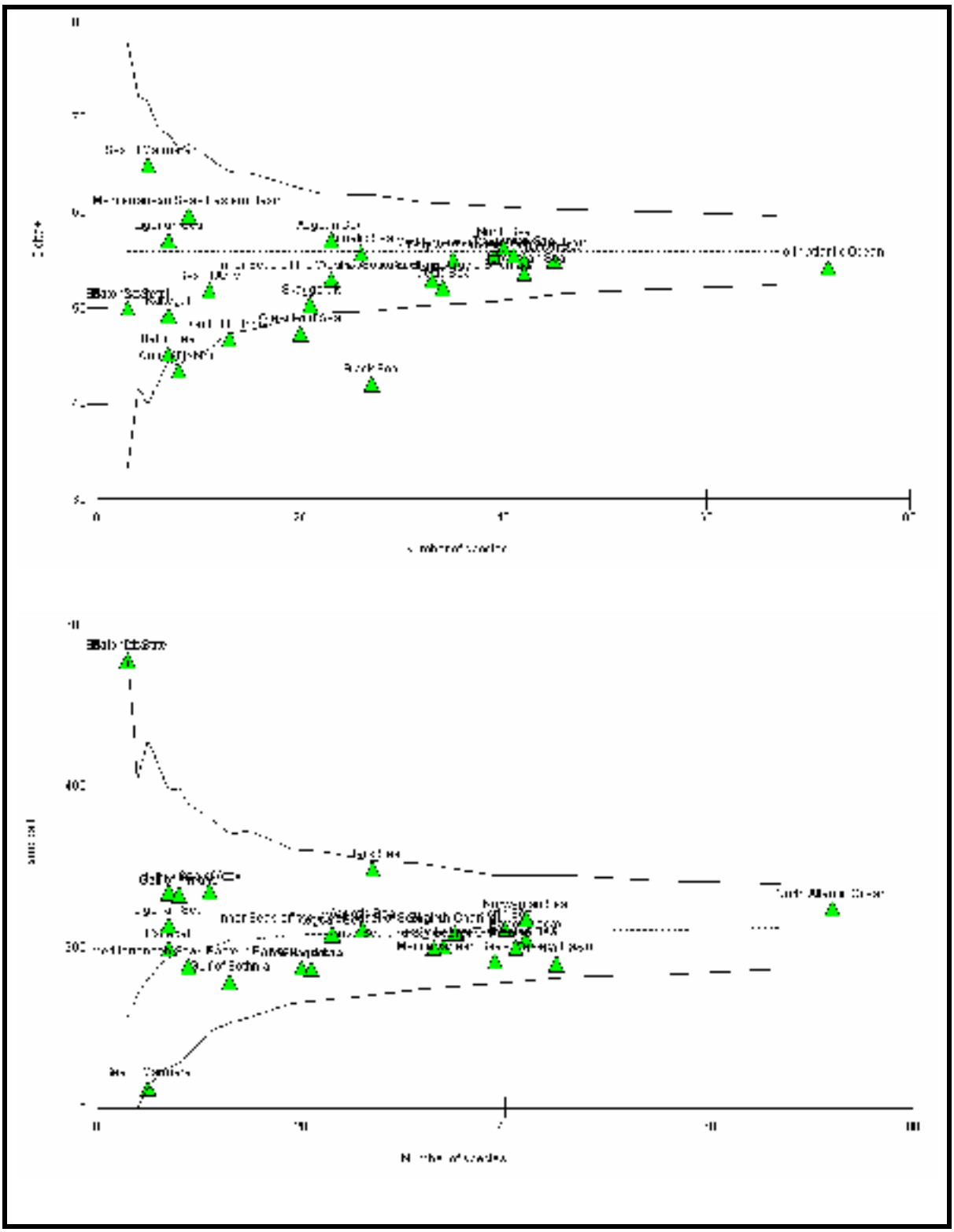


Figure 36. 95% probability funnels for Average Taxonomic Distinctness and Variation in Taxonomic distinctness plotted against the number of species for different mysida assemblages in European marine waters. Dashed lines indicate the simulated Delta + and Lambda + from 1000 random selections from the master list of 1086 species.

5. Discussion

In this study, the first part of the question formulated in the introduction of this chapter 'Where do Mysida occur ? ' is answered from different points of view. The second part of this first question ' … and why do they occur in this range?' is much more difficult to answer, because it can be interpreted in two ways: (1) the reasons for the occupied range can lay in the biology of the species, or (2) the distributions can be explained by a number of environmental changes on a long or short term. Both reasons are strongly related to each other. As this study does not focus on biological aspects of distinct species, species-related reasons will not be discussed.

The biogeography of a higher taxonomic marine group on a global scale is not often studied. Recently, a few studies mainly based on molecular phylogenetic data (Anderson, 2000; Bellwood & Wainwright, 2002; Colborn *et al*. 2001; Howes, 1991), were published, mostly focusing on fish. Comparing the Mysida biogeography with closely related groups is not possible yet.

The questions concerning Mysida biogeography will remain partly unresolved. The conclusions drawn (see above and further) are strongly dependant on the quality of the used dataset. Most statistical analyses (e.g. ANISIM analysis, many nMDS-plots) also give results with rather low statistic relevance. The reasons for this were already given, although many others may have an influence.

(1) **strong relation with research effort**: it is shown that many of the observed patterns in the dataset are strongly related with the amount of research in particular regions. When analyzing global datasets, this problem appears regularly (Dumont, 1983; Funk *et al.*, 2005). At first sight, some habitat-rich areas, often recognized as hotspots of biodiversity, appear not to be unusual in the total picture (for example Madagascar, Great Barrier Reef) (Meyers *et al.*, 2000). This effect can only partly be tackled by using effort independent statistical analysis techniques. One of the methods often proposed is the 'rarefraction' diversity index (Caprariis, 1984). Although this technique leads to promising results in many cases, it has a few restrictions by which it becomes irrelevant for this dataset. It requires standardized sampling

methods in all research areas. It also assumes samples being randomly dispersed. Both requirements are not fulfilled in this study. To overcome the 'research effort'-related limitations of this dataset, the analysis of average taxonomic distinctness and variation of average taxonomic distinctness is used. This technique is based on presence/absence data and is the only technique taking which also takes higher taxonomic levels into account (Warwick & Clarke, 1995). A third relatively simple way of eliminating the research effort problem is splitting the dataset in sufficiently large regions with enough samples over the complete area or by working with sufficiently small regions. Although results are highly influenced by research effort, these problems may be considered as a result of the study as well. It helps to determine regions of prior interest for future research.

(2) **Relation with systematic history**: the uniqueness of this dataset is its literature based origin. However, this is also a main problem when comparing data. For example: 60 years ago, certain specimens were identified as speciesX. Recently speciesX may have been split up in 6 other species, previously all recognized as variations of speciesX. Except for taxonomic publications, identifications of species are based on the taxonomy of that particular period (example: before 1992, *Mesopodopsis slabberi* was regularly reported from European waters and South African waters. In 1992, Wittmann split the species in a number of distinct species of which *M. wooldridgei* is recognized as the formerly known *M*. *slabberi* of South African waters.). Many identifications up to species level may be doubtful. Nevertheless the identifications up to genus level are much more reliable. For this reason, most area-models and latitudinal patterns were tested with genus-distribution data. Another way to handle this problem is by comparing similar random sets of records in different time periods, and looking at changes in taxonomic composition. Such methodology requires a minimum number of records randomly spread over all studied areas in the selected periods. Another consequence of the literature based origin of the dataset is the 'author-effect'. Each data record relies on the data-originator, who are (in many cases) the authors of the publication. The correctness of the identification of the specimens depends on the scientific capacities of the

authors. Verifying the correctness of historical identifications is mostly impossible. 'Mismatch' distributions may be an indication of misidentified specimens.

(3) **Efficiency of sampling methods:** Several factors influence whether mysid species are trapped or not during sampling. The most important one is the used sampling methodology. Many older publications do not supply sufficient data on used gear and methodology. Consequently, the representation of the true fauna in a sample is very uncertain. Additionally, many species live in schools (Mauchline, 1980), meaning that only by sampling regularly, a representative view of the fauna on a certain spot can be obtained. A study, conducted along a South-African beach, clearly showed this effect. From literature (Wooldridge, 1988), it was known that *Gastrosaccus bispinosa* occurred in the swash zone of that particular beach. In total, 12 samplings with a small hyperbenthic sledge were performed before catching the focused species (Deprez, unpublished data).

(4) **Availability of the data**: for many regions much more data is available than is known. A problem with this data is that it is published in publications with a non-taxonomical or non-biogeographical scope, or even not published. Many ecological research results are published without mentioning exact species identification details. Finding relevant publications, which mention a species name in the text but not in title, abstract or keywords, is impossible through classical library indexes. (for example: Oh *et al*. describe feeding aspects of *Crangon crangon* (2001) and report *Schistomysis spiritus*, a mysid as part of the diet. Through the key words or the title no indication of record of *S. spiritus* could be retrieved.) Creating indexed electronic catalogues, including the text of the publication should solve this problem.

▪ 5.1. GLOBAL PATTERNS

Although there are many (hidden) problems in this dataset, some patterns were retrieved. The fauna of the Northern hemisphere differs from the fauna of the Southern hemisphere. This may be mainly due to the latitudinal limited range of most of the genera. Latitudinal ranges are closely related with ranges in sea surface temperature. Temperature may be considered as one of the determining borders in the geographical range of many species. Well known biogeographical borders like the southern entrance of the Red Sea (depth and salinity) (Cox & Moore, 2005) do also influence species biogeographical ranges. Another important factor, for many species limited to the continental shelf, is the substrate type of the sea floor. Many large rivers influence the constitution of this substrate and many chemical properties in its surroundings. The river mouth of the Orinoco and the Amazon may influence the taxonomic composition in surrounding areas a lot. For these specific areas, not enough data is available yet to prove the correctness of this theory for Mysida.

The high mobility (active swimming) of many species enlarges their dispersal capacities. However, the lack of a planktonic larval phase in the Mysida restricts the dispersal capacities through passive transport with sea surface currents. This passive transport is documented for many other taxa (Luschi *et al*. 2003).

Explaining observed ranges is only possible by taking into account all kinds of processes (on small and large geographic scales and over short and long periods in time).

Of all tested area models, two models fitted the dataset relatively well: the ‘Mauchline’ model using grid with large ocean-related areas, and the “Briggs” marine coastal areas.

Mauchline area model (1980): Mysid genera and species are linked to a certain oceanic water body. This also means that all oceans have a number of genera which are unique to that ocean. From an evolutionary point of view this can be interpreted in two ways: (1) these genera were formerly also present in other oceans and subsequently became extinct in these neighbor oceans or (2) these genera did evolve in the ocean after it was formed. As mainly coastal species are studied, with

less exchange capacities to other oceanic areas, the second interpretation may be most plausible. Concerning the number of oceanic 'endemic' genera, the Australasian area, the Western Indian Ocean area and the North Atlantic Ocean have the largest number of 'endemics'. When including all genera, only the Australasian area and the Western Indian Ocean area exceed, one fifth of their genera being 'endemic'. The large number of regional genera in the North Atlantic is most probably also due to the research effort in that particular area. As the species-description-rate curve in the Indian Ocean area has not reached an asymptotic plateau yet, it may be expected that the amount of 'endemic genera' for both the Indian Ocean and the Australasian area further increases in the future.

Two thirds of all genera occur in more than one oceanic region. Twenty genera have representatives in all oceanic basins, 30 genera occur in 2 basins. The remaining genera are limited to only one ocean. A possible reason may be found in the tectonic history of the oceanic basins. Many genera may have existed for many million years. During the Jurassic and Cretaceaous era (150 million years – 80 million years ago) all precedents of the current oceanic basins were connected by a Tethyan Seaway (Cox & Moore, 2005). The present continents, forming the borders of the current oceanic basins could in these periods be considered as islands with a continuous coastline. The current coastal borders of North and South America were connected, the West African and East African borders were connected, and European coastlines were connected with the North American ones. This last connection is existed before the beginning of seafloor spreading in the Northern Atlantic area. Current distributions of genera like *Parerythrops*, *Praunus*, *Katherythrops*, *Mysideis* might be explained by this northern connection between the present North East Atlantic and North West Atlantic coasts. Distributions of some other genera in the 'Mauchline Area model' may also be explained by tectonic events. *Gastrosaccus* is known from North-East Atlantic, East Atlantic and Western Indian Ocean waters. This genus may have developed after the breakup of the North East and North West Atlantic coast lines about 50 million years ago. During this period a connection between the North East Atlantic and the Western Indian Ocean still was present. A global ancestral form of the genus probably existed much earlier. The sister genus *Bowmaniella* is reported from American waters and

Archaeomysis and *Haplostylus* are reported from Indian Ocean, European and Indo-Pacific waters.

Three genera are found to be dominant in all analyses: *Siriella, Anchialina* and *Boreomysis*. These three can be defined as cosmopolitan genera. *Anchialina* and *Siriella* are discussed in more detail in the following chapters.

The second model matching the dataset is the biogeographical **area model as described by Briggs (1974)**. For all tropical provinces a high number of endemics is, similarly as for fish and corals, found for the Mysida. Based on taxon composition, certain geographically related regions cluster, relatively close together. They might have a similar history, or exchange between regions might have occurred. The Red Sea clusters relatively well together with Australian areas. The high similarity in genus composition may be due to a relatively large number of globally common genera in all regions. However, the species composition of both regions clearly differs.

The taxonomic distinctness analysis shows that some of the provinces are taxonomically more diverse than expected. Most of these provinces are related to the 'East Indies Triangle' (Briggs, 2005a; Briggs, 2005b). This region is described as the most important driving engine for speciation in the entire Indo-Pacific area. For many other marine taxa it has been proven that, due to both sympatric and allopatric processes, this region is a true 'center of origin' (Fishes: Allen & Adrim, 2003; Corals: Veron, 1995). The history of the region is of main importance to explain this. Originally the region was situated in between the African and Eurasian continent. It moved to its current location due to plate tectonics and is relatively isolated from other regions in the area. The features, which drive speciation, are for example an ideal climatological history, or a high number of habitat types. The Large Marine Ecosystem model also demonstrates this region as distinctly diverse. Because up to now the research effort in this region was relatively low, it may be expected that many more new mysid species will be described from this area. The 'East Indies Triangle' may be considered as a center of origin for the order Mysida. The Darwin-Wallace dispersal paradigm with a center of origin, as the general descriptor for global biogeographical patterns, may be essential for explaining Mysida biogeography.

In order to confirm the East-Indies as a center of origin for Mysida, molecular study of specimens from the region, with the aim of determining the evolutionary age of East-Indies species, may be useful. Currently, no species from the East-Indies have been included in molecular phylogenetic analyses (Remerie *et al.*, 2004).

Another region of particular interest is the Caribbean area. In both the LME model and the WWF model, the area clearly is separated from other provinces. The analysis with the Briggs (1974) model supports this less clearly, although in the presented cluster analysis, the region is grouped in a separate branch, together with its neighboring regions. Currently, it can not be concluded that the taxonomic diversity of the Caribbean area is higher than in other regions. Briggs (2006) describes this region, also as a centre of origin, similar to the East-Indies, although less clearly pronounced.

Other areas, recognized as centers of origin, are Antarctica and the North Pacific (Heads, 2005; Briggs, 2006). Antarctica is separated from other areas in all performed analyses, although this is mainly due to the large proportional influence of the genus *Antarctomysis*. Currently, the available data is limited to the Weddell Sea and Prydz Bay. Data from less researched regions should give a better view on the number of endemics of the Antarctic waters.

All Northern Polar regions were found to be different from other regions in all analyses. This proves that Mysida species are limited to a specific temperature range. The most abundant genera in these colder areas are: *Boreomysis, Pseudomma, Erythrops, Amblyops, Mysis,* and *Dactylamblyops*. In total, about 100 species are reported from the area North of 60° latitude. Mauchline (1980) reports only 8 species from the Arctic Ocean. The current dataset updates this list with another 32. This is mainly due to the consultation of a much higher number of published sources from the area (Geiger, 1969; Shih & Laubitz, 1978; Ohlin, 1901; Stephensen, 1933; Faxon, 1895; Stephensen, 1943; Just, 1970; Holt & Tattersall, 1906).

Although Mauchline (1980) stated that mapping of records is of limited value, the presented dataset shows, that even with a rather problematic dataset, it is valuable to examine a number of biogeographical issues. Examining the global distribution

through an area-model and using recent statistical sample-size-independent techniques, allows recognizing some global patterns. Although these patterns are not fully defined, we conclude that the distribution patterns of the Mysida have the following characteristics:

(1) **Distributions of Mysida reflect the history of the oceanic basins**. Certain 'older genera' can be distinguished as occurring in different oceanic basins and some 'younger taxa' as limited to one ocean. They thus came into existence after the formation of the oceanic basins (cfr. Mauchline area model p. 221).

(2) **Three large global regions of high or distinct diversity are recognised**, and therefore also play an evolutionary important role: **East Indies, Caribbean Area, Antarctica**.

(3) **Many small areas with a distinct diversity (on species level) are found**. They are, mainly due to the lack of a sufficient amount of data, sometimes dubious: Red Sea, Agulhus current area, Mediterranean Sea, Californian Coast, W-Australia, North West Pacific. All these regions are enclosed areas, or are influenced by major currents. These currents play an important role as temperature and salinity barriers, and can determine the productivity of the ecosystem of an area (transport of food resources).

(4) **Temperature is a limiting factor** for the distribution of many genera/species (cfr. Polar fauna).

(5) **Eastern and Western coastal faunas of oceans do not have much taxa in common.** Mysids do not disperse (except for oceanic taxa) by making use of oceanic currents.

(6) **The Darwin-Wallace paradigm,** based on a long tectonical history perspective, is the main process to explain Mysida biogeography.

Mysida biogeography fits with some generally accepted biogeographical theories. Adey and Steneck (2001) found similar results for benthic marine algae and tried to build a model, explaining and even predicting distributions. Three major parameters

were included in this model: temperature, time and space. Although it explains well some of their observations, it is relatively limited in time (18000 years) and restricted to one habitat type (rocky shores). A similar model, using a larger time frame and taking into account some of the area models, should allow to predict faunas in less researched areas. A Mysida predictive model should, as no planktonic stages exist, take long distance dispersal into account as well. Cook and Crisp (2005) discuss that these long-distance dispersal mechanisms often lead to doubtful interpretations of distributions. An ideal model should also take phylogenetic relationships into account as well. Predicted faunas for regions can as such be checked with phylogenetic area models (Veller, 2001).

▪ 5.2. EUROPE

The European mysid fauna is well known. Consequently, recent work in this area is no longer taxonomically oriented, but focuses mainly on ecological and environmental aspects (e.g. Roast *et al*., 2002; Verslycke *et al*., 2003), life history (Gorokhova, 2002) and molecular aspects (Remerie, 2005; Remerie *et al*., 2004). Although the fauna is well known the recent availability of distributional datasets still makes an analysis valuable.

The dataset used for analysing the mysid fauna of European waters, combining published sources and research datasets, may be discussable. Duplication of data (through publications based on present research datasets) is possible. However, analysis of the locations did not show duplication, except for some estuary bound datasets. Moreover, the amount of data in the EurOBIS database is much smaller than in the NeMys dataset. The EurOBIS records may be considered as an addition to the NeMys records, adding data for a few uncovered areas in NeMys (for example the Northern North Sea and the North East Atlantic Ocean).

The latitudinal gradient, as already illustrated for the global analyses, also matches the European fauna. Almost all regions are clearly arranged along this gradient. Four European provinces are distinguished based on faunal composition. Three of them (Scandinavian-Baltic area, Mediterranean Sea and Black Sea) are semi-enclosed areas, with limited possibilities of exchange in fauna. The Mediterranean and Black Sea also have a particular history. The North East Atlantic fauna is the least distinct on a global scale. Next to these four areas, certain other distinct northern faunal areas can be distinguished.

An ecological relevance for biogeographical patterns requires quantitative field data and species assemblage studies. Currently, the faunal distribution patterns of many groups are studied through the European Marbef Project (http://www.marbef.org). Repeating the analyses with additional environmental data would be valuable. It should possibly lead to the development of predictive models.

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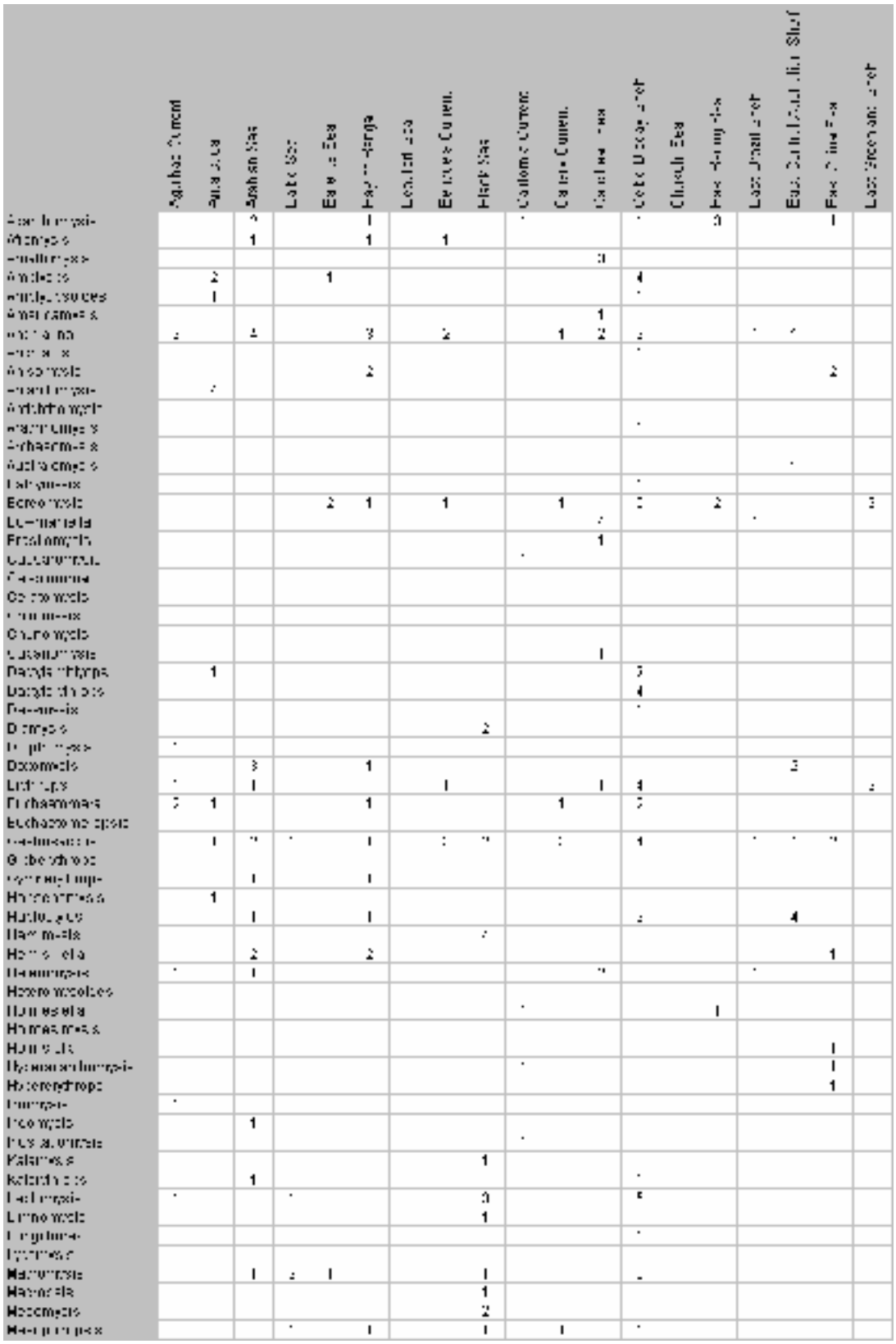
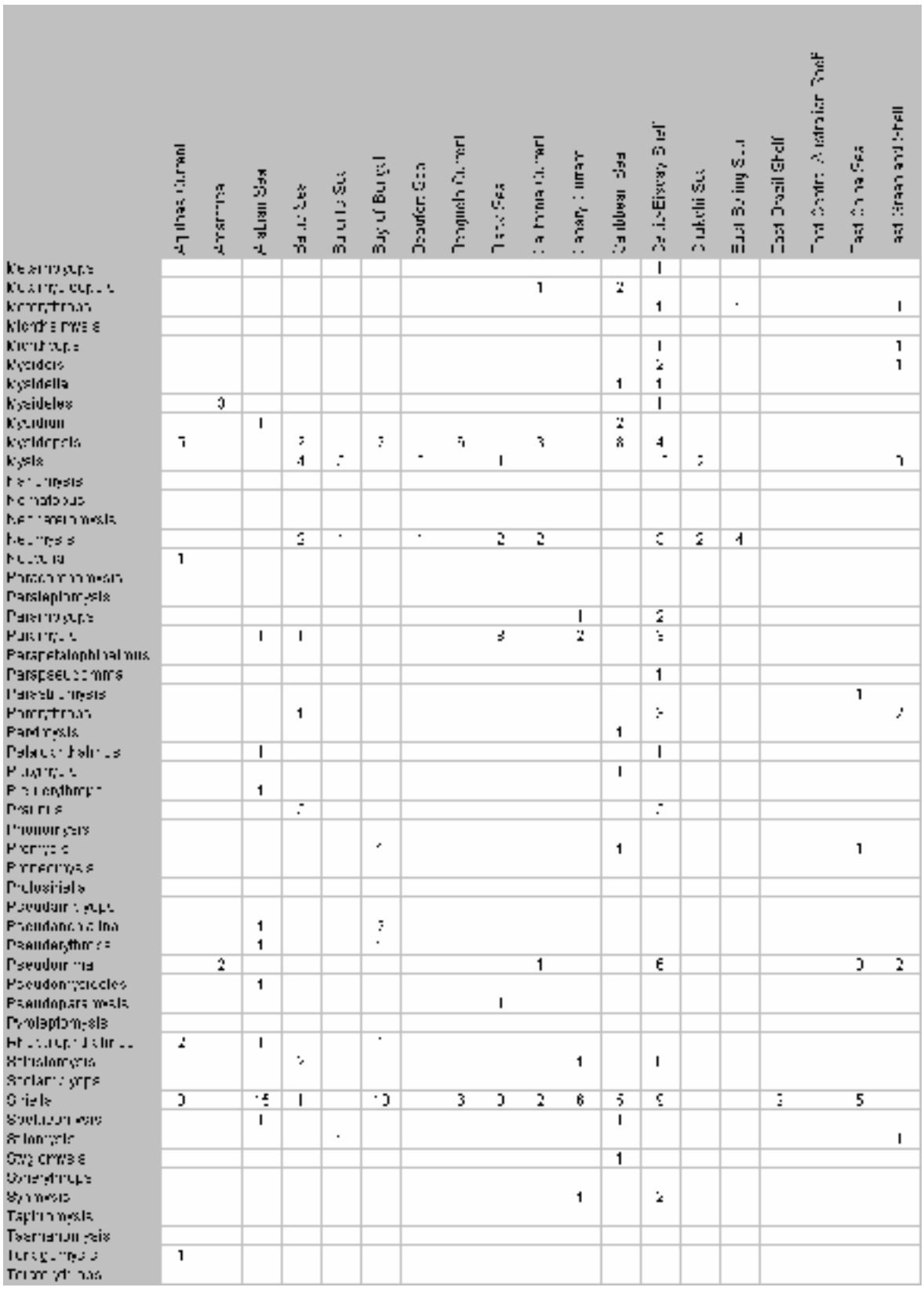
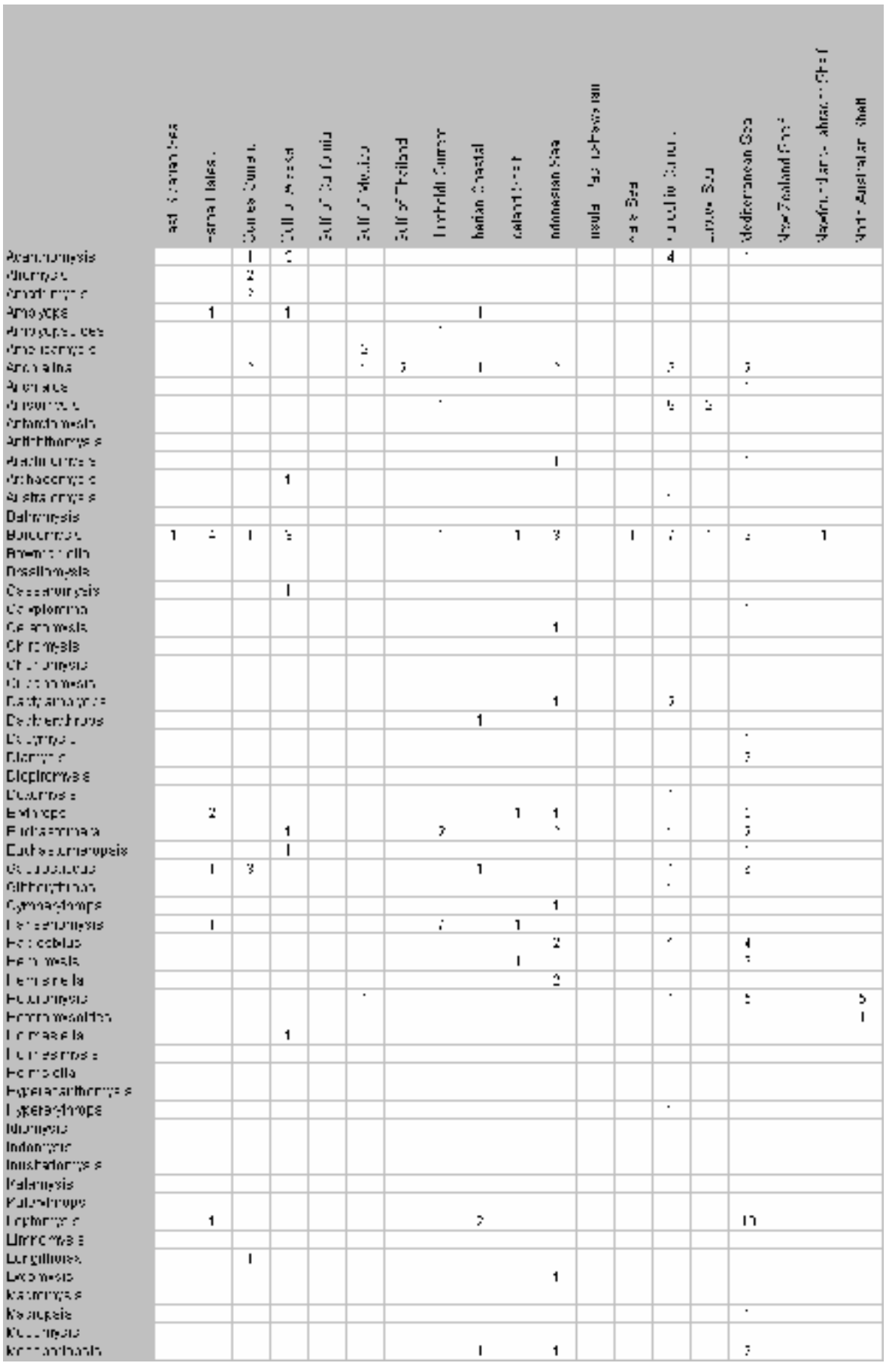
8. Appendices

8.1. APPENDIX 1. LME GENUS PRESENCE TABLES



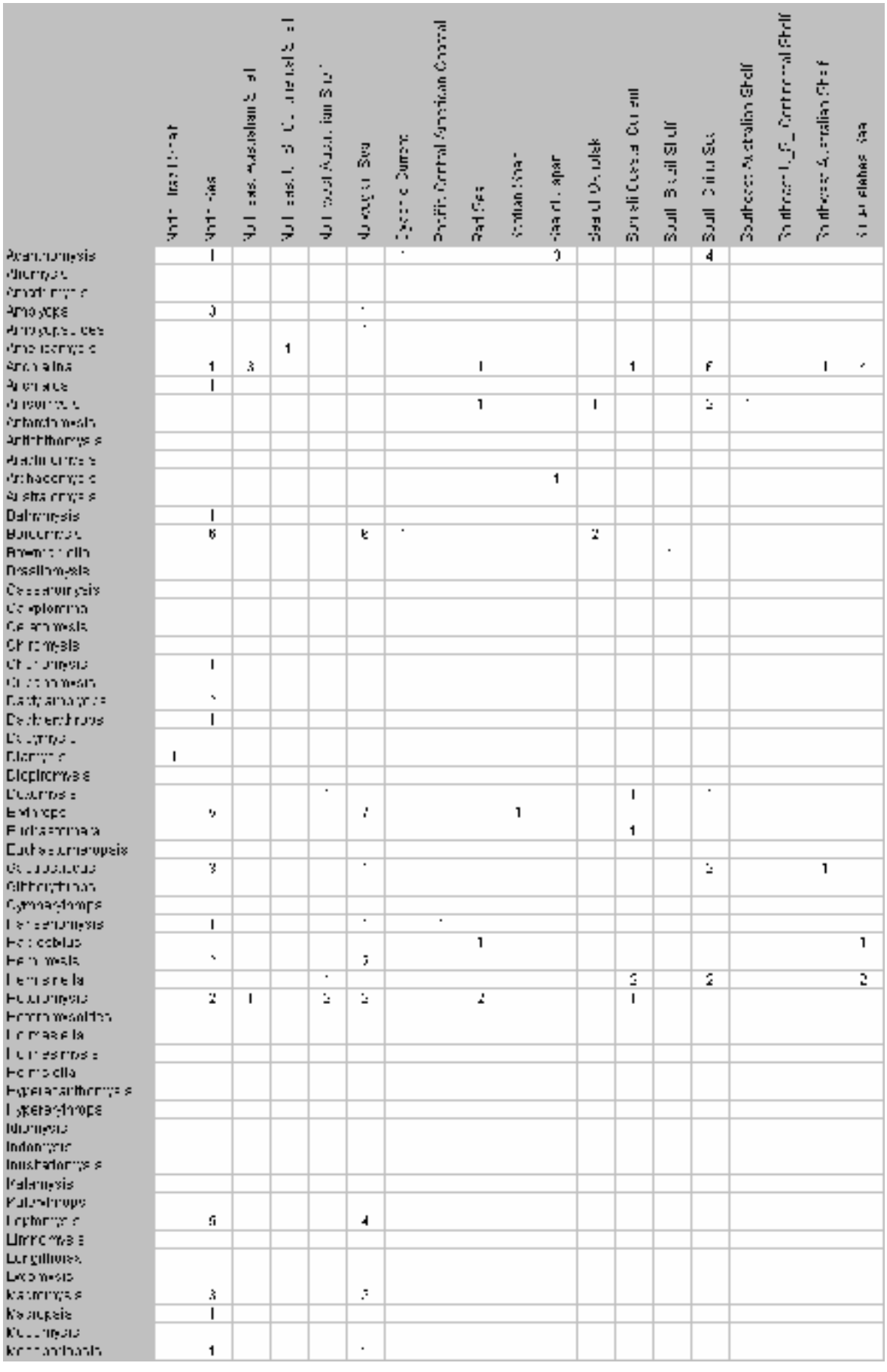


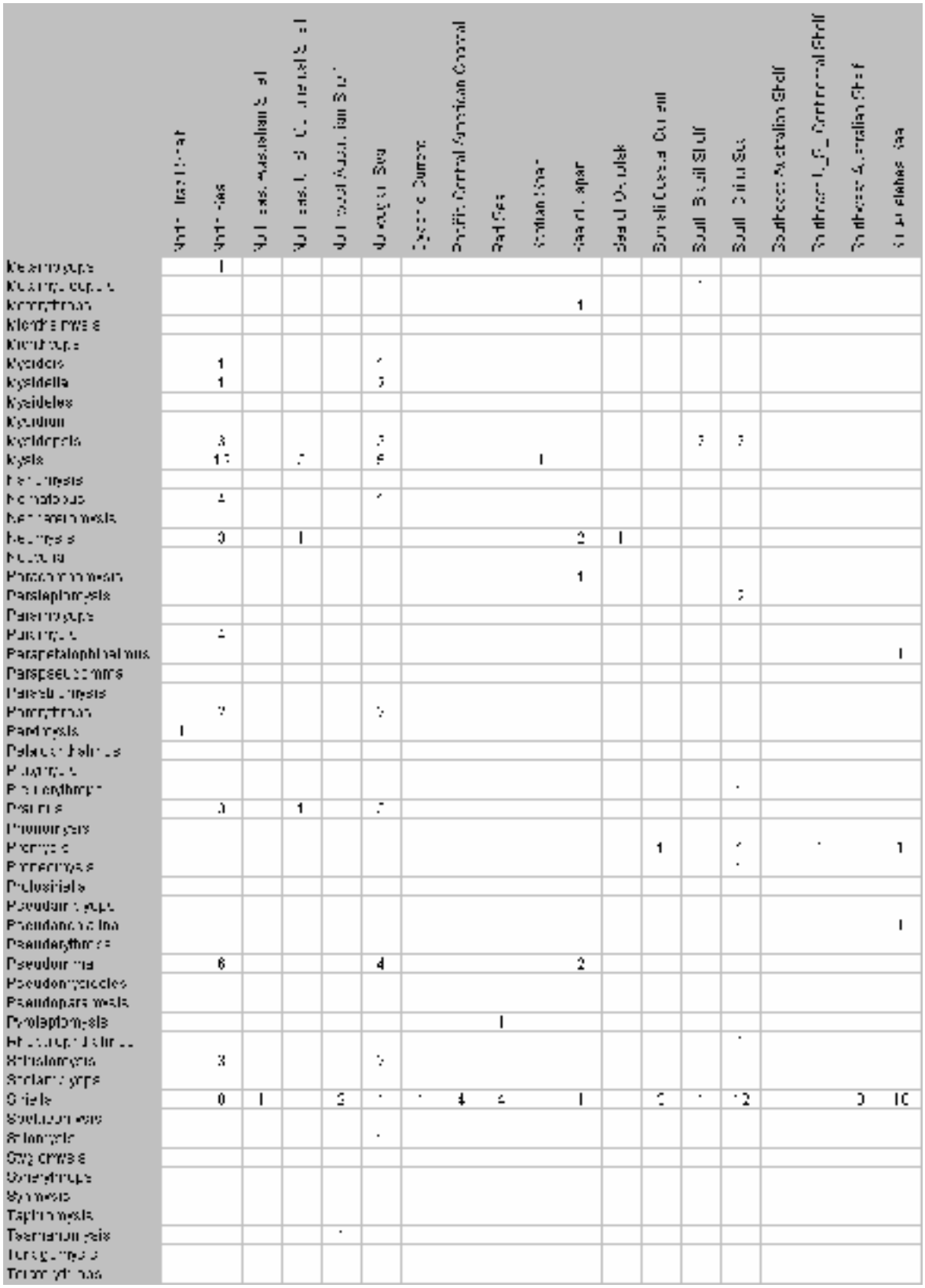
	Agulhas Current	Arabian Sea	Baltic Sea	Barents Sea	Bay of Bengal	Benguela Current	Black Sea	California Current	Canary Current	Caribbean Sea	East China Sea	East Siberian Sea	Gulf of Alaska	Gulf of Mexico	Kara Sea	Laptev Sea	Mediterranean Sea	Red Sea	Sea of Japan	Sea of Okhotsk	South China Sea	Southeast Australian Shelf	Southeast Brazil Shelf	Weddell Sea
Mesomysis												1												
Metamysidopsis								1		2														
Monomysis												1							1					1
Mysidella																								
Mysidetes												1												1
Mysidopsis												2												1
Mysidella										1		1												
Mysideles		3										1												
Mysidium		1								2														
Mysidopsis	1		2		2		5		3	8		4		2										
Mysis			4	2		1		1				1												1
Neomysis																								
Neomysidopsis																								
Neomysis																								
Neomysis			2	1		1		2	2			2	2	4										
Nouvelia	1																							
Paracanthomysis																								
Parastephomysis																								
Paramysis									1			2												
Paramysis		1	1					3	2			1												
Parapetalophthalmus																								
Parapseudomma												1												
Paraspelaeomysis																								
Paramysis																		1						
Pimeyptron			1									1												1
Pseudomysis										1														
Petalophthalmus		1										1												
Platymysis										1														
Polymysis		1																						
Porcellio			1									1												
Promysis					1																1			
Pseudomysis										1														
Prolosiella																								
Pseudomysis																								
Pseudomysidopsis		1			2																			
Pseudorythrops		1			1																			
Pseudomma			1						1			6									3			2
Pseudomysidopsis		1																						
Pseudoparamysis							1																	
Pycnolepidomysis																								
Rhopalopsyllus	2	1			1																			
Schistomysis			2						1			1												
Stenomysis																								
Siriella	3	15	1		10		3	3	2	6	5	2				1		5						
Spelaeomysis		1									1													
Stilomysis				1																				1
Stygomysis											1													
Synmysis																								
Taphromysis									1			2												
Tenagomysis																								
Tenagomysis	1																							
Tenagomysis																								



	Red Sea	Persian Gulf	Arabian Sea	Bay of Bengal	Gulf of Thailand	Andaman Sea	Indonesian Seas	Arafura Sea	Australian Shelf	Tasman Sea	New Zealand Shelf	Mediterranean Sea	Atlantic Ocean	Pacific Ocean	Antarctic Shelf
Acanthomysis			1	2									4		
Alienomysis			2												
Amorphomysis			2												
Amblyops		1		1			1								
Amblyopsoides															
Anisomysis						2									
Anomalina			2			3	1						3		
Arachnomysis															
Arthrorhynchus													5	2	
Arthrorhynchus															
Antitheromysis															
Austromysis							1								
Archaeomysis				1											
Australomysis													2		
Dalmonysis															
Boreomysis	1	2	1	3			3	1		1			7	1	
Brevimysis															
Dasythrix															
Caesaromysis				1											
Caspiomysis															
Caspiomysis							1								
Chiromysis															
Chiromysis															
Chiromysis															
Dactylamblyops							1						3		
Dactylopsis						1									
Diamysis													2		
Diamysis													3		
Diaphanosoma															
Diastylis													2		
Lamprops		2					1	1					2		
Pontoporeia				1		2		3					3		
Eucheta				1									2		
Gastrosaccus		1	3				1						2		
Gastrosaccus													2		
Gymnodiaptomus							1								
Heterocuma		1				2									
Hemimysis							2						4		
Hemimysis							1						3		
Hemimysella							2								
Holmesimysis					2								2		5
Hormomysis															1
Limnomysis				1											
Limnomysis															
Heterocuma															
Hyperacanthomysis															
Hyperacanthops													2		
Idiomysis															
Indomysis															
Inusitatomysis															
Kalamysis															
Katamysis															
Katharopsis		1				2							17		
Limnomysis															
Longithorax			1												
Lycomysis							1								
Katamysis															
Mesopsis													2		
Mysidopsis															
Mysidopsis						1	1						2		

	East Siberian Sea	Faroe Islands	Guinea Current	Gulf of Alaska	Gulf of California	Gulf of Mexico	Gulf of Thailand	Humboldt Current	Iberian Coastal	Iceland Shelf	Indonesian Sea	Insular Pacific-Hawaiian	Kara Sea	Kuroshio Current	Laptev Sea	Mediterranean Sea	New Zealand Shelf	Newfoundland-Labrador Shelf	North Australian Shelf
Metamblyops																			
Metamysidopsis						1													
Meterythrops		1		1						1	1		1	1					
Michthyomysis										1									
Michthyops																			
Mysideis		1								1						1			
Mysidella														1					
Mysidetes								1								1			
Mysidium																			
Mysidopsis		1	1			3				1	1					3			
Mysis	2									1					2	4		1	
Nanomysis											1								
Nematobous																			
Neoheteromysis																			
Neomysis				6					1					2		2			
Nouvelia																			
Paracanthomysis														4					
Paraleptomysis																3			
Paramblyops		1														1			
Paramysis									1							5			
Parapetalophthalmus																			
Parapseudomma																			
Parastilomysis														2					
Parerythrops		2							1	1						1			
Pardimysis																			
Petalophthalmus					1														
Platymysis																			
Pleurerythrops																			
Praunus		1								1									
Proneomysis														1					
Promysis																			
Prionomysis				1										4					
Prolusiniella																1			
Pseudamblyops														1					
Pseudanchialina											1			1					
Pseuderythrops																			
Pseudomma		4		2		1				2			1	15		3			
Pseudomysidetes																			
Pseudoparamysis																			
Pyroleptomysis																			
Rhopalophthalmus			2						1		1					1			
Schistomysis		1							2	1						2			
Scolamblyops														1					
Siriella			1			4		3	2		11	2		19		12			3
Spelaeomysis																			
Stilomysis																			
Stygiomysis																			
Synerythrops											1								
Synmysis																			
Taphromysis						3													
Tasmaniomysis																			
Tenagomysis																	3		
Teraterythrops														1					

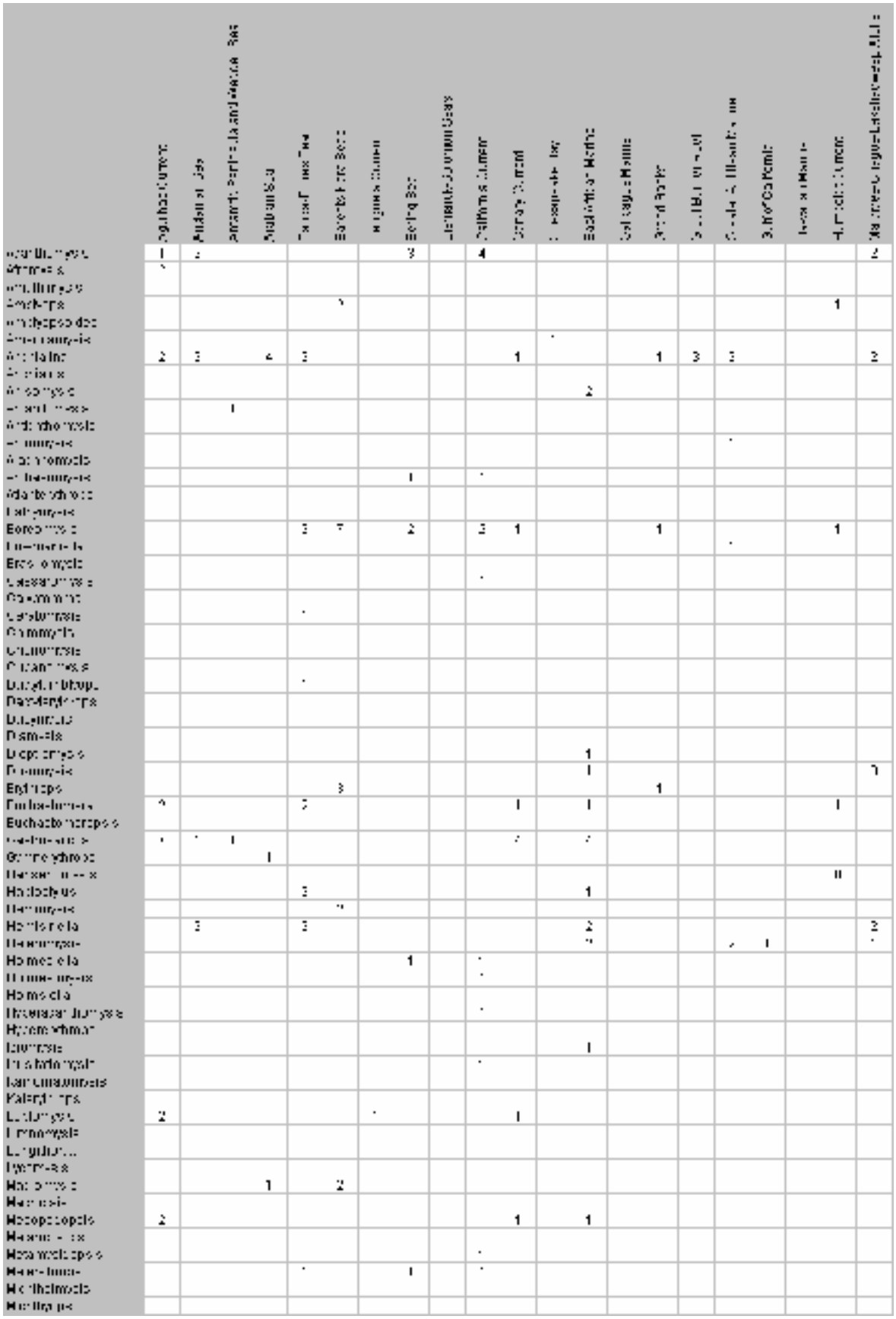


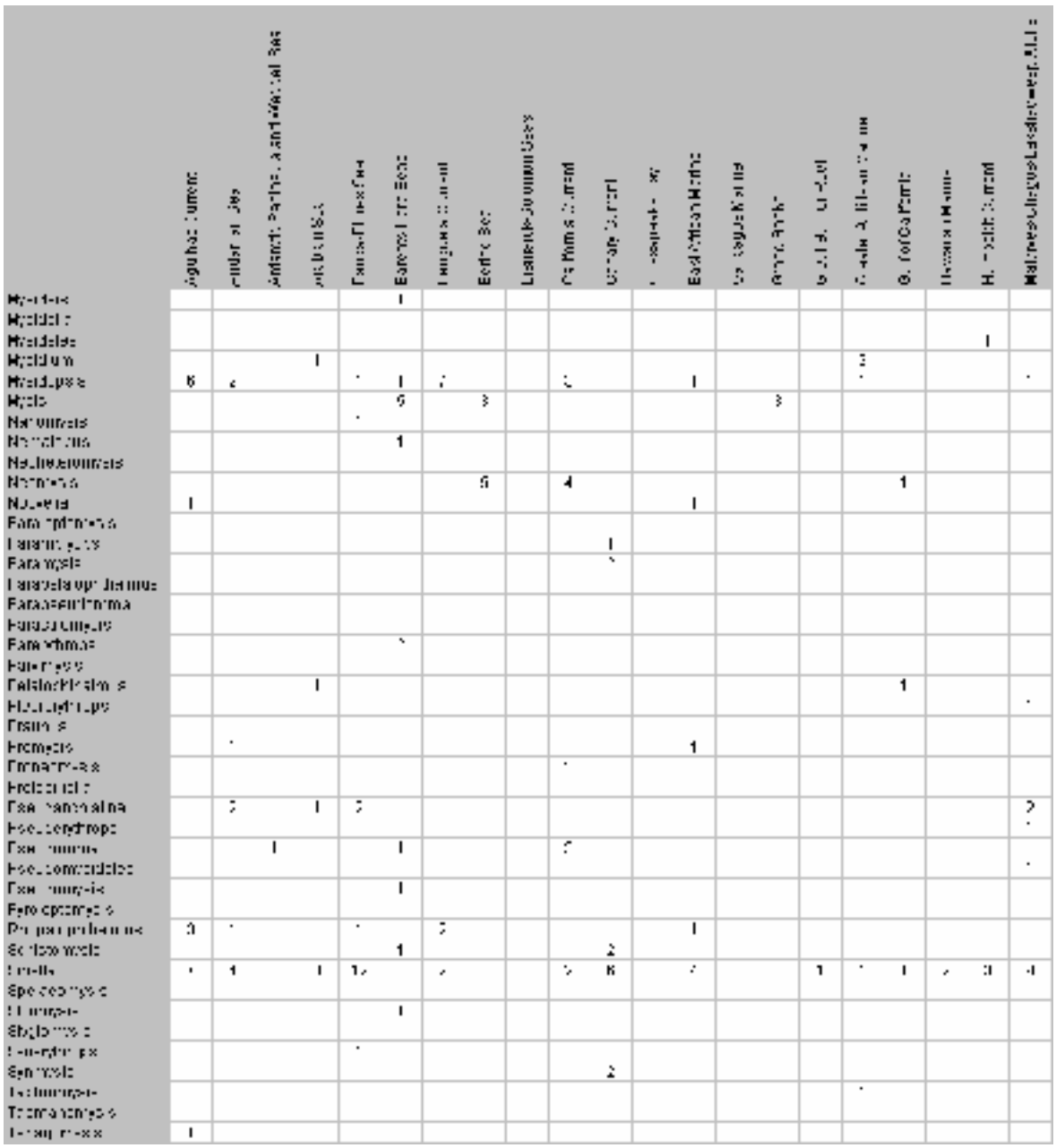


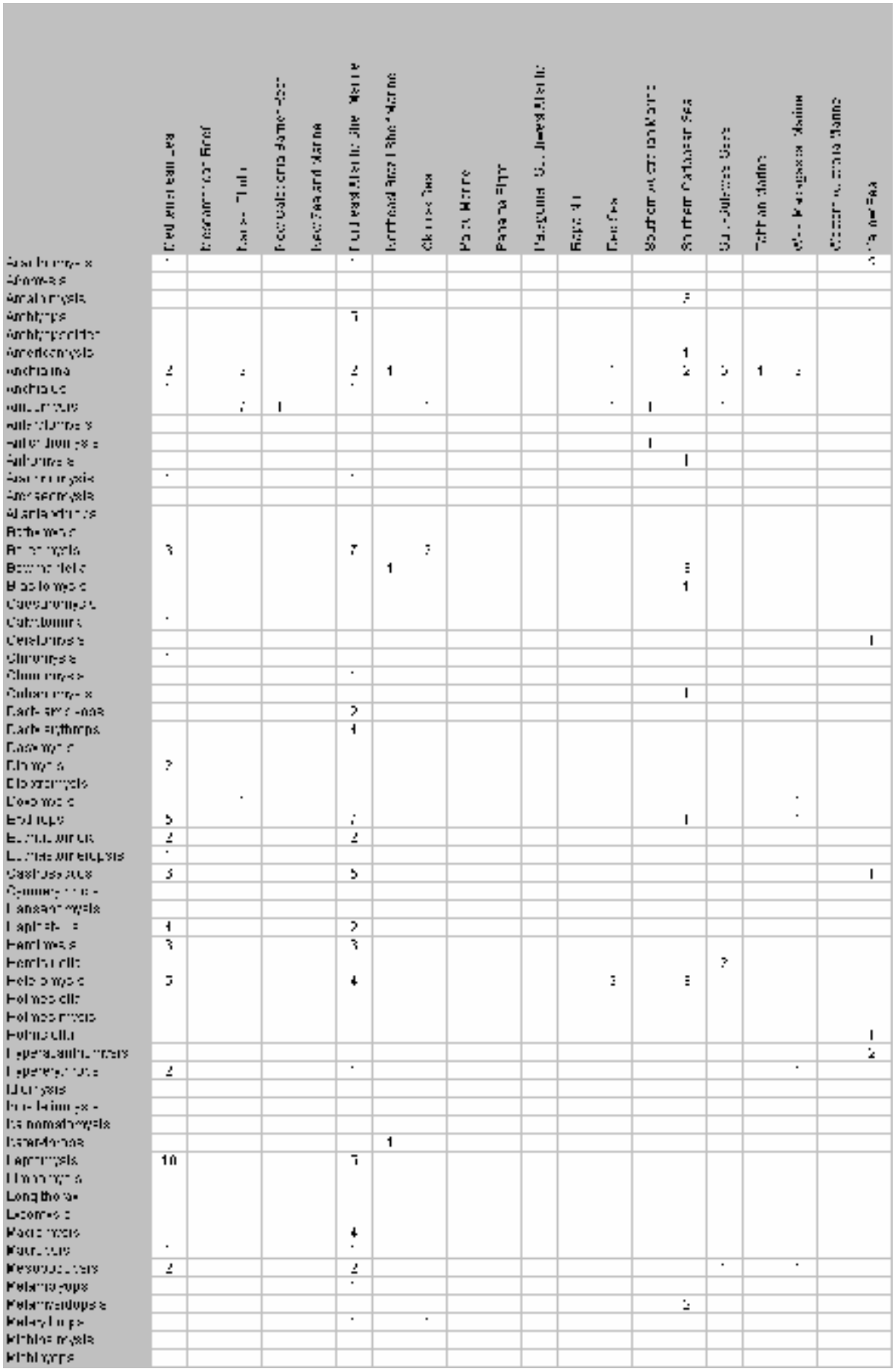
	West Bering Sea	West Chukchi Sea	West Beaufort Sea	Yellow Sea
Acanthomysis				2
Afromysis				
Amathimysis				
Amblyops				
amblyopsidae				
Amorsimysis				
Anchialina				
Anchialus				
Anisomysis				
arenicolamysis				
Anisomysidae				
Arachnomysis		1		
Archaeomysis	1			
Australomysis				
Bathymysis				
Boreomysis			2	
Bowmaniella				
Brasilomysis				
Caesaromysis				
Calyptomysis				
Caspiomysis				
Chloromysis				
Chunomysis				
Cuberomysis				
Dactylamblyops				
Dactylerythrops				
Dasymysis				
Diamysis				
Diastylomysis				
Dimorphostylis		1		
Dioptromysis			2	
Eirchaetomera				
Escherichiomysis				
Gastrosaccus				1
Gnathomysis				
Gonerythrops				
Hansenomysis				
Haplostylus				
Heteromysis				
Holmesimysis				
Holmesimysoides				
Holmesina				
Iberoleptomysis				2
Hypererythrops				
Iranomysis				
Irenomysis				
Iroimysis				
Katamysis				
Katerythrops				
Limnomysis				
Longithorax				
Lycomysis				
Macromysis				
Mancomysis				
Meschrella				
Mesopodopsis				

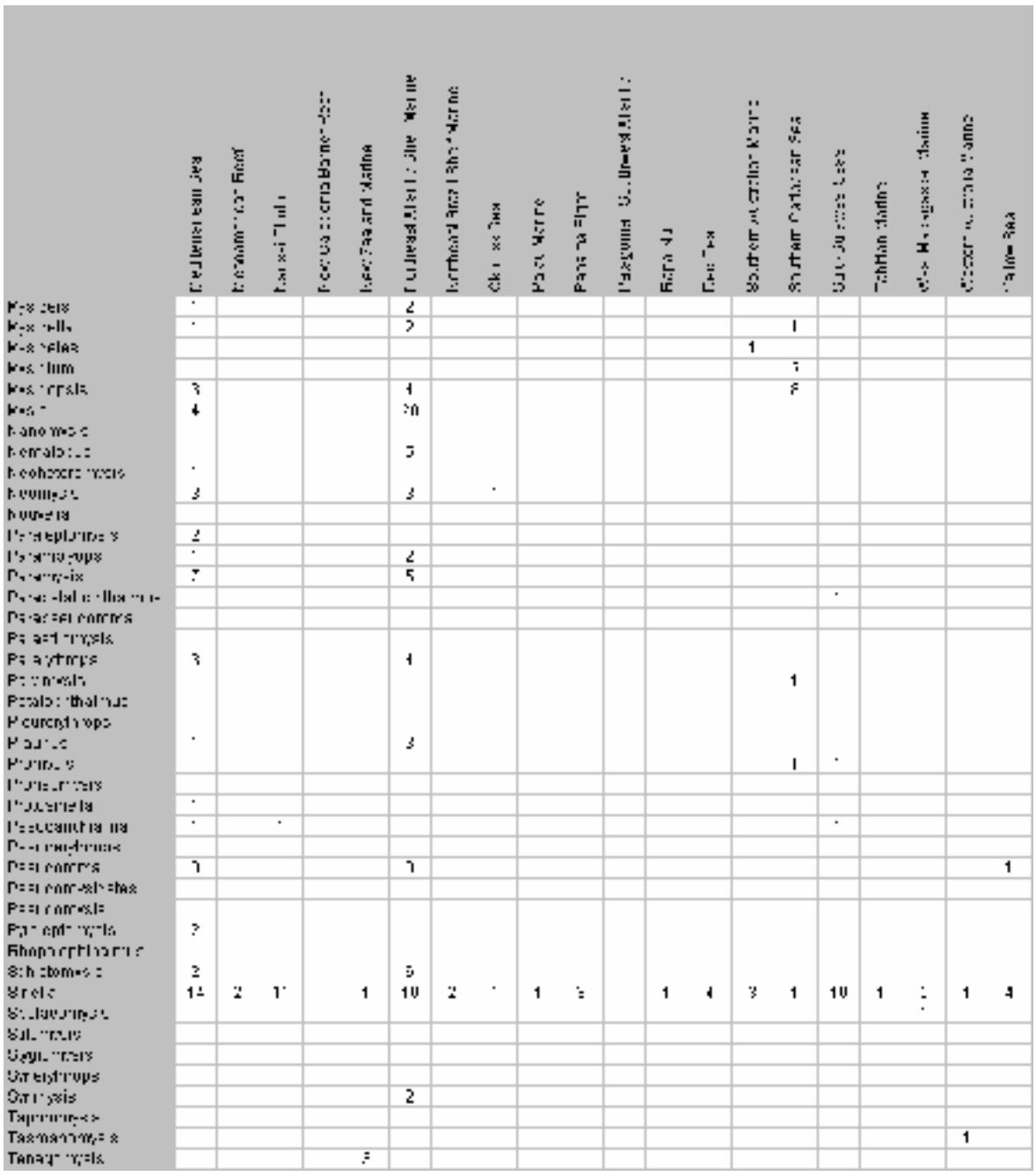
	West Bering Sea	West Chukchi Sea	West Beaufort Sea	Other Seas
Metamysidopsis				
Metamysinopsis				
Meterythrops			1	
Michthalmysis				
Michthyops				
Mysidella				
Mysidetes				
Mysidopsis				
Mysidium				
Mysidocosta				
Mysis				
Narmonella				
Nematocuma				
Neomysidopsis				
Nipponomysis				
Novamysis				
Orientomysis				
Paramblyops				
Paramysidopsis				
Parastilomysis				
Paravalenciella				
Parvimysis				
Petalophthalmus				
Phallocryptops				
Pharamysis				
Pseudamblyops				
Pseudomysidetes				
Pseudoparamysis				
Pyralopsis				
Rhopalophthalmus				
Schistomysis				
Siriella				
Siriellidae		3		3
Spelaeomysis				
Stilomysis				
Synmysis				
Synerythrops				
Syrrhoe				
Tenagomysis				
Tenagomysoides				
Tetrapleuromysis				

▪ 8.2. APPENDIX 2. WWF GENUS PRESENCE TABLES









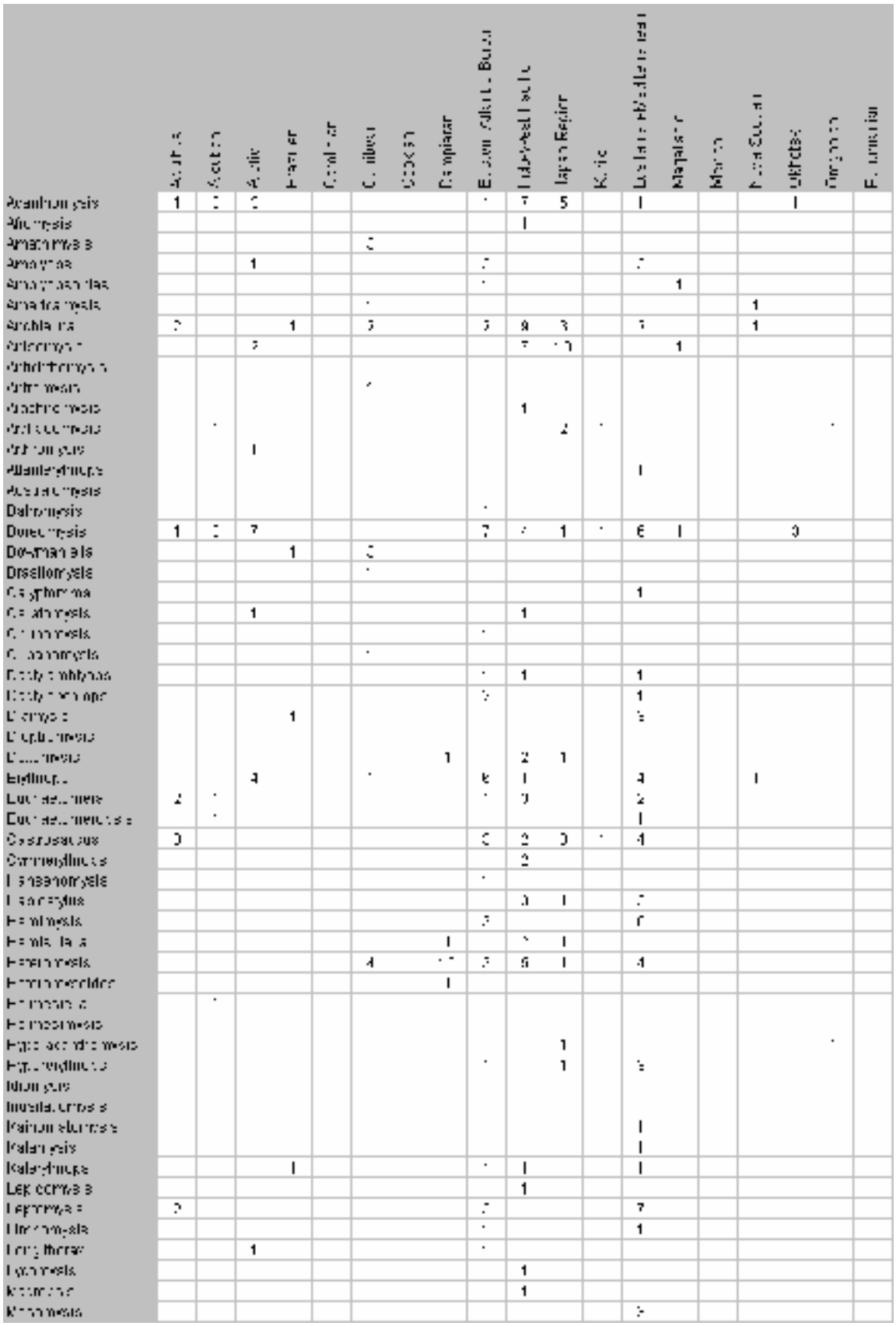
Mysidae					2														
Mysinella					2								1						
Mysinilas												1							
Mysinium													1						
Mysinopsis	3				4								2						
Mysis	4				20														
Nanomysis																			
Neomysis					5														
Neotenomysis	1																		
Pacifacanthomysis	3				3		1												
Paramysis																			
Parastilomysis	2																		
Pseudomysis	1				2														
Pseudomysis	7				5														
Pseudomysis														1					
Pseudomysis																			
Pseudomysis	3				4														
Ptilomysis													1						
Ptilomysis																			
Ptilomysis	1				3														
Ptilomysis													1	1					
Pyramimysis																			
Pyramimysis	1																		
Rhopalophthalmus																			
Schistomysis	2				5														
Siriella	14	2	17	1	10	2	1	1	5	1	4	3	1	10	1	1	1	4	
Stilomysis																			
Sulcimysis																			
Syspicomysis																			
Streptomysis																			
Synmysis					2														
Taphromysis																			
Tasmanomysis																	1		
Teneriomysis				3															

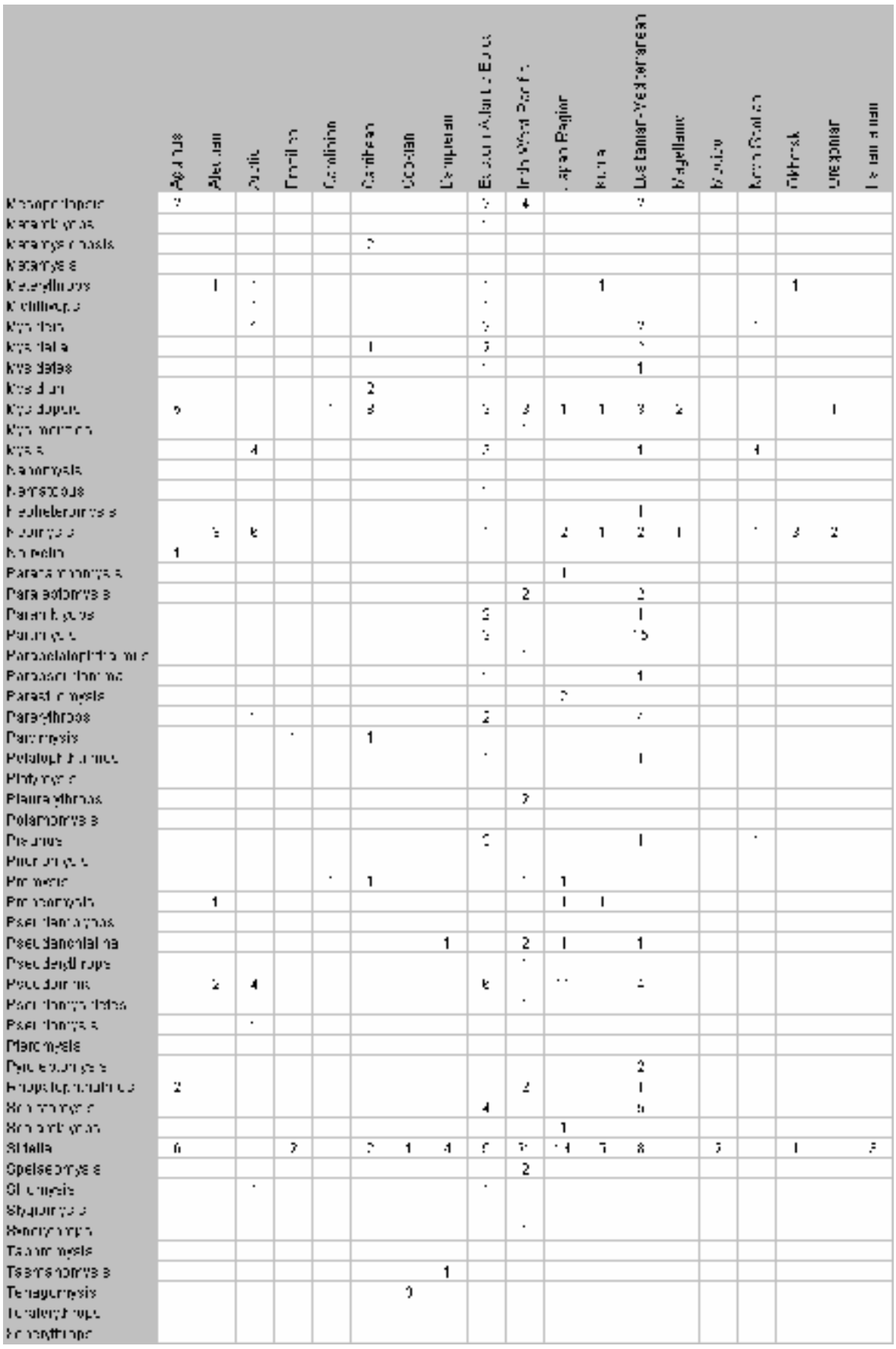
8.3. APPENDIX 3. MAUCHLINE GENUS PRESENCE TABLES

	Australasian	East Asian	East Pacific	Eastern Indian	North East Atlantic	North Pacific	North West Atlantic	South Atlantic	South Indian	South Pacific	West Atlantic	West Pacific	Western Indian
Acanthomysis	18	17	1	3	1	6							2
Afromysis		9		1								1	3
Amblyops		2									4		
Amblyspina		1	1		7	1				1			
Anisomysis					1			1	2	1			
Antromysis							1				1		
Archaeomysis	10	3	2	3	2		1				2	2	7
Archamysis		1			1								
Arthromysis	13	2	1	1		2						4	3
Arthrorhynchus								1	2				
Australomysis												1	
Avetilerius											1		
Bacillomysis	1			1	1								1
Boreomysis	2	2	1			1							
Bowmaniella							1						
Brasilomysis					1								
Caesaromysis	2												
Calyptomysis					1								
Caspiomysis						5	5	3	2	3			
Chaceon		1									2		
Chelomysis		1									1		
Chlamydopleon			1			1							
Chlamydopleoncopis	1						1						
Chunomysis					1								
Cnidocarpus											1		
Deltamysis	3	2			2					1			
Dioptromysis					2								
Diastylopsis					1								
Diamysis		2									1		
Dioptromysis													1
Doxomysis	7												3
Dyroamysis	1	7			3		3				1		2
Eucopiopsis	3	9	2	2	2	1				1	2		3
Euchaetomera						1							
Gastrosaccus	3	15		3	5						1		12
Gibborhynchus	1	1											
Gymnorhynchus	1												1
Heteromysis			6		1					1			
Holmesimysis	2			2	2							1	4
Hyperacanthomysis		3			5								
Hyperapseudes	2	1		2									
Hyperastacus	11	2	1		4						6		1
Hyperbenthos	1												
Hypermysis			1			1							
Hypsimysis			1										
Idiomysis	1												
Iphimedia	2	1	1										
Iphinoe													1
Isomysis													1
Katamysis		1											
Katerythropus		1			1						3		1
Leptomysis													1
Limnomysis		5			1								2
Limnomysis		1			1								
Longithorax		1			1		1						1
Lycomysis	1	1											

	Australasian	East Atlantic	East Pacific	Eastern Indian	Mid Eastern Atlantic	Mid Northern Pacific	Mid Western Atlantic	North Atlantic	South Indian	South Pacific	Western Atlantic	West Pacific	Worldwide
Macromysis		2			4		1				1		1
Mesomysis		1		1	1								
Metamysidopsis		3			1								
Mesopodopsis	3	1		1	1								1
Mesorhoptrops					1								
Mesomysidopsis			1								1		
Mesopsis		1											
Metacanthops	1	3			2	1	1						1
Metamysidopsis		1			1								
Michthops					2								
Mysidella		3			3		1						
Mysidetes	1	1			2						1		
Mysidopsis			1		1			2	1	1		1	
Mysidium											1		
Mysidopsis	1	10	7	2	4			1			15		3
Mysimandibas													
Mysis		2			33	5	9			1			
Neomysis													
Paramysidopsis					6								
Neomysis	1	11	4		2	1	2				1	1	
Nouvelia													
Pakaroidiomysis	1	2										1	
Paramysidopsis	2												
Parastilomysis		1			2			1					
Paramysis		7			2								
Paravetuscimysis	1												
Paramysidopsis		1			1								
Parastilomysis	2												
Pseudomysis		1			5		1				2		
Paramysis													
Petalophthalmus			1		1								2
Platymysis											1		
Pleurerythrops	1												1
Polymeromysis				1									
Proneomysis		3			2		1						
Promysis	1	1											
Pseudomysis				1							1		
Pseudomysidopsis	1	2				1							
Pseudomysis		1											
Pseudocuma	1	1		2									2
Pseudomysis	1												1
Pseudomysis	10	10	1		8	2	2	2		1	1		
Pseudomysidopsis													1
Pseudomysis					1								
Pseudomysidopsis		1											
Platymysis		1											
Pycnoplumosis													1
Rhopalophthalmus	1	3		1									4
Schistomysis		7			6								
Siriella	1												
Siriella	30	10	9	11	17		1		1	1	11	7	11
Spelaeomysis											1		3
Stilomysis		1			1							1	
Stygomysis											1		
Xenacanthomysis	1												
Synmysis		2			2								
Taphromysis		1									2		
Taphromysis													
Tenagomysis	1									2			1
Tenagomysis		1											
Typhlomysis		1											
Venemysis		1											

▪ 8.4. APPENDIX 4. BRIGGS GENUS PRESENCE TABLES





	Peru-Chilean	Pacific	San Diego	SE Australian	SE South Australian	South African	SW Australian	Tasmanian	West African	West Indian	West Indian Pacific
Anarthromysis			[illegible]						14		
Anchialomysis						1			3		[illegible]
Annandalomysis									2	2	
Amblyops	1								2		
Amblyopsibidae											
Amblyopsis										[illegible]	
Anchialina		[illegible]		1		1	1		2	[illegible]	[illegible]
Antromysis		[illegible]						[illegible]	2		[illegible]
Antrobiotic								[illegible]			
Antromysis										1	
Arachnomysis											
Archaeomysis									2		
Atlantomysis											
Australomysis											
Australomysis				1							
Bathymysis											
Boreomysis	1					1			7		
Boreomysidae					[illegible]				1	[illegible]	
Brasilomysis					[illegible]				1		
Caspiomysis									1		
Centromysis											
Chiromysis											
Circomysis										1	
Dactylamblyops									1		
Dactylerythrops											
Diamysis									2		
Diaphromysis											[illegible]
Docosomysis				2							[illegible]
Erythrops						1			9		[illegible]
Eucopiamorpha	[illegible]								1		[illegible]
Eucopiidae											
Gastrosaccus				2		3	1		7		0
Gymnomysinops											[illegible]
Haplomysis	0										
Hastigerella		[illegible]		[illegible]			1				[illegible]
Heteromysis									3		
Heteromysoides									1		2
Heteromysis		2							1	4	[illegible]
Heteromysoides											
Holmesella			1								
Holmesimysis			1								
Hyperacanthomysis									1		
Hypererythrops											[illegible]
Iodomysis											[illegible]
Inusitatomysis			1						1		
Kamomysis											
Katamysis									1		
Kuderiopsis									1		
Leptomysidae											
Leptomysis						1			2		[illegible]
Limnomysis									1		
Longithorax									1		
Lycomysis									1		
Mesopsis											
Mesomysis									3		

	East Pacific	Eastern Asia	Eastern Atlantic	Eastern Australian	Eastern South America	New Zealand	New South Australian	Tasmanian	Western African	Western Indian	Western Indian Ocean
Mesopodopsis									1		3
Metamysidopsis											
Metamysidopsis			1		1					2	
Metamysis									1		
Michthyops									3		1
Michthyops											
Mychotrochus									4		
Mysidella									1		
Mysidella	1							1			
Mysidium										4	
Mysidopsis			3		3	3			3	2	2
Mysidopsis									2		
Mysis											
Neomysis											
Neomysis											
Neomysis			2						1		
Neomysis											1
Parastenomysis									2		
Parastenomysis											
Paramysopsis									1		
Parastenomysis									3		
Parastenomysis											
Pseudomysidella									1		
Pseudomysis											
Pseudomysis									1		
Pseudomysis											
Pseudomysis											2
Rhopalophthalmus										1	
Rhopalophthalmus											
Siriella									2		
Siriella					1					1	1
Siriella									2		
Siriella									1		
Siriella									1		1
Siriella											
Siriella									1		
Siriella		1									
Rhopalophthalmus						2			2		3
Stilomysis									1		
Gastrosaccus											
Siriella	2	3	1	2		2	4		11	4	1
Spelaeomysis										1	1
Stilomysis									1		
Hyperacanthomysis										1	
Synmysidopsis									1	2	
Tenagomysis											
Tenagomysis											1
Synmysidopsis									1		
Xenacanthomysis									1		

CHAPTER 5 - A REVIEW OF THE GENUS *ANCHIALINA*

Authors: Tim Deprez & Merlijn Jocqué

1. Abstract

This study gives a detailed overview of the 16 species belonging to the genus *Anchialina*. For each species a morphological and biogeographical overview is given and two dichotomous keys (the first one on the sexually dimorphic third male pleopod, the second one on a mixing of somatic and sexually dimorphic characters), and one polytomous digital identification key are made. Although most of the information presented is based on literature, new additions through observations on specimens help to solve most of the difficulties in this genus. The two groups currently accepted in this genus (the 'typica-group' and the 'grossa-group') (Nouvel, 1969; Ii, 1964) are, based on a phylogenetic morphological analysis, found to be stable and well-defined.

2. Introduction

The genus *Anchialina* belongs to the *Gastrosaccinae*, a subfamily of one of the seven families of the order Mysida, together with the genera *Gastrosaccus*, Paranchialina, *Bowmaniella*, *Haplostylus*, *liella* and *Archaeomysis*. The 16 (17) species in *Anchialina* are morphologically very similar and identification is made difficult due to the continuation of growth long after sexual maturity is reached. In spite of the worldwide distribution of *Anchialina* (see chapter 4), no global surveyor overview has been published yet. Some geographical limited studies were done: the most recent one by Wang & Liu (1987) on the *Gastrosaccinae* of the China Sea. However, these studies mostly confine themselves to merely mentioning the present species in the studied area.

The genus is a clearly monophyletic genus in the paraphyletic subfamily Gastrosaccinae. Remerie *et al*. (2005) showed through phylogenetic analysis of 18SrDNA that the genus is clustering clearly apart from the other representatives of the family. The sequenced species in this analysis was *A. agilis*. Figure 1 shows the relationships of four genera of the subfamily. The subfamily may thus be splitted in two major sister goups of genera. A first group includes all *Gastrosaccus* related

genera: *Gastrosaccus*, *Bowmaniella, liella, Archaeomysis, Eurobowmaniella,* and *Haplostylus*. The second group includes all *Anchialina* related genera: *Anchialina*, *Paranchialina* and *Pseudanchialina*. A hypothetic phylogenetic tree making use of morphological features, geographical distributions and molecular findings (after Remerie *et al*. 2005, and Deprez unpublished work) is presented in figure 2.

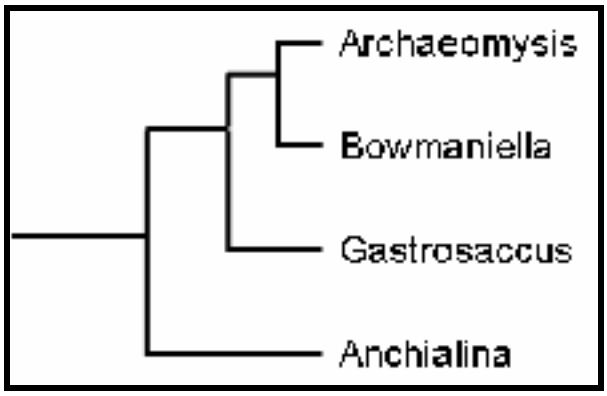


Figure 1. phylogenetic position of anchialina in the subfamily Gastrosaccinae (after Remerie *et al*, 2005)

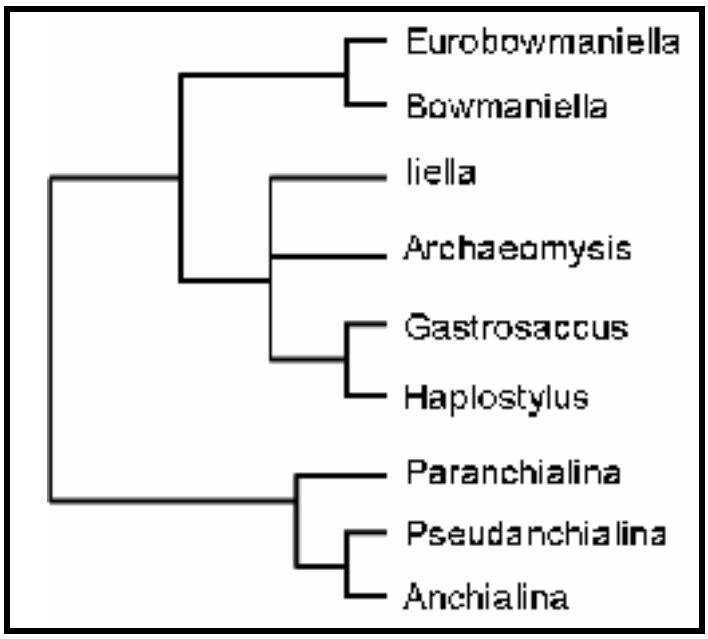


Figure 2. Hypothetic phylogenetic tree of the subfamily Gastrosaccinae

3. Materials en methods

In this study the literature on *Anchialina* with information on morphology, distribution and taxonomic position of the species and genus is handled. The personal notes of Nouvel about *Anchialina*, made available by Jean-Paul Lagardere added valuable information for several species.

Material for *A. typica* was available for study. It was possible to correlate observations with data extracted from the literature. For four species (*A. agilis*, *A. penicillata*, *A. obtusifrons* and *A. truncata*) new information has been added to literature based description.

All figures are hand drawn with ink, most of them after published figures. Figures 5.7 and 11.1 are new drawings of the third male pleopod of *A. agilis* and *A. truncata*. The figures have two possible scale indications. The first is a scale line under the drawing, the second the magnification used by the author of the original, represented as (x "magnification") and mentioned in the legend.

The numeration of the segments in the pleopods starts from the extremity, based on an observation from Nouvel (1969). He remarked that the differentiation of the pleopods in immature animals starts from the extremities. This method keeps the numeration of the segments invariable.

All geographical, bibliographical and morphological data was also added to the online world Mysida database hosted on the NeMys biological information system (Deprez *et al.*, 2004) (http://www.nemys.ugent.be). For each species the url is mentioned. On the website a distribution map for each species can be consulted. The NeMys database was also used to host a polytomous identification key.

The cladistic analysis was based on parsimony and carried out with NONA (Goloboff, 1998), which is similar to Hennig86 (Farris, 1975) but runs under WINCLADA (Nixon, 1999) facilitating screening and layout of trees.

As outgroups *Gastrosaccus trilobatus* Murano & Mclachlan 1998 and *Archaeomysis grebnitzkii* Czerniavsky 1882 were chosen. Both are well defined species and thus

representing the genera *Gastrosaccus* and *Archaeomysis* (from the “Gastrosaccus” sister-group) belonging to the Gastrosaccinae. For both taxa, enough reliable information was available to score all the characters of the in-group. Twelve out of the 23 characters are somatic, the other eleven are all sexual dimorphisms of the male. All characters were given equal weight and were treated as unordered (non-additive) if different states were present for one character. The analysis was done through the WINCLADA-interface with the ‘Heuristic’ option. The maximum number of trees to hold was set to 1000, with 100 replications. Only the strict consensus tree was held. Bootstrap trees were calculated in order to have a numerical value for the reliability of the branches shown in the tree.

A second analysis was done by adding the geographical distributions to the dataset as additional characters.

▪ 3.1. CHARACTERS USED IN THE ANALYSIS

[1] **Antennal scale length to width ratio:** This character probably is a sexual dimorphism. However, in most of the descriptions it was not mentioned. If so, measurements on the male were used. The possible character states are: length to width ratio is equal or smaller than two (state 0), bigger than two (state 1), equal to three (state 2) or equal or larger than three (state 3).

[2] **Telson-uropod endopod**: The length of the telson in both sexes compared with the length of the endopod of the uropod. The telson can be smaller (state 0), equal (state 1) or longer (state 2) than the endopod of the uropod.

[3] **Telson length to width ratio:** The length of the telson in both sexes divided by the width at the base in both sexes. This ratio varies around three times as long as wide, and can be smaller (state 0), exact three times as long as wide (state 1) or larger (state 2).

[4] **Cleft length:** The length of the cleft as a part of the length of the telson. Normally the cleft length is 1/sixth of the telson length (state1), but can be smaller (state0), or longer (state2).

[5] **Number of segments in the tarses of the thoracic limbs:** The number of tarses from the third to eightest thoracic limb in both sexes. The tars consists of the carpus, propodus and dactylus of the endopod of the thoracic limbs. There are three (state 2) or four (state 1) segments. An exception is *A. latifrons* with two tarses as mentioned by Nouvel (unpublished data). However, publications on this species show three segments (Nouvel 1971). The members of the outgroup have more than four segments (state 0).

[6] **Large lamellar process of the third segment in the third male pleopod:** Whether (state 1) or not (state 0) there is a process covering at least the whole third and second segment. This character makes the main difference between the "*typica*-group" and the "*grossa*-group".

[7] **Trifid spine on the second segment of the exopod of third male pleopod:** The second segment bears a trifid spine or a spine with two subsidiary spines (state 1) on the internal side. The alternative is a single or bifid spine (state 0).

[8] **Terminal process on distal segment of exopod in third male pleopod**: The terminal process exceeds all other processes and the end of the first segment (state 1). Such a process is absent or much smaller (state 0).

[9] **Number of setae on the distal segment of the exopod of third male pleopod:** This is two (state 0) or three (state 1).

[10] **Expansion of the merus (fifth segment) of male endopod of second thoracic limb:** The merus has a lamellar expansion directed forward (Figure 9.2) (state 1), a widened expansion with the distal side truncated (Figure 6.1) (state 2) or no expansion at all (state 0).

[11] **Male endopod of third thoracic limbs distally with modified setae:** The sixth segment of the male endopod is truncated with (Figure 6.3) (state 0) or without (state 1) modified setae (Figure 4).

[12] **Mandibular palp with modified setae:** The male palp distally bears two modified setae (Figure 8.3 & 8.4) (state 1) or not (state 0).

[13] **Pseudobranchial lamellae:** can be single and more triangular (state 1), bilobed and rounded (state 2) or absent.

[14] **Segments of exopod of third male pleopod:** The segments of the exopod of the third male pleopod vary from 7 to 16, three arbitrary categories are used: less than five segments (state 0), between five and ten segments (state 1) and more than ten segments (state 2).

[15] **Rostrum:** Mostly in both sexes the rostrum is triangular and pointed (state 0). In some species the rostrum has a trapezoidal or truncated shape (state 1).

[16] **Antennule with additional hairs:** The third segment of the male antennule bears a dens additional bush of curved hairs (Figure 8.1) (state 1), or not (state 0).

[17] **Antennal base with large spine:** The antennal base in both sexes bears a large spine (state 1), mostly with subsidiary dentic1es (Figure 10.1, 10.2 & 10.3), or not (state 0).

[18] **Exopod -telson:** The length of the telson in both sexes compared with the length of the exopod of the uropod. The telson can be smaller (state 0), equal (state 1) or longer (state 2) than the exopod of the uropod.

[19] **First thoracic limbs with nail:** Whether (state 1) or not (state 0) there is a (large) nail on the dactylus of the fust thoracic limbs in both sexes.

[20] **Second thoracic limbs with nail:** Whether (state 1) or not (state 0) there is a (large) nail on the dactylus of the second thoracic limbs in both sexes.

[21] **Posterior edge of carapace nearly straight:** The carapace may be straight (state 1) or not (state 0).

[22] **Large lamellar process of the second segment in the third male pleopod:** Whether (state 1) or not (state 0) there is a process covering at least the second and first segment.

[23] **Bent (90°) modified setae on the exopod of third male pleopods:** Distally on the internal side of the male exopod there may be remarkably modified setae (state 1), bent 90° (Figure 5.1, 5.2, 5.3, 5.5 & 5.6), or not (state 0).

▪ 3.2. GEOGRAPHICAL CHARACTERS USED IN A SECOND ANALYSIS

[24] Red Sea, [25] Madagascar, [26] Indian waters, [27] Atlantic Ocean, [28] Carribean, [29] East Indies, [30] East Indies – West, [31] East Indies – East (Pacific), [32] Western – Australia, [33] Eastern – Australia, [34] Mediterranean

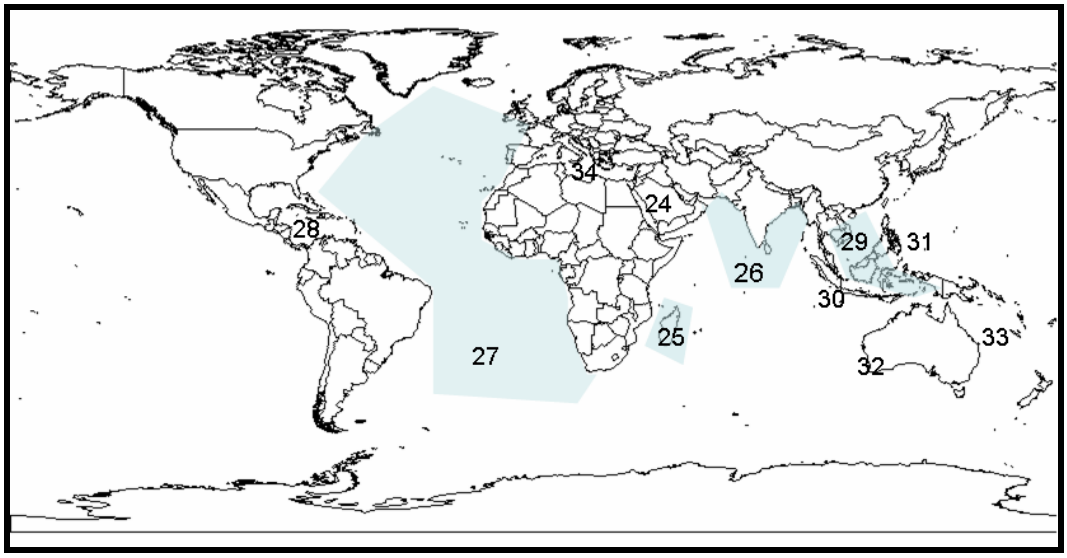


Figure 3. Geographical areas used in second phylogenetic analysis

▪ 3.3. ABBREVIATIONS AND ACRONYMS

F: female; **LW**: length to width; **M**: male; **NHM**: Natural History Museum (London); **Not**: Unpublished notes from Nouvel made available by Lagardere; **Obs**: personal observation; **Drw**: information derived from drawings; **USNM**: United States National Museum (Washington)

▪ 3.4. CHECKLIST OF SPECIES

Anchialina agilis (Sars G.O. 1877)

Anchialina dantani Nouvel 1944

Anchialina dentata Pillai 1964

Anchialina flemingi Tattersall W.M. 1943

Anchialina grossa Hansen 1910

Anchialina latifrons Nouvel 1971

Anchialina lobatus Panampunnayil 1999

Anchialina madagascariensis Nouvel 1959

Anchialina media Ii 1964

Anchialina obtusifrons Hansen 1912

Anchialina oculata Hoenigman 1960

Anchialina penicillata Zimmer 1915

Anchialina pillai Jo & Murano 1992

Anchialina sanzoi Coifman 1937

Anchialina truncata (Sars G.O. 1883)

Anchialina typica (Kroyer 1861)

subspecies: *Anchialina typica orientalis* Nouvel, 1971 and *Anchialina typica typica* Brattegard, 1969

Anchialina zimmeri Tattersall W.M. 1951

▪ 3.5. SYNONYMIES AND TRANSFERS:

Anchialus angustus Sars G.O. 1883 = *Paranchialina angusta* Sars G. O. 1883, see Hansen (1910).

Anchialina frontalis Zimmer 1915 = *Anchialina grossa* Hansen 1910 see Tattersall W.M. (1922).

Anchialina mediterranea Colosi 1922 = *Anchialina agilis* Sars G. 0.1877, see Colosi (1929).

Anchialina parva Ii 1964 = *Anchialina dentata* Pillai 1964, see Pillai (1973).

4. Systematic account

▪ 4.1. GENUS *ANCHIALINA* NORMAN & SCOTT 1906

Anchialus Kroyer 1861: 58

Anchialina Norman & Scott 1906: 24 (new name for *Anchialus* preoccupied)

Anchialina Hansen 1910: 50; Tattersall & Tattersall 1951: 179, Figs. 6-9; Ii 1964: 186; Pillai 1965; Wang & Uu 1987: 218; Jo & Murano 1992: 1.

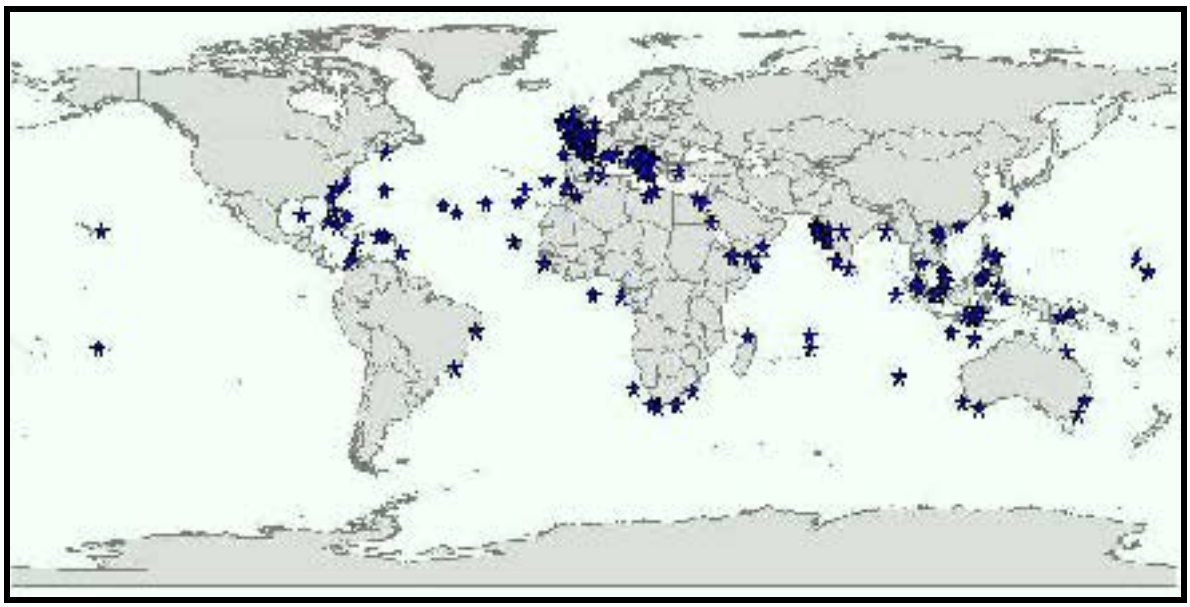
Description:

Body short, robust. Carapace usually covering all thoracic segments and sometimes part of the first abdominal somite. Posterior margin straight or slightly concave (figure 14). Anterior margin with well developed rostrum, often triangular with sexual dimorphism (figures 8.1 & 8.2).

Eyes large. Mandibles with laciniae mobilis, spine row and molar tubercle. Palp on mandibles with somewhat expanded second segment, third segment oblong (figures 8.3 & 8.4). Base of outer flagellum of antennule in male swollen (figures 8.1 & 8.2). Antennal scale with small distal segment and small outer terminal denticle (figures 10.1 & 10.2), outer margin naked. Second segment of antennal peduncle longer and thicker in the male (figure 10.1) than in the female (figure 10.3). Basal segment from which the antennal scale arises with large spine, covered with spinules (figures 10.1, 10.2 & 10.3). First pair of thoracic limbs with strong long claw (figures 10.4 & 10.5). Second pair of endopod of male thoracic limbs with second segment large and long claw, merus (fifth element) expanded internally as a lamellar process (figure 9.2) or a blunt process with truncate distal side (figure 6.1). Endopod in female unmodified (figure 9.1). Third pair of thoracic limbs with flattened sixth segment with (figure 6.3) or (figure 4) without modified setae. The five anterior abdominal somites in the male with more or less developed pleura (figure 13). In female only the first abdominal somite with small pleura. Female with two pairs of oostegites. First pair of pleopods in female small and unsegmented, remaining pleopods rudimentary. Pleopods of

male well developed and natatory, biramous (figure 6.2) except the first pair, with the endopod lacking. Pseudobranchial lobes large and lamellar, either single or bilobed (figure 6.2). Exopod of the third male pleopod modified, characteristic for a species. Telson about three times as long as broad at the base, sides almost straight, laterally armed with spines (figure 9.3), distal spines furnished with subsidiary spines. Apical cleft small, usually around 1/6 of telson length (figure 9.3). Exopod of uropod smaller than endopod, outer margin armed with small spines (figure 9.3 & 9.4). Spines on endopod and telson usually in series, two long spines with several little spines between, arming at least the distal half of inner margin (figure 9.4). Small statocyst on endopod (figures 9.3 & 9.4).

Weblink: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina



Map 1. Currently known distribution of the genus *Anchialina*

▪ 4.2. DESCRIPTION OF THE SPECIES:

4.2.1. Anchialina agilis (Sars G.O. 1877)

Anchialus agilis Sars G.O. 1877: 78, Figs. 26-28; Carus 1885: 468; Norman 1892: 157; Holt & Beaumont 1900: 230; Calman 1901: 23; Scott 1901: 331; Walker 1901: 293;

Anchialina agilis Norman & Scott 1906: 24;

Anchialus agilis Gough 1907: 198;

Anchialina agilis Norman 1907: 389; Tattersall W.M. 1908: 193; Tattersall W.M. 1909: 141;

Anchialus agilis Zimmer 1909: 66, Figs. 114-118;

Anchialina agilis Tesch 1910: 52; Massy 1912: 70;

Anchialus agilis Tattersall W.M. 1912: 5;

Anchialina agilis Kramp 1913: 554; Riddel 1913: 243; Farran 1914: 5;

Anchialina meditterranea Colosi 1922: 15. Figs. 3a-c;

Anchialus agilis Russel 1925: 780, 797, Fig. 6;

Anchialina agilis Colosi 1929: 411, Figs. 5-6; Zimmer 1933: 30,41,56,57, Figs. 3-4;

Anchialus agilis Bacescu 1941: 9;

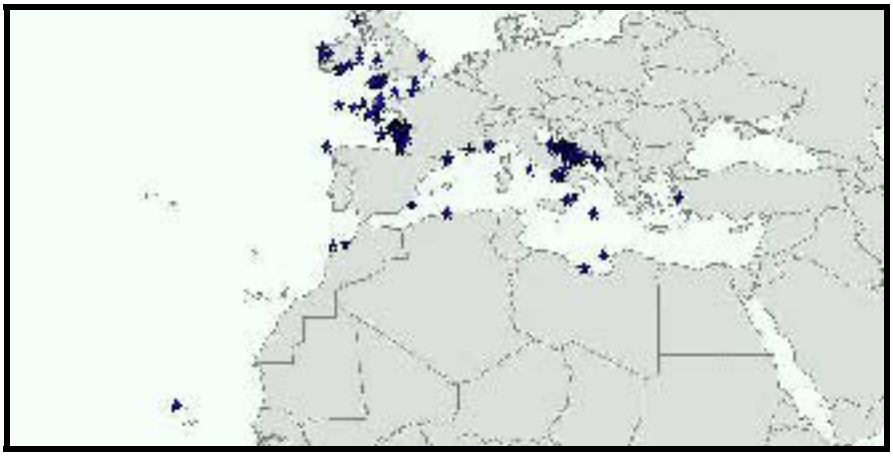
Anchialina agilis Nouvel 1943: 71, Figs. 11-112; Tattersall O.S. 1949: 781,782; Nouvel 1950: 3, Figs. 82-89, Tattersall W.M. 1951: 105; Tattersall & Tattersall 1951: 180, Fig. 34B, 37A-L, 38A-F; Hoenigman 1954: 106, Fig. 9; Furnestin 1960: 158, 185, Figs. 37-38; Tattersall O.S. 1961: 153; Hoenigman 1963: 603, 605, 611, 614; Macquart & Moulin 1965: 147, 188; Hoenigman 1968: 449; Vives 1968: 459; Mauchline 1971: 9,20, Fig. E; Ariani & Spagnuolo 1975: 467, Fig. 18.

Material examined: 1M 2F 1 juv.: Plymouth, 1956.02.27, night, Tattersall O.S. (NHM).

Diagnosis: Both sexes of *A. agilis* can be recognized by the fact that the entire animal is covered with tiny bristles, especially dense on telson and appendages.

Description: Length: M 9 mm F 7-8mm **Carapace**: partially covering first abdominal somite, posterior margin straight. **Rostrum**: triangular, acuminated, bent downward, in female eyestalks partially covered. **Eyes**: dorsal side of peduncle with papilla (look from aside!) in variable shape, mostly oval. **Antenna**: scale small, extending slightly beyond first segment of peduncle.**Thoracic limbs**: endopod of second male pair with basal segment large, fifth segment widened and with oblong-triangular, distally blunt lamellar process directed inward and forward, irregular, endopod of third male pair distally with seven modified setae, tars of thoracic limbs with four segments. **Pleopods:** pseudobranchial lamellae single. Third male pleopod: (figures 5.7, 11.3 & 11.4) exopod 12 segments. **Telson**: laterally with 25-30 spines. **Cleft**: 1/7 of telson, with 25 teeth on each margin. **Uropod**: endopod laterally with 54 spines, exopod laterally with 22 spines.

Distribution: North East Atlantic: West Coast of Ireland (Holt & Beaumont 1900), Irish Coast (Gough 1906); North Sea: Devon, Cornwall (Norman 1906); Channel: English Channel (Gough 1905) Channel Islands (Walker & Thornell 1896), Coast of Normandy (Bazin 1966); Mediterranean: South and West of Italy (Bacescu 1941), Algeria (Tattersall W.M. 1927), Marseille (Champalbert & Macquart-Moulin 1970), Lybia (Bacescu 1976), Morocco (Furnestin 1959).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=agilis

4.2.2. Anchialina dantani Nouvel 1944

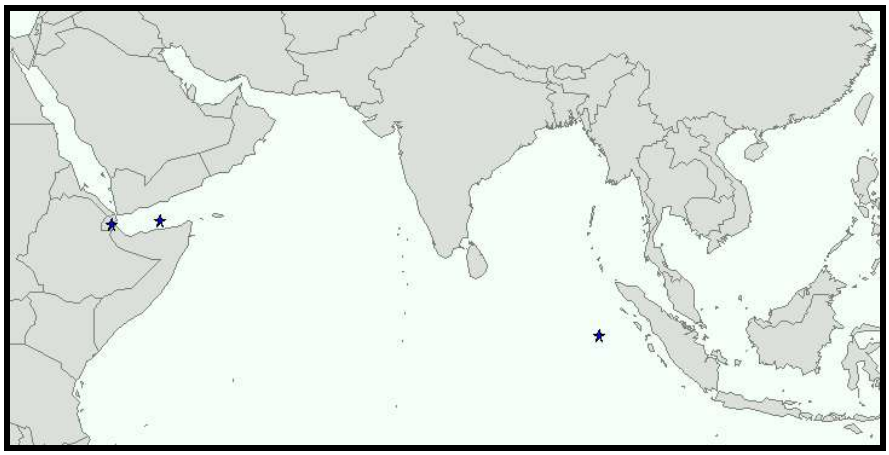
Anchialina dantani Nouvel 1944: 265, Figs. 8A-B; Nouvel 1959: 218, Figs. 69-81.

Diagnosis: *A. dantani* shares the typical dense setae covering with *A. penicillata* but differs from this species by the exopod of the third male pleopod. *A. dantani* is the only species in which the distal process is not smooth but bears saw tooth like tuberculate expansions.

Description: Length: M 6-6.5 mm F 5.5-6.5 mm **Carapace**: first abdominal somite partially to totally covered. **Rostrum**: triangular, pointed, bent downward, covering proximal half of eyestalks in female, in male eyestalks uncovered, rostrum covered with very short setae. **Antennule**: distal segment of peduncle in female with strong spine on internal side, in male internal side of second and third segment and dorsal side of first and second segment densely covered with short setae. **Antenna**: scale with long spine, distal segment slightly longer than wide. **Mandibles**: last two setae on mandibular palp in male modified. **Thoracic limbs**: fifth segment of second male pair with lamellar expansion, tars of thoracic limbs with four segments. **Pleopods**: pseudobranchial lamellae bilobed. Third male pleopod: (Figure 15.2) exopod seven segments, third segment with large lamellar process on external side, external spine of first segment long, saw tooth like tuberculate expansions with soft tops, two closely set short slender straight and naked unequal spines on inner margin, small smooth spine above implantation of terminal spine, internal spine on second

segment forms trident. **Telson**: laterally with 13-17 spines in female, 18-24 in male. **Uropod**: endopod equally long as telson, laterally with 30 spines, two last spines form 900 angle, exopod laterally with 11-15 spines in male or 9-13 in female.

Distribution: East Indian Ocean, Gulf of Aden, Bay of Tadjoura (Nouvel 1944, 1959).



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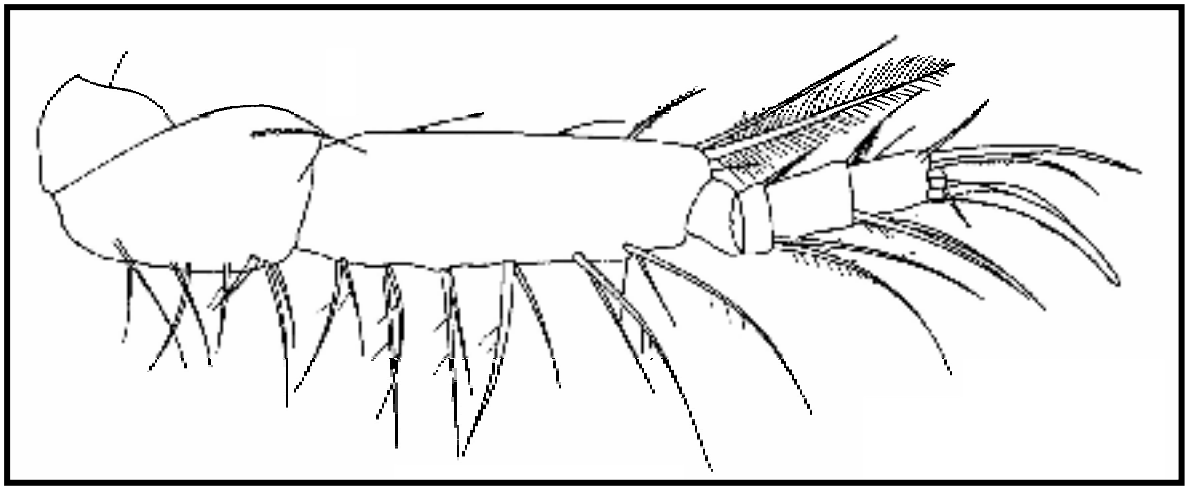


Figure 4. *A. dantani*, distal part of the third thoracic limb in male, posterior view (x120) (after nouvel 1969)

4.2.3. Anchialina dentata Pillai 1964

Anchialina dentata Pillai 1964: 19, Figs. 11a-f;

Anchialina parva Ii 1964: 196, Figs. 50 A-K, 51 A-O;

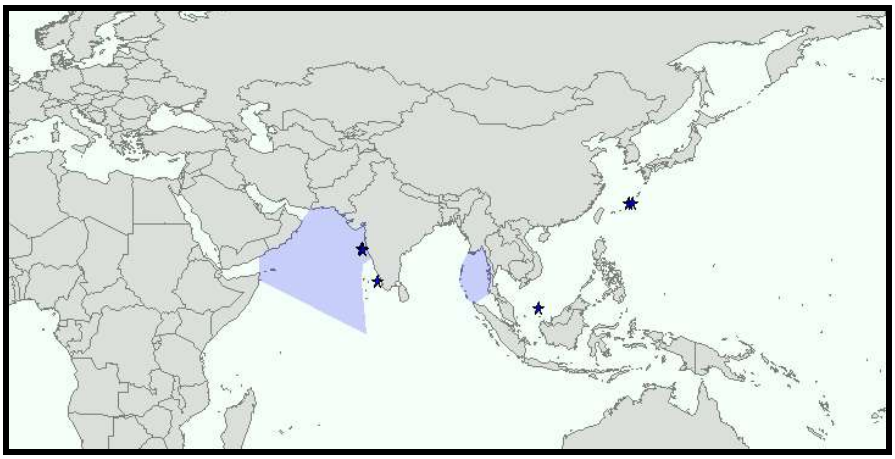
Anchialina dentata Pillai 1965: 1702, Figs. 42-45; Pillai 1973: 70, Figs. 33-34.

Diagnosis: *A*. *dentata* is very similar to *A*. *typica* and *A*. *agilis*, but can easily be distinguished from the latter by the third thoracic endopod in the male: in *A*. *agilis* the distal border of the expansion is straight but oblique and cut into two teeth intervened by two shallow concavities. In *A*. *dentata* there is a row of teeth arming the deeper excavation. *A*. *dentata* differs from *A*. *typica* by the shape of the rostrum, a lesser number of lateral spines on the telson and by the exopod of the third male pleopod, which is ten-segmented in *A*. *dentata*. Remarks: *A*. *dentata* has a spiny surface (Tattersall O.S. 1965; Pillai 1973) of very minute bristles; Ii (1964) did not observe these.

Description: Length: M 6 mm F 4.3-5 mm **Carapace**: first abdominal somite covered in female, uncovered in male, posterior margin straight. **Rostrum:** triangular, moderate anteromedian point, bent forward, eyestalks uncovered in both sexes. **Antennule:** third segment of peduncle slightly longer than wide. **Antenna:** tooth on scale very small, second segment of peduncle in male longer than scale, in female about as long as scale. **Thoracic limbs:** second pair in male with merus strongly dilated internally, distal extremity truncated with seven sharp teeth, third pair in male with six modified setae on distal segment, tars of thoracic limbs with four segments (Nouvel, unpublished data). **Abdomen:** pleural plates well developed. **Pleopods:** pseudobranchial lamellae single, nearly semicircular with four setae at inner distal angle. Third male pleopod: (figure 5.8) exopod of male ten segmented, last three segments with modified external setae, first segment distally with three smooth setae, external seta of second segment with spinules in distal half, extending to tip of inner terminal seta, external seta of third segment: slender, naked, as long as third segment, external seta of fourth segment: thin, naked, short (smaller than half the length of the segment). **Telson:** laterally about 20 spines Cleft: 1/6

length of telson, 28 teeth on each margin. **Uropod:** endopod as long as tip of terminal spine of telson, exopod laterally with 20 short spines.

Distribution: West Pacific: South China Sea (Ii 1964), Ryukyu Islands, Japan (Murano 1990); East Indian Ocean: Arabian Sea (Pillai 1964, 1973), Andaman Sea, South of Java (Pillai 1973).



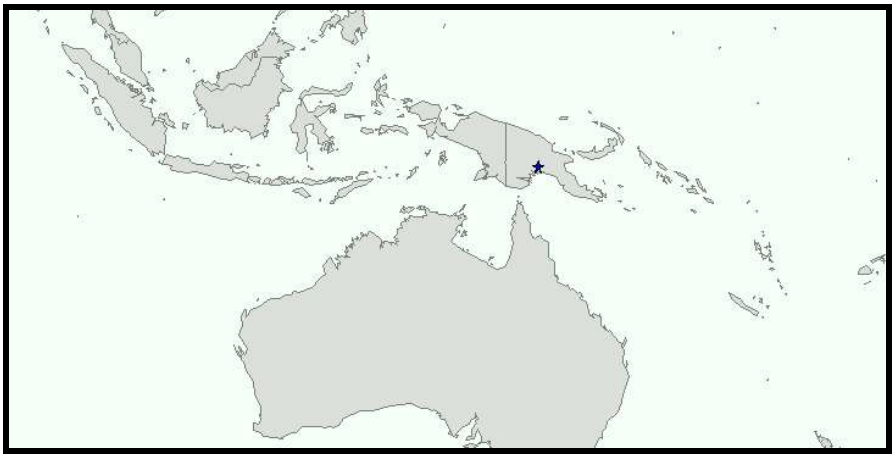
Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=dentata

Anchialina flemingi Tattersall W.M. 1943: 66, Figs. 1 A-B, 2 A-B, 3 A-C.

Diagnosis: The differences with related species, mainly *A. agilis* are based on the shape of the rostrum in both sexes, slight differences in the second thoracic limbs of the male and details of the exopod of the third male pleopod. Remark: description by Tattersall was based on one damaged adult male, and two immature specimens.

Description: Length: M 6 mm **Rostrum:** long triangular, acutely pointed, rostrum longer than first segment of antennular peduncle, slightly covering eyestalks. Antenna: second segment of peduncle longer than scale, twice as long as wide. Thoracic limbs: second pair in male with merus strongly dilated internally, distal extremity truncated with six to seven minute teeth. **Pleopods:** pseudobranchial lamellae single, triangular, inner angle broadly rounded, outer angle with single seta. Third male pleopod: (figure 5.4) exopod nine segments, last four setae on outer and last three setae on inner side modified. **Telson:** laterally with 33 spines. **Uropod:** endopod longer than telson, about 66 spines in series, exopod laterally with 23 spines.

Distribution: West Pacific: Samoa (Tattersall W.M. 1943).



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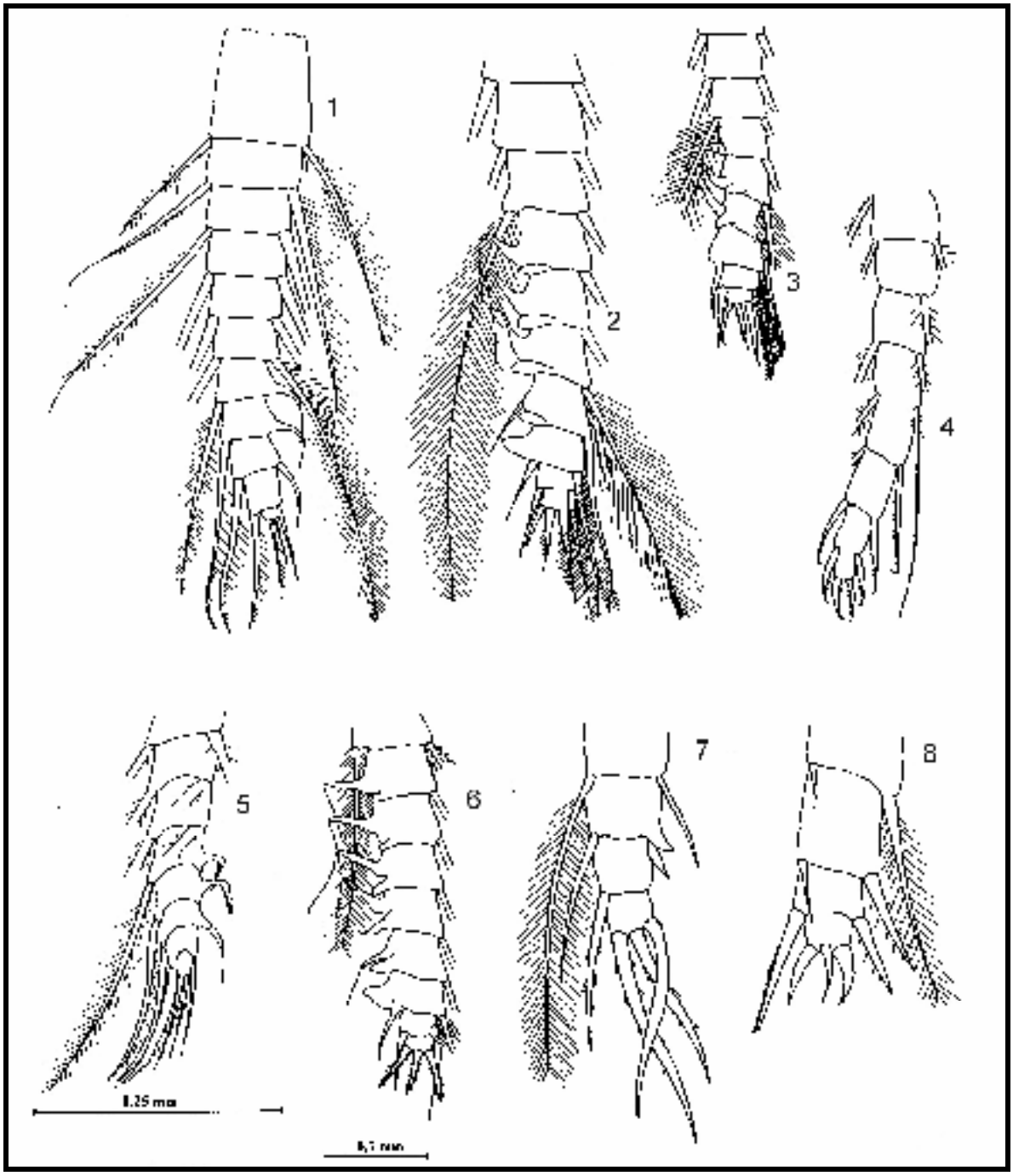


Figure 5. 1. *A. latifrons*, distal end of left exopod of third male pleopod, posterior view (x 120) (after Nouvel 1971) 2. *A. typica typica*, distal end of left exopod of third male pleopod (5.8 mm) from Nosy-be (x 182) (after Nouvel 1971) 3. *A. typica orientalis*, distal end of left exopod of third male pleopod (7 mm) from the NW Atlantic (x 120) (after Nouvel 1971) 4. *A. fleminghi* distal end of exopod of third male pleopod (x 70) (after Tattersall 1943) 5. *A. pillai*, distal end of exopod of third male pleopod (after Jo & Murano 1992) 6. *A. typica*, distal end of exopod of third male pleopod (after Pillai 1964) 7. *A. agilis*, distal end of exopod of third male pleopod (x 40) (after Tattersall 1951) 8. *A. dentata*, distal end of exopod of third male pleopod (scale unknown) (after Pillai 1973).

4.2.5. Anchialina grossa Hansen 1910

Anchialina grossa Hansen 1910: 54, Figs. 3a-h, 1a-d; Hansen 1912:196;

Anchialina frontalis Zimmer 1915b: 159, Figs. 1-5;

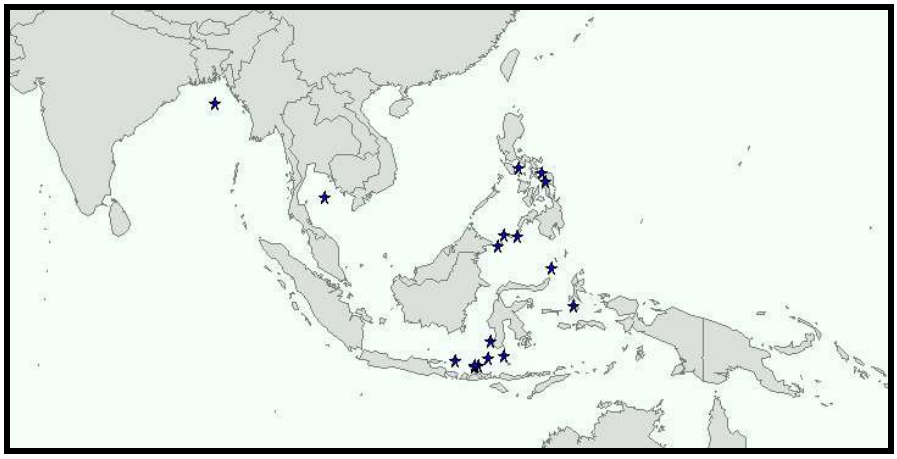
Anchialina grossa Tattersall W.M. 1922: 458, Fig.6; Illig 1930: 566; Tattersall W.M. 1936: 148; Tattersall W.M. 1951: 102; Tattersall O.S.: 166, 176; Ii 1964: 202, Figs. 53K-M, 53P; Pillai 1965: 1701, Figs. 35-38; Wang & Liu 1987: 218, Figs. 7,1-12.

Diagnosis: *A. grossa* is characterized by a typical lamellar process of the exopod of the third pleopod in the male, but there is possible confusion with *A. obtusifrons*. Distinguishing features from the latter are the triangular pointed rostrum in both sexes and the length of the endopod of the uropod. In *A. grossa* the telson exceeds the endopod in length, where in *A. obtusifrons* the endopod equals or does not reach the tip of the telson. (see also diagnosis *A. obtusifrons*)

Description: Length: M 9.2 mm F 7 mm **Carapace:** first abdominal somite only partially covered, posterior margin emarginate. **Rostrum:** triangular, acuminated, bent downward, in female eyestalks partially covered. **Antenna:** scale two and a half times as long as wide, second segment shorter than width of scale in female, in male shorter than length of scale. **Thoracic limbs:** endopod of second male pair with second segment enlarged, fifth segment with lamellar process directed inward and forward, sixth segment broad, tars of thoracic limbs with four segments. **Pleopods:** pseudobranchial lamellae large, bilobed, outer lobe three to four times larger as inner, no sharp angles. **Third male pleopod:** (figure 11.6) terminal process near the base with one short spine, large lamellar hook-shaped process from third segment covers segments two and one, internal spine on second segment trifurcate. **Telson:** laterally with 21-27 spines (Nouvel, unpublished data). **Uropod:** endopod longer than telson, exopod laterally with 16 spines (Nouvel, unpublished data), end broadly rounded, almost truncate.

Distribution: North East Indian Ocean: Bay of Bengal (Hansen 1910; Zimmer 1915), Gulf of Siam (Hansen 1910; 1912), Gilbert Islands (Hansen 1912), India

(Tattersall, W.M. 1922), North West Australia: Great Barrier Reef (Tattersall W. M. 1936); West Pacific: Philippines (Tattersall W. M. 1951).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=grossa

4.2.6. Anchialina latifrons Nouvel 1971

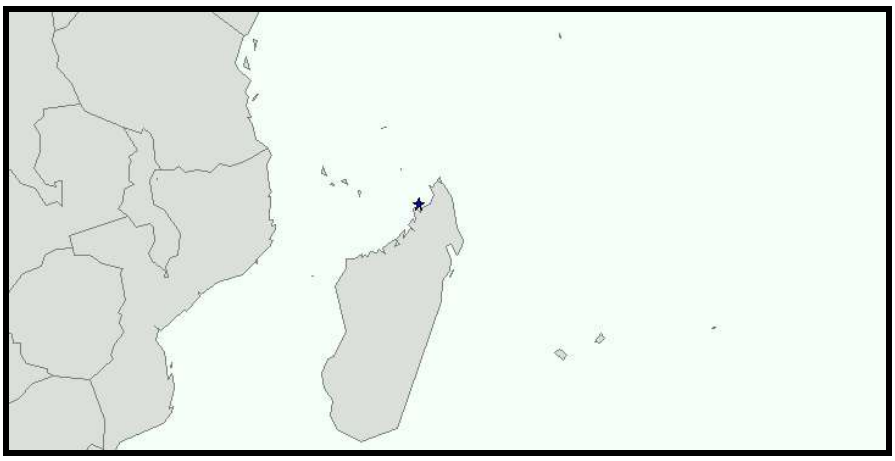
Anchialina latifrons Nouvel 1971: 329, Figs. 10-29.

Diagnosis: Very close to *A. pillai*, but separated from that species by details of the rostrum, second thoracic limb, te1sonand third male p1eopod. (see also diagnosis *A. pillai*).

Description: Lenght: M 5.3-7.2 mm F 5.3-7.2 mm **Carapace:** first abdominal somite partially covered in female, totally covered in male. **Rostrum:** strongly curved with anteromedian small tooth, slightly bent forward. **Antennule:** median segment of the peduncle on the distal side with 4-5 spines in both sexes, separated by denticulations, internal side of second and third segment with one single seta Antenna: scale small in both sexes, smaller than second segment. **Thoracic limbs:** merus (fifth segment) of endopod of second male pair strongly dilated to internal side, distal extremity truncated and sinuous, third pair in male with four modified setae on distal segment, carpopropodus formed by two segments, tars of endopod of third (female) or fourth (male) to eight thoracic limbs with three segments. **Pleopods:** pseudobranchial lamellae rounded, single. **Third male pleopod:** (figure 5.1) exopod 11 segments, segments one-five with modified setae, external spine on

fust segment long, denticulated, internal spine on first segment smooth, segment two, three and four internally with slightly curved, barbed seta ending in soft point, extremities ending at the same point, external seta of segment two simple, segment three, four and five with smooth obtusely curved setae, seta on segment three less curved. **Telson:** 22-30 lateral spines in male, 14-20 in female. **Uropod:** endopod equally long as telson, exopod laterally with 20-26 spines, and distally truncated, distal spine of external side forms obtuse angle.

Distribution: Madagascar: Nosy-be (Nouvel 1971).



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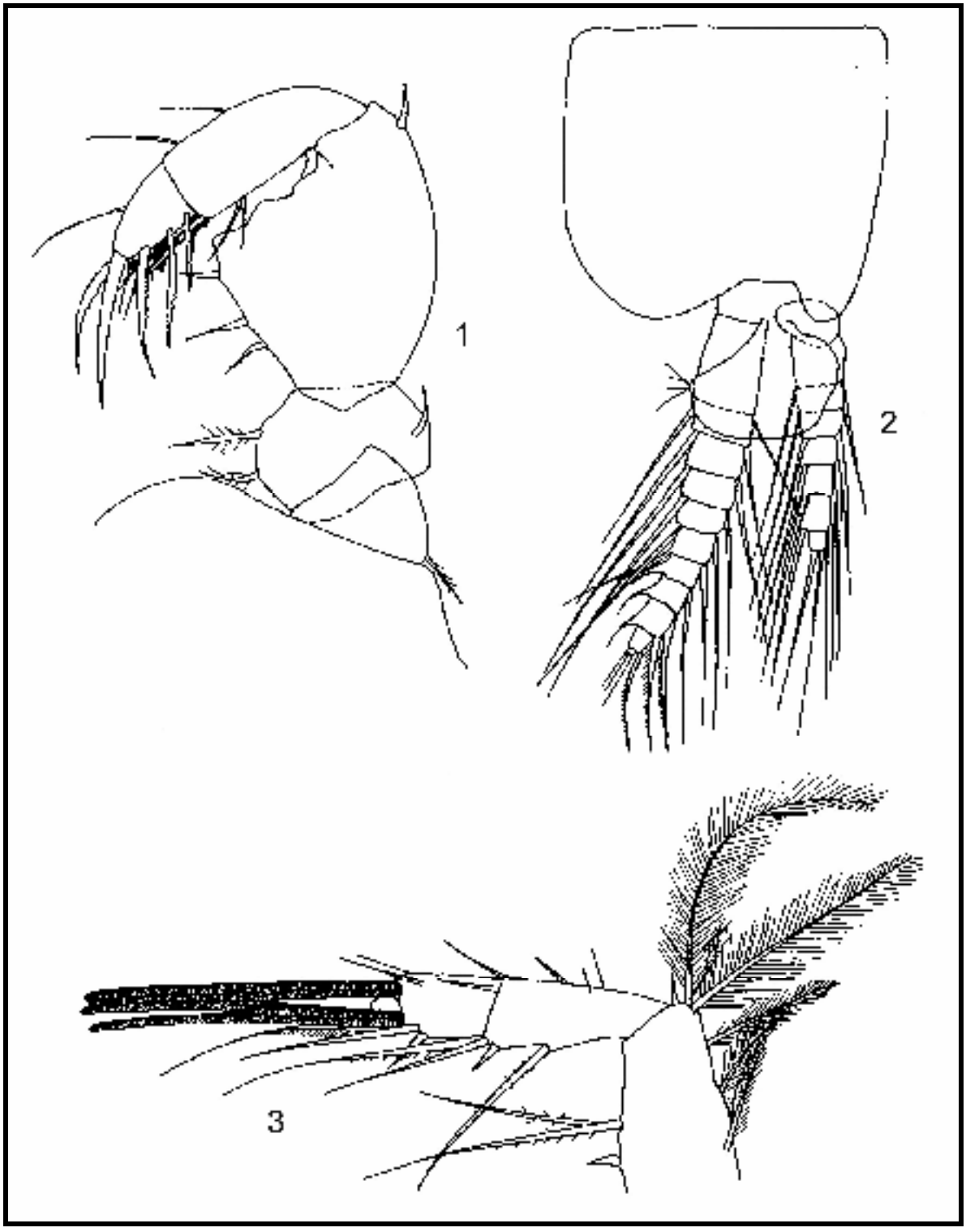


Figure 6. 1. *A. latifrons*, endopod of left second thoracic limb in male, posterior view (xI20) (after Nouvel 1971) 2. left pleopod of the third pair in male, posterior view (xI20) (after Nouvel 1971) 3. , distal part of the left third thoracic limb in male, posterior view (x120) (after nouvel 1971)

Anchialina lobatus Panampunnayil 1999: 685, Figs. 1-39.

Diagnosis: *A. lobatus* belongs to the "grossa-group" and is easy distinguished from the other species by the presence of a large middorsal hairy lobe on the first segment of the antennule, the modified setae on the mandibular palp and the exopod of the third male pleopod.

Description: Length: M 8-8.2 mm F 5.7-6.3 mm **Carapace:** posterior margin nearly straight. **Rostrum:** triangular, pointed, in male bent downward, in female straight. **Antennule:** first segment in male with large middorsal hairy lobe, extending to middle of third segment. Antenna: scale three times as long as wide. **Mandible:** mandibular palp with two modified setae. **Thoracic limbs:** first thoracic limbs without sexual dimorphism, fifth segment of second male thoracic limbs with lamellar expansion, tars of thoracic limbs with four segments. **Pleopods:** pseudobranchial lamellae bilobed, rounded. Third male pleopod: (figure 7) exopod 14 segments, segments three, four en five externally with lobes, third segment as long as preceding three segments combined, inner distal angle with one long spine and one middorsal spine, second segment short with one thick granulated spine on outer distal comer and one slender spine on inner distal comer, fust segment terminating in one short and two long spines. **Telson:** laterally with 30-32 spines in male, 20-22 in female. Cleft: 30-35 spines on each margin in male, 20-25 in female. **Uropod:** endopod longer than telson, exopod laterally with 19-21 spines.

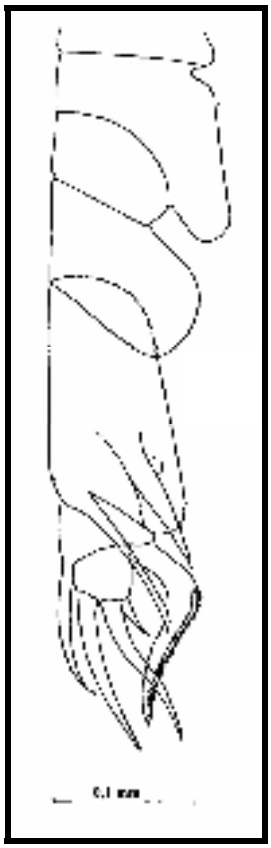
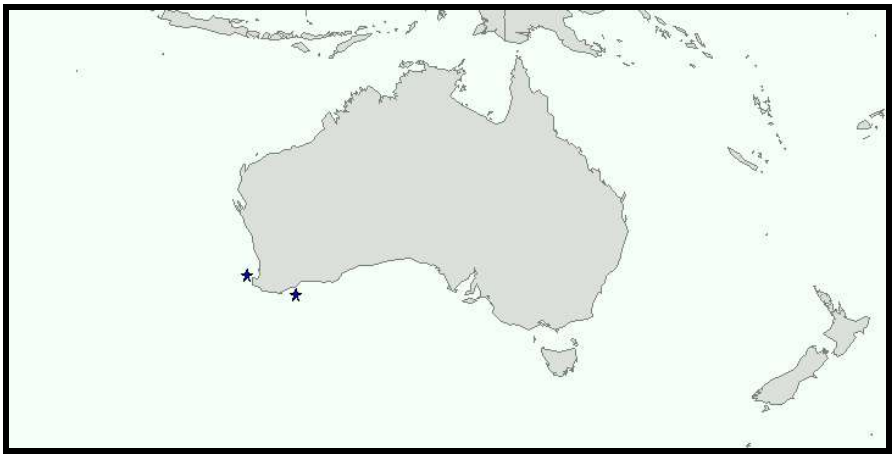


Figure 7. *A. lobatus*. distal end of exopod of third pleopod in male (after Panampunnayil 1999).

Distribution: South West Australia (Panampunnayil 1999).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=lobatus

4.2.8. Anchialina madagascariensis Nouvel 1969

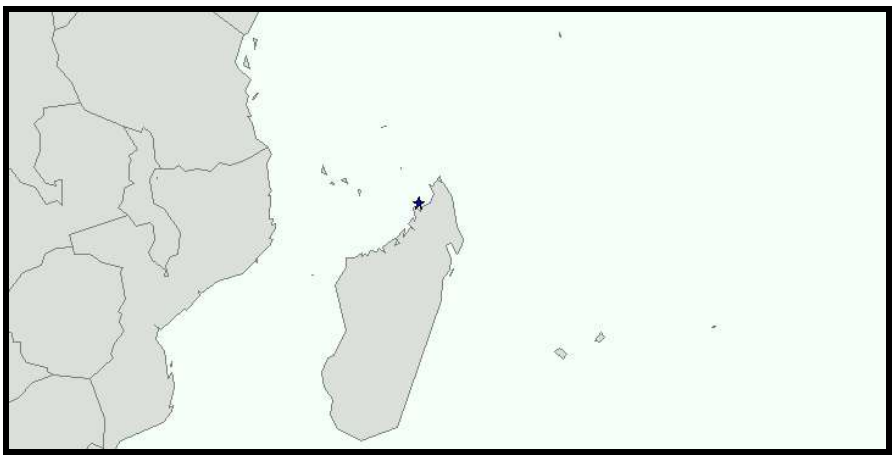
Anchialina madagascariensis Nouvel 1969: 340, Figs. 1-32.

Diagnosis: *A. madagascariensis* is possibly confused with *A. sanzoi*. Specimens of *A. madagascariensis* are characterized by the mandibular palp and the number of spines on the exopod of the uropod and telson. Nouvel (1969) made a full morphological study on the number of spines linked to the body length of *A. sanzoi* and *A. madagascariensis*, and found a higher number of spines in *A. sanzoi*. The males are further recognized by differences in the exopod of the third pleopod.

Description: Length: M 7.1-9.3 mm F 6-7.5 mm **Carapace:** first abdominal somite partially covered, posterior margin slightly concave. **Rostrum:** triangular, sharply pointed, proximal half with slightly convex margins, covering the proximal half of the eyestalks in female, in male eyestalks uncovered, rostrum more obtuse, more bent downward. **Antennule:** distal two segments from peduncle armed with many slender setae. Antenna: peduncle in male longer, in female shorter than scale, second segment slightly shorter than scale. **Mandibles:** last two setae on mandibular palp in male modified. **Thoracic limbs:** endopod of second male pair with lamellar expansion, third pair in male lacking particular modified setae, tars of endopod of third (female) or fourth (male) to eight thoracic limbs with four segments.

Pleopods: pseudobranchial lamellae rounded, bilobed, except fifth pair simple, subtriangular. Third male pleopod: (figure 15.4) exopod 14-15 segments, third segment with large lamellar process on external side, external spine on third segment long, with spinules, displaced, in middle of posterior side of segment, internal spine on third segment short, more spine like, smaller than second segment, second segment smal, external development, external spine on second segment displaced, in middle of posterior side of segment, curved and slightly barbed, internal spine on second segment trifid, one spine longer than other two, first segment displaced, external spine on first segment smooth, sinuous, forming the terminal process, internal spine on first segment, short. **Telson:** laterally with 30-34 spines in male, 22-26 in female. **Uropod:** endopod longer than telson, laterally with 40 spines, exopod laterally with 16-20 in male, 13-15 in female, rounded, one side truncated, distal side makes sharp angle with last spine of external side.

Distribution: Madagascar: Nosy-be (Nouvel 1969).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=madagascariensis

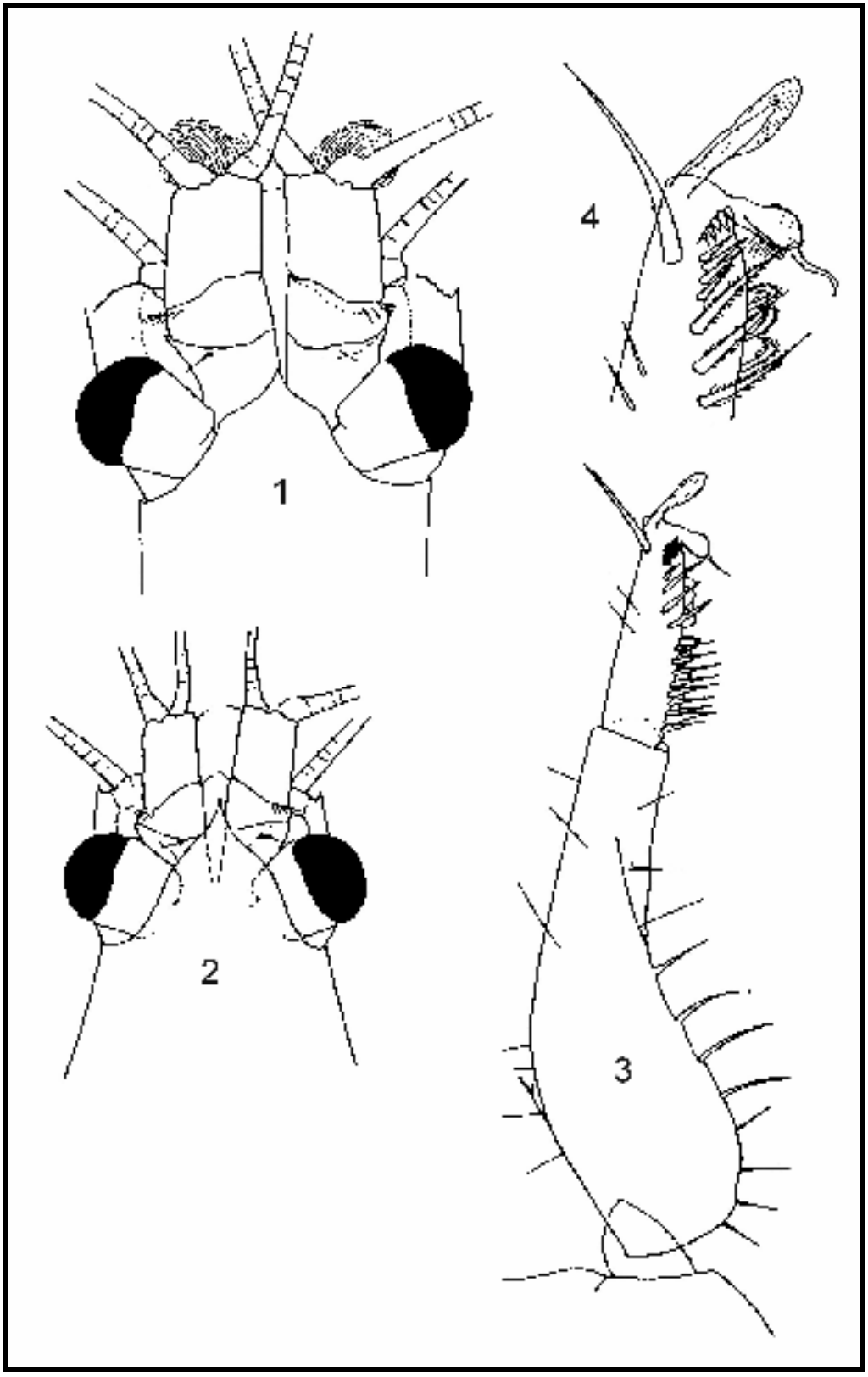


Figure 8. 1.*A. madagascariensis*, anterior part of male (9.3 mm), dorsal view (x28) (after Nouvel 1969) 2. anterior part of female (7.1 mm), dorsal view (x28) (after Nouvel 1969) 3. left mandibular palp of male, ventral view (x60) (after Nouvel 1969) 4. Extermity of the same palp (xI83) (after Nouvel 1969)

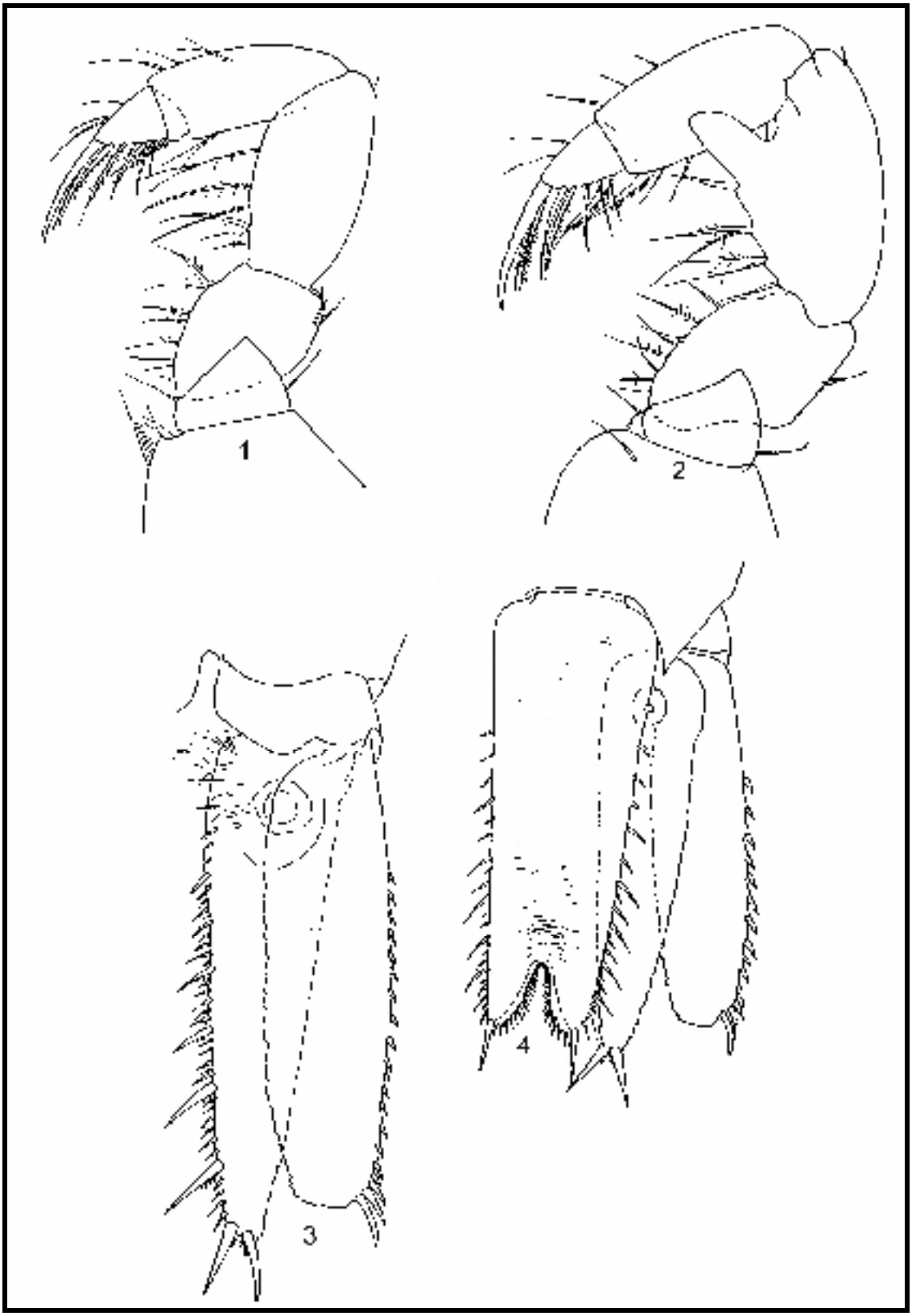


Figure 9. 1. *A. madagascariensis*, endopod of left second thoracic limb in female, posterior view (xI20) (after Nouvel 1969). 2. endopod of left second thoracic limb in male, posterior view (xI20) (after Nouvel 1969). 3. left uropod of male (8.1 mm), ventral view (x60) (after Nouvel 1969). 4. A. madagascariensis, telson and left uropod of female (x60) (after Nouvel 1969)

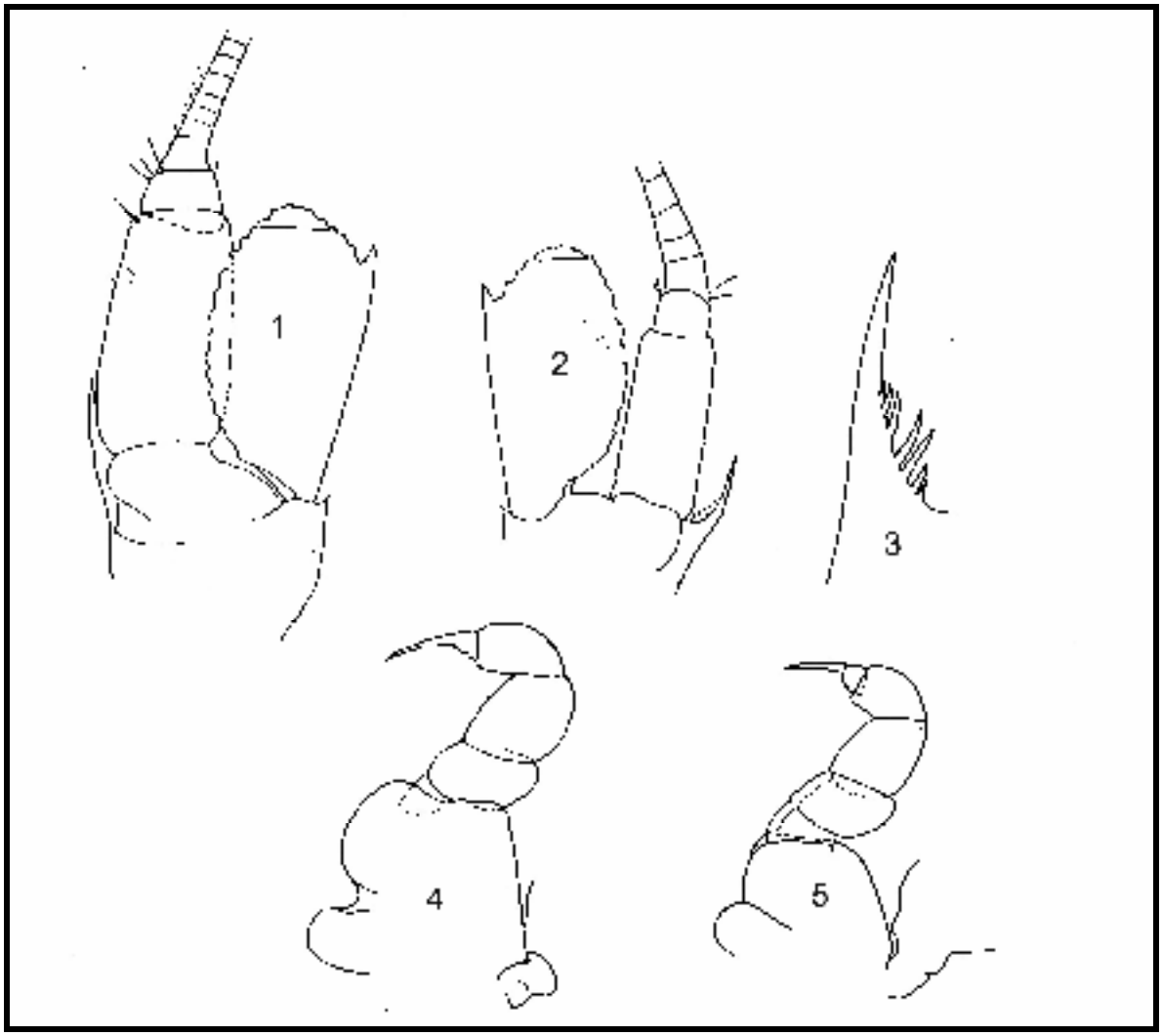


Figure 10. 1. *A. madagascariensis*, base of right antenna of male, dorsal view (x60) (after Nouvel 1969) 3. spine on base of right antenna of male, dorsal view (xI83) (after Nouvel 1969). 2. base of left antenna of female, dorsal view (x60) (after Nouvel 1969). 4. left ftrst thoracic limb of male, posterior side (x60) (after Nouvel 1969). 5. left first thoracic limb of female, posterior side (x60) (after Nouvel 1969).

4.2.9. Anchialina media Ii 1964

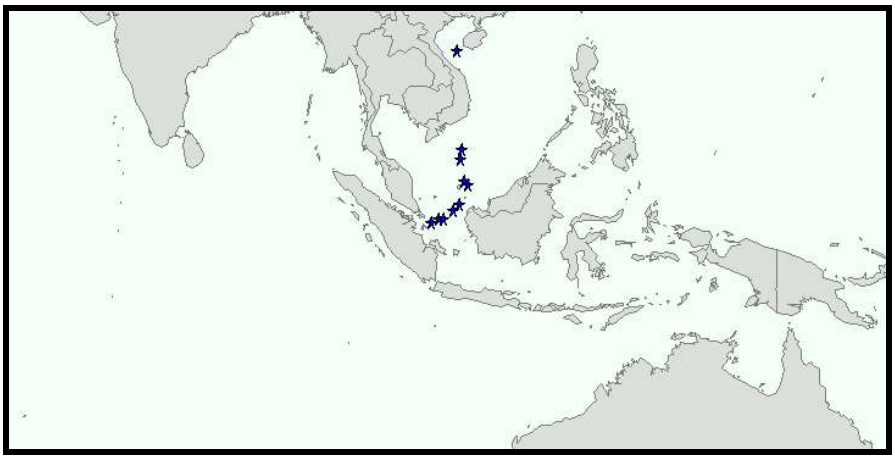
Anchialina media Ii 1964: 204, Figs. 52 A-Q, 53 A-J, 54A-P.

Diagnosis: *A. media* differs from *A. grossa* and *A. sanzoi* by the relative size of the antennal peduncle in the female, and the third male pleopod. These species are so closely allied that Ii (1964) suggested the species *A. media*, *A. grossa*, and *A. sanzoi* to be different growth stages of one species, *A. grossa* , based upon the very similar armature of the third male pleopod and the known morphological variations depending on size and maturity (Nouvel 1971, Tattersall W.M. 1922).

Description: Length: M 7 mm F 7 mm **Carapace:** first abdominal somite uncovered, posterior margin slightly concave. **Rostrum:** triangular, proximal half with convex margins, covering proximal half of eyestalks in female, distal half with slightly concave margins and bent downward, in male eyestalks uncovered, rostrum smaller, narrower and more bent downward. **Antennule:** distal two segments of peduncle armed with many slender setae. **Antenna:** peduncle in male longer than scale, second segment slightly shorter than scale, peduncle in female shorter than scale, second segment 1 ½ as long as width of scale, second segment of antennal peduncle always four times as long as third. **Mandibles:** terminal two setae on mandibular palp in male modified. **Thoracic limbs:** fifth segment of second male endopod with large lamellar expansion, distal margin nearly straight, tars of endopod of third (female) or fourth (male) to eight thoracic limbs with four segments, exopod of thoracic limbs with small spine at distal outer comer of basal plate in all pairs. **Pleopods:** pseudobranchial lamellae rounded, bilobed, outer lamella bigger than inner, pleural plate on first abdominal somite in female triangular with rounded angles. Third male pleopod: (figure 15.1) exopod 15 segments, third segment with large lamellar process on external side, slightly curved inward, bilobate at distal end, each end with rounded apex, second segment with stout internal spine, spinous with single stout subsidiary spine at middle and densely spinous in distal half, external spine on second segment short slender simple spine (Ii, 1964), second segment with two setae at inner distal comer, ventral seta trifurcated and minutely spinous near the end, dorsal seta shorter and naked, fust segment ends in long terminal spine in S-shape, two closely set short, slender, straight and naked spines on inner

margin, one about twice as long as the other. **Telson:** laterally with 35 spines. Cleft: 38 teeth on each margin. **Uropod:** endopod equally long as telson, dense row of gradually increasing spines, 39 on inner margin, spines barbed with spinules, exopod laterally with 15-19 spines, rounded, one side truncated.

Distribution: Indian Ocean: South China Sea (li 1964).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=media

4.2.10. Anchialina obtusifrons Hansen 1912

Anchialina obtusifrons Hansen 1912: 197, Figs. 4a-c; Illig 1930: 566; Tattersall W.M. 1951: 102; Ii 1964: 202, Fig. 53c.

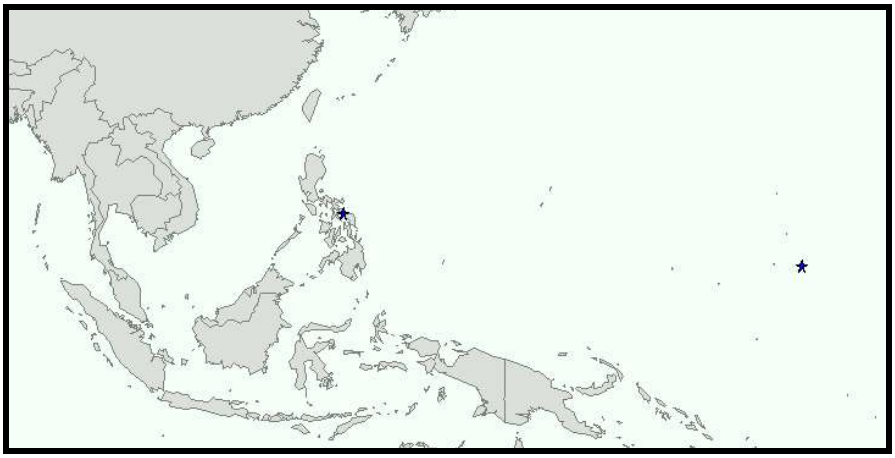
Material examined: 4M 2F: Arno Atoll, Marshall Islands, 1900.01.24-26, surface, Tattersall W.M. (USNM)

Diagnosis: *A. obtusifrons* is closely allied and similar to *A. grossa* (Hansen 1912), males can be distinguished by the exopod of the third pair of pleopods, the shape of the rostrum which is triangular in *A. grossa*, and by the third antennular segment. In *A. obtusifrons* the distal segmentof the antennular peduncle is conspicuously longer in proportion to its width where in *A. grossa* it is about half as long as wide.

Remark: Original description was based on two males.

Description: Length: M 7.5 mm. **Rostrum:** long, in male reaching beyond eyes, eyestalks uncovered, looks truncate but tenninal triangular portion bent downward, lateral margins slightly concave. **Thoracic limbs:** fifth segment of endopod of second male pair with large lamellar expansion, directed forward. **Third male pleopod:** (figure 11.5) large lamellar process on external side, slightly curved inward, narrowed before end, second segment long, with tenninal expansion covering insertion of spines on this segment, internal spine on second segment trifurcate, external spine on second segment distal half very slender, internal spine on first segment with saw like teeth and distal half very slender. **Uropod:** endopod equally long as telson or slightly longer, exopod laterally with 15-17 spines. Female unknown.

Distribution: South West Pacific: Gilbert Islands (Hansen 1912).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=obtusifrons

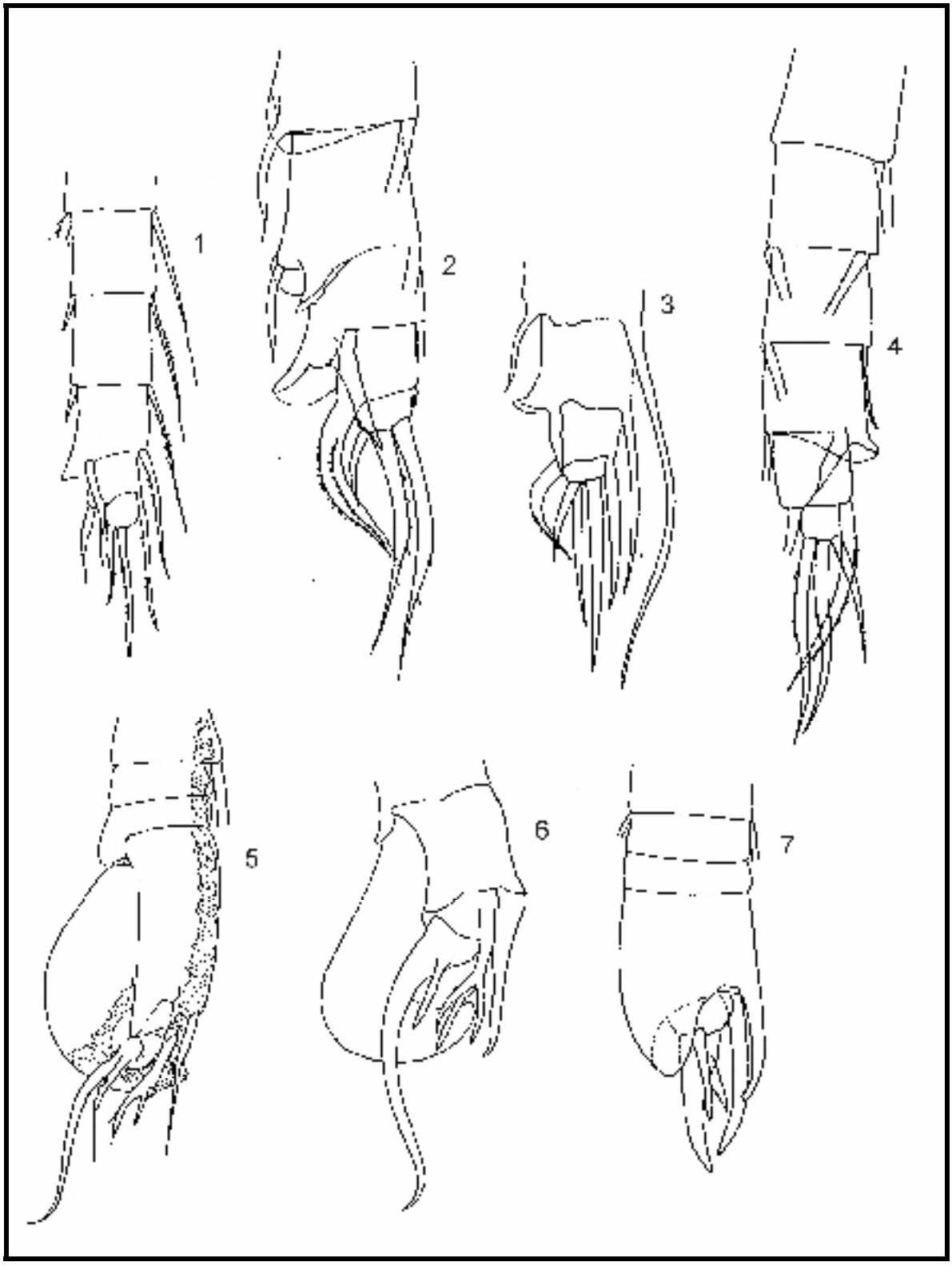


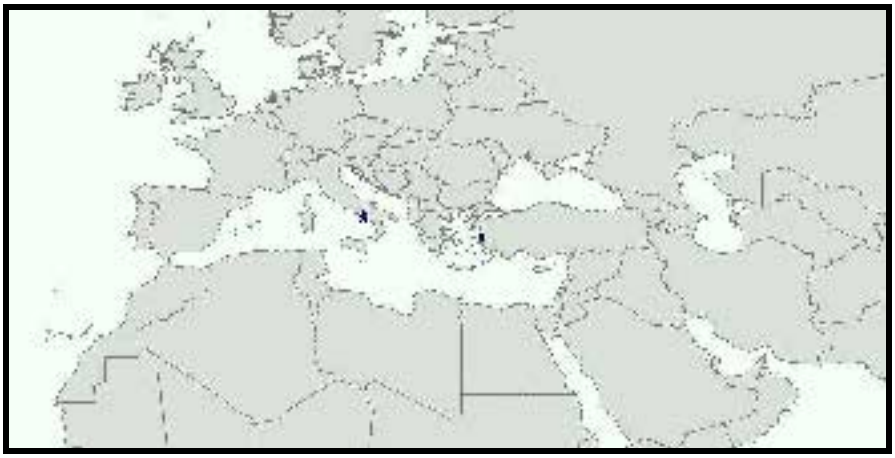
Figure 11. 1. *A. truncata*, distal end of exopod of third male pleopod (after Sars 1885) 2. *A. truncata*, distal end of exopod of third male pleopod (x 250) 3.. *A. agilis*, distal end of exopod of third male pleopod (after Sars 1877) 4. *A. agilis*, distal end of exopod of third male pleopod (x250) 5. *A. obtusifrons*, distal end of exopod of third male pleopod (x 185) (after Hansen 1912) 6. *A. grossa*, distal end of exopod of third male pleopod (x 125) (after Hansen 1910) 7. *A. frontalis*, distal end of exopod of third male pleopod, anterior view (x 200) (after Zimmer 1915).

4.2.11. Anchialina oculata Hoenigman, 1960

Anchialina oculata Hoenigman 1960: 339; Hoenigman 1963: 612; Hoenigman 1964: 141; Hoenigman 1968: 449; Ariani & Spagnuolo 1975: 468, Fig. 19.

Description: a variant of *A. agilis*, no papillae on eye peduncle, sixth abdominal somite larger, lesser spines on exopod of telson.

Distribution: Central Adriatic Sea, Palagruza Islands (Hoenigman 1960).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=oculata

4.2.12. Anchialina penicillata Zimmer 1915

Anchialina penicillata Zimmer 1915b: 161, Figs. 7-12; Tattersall W.M. 1940: 331; Tattersall W.M. 1951: 103; Tattersall a.s. 1960: 166, 176; Ii 1964: 201,579; Pillai 1965: 1702, Figs. 39-41.

Material examined: 1M 1F 1juv.: NW Australia, Stephens Bay, 1964.01.21, Tattersall collection (NHM).

Diagnosis: *A*. *penicillata* shares the typical dense covering on the peduncle of the antennules in the male with *A*. *dantani*, distinguishable by the exopod of the third male pleopod. (see also diagnosis *A*. *dantani*)

Description: Length: 7-8 mm **Rostrum:** triangular, acuminated, bent downward, in female eyestalks partially covered. **Antenna:** peduncle barbed, first segment inside smooth, dorsally with triangular pattern, base at distal side, second segment inside barbed forming triangular pattern, dorsal triangular pattern with base on internal side, third segment internal side barbed, dorsal side smooth. Scale smaller than second segment of peduncle. **Thoracic limbs:** fifth segment of second pair in male widened and with oblong-triangular, distally blunt lamellar process directed inward and forward, carpus of third thoracic endopod very long, twice as longas the combined length of the propodal segments. Third male pleopod: (figure 12) 13 segments, fifth segment with oval lamella partially covering the fourth segment with small rounded extrusion, third segment small, second segment large with distal spine on inner side, other side with elongation ending in strong spine, distal segment with distally two spines. **Telson:** laterally with 23-24 spines. **Uropod:** endopod smaller than telson, exopod laterally with 13 spines (Nouvel, unpublished data).

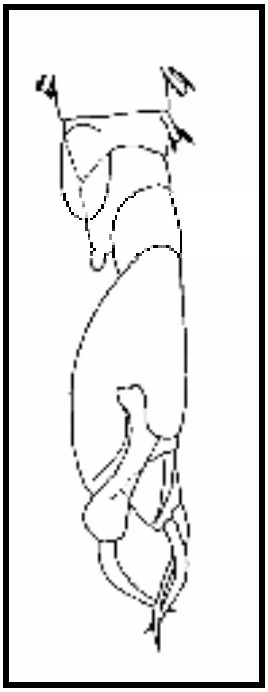
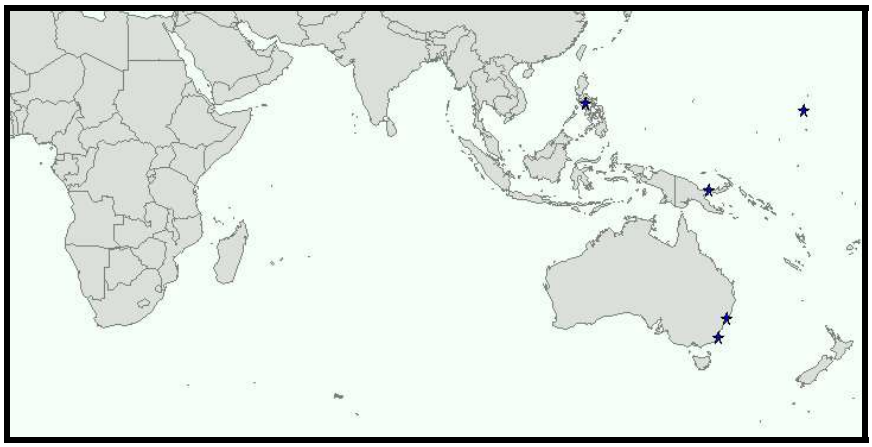


Figure 12. *A. penicillata.* distal end of exopod of third pleopod in male, (x 155) (after Zimmer 1915).

Distribution: Indian Ocean: New South Wales (Tattersall W.M. 1940), between Ceylon and Dampier (Zimmer 1915); Central and South West Pacific: Marshall Islands and Philippine Islands (Tattersall W.M. 1951).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=penicillata

Anchialina pillai Jo & Murano 1992: 192, Figs. 5-7.

Diagnosis: Very closely related to *A. latifrons* but separable by the rostrum which does not extend beyond the first antennular segment in *A. latifrons* and the merus of the second thoracic limb in the male where the projection of the inner margin makes a right angle. In *A. pillai* the inner angle of the merus is produced into an obtuse angle at about its middle. The telson extends beyond the exopod of the uropod in *A. pillai*, where in *A. latifrons* the telson is smaller or equally long. The male exopod of the third pleopod cannot be used to separate these two species.

Description: Length: M 5.5-6.9 mm **Carapace:** first abdominal somite covered, eyestalks partially covered, posterior margin convex. **Rostrum:** triangular, sharply pointed, extends beyond distal margin of first segment of antennular peduncle. **Antenna:** scale small, reaching 2/3 of second segment of antennal peduncle, second segment of peduncle five times longer than third, spine with spinules along inner and outer margins. **Labrum:** with long and median process armed with 10 or 11 pairs of teeth. **Mandible:** right mandible with three processes, left without any, palp distally with two modified setae.

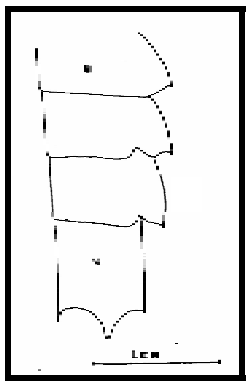
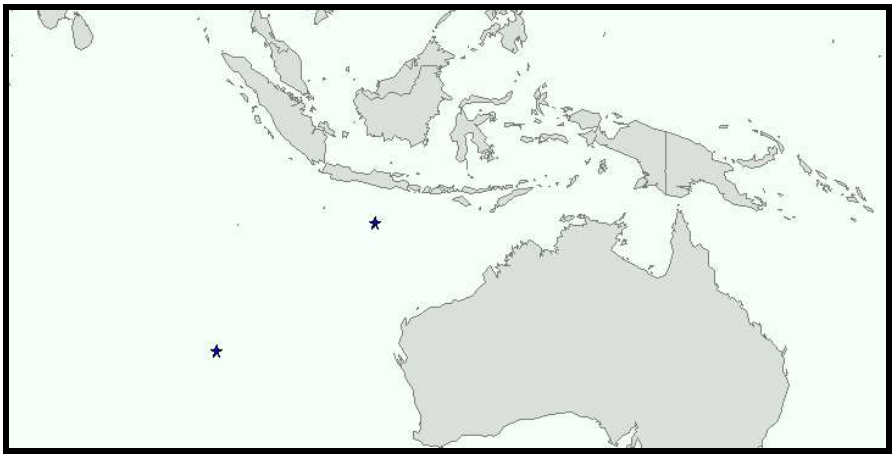


Figure 13. *A. pillai*, abdominal somites (after Jo & Murano 1992)

Thoracic limbs: endopod of second pair in male with merus broadened, distal side truncated with two rounded teeth on distal half of inner border, endopod of third male pair with carpopropodus 3-segmented, with distally four modified setae, tars of thoracic limbs with three segments, pleural plates well developed with apical spine directed backward. **Pleopods:** pseudobranchial lamellae single, almost circular. Third male pleopod: (Figure 5.5) exopod 11 segmented, last five segments with modified setae. **Telson:** laterally with 29-32 spines, cleft 29-32 spines on each margin. **Uropod:** telson longer than endopod, endopod laterally with 52 spines, exopod laterally with 15-20 spines.

Distribution: Southeastern Indian Ocean (Pillai 1973), North West Coast of Australia (Jo & Murano 1992).



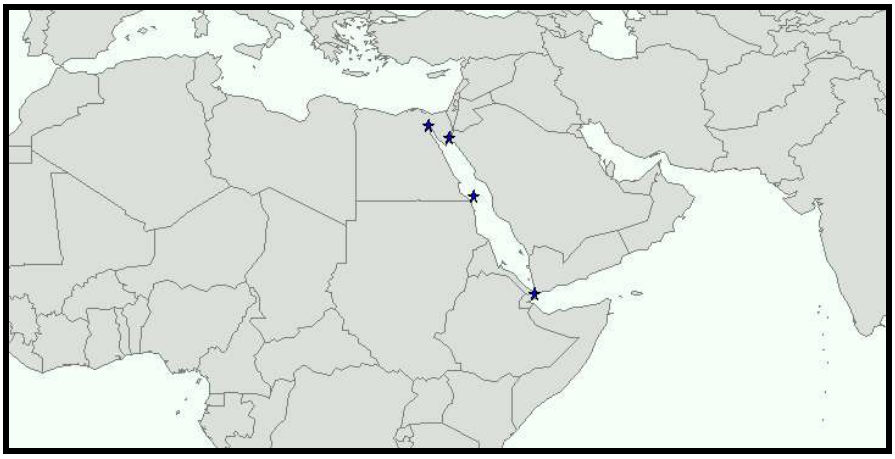
Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=pillai

4.2.14. Anchialina sanzoi Coifmann 1937

Anchialina sanzoi Coifmann 1937: 26, Figs. 15f, 15g-h; Nouvel 1944: 255; Nouvel 1959: 217; Ii 1964: 210, Fig. 53; Nouvel 1969: 351, Figs. 31-37.

Diagnosis: Close to *A. madagascariensis*. (see diagnosis *A. madagascariensis*) **Description:** Length: M 8-9 mm F 5-7 mm **Carapace:** covers partially (Coifmann 1937) or totally (Nouvel 1959) the first abdominal somite. **Rostrum:** triangular, sharply pointed, bent downward. **Antennula:** internal side of second and third segment of peduncle, distally with spinein both sexes. **Antenna:** scale larger than third segment peduncle. **Mandibles:** last two setae on mandibular palp in male modified. **Thoracic limbs:** second pair in male with digital expansion on fifth segment, tars of thoracic limbs with four segments. **Third male pleopod:** (figure 15.3) exopod 12 segments (Nouvel, unpublished data), third segment with large lamellar process on external side, slightly inwardly curved, external spine on third segment and external spine on second segment long, denticulated, external spine on first segment very long, forming distal process. **Telson:** laterally with 30-33 spines. **Uropod:** endopod equally long as telson, exopod laterally with 19-23 spines.

Distribution: Red Sea: Bab-El-Mandab (Coifmann 1937), Gulf of Akaba (Nouvel 1959), Gulf of Suez (Nouvel 1959).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=sanzoi

4.2.15. Anchialina truncata (Sars G.O. 1883)

Anchialus truncatus Sars G.O. 1883: 38;

Anchialus typicus Sars G.O. 1885: 193; Figs. 4-24; Ortmann 1905: 972;

Anchialina truncata Hansen 1910: 51, 53; Zimmer 1912: 10; Tattersall O.S. 1955: 90; Ii 1964: 195.

Material examined: 2M 2F 2juv.: Discovery exp., 1985.11.19, Tattersall collection (443), (NHM); 2M 2F Discovery exp., 1985.11.19, Tattersall collection (423), (NHM).

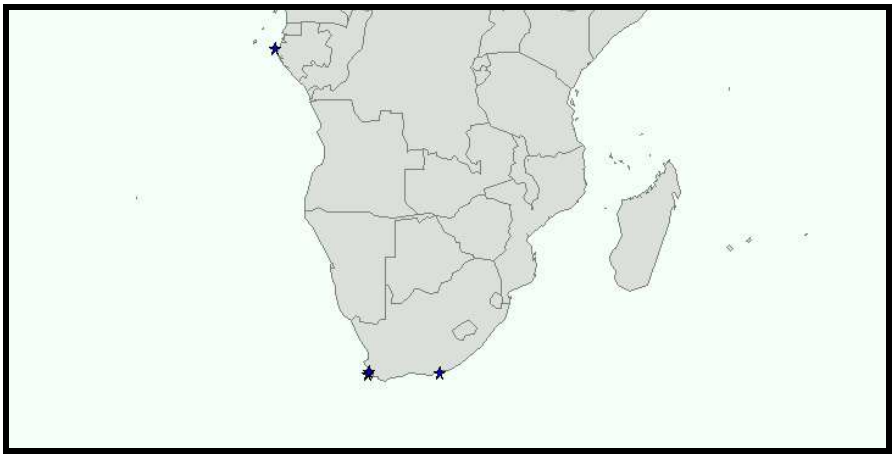
Diagnosis: Recognizable by the armature of the third male pleopod, and the truncated rostrum in both sexes.

Remark: *A. truncata* has three setae on the distal segment of the exopod of the third male pleopod, and not two as mentioned by Nouvel (1971).

Description: Length: F 9 mm **Carapace:** posterior margin straight. Rostrum: truncated, bent downward, when lifted up slightly convex (obs). **Antennule:** last segment in peduncle as long as two preceding ones together. **Antenna:** scale about two times as long as broad (obs), smaller than second segment of peduncle.

Thoracic limbs: (obs) second male pair with fifth segment expanded, distal side truncated, sixth segment of endopod of third male pair truncated with 10 modified setae, tars of thoracic limbs with four segments. **Pleopods:** (obs) pseudobranchial lamellae single. **Third male pleopod:** (figures 11.1 & 11.2) (obs) exopod 12 segments, second segment with strong curved spine/process with double row of denticulations, third segment with expansion covering distal end of fourth segment, expansion with gently rounded bulb and one long sharp lamellar processus, unequally narrowing at end, fourth segment with expansion covering distal end of second segment, smaller than on third segment, consisting of gently rounded bulb with sharp triangular process. **Telson:** (obs) laterally with 40 spines in male. Cleft: 36 spines on each margin. **Uropod:** (obs) endopod longer than telson, laterally with 72-78 spines, exopod laterally with 26 spines in male.

Distribution: South Africa: Port Elizabeth to Cape Peninsula (Tattersall W.M. 1951), Cape Town (Sars G.O. 1883; Zimmer 1912); Coast of Gabon: Cape Lopez (Tattersall W.M. 1951).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=truncata

4.2.16. Anchialina typica Kroyer, 1861

Anchialus typicus 1861: Kroyer: 53, Figs. 7a-b;

Anchialina typica Hansen 1910: 52, Figs. 2a-k; Hansen 1912: 196; Colosi 1918: 7; Colosi 1920:237; Tattersall W.M. 1922: 457; Tattersall W.M. 1923: 282;

Anchialus typica Hansen 1925: Fig. 6a;

Anchialina typica Tattersall W.M. 1926: 9; Tattersall W.M. 1936a: 148; Tattersall 1936c: 279;Tattersall 1936b: 96; Delsman 1939: 166, Fig. 18; Nouvel 1943: 70, Figs. 109-110; Tattersall W.M. 1951: 100; Banner 1954: 580; Tattersall O.S. 1955: 89,183, Figs. 15A-M; Tattersall O.S. 1960: 166, 176; Tattersall O.S. 1962: 230; Ii 1964: 188,579, Figs. 48A-L, 49A-C; Pillai 1964: 18, Figs. 10 a-i; Tattersall O.S. 1965: 82; Pillai 1966: 1700, Figs. 32-34; Brattegard 1970: 24, Figs. 6A-D; Wigley & Bums 1971: 722, Fig. 4; Nouvel 1971: 325; Lagardere 1972: 669; Brattegard 1973: 16; Bacescu & Ortiz 1984: 16, Fig. 1B; Wang & Liu 1987: 222, Figs. 9,1-14.

Diagnosis: the best diagnostic character of this species is the modification of the third male pleopod. **Description: Length:** M 5-7 mm, F 4.5-5 mm **Carapace:** partially covering first abdominal somite, posterior margin nearly straight. **Rostrum:** short, trapezoidal with rounded angles,concave along the mid-line, anteriorly slightly bent forward, in female covering base ofeyestalks. **Antenna:** scale smaller than second segment of peduncle. **Thoracic limbs:** endopodof second male pair with fifth segment expanded, ending in rounded process, margin betweenprocess and insertion of sixth segment concave, tars of thoracic limbs with three segments,endopod of third male pair with sixth segment widened, truncated, with six modified setae. **Pleural plate:** well developed.

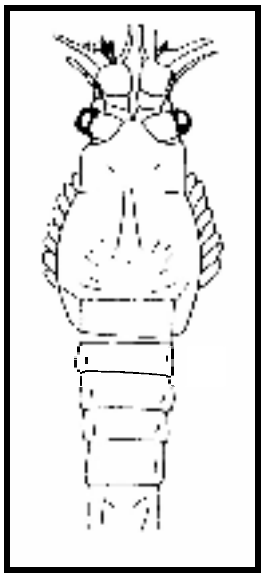


Figure 14. A. typica, dorsal view, (after Ii 1964)

Pleopods: pseudobranchial lamellae single, semicircular (triangular), outer margin nearly straight, inner margin evenly rounded. **Third male pleopod:** (figures 5.2, 5.3 & 5.6) exopod 11-13 segments, first segment distally with three barbed setae, second segment with two simple setae, segments three-seven (eight) with protuberance on outer distal corner, oblong triangular with bluntly rounded apex, third segment with short slender setae distally spinulated at inner distal side of protuberance, fourth segment with short simple seta slightly bent inward, segments five, six, seven and sometimes eight, external setae demarcated into a peduncle and a flagellum, forming 90° angle, internal plumose setae on distal inner corner of third and fourth segment shorter than on the proximal segments and with stouter subsidiary hairs. **Telson:** laterally with 25 spines in series with secondary spinules. Cleft: 1/6 of telson length, 33 teeth on each margin. **Uropod:** endopod equally long or slightly longer than telson, exopod laterally with 15-20 spines with secondary spinules.

Distribution: Tropical, around the equator: Indian Ocean: Gulf of Siam, Bay of Rayong (Ortmann 1902), North West Madagascar, Nosy-be (Nouvel 1971), Northern regio of Malacca Strait (Tattersall O.S. 1965); Tropical Atlantic: 14°N (Kroyer 1861), Rio De Janeiro (Tattersall W.M. 1923), Western Cuban shelf waters (Bacescu & Ortiz 1984), Gulf of Mexico (Modlin 1984; Price *et al*. 1986; Briones & Soto 1991), Western Atlantic near Bermuda and Bahama (Tattersall W.M. 1922 and 1936b); Pacific Ocean: Hawaiian Islands (Ortmann 1902), Gilbert Islands, Andaman Islands (Tattersall W.M. 1922), Gulf of Manaar (Tattersall W.M. 1922), Great Barrier Reef (Tattersall W.M. 1936a,c), Philippine Islands (Tattersall W.M. 1951); Caribbian Sea (Colosi 1918 and 1920), Caribbian coast of Colombia (Brattegard 1974), Carribean region (Brattegard 1975); Mid-Atlantic and Benguela Current (Tattersall O.S. 1955), English channel (Gough 1905).

Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=typica

4.2.17. Anchialina typica typica Brattegard, 1969

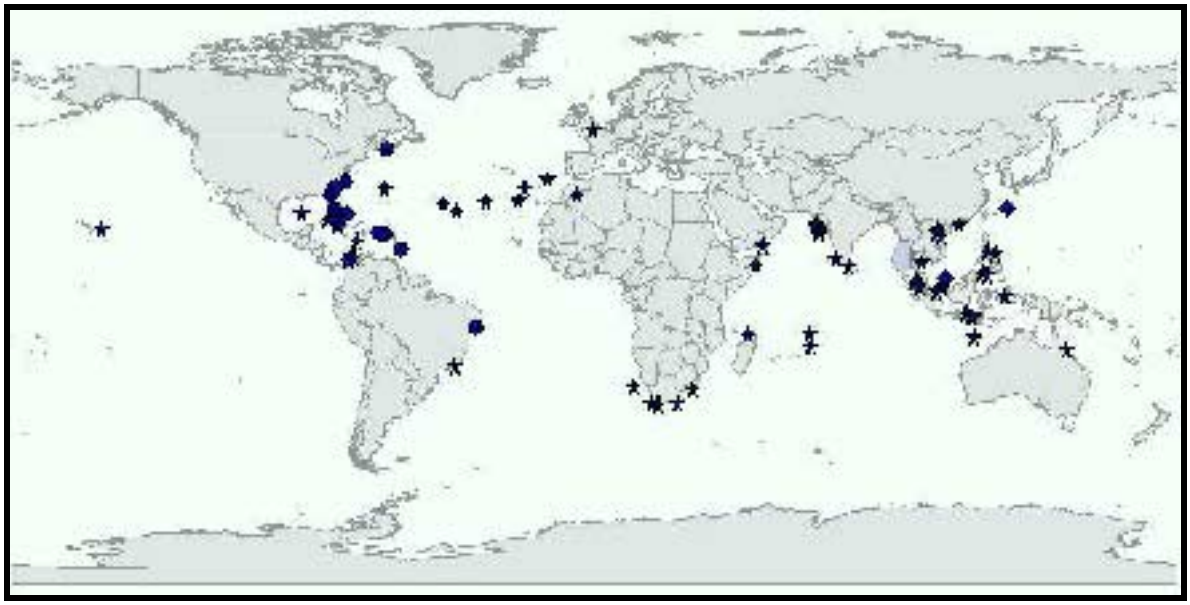
Description: Length: F 3.9-5.6mm M 3.9-5.8mm **Third male pleopod:** (figure 5.2) segment five, six, seven (sometimes eight): setae with angle of 90°, segment four always a spiny seta but never with an angle of 90°, second and third segment with spined, straight setae, third segment very large and internal distal comer elongated in a rounded point.

Distribution: Western Tropical Atlantic: Coasts of Brazil, Colombia, Barbados, Virgin Islands, Puerto Rico, Cuba, Bahamas, Southern and North Eastern Horida, South Carolina, North Carolina, Nova Scotia (Hansen 1910; Tatersall, W.M. 1923, 1951, Nouvel 1943, Lewis & Fish 1969, Brattegard 1970, Wigley and Bums 1971), The Mid-Atlantic just north of the equator (Tattersall O.S. 1955).

4.2.18. Anchialina typica orientalis Nouvel, 1971

Description: Length: M 4.9-5.2 mm **Rostrum:** dorsal view truncated with concave margin, the real anterior margin (bent downward) slightly convex, never pointed forward in a relevable point. **Thoracic limbs:** carpopropodus from third to eighth pair with three segments. **Third male pleopod:** (figure 5.3) segment four, five, six: external setae with angle of 90°, external setae of the second and third segment strongly curved, no angle of 90°, internal setae of the second, third and fourth segment with normal hairs, third segment not dilated on external side.

Distribution: Indian Ocean (Hansen 1910, 1912; Pillai 1964, 1973), South China Sea (Ii 1964; Nouvel 1971; Jo 1991); West-Pacific: Nansei Islands of Japan (Jo 1991), Ryukyu Islands (Fukuoka & Murano 1997).



Map 2. Distribution map *of A. typica* (star), *A. typica typica* (circles), *A. typica orientalis* (rhomb)

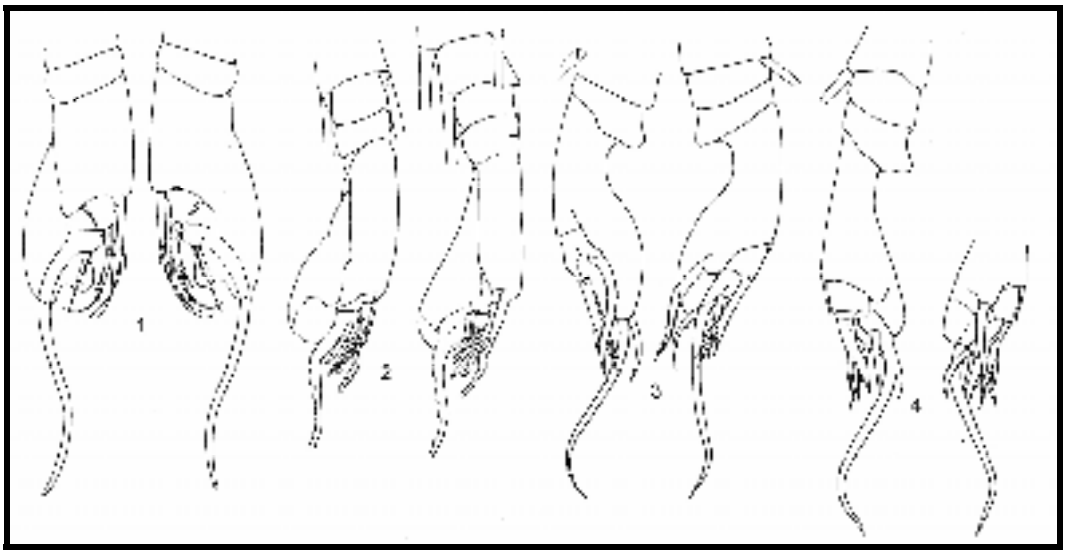


Figure 15. 1. *A. media*, distal end of exopod of third male pleopod (7.5 mm), anterior view (right), posterior view (left) (x 270) (after Li 1964) 2. *A. dantani*, distal end of right exopod of third male pleopod (6 mm), anterior view (right), posterior view (left), (x 366) (after Nouvel 1944) 3. *A. sanzoi*, distal end of left exopod of third male pleopod (7.5 mm), posterior view (left), anterior view (right), (x 183) (after Nouvel 1969) 4. *A. madagascariensis*, distal end of left exopod of third male pleopod, anterior view (left), posterior view (right) (x 183) (after Nouvel 1969).

Anchialina zimmeri Tattersall W.M. 1951: 103, Figs. 31A-G; Ii 1964: 201; Wang & Liu 1987: 224, Figs. 10, 1-11.

Diagnosis: Closely allied with *A. penicillata*. The third pleopod of the male is the main distinguishing feature. Other differences are the presence of microscopic spinules on the outer part of the third segment of the antennular peduncle in *A. zimmeri*, the antennal scale in *A. zimmeri* is three times as long as broad, in *A. penicillata* only two times. And the two segments of the propodus of the endopods of the 3-8 thoracic limbs are subequal to the carpal segment in *A. zimmeri*.

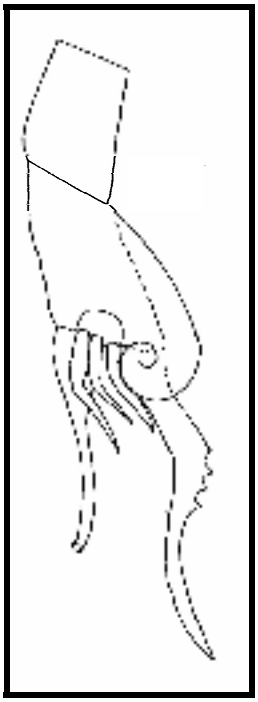
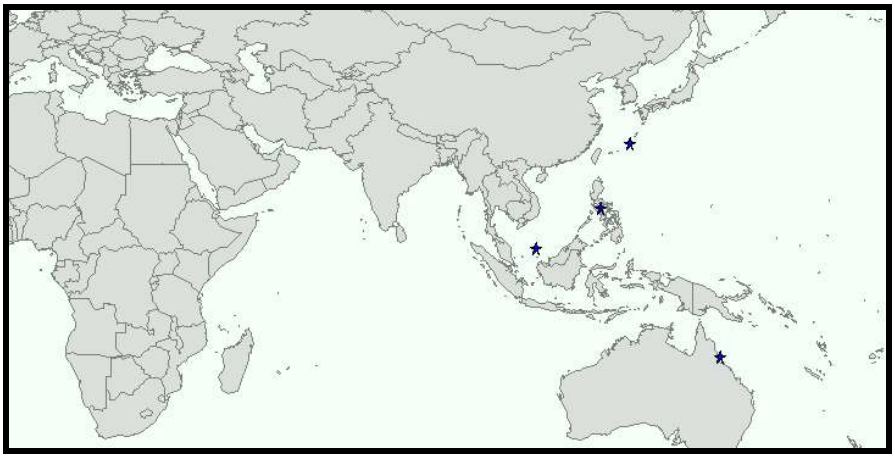


Figure 16. A. zimmeri, distal end of exopod of third pleopod in male (x 39) (after Tattersall 1951)

Description: Length: M 6-7 mm F 5.2-7 mm **Antennule:** microscopic spinules on the external side of the third segment of peduncle. **Antenna:** microscopic spinules on the outer part of the second segment of the peduncle, scale three times as long as broad. Thoracic limbs: iuth segment of second male pair with lamellar expansion, tars of thoracic limbs with three segments, the two segments of the propodus of the endopods of the 3-8 thoracic limbs sub equal to the carpal segment.

Third male pleopod: (figure 16) exopod 11 segments, segment two typical large swollen shape, external spine on second segment long, strong, gently curved in S-shape with tubercles on its outer margin, internal spine on second segment slightly curved, longer than spines on terminal segment, segment one with three sub equal spines, all shorter than the external and internal spine on the second segment.

Distribution: West Pacific: Philippine Islands, Mindano Strait (Tattersall W.M. 1951), The Great Barrier Reef (Bacescu 1979), South China Sea (Wang and Liu 1987), Ryukyu Islands (Fukuoka & Murano 1997).



Web link: http://intramar.ugent.be/nemys/nemys.asp?genus=anchialina&species=zimmeri

5. Cladistic analysis

The data matrix with character states for every species can be found in appendix 1 and 2.

The analysis yields 40 trees of equal length (L: 55; CI 56; RI: 73). The strict consensus tree collapses ten nodes and results in a fairly uninformative tree (figure 17). However, some patterns can be derived.

The tree shows that the genus *Anchialina* is well defined by a long series of characters (this is also proved by high bootstrap values in the tree displayed in figure 18).

The analysis confirms the existence of the two groups that are currently recognized by several authors. These were formerly known as the "*typica*-group" and the "*grossa*-group". The "*grossa*-group" including *A. media*, *A. madagascariensis*, *A. dantani*, *A. obtusifrons*, *A. sanzoi* and *A. grossa*, is well defined by the characters 1, 7, 8 and 9 which are all except for 1 (the length of the antennal scale) features of the armature of the third pleopod in the male. *Anchialina lobatus*, normally classified in the "grossa-group" forms an intermediate form between the "*grossa-group*" and the "*typica-group*", by sharing a more primitive distal part of the pleopod, together with some larger expansions of the third-sixth segment. These expansions are not so prominent as within the members of the "typica-group".

Remarkable in the tree is the presence of *A. zimmeri* and *A. penicillata* in the "*typica*-group", and not in the "*grossa*-goup" as expected, for not sharing the character states 6(1), 10(1), 11(0), 12(1), 13(2), 16(1). These characters are well described: especially the differences in the second (10), and third (11) thoracic endopod in the male and the pseudobranchial lamellae (13).

A. penicillata clearly belongs in the "*typica*-group". The situation of *A. zimmeri* is not as clear, partially by lack of information, and otherwise as a result of a heterogeneous distribution of characters. *A. zimmeri* will probably take a position similar to *A. lobatus*, not really classifiable in one of the two groups.

To be able to get a more detailed view on the relationships within both groups, 10 additional characters were added describing the geographical distribution of all taxa.

This second analysis yields 556 trees of equal length (L: 113; CI 37; RI: 39). The strict consensus tree collapses nine nodes. The retrieved tree (figure 19) shows a similar pattern. This implies adding the geographical distributions did not influence the phylogenetic relationship. It may be concluded that the geographical distributions observed match more or less the morphologically observed data. The bootstrap tree plotted in figure 20 proves the genus is well defined (high value – 99), and also the "*grossa*"-branch is relatively well reliable.

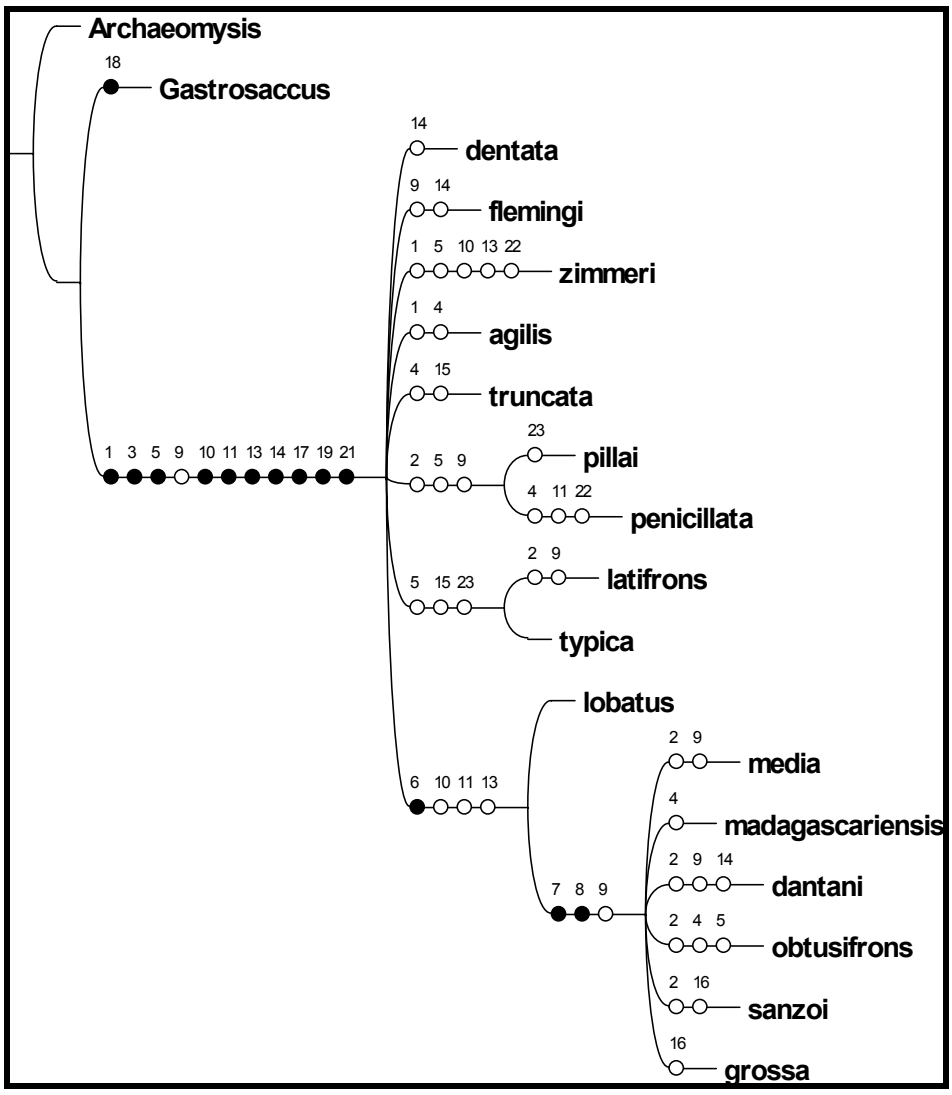


Figure 17. Strict consensus tree based on morphological data

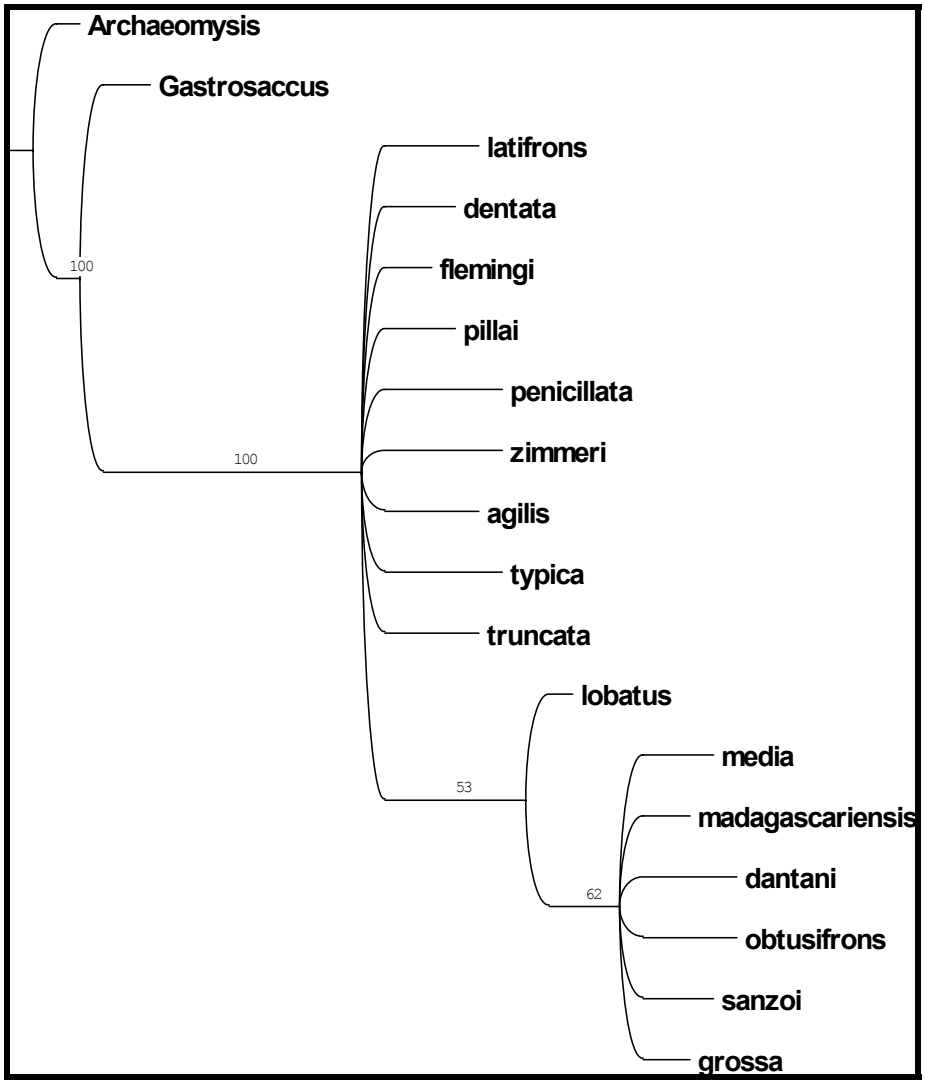


Figure 18. Bootstrap tree morphology

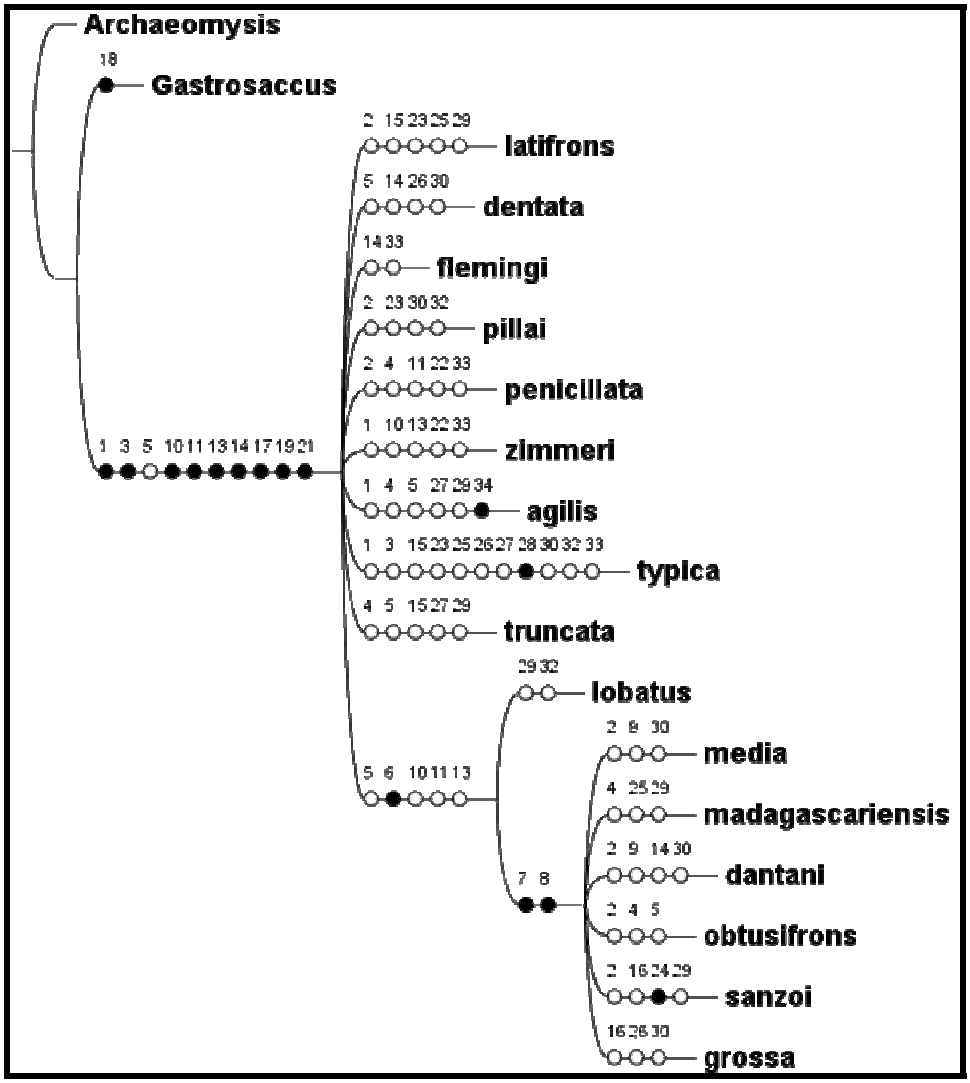


Figure 19. Strict consensus tree based on morphological and geographical characters

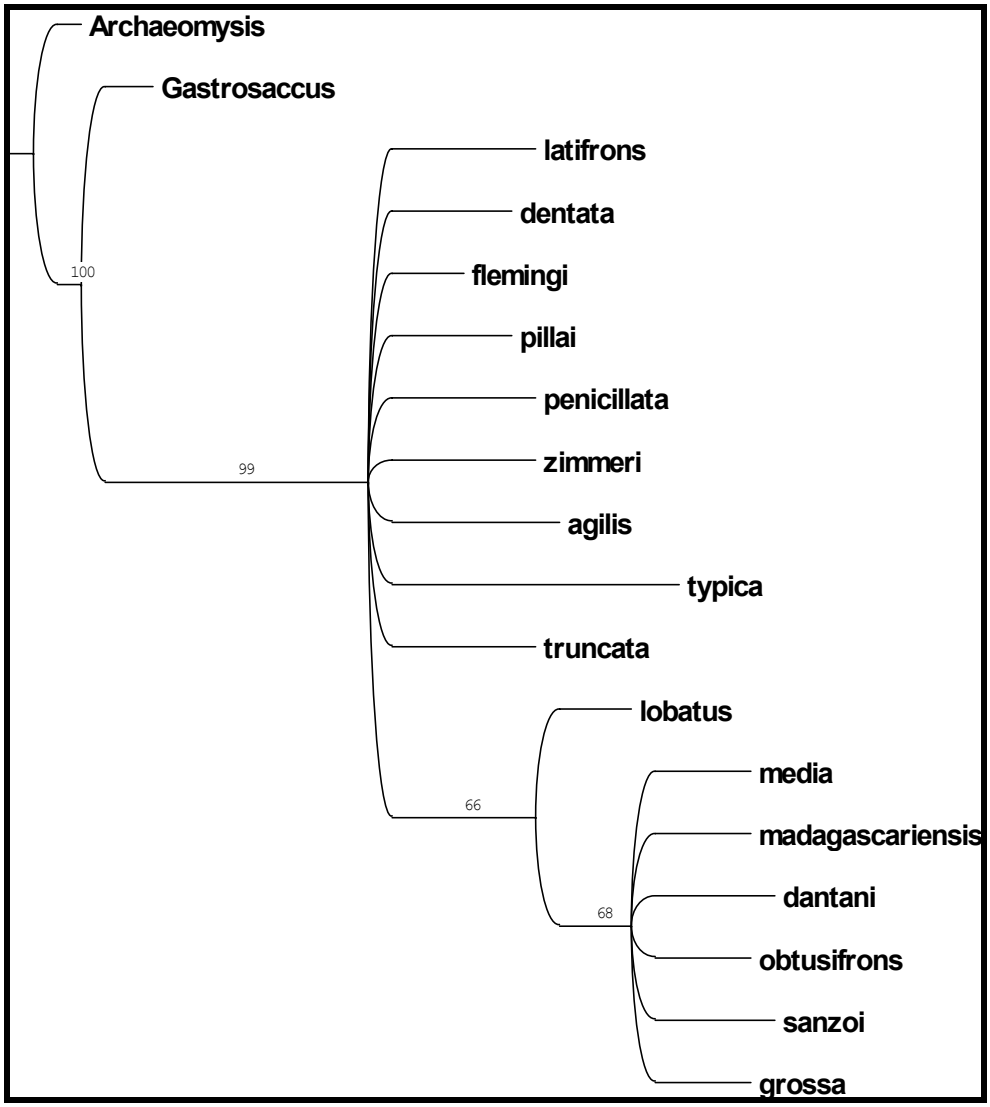


Figure 20. Bootstrap tree morphology + geography

6. Identification keys

Three identification keys are presented, two of them are classical dichotomous keys, the third is a digital polytomous version. The first is based on the main distinguishing characteristic for this genus, being the third male pleopod. A second key uses more general characteristics.

The identification keys should be used with care and it should always be kept in mind that they are mainly based on literature. The more recently described species *A. pillai* (Jo & Murano 1992), *A. lobatus* (Panampunnayil 1999) and also the species described by Nouvel (*A. madagascariensis, A. latifrons, A. dantani*) have a detailed description with an analysis of the important characters. More problematic are the species only known from older descriptions, in which in most cases not the crucial characters are studied or mentioned. (*A. zimmeri, A. penicillata,* and *A. obtusifrons*). Another problem arises with *A. flemingi* for which the description is based on one damaged male (and four females). For *A. truncata* the most current description is still the original one from Sars G.O. (1883) and the erroneous description off *A. typicus* (Sars G.O. 1885), which turned out to be *A. truncata* later on. The information for *A. truncata* is derived from personal observations, as the original description could not yet be retrieved.

The digital polytomous key uses the NeMysKey application. A matrix (similar to the one used for the phylogenetic analysis) is built having all morphological features documented. Doubtfull observations are marked by having the surrounding values also checked. The key can be consulted through the NeMys website at http://intramar.ugent.be/nemys/ident/iden.asp?t=8888&k=2.

▪ 6.1. IDENTIFICATION KEY FOR ANCHIALINA ON THE EXOPOD OF THE THIRD MALE PLEOPOD.

1. - Third pleopod of the male with an elongation of the second segment (minimum three times the first segment) or large third segment (clearly longer than two first segments together) with large lamellar expansion .....…2

   - Third pleopod of male primitive, not with these elongations or expansions, or much smaller, third segment smaller …….10

2. - Third segment with lamellar expansion not exceeding the distal end of the second segment (without spines). Second segment with thick granulated spine on distal outer comer (figure 7)……..……...*A. lobatus*

   - Lamellar expansion of third segment larger, exceeding first segment or absent, second segment with no such spine……..…3

3. - Lamellar expansion of third segment, internal spine on second segment trifurcated or one big spine with two subsidiary spines close together. …….5

   - No lamellar expansion of the third segment, second segment very large. No trifurcated internal spine (on second segment)……...……. ……..4

4. - Expansion of the second segment spirally twisted, proximal segments not with expansion (figure 16)….……*A. zimmeri*

   - Expansion of the second segment not spirally twisted. Fifth segment with oval expansion (figure 12)…….*A. penicillata*

5. - Terminal process dentated (soft denticles) (figure 15.2)…….. .*A. dantani*

   - Terminal process smooth…… 6

6. - Two spines at base of terminal expansion (1 small). Internal and external spine on second segment and external spine on third segment distally strongly

curved (figure 15.1)…..……..... *A. media*

- Only one spine at base of terminal expansion. Spines not strongly curved… 7

7. - Lamellar expansion of third segment longer or almost as long as all spines except for the terminal process. ……. .8

- Lamellar expansion much shorter than spines on first and second segment .9

8. - Spine at base of terminal process dentated and distal half very slender. Second segment large covering base of first segment and base of spines on first segment (figure 11.5)……... *A. obtusifrons*

- Spine at base of terminal process normal. Second segment normal (figure 11.6)……..…… *A. grossa*

9. - Internal spine on third segment about as long as second segment, lamellar process of third segment irregular in form (figure 15.4)..... *A. madagascariensis*

- Internal spine on third segment half as long as second segment. Lamellar process of third segment elongate, more regularly rounded (figure 15.3) …….*A.sanzoi*

10. - Distal external side with short strongly curved setae (90°). ……14

- No such setae……..11

11. - Third segment with an expansion covering the distal end of the fourth segment. This expansion consists of a gently rounded bulb and one long sharp lamellar process, unequally narrowing at the end. ……..12

- Third segment simple, no such expansion. ……13

12. - Fourth segment with an expansion covering the distal end of the second segment. This expansion smaller than the one on the third segment, but also consisting of a gently rounded bulb and with one sharp triangular process (figures 11.1 & 11.2)…….. *A. truncata*

    - Fourth segment simple, no such expansion (figures 5.7, 11.3 & 11.4) *A. agilis*

13. - Terminal segment with two setae. Modified setae on distal segments with minute hooks at tips (figure 5.4)……... *A.flemingi*

    - Terminal segment with three setae. Modified setae on distal segments with normal pointed tips (figure 5.8)…….....*A. dentata*

14. - Distal segment ending in three spinose setae (figures 5.2, 5.3 & 5.6)……... .*A. typica* and *A. oculata*

    - Distal segment ending in two spinose setae (figures 5.5 & 5.1)…….. *A. pillai* and *A. latifrons*

▪ 6.2. GENERAL IDENTIFICATION KEY FOR THE GENUS ANCHIALINA.

1. - Endopod of second male thoracic limb, with large lamellar expansion of merus (fifth segment). Pseudobranchial lamellae bilobed. ……2

   - Endopod of second male thoracic limbs, with large obtuse expansion of merus (fifth segment). Pseudobranchial lamellae single. ……..9

2. - First segment of antennular peduncle in male with large middorsal hairy lobe, extending to middle of third segment. ……..*A. lobatus*

   - No such hairy lobes on antennular peduncle, or much smaller. …….3

3. - Exopod of third male pleopod with second segment large and with large spirally twisted expansion ……..*A. zimmeri*

   - Second segment different. ... ... ……..4

4. - Long terminal process on with base two spines (one possibly small!). …….5

   - Long terminal process on base with one spine. ……6

5. - Exopod of third male pleopod with 14-15 segments ……..*A. media*

   - Exopod of third male pleopod with seven segments, dense covering with setae in the adult male on antennular peduncle and rostrum. ……..*A. dantani*

6. - Endopod of uropod smaller than telson, not reaching the tip of the telson. ...7

   - Endopod of telson as long or longer than telson. ……..8

7. - Exopod of third pleopod of male with large lamellar expansion, longer or almost as long as all spines except for the terminal processus. No hairs on distal antennular peduncle in male……. *A. grossa*

   - Exopod of third pleopod of male with lamellar expansion of third segment clearly shorter than spines on first and second segment. Distal segment of antennular peduncle in male with busch hairs. ……..*A. madagascariensis*

8. - Rostrum truncate (when lifted up, triangular). Tars of endopod of third (female) or fourth (male) to eight thoracic limbs with three segments……. *A. obtusifrons*

   - Rostrum triangular. Tars of endopod ofthird (female) or fourth (male) to eight thoracic limbs with four segments. ……...*A. sanzoi*

9. - Rostrum not triangular, trapezoidal, truncate or curved with anteromedian point. ……10

   - Rostrum triangular. ……..12

10. - Distal segment of exopod of third male pleopod with three setae. Third thoracic limb in male with six modifled setae on sixth segment. ……..*A. typica*

    - Distal segment of exopod of third male pleopod with two setae. Third thoracic limb in male with four or ten modifled setae on sixth segment……. 11

11. - Third thoracic limb in male with four modifled setae on sixth segment. ……*A. latifrons*

    - Third thoracic limb in male with 10 modifled setae on sixth segment……. *A. truncata*

12. - Exopod of third male pleopod with second segment very large, longer than segment three and four together. ……...*A. penicillata*

    - Second segment primitive, not that large smaller than third segment……. 13

13. - Exopod ofthird male pleopod with two setae on distal segment. ……..14

    - Exopod ofthird male pleopod with three setae on distal segment. ……...15

14. - Tars of endopod of third (female) or fourth (male) to eight thoracic limbs with four segments. Third thoracic limb in male with seven modified setae on sixth segment. Exopod of third male pleopod with 12 segments. ……15

    - Tars of endopod of third (female) or fourth (male) to eight thoracic limbs with three segments. Third thoracic limb in male with six modified setae on sixth segment. Exopod of third male pleopod with ten segments. ……..*A. dentata*

15. - Papilla on the eye peduncle. …….*A. agilis*

    - No papilla on the eye peduncle. …….*A. oculata*

16. - Endopod of uropod smaller than telson. Exopod of third male pleopod distal setae not strongly curved…….. *A.flemingi*

    - Endopod of uropod larger than telson. Exopod of third male pleopod with strongly curved setae (90°), consisting of a base and a backwards directed hair, on segment three-five. …….*A. pillai*

7. Discussion

A problem with identification of species of this genus *Anchialina* is that much existing keys do not use enough detail morphological features, or only use characters without appropriate distinguishing value on species level. Most former keys are based on somatic characters. These are easy observable, although may vary a lot within one species. As mentioned by Nouvel (1969) and Ii (1964), many morphological features keep changing during the development.

Unless an intensive morphological study has been done, somatic characters should only be used as additional information or secondary characters. Nouvel (1971) proved the variability of many somatic characters through an intensive study on the spines on the lateral side of the telson in both *A. sanzoi* and *A. madagascariensis*, and could prove statistically *A. sanzoi* has a higher amount of spines. No other species have been similarly studied, and thus less is known about variation of morphological characters within a species.

A problem with older descriptions is that only a limited set of characters is described. Characters giving reliable results and neccesary for future descriptions are: the antennule, and more specific the relative difference in size and the ornamentations of the peduncle in both sexes, and the presence or absence of (two) modified setae on the distal segment of the mandibular palp. Modifications of the first, second and third thoracic male endopod also give valuable distinguishing information.

All authors agree on the two morphologically clearly defined "groups" in the genus *Anchialina*: the "*typica*-group" and the “*grossa*-group”. The “*typica*-group” is formed by *A. typica, A. agilis, A. dentata, A. pillai, A. flemingi, A. truncata* and *A. latifrons*. The other species: *A. grossa, A. obtusifrons, A. penicillata, A. sanzoi, A. dantani, A. zimmeri, A. media, A. madagascariensis* and *A. lobatus* belong in most cases to the "*grossa*-group".

The "*grossa*-group" is distinguished by a typical armature on the terminal part of the exopod of the third male pleopod. It consists of a large expansion of the third segment, and a long modified process with a subsidiary spine near its base on the

first segment. The third male thoracopod has a lamelliform expansion of the merus forward.

The "*typica*-group" has the merus expanded internally with a truncated distal side. The species in the "*grossa*-group" are also characterized by bilobed pseudobranchial lamellae, the presence of modified setae on the mandibular palp in the male, and the absence of modified setae on the sixth segment of the third thoracic endopod in the male. They also have the exopod of the uropod broadly rounded in contrast with a truncated exopod (Ii 1964). The species of the "*typica*-group" have single pseudobranchiallamellae, no modified setae on the mandibular palp and modified setae on the sixth segment of the third thoracic endopod in the male.

The devision in two clear morphological groups is somewhat reflected in the presented phylogenetic analysis: all members of the “*grossa*-group” clearly differentiate from the rest (except for *A. penicellata* and *A. zimmeri*). Although the display of this group in the analysis is rather logical as it is also based on morphological features, it gives a more nuanced view on the structure of the genus.

The analysis shows there is one general form of *Anchialina* with for each species a set of typical species-own characteristics. From this general form the “grossa-group” evolved. The “*grossa*” branch is characterised by a large lamellar process on the third segment in the third male pleopod. The expansion of the merus of the second male endopod has a lamellar forward directed expansion, and the third male pleopod endopod has on the sixth segment modified setae.

Geographically there is no clear distinction between both groups, although the “grossa-group” is strictly related to the Indian Ocean area, and is in these areas bound to the more tropical regions. Whether or not this group is also evolutionary of importance is with the current knowledge unsure.

Although the genus *Anchialina* is considered as cosmopolitan, more detailed analysis shows that except for *A. typica* and *A. agilis* and *A. oculata* (often considered as synonyms of *A. agilis*) all species are restricted to areas somehow related to the Indian Ocean and South West Pacific. *A. agilis* may be considered as

the European member of the genus, *A. typica typica* as the Caribbean representant and *A. truncata* as the Agulhas Current and West Africa related species.

All records found in the literature are restricted to the continental shelve except for *A. typica*. The area with the largest number of species is clearly the East-Indies triangle, which is the hotspot of diversity for the whole Mysida fauna (see chapter 4). The observed distribution may be interpreted from an hypothetical evolutionary point of view: Originally the ancestors of the genus may have been originated in the East-Indies Area. This region was about 450 MA ago still connected with the coastal areas of the African and Indian plate. After the formation of the Indian Ocean basin most of the anchialina species stayed in the surroundings of the East-Indies coasts. A few new species originated along the nowadays African coast line. The two Madagascar species (*A. madagascariensis* and *A. latifrons*) may be relict witnesses of this hypothetic scenario. Species like *A. sanzoi* and *A. agilis*, which are restricted to an enclosed sea, may have speciated in it. The exception on this rule is *A. typica*, a species which was able to live in oceanic environments and as such could with oceanic currents spread from the East Indies, through the Agulhas Current to the atlantic and finally to the east coast of Central and South America. The Caribbean, often also recognised as an evolutionary engine may have lead to the speciation of *A. typica typica* (Heads, 2005).

Another hypothesis would be that the genus originated in the East Indies and that all species in areas not related to the East Indies have evolved through the wide spread areal of *A. typica*. Possible evidence for this can be found in the currently observed distribution of *A. typica*. It occurs globally well-spreaded. In many cases the species has also been caught in the neighborhood of other species. This would implement that all non-East-Indies species are phylogenetically closely related with *A. typica*. The morphological phylogenetic analysis does not prove any of both hypotheses yet. Molecular research on this interesting group will be the only possible way to understand the distributional patterns of the genus.

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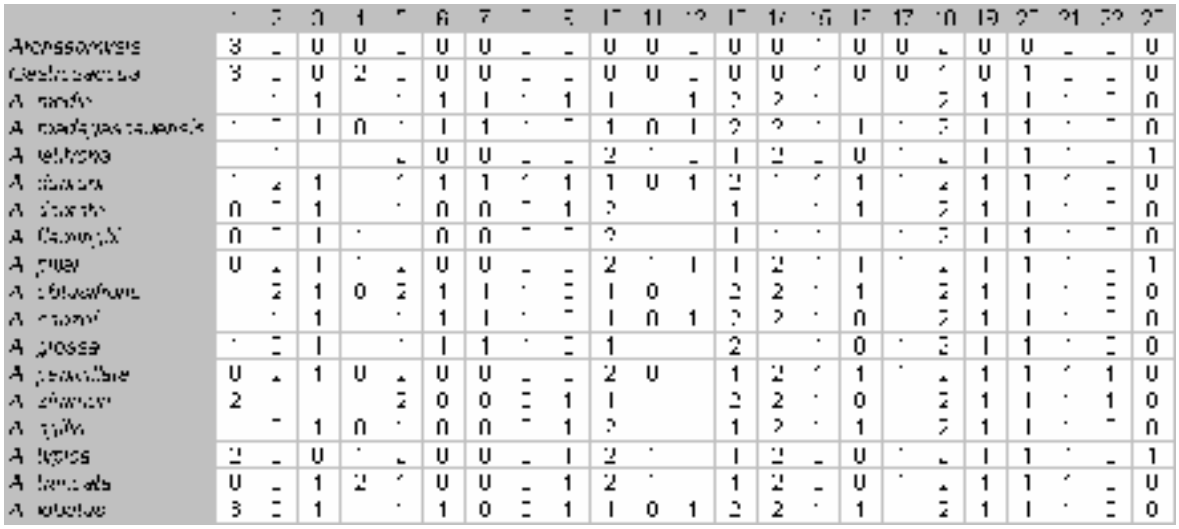
9. Appendices

9.1. Appendix 1: Morphological data matrix used for phylogenetic analysis



9.2. Appendix 2: Additional geographic data matrix used for phylogenetic analysis

	24	25	26	27	28	29	30	31	32	33	34
Aroneesomysis											
Gastrosaccus											
A. media	C	0	0	0	0	-	-	-	?	C	C
A. mediapectinata	C	1	0	0	0	?	?	?	?	C	C
A. sindus	C	1	0	0	0	?	?	?	?	C	C
A. dentex	1	11	11	11	11	?	?			1	1
A. davisae	L	U	1	U	U	?	?	?	-	L	L
A. Derwentia	L	U	U	U	U	?	?	?	-	1	L
A. gilli	C	0	0	0	0	-	-	?	1	C	C
A. obtusifrons	C	0	0	0	0	-	?	-	?	C	C
A. sandi	1	0	0	0	0	?	?	?	?	C	C
A. spinosa	C	0	1	0	0	-	-	-	?	C	C
A. spinulata	C	0	0	0	0	-	?	-	-	1	C
A. zimmeri	C	0	0	0	0	-	?	-	-	1	C
A. agilis	1	11	11	1	11	1	1			1	1
A. hystrix	1	1	1	1	11	?	?	?	1	1	1
A. brucicola	L	U	U	1	-	?	?	-	-	L	L
A. lobatus	L	U	U	U	U	?	?	-	1	L	L

CHAPTER 6 - A REVIEW OF THE GENUS *SIRIELLA*

Authors: Tim Deprez & Bea Merckx

1. Abstract

This study examines all 66 species belonging to the globally occurring genus *Siriella*. A morphology based phylogenetic analysis is presented testing the six groups of species as proposed by Ii (1964). All groups, except the 'Anomala' and 'Aequiremis' group, were found to be well defined in the phylogenetic analysis. A biogeographical study was carried out and compared with the phylogenetic results. The distribution of this genus fits well with the biogeographic model designed by Briggs (1974). Comparing the distributional patterns with the phylogenetic results leads to the conclusion that the evolution of the genus knows a long history probably driven by tectonic processes and vicariant speciation. Variations in morphology were reported for *S. pacifica*, *S. roosevelti, S. panamensis* and *S. thomposoni*. Additions to the original description of *S. paulsoni* were made. The variability of *S. jaltensis* is discussed.

2. Introduction

The genus *Siriella* is with 66 described species the most speciose genus of the order Mysida. It has also the largest distribution. A general revision of this group does not exist. Identification of specimens of the genus is considered as very hard. A proof of this may be that many specimens of the genus *Siriella* in natural history collections are not identified.

The genus *Siriella* is distinguished from other Mysida by a number of clear morphological features: females have three oostegites on the marsupium, the exopod of the uropod is divided in two segments, of which the proximal one mostly bears spines and no setae. The endopod of the third thoracopod is similar to other thoracopods. Pleopods of the female are reduced. The outer margin of the antennal scale is mostly naked, and distally a tooth is present. Male pleopods have mostly well developed pseudobranchiae, and endopods and/or exopods may bear modified setae (Ii, 1964; Mauchline, 1980; Hansen, 1910).

Members of the genus occur globally mainly in marine coastal waters, although *S. clausi* is reported from brackish waters and *S. gracilipes* is found in caves (Fossi *et*

al., 2001). Most species are reported from shallow waters. However, oceanic species as *S. thompsoni* are reported from depths up to 3000 m (Zimmer, 1914). Many species show a daily vertical migration. During the night they are found in the upper water layers, during the day they move to deeper (darker) water layers (Champalbert & Macquart-Moulin, 1970; Mauchline, 1980; Macquart-Moulin, 1972). Allmost all species form close aggregations with exception of *S. jaltensis.* It is mostly reported with one or few specimens in one sample (Mauchline, 1971). Most known predators are fish. Analysis of stomach content of economically important species as *Clupea harengus harengus*, *Gadus morhua*, *Raja clavata* and *Lepidorhombus boscii* showed that members of this genus are part of their diet (Tattersall & Tattersall, 1951; Mauchline, 1980)

Pillai (1961) recognised that species of the genus keep growing after reaching maturity. This implies modifications of morphological characters throughout the whole life-cycle. This and also the relative morphological uniformity of the genus make identification currently a hard task. Most existing keys are limited to small regions and as such do only treat a small number of species (Hansen, 1910; Ii, 1964; Pillai, 1965; Tattersall, 1927). Females are very similar for all species and hence can hardly be identified.

Hansen (1910) divided the genus in four groups, which were further defined by Ii (1964) (six groups). This division was a first global attempt to put some structure in this extremely species rich genus. The classification is based on clear morphological mostly male characters. The classification according to Hansen (1910) and Ii (1964) is presented in table 1. Since the work of Ii, eleven new species were described (Panampunnayil, 1981; Panampunnayil, 1995; Udrescu, 1981; Ariani & Spangnuolo, 1975; Murano, 1986; Fukuoka & Murano, 1996; Da Silva, 1974). These new *Siriella* species were however never matched with the classifications of Hansen and Ii.

The difficulties in this genus offer enough arguments to create a review of the current knowledge, in combination with new observations. The consistency of the morphological species will be checked through a morphology based phylogenetic analysis. This analysis facilitates the understanding of phylogenetic relations between species. The results presented are based on a profound analysis of all available literature on the genus, and morphological studies on collection material

provided by several museums. This study aims to review the classification presented by Hansen (1910) and Ii (1964) and may lead to a comprehensive overview of the genus. A digital identification key is presented and biogeographical analysis is done for all members of the genus. Some systematic problematic issues will be highlighted and possible changes will be proposed.

Thompsoni-group	Armata-subgroup	*S. aramata, S. clause, S. dayi, S. frontalis, S. jaltensis, S. jaltensis brooki, S. norvegica*
	Thompsoni-subgroup	*S. affinis, S. lingvura, S. trispina, S. australis, S. longidactyla, S. vincenti, S. brevicaudata, S. longipes, S. vulgaris, S. gracilis, S. nodosa, S. vulgaris rostrata, S. halei, S. okadai, S. wadai, S. hanseni, S. pondoensis, S. watasei, S. japonica, S. quadrispinosa, S. watasei koreana, S. japonica izuensis, S. sinensis, S. watasei macropsis, S. japonica sagamiensis, S. singularis, S. denticulate*
Inornata-group	*S. inornata, S. media, S. plumicauda, S. serrata*	
Dubia-group	*S. dubia*	
Pacifica-group	*S. chierchiae, S. pacifica, S. panamensis, S. roosevelti*	
Aequiremis-group	*S. aequiremis, S. conformalis, S. distinguenda*	
Anomala-group	*S. anomala*	

Table 1. original grouping of the species of *Siriella* accoring to Ii (1964)

3. Materials en methods

A study of the state of art of the genus has been conducted through the 'Mysida dataset' running on the online biological information system NeMys (http://www.nemys.ugent.be). All literature was linked to the system and relevant data (morphometry, morphology and geography) was extracted for all 66 species. Where possible data of multiple data-sources was used and compared.

Specimens of 28 species were studied (table 2). It was not possible to obtain material for all 66 described species.

Morphological data used for the phylogenetic analysis originates from both literature data and observations on specimens. Where possible, data on morphological intraspecific variation was included. Part of the data-matrix used for the cladistic analysis was also used to develop a polytomous identification key. This key running on the NeMysKey© platform illustrates that data gathered for phylogenetic analysis can be reused for other implementations, like identification keys.

Species	Collection-number	Institution
Siriella aequiremis	82685	SMIT
Siriella affinis	82614	SMIT
Siriella anomala	82393	SMIT
Siriella armata	211160	SMIT
Siriella chierchiae	11481	SMIT
Siriella distinguenda	82493	SMIT
Siriella frontalis	128552	SMIT
Siriella gracilis	45423	SMIT
Siriella inornata	82579	SMIT
Siriella jaltensis gracilipes	211162	SMIT
Siriella media	82752	SMIT
Siriella mexicana	137793	SMIT
Siriella norvegica	99237	SMIT
Siriella pacifica	101829	SMIT
Siriella roosevelti	79279	SMIT
Siriella thompsoni	82600	SMIT
Siriella vulgaris	82793	SMIT
Siriella vulgaris rostrata	82497	SMIT
Siriella conformalis	ZMUC Crustacea 5905	COP
Siriella nodosa	ZMUC Crustacea 5903	COP
Siriella plumicauda	ZMUC Crustacea 5892	COP
Siriella quadrispinosa	ZMUC Crustacea 5908	COP
Siriella serrata	ZMUC Crustacea 5902	COP
Siriella wolffi	ZMUC Crustacea 5893	COP
Siriella halei	J5389	VICT
Siriella vincenti	J43693	VICT
Siriella clausi		HAM
Siriella media		HAM
Siriella vulgaris		HAM
Siriella thompsoni		HAM

Table 2 Overview of analyzed specimens (SMIT: Smithsonian Institution, USA; COP: Zoological Museum of the University of Copenhagen, Denmark; VICT: National museum of Victoria, Australia; HAM: University of Hamburg, specimens obtained by A. Brandt.

- *3.1. PHYLOGENETIC ANALYSIS*

All phylogenetic analyses where conducted based upon 74 morphological characters (listed below).

Originally, many more characters (172) were defined. However, during the setup of the data matrix, many characters had to be dropped out, because of: (1) too high intraspecific variation; (2) not all data was available for all species; (3) too high interspecific variability (i.e. each species has a different character state).

Measured characters were divided in classes with the package Morphocode©, using the 'Gap-Weighting' technique (Schols *et al*., 2004).

The cladistic analysis was based on the parsimony criterion and carried out with NONA (Goloboff, 1998), which is similar to Hennig86 (Farris, 1975) but runs under WINCLADA (Nixon, 1999) facilitating screening and layout of trees.

Anchialina typica was used as outgroup for the analysis. Remerie *et al*. (2004) found that this species clusters relatively close to members of the genus Siriella. Sixty out of the 74 characters were relevant and thus could be defined for the species.

All analyses were done through the WINCLADA-interface using the 'Heuristic search' option. A maximum of 1000 trees were kept for each search using 100 replications. Only the strict consensus tree was held. Characters were treated as unordered and unweighted. A bootstrap analysis (100 replications) was done to check the reliability of the found branches in the resulting tree.

- *3.2. CHARACTERS USED IN THE ANALYSIS*

The characters used in this analysis are listed below. All of them are considered as independent. Characters are taken from all regions of the body: head-region (22 characters), thoracal region (13 characters) and abdominal region (33 characters). The abdominal region is considered as morphologically very important, as for most species, the clearest distinguishing characters are located in it (pleopods, uropods, telson).

[0] **Form of pseudobranchia on male pleopod 2:** (0) small and bilobed, not clearly developed; (1) straight; (2) G-shaped; (3) spirally coiled.

[1] **Form of pseudobranchia on male pleopod 3:** (0) small and bilobed, not clearly developed; (1) straight; (2) G-shaped; (3) spirally coiled

[2] **Form of pseudobranchia on male pleopod 4:** (0) small and bilobed, not clearly developed; (1) straight; (2) G-shaped; (3) spirally coiled

[3] **Modified terminal setae on endopod of male pleopod 3:** (0) No modified setae present; (1)2 setae on ultimate joint (1 strongly bent and 1 straight modified seta) + (penultimate joint sometimes with 1 modified seta); (2) 2 terminal setae longer and more produced than the other setae, only slightly modified; (3) 2 or 3 straight modified setae, about equal in length and about the same length as the ultimate joint + rudimentary setae on penultimate joint; (4) 2 straight setae (1 large blunt, 1 smaller more acute one); (5) 2 straight setae (1 short blunt (same length as ultimate joint), 1 longer more acute one); (6) 1 straight seta on ultimate joint (+ 1 on penultimate joint); (7) 2 straight setae (both blunt, 1 longer than the other); (8) 2 straight modified setae (about equal in length: one stout & one more slender and plumose at the distal end)

[4] **Form of terminal setae on endopod of male pleopod 4:** (0) No modified setae present; (1) 2 on ultimate joint (1 long and 1 short (1/4-2/3)) + 1 very long straight seta on penultimate joint; (2) 2 on ultimate joint (1 long + 1 shorter (3/4)) + 2 straight seta on penultimate joint (both longer than setae on ultimate joint); (3) 2 on ultimate joint (± equal in length); (4) 1 very long seta on the ultimate joint (+ sometimes the 3 preceding joints with a long and strong blunt spine); (5) 2 on ultimate joint (± equal in length) + 2 on penultimate jnt (1 very long & 1 very short) + 1 very long on antepenultimate joint (+ sometimes 1 short); (6) 2 more or less straight setae on ultimate joint (1 short (1/4-2/3) and 1 long); (7) 2 on ultimate joint (1 long and 1 short (<1/2)); (8) 2 straight setae on ultimate joint (± equal in length) + 1 very long on penultimate joint (+sometimes a very small one); (9)2 on ultimate joint (1 long + 1 shorter (> 3/4) + 2 on penultimate joint (1 long + 1 short) + (sometimes 1 short naked seta on penultimate joint)

[5] **Growth of spines on the proximal joint of exopod of uropod:** (0) extending proximally considerably beyond the middle of the outer margin; (1) confined distally between 1/2 and 1/3 of the outer margin of the proximal joint; (2)confined distally between 1/3 and 1/6 of the outer margin of the proximal joint; (3) confined distally to about or less than 1/6 of the outer margin of the proximal joint.

[6] **Relative length of exopod and endopod of uropod:** (0) exopod shorter than endopod; (1) exopod about as long as endopod; (2) exopod distinctly longer than endopod

[7] **Size of the eyes:** (0) small (width of the cornea less than 1/2 of the width of the carapax)(dorsal view); (1) moderate size (width of the cornea between 1/2 and 2/3 of the width of the carapax)(dorsal view); (2) large (width of the cornea about or more than 2/3 of the width of the carapax)(dorsal view)

[8] **Length relative to width of the total antennal scale of the male:** (0) short, less than 3,2 times as long as broad; (1) between 3,2 and 3,8 as long as broad; (2) between 3,8 and 4,5 times as long as broad; (3) long and slender, more than 4,5 times as long as broad or more.

[9] **Eye- Stalk length (only broadend part, measured at max width and length)**: (0)very short, at most half as long as broad; (1) short, between 0,5 and 0,8 time as long as broad; (2) almost square; (3) elongated, between 1,2 and 2 times s long as broad

[10] **Relative size of the telson:** (0) short, clearly less than 2 times as long as broad; (1) medium length, between 2 and 2,6 times as long as broad at base; (2) slender, between 2,6 and 3,2 times as long as broad; (3) very slender, more than 3,2 times as long as broad.

[11] **Shape of the spines on the telson:** (0) barbed, with secondary spinules; (1) normal and smooth, without secondary spinules

[12] **Number of dorsal proteburances on the carapax of the female:** (0) female without proteburances; (1) female with 1 proteburance anterior to the cervical groove; (2) female with 2 proteburances, one pre-cervical and one post-cervical, immature females with one postcervical proteburance.

[13] **Length relative to width of terminal lobe of antennal scale of male:** (0) H/W less or about ¾; (1) H/W between 3/4 and 2; (2) elongated (L/W more than 2).

[14] **Relative length of the 2 pairs of spines lateral to the (normally) three apical spines on the telson:** (0) Outer pair longer than inner pair; (1) Outer pair as long as inner pair; (2) Outer pair bigger than 2/3 of the inner pair, but still clearly smaller; (3) Outer pair between 1/3 and 2/3 as long as inner pair; (4) Outer pair much smaller than inner pair (less or about 1/3).

[15] **Form of apex of rostrum:** (0) acutely pointed or pointed; (1) bluntly pointed; (2) acutely or narrowly rounded; (3) bluntly rounded; (4) bluntly rounded with a spiniform pseudorostral process beneath it; (5) pointed, but bended downwards.

[16] **Length of dactylus and claw compared to carpopropodus of thoracopod 2:** (0) short (less than 1/3 of the carpopropodus); (1) moderate (Between half of the length and 1/3 of the carpopropodus); (2) long (More than half of the length of the carpopropodus).

[17] **Form of rostral plate:** (0) very low triangular (hight smaller than 1/3 of the base); (1) low triangular (higth of the triangle between 1/3 and 1/2 of the base); (2) medium triangular (hight of the triangle more than 1/2 of the base); (3) long triangular (higth of the triangle bigger than the base).

[18] **Form of apical spines on telson:** (0) 2 small spines; (1)3 small spines, about equal in length; (2) 3 small spines, inner spine longer than lateral ones (till about 2 times longer); (3) 3 spines forming a tridentate plate, about equal in length, but longer than the spines on the lateral side of the telson; (4) 4 or 5 small spines; (5) without small spines, but with 2 to 4 setae

[19] **Number of spines on the proximal joint of exopod of uropod:** (0) less than 6; (1) 6 to 8; (2) 9 to 12; (3) 13 to 17; (4) more than 17.

[20] **Form of antennular inner flagellum of the male:** (0) normal and slender; (1) male: swollen and/or contorted (and possibly densely hirsute) near the base

[21] **Relative form of lateral spines on telson or groups of spines:** (0) alternate arrangement of larger and smaller spines (also the last spines!); (1) grow longer posteriorly or more or less the same length (no clear grouping)

[22] **Do the apical plumose setae on the telson have conspiciously long hairs?** (0) no, with usually fine secondary hairs; (1) yes, with conspiciously strong secondary hairs

[23] **Form of terminal setae on exopod of male pleopod 4:** (0) No modified setae present; (1) 2 setae on ultimate joint (1 long curved and 1 small (about 1/3 of the

other)); (2) 1 extremely long (normal setae not reaching 1/2 of it) (+ 1 normal seta)+ 1 straight on penultimate joint; (3) 2 straight on ultimate joint (1 long and 1 short (< 1/2)), normal setae not reaching 1/2 of the modified seta + 1 straight on penultimate joint; (4) 2 straight on ultimate joint (1 long & 1 short (± 1/5) seta), normal setae reaching beyond 3/5 of the modified seta + 3 modified on penultimate joint; (5) 2 curved setae on ultimate joint + 3 modified setae on penultimate joint (one curved, two straight ones on inner corner); (6) 2 straight setae on ultimate joint (1 long and 1 short (<= 1/3)), normal setae reaching ± 1/2 of the modified seta or further+ 1 straight on penultimate joint; (7) 2 modified setae on the ultimate joint (1 straight and one curved, more or less equal in length) + 1 on penultimate joint (+ 2 normal setae); (8) 2 setae on ultimate joint (1 short and 1 extremely bent) + 1 straight seta on the penultimate joint; (9) 1 long on the ultimate joint (normal setae reaching 2/3 or further)(+ 1 scarcely or not modified seta) + 1 on penultimate joint.

[24] **Outgrows on outer margin of proximal joint on exopod of uropod:** (0) both spines and plumose setae; (1) spines only.

[25] **Length/width of distal segment of exopod of uropod for a female:** (0) female: very short, less than 1,5 as long as broad; (1) female: short, between 1,5 and less than 2 times as long as broad; (2) female: between 2 and less than 2,5 as long as broad; (3) female: long, 2,5 or more as long as broad.

[26] **How many spines are there on the outer margin of the antennal scale?** (0) 1 (terminal denticle included); (1) 4-5; (2) 13-15

[27] **Length of unarmed margin compared to the width (measured at maximum width):** (0) More than 1/2 of the width; (1) Smaller than 1/2 of the width.

[28] **Form of the rostral margins of the rostral plate of the female:** (0) with concave margins and somewhat acuminated at the apex; (1) straight margins and not acuminated at the apex or convex margins.

[29] **Distal joint visible at the distal end of the antennal scale?** (0) Yes; (1) No.

[30] **Where is the tip of the terminal spine of the antennal scale situated?** (0) The tip is situated almost half-way the antennal scale (only applicable for male

specimens); (1) The tip clearly doesn't reach the distal joint ; (2) The tip reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible); (3) The tip reaches beyond the apex of the antennal scale.

[31] **Length of the 2nd segment of the peduncle of the antenna/length of the 3th:** (0) about or more than three times as long as the 3rd; (1) between 2 and 3 times longer than the 3rd; (2) less than twice as long as the 3rd.

[32] **Length of the antennal scale compared to the antennular peduncle for the male:** (0) Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle; (1) Antennal scale reaches beyond the antennular peduncle.

[33] **Length of the antennal scale in comparison with the antennal peduncle:** (0) peduncle more than 2/3 of the antennal scale; (1) peduncle (2nd and 3rd segment) less or about 2/3 of the antennal scale.

[34] **Number of plumose setae on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female:** (0) 0; (1) 1; (2) 2; (3) 3; (4) 4; (5) 5 or more.

[35] **Color of the eyes:** (0) black; (1) brown; (2) purple; (3) red.

[36] **Modified terminal setae on exopod of male pleopod 3:** (0) No modified setae present; (1) 2 straight setae (about equal in length: one stouter & one more slender and plumose at the distal end); (2) 1 thick long spiniform seta and 1 normal seta on the ultimate joint (+ sometimes an aditional smaller one on penultimate joint); (3) 1 thick blunt seta and 1 short plumose seta (clearly shorter than normal setae) + sometimes a smaller one on the penultimate joint; (4) 2 setae (1 strongly bent and 1 straight modified seta), penultimate joint with 1 modified setae (+ sometimes a smaller one)

[37] **Carapax-form of the lateral margins at the anterior end of the carapax:** (0) Lateral margins grow anteriorly; (1) Lateral margins show no tendency to grow anteriorly; (2) Pointed shoulders are clearly visible.

[38] **Length of dactylus and claw compared to the carpopropodus of thoracopod 8:** (0) long (More than half of the length of the carpopropodus); (1) moderate (between half of the length and 1/3 of the carpopropodus); (2) short (less than 1/3 of the carpopropodus)

[39] **Is thoracopode 2 subchelate?** (0) No; (1) Yes.

[40] **Relative length of the carpus and he propodus of the 8th thoracopod:** (0) Carpus less or about 1/3 of the propodus; (1) Carpus between 1/3 and half of the length of the propodus; (2) Carpus shorter than propodus, but more than half of the propodus; (3) Carpus about the same length or longer than the propodus; (4) Carpopropodus undivided.

[41] **Relative size of the carpopropodus of the endopod of 8th thoracopod:** (0) Robust (carpopropodus smaller than 6 times as long as broad); (1) Normal (carpopropodus between 6 and 8 times as long as broad); (2) Slender (carpopropodus between 8 and 12 times as long as broad); (3) Extremely slender (carpopropodus more than 12 times as long as broad)

[42] Denticle on **base of outer margin of thoracopod 8 exopod?** (0) No; (1) Yes.

[43] **Relative size of the dactylus:** (0)Longer than broad; (1) Broader than long or nearly square.

[44] **Is the 5th thoracopod elongated?** (0) No; (1) Yes.

[45] **Form of the male copulatory organ:** (0) Not pointed; (1) Pointed.

[46] **General form of the telson:** (0) Linguiform; (1) Triangular; (2) Trapezium.

[47] **Does the telson reach the margin of the distal joint of the exopod?** (0) Yes, the telson overreaches the margin of the distal joint of the exopod; (1) No, the telson doesn't reach the margin of the distal joint of the exopod

[48] **Length-width ratio of distal segment of exopod of uropod a male:** (0) very short, less than 1,5 as long as broad; (1) short, between 1,5 and less than 2 times

as long as broad; (2) between 2 and less than 2,5 as long as broad; (3) long, 2,5 or more as long as broad

[49] **Dispersal of lateral spines on endopod of uropod:** (0) Distal spines not in groups, no smaller spines in between them; (1) Spines in groups, also between the last distal spines; (2) No spines in groups, spines grow longer distally

[50] **Black or brown spots visible laterally on the abdomen?** (0) No; (1) Yes

[51] **Is the distal one third of the 6th segment of the endopod of thoracopod 2 excavated?** (0) No; (1) Yes

[52] **Relative length of the three segments of the antennular peduncle of the male:** (0) Segment 1 and 2 equal more or less segment 3; (1) Segment 1 equals more or less segment 3; (2) Segment 2 and 3 equal more or less segment 1; (3) Segment 1 is longer than segment 2 and 3 together

[53] **Rostrum covering any part of the eye (including eyestalk)?** (0) Yes; (1) No

[54] **Terminal lobe of the antennular peduncle hirsute?** (0) Yes; (1) No

[55] **Form of setae on the male copulatory organ:** (0) All setae the same form: all long or all short; (1) Some short curved setae and 1 to 4 long straight setae; (2) Some short curved setae and 5 or more long straight setae; (3) The usual setae and strong spirally coiled setae

[56] **Is the eye clearly broader than the eyestalk?** (0) No, eye about as broad as eyestalk; (1) Yes, eye clearly broader than eyestalk

[57] **Are there any lateral spines growing next to the statoyst?** (0) Yes, there are spines next to statocyst; (1) No, spines start growing more distally than statocyst

[58] **Are the spines on the inner uropod barbed?** (0) Yes, the spines have secondary spinules; (1) No, the spines don't have secondary spinules

[59] **Length relative to width of the total antennal scale of the female:** (0) short, less than 3,2 times as long as broad; (1) between 3,2 and 3,8 as long as broad; (2)

between 3,8 and 4,5 times as long as broad; (3) long and slender, more than 4,5 times as long as broad or more

[60] **Length relative to width of terminal lobe of antennal scale of female:** (0) H/W less or about ¾; (1) H/W between 3/4 and 2; (2) elongated (L/W more than 2)

[61] **Length of the 6th abdominal segment compared to the 5th:** (0) 6th segment less than 1,75 times the 5th segment; (1) 6th segment more than 1,75 times the 5th segment

[62] **Number of somites not covered by carapax dorsally:** (0) Less than 2 somites are visible dorsally; (1) Between 2 and 3 somites are visible dordally; (2) 3 or more somites are visible dorsally

[63] **Number of somites not covered by carapax laterally:** (0) Less than 1 somite is visible laterally; (1) Between 1 and 2 somites are visible laterally; (2) 2 or more somites are visible laterally

[64] **Length of adult female (tip rostrum till end of telson) - size can be very variable:** (0) smaller than 7 mm; (1) between 7 and 12 mm; (2) between 12 and 17 mm; (3) more than 17 mm

[65] **Length of male (tip rostrum till end of telson) -size can be very variable:** (0) smaller than 7 mm; (1) between 7 and 12 mm; (2) between 12 and 17 mm; (3) more than 17 mm

[66] **Are there any plumose setae on the sympode of the first pleopode?** (0) No, there are no plumose setae; (1) Yes, there are plumose setae present.

[67] **Number of basal spines on the telson:** (0) 0; (1) 1; (2) 2; (3) 3; (4) 4; (5) 5; (6) 6 or more

[68] **Number of lateral spines at one side (including basal spines and spines next to the 3 apical spines):** (0) < 20; (1) 20 – 39; (2) 40 – 60; (3) > 60

[69] **How many lateral spines on the endopod of the uropod?** (0) < 20; (1) 20 – 39; (2) 40 – 60; (3) > 60

[70] **Length of the proximal joint of the exopod of the uropod/length of the distal joint of the male:** (0) Proximal joint less than 2,2 times longer than distal joint; (1) Proximal joint between 2,2 and 2,8 times longer than distal joint; (2) Proximal joint between 2,8 and 3,5 times longer than distal joint; (3) Proximal joint more than 3,5 times longer than distal joint

[71] **Are there any modified setae present on the exopod or endopod of the 4th pleopod?** (0) No; (1) Yes

[72] **Are there any modified setae present on the exopod or endopod of the 3th pleopod?** (0) No; (1) Yes

[73] **Are there any modified setae present on the exopod or endopod of the 2nd pleopod?** (0) No; (1) Yes

- *3.3. SYSTEMATIC ACCOUNT*

All morphological characters were entered in the NeMys-Mysida database. Based on the entered data, diagnostic features for each species were listed up, and transformed to a text based description. All specimens examined were checked with the original description and for some species (*S. jaltensis, S. paulsoni, S. roosevelti, S. panamensis,* and *S. thompsoni*) additions to the original description are reported. Variations were photographed. For *S. paulsoni* additional drawings, completing the rather poor original description by Kossmann (1877), were made.

- *3.4. BIOGEOGRAPHIC ANALYSIS*

Biogeographical records for all species were derived from the literature and entered in the NeMys-Mysida dataset. Exact coordinates were assigned to each reported location. Extra records were retrieved from the OBIS-portal (http://www.iobis.org). Although many records are available on the OBIS-portal site, only few could be used. Exact coordinates are lacking for most records, many even don't include text-based location data.

- *3.5. CHECKLIST OF SPECIES AND SYNONYMIES*

Siriella aequiremis Hansen, 1910

Siriella afinis Hansen, 1910

Siriella africana Panampunnayil, 1981

Siriella anomala Hansen, 1910

Siriella armata Milne-Edwards, 1837

Synonyms: *Cynthia armata; Rhinomysis armata; Cynthia flemingii; Mysis rostrata; Mysis griffithsiae; Rhinomysis griffithsae; Rhinomysis rostrata; Mysis productus; Rhinomysis producta; Siriella flemingii; Mysis frontalis; Pseudosiriella frontalis; Rhinomysis frontalis; Rhinomysis sarsi; Siriella frontalis; Siriella intermedia; Themisto longispinosa.*

Siriella australiensis Panampunnayil, 1995

Siriella australis Tattersall, 1927

Siriella bacescui Udrescu, 1981

Siriella brevicaudata Paulson, 1875

Synonym: *Siriella gibbosa*

Siriella brevirostris Nouvel, 1944

Siriella castellabatensis Ariani & Spagnuolo, 1975

Siriella chessi Murano, 1986

Siriella chierchiae Coifmann, 1937

Synonym: *Siriella occidentalis*

Siriella clausi Sars, 1877

Synonyms: *Siriella messinensis; Siriellides clausi; Cynthilia clausii.*

Siriella conformalis Hansen, 1910

Siriella dayi Tattersall, 1952

Siriella denticulata Thompson, 1880

Siriella distinguenda Hansen, 1910

Siriella dollfusi Nouvel, 1941

Siriella dubia Hansen, 1910

Siriella gracilipes Nouvel, 1942

Synonym: *Siriella adriatica*

Siriella gracilis Dana, 1852

Siriella halei Tattersall, 1927

Siriella hanseni Tattersall, 1922

Siriella inornata Hansen, 1910

Siriella intermedia Panampunnayil 1981

Siriella jaltensis Czerniavsky, 1868

Synonyms: *Protosiriella jaltensis; Cynthia brooki; Siriella brooki; Cynthia crassipes; Cynthia jaltensis; Siriella aculeata; Siriella gordonae; Siriellides crassipes; Protosiriella jaltensis*

Siriella japonica Ii, 1964

Siriella japonica izuensis Ii, 1964

Siriella japonica sagamiensis Ii, 1964

Siriella jonesi Pillai, 1964

Siriella lingvura Ii, 1964

Siriella longidactyla Tattersall, 1940

Siriella longipes Nakazawa, 1910

Siriella macrophthalma Murano, 1986

Siriella media Hansen, 1910

Siriella melloi da Silva, 1974

Siriella mexicana Brattegard, 1970

Siriella nodosa Hansen, 1910

Siriella norvegica Sars, 1869

Siriella okadai Ii, 1964

Siriella pacifica Holmes, 1900

Siriella panamensis Tattersall, 1951

Siriella paulsoni Kossmann, 1877

Siriella plumicauda Hansen, 1910

Siriella pondoensis Tattersall, 1962

Siriella quadrispinosa Hansen, 1910

Siriella quilonensis Pillai, 1961

Siriella robusta Pillai, 1964

Siriella roosevelti Tattersall, 1941

Siriella serrata Hansen, 1910

Siriella sinensis Ii, 1964

Siriella singularis Nouvel, 1957

Siriella spinula Panampunnayil, 1995

Siriella tadjourensis Nouvel, 1944

Siriella thompsoni Milne-Edwards, 1837

Synonyms: *Siriella brevipes, Heterosiriella galatheae; Siriella inermis; Siriella indica; Cynthia thompsonii.*

Siriella trispina Ii, 1964

Siriella tuberculum Fukuoka & Murano, 1996

Siriella vincenti Tattersall, 1927

Siriella vulgaris Hansen, 1910

Synonym: *Siriella suluensis*

Siriella vulgaris rostrata Tattersall, 1951

Siriella wadai Ii, 1964

Siriella watasei koreana Ii, 1964

Siriella watasei macropsis Ii, 1964

Siriella watasei Nakazawa, 1910

Siriella wolffi Tattersall, 1961

4. Systematic account

4.1. Siriella aequiremis Hansen, 1910

Diagnosis : Female (adult) between 7 and 12 mm, male between 7 and 12 mm. Carapax of female without protuberances. Between 2 and 3 thoracal somites are visible dorsally. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin with one terminal denticle. Female scale between 3,2 and 3,8 as long as broad. Terminal lobe about 3/4 as long as broad ane hirsute. The tip of the terminal spine reaches the distal joint but does not reach beyond the apex. Male antennular flagellum normal. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eye broader than eyestalk. Rostrum with concave margins. Second thoracopod subchelate. Thoracopod five equal in length to others. Total length of dactylus and claw of thoracopod 8 moderate (between half of the length and 1/3 of the carpopropodus). Dactylus longer than broad, carpopropodus slender (carpopropodus between 8 and 12 times as long as broad), carpus shorter than propodus, but more than half of the propodus. Copulatory organ bluntly shaped with short curved setae and 1 to 4 long straight setae. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod straight. Third male pleopod with straight pseudobranchia, no modified setae on either endopod nor exopod. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint + 2 straight setae on penultimate joint (both longer than setae on ultimate joint). No modified setae on exopod. All spines on uropod endopod ordered in groups. Exopod about as long as the endopod. Proximal joint with only spines (no setae) and shorter than 2,2 times the length of the distal segment. Apical plumose setae on telson look normal. Three apical spines, equal in length. First two pairs of subapical spines are about 1/3 to 2/3 as long as the apical spines. Lateral spines are alternately arranged in length. No secondary spinules. Unarmed part of telson margin is less than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Coiffmann (1937), Hansen (1910), Ii (1964), Pillai (1965), Pillai (1973), Tattersall (1943)

4.2. Siriella affinis Hansen, 1910

Diagnosis : Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Less than 1 somite visible laterally. Lateral margins of carapace grow anteriorly. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin with one terminal denticle. Distal joint visible. Second segment of antennular peduncle between 2 and 3 times longer than the third. Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes not covered by the rostrum. Rostrum is acutely pointed with concave margins. Second thoracopod normal. Distal one third of the 6th segment of the endopod not excavated. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate. Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod slender (carpopropodus between 8 and 12 times as long as broad) Carpus of eight thoracopod shorter than propodus, but more than half of the propodus. Base of outer margin of exopod of thoracopod eight normal. Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Uropod exopod proximal joint with only spines. Distal segment of female uropod exopod short (between 1,5 and less than 2 times as long as broad). Three apical and two basal spines, equal in length on the linguiform telson. No secondary spinules. Telson overreaches the margin of the distal joint of the exopod.

Used literature: Hansen (1910), Pillai (1965), Shyamasundari (1973), Tattersall (1922)

4.3. Siriella africana Panampunnayil, 1981

Diagnosis : Male between 7 and 12 mm. Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Lateral margins of carapace show no tendency to grow anteriorly. Less than 1 somite is visible laterally. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin with more than twelve spines. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the scale. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. Male antennular flagellum normal. Segment 2 and 3 of the antennular peduncle of the male more or less same size as segment 1. Eyes are small. Eye about as broad as eyestalk. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum has a long triangular shape (higth of the triangle bigger than the base). Rostrum with concave margins. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Carpopropodus robust (carpopropodus smaller than 6 times as long as broad). Carpus between 1/3 and half of the length of the propodus. Modified setae on third pleopod. Modified setae on fourth pleopod. Lateral spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 13 and 17 spines. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Telson linguiform, with normal apical plumose setae and three apical spines, equal in length. Four basal spines on the telson. Telson slender, between 2,6 and 3,2 times as long as broad. Unarmed part of telson margin is less than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Panampunnayil (1981)

Diagnosis : Female between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Less than 1 somite is visible laterally. Antennal scale reaches beyond the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the antennal scale. Terminal lobe of male antennal scale is longer than two times the width. Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyestalks very short. Eye clearly broader than eyestalk. Rostrum is acutely pointed. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Rostrum with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Copulatory organ blunt. Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are clearly straight. Endopod of the third male pleopod with 2 or 3 straight modified setae, about equal in length and about the same length as the ultimate joint. Rudimentary setae on penultimate joint. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (1 long + 1 shorter (> 3/4) + 2 on penultimate joint (1 long + 1 short) + (sometimes 1 short naked seta on penultimate joint). No modified setae on exopod of male fourth pleopod. Modified setae on fourth pleopod. Lateral spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Telson with linguiform shape with three basal spines and others alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson

width. The telson overreaches the margin of the distal joint of the exopod No black spots on lateral side of the abdomen.

Used literature: Fukuoka & Murano (1997), Hansen (1910), Ii (1964)

4.5. Siriella armata (Milne-Edwards, 1837)

Diagnosis : Carapax of female without protuberances. Lateral margins of carapace show no tendency to grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the antennal scale. Female antennal scale (between 3,2 and 3,8 as long as broad). Antennal scale is long and slender. Terminal lobe of antennal scale between 3/4 and two times long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. Four plumose setae on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Black eyes. Eyestalks are clearly elongated. Eye about as broad as eyestalk. Rostrum is acutely pointed. Rostrum has a long triangular shape (higth of the triangle bigger than the base). Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Carpus of eight thoracopod about the same length or longer than the propodus. Denticle on base of outer margin of exopod of thoracopod eight. Copulatory organ blunt . Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Between 20 and 39 spines on the uropod exopod. Endopod of uropod without

barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod more than 3,5 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears more than seventeen spines. Distal segment of female uropod exopod very short (less than 1,5 as long as broad). Apical plumose setae on telson look normal. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Ariani (1967), Colosi (1929), Ii (1964), Milne-Edwards (1837), Sars (1877), Tattersall & Tattersall (1951), Zimmer (1909)

4.6. Siriella australiensis Panampunnayil, 1995

Diagnosis : Male between 7 and 12 mm. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. No distal joint on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Segment 2 and 3 of the antennular peduncle of the male more or less same size as segment 1. Terminal lobe of the antennular peduncle hirsute. Eyes of moderate size. Eye clearly broader than eyestalk. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Dactylus and claw of second thoracopod are between half and 1/3 the length of the carpopropodus. Second thoracopod normal. Thoracopod five is elongated. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Carpopropodus of eight thoracopod normal (carpopropodus between 6 and 8 times as long as broad). Eight thoracopod carpopropodus undivided Denticle on base of outer margin of exopod of thoracopod eight.

Copulatory organ blunt . All setae on the male copulatory organ have the same form. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. One thick long spiniform seta and one normal seta on the ultimate joint of the male third pleopod exopod. Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 straight setae on ultimate joint (± equal in length) + 1 very long on penultimate joint (+sometimes a very small one). Exopod of male fourth pleopod with 2 modified setae on the ultimate joint (1 straight and one curved, more or less equal in length) + 1 on penultimate joint (+ 2 normal setae). Modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. No spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,8 and 3,5 times longer than the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 13 and 17 spines. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Telson with three basal spines. Telson with linguiform shape. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width. The telson overreaches the margin of the distal joint of the exopod

Used literature: Panampunnayil (1995)

Diagnosis : Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Second segment of antennular peduncle between 2 and 3 times longer than the third. No distal joint on the antennal scale. Antennal scale short, less than three times as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Black eyes. Eyes of moderate size. Eyestalks are short. Eye about as broad as eyestalk. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Dactylus and claw of second thoracopod are between half and 1/3 the length of the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Carpus of eight thoracopod shorter than propodus, but more than half of the propodus. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. No spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of uropod exopod of the male very short. Three apical spines, equal in length on the telson. First two

pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Two basal spines on the telson. Telson with linguiform shape. Less than 20 lateral spines on the telson (including basal spines and spines next to the 3 apical spines). Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Tattersall (1927)

4.8. Siriella bacescui Udrescu, 1981

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Antennal scale short, less than three times as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. Eyes of fresh specimens red. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod long (More than half of the length of the carpopropodus). Eight thoracopod carpopropodus undivided No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines including the distal spines on uropod endopod ordered in groups. No spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of

uropod without barbed spines. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,2 and 2,8 times longer than the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of uropod exopod of the male very short. Three apical spines, equal in length on the telson. Two basal spines on the telson. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width.

Used literature: Udrescu (1981)

4.9. Siriella brevicaudata Paulson, 1875

Diagnosis : Female (adult) smaller than 7 mm. Male smaller than 7 mm. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. No distal joint on the antennal scale. Antennal scale short, less than three times as long as broad. Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Black eyes. Parts of the eye are covered by the rostrum. Rostrum with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Eight thoracopod carpopropodus undivided Copulatory organ blunt . All setae on the male copulatory organ have the same form. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of

male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral uropod endopod spines not gouped. Lateral spines next to the statocyst. Less than 20 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of uropod exopod of the male very short. Apical plumose setae on telson look normal. Telson with trapezium shape. Telson is less than two times as long as broad. Less than 20 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Coifmann (1937), Nouvel (2004), Paulson (1875), Tattersall (1922)

4.10. Siriella brevirostris Nouvel, 1944

Diagnosis : Male between 7 and 12 mm. Carapax of female bears one protuberance anterior to the cervical groove. Lateral margins of carapace show no tendency to grow anteriorly. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. Eyes of moderate size. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum with straight margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpus less or about 1/3 of the propodus Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt . Some short curved setae and 1

to 4 long straight setae on the male copulatory organ. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral uropod endopod spines not gouped. Lateral spines next to the statocyst. Less than 20 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Apical plumose setae on the telson have extreme long secondary hairs. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Two basal spines on the telson. Telson with linguiform shape. Telson is between 2 and 2.5 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines). No secondary spinules present. Unarmed part margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Nouvel (1944), Nouvel (1959), Nouvel (2004)

Diagnosis : Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Three or more somites are visible dorsally. Between 1 and 2 somites are visible laterally. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle less than twice as long as the third. Distal joint visible on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Segment 2 and 3 of the antennular peduncle of the male more or less same size as segment 1. Terminal lobe of the antennular peduncle hirsute. Two plumose setae on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of fresh specimens brown. Eyes of moderate size. Eye about as broad as eyestalk. Eyes are not covered by the rostrum. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Rostrum with concave margins. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod normal (carpopropodus between 6 and 8 times as long as broad). Carpus of eight thoracopod shorter than propodus, but more than half of the propodus. Denticle on base of outer margin of exopod of thoracopod eight. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without

barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,2 and 2,8 times longer than the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 13 and 17 spines. Distal segment of female uropod exopod normal (between 2 and less than 2,5 as long as broad). Apical plumose setae on telson look normal. Three apical spines on the telson of which middle one about twice as long as outer pair. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Four basal spines on the telson. Telson with linguiform shape. Telson is very long, more than 3,2 times as long as broad. Between 40 and 60 lateral spines on the telson. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Ariani & Spagnuolo (1975)

4.12. Siriella chessi Murano, 1986

Diagnosis : Male between 7 and 12 mm. Carapax of female without protuberances. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe of antennal scale between 3/4 and two times long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of moderate size. Eyestalks are short. Eye about as broad as eyestalk. Parts of the

eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Rostrum with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod normal (carpopropodus between 6 and 8 times as long as broad). Carpus less or about 1/3 of the propodus Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. Plumose setae on the sympod of the first pleopod. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. The endopod of the third male pleopod bears one straigt modified seta on the terminal segment. One thick long spiniform seta and one normal seta on the ultimate joint of the male third pleopod exopod. Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (1 long and 1 short (1/4-2/3)) + 1 very long straight seta on penultimate joint. Exopod of male fourth pleopod with 1 long on the ultimate joint (normal setae reaching 2/3 or further) with one scarcely or not modified seta + 1 on penultimate joint. Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines on uropod endopod ordered in groups. No spines next to the statocyst. Between 20 and 39 spines on the uropod exopod. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of the uropod exopod bears between 6 and 8 spines. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Telson with three basal spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines). Spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width.

Used literature: Murano (1986)

4.13. Siriella chierchiae Coifmann, 1937

Diagnosis : Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Sixth segment more than 1,75 times as long as fifth segment. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the antennal scale. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. No plumose setae on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Black eyes. Eye clearly broader than eyestalk. Rostrum is acutely pointed. Rostrum with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod robust (carpopropodus smaller than 6 times as long as broad). Base of outer margin of exopod of thoracopod eight normal (no denticle). The usual setae and strong spirally coiled setae on the male copulatory organ. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. The endopod of the third male pleopod bears two slightly modified setae terminally. These are slightly longer and more produced than the other setae present. One thick blunt seta and one short plumose seta on the exopod of the third male pleopod. Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 straight setae on ultimate joint (± equal in length) + 1 very long on penultimate joint (+sometimes a very small one). Exopod of male fourth pleopod with 2 straight setae on ultimate joint (1 long and 1 short (<= 1/3)), normal setae reaching ± 1/2 of the modified seta or further+ 1 straight on penultimate segment. Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines.

Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Distal segment of female uropod exopod short (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Telson with linguiform shape. Telson spines are alternately arranged in length. No secondary spinules present on the telson. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Brattegard (1970), Coifmann (1937), Nouvel (2004), Tattersall (1951)

4.14. Siriella clausi Sars, 1877

Diagnosis : Carapax of female without protuberances. Lateral margins of carapace show no tendency to grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the antennal scale. Female antennal scale (between 3,2 and 3,8 as long as broad). Terminal lobe of antennal scale between 3/4 and two times long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Black eyes. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt . Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third

pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Apical plumose setae on telson look normal. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Telson with linguiform shape. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines are alternately arranged in length. No secondary spinules present on the telson. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Sars (1877), Czerniavsky (1883), Zimmer (1909), Colosi (1929), Bacescu (1941), Tattersall & Tattersall (1951), Genovese (1956), Ariani (1967)

4.15. Siriella conformalis Hansen, 1910

Diagnosis : Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal scale is between 3,8 and 4,5 times as long as broad. Black eyes. Eyes of moderate size. Eyestalks very short. Eye clearly broader than eyestalk. Rostrum is acutely pointed. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). No modified setae on second pleopod. Pseudobranchia on second male pleopod are clearly straight. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Third male pleopod has straight pseudobranchia. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (1 long + 1 shorter (3/4)) + 2 straight seta on penultimate joint (both longer than setae on ultimate joint). No modified setae on exopod of male fourth pleopod. Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are straight. Exopod of the uropod longer than the endopod. Proximal

segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 9 and 12 spines. Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Three apical spines, equal in length on the telson. Telson with three basal spines.

Used literature: Hansen (1910)

4.16. Siriella dayi Tattersall, 1952

Diagnosis : Male between 7 and 12 mm. Lateral margins of carapace show no tendency to grow anteriorly. Antennal scale reaches beyond the antennular peduncle, outer margin with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Terminal lobe length of male antennal scale is between 3/4 and two times its width. Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle normal (without hairs upon). Eyes are small. Eyestalks square-like. Eye about as broad as eyestalk. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). No modified setae on second pleopod. Pseudobranchia on second male pleopod are G-shaped. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are G-shaped. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Lateral uropod endopod spines not gouped. Pseudobranchia of fourth male pleopod are G-shaped. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 13 and 17 spines. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad).

Apical plumose setae on telson look normal. Three apical spines on the telson of which middle one about twice as long as outer pair. First two pairs of subapical spines on the telson shorter than 1/3 the length of the apical spines. Four basal spines on the telson Telson with triangular shape. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Tattersall (1952)

4.17. Siriella denticulata (Thompson, 1880)

Diagnosis : Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Sixth segment more than 1,75 times as long as fifth segment. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle less than twice as long as the third. No distal joint on the antennal scale. Antennal scale short, less than three times as long as broad. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex. Segment 1 of the antennular peduncle of the male is longer than segment 2 and 3 together. Eyes of moderate size. Eye clearly broader than eyestalk. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Dactylus and claw of second thoracopod are between half and 1/3 the length of the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod exopod grow between 1/2 and 1/3 of the distal outer margin. Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Telson with linguiform shape and slender. Between 20 and 40 lateral spines growing distally longer. Unarmed part of telson margin is more than half the telson width.

Used literature: Thomson (1900), Nouvel (2004)

4.18. Siriella distinguenda Hansen, 1910

Diagnosis : Female between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Less than 2 somites are visible dorsally. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. Terminal lobe of the antennular peduncle hirsute. Two plumose setae on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyestalks very short. Eye clearly broader than eyestalk. Rostrum is acutely pointed. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Second thoracopod normal. No modified setae on second pleopod. Pseudobranchia on second male pleopod are clearly straight. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Third male pleopod has straight pseudobranchia. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (1 long and 1 short (1/4-2/3)) + 1 very long straight seta on penultimate joint. No modified setae on exopod of male fourth pleopod. Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are straight. Spines including the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 9 and 12 spines. Distal segment of female uropod exopod normal (between 2 and less than 2,5 as long as broad). Distal segment of uropod exopod of the male long (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Telson with three basal spines. Telson with linguiform shape.

Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Hansen (1910), Bacescu (1979)

4.19. Siriella dollfusi Nouvel, 1941

Diagnosis : Female between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Less than 1 somite is visible laterally. Lateral margins of carapace show no tendency to grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of fresh specimens red. Eyestalks are short. Eye about as broad as eyestalk. Parts of the eye are covered by the rostrum. Rostrum with straight margins. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpus of eight thoracopod shorter than propodus, but more than half of the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. The endopod of the third male pleopod bears two slightly modified setae terminally. These are slightly longer and more produced than the other setae present. One thick long spiniform seta and one normal seta on the ultimate joint of the male third pleopod exopod. Modified setae on third pleopod.

Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (± equal in length). Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines excluding the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Distal segment of female uropod exopod normal (between 2 and less than 2,5 as long as broad). Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Nouvel (1944), Nouvel (1959), Nouvel (2004)

4.20. Siriella dubia Hansen, 1910

Diagnosis : Carapax of female without protuberances, lateral margins growing anteriorly. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of scale with one terminal denticle. Peduncle more than 2/3 of the antennal scale length. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe of antennal scale between 3/4 and two times long as broad. The tip of the terminal spine doesn't reach the distal joint. Male antennular flagellum normal. Segment 1 of the antennular peduncle of the male is longer than segment 2 and 3 together. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Black

eyes. Eyestalks square-like. Eye about as broad as eyestalk. Second thoracopod normal. Distal third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Eight thoracopod carpopropodus undivided. No modified setae on second pleopod. The endopod of the third male pleopod bears one straigt modified seta on the terminal segment. No modified setae on the male third pleopod exopod. No modified setae on exopod of male fourth pleopod. Modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. Endopod without barbed spines. Exopod proximal joint with spines and plumose setae. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears less than six spines. Distal segment of female uropod exopod long (2,5 or more as long as broad). Distal segment of uropod exopod of the male long (between 1,5 and less than 2 times as long as broad). Apical plumose setae on the telson have extreme long secondary hairs. Telson trapezium shaped. Spines grow distally longer. No secondary spinules present on the telson.

Used literature: Hansen (1910), Tattersall (1922), Ii (1964), Pillai (1964), Pillai (1965), Pillai (1973), Panampunnayil (1995)

4.21. Siriella gracilipes Nouvel, 1942

Diagnosis : Carapax of female without protuberances. Less than 2 somites are visible dorsally. Antennal scale reaches beyond the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale is between 3,2 and 3,8 times as long as broad. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Segment 1 of the antennular peduncle of the male is longer than segment 2 and 3 together. Terminal lobe of the antennular peduncle hirsute. Black eyes. Dactylus and claw of second thoracopod are longer than the

carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Denticle on base of outer margin of exopod of thoracopod eight. Copulatory organ blunt . Plumose setae on the sympod of the first pleopod. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Lateral uropod endopod spines not gouped. Pseudobranchia of fourth male pleopod are spirally coiled. Between 20 and 39 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Apical plumose setae on telson look normal. Three apical spines on the telson of which middle one about twice as long as outer pair. Telson spines are alternately arranged in length. No secondary spinules present on the telson. The telson overreaches the margin of the distal joint of the exopod No black spots on lateral side of the abdomen.

Used literature: Nouvel (1942), Tattersall & Tattersall (1951), Hoenigman (1960), Ariani (1967), Ariani & Spagnuolo (1975)

4.22. Siriella gracilis Dana, 1852

Diagnosis : Female (adult) smaller than 7 mm. Carapax of female without protuberances. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Second segment of antennular peduncle between 2 and 3 times longer than the third. Female antennal scale short (less than 3,2 times as long as broad). Terminal lobe length of male antennal scale is between 3/4 and two times its width. Male antennular flagellum normal. Segment 1 and 2 of the antennular

peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes are small. Eye about as broad as eyestalk. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Thoracopod five equal in length to others. Eight thoracopod carpus between 1/3 and half of the length of the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Exopod of the uropod is shorter than endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Telson with linguiform shape. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod Black spots on the lateral side of the abdomen.

Used literature: Coifmann (1937), Ii (1964), Pillai (1965), Nouvel (2004)

4.23. Siriella halei Tattersall, 1927

Diagnosis : Female (adult) between 12 and 17 mm. Male between 12 and 17 mm. Carapax of female without protuberances. Pointed shoulders are clearly visible on lateral margins of the carapace. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle less than twice as long as the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale short, less than three times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Segment 2 and 3 of the antennular peduncle of the male more or less same size as segment 1. Five or more plumose setae on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Black eyes. Eyes are small. Eyestalks square-like. Eye about as broad as eyestalk. Eyes are not covered by the rostrum. Rostrum bluntly rounded with a spiniform pseudorostral process beneath it Rostrum lowly triangular (hight smaller than 1/3 of the base). Rostrum with concave margins. Dactylus and claw of second thoracopod are between half and 1/3 the length of the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Dactylus of thoracopod eight broader than long or nearly square Carpopropodus of eight thoracopod robust (carpopropodus smaller than 6 times as long as broad). Eight thoracopod carpus between 1/3 and half of the length of the propodus. Denticle on base of outer margin of exopod of thoracopod eight. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia

of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod exopod grow between 1/2 and 1/3 of the distal outer margin. Proximal segment of the uropod exopod bears between 9 and 12 spines. Distal segment of female uropod exopod very short (less than 1,5 as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Telson with three basal spines. Telson with triangular shape. Telson is between 2 and 2.5 times as long as broad. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Tattersall (1927)

4.24. Siriella hanseni Tattersall, 1922

Diagnosis : Female (adult) smaller than 7 mm. Male smaller than 7 mm. Carapax of female without protuberances. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. No distal joint on the antennal scale. Terminal lobe of antennal scale between 3/4 and two times long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. Male antennular flagellum normal. Eyes of moderate size. Eyestalks square-like. Eye about as broad as eyestalk. Eyes are not covered by the rostrum. Rostrum bluntly rounded with a spiniform pseudorostral process beneath it Rostrum lowly triangular (hight smaller than 1/3 of the base). Rostrum with concave margins. Eight thoracopod carpopropodus undivided No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod

are spirally coiled. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral uropod endopod spines not gouped. Lateral spines next to the statocyst. Less than 20 spines on the uropod exopod. Endopod uropod without barbed spines. Exopod longer than the endopod. Exopod proximal joint with only spines growing distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of female uropod exopod very short (less than 1,5 as long as broad). Distal segment of uropod exopod of the male very short. Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Telson with three basal spines. Telson with linguiform shape. Telson is less than two times as long as broad. Less than 20 lateral spines on the telson. Spines grow distally longer. No secondary spinules present on the telson. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Tattersall (1922), Tattersall (1960), Ii (1964), Pillai (1965)

4.25. Siriella inornata Hansen, 1910

Diagnosis : Less than 1 somite is visible laterally. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Distal joint visible on the antennal scale. Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. Black eyes. Eyes of moderate size, broader than eyestalk. Eyestalks very short. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpopropodus extremely slender (carpopropodus more than 12 times as long as broad). Carpus about the same length as propodus. Base of outer margin of exopod of thoracopod eight normal. Copulatory organ blunt. Plumose setae on the sympod of the first pleopod. No

modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 more or less straight setae on ultimate joint (1 short (1/4-2/3) and 1 long). Exopod of male fourth pleopod with 2 straight on ultimate joint (1 long and 1 short (< 1/2)), normal setae not reaching 1/2 of the modified seta + 1 straight on penultimate joint. Modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. More than 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 13 and 17 spines. Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width.

Used literature: Hansen (1910), Fukuoka & Murano (1997)

4.26. Siriella intermedia Panampunnayil, 1981

Diagnosis : Female (adult) between 7 and 12 mm. Carapax of female without protuberances. Sixth segment more than 1,75 times as long as fifth segment. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. No distal joint on the antennal scale. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Eyes of moderate size. Eye clearly broader than eyestalk. Parts of the eye are covered by the rostrum. Rostrum bluntly rounded. Rostrum lowly triangular (hight smaller than 1/3 of the base). Rostrum with

straight margins. Total length of dactylus and claw of eight thoracopod long (More than half of the length of the carpopropodus). Carpopropodus of eight thoracopod normal (carpopropodus between 6 and 8 times as long as broad). Eight thoracopod carpopropodus undivided Denticle on base of outer margin of exopod of thoracopod eight. Spines excluding the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,2 and 2,8 times longer than the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. No apical spines on the telson. Two to four setae present. First two pairs of subapical spines on the telson shorter than 1/3 the length of the apical spines. Telson with three basal spines. Telson with linguiform shape. Telson is less than two times as long as broad. Less than 20 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Panampunnayil (1981)

4.27. Siriella jaltensis Czerniavsky, 1868

Diagnosis : Carapax of female without protuberances. Lateral margins of carapace show no tendency to grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin with one terminal denticle. Peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the scale. The tip of the terminal spine doesn't reach the distal joint. Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. Black eyes. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Denticle on base of outer margin of exopod of thoracopod eight. Copulatory organ blunt. Sympod of first pleopod without plumose setae. No modified setae on second

pleopod. No modified setae on third and fourth pleopod. Lateral uropod endopod spines not gouped. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Apical plumose setae on telson look normal. Telson spines are alternately arranged in length. No secondary spinules present on the telson. No black spots on lateral side of the abdomen.

Remarks: The species is known for its large intraspecific variation. Seven studied characteristics were very variable and varied over three classes (used in phylgenetic analysis): The male and female habitus length, the number of feathered setae at the inner border of the female antennular peduncle, carpus-propodus length ratio of the eight thoracopod, number of basal spines on the telson, relative length of the telson compared to the total body length and the number of spines on the uropod endopod. 24 other morphological characters varied over two classes.

A detailed study on specimens from one population showed even a variation in the number of terminal spines on the telson. In the literature it is agreed that *S. jaltensis* is characterized by three spines, although one fifth of the specimens studied from the available material originating from one population had two spines. (see Figure 1)

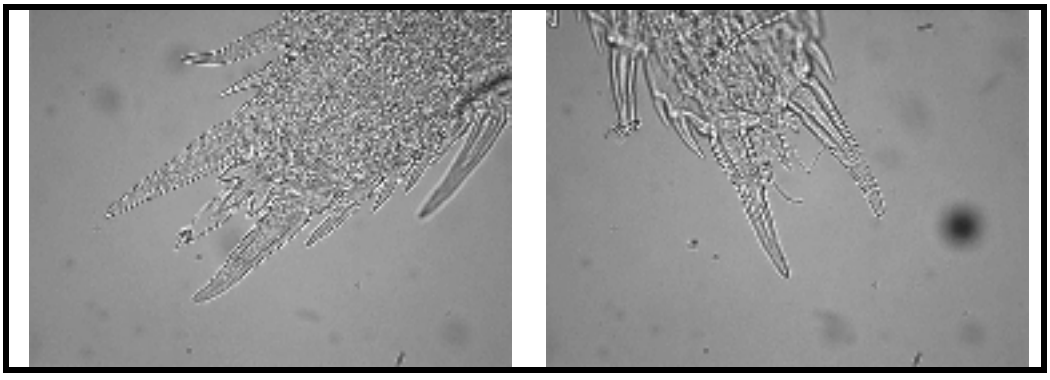


Figure 1. variation in terminal spines on the telson of S. jaltansis

Used literature: Czerniavsky (1868), Sars (1877), Czerniavsky (1882), Czerniavsky (1883), Norman (1887), Zimmer (1909), Zimmer (1932), Bacescu (1940), Nouvel (1942), Bacescu (1954), Zakutskiy (1970), Nouvel (2004)

4.28. Siriella japonica Ii, 1964

Diagnosis: Female between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Second segment of peduncle between 2 and 3 times longer than the third. Distal joint visible on the scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale short, less than three times as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint. Flagellum on male second antenna is swollen near the base. Eyes of moderate size, broader than eyestalk. Eyestalks short. Parts of the eye covered by the rostrum. Rostrum is acutely pointed and medium triangular (hight of the triangle more than 1/2 of the base), with straight margins. Thoracopod five equal in length to others. Eight thoracopod carpus between 1/3 and half of the length of the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on third and fourth pleopod. Pseudobranchia of third male pleopod are spirally coiled. Spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod spirally coiled. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally between 1/3 and 1/6 of the outer margin. Proximal segment of the uropod exopod bears between 6 and 8 spines. Apical plumose setae on telson normal. Three apical spines are equal in length. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Two basal spines on the telson. Telson linguiform and slender. Between 20 and 40 lateral spines on the telson. No secondary spinules present. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Ii (1964)

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale short, less than three times as long as broad. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. Black eyes. Eyestalks are short. Eyes are not covered by the rostrum. Rostrum is acutely pointed and medium triangular with concave margins. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpopropodus slender (carpopropodus between 8 and 12 times as long as broad) No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. No spines next to the statocyst. More than 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally between 1/3 and 1/6 of the outer margin. Proximal segment of the uropod exopod bears between 6 and 8 spines. Apical plumose setae on telson look normal. Telson similar to *S. japonica* .

Used literature: Ii (1964)

Diagnosis: Female between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Lateral margins of carapace show no tendency to grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint. Male antennular flagellum normal. Segment 1 of the antennular peduncle of the male is longer than segment 2 and 3 together. Terminal lobe of the antennular peduncle normal (without hairs upon). One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of moderate size. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Dactylus and claw of second thoracopod are between half and 1/3 the length of the carpopropodus. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpopropodus slender. Carpus shorter than propodus, but more than half of the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are G-shaped. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are G-shaped. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are G-shaped. Spines excluding the distal spines on uropod endopod ordered in groups. More than 60 spines on the uropod exopod. Endopod without barbed spines. Exopod longer than the endopod. Exopod proximal joint with only spines with proximal segment shorter than 2,2 times the

length of the distal segment. Spines on the proximal segment of the uropod grow distally between 1/3 and 1/6 of the outer margin. Proximal segment of the uropod exopod bears between 6 and 8 spines. Telson similar to *S. japonica*.

Used literature: Ii (1964)

4.29. Siriella jonesi Pillai, 1964

Diagnosis: Female (adult) smaller than 7 mm. Sixth segment more than 1,75 times as long as fifth segment. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Distal joint visible on the antennal scale. Antennal scale is between 3,8 and 4,5 times as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. Eyes are small. Eye about as broad as eyestalk. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Dactylus of thoracopod eight longer than broad. Denticle on base of outer margin of exopod of thoracopod eight. Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. No modified setae on second pleopod. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Lateral uropod endopod spines not gouped. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Apical plumose setae on the telson have extreme long secondary hairs. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Two basal spines on the telson. Telson with

linguiform shape. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Pillai (1964), Pillai (1965), Pillai (1973)

4.30. Siriella lingvura Ii, 1964

Diagnosis: Male smaller than 7 mm. Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Lateral margins of carapace show no tendency to grow anteriorly. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle less than twice as long as the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe of antennal scale between 3/4 and two times long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Fresh specimens have purple eyes. Eyestalks are short. Eye about as broad as eyestalk. Eyes are not covered by the rostrum. Rostrum bluntly rounded with a spiniform pseudorostral process beneath it Rostrum lowly triangular (hight smaller than 1/3 of the base). Rostrum with straight margins. Second thoracopod normal. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpus less or about 1/3 of the propodus Copulatory organ blunt . All setae on the male copulatory organ have the same form. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod

are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Lateral uropod endopod spines not gouped. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. Less than 20 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Telson with linguiform shape. Telson is less than two times as long as broad. Less than 20 lateral spines on the telson (including basal spines and spines next to the 3 apical spines). Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Ii (1964), Valbonesi & Murano (1980), Fukuoka & Murano (1997)

4.31. Siriella longidactyla Tattersall, 1940

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Second segment of antennular peduncle about or more than three times as long as the third. No distal joint on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Black eyes. Eyes of moderate size. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Total length of dactylus and claw of eight thoracopod long (More than half of the length of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod slender (carpopropodus between 8 and 12 times as long as broad) Carpus of eight thoracopod shorter than propodus, but more than half of the

propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ pointed. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. No spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod exopod grow between 1/2 and 1/3 of the distal outer margin. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Two basal spines on the telson. Telson with triangular shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Secondary spinules on the telson. Unarmed part of telson margin is less than half the telson width.

Used literature: Tattersall (1940)

4.32. Siriella longipes Nakazawa, 1910

Diagnosis: Female between 12 and 17 mm. Male between 12 and 17 mm. Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Lateral margins of carapace grow anteriorly. Between 1 and 2 somites are visible laterally. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint

visible on the antennal scale. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Segment 1 and 2 of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. Eyes of fresh specimens brown. Eyestalks square-like. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod short (less than 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus extremely slender. Carpus about the same length as the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt. Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on third and fourth pleopod. Pseudobranchia of third male pleopod are spirally coiled. Pseudobranchia of fourth male pleopod are spirally coiled. Spines excluding the distal spines on uropod endopod ordered in groups. No spines next to the statocyst. More than 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Distal segment of female uropod exopod long (2,5 or more as long as broad). Distal segment of uropod exopod of the male long (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Four basal spines on the telson Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Nakazawa (1910), Ii (1964)

4.33. Siriella macrophthalma Murano, 1986

Diagnosis: Female (adult) between 7 and 12 mm. Carapax of female without protuberances. Sixth segment more than 1,75 times as long as fifth segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal scale is between 3,8 and 4,5 times as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Segment 2 and 3 of the antennular peduncle of the male more or less same size as segment 1. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes are large (cornea is about 2/3 of carapax width dorsally seen). Eyestalks are short. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum with concave margins. Dactylus and claw of second thoracopod are between half and 1/3 the length of the carpopropodus. Second thoracopod normal. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod extremely slender (carpopropodus more than 12 times as long as broad). Carpus of eight thoracopod about the same length or longer than the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt . Some short curved setae and 5 or more long straight setae on the male copulatory organ. Plumose setae on the sympod of the first pleopod. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. Third male pleopod endopod with two setae on ultimate segment (1 strongly bent and 1 straight modified seta). Penultimate segment sometimes with 1 modified seta. Third male pleopod exopod with two setae (1 strongly bent and 1 straight modified seta) Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (± equal in

length) + 2 on penultimate jnt (1 very long & 1 very short) + 1 very long on antepenultimate jnt (+ sometimes 1 short). Exopod of male fourth pleopod with 2 straight on ultimate joint (1 long & 1 short (± 1/5) seta), normal setae reaching beyond 3/5 of the modified seta + 3 modified on penultimate joint. Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines excluding the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Telson with three basal spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Murano (1986)

4.34. Siriella media Hansen, 1910

Diagnosis: Carapax of female without protuberances. Less than 1 somite is visible laterally. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Second segment of antennular peduncle about or more than three times as long as the third. Distal joint visible on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of

the female. Black eyes. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod slender (carpopropodus between 8 and 12 times as long as broad) Denticle on base of outer margin of exopod of thoracopod eight. Copulatory organ blunt . No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 straight setae on ultimate joint (± equal in length) + 1 very long on penultimate joint (+sometimes a very small one). Exopod of male fourth pleopod with 2 curved setae on ultimate joint + 3 modified setae on penultimate joint (one curved, two straight ones on inner corner) Modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 13 and 17 spines. Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Telson spines are alternately arranged in length. No secondary spinules present on the telson. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Hansen (1910), Hansen (1912), Ii (1964), Fukuoka & Murano (1997)

4.35. Siriella melloi da Silva, 1974

Diagnosis: Male between 7 and 12 mm. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle about or more

than three times as long as the third. No distal joint on the antennal scale. Antennal scale is long and slender. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Eyes of moderate size. Eye clearly broader than eyestalk. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). No modified setae on second pleopod. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are straight. Spines including the distal spines on uropod endopod ordered in groups. Endopod of uropod without barbed spines. Exopod of the uropod is shorter than endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,8 and 3,5 times longer than the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are longer than apical spines. Two basal spines on the telson. Telson with linguiform shape. Telson spines grow distally longer. No secondary spinules present on the telson.

Used literature: Da Silva (1974)

4.36. Siriella mexicana Brattegard, 1970

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal

scale is between 3,8 and 4,5 times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Segment 1 of the antennular peduncle of the male is longer than segment 2 and 3 together. Terminal lobe of the antennular peduncle normal (without hairs upon). One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of fresh specimens brown. Eyes of moderate size. Eye clearly broader than eyestalk. Parts of the eye are covered by the rostrum. Rostrum bluntly pointed. Rostrum lowly triangular (hight smaller than 1/3 of the base). Rostrum with straight margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod extremely slender (carpopropodus more than 12 times as long as broad). Carpus of eight thoracopod about the same length or longer than the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. The endopod of the third male pleopod bears two slightly modified setae terminally. These are slightly longer and more produced than the other setae present. Third male pleopod exopod with two setae (1 strongly bent and 1 straight modified seta) Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (± equal in length) + 2 on penultimate jnt (1 very long & 1 very short) + 1 very long on antepenultimate jnt (+ sometimes 1 short). Exopod of male fourth pleopod with 2 straight setae on ultimate joint (1 long and 1 short (<= 1/3)), normal setae reaching ± 1/2 of the modified seta or further+ 1 straight on penultimate segment. Modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod

proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Distal segment of female uropod exopod normal (between 2 and less than 2,5 as long as broad). Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Brattegard (1970)

4.37. Siriella nodosa Hansen, 1910

Diagnosis: Female (adult) smaller than 7 mm. Male smaller than 7 mm. Carapax of female bears two protuberances: one pre-cervical and one post-cervical. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle less than twice as long as the third. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale short, less than three times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Eyes of fresh specimens red. Eyes are small. Eye clearly broader than eyestalk. Parts of the eye are covered by the rostrum. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Thoracopod five is elongated. Eight thoracopod carpopropodus undivided No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No

modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. Endopod of uropod without barbed spines. Exopod of the uropod is about as long as the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,8 and 3,5 times longer than the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of female uropod exopod short (between 1,5 and less than 2 times as long as broad). Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson shorter than 1/3 the length of the apical spines. One spine on the telson basis. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Hansen (1910), Ii (1964), Bacescu (1979), Murano (1990)

4.38. Siriella norvegica Sars, 1869

Diagnosis: Carapax of female without protuberances. Three or more somites are visible dorsally. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Terminal lobe of antennal scale between 3/4 and two times long as broad. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Terminal lobe of the

antennular peduncle hirsute. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Dactylus of thoracopod eight longer than broad. Denticle on base of outer margin of exopod of thoracopod eight. Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,2 and 2,8 times longer than the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Apical plumose setae on telson look normal. Three apical spines on the telson of which middle one about twice as long as outer pair. Telson with linguiform shape. Telson is very long, more than 3,2 times as long as broad. Between 40 and 60 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Sars (1879), Czerniavsky (1883), Zimmer(1909), Zimmer (1932), Bacescu (1941), Tattersall & Tattersall (1951), Furnestin (1960), Ariani (1967), Ariani & Spagnuolo (1975), Lagardere & Nouvel (1980)

4.39. Siriella okadai Ii, 1964

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Less than 1 somite is visible laterally. Lateral margins of carapace grow anteriorly. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Flagellum on male second antenna is swollen near the base. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of moderate size. Eyestalks are short. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Thoracopod five equal in length to others. Eight thoracopod carpus between 1/3 and half of the length of the propodus. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines excluding the distal spines on uropod endopod ordered in groups. No spines next to the statocyst. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of uropod

exopod of the male normal (between 2 and less than 2,5 as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Two basal spines on the telson. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: li (1964)

4.40. Siriella pacifica Holmes, 1900

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Lateral margins of carapace grow anteriorly. Less than 1 somite is visible laterally. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod long (More than half of the length of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod normal (carpopropodus between 6 and 8 times as long as broad). Carpus less or about 1/3

of the propodus Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ pointed. The usual setae and strong spirally coiled setae on the male copulatory organ. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. The endopod of the third male pleopod bears one straigt modified seta on the terminal segment. One thick long spiniform seta and one normal seta on the ultimate joint of the male third pleopod exopod. Modified setae on third pleopod. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (± equal in length). Exopod of male fourth pleopod with 2 setae on ultimate segment (1 short and 1 extremely bent) + 1 straight seta on the penultimate joint. Modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. More than 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Between 40 and 60 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines are alternately arranged in length. No secondary spinules present on the telson. The telson overreaches the margin of the distal joint of the exopod No black spots on lateral side of the abdomen.

Used literature: Holmes (1900), Hansen (1913), Tattersall (1951)

4.41. Siriella panamensis Tattersall, 1951

Diagnosis: Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle less than twice as long as the third. Distal joint visible on the antennal scale. Female antennal scale (between 3,2 and 3,8 as long as broad). Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the

antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Black eyes. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod long (More than half of the length of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod robust (carpopropodus smaller than 6 times as long as broad). Carpus less or about 1/3 of the propodus No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. Third male pleopod endopod with two setae on ultimate segment (1 strongly bent and 1 straight modified seta). Penultimate segment sometimes with 1 modified seta. Third male pleopod exopod with two setae (1 strongly bent and 1 straight modified seta) Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (± equal in length). Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines including the distal spines on uropod endopod ordered in groups. No spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,2 and 2,8 times longer than the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 9 and 12 spines. Distal segment of female uropod exopod normal (between 2 and less than 2,5 as long as broad). Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Telson with three basal spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width.

Used literature: Tattersall (1951)

Diagnosis: Male between 7 and 12 mm. Carapax of female without protuberances. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the antennal scale. Female antennal scale (between 3,2 and 3,8 as long as broad). Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. Eyes of moderate size. Eye clearly broader than eyestalk. Rostrum with concave margins. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod slender (carpopropodus between 8 and 12 times as long as broad) Base of outer margin of exopod of thoracopod eight normal (no denticle). Plumose setae on the sympod of the first pleopod. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. The endopod of the third male pleopod bears one straigt modified seta on the terminal segment. One thick long spiniform seta and one normal seta on the ultimate joint of the male third pleopod exopod. Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 more or less straight setae on ultimate joint (1 short (1/4-2/3) and 1 long). Exopod of male fourth pleopod with 1 long on the ultimate joint (normal setae reaching 2/3 or further)(+ 1 scarcely or not modified seta) + 1 on penultimate joint. Modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Three apical spines, equal in length on the telson. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical

spines) No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width.

Remarks: Unidentified material collected from the red sea was identified as *S. paulsoni*. Almost all morphological characteristics matched the description made by Nouvel (1959). Nevertheless, variations in the modified setae of the fourth male pleopod were found. The setae are much more bent than described by Nouvel. Relative length of the setae equals the description by Nouvel. In addition to the description of Nouvel. Drawings of the third and fourth male pleopod, exopod of the uropod, telson and male copulatory organ which were lacking in the original description were made.

Used literature: Kossmann (1880), Coifmann (1937), Nouvel (1944), Nouvel (1959), Nouvel (2004)

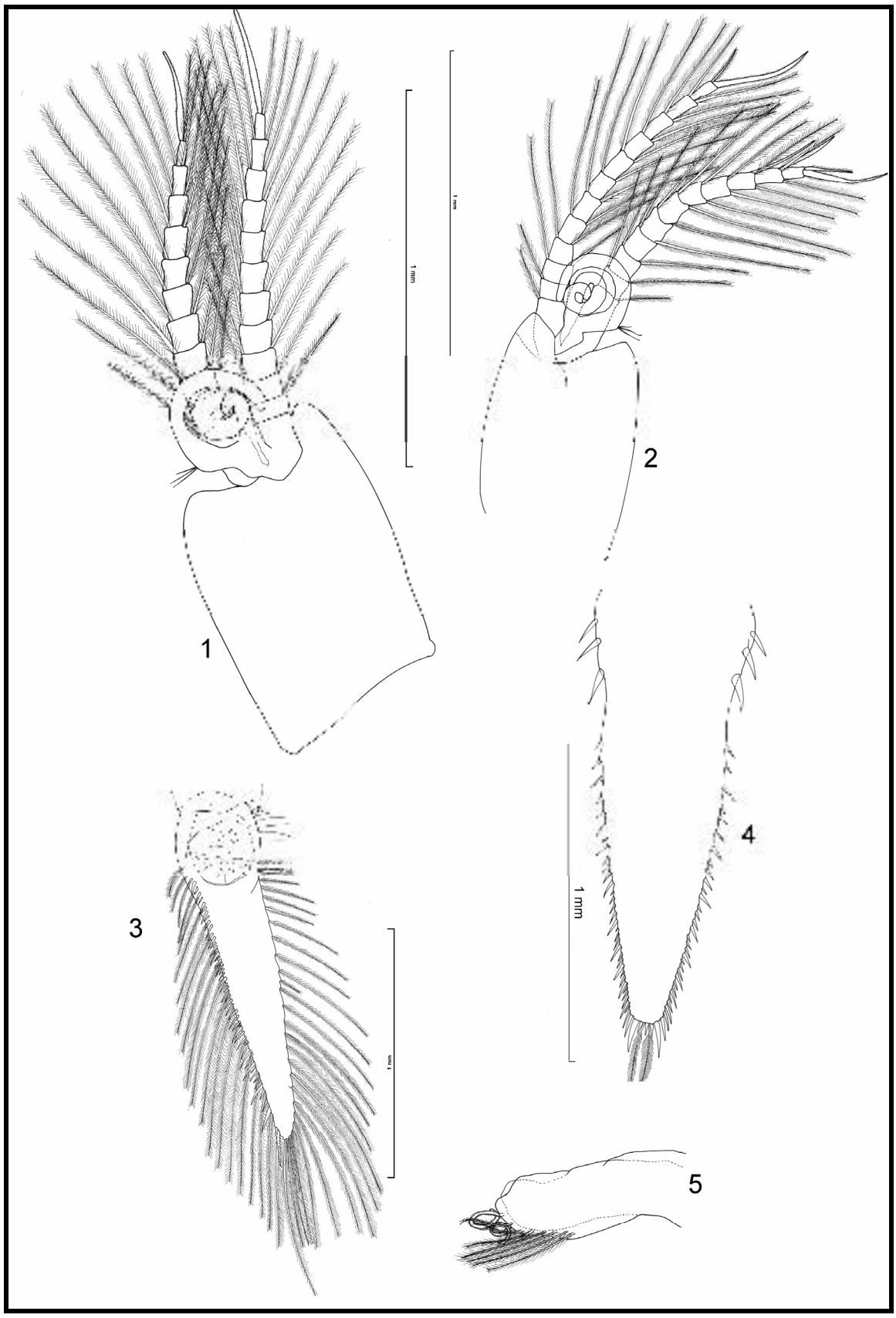


Figure 2. *S. paulsoni* 1. third male pleopod, 2. fourth male pleopod, 3. uropod exopod, 4. telson, 5. male copulatory organ

Diagnosis: Less than 2 somites are visible dorsally. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Less than 1 somite is visible laterally. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle about or more than three times as long as the third. Distal joint visible on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Eyes of moderate size. Eyestalks very short. Eye clearly broader than eyestalk. Rostrum is acutely pointed. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Carpopropodus of eight thoracopod extremely slender (carpopropodus more than 12 times as long as broad). Carpus of eight thoracopod about the same length or longer than the propodus. Copulatory organ blunt . Some short curved setae and 5 or more long straight setae on the male copulatory organ. Plumose setae on the sympod of the first pleopod. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 straight setae on ultimate joint (± equal in length) + 1 very long on penultimate joint (+sometimes a very small one). Exopod of male fourth pleopod with 2 curved setae on ultimate joint + 3 modified setae on penultimate joint (one curved, two straight ones on inner corner) Modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. No spines next to the statocyst. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 13 and 17 spines. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Apical

plumose setae on the telson have extreme long secondary hairs. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines are alternately arranged in length. No secondary spinules present on the telson. No black spots on lateral side of the abdomen.

Used literature: Hansen (1910)

4.44. Siriella pondoensis Tattersall, 1962

Diagnosis: Female (adult) smaller than 7 mm. Male smaller than 7 mm. Carapax of female without protuberances. Three or more somites are visible dorsally. Two or more somites are visible laterally. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale short, less than three times as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of fresh specimens brown. Eyes are small. Eyestalks square-like. Eye about as broad as eyestalk. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum with concave margins. Thoracopod five equal in length to others. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the male third pleopod exopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. No spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod is shorter than endopod. Uropod

exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,2 and 2,8 times longer than the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Two basal spines on the telson. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines grow distally longer. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod Black spots on the lateral side of the abdomen.

Used literature: Tattersall (1962)

4.45. Siriella quadrispinosa Hansen, 1910

Diagnosis: Carapax of female without protuberances. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. Rostrum with concave margins. Dactylus and claw of second thoracopod are between half and 1/3 the length of the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod normal (carpopropodus between 6 and 8 times as long as broad). Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No

modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. No spines next to the statocyst. Endopod of uropod without barbed spines. Uropod exopod proximal joint with only spines. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are longer than apical spines. Two basal spines on the telson. Telson with linguiform shape. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. No black spots on lateral side of the abdomen.

Used literature: Hansen (1910), Tattersall (1922), Ii (1964), Pillai (1965), Murano (1990)

4.46. Siriella quilonensis Pillai, 1961

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Terminal lobe length of male antennal scale is about 3/4 its width. Male antennular flagellum normal. Segment 1 and 2 of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. Eyes are small. Eyestalks square-like. Eye about as broad as eyestalk. Parts of the eye are covered by the rostrum. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Rostrum with concave margins. Eight thoracopod carpus between 1/3 and half of the length of the propodus. No modified setae on second pleopod. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Third male pleopod has straight pseudobranchia. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth

male pleopod are straight. Spines including the distal spines on uropod endopod ordered in groups. Endopod of uropod without barbed spines. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson equal in length to apical spines. Two basal spines on the telson. Telson with linguiform shape. Telson is between 2 and 2.5 times as long as broad. Less than 20 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Pillai (1961), Pillai (1965)

4.47. Siriella robusta Pillai, 1964

Diagnosis: Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Distal joint visible on the antennal scale. Antennal scale is between 3,8 and 4,5 times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Segment 2 and 3 of the antennular peduncle of the male more or less same size as segment 1. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of moderate size. Eyestalks very short. Eye clearly broader than eyestalk. Rostrum acutely or narrowly rounded. Rostrum with concave margins. Thoracopod 2 subchelate. Distal one third of the 6th segment of the endopod of second thoracopod is excavated. Thoracopod five is elongated. Eight thoracopod carpus between 1/3 and half of the length of the propodus. No modified setae on second pleopod. Pseudobranchiae on second male plepod small and bilobed. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchiae

on third male plepod small and bilobed. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchiae on fourth male plepod small and bilobed. Endopod of uropod without barbed spines. Exopod of the uropod is about as long as the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 9 and 12 spines. Apical plumose setae on the telson have extreme long secondary hairs. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Telson with three basal spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width.

Used literature: Pillai (1964), Pillai (1965)

4.48. Siriella roosevelti Tattersall, 1941

Diagnosis: Male between 7 and 12 mm. Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Distal joint visible on the antennal scale. Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Black eyes. Eyestalks are short. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod long (More than half of the length of the carpopropodus). Dactylus of thoracopod eight longer than broad. Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ pointed. The usual setae and strong spirally coiled setae on the male copulatory organ. Sympod of first pleopod without plumose setae. No modified

setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (1 long and 1 short (1/4-2/3)) + 1 very long straight seta on penultimate joint. Exopod of male fourth pleopod with 2 setae on ultimate joint (1 long curved and 1 small (about 1/3 of the other)) Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Distal segment of female uropod exopod short (between 1,5 and less than 2 times as long as broad). Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Tattersall (1941)

4.49. Siriella serrata Hansen, 1910

Diagnosis: Male between 7 and 12 mm. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with 4 or 5 spines. Antennal scale is between 3,2 and 3,8 times as long as broad. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 1 very long seta on the ultimate joint (+ sometimes the 3 preceding joints with a long and strong blunt spine). Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Uropod exopod proximal joint with only spines.

Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 9 and 12 spines. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are about 1/3 to 2/3 as long as the apical spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines are alternately arranged in length. No secondary spinules present on the telson. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Hansen (1910)

4.50. Siriella sinensis Ii, 1964

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle more than 2/3 of the antennal scale length. Second segment of antennular peduncle about or more than three times as long as the third. Distal joint visible on the antennal scale. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Male antennular flagellum normal. Segment 1 and 2 of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. Black eyes. Eyes of moderate size. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Total length of dactylus and claw of eight thoracopod moderate (between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod extremely slender (carpopropodus more than 12 times as long as broad). Carpus of eight thoracopod shorter than propodus, but more than half of the propodus. Copulatory organ blunt . Some short curved setae and 5 or more long straight setae on the male copulatory organ. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No

modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. No spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally between 1/3 and 1/6 of the outer margin. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson are bigger than 2/3 the length of the apical spines, but still smaller. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: li (1964)

4.51. Siriella singularis Nouvel, 1957

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Less than 1 somite is visible laterally. Lateral margins of carapace grow anteriorly. Outer margin of antennal scale with one terminal denticle. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal scale is long and slender. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Segment 2 and 3 of the antennular peduncle of the male more or less same size as segment 1. Terminal lobe of the antennular peduncle hirsute.

One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes are small. Eye clearly broader than eyestalk. Parts of the eye are covered by the rostrum. Rostrum lowly triangular (hight smaller than 1/3 of the base). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod slender (carpopropodus between 8 and 12 times as long as broad) Carpus of eight thoracopod shorter than propodus, but more than half of the propodus. Denticle on base of outer margin of exopod of thoracopod eight. Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. Modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. The endopod of the third male pleopod bears two straight blunt modified setae terminally, one longer than the other. No modified setae on the male third pleopod exopod. Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. No modified setae on exopod of male fourth pleopod. Modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines excluding the distal spines on uropod endopod ordered in groups. No spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod exopod grow between 1/2 and 1/3 of the distal outer margin. Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Apical plumose setae on the telson have extreme long secondary hairs. Three apical spines, equal in length on the telson. Telson is between 2 and 2.5 times as long as broad. Less than 20 lateral spines on the telson (including basal spines and spines next to the 3 apical spines). Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Nouvel (1957), Tattersall (1960)

4.52. Siriella spinula Panampunnayil, 1995

Diagnosis: Female (adult) smaller than 7 mm. Male smaller than 7 mm. Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. No distal joint on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes are small. Eyestalks are short. Eye about as broad as eyestalk. Eyes are not covered by the rostrum. Rostrum bluntly rounded with a spiniform pseudorostral process beneath it Rostrum with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Total length of dactylus and claw of eight thoracopod long (More than half of the length of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod normal (carpopropodus between 6 and 8 times as long as broad). Eight thoracopod carpopropodus undivided Base of outer margin of exopod of thoracopod eight normal (no denticle). No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral uropod endopod spines not gouped. Lateral spines next to the statocyst. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,2 and 2,8 times longer than the length of the distal segment. Spines on the proximal segment of the uropod

grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of uropod exopod of the male very short. Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Less than 20 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Panampunnayil (1995)

4.53. Siriella tadjourensis Nouvel, 1944

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eye clearly broader than eyestalk. Rostrum with straight margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Base of outer margin of exopod of thoracopod eight normal (no denticle). Some short curved setae and 5 or more long straight setae on the male copulatory organ. Plumose setae on the sympod of the first pleopod. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. The

endopod of the third male pleopod bears one straigt modified seta on the terminal segment. One thick long spiniform seta and one normal seta on the ultimate joint of the male third pleopod exopod. Modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Terminal setae on endopod of male pleopod 4: 2 more or less straight setae on ultimate joint (1 short (1/4-2/3) and 1 long). Exopod of male fourth pleopod with 1 long on the ultimate joint (normal setae reaching 2/3 or further)(+ 1 scarcely or not modified seta) + 1 on penultimate joint. Modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Distal segment of female uropod exopod normal (between 2 and less than 2,5 as long as broad). Apical plumose setae on the telson have extreme long secondary hairs. Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod. No black spots on lateral side of the abdomen.

Used literature: Nouvel (1944), Nouvel (1959), Nouvel (2004)

4.54. Siriella thompsoni (Milne-Edwards, 1837)

Diagnosis: Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Second segment of antennular peduncle about or more than three times as long as the third. Male antennular flagellum normal. Terminal lobe of the antennular peduncle hirsute. Eye clearly broader than eyestalk. Rostrum with concave margins. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Total length of dactylus and claw of eight thoracopod short (less than 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus slender. Copulatory

organ blunt . Sympod of first pleopod without plumose setae. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on third and fourth pleopod. Pseudobranchia of third male pleopod are spirally coiled. Spines including the distal spines on uropod endopod ordered in groups. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. More than 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Uropod exopod proximal joint with only spines. Distal segment of female uropod exopod short (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Telson spines grow distally longer. No secondary spinules present on the telson. The telson overreaches the margin of the distal joint of the exopod.

Remarks: Variations on the shape of the terminal spines of the telson were observed. According to the description (Coifmann, 1937) all three spines are equally developed. However, studied specimens showed twice a remarkably strongly developed median spine.

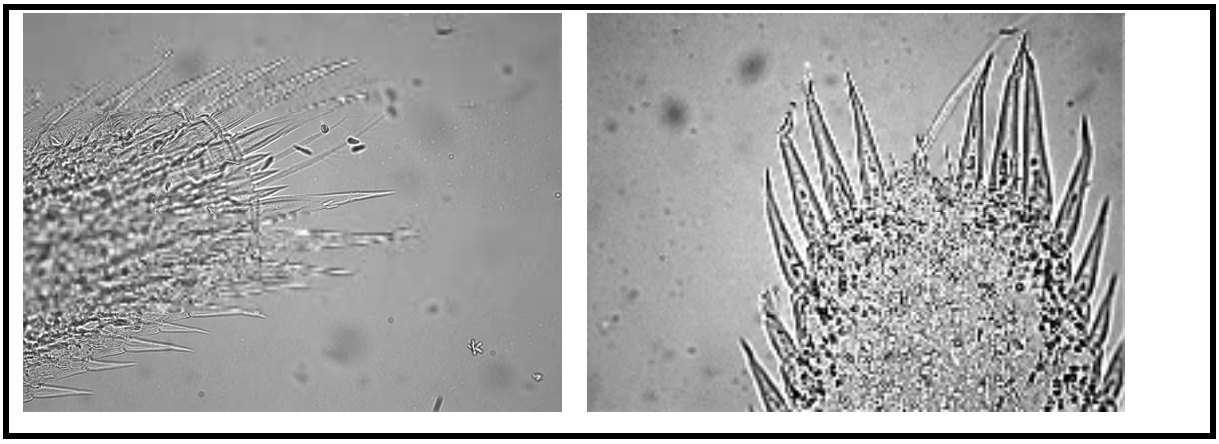


Figure 3 *S. thompsoni*: Light microscope photographs of variations in terminal spines on the telson: Left normal development, Right modified form

Used literature: Milne-Edwards (1837), Dana (1852), Paulson (1875), Czerniavsky (1882), Czerniavsky (1883), Hansen (1912), Coifmann (1937), Ii (1964), Pillai (1965), Pillai (1973), Stuck, Perry & Heard (1979)

4.55. Siriella trispina Ii, 1964

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Lateral margins of carapace grow anteriorly. Less than 1 somite is visible laterally. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Segment 1 and 2 of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. Eyestalks are short. Eye clearly broader than eyestalk. Rostrum bluntly rounded. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Rostrum with straight margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is excavated. Thoracopod five is elongated. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod slender (carpopropodus between 8 and 12 times as long as broad) Eight thoracopod carpus between 1/3 and half of the length of the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral uropod endopod spines not gouped. Lateral spines next to the statocyst. Between 20 and 39 spines on the uropod exopod. Uropod endopod with barbed spines. Exopod of the uropod

longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod grow distally between 1/3 and 1/6 of the outer margin. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Three apical telson spines forming a tridentate plate. First two pairs of subapical spines on the telson shorter than 1/3 the length of the apical spines. Telson with linguiform shape. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. No black spots on lateral side of the abdomen.

Used literature: li (1964)

4.56. Siriella tuberculum Fukuoka & Murano, 1996

Diagnosis: Female (adult) smaller than 7 mm. Male smaller than 7 mm. Carapax of female bears one protuberance anterior to the cervical groove. Lateral margins of carapace show no tendency to grow anteriorly. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale is between 3,2 and 3,8 times as long as broad. Terminal lobe of antennal scale about 3/4 as long as broad. Terminal lobe length of male antennal scale is about 3/4 its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle normal (without hairs upon). One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of moderate size. Eyestalks very short. Eye clearly broader than eyestalk. Eyes are not

covered by the rostrum. Rostrum is bluntly triangular (higth of the triangle between 1/3 and 1/2 of the base). Rostrum with straight margins. Second thoracopod normal. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod slender (carpopropodus between 8 and 12 times as long as broad) Eight thoracopod carpopropodus undivided Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Lateral uropod endopod spines not gouped. Pseudobranchia of fourth male pleopod are spirally coiled. Lateral spines next to the statocyst. Between 20 and 39 spines on the uropod exopod. Uropod endopod with barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Distal segment of female uropod exopod short (between 1,5 and less than 2 times as long as broad). Three apical spines, equal in length on the telson. Two basal spines on the telson. Telson with linguiform shape. Telson is between 2 and 2.5 times as long as broad. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Fukuoka ; Murano (1996)

4.57. Siriella vincenti Tattersall, 1927

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. No distal joint on the antennal scale. Terminal lobe of antennal scale between 3/4 and two times long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Black eyes. Eyes are small. Eyestalks square-like. Eye about as broad as eyestalk. Rostrum bluntly rounded with a spiniform pseudorostral process beneath it Rostrum lowly triangular (hight smaller than 1/3 of the base). Rostrum with straight margins. Second thoracopod normal. Eight thoracopod carpopropodus undivided No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on third and fourth pleopod. Pseudobranchia of third male pleopod are spirally coiled. Lateral uropod endopod spines not gouped. Pseudobranchia of fourth male pleopod are spirally coiled. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod between 2,2 and 2,8 times longer than the length of the distal segment. Spines on the proximal segment of the uropod grow distally to about or less than 1/6 of the outer margin. Proximal segment of the uropod exopod bears less than six spines. Three apical spines, equal in length on the telson. First two pairs of subapical spines on the telson equal in length to apical spines. Telson with three basal spines. Telson shape linguiform. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. Telson doesn't reach the margin of the distal joint of the exopod.

Used literature: Tattersall (1927)

4.58. Siriella vulgaris Hansen, 1910

Diagnosis: Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of scale with one terminal denticle. Female scale short. Terminal lobe of antennal scale between 3/4 and two times long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes are small. Eyestalks are short. Eye about as broad as eyestalk. Eyes are not covered by the rostrum. Rostrum with concave margins. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Total length of dactylus and claw of eight thoracopod moderate (Between half of the length and 1/3 of the carpopropodus). Dactylus longer than broad. Carpopropodus slender (carpopropodus between 8 and 12 times as long as broad) Carpus shorter than propodus, but more than half of the propodus. Base of outer margin of exopod of thoracopod eight normal. Copulatory organ blunt. Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. Sympod of first pleopod without plumose setae. No modified setae on second, third and fourth pleopod. Pseudobranchia on second male pleopod spirally coiled. Pseudobranchia of third male pleopod spirally coiled. Pseudobranchia of fourth male pleopod spirally coiled. Lateral spines next to the statocyst. Between 40 and 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Distal segment of female uropod exopod short (between 1,5 and less than 2 times as long as broad). Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Two basal spines on the telson. Telson with linguiform shape. Telson spines grow distally longer. No secondary spinules. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Hansen (1910), Pillai (1965), Murano (1990)

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Sixth abdominal segment less than 1,75 times the length of the 5th segment. Between 1 and 2 somites are visible laterally. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale short, less than three times as long as broad. Terminal lobe of antennal scale between 3/4 and two times long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. Male antennular flagellum normal. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes are small. Eyestalks are short. Eye about as broad as eyestalk. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum with concave margins. Dactylus and claw of second thoracopod are longer than the carpopropodus. Second thoracopod normal. Distal one third of the 6th segment of the endopod of second thoracopod is not excavated. Thoracopod five equal in length to others. Dactylus of thoracopod eight longer than broad. Carpopropodus of eight thoracopod normal (carpopropodus between 6 and 8 times as long as broad). Eight thoracopod carpus between 1/3 and half of the length of the propodus. Base of outer margin of exopod of thoracopod eight normal (no denticle). Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. Plumose setae on the sympod of the first pleopod. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines including the distal spines on uropod endopod ordered in groups. Endopod of uropod without

barbed spines. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod grow distally between 1/3 and 1/6 of the outer margin. Distal segment of uropod exopod of the male short (between 1,5 and less than 2 times as long as broad). Apical plumose setae on telson look normal. Three apical spines, equal in length on the telson. Two basal spines on the telson. Telson with linguiform shape. Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod No black spots on lateral side of the abdomen.

Used literature: Tattersall (1951)

4.59. Siriella wadai Ii, 1964

Diagnosis: Carapax of female without protuberances. Outer margin of antennal scale with one terminal denticle. Distal joint visible on the antennal scale. Female antennal scale short (less than 3,2 times as long as broad). Antennal scale short, less than three times as long as broad. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Spines including the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. Uropod endopod with barbed spines. Three apical spines, equal in length on the telson. Secondary spinules on the telson.

Used literature: Ii (1964)

4.60. Siriella watasei Nakazawa, 1910

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Distal joint visible on the antennal scale. Female antennal scale (between 3,8 and 4,5 times as long as broad). Antennal scale is between 3,8 and 4,5 times as long as broad. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Flagellum on male second antenna is swollen near the base. Eyes are small. Eyestalks are short. Eyes are not covered by the

rostrum. Rostrum is acutely pointed. Base of outer margin of exopod of thoracopod eight normal (no denticle). No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Proximal segment of the uropod exopod bears between 9 and 12 spines. Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Nakazawa (1910)

Siriella watasei koreana Ii, 1964

Diagnosis: Female (adult) between 7 and 12 mm. Male between 7 and 12 mm. Carapax of female without protuberances. Between 2 and 3 somites are visible dorsally. Lateral margins of carapace grow anteriorly. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Second segment of antennular peduncle between 2 and 3 times longer than the third. Distal joint visible on the antennal scale. Antennal scale is between 3,8 and 4,5 times as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Flagellum on male second antenna is swollen near the base. Segment 2 and 3 of the antennular peduncle of the male more or less same size as segment 1. Terminal lobe of the

antennular peduncle hirsute. Eyes of fresh specimens brown. Eyes are small. Eyestalks square-like. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Second thoracopod normal. Thoracopod five equal in length to others. Carpopropodus of eight thoracopod slender (carpopropodus between 8 and 12 times as long as broad) Carpus of eight thoracopod shorter than propodus, but more than half of the propodus. Copulatory organ blunt . Some short curved setae and 1 to 4 long straight setae on the male copulatory organ. No modified setae on second pleopod. Pseudobranchia on second male pleopod are spirally coiled. No modified setae on the endopod of the third male pleopod. No modified setae on the male third pleopod exopod. No modified setae on third pleopod. Pseudobranchia of third male pleopod are spirally coiled. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Pseudobranchia of fourth male pleopod are spirally coiled. Spines excluding the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. More than 60 spines on the uropod exopod. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod exopod grow between 1/2 and 1/3 of the distal outer margin. Distal segment of uropod exopod of the male normal (between 2 and less than 2,5 as long as broad). Three apical spines, equal in length on the telson. Four basal spines on the telson Telson with linguiform shape. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: li (1964)

Diagnosis: Carapax of female without protuberances. Antennal scale doesn't reach or hardly reaches the apex of the antennular peduncle. Outer margin of antennal scale with one terminal denticle. Antennular peduncle (2nd and 3rd segment) less or about 2/3 length of the antennal scale. Distal joint visible on the antennal scale. Antennal scale is between 3,8 and 4,5 times as long as broad. Terminal lobe length of male antennal scale is between 3/4 and two times its width. The tip of the terminal spine of the antennal scale clearly doesn't reach the distal joint Flagellum on male second antenna is swollen near the base. Segment 1of the antennular peduncle of the male more or less same size as segment 3. Terminal lobe of the antennular peduncle hirsute. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes of fresh specimens brown. Eyes are small. Eye clearly broader than eyestalk. Eyes are not covered by the rostrum. Rostrum is acutely pointed. Rostrum medium triangular (hight of the triangle more than 1/2 of the base). Rostrum with concave margins. Thoracopod five equal in length to others. Sympod of first pleopod without plumose setae. No modified setae on second pleopod. No modified setae on third pleopod. Endopod of fourth male pleopod does not bear modified setae terminally. No modified setae on exopod of male fourth pleopod. No modified setae on fourth pleopod. Spines excluding the distal spines on uropod endopod ordered in groups. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Proximal segment of uropod exopod shorter than 2,2 times the length of the distal segment. Spines on the proximal segment of the uropod exopod grow between 1/2 and 1/3 of the distal outer margin. Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Telson slender, between 2,6 and 3,2 times as long as broad. Between 20 and 40 lateral spines on the telson (including basal spines and spines next to the 3 apical spines) Telson spines grow distally longer. No secondary spinules present on the telson. Unarmed part of telson margin is more than half the telson width. The telson overreaches the margin of the distal joint of the exopod.

Used literature: Ii (1964)

4.61. Siriella wolffi Tattersall, 1961

Diagnosis: Female (adult) between 7 and 12 mm. Carapax of female without protuberances. Outer margin of antennal scale with one terminal denticle. Distal joint visible on the antennal scale. The tip of the terminal spine of the antennal scale reaches the distal joint but does not reach beyond the apex or doesn't reach the apex (if no distal joint is visible) Male antennular flagellum normal. Segment 1 of the antennular peduncle of the male is longer than segment 2 and 3 together. One plumose seta on the inner margin (not at the corner) of the 3rd segment of the antennular peduncle of the female. Eyes are large (cornea is about 2/3 of carapax width dorsally seen). Eyestalks are short. Eye clearly broader than eyestalk. Parts of the eye are covered by the rostrum. Rostrum is acutely pointed. Rostrum lowly triangular (hight smaller than 1/3 of the base). Rostrum with concave margins. Total length of dactylus and claw of eight thoracopod long (More than half of the length of the carpopropodus). Terminal setae on endopod of male pleopod 4: 2 on ultimate joint (1 long and 1 short (<1/2)). Modified setae on fourth pleopod. Spines including the distal spines on uropod endopod ordered in groups. Lateral spines next to the statocyst. Endopod of uropod without barbed spines. Exopod of the uropod longer than the endopod. Uropod exopod proximal joint with only spines. Spines on the proximal segment of the uropod extending proximally considerably beyond the middle. Proximal segment of the uropod exopod bears between 13 and 17 spines. Distal segment of female uropod exopod normal (between 2 and less than 2,5 as long as broad). Three apical spines, equal in length on the telson. Telson with three basal spines. Telson with linguiform shape. Telson spines are alternately arranged in length. No secondary spinules present on the telson. Unarmed part of telson margin is less than half the telson width.

Used literature: Tattersall (1961)

Tattersall (1951b) stated that the three pacific species *S. roosevelti, S. panamensis* and *S. pacifica* are closely related. According to Tattersall *S. panamensis* differs from the other species by its hooked terminal setae on the third pleopod.

S. roosevelti is described by Nouvel (1959) with relative straight setae on the third pleopod. A study on the available collection material of *S. roosevelti* (see Table 1) showed a large variation in the shape of terminal setae of the third pleopod. Observed variations are shown in figure 4, 5 and 6.

Similar observations were made on specimens identified as *S. pacifica*. A picture of the terminal setae on the third and fourth male pleopods is given in figure 7.

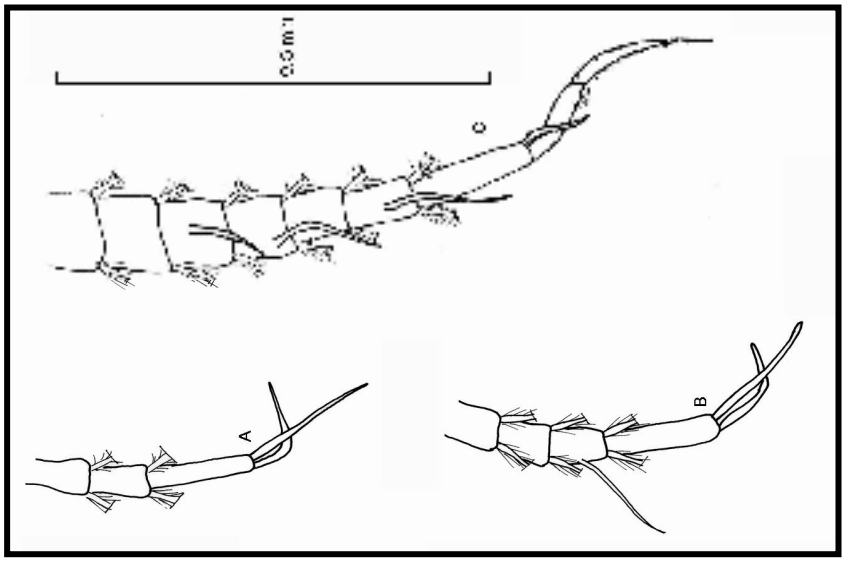


Figure 4. *S. roosevelti* a. modified setae on exopod of third male pleopod, b. modified setae on endopod of third male pleopod, c. exopod of fourth male pleopod

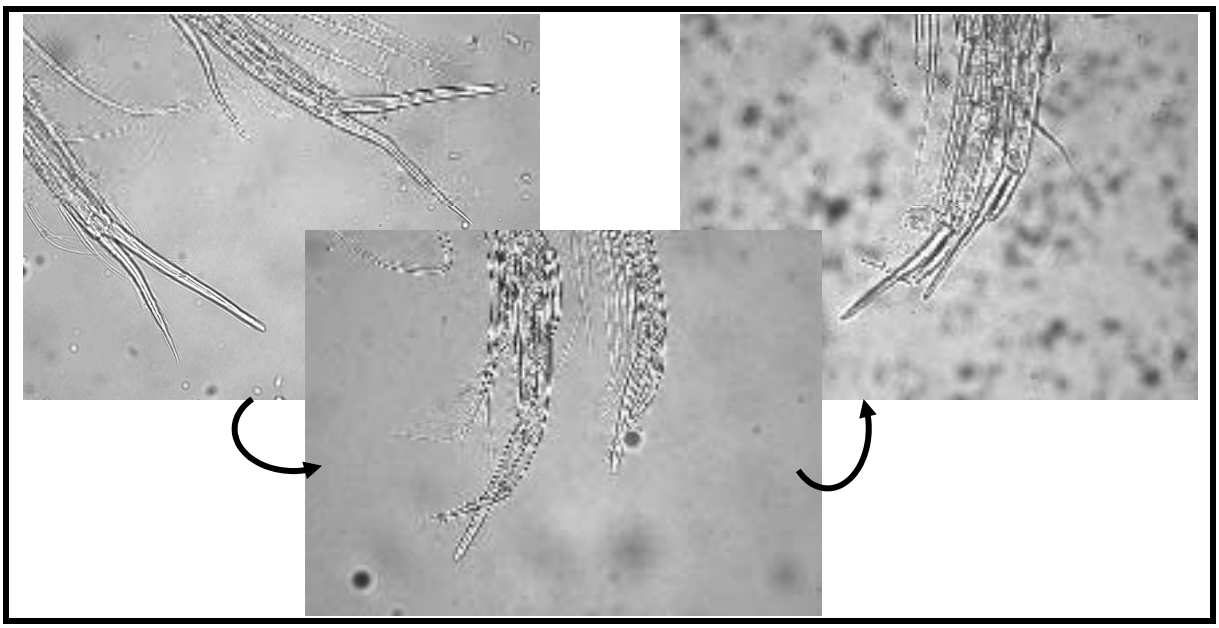


Figure 5. : *S. roosevelti*: different shapes of terminal setae on third male pleopod (x 200)

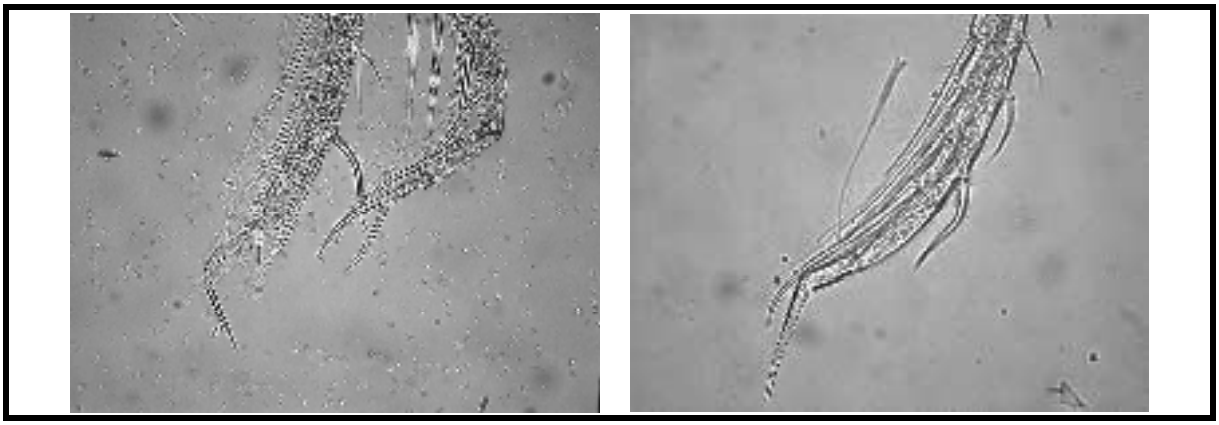


Figure 6. *S. roosevelti*: modified setae on fourth male pleopod (left:: exopod and endopod, right: endopod)

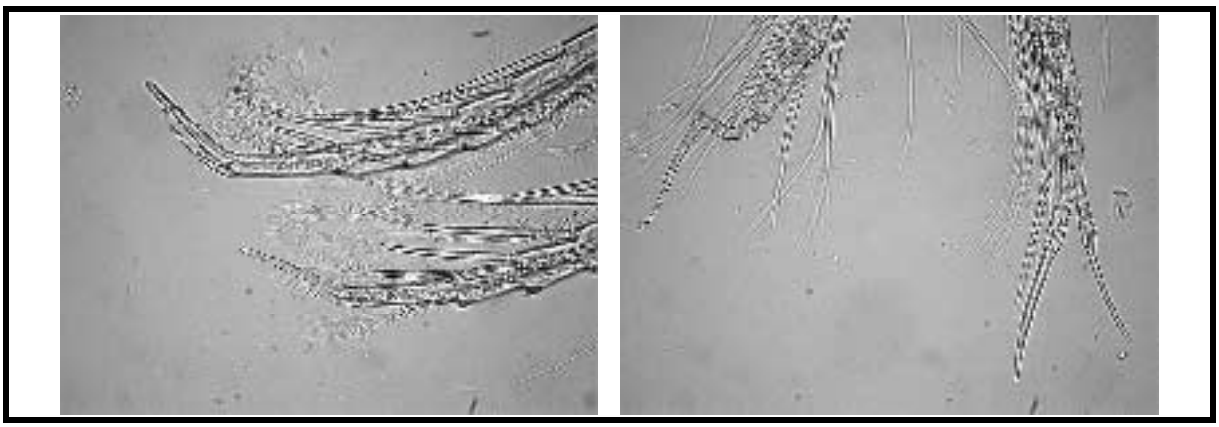


Figure 7. *S. pacifica*: Left: Modified setae on third male plepod (left endopod, right exopod), Right: modified setae on fourth male pleopod (left exopod, right endopod) (x 200)

5. Cladistic analysis

The parsimony analysis yields 16 trees of equal length (L: 527, CI: 31, RI: 55). When calculating the strict consensus tree, seven nodes collapsed. The resulting tree is displayed in figure 8.

Twelve species in the used matrix have a dubious place in the tree. For *S. conformalis, S. denticulate, S. intermedia, S. serrata, S. wadai, S. watasei* and *S. wolffi* less than 50% of all characters could be defined. *S. dubia, S. jaltensis, S. mello, S. paulsoni* and *S. thompsoni* have a high number of polymorphic characters and unknown characters.

In the presented tree eight monophyletic groups of species can be distinguished. Almost all branches are supported by moderate to high bootstrap values.

Group1: *S. armata*, *S. castellabatensis*, *S. clausi*, *S. dayi*, *S. gracilipes*, *S. jaltensis* and *S. norvegica* form a monophyletic group. Ii (1964) grouped these species in the the '*Thompsoni – armata*' group. Morphologically all species are characterized by a long and slender telson with three apical spines and between 40 and 60 lateral spines. Two plumose setae are present on the inner margin of the third segment of the antennular peduncle of the female. A denticle on the base of the outer margin of the exopod of eight thoracopod, at least three somites dorsally not covered by the carapax, and less than 20 lateral spines on the endopod of the uropod, are also typical features. Geographically all members except *S. dayi* occur in coastal European waters.

Group2: A second monophyletic group consists of *S. brevicaudata*, *S. halei*, *S. hanseni*, *S. lingvura*, *S. spinula, S. nodosa, S. jonesi, S. intermedia* and *S. vincenti*. The morphological distinguishing features of this group are: very short eyestalk, the antennal peduncle second segment is less than twice as long as the third segment, the total peduncle length is up to 2/3 the antennal scale length, the carpopropodus of the eight thoracopod is undevided, the carapax does not cover the last two or three thoracal segments, no modified setae on the third male pleopod, and the uropod exopod is longer than the endopod.

Group 3: The third clearly monophyletic group is formed by *S. aequiremis*, *S. anomala*, *S. conformalis*, *S. distinguenda*, and *S. robusta*. Most species are reported from the tropics and subtropics, both from coastal and oceanic areas. This group is morphologically characterized by straight pseudobranchia on the second, third and fourth male pleopod, enopod of third male pleopod without modified setae, two modified setae (1 long, 1 short) on the ultimate joint and one on the penultimate joint of the endopod of the fourth male pleopod, exopod of fourth male pleopod without modified setae, short eye stalks, exopod of uropod with 9 to 12 spines on the proximal joint, length of carpus of eight thoracopod between half length of propodus and length of propodus, slender carpopropodus of eigth thoracopod endopod, short distal segment of endopod uropod (male), distal end of sixth segment of the second thoracopod endopod excavated, segments 2 and 3 of male antennular peduncle equal in length to first segment, 1 to 4 long and some short setae on male copulatory organ.

Group 4: *S. chessi, S. roosevelti, S. pacifica, S. panamensis* and *S. chierchiae* form also a monophyletic branch characterized by the following morphological features: distal segment of exopod of uropod female between 1,5 and 2 as long as broad, the total length of the dactylus and claw of thoracopod 8 is more than half the length of the carpopropodus, carpus is about 1/3 of propodus length, carpopropodus is robust (smaller than 6 times as long as broad), the penis has a pointed shape, with strong spirally coiled setae, sympod of first male pleopod without plumose setae, third male pleopod with modified setae, and most of the species have the uropod exopod first segment between 2.2 and 2.8 as long as the second segment.

Group 5: A fifth monophyletic clade consists of *S. paulsoni, S. dollfusi* and *S. tadjourensis*. Mainly the carpus length of the eighth thoracopod which is between ½ and 1/3 the length of the propodus, and the shape of the distal segment of the male uropod exopod (between 2 and 2.5 as long as broad) define this group. Although the morphological evidence is not explecitely pronounced, all three species occur in Red Sea related waters. This areal is not unique for these three species.

Group 6: This small group also consists of three species: *S. mexicana, S. denticulate* and *S. macrophthalma*. The antennal scale of all species is between 3,8 and 4.5 times as long as broad, peduncle with segment 1 longer than total length of segment 2 and 3. Eight thoracopod endopod has an extremely slender carpopropodus. The male third pleopod exopod bears modified setae on each joint: two on the ultimate joint (1 strongly bent and one straight), one on the penultimate joint (sometimes with some additional smaller ones). Male pleopod 4 has 2 terminal setae on the ultimate joint, equal in length. On the penultimate joint one long and one short seta are present. The antepenultimate joint bears one very long terminal seta. Distal segment of male uropod exopod between 2 and 2.5 times as long as broad. The uropod endopod lateral spines are not grouped, no smaller spines in between large ones. All lateral telson spines are equal in size or in some cases grow longer posteriorly.

Group 7: This clade is formed by *S. trispina, S. tuberculum* and *S. brevirostris*. The rostrum of these species is described having straight margins. The telson is clearly shorter than the uropod exopod. It does not overreach the margin between the two segments. There are between 20 and 39 spines on the uropod endopod which are not grouped and distally clearly longer. Each of the species in this clade is has a long series of unique distinguishing characters, meaning species are morphologically grouped but still differ a lot from each other.

Group 8: Three species take part in this branch: *S. longidactyla, S. meltoi* and *S. thompsoni*. The antennal scale does not have a visible distal joint and the second peduncular segment is about or more than three times the length of the third segment. This branch is not supported in the bootstrap tree and hence it may be considered as a dubious group.

Group 9: This group is formed by *S. longipes, S. sinensis, S. japonica ,S. watasei, S. watasei macropsis, S. watasei koreana, S. japonica sagamiensis* and *S. japonica izuensis*. All species are only reported from Japanese waters. The exopod of the uropod only bears spines on the distal half of the proximal segment. Between 1 and 2 thoracal segments are not covered by the carapace. The antennal scale does not overreach the length of the antennular peduncle.

Group 10: This monophyletic clade is formed by *S. australis, S. quilonensis, S. singularis* and *S. dubia.* The rostrum is short bluntly triangular, and covers partly the eyes which are equally broad and long. The telson has less than 20 spines on the lateral side.

All other species are not clearly grouped with other species. Although *S. gracilis* and *S. pondoensis* form a small monophyletic pair, morphological evidence is very poor and dubious (spots on the carapace, number of segments not covered by the carapace). Other problematic species are *S. wadai, S. vulgaris, S. quadrispinosa, S. bacecui, S. okadai, S. afinis, S. wolffi, S. africana* and *S. australiensis*. Some of these species were already reported as problematic due to the low number of characters entered.

The genus *Siriella* is well defined by a large number of apomorphic characters (10). *S. wadai* is only poorly characterized and as a result is displayed as a sister taxon of all other species.

Group 2 forms a sister group of all other groups. Group 9 and 10 form a morphological related clade of which group 9 (including *S. okadai*) is typically bound to Japanese waters, while group 10 has a broader geographic range bound to eastern side of the Indian Ocean. Group 7 and 8 form two small clusters of species clearly differing from the largest clade in the tree. This clade is formed by three monophyletic groups: group 1 which is geographical bound to European coastal waters, group 3 which is mainly found in the East-Indies region (except *S. robusta* which reported from Indian coastal waters and *S. aequiremis* which globally also occurs in tropical oceanic waters). The the third group is less clear and consists of groups 4, 5 and 6.

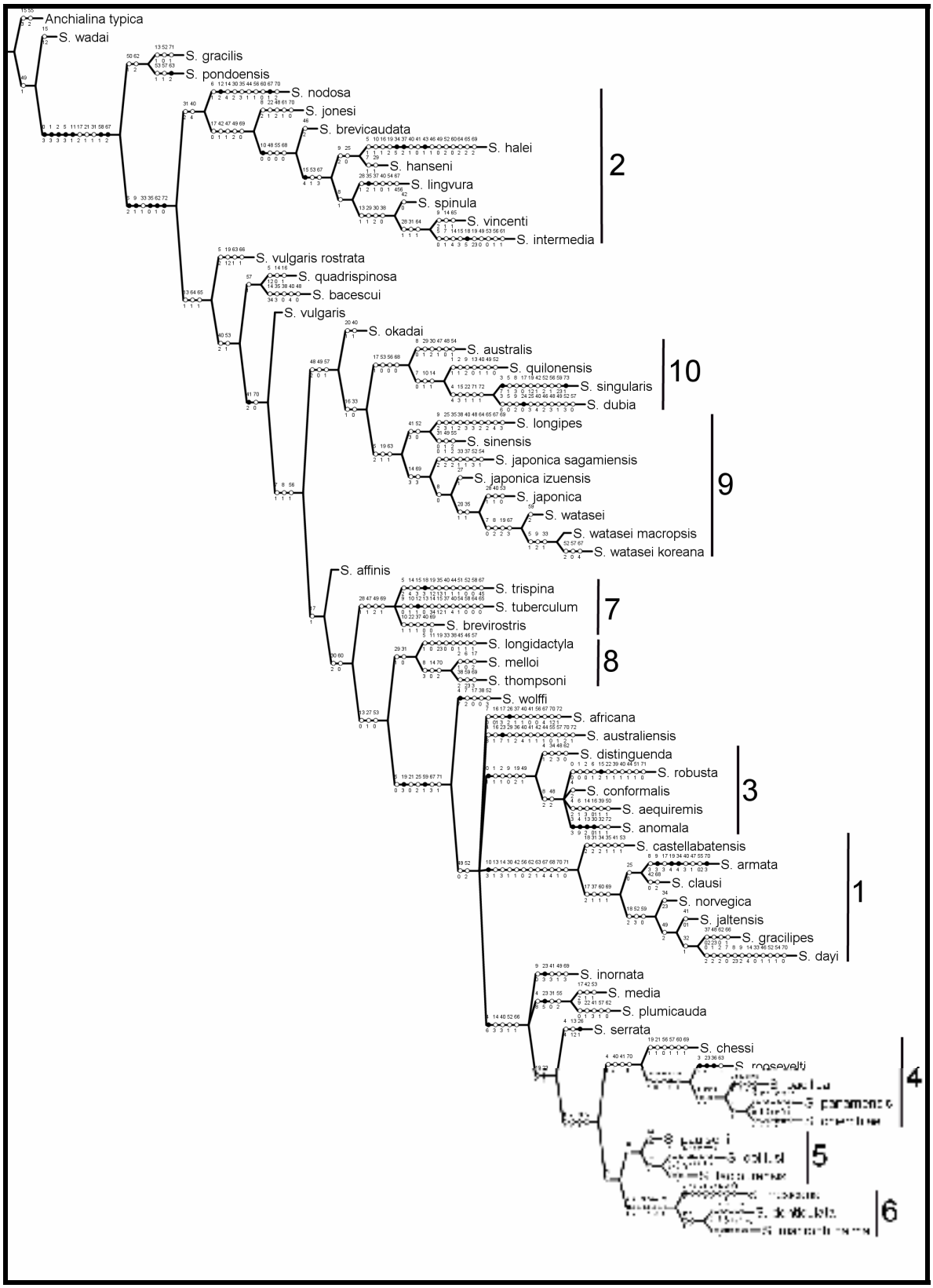


Figure 8. Strict consensus tree based upon morphological data without weighting of characters

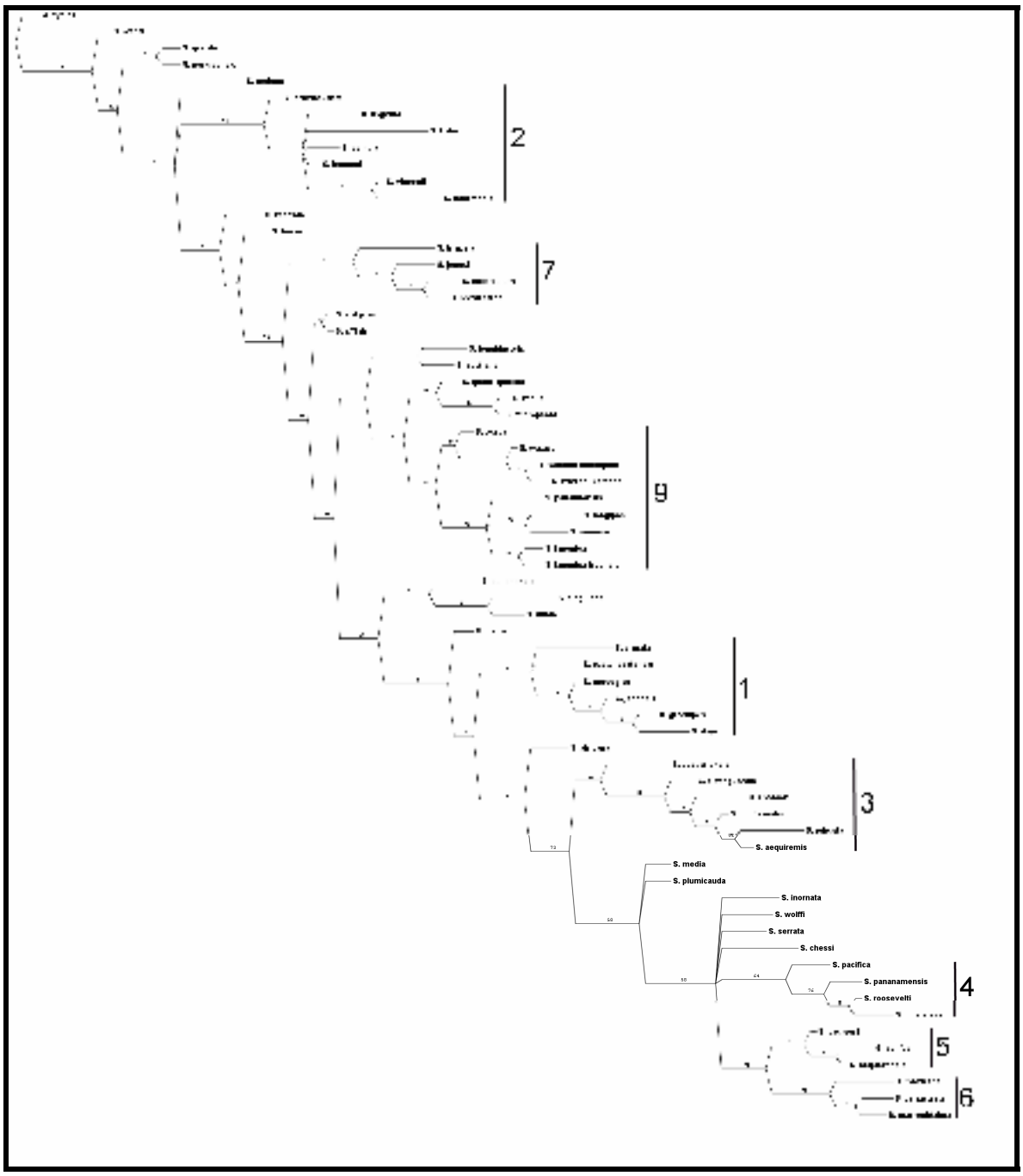


Figure 9. Bootstrap tree morphology

A comparison between the classification of Ii and the found phylogenetic groups is together with the distributions shown in table 3.

The '*Armata*' - group is a well defined monophyletic group, geographically distinct from all other *Siriella* species. It is strictly bound to European and East Atlantic coastal waters. The biogeographic border of this group is formed by the Agulhas Current, deviding hydrogeographically the Atlantic Ocean from the Indian Ocean. The '*Thompsoni*' – group is clearly paraphyletic and consists of 5 clades: (1) 'Group 2' is bound to Australian and Indo-pacific waters, (2) 'Group 7' has a strange distributional pattern (2 species are reported from Japanese waters, 1 species from the entrance of the Red Sea), (3) 'Group 9' grouping species all reported from Japanese waters, (4) 'Group 10' is bound to Central Indian Ocean, (5) 'Group 8' consisting of *S. thompsoni*, having a broad geographic distribution and *S. melloi* reported from South West Atlantic coastal waters.

The '*Australiensis*' – group is phylogenetically well supported and consists of three sister groups: 'Group 4', 'Group 5' and 'Group 6'. Geographically the '*Australiensis*' - group is globally spread with 'Group 4' being related to the East and West side of the Northern American continent, 'Group 5' occurring in the Red Sea and 'Group 6' reported from Australia and the Western Atlantic.

The '*Aequiremis*' - and '*Anomala*' - group form one monophyletic clade mainly occurring the West-Indies area, except for *S. aequiremis.*

Species described since the publication of the Ii-groups (1964) can based upon the phylogenetic analysis be assigned to a distinct group: *S. robusta* is assigned to the '*Aequiremis*'-group, *S. quilonensis* is assigned to the '*Thompsoni*' group, *S. denticulate* and *S. intermedia* are assigned to the '*Australiensis*'-group.

	II	Phylogeny	Geografic region
Siriella armata	Armata	1	North East Atlantic Ocean
Siriella clause	Armata	1	North East Atlantic Ocean
Siriella gracilipes	Armata	1	North East Atlantic Ocean
Siriella norvegica	Armata	1	North East Atlantic Ocean
Siriella castellabatensis	Armata	1	North East Atlantic Ocean + Mediterranean
Siriella jaltensis	Armata	1	North East Atlantic Ocean & South-Africa
Siriella dayi	Armata	1	East Atlantic ocean & South Africa
Siriella vincenti	Thompsoni	2	Southern Australia
Siriella halei	Thompsoni	2	Southern Australia
Siriella spinula	Thompsoni	2	Southern Australia
Siriella hanseni	Thompsoni	2	Indo-Pacific region
Siriella lingvura	Thompsoni	2	Indo-Pacific region
Siriella brevicaudata	Thompsoni	2	Indo-Pacific region
Siriella robusta	-	3	Indo-Pacific region
Siriella aequiremis	Aequiremis	3	Common
Siriella conformalis	Aequiremis	3	Indo-Pacific region
Siriella distinguenda	Aequiremis	3	Indo-Pacific region
Siriella anomala	Anomala	3	Indo-Pacific region

Siriella jonesi	Thompsoni		Indo-Pacific region
Siriella trispina	Thompsoni	7	Indo-Pacific region
Siriella tuberculum	Thompsoni	7	Indo-Pacific region
Siriella brevirostris	Thompsoni	7	Indo-Pacific region – Red Sea
Siriella watasei	Thompsoni	9	Indo-Pacific region
Siriella watasei koreana	Thompsoni	9	Indo-Pacific region
Siriella watasei macropsis	Thompsoni	9	Indo-Pacific region
Siriella japonica	Thompsoni	9	Indo-Pacific region
Siriella japonica izuensis	Thompsoni	9	Indo-Pacific region
Siriella japonica sagamiensis	Thompsoni	9	Indo-Pacific region
Siriella longipes	Thompsoni	9	Indo-Pacific region
Siriella sinensis	Thompsoni	9	Indo-Pacific region
Siriella quilonensis	-	10	Indo-Pacific region
Siriella australis	Thompsoni	10	Southern Australia
Siriella thompsoni	Thompsoni	8	Common
Siriella melloi	Thompsoni	8	West Atlantic
Siriella macrophthalma	Australiensis	6	West Atlantic
Siriella mexicana	Australiensis	6	West Atlantic
Siriella denticulata	-	6	Southern New Zealand
Siriella dollfusi	Australiensis	5	Indo-Pacific region – Red Sea
Siriella paulsoni	Australiensis	5	Indo-Pacific region – Red Sea

Siriella tadjourensis	Australiensis	5	Indo-Pacific region – Red Sea
Siriella pacifica	Australiensis	4	Eastern Pacific – California
Siriella panamensis	Australiensis	4	Eastern Pacific – Tropical
Siriella roosevelti	Australiensis	4	Eastern Pacific – Tropical
Siriella chessi	Australiensis	4	Western Atlantic Ocean
Siriella chierchiae	Australiensis	4	Western Atlantic Ocean
Siriella australiensis	Australiensis		Southern Australia
Siriella Africana	-		Eastern Atlantic Ocean – South Africa
Siriella wolffi	-		Eastern Atlantic Ocean – West coast Africa
Siriella quadrispinosa	Thompsoni		Indo-Pacific region
Siriella okadai	Thompsoni		Indo-Pacific region
Siriella intermedia	-		Indo-Pacific region
Siriella singularis	-		Indo-Pacific region
Siriella dubia	Dubia	10	Indo-Pacific region
Siriella gracilis	Thompsoni		Common
Siriella pondoensis	Thompsoni		Indo-Pacific region - Zuid-Afrika
Siriella inornata	Inornata		Indo-Pacific region
Siriella media	Inornata		Indo-Pacific region
Siriella plumicauda	Inornata		Indo-Pacific region
Siriella serrata	Inornata		Indo-Pacific region – Red Sea
Siriella bacescui	Thompsoni		Indo-Pacific region - North-Australia

Siriella longidactyla	Thompsoni	8	Eastern Australia
Siriella affinis	Thompsoni		Indo-Pacific region
Siriella nodosa	Thompsoni		Indo-Pacific region
Siriella vulgaris rostrata	Thompsoni		Indo-Pacific region
Siriella wadai	Thompsoni		Indo-Pacific region
Siriella vulgaris	Thompsoni		Indo-Pacific region + West South America

Table 3. Summarising table showing Ii groups, phylogenetic groups and geographical distributions

6. Geographical distributions

The distribution of Siriella species is latitudinally restricted (Figure 10). The most Northern record is at 63° North (Tattersall, 1951), while the most Southern record is reported from 47° South (Tattersall, 1957). A comparison of the found distribution with the biogeographical marine regions as used by Proches (2001) (after Briggs (1974)) shows that *Siriella* does not occur in the Arctic zone, the Sub-Antarctic zone, the Southern South America zone, and the Antarctic zone. Borders of these zones, based upon hydrographic characteristics (e.g. temperature), follow the distribution of the genus.

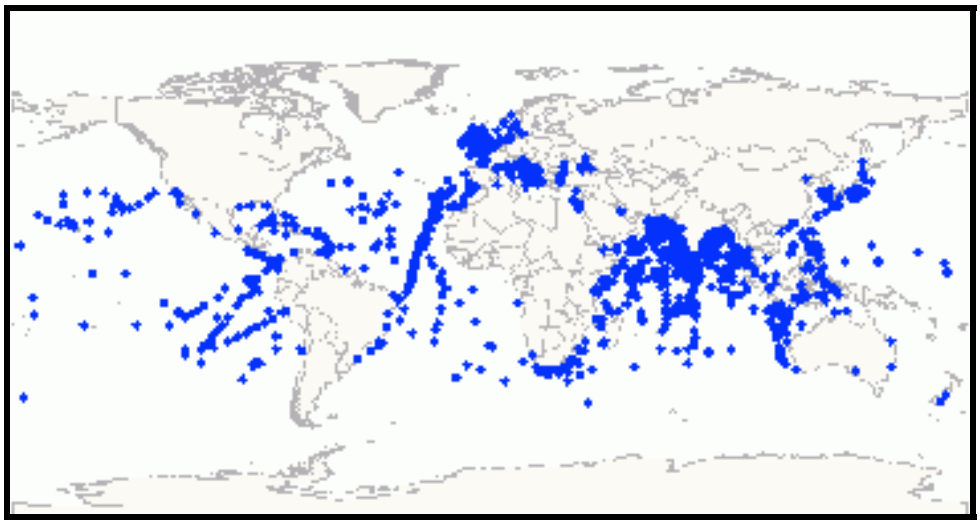


Figure 10. Distribution records of the genus *siriella*

Table 4 summarises the most species rich seas. When also taking into account the surface of these areas, it is clear that the East-Indies (Philippine Sea, South China Sea, Flores Sea, Sulu Sea, Celebes Sea) are the most species rich area.

The 4513 available distribution records were assigned to the Briggs biogeographical regions (Briggs, 1974). When species compositions were equal, the neighbouring regions were combined in one region. The East Atlantic Boreal zone and the Mediterranean Atlantic zone were grouped as the East Atlantic Northern Zone. The tropical westatlantic and the Northern part of the Gulf of Mexico were combined as the West Atlantic Zone. A third combined zone is the Indo-Pacific zone consisting of Japan, the Western Pacific Boreal Zone and the Indo-West Pacific zone. The Red

Sea fauna and the fauna of Northern Australia were remarkely different and are thus treated as separate zones.

Area	# species
Philippine Sea	16
South Atlantic Ocean	14
North Pacific Ocean	13
South China Sea	10
Flores Sea	9
Eastern China Sea	9
North Atlantic Ocean	9
Sulu Sea	8
Laccadive Sea	8
Indian Ocean	8
Celebes Sea	7

Table 4. Top species rich seas

Three species have a wide distribution: *S. aequiremis, S. gracilis*, and *S. thompsoni.*

The largest species diversity is observed in the Indo-Pacific region with 39 species. Except for *S. vulgaris* and *S. jaltensis,* all species are restricted to one biogeographical zone. *S. vulgaris* does occur in both the Indo-Pacific region and the West-Coast of South America (1 observation). *S. jaltensis* is common for European waters but is also reported from South-African waters.

7. Identification key

Through the NeMysKey© hosted on the NeMys biological information system, a polytomous identification key was created. This key uses 82 characters, of which many equal those used for the phylogenetic analysis.

Eastern Atlantic Ocean	Northern zone	*S. armata, S. clausi, S. castellabatensis, S. gracilipes, S. jaltensis, S. norvegica*
	West Coast Africa	*S. wolffi*
	South Africa	*S. africana, S. jaltensis, S. dayi*
Western Atlantic Ocean	Tropical region	*S. chessi, S. chierchiae, S. macrophthalma, S. melloi, S. mexicana*
Eastern Pacific Ocean	California region	*S. vulgaris, S. pacifica*
	Tropical region	*S. panamensis, S. roosevelti*
Western Pacific Ocean	North Australia	*S. bacescui, S. wadai*
	Indo-West pacific	*S. affinis, S. japonica sagamiensis, S. robusta, S. anomala, S. jonesi, S. sinensis, S. brevicaudata, S. lingvura, S. singularis, S. conformalis, S. longipes, S. trispina, S. distinguenda, S. media, S. tuberculum, S. dubia, S. nodosa, S. vulgaris rostrata, S. hanseni, S. okadai, S. wadai, S. inornata, S. pondoensis, S. watasei, S. intermedia, S. plumicauda, S. watasei koreana, S. japonica, S. quadrispinosa, S. watasei macropsis, S. japonica izuensis, S. quilonensis*
	Southern Australia	*S. australiensis, S. australis, S. halei, S. longidactyla, S. spinula, S. vincenti*
	Southern New Zealand	*S. denticulate*

Table 5. Species composition of biogeographic zones (after Briggs, 1974)

8. Discussion

8.1. COMMENTS ON THE USED METHODOLOGY

The most accurate scientific way for assessing morphological phylogenetic patterns is by studying the specimens of each species in a standardized way. Phylogenetic analyses currently are mostly performed on molecular datasets, in few cases combined with morphological data. (Schubart *et al.*, 2000; *Giribet et al.*, 2001). During the setup of this study, it was attempted to obtain specimen material for as many as possible species. Only four of the about hundred contacted museums were able to provide specimens. This may be one of the reasons why no revisional study on this group of mysid shrimps has been done yet. Moreover, type material could hardly be found in these collections, and if available, it was not allowed to be used for morphological studies requiring the *dissection* of the specimen. As only a limited amount of data could be retrieved through the study of specimens, the dataset was completed with data derived from literature. This implies that data quality of the presented dataset is strongly related to the quality of the observations of the different authors of the studied literature. Older publications often lack detailed descriptions of all morphological features (e.g. Hansen, 1910) and many species have not been revised since the original publication (e.g. *S. conformalis, S. plumicauda, S. wolffi*…).

The biogeographical dataset, also based upon a combination of literature and collection data, has similar problems concerning data quality. The main problem with geographical data is the limited research effort for many regions (see chapter 4). Hence, the observed distributional patterns need to be interpreted with some scepsis. It is clear that regions, which were scoped for much research, also show a much clearer picture of biogeographical patterns. Only species presence can as such be taken into account (for most regions no absence data is available). The observed distributional patterns may lead to the conclusion that for many more unexplored regions still more new species may be found and more records of known species will be added.

The used phylogenetic method for calculation of trees can be discussed. However, there is no consensus on which methodology to use for this kind of studies. Some publications use 'Strict consensus' trees (Ariani, 2002), while others use 'Majority rules' trees (Bitsch & Bitsch 2002). Also the used parameters (number of replications, number of trees to hold, methodology of tree calculation) differ in the available literature (Richter & Scholtz, 2001; Arango, 2002; Bosselaers & Jocqué, 2002; Carvalho & Salles, 2004). During the preparation of this study different methods have been tested and compared. The presented tree uses the parameters resulting in the most parsimonious trees for this particular dataset. Tree generation strategies can easily be changed, in order to get a tree showing nice phylogenetic patterns. A common methodology on how to calculate trees for different types of datasets would be very usefull.

Most currently published phylogenetic analyses use data matrices with each character having only few states, with a bias to characters having only one matching state for each taxon. The presented dataset uses many polymorphic multiple state characters. Notwithstanding this rare method, the analysis resulted in usefull phylogenetic patterns. This proves that characters with multiple states are also phylogenetically relevant as stated earlier by Wiens (1999).

The value of a boostrap tree is discussable: depending on the used parameters for calculating the trees, both nice trees and unrelevant trees can be found. Scotland (2003) puts forward that morphology based dataset will hardly produce nice bootstrap values, as the number of characteristics used is much lower than in molecular based phylogenetic studies.

▪ 8.2. BIOGEOGRAPHY

The interpretation of the geographical patterns is strongly related with the number of records and the number of studies conducted in each region. This study only focuses on one genus, and as a consequence it is impossible to use research-effort-independent techniques (i.e. Taxonomic Distinctness Diversity index (Clarke & Warwick, 1998)) These techniques relay on the variation in higher taxonomic levels of the observed taxa in a region.

However, there are some clear conclusions that can be drawn: (1) the distribution of members of the genus is restricted to warm and moderate waters, (2) the East-Indies area is the most speciose area, (3) many species have a distribution bound to hydrographic boundaries.

As shown in the results section, *Siriella* species occur only in a limited lattitudinal range, matching the biogeographical areas defined by Briggs (1974) (except the most Southern and Northern ones). The Northern species can occur in relatively colder waters. Southern species are observed in warmer waters, although this may be related to the lower research effort in the area.

Some species are bound to rather small areas. The Gulf of Aden is known as an area of faunal change. The entrance to the Red Sea is very shallow. This may be a geographical barrier for many taxa. Due to strong evaporation, he Red Sea is more saline than the surrounding areas (Cox & Moore, 2005). Five species of the genus *Siriella* are endemic to this area.

The eastern coastal areas of South America also show clear barriers. The mouth of the Orinoco and Amazone largely influence the salinity and sedimentology of the neighbouring coastal areas. No *Siriella* species are currently reported from these areas, although many data is available from the neighbourhoods of these two rivers (see http://www.nemys.ugent.be). A same influence could be expected from the Yang Tsé River, having its mouth in the Eastern Chinese Sea. Yet a shift in species composition is not observed. This may be explained by the much broader continental shelf area in the Chinese Sea compared to the South American

coastline. Data from similar regions, like the mouth of the Congo-river are not available yet.

Two species are reported from the Suez Canal: *S. brevicaudata* and *S. serrata*. This observation proves that the Suez Canal may act as a migration route between the Indian Ocean and the Mediterranean Sea. No records from these species are however available yet from the Mediterranean Sea. This possible migration route was also described for 50 fish species, 40 molluscs and 20 other crustaceans (Cox & Moore, 2005). Species crossing the Suez Canal need to be adapted to hypersaline muddy conditions.

A similar migration route could be expected in the Panama Canal, connecting the Atlantic and Pacific Ocean. However, this has not been described yet. Possible reasons for this are the freshwater environment in the canal and the large number of physical barriers (sluices).

In general it is assumed that biodiversity of continental shelve regions is much richer than the diversity of oceanic regions (Cox & Moore, 2005). Also for the genus *Siriella* and many other Mysid-genera this seems to be true (see chapter 4). Only three species were reported from oceanic waters while all others are restricted to coastal waters. The three oceanic species were also reported from coastal areas.

Fossil records of the genus *Siriella* from about 160 MA (Middle Jurassic) (*Siriella antiqua* and *Siriella carinata*) strongly resemble the current known *Siriella* species (Fisher, 2003 & http://paleodb.org/cgi-bin/bridge.pl?action=displayCollectionDetails&collection_no=58221). This illustrates that some *Siriella* species might already exist for about 160 -180 Million Year. Secretan and Riou (1986) even suggest that for many recent crustacean groups the morphological features are relatively stable since the Jurassic period. During the Jurassic all continents were still connected and as such all coastal areas were still connected. The age of *Siriella* species and the observed distributions may be explained following some of the concepts stated by Heads (2005). He suggests that current observed patterns in marine biogeography are mainly due to the Darwin-Wallace biogeographical paradigma (spreading from a center of origin) and the vicariance hypothesis. The vicariance hypothesis argues that speciation takes place

when populations break up due to changes in the environment (for example tectonic events). According to the Darwin-Wallace paradigma the East-Indies are considered as the marine center of origin. The distributional areas of the observed phylogenetic groups (Indian Ocean, Pacific Ocean and Atlantic (Thetys) ocean) cross this region and may hance be indicative for the vicariance hypothesis.

Assuming the East Indies are indeed the center of origin for these species about 160 million years ago some of the observed distribution patterns may be explained:

(1) Phylogenetic 'Group 1' is a relatively old branch, originated during the middle Jurrasic period, and speciated due to the existence of the Atlantic Ocean and the closing of the connection between the East-Indies area and the current Northern Atlantic areas. The close relationship with other small groups linked with the current East-Indies may prove this.

(2) 'Group 5' clearly speciated during the formation of the Red Sea area. Members of this group are morphologically variable. This may be explained by the high number of specialised habitats in this area.

(3) 'Group 4' was formed before the closing of the Panama Isthmus. Representatives of this group occur at both sides of this Isthmus.

(4) 'Group 8' and 'Group 6' are probably formed after the closing of the Panama-Isthmus. Both groups have representatives from the Western Atlantic, but are not reported from the Eastern Pacific coast.

The distributions of *S. jaltensis* and *S. vulgaris* are difficult to explain with the presented hypotheses. *S. jaltensis* is known for its large morphological variability. Measurements even showed that the variation within a population is analogue to the variation between two other species. Possibly *S. jaltensis* is not one species but consists of several cryptic species. *S. gracilipes* was formerly also described as a variation of *S. jaltensis*. The records from South Africa may belong to a cryptic species resembling *S. jaltensis*, or may be a misidentification. *S. dayi* was also described from South Africa and is very similar to *S. jaltensis*. The records of Tattersall (1958) may be *S. dayi* or a cryptic *S. jaltensis* - like species. Only molecular pylogenetic analysis on all members of the *S. jaltensis* species

complex may prove this. *S. vulgaris* is reported once from South America. A possible misidentification may explain the strange biogeographical distribution of this species. More records from the South American coastline may prove whether this species indeed occurs in this region.

The combination of the Darwin-Wallace concept and the vicariance hypothesis can explain the observed distributions for this genus. Not using the vicariance hypothesis would imply that species have cross-ocean dispersal mechanism. In order to prove whether the explained hypothesis indeed explain the distributions of this genus, a molecular study using molecular clocks should be conducted.

- *8.3. PHYLOGENY*

Although all goups are well supported, the original classification by Ii (1964) and Hansen (1910) may, based on the found phylogenetic patterns, be slightly adopted.

The '*Australiensis*' - group is well supported by the phylogeny and consists of three smaller groups with a distinct biogeographical range.

The '*Armata*' - group is also well-defined as one monophyletic branch in the tree.

The '*Thompsoni*' - group consists of five monophyletic groups (2, 7, 8, 9, 10). However these five groups are not all sister-groups and consequently the '*Thompsoni*' - group may be treated as paraphyletic. Dividing the '*Thompsoni*' group in three groups is in terms of morphological clear characters rather difficult. It is impossible to find one clear characteristic unique for each group. Only a long combination of morphological features can describe each sub-group. As such the definition of the '*Thompsoni*' - group is remained.

The '*Aequiremis*' - and '*Anomala*' - group are not distinguishable from each other. The '*Anomala*' - group has only one representant and both *S. anomala* and the members of the '*Aequiremis'* - group occur in the Indo-Pacific region. Consequently it is not longer supported to maintain the two 'Ii' groups.

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10. Appendix 1: Morphological data matrix used for phylogenetic analysis

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
A. nigra	?	?	0	0	0	0	?	0	0	?	?	?	0	0	?	A	?	1	?
S. aspersa	1	1	?	0	2	031	1	132	?&2	021	023	1	0	0	2	031	03?	03?	1
S. bilobata	?	?	?	0	0	25?	1?&	021	031	121	?&2	1	0	031	25?	0	1?&	??	1
S. cristata	?	?	?	?	^	0	?	0	031	0?0?0	?	1	0	0	0?0	0	?0?	?	1
S. crystallina	1	1?&	1?0	0	?	0	?	1?2	023	0	023	1	0	2	?	0	?	1	1
S. dentata	?	?	?	0	0	0	?	021	?	?	1?2	1	0	1	5??	0	?	?	?21
S. eurystoma	?	?	0	0	0	0	?	?	1	?	?0?	1	^	0	?	0	1	1	1
S. expansa	3	?	^	0	0	?	?	?	0	1	?&2	1	0	1	?	0	1	1	1
S. fimbriata	3	?	?	0	0	3	1?&	?	0	021	2	1	0	1	5??	0	?	?	1
S. brandaueriana	?	?	0	0	0	0	?	?21	0	?02	0	1	031	031	230	0??	?	1?&	?2
S. hemistoma	3	?	?	0	0	?	_	?	1	121	1	1	1	031	_	031	_	1??	1
S. nanocarinata	3	?	?	0	0	0	?		1	1?2	3	1	0	1	?	031	?	1	?
S. obtusa	?	?	0	0	1	0	?	?	1	1	?	1	0	0	?	0	?	1	1
S. otostoma	3	?	?	1	?	0	_	121	031	03?&2	123	1	0	0	12?&?	0	_	03?&2	1
S. planospira	?	?	?	0	0	0	?	?21	031	?02	?0?	1	0	1	?	0	?	?	?A ?A1
S. rotundata	1	1	?	0	?	0	?	?	?	?	^	?	^	031	?	0	?	1	1
S. step	?	?	?	0	0	0	?	0	25?	?	?2?	1	?	1	1	0	?	?	?
S. striatula	?	?	?	?	'	1	?		0	?02	?	?	'	031	?	0	1	1	1
S. strigella	1	1	?	0	1	0	?	132	1	?	?	1	0	0	?	0	?	1	1
S. subtilis	?	?	?	?	?	0	?	?21	031	1	?	1	0	0	?	?0?&?	?	??	1
S. sulcata	?10	?10	?10	0	1?&?1	0	1??	?21	?	?	??	1	0	031	?0?	11?10	1??	?0?	1??
S. ventricosa	3	?	?	0	0	0	?	?21	1	132	?&2	1	0	031	03A	035	?	1??	?
S. zonata	?	?	?	0	0	?	_	0	031	1?2	?&2	1	0	1	25?	?&1?2	?	?	1
A. bella	1	?	0	0	0	1	?	0	0	?	1	1	0	0	?	A	1	?	1
A. lamarcki	3	?	?	0	0	?	?	?	031	?	0	1	0	0	?	A	?	?	1
A. lamellata	3	?	?	0	?	0	?		?2	?	?	1	?	031	25?	0	?	?	1
A. leucostoma	?	?	?	?	^	0	?	?	^	?	0	1	0	^	A	0	?	?	5
A. pulchra	0?0	0?0	0?&	0	0	0	_	1?1	031	1?2	1?2?&	1	0	031	03A	031	_	0?0	0?2
A. pygmaea	3	?	?	0	0	?	?		0	1	?	1	0	1	?	0	?	?	1
A. pygmaea brevis	?	?	0	0	0	?	?	?	0	1	?	1	0	1	?	0	?	?	1
A. pusilla	0?0	0?0	0?&	0	0	?	1?&	0	?	1?2	?&2	1	^	0	?	1?1?0	1?&	0??	1
A. rupestris	?	?	?	0	0	^	?	?21	?	1	?	1	0	^	?&1	A	?	?	1
A. scalaris	3	?	?	0	?	0	?	?21	1	1?2	?&2	1	0	031	230	0	?	?	1
A. similis	?	?	?	0	0	?	?	?	?	?	?	1	^	0	?	0	?	1	1
A. solida	3	?	?	1	?	0	?	0	0	?21	0	1	0	031	?	031	?	?	1
A. subcarinata	?	?	?	0	0	?	?	?21	031	1?2	?&2	1	0	1	?	0	?	?	1
A. subplana	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
A. subrugosa	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. sulcata	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. tenuicostata	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
A. tenuilabris	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
A. tenuis	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. tumida	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. turbinata	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. turgida	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. umbilicata	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. umbrosa	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. undulata	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. vicina	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. vicinoides	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. vitrea	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. vitrinoides	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1
A. zonata	3	?	?	0	0	?	?	?	0	?	?	1	0	031	25?	0	?	?	1

	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61
A. lignicolor	0	0	0	0	0	0	0	0	0	0	0	0	-	0	0	0	0	0	0	0	0
C. nodulosa	2	2	0&1	0	0	0	0&1	0	2		1	0&1	0&2	0&1	1	1	1	0	1	1	1
D. subtilis	2	2	0	0	0	0	0	0	0&1	0&1&2	0	0	0&1	-	0	1	0&1	0	1	0	0&1
G. citrinum	1	0	0	0	0	0	0	0	1	0&2	0	0	2	0	0	0	0	0	1	0&1	0
H. cinereus	2&3	2&3	0&1	0	0	0	0	0	2&3	0&1	0	0	0&2&3	0&1	1	1	1	0	1	0&1	0&1
H. cremeus	3	0&1&2&3	1	0&1	0	0	0&1	1	0&1&2	0&2	0&1	0	0&2&3	0&1	0	0&2	0	0&1	1	1	1
H. versiformis	4	1	1	0	1	0	0	0	0&1	0	0	0	2	0	0	0	1	-	1	0	0
H. varians	2	-	0	0	-	0	0	1	0	0	0	0		0	0	0	0		1	0	0
H. pseudocinereus	4	0&1	0	0	0	0	0	0	0	-	0	0	0	-	0	0	0	-	1	0	0
P. multiseptata	4	1&2&3	0&1	0	0	0	0	1	0	0	0&1	0	0&2&3	0	0	0	0&1	0	1	0	0
S. acuminatus	0	0&2	0	0	0	0	0	1	1	2	0	0	0&1	-	0	1	1	0	1	0	0
S. cucullatus/cucullatus	2	1	1	0	0	0	0	0	0	0&2	0	0	2	-	0	0	0	0&1	1	0&1	0
S. dentata	0	1	0	0	0	0	0	0	1	0	0	0		0	0	1	0		1	0	1
S. dentatus	0&1	0	0	0	0	0&1	0	0	0&1	0&1	0	0	1&2	0&1	0	0	1	0	1	0&1	0
S. emodi	2&3	2&3	0	0	0	0	0	0	0&1	0	0&1	0	2&3	0	0&1	0	2&3	0&1	1	1	1
S. fasciculata	-	-	?	?	-	?	-	?	?	-	?	-	-	-	?	?	1	-	?	?	?
S. fusi	0	0	?	?	0	?	1	0	1	2	?	0	-	0	1	0	0	0	1	?	0
S. globulosa	0	0	?	?	0	?	0	?	0	?	?	0	0	0	?	?	1	0	?	0	0&1
S. heterosporus	0	0&2	0	0	0	0	0	0	2	0	0	0	-	0	0	0	0	0	1	0&1	0
S. indica	4	-	0&1	?	0	?	?	0&1	3		?	0	3	0&1	0	0&1	0	0	1	?	0
S. javanica	2&3	1&2&3	1	0	0	0	0&1	0	2&3	2	0	0	2	0&1	0	0	0&1	0&1	1	0	0&1
S. jenkinii	1	0	0	0	0	0	0	0	0&1	0&1	1	0	0	0&1	0	0	0	0	1	0	0&1
S. kamatii	1	0	1	1	0	?	1	1	-	0	?	0	>		?	?	0	0	1	0	0
S. kenyana	4	-	0	0	-	0	0	1	0	2	0	-	2	-	0	0	0	0	1	0&1	1
S. kiliensis	0	0	0	0	0	0	0	0&1	0&2	-	0	0	-	0	0	0	1	0	1	0	0
S. leptocephala	4	1	1	?	-	?	0	1	-	0	?	-	-	0	?	?	1	0	1	0&1	0&1
S. longicollis	0&1&2	0&1	1	0	0	0	0&1	0&1	0&2	2	0	0	0&2&3	0&1	0	0&1	0&1	0&1	1	0&1	0&1
S. longipes	1	^	0	0	0	0	0	0	0&2	0	0	^	-	0	0	0	1	0	?	0	0
S. longipes var. brevipes	v	2	0	0	0	0	0	0	0&2	0	0	v	-	-	0	0	1	-	1	0	1
S. lunata	0&4	0&2	1	0	0&1	0	0	1	2	2	0	0	1&2	0&1	0	1	0	0	1	0	0
S. lutea	0	0&1	0&1	0	0	0	0	1	0&1	>	?	-			?	0	0	0	1	0	1
S. magnibrachiata	2	2	0	0	v	1	1	0	1	-	0	v	0	0	0	0	0	-	1	0	0
S. megalocephala	0	0	0	0	0	0	0	0	0	0	0	^	0	-	0	1	1	-	1	0	0
S. mesenterica/mesenterica	3	3	0	0	0	0	0	0	2	0	?	-	2		0	2	1	0	1	?	?
S. nivalis	2&3	2	1	0	0	0	0	0	0&2	0	0	0	0&2	-	0	0&2	1	0	1	0	0
S. nodosa	^	^	?	?	^	?	0	?	^	-	?	^	0	0	?	?	1	0	1	1&2	?
S. obovata	3	3	0	0	0	0	0	0	2	0	0	v	0	0	1	1	1	0	1	1&2	0
S. ovalis	4	-	?	?	1	?	0	0	1	-	?	-	^	0	?	?	1	^	1	0	0
S. pachypleura	2&3	2	0&1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
S. parasitica	0	1	0	0	0	1	0	0	1	-	0	0	0&2	-	0	0	0&1	0	1	0&1	0
S. pedicellata	2	2	1	0	0	?	0	0	0&2	0	?	-	3		1	?	1	0&1	1	0	1
S. pedicellata	0	0	0	0	0	0	0	0	2	-	0	0	0	-	0	0	0	-	1	1	0
S. pendula	0&2	2	0	0	0	0	0	0	0&2	0	0	^	0&2&3	0&1	0	0	1	0&1	1	1	0
S. pseudocinerea	3	3	?	?	-	0	0	0&1	1	0	0	-	-	-	?	2	1		?	?	?
S. pseudocinerea	2&3	1	0	0	0	0	0	0	0&1	-	0	0	0&1	0&1	0	1	2&3	-	1	0	0
S. pulchra	1	v	0	0	v	0	0	0	2	-	0	v	0	0	0	0	0	0	1	0	0&1
S. pulchra	1	^	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
S. pulchrella	0&1	0&1	1	0	0	1	0	0	1	0&1	0	0	0&1	0&1	0	0	0	0&1	1	0	0&1
S. punctata	1	1	0	0	0	0	0	0	1	-	0	0	0	0	0	0	0	0&1	1	0	0
S. pusilla	^	^	?	?	^	?	0	?	^	-	?	^	?	0	?	?	?	?	?	?	?
S. quadrifida	2&3	1	0	0	0	0	0	0&1	0&1	-	0	0	0&1	0&1	0	1	2&3	-	1	?	?
S. quadrifida	1	v	v	v	v	v	0	0	2	-	v	v	0	0	0	v	0	v	1	v	0&1
S. quercina	1	^	?	?	1	?	0	?	^	^	?	^	2	0&1	?	?	1	^	1	?	0
S. recondita	0&1	0&1	1	0	0	1	0	0	1	0&1	0	0	0&2	0&1	0	0	0&1	0&1	1	0&1	0&1
S. recondita	1	1	0	0	0	0	0	0	1	-	0	0	-	0	0	1	0	0&1	1	0	1
S. rostrata	^	^	?	?	^	?	0	0	0&2	?	?	^	?	0	?	?	?	?	?	?	?
S. rostrata	3	3	0&1	0	0	0	0	0	2		?	0	0		0	2	1		1	?	?
S. rugosa	2	2	1	0	v	0	0&2	0	2	0	0	v	2	0	0	1	1	-	1	0&1	0&1
S. spinosa	4	1	0	0	^	?	0	1	0	2	?	0	-	-	0	?	0	0	?	?	?
S. stipitata/stipitata	0&2	0&2	0	0	?	0	0	0	0&2	0	0	0	0&2	0&1	0	0&2	1	0	1	0	0
S. stoveae	0&2	2	0&1	0	0&1	0	0&2	0	0&1&2	-	0&1	0	1&2	0&1	0	1&2	1	0	1	0&1	0&1
S. subtilis	1	>	0	0	1	<	0	0&1	1	>	0	1	0	0&1	0	<	1	0	0	<	?
S. subvinosa	4	2	0	0	v	0	0	1	v	2	0	v	-	-	1	1	1	0	0	0	0
S. tenuis	4	^	?	?	^	?	0	1	0&1	2	?	^	?	0&1	?	?	0	?	1	0&1	1
S. vaginata	2	2	0	0	0	0	0	0	1	0&1	0	0	0&1		0	1	0	0	1	0	0
S. vinosa	v	v	0	0	v	0	v	0	v	-	0	v	0	0	0	0	0	0	0	0	0
S. vulgaris	^	^	0	0	^	0	0	0	0&2	?	0	^	?	-	0	0	0	?	0	2	0
S. xylophila/xylophila	2	2	0&1	0	0	0	0	0	2	0	0	0	2		0	1	1	0	1	?	?
S. zahlbruckneri/zahlbruckneri	0&2	0	?	?	0	0	0	0	2&3	0	0	0	-	-	0	0	1	0	1	0	0
S. zeolitis	^	^	?	?	^	?	0	?	^	-	?	^	0	0	?	?	1	0	1	1&2	?

	G2	G3	G4	G5	G6	T1	T2	T3	T4	T5	T6	T7	T8
S. aquensis	0	0	0	C	0	0	0	E	E	?	C	I	0
S. aquensis	0&1	1	0&1	1	1	0	0&E	C&4	2&3	0	1	0	0
S. aliibis	0	1	0	0&1	C&1	0	0	C&C	1&2	0&1	C	0	0
S. aliviscus	0&1	1	0	1&C	1	?	?	C&4	2	1&2	1	I	?
S. aquensis	1&1	1 &1	1	1	1	I	1	>&a	?	1	1	I	1
S. aureus	0&1	C&1&2	1&2	M&C&2	1&2&3	0	4&E&6	4&C	1	3	C	0	0
S. aurelianensis	^	?	^	?	1	0	0	E	E	E	1	I	0
S. aurelii	0	?	^	1	1	?	E	C	E	0	C	0	0
S. baccarini	*	?	*	1	1	?	0	C&C	2	1	C	0	0
S. bavaricoides	0&1	1&2	0&1	C	0	0&1	2&3	C	0	1&2	C	0&1	0
S. bavaricus	v	v	v	v	1	v	?	>	1	1	1	1	1
S. caudatobaccatus	0	>	1	1	1	1	<	d	>		C	0	0
S. clavus	0&1	1&2	^	?	1	1	0	E	1	1	1	I	0
S. clavicornis	1	C01	0&1&2	1	1	0	0&4	E&4	1&2&3	1&2&3	1	I	0
S. clavus	0&1	1&2	0&1	0&1	C&1	0	0&4	C	1&2	1&2	C	0	0
S. costulensis	*	?	*	?	1&2	?	?	?	?	0	1	0	0
S. cryx	v	v	v	v	1	v	<	>&a	v	1	1	1	1
S. curvicornis	1	?	1	1	1	?	1	?	?	1	?	1	1
S. distinguenda	0	0	1	1	1	?	3	E	E	0	1	0	0
S. dudleyi	^	C01	0	1	1	?	0&4	E&4	E&0	0	1	1	0
S. dubia	0	?	*	0&1	C&1	?	0&E	C&C	1&2	0	1	1	0
S. gracilipes	0&1	0	0&1	1&C	1&2	1	0&4	C&4	1	0&1	C	0	0
S. gracilis	0&1	1&2	0&1	C	C&1	v	1&2	C&C	2&3	0&1	1	1	0
S. hajeki	0	?	1&1	2	2	?	1	C&A&2	?	A2	C	0	0
S. hassalli	1	?	1	C	0	?	3	C	0	0&1	C	0	0
S. hermesia	0&1	C01	0	1&E	1&2	1	0&4	E&4	0	0&1	1	0	0
S. intermedia	1	?	*	1	?	?	0	C	?	1	?	*	?
S. jahnsoni	0&1	1&2	0&1	1&2&3	1&2&3	0	0&4&5	C&4	2&1&2	0&1	C	0	0
S. javanus	0	1	1&2	1	1	v	2	>	v	0	C	0	0
S. javanus curvicornis	v	v	v	1	1	v	?	>	<	1	1	1	1
S. javeti	1	?	1	C	C&1	?	2	E	C&1	0	C	0	0
S. legeri	0	1	0&1	0&1	0	?	4&E&6	C	0	0&1&2	C	0	0
S. longicornis	*	?	*	1	1	?	0	C	2	0	C	0	0
S. longipes	0&1	1	1	C	0	?	A	C&4	3	0	C	0	0
S. macrophthalma	1	v	v	1	1&2	1	?	1&4	2	0	1	1	0
S. major	1&1	1&v	1	1&1*	1&v	1&1	1	>&a	v&1	1&1&2	1	1	1
S. malloi	'	?	'	?	1	?	2	C&2	?	2	C	0	0
S. marianus	^	C01	^	1	1	?	0	E&4	1&2	0	1	1	0
S. mauensis	^	?	^	C	0	?	'	E	?	E	C	0	0
S. meregalli	0&1	2	0&1	C&1&2&3	C&1&2&3	0	4&E&6	4	1&2	'	C	0	0
S. nebulosa	0	1	0	1	1	?	2	2	2&3	0	C	0	0
S. nevadensis	1	1	1	1	1	1	1	d	<	1&2	1	1	1
S. pacifica	0&1	1	1&2	1	1	0	1&4	>	>	0	C	0	0
S. pallidula	1	C01	0	0&1	C&1	1	0	E&4	1&2	0	1	1	0
S. pallipes	0&1	1&2	0&1	C	0	?	3	C	C&1	0&1	C	0	0
S. palustris	0&1	C&1&2	0&1	1	1	1	0	E&4	2&3	0	1	1	0
S. pectinicornis	0&1	C&1&2	0&1	0&1	C&1	0	1&C&0	C&C	3	1&2	C	0	0
S. peregrina	0&1	1&2	0	1	1	?	2&3	2	1	0	C	0	0
S. pharaonica	0	1&2	v	1&C	0	v	2	C&4	1	0&1	C	0	0
S. planicollis	1	v	v	1	1	v	1	1&>	1&1	1	1	1	1
S. pulchra	0	1	0&1	0&C	C&1	0	2	C&4	1&2	0	C	0	0
S. punctata	0&1	1&2	0&1	1	1	0	0&4	C&4	1	0	C	0	0
S. pygmaea	0	1	0&1	0&C	C&1	0	2	C&4	2	0	C	0	0
S. quadrifoveolata	^	?	^	?	?	?	?	?	?	?	?	^	?
S. reitteri	*	?	*	1	1	?	0	C	?	0	C	0	0
S. reitterelloides	0&1	1	0&1	1	1	?	A	C	3	0&1	C	0	0
S. rufomarginata	v	v	v	1&C	1&2	0	?	1&4	v	0	C	0	0
S. rugosa	v	v	v	1	v	v	1	>&a	1&v	v	1	1&1	v

CHAPTER 7 – BIOLOGICAL INFORMATION SYSTEMS AS TOOLS FOR TAXONOMIC AND BIOGEOGRAPHICAL RESEARCH

1. Introduction

The aim of this Ph.D. project was to create a systematic, geographic, and morphological overview of the world Mysida fauna. Instead of solving this question by taking samples following a specific strategy it was chosen to base it on published sources. A large amount of literature was brought together and digitally combined. This methodology resulted in the largest currently existing literature collection on Mysida. Systematic, geographic and morphological data was extracted from this literature and digitally linked, using the Biological Information System NeMys (Deprez, *et al.* 2004).

By using this methodology, a number of outcomes could be produced: (1) a digital catalogue on different aspects of Mysida shrimps, (2) a biogeographical analysis of Mysida distributions, (3) two taxonomic phylogenetic genus reviews and (4) the experience of developing and working with a biological information system. The large variety of outcomes illustrates that using a biological information system helps in the production of scientific results.

This chapter aims to discuss some topics related with the use of digital biological information systems. Whether or not biological information systems facilitate taxonomic research, and how taxonomic research may benefit in the most efficient way from these new digital developments, is emphasized in the following.

2. Taxonomic research

The science of ordering biological names in a coherent way that reflects their evolution is known as taxonomy (after Guiry, 2005). This ordering may be based on morphological characteristics, although recently also molecular results play an important role. Although these molecular techniques are able to solve many problems faced with classical morphology based classifications, they do have some major constraints (for example Uilenberg *et al.*, 2004). Molecular biology requires molecules, and thus specimens, being preserved in good conditions. It also uses a methodology, which is due to many reasons, not for every taxonomist available. To some extend some of these techniques are still experimental. Results derived from

pure molecular taxonomy are in some cases controversial (Kipling & Rubinoff, 2004; Wiens, 2004). Classifications based on morphological features will for these reasons remain important. Identification of organisms still relays on the investigation of morphological distinguishing features. Molecular taxonomy may help to solve problematic issues in taxonomy, but mostly does not lead to systematic reorganizations influencing the identifications of species.

Taxonomy is a living science building upon existing classifications and descriptions of species. The longer the history of taxonomic research, the more data becomes available, and mostly the more complex the total picture becomes. The access to original species descriptions and taxonomic reviews, in combination with the access to specimens is as such essential for taxonomic research. Often, publications are widespread over journals, kept in different institutions and libraries. Collecting the full bibliographic taxonomic history is a first major problem in taxonomy. For this Ph.D. project, much time and effort were paid to collecting the literature on the Mysida. Although the majority of taxonomy-oriented papers were collected still a lot of literature, mostly on non-taxonomic issues, is lacking in the archive.

Specimens are, next to the literature, the basis of the definition of a species. The concept of a morphological species, falls or stands with its linked specimen (holotype, paratype). A major problem with the Mysida is the lack of type material for many species. It is for many species (mostly described long ago) dubious whether type material still exists. Even when it is available and localized the state of many specimens is bad. *Anchialina typica*, the type species of this genus, can be taken as an example. Type material was found in the collections of the Natural History Museum of London. A study of the specimens however was not possible due to the bad conservational status of the specimens.

The two presented problems (‘lack of specimens’ and ‘lack of literature’) could possible be handled by using innovative technologies. The presented methodology (the use of a biological information system for taxonomic research) and its implementation for the Mysida, opens a number of possibilities for taxonomic research on many other groups, facing similar problems as for the Mysida.

3. The optimal biological information system

The term “Biological Information System (BIS)” is until now rather vaguely defined. The use of it depends strongly on the research field in which it is implemented. When used in a biodiversity research context it should be seen as set of tools, opening biological information in its broadest sense to the user community. The way of presenting the information should be directed by the targeted user. As such BIS may exist for well skilled taxonomists, while at the other extreme, other systems may exits for young school children. The ideal situation would be a system presenting biodiversity data in a format depending on the queries and expectations of the users. Current technological developments facilitate the construction of BIS’s based on digital information.

A ‘taxonomic’ BIS (i.e. the users of the system are ‘experienced’ taxonomists) should fulfill the following requirements: (1) the ability to store systematic data and its history, (2) possibilities to link data with the literature, if possible in a digital way, (3) any kind of data should fit in the data model, (3) presentation of the data must be useful for a genuine taxonomist, (4) communication between taxonomists should be encouraged, (5) genericity on all levels should be implemented.

As described in chapter one and two of the thesis, NeMys was developed aiming to give answer to these requirements. Some of the requirements were answered although many features of this system are still a point of discussion and development.

Next to NeMys also a series of other tools exist. The systems fitting best the requirements listed above are currently Linnaeus (Schalk, 2005) and Taxis. Beside the all-round systems a large group of packages exist answering one or few of the requirements of a BIS. Among these packages, identification keys, bibliographic management systems, and geographic information systems are most prominent. Integrating the data hosted on all these systems, may be the most efficient way to get to a genuine BIS. Data portals such as GBIF (Edwards *et al.*, 2000) and OBIS (Grasle, 2000) may play an important role in this integration process. A number of web services developed by UBio (Remsen *et al.*, 2006; Kennedy *et al.*, 2005) can

facilitate the intelligent automated creation of links between different parts of the total puzzle. Crucial in this integration process are agreed standards and formats making communication between different entities work. A number of standards developed by the TDWG (Taxonomic Databases Working Group – http://www.nhm.ac.uk/hosted_sites/tdwg/) are a good step forward. Currently formats exist for the exchange of taxonomic, bibliographic, geographic and morphological data (for example SDD (Structure of Descriptive Data) (see http://wiki.tdwg.org/twiki/bin/view/SDD/Version1dot1) and Darwin Core 2 (see http://darwincore.calacademy.org/)). The final optimal BIS however, would require many more exchange protocols (for example for ecological data, molecular data, images, specimens …).

The last few years, there has been a change in mind concerning the use of BIS's. The relative large number of publications on this topic, and the successful establishment of some biodiversity data portals may have played a role in this change of mentality. From 2000 onwards, articles related to BIS's were published in high impact journals. A few examples are Bisby (2000), Godfray (2002), Stein (2002), Gewin (2002); Polaszek *et al.* (2005) all describing in more or less detail a digital webbased service providing biological information on taxa. The success of some species databases, of which Fishbase (Froese & Pauly, 2005) is the best known one, may have convinced some decision makers that financing of this type of research is valuable.

4. What tools are needed in a BIS?

The success of a BIS will depend on the tools offered for data exploration and data management. Once the critical amount of data in a BIS is reached, people start using it. This critical data amount issue was experienced for several datasets running on NeMys. The tools required in a BIS are strongly related to the emphasized research topic.

For answering biogeographical questions very specific data is needed. The presented biogeographical analysis of the Mysida distributions (chapter 4) shows that the nature of the data hosted on a BIS strongly influences the research questions that can be answered with it. For the presented example only presence/absence data, derived from literature, was available. Many regions were distinguished as insufficiently sampled. Moreover, a strong correlation between the research effort and the number of observed species was found. As a consequence of the status of the dataset only large scale processes could be studied. Unraveling processes on a small geographic scale on a limited set of taxa is with the current setup of the Mysida database impossible. Beside limitations related to data quality, limitations of a BIS are also strongly related with the availability of tools.

Following tools should get attention in the development of BIS:

(1) for biogeography: biogeography analysis tools such as mapping tools, data export tools and in a further stage also statistical tools.

(2) for taxonomy: library exploration tools, morphological analysis tools and digital documentation tools.

A large role for the development of toolboxes could be played by international biodiversity portals (for example GBIF). Currently these portals are limited to grouping and displaying biodiversity information. The setup of outside accessible tools would be an efficient solution for carrying out taxonomic research making use of a BIS. Not every BIS would as such necessarily have to develop his own set of devices, but could use those developed by the portal. If possible these tools (web services) should be easy to integrate in the interface environment of a particular BIS.

Two possible examples could be a GIS mapping tool or a bibliographic facility linked with open archives accessible by or hosted by these portals. Concerning GIS tools a number of initiatives are checking the possibilities of central freely accessible web-based mapping tools. Some preliminary examples are for available from the OBIS website (http://www.iobis.org – C–Squares mapper).

Some other possibly useful tools were developed in the framework of the NeMys toolbox: a glossary, a methodological unit, a language module, a private taxonomic workbench.

This last tool will be essential for the future of NeMys. It is an environment developed for taxonomists, allowing them to use NeMys as a daily research tool. Research data can be entered in a strictly private environment and be integrated with formerly published data. In this way, it is hoped to stimulate taxonomic research with the advantage that starters will have a guaranteed link with the literature.

▪ 4.1. TOWARDS DIGITAL REFERENCE COLLECTIONS

The lack of Mysida specimens is a major problem for a taxonomic review of the group. For *Anchialina* and *Siriella* almost no valuable specimens could be retrieved. Setting up digital reference collections would prevent the future loss of specimens. A digital reference collection should be much more than a simple collection management system (like for example Biotica or Specify – see chapter 1). A digital reference collection should not only give some basic specimen metadata parameters (where and when has it been collected), but should through digital visualization techniques show all distinguishing features of a species. In the future one could even think of a hologram representation of a specimen. Some work on digital collections was already started for a number of groups. The 3D imaging of extinct birds of the 'Naturalis' Museum in the Netherlands carried out by ETI (http://www.eti.uva.nl/) offers a good view on the possibilities of three dimensional visualization of specimens (Veldhuyzen *et al.*, 2005; Leslie, 2005a). The technique using movies described by Deley & Bert (2002) also gives a nice example of transforming three dimensional structures into a two dimensional medium.

Digital reference collections would also help to set up networks of taxonomists on a global scale. It would offer taxonomists from developing countries the facilities to consult specimens often stored in natural history collections of developed countries.

Although this is an enormous task, the development of a fixed methodology for a number of taxa may help to raise the efficiency of it. Digital imaging of specimens not necessarily requires skilled specialist taxonomists. It can in many cases be carried out by well trained technicians, and as such lower the cost of such projects.

5. What data is required in a BIS to use it as a research tool?

This Ph.D. project has illustrated at several points that taxonomic oriented BIS's can be valuable tools for taxonomic research. Although tools play an important role in a research project, the quantity and quality of the data is much more important.

For the particular case of Mysida, it was chosen to base the study on published data. Extraction and standardization of this published data lead to a dataset with a large number of morphological and geographical records. The biogeographical analysis on this data did show some large global patterns, but much more it showed that still many regions are not investigated yet. A more accurate picture of the biogeography of the Mysida would thus be possible when more data becomes available. As published data is already included, this new data should come from new research. As many as possible variables, possibly explaining the distributional range of a species, should be recorded. Sampling should be as much as possible standardized. A standardized sampling methodology would allow comparing data from different sampling campaigns.

Standardized methodologies are of huge importance when trying to compare data from different sources. Documentation of used methodologies would be an immense step forward in order to interpret data in BIS's. At least as important in a BIS as data is metadata.

A standardized methodology for the description of new species would ease comparing species in a BIS. The study of the genera *Anchialina* and *Siriella* showed large differences in the different descriptions (see chapter 5 & 6). Additional study of specimen material was needed in order to understand some of the descriptions. The dataset used to do the morphological phylogenetic analysis showed for many characteristics large gaps as certain features were not documented at all for some species.

Setting a number of standardized characters for the description of a species would open promising possibilities for morphology based phylogenetics. New species would at the point of description, if all characters of all other members of a genus

are known, immediately be seen in an evolutionary perspective. The current way of describing new taxa through a text and some figures (mostly drawings which are in se interpretations of the reality by the author), in many cases does lead to interpretation problems. Interpretation of certain English terms often used in species descriptions depends largely on the reader. Vague terms like 'large', 'small', 'broad', 'long' should be forbidden, if they are not clearly defined. BIS may facilitate these problems by the development of a new strategy for publishing new species. Instead of using the classic peer-reviewed publication based method, a standardized peer reviewed open format would be much more favorable. Similar to molecular publications, a taxonomic publication on a new species should only be accepted if the description is submitted to a global taxonomy database. This database should hold descriptions of species in an undubious way, if possible illustrated by drawings and digital images of all distinguishing features on the submitted type specimens. Organizations like TDWG (Taxonomic Databases Working Group - http://www.nhm.ac.uk/hosted_sites/tdwg/) or the International Commission on Zoological Nomenclature (http://www.iczn.org) could play an important role in this matter. Currently a number of initiatives are ongoing. Zoobank for example aims to set up an obligatory registration system for new zoological descriptions, similar to Genbank (http://www.afriherp.org:8000/ZooBank/Zoobank.htm) (Polaszek *et al.*, 2005 a & b).

When changing the rules on data delivery, also the minds of the data deliverers should be changed. This process of changing the minds will take a long time. A first step is to introduce taxonomists to the concept of a BIS and let them taste the advantages of these systems.

6. A classification of biological information systems

The development of one global overall taxonomic biological information system is possibly not the best way of really getting to one global system with global information on biodiversity. Many systems do already exist, and many have a number of advantages and disadvantages. Advantages and disadvantages strongly depend on the needs of the user and as such cannot be discussed objectively. NeMys for example is an online maintained system. For certain scientists this may be an advantage, although others may argue that for example for data property issues, an online system is not the best option.

A classification of biological information systems would be interesting in order to get an overview of existing research in this field. Such classification could be based on the characteristics of a BIS. These characteristics could include information on target users, types of data, taxonomic range, …

The existence of different 'concurent' systems encourages the development of new features. It also keeps developers critical enough on features of the own and other existing systems. Although a kind of 'concurrence' in layout and setup may be positive, standard methodologies must be constructed to enable data exchange between different levels in this BIS classification. Whether or not a BIS implements these exchange formats would be an additional valuable criterion in evaluating different systems. Exchange of data should be multi-directional. One can for example be used to work with the identification keys developed by ETI (Linnaeus©). Exchange of keys would in this case mean that for example the identification key on marine Nematodes developed in the NeMysKey environment can be uploaded to the Linnaeus package and vice versa for keys developed with Linnaeus©. Standards exchange formats for a whole series of biological data are critical in the construction of a global BIS infrastructure. Some standards for data exchange are recently finalized by TDWG: ABCD (Access to Biological Collections Data), SDD (Structure Descriptive Data), TCS (Taxonomic Concept Transfer Schema). (for details on this see: http://www.nhm.ac.uk/hosted_sites/tdwg/TDWGStandardsBallot2005Result.htm)

7. The added value of biological information systems

Biological Information Systems may have next to the purely scientific values, which were already extensively discussed, also their value concerning the awareness of the broader public on biodiversity. In Europe for example currently about half of the inhabitants have access to the internet (Eurostat, 2006). This means access to data hosted on the internet is no longer a privilege for the richer educated group of the population. A much broader group than for instance ten years ago of potential users of online BIS is now available. People interested in matters on biodiversity are through BIS able to consult scientific data.

Thanks to the communication power of internet, it is the first time in history that academic science is able to communicate (in a passive way) with the broad public. Currently this communication is mostly only used from scientist to user, by presenting data through for example a BIS. A step further would be that communication in the other direction becomes an integrated part of certain BIS. This would mean that data on organisms provided by a non-academic public integrates through a web-based information facility with the available academic scientific data. A promising example of such tool is the website http://www.waarneming.nl offering a facility to add observational data on organisms (insects, birds) making use of cell phones. A similar system, although guided by the INBO (Instituut voor Natuur en Bosonderzoek – Belgium) (http://www.inbo.be), has been setup for field observations on ladybirds. Data is after a data quality control monthly added to the NeMys Eurocox website (chapter 1). Another integrative project on biodiversity information is the WikiSpecies project initiated by the Wikipedia online free encyclopedia (http://species.wikimedia.org/wiki/Main_Page). This project allows to anyone adding and editing data on species, and as such create an open directory on species information (Leslie, 2005b).

Beside communication possibilities of BIS also a number of other implementations can be thought of. First of al BIS can be valuable tools for educational purposes. The NeMys database for example is used in a number of courses conducted at the Ghent University (see chapter 1). Secondly these tools may be supportive to

decision makers. They allow getting a fast overview of species related topics, and may facilitate communication from the scientific community towards decision makers.

BIS's may be the future tools to get taxonomy, and biological academic science, out of the ivory tower. The implementation of an information system may as such not only be valuable for biological science but for many more fields (in science or the public domain).

8. Conclusions

A number of conclusions on the use of BIS in taxonomic research can be drawn:

- Taxonomic research gains efficiency when making use of freely accessible (preferably online) BIS.
- Using a BIS for answering biogeographical research questions is possible, although results strongly depend on the type of data in the BIS.
- New methodologies for descriptive taxonomy should be developed, making use of the strengths of BIS.
- Exchange formats between BIS are needed, to encourage a wide range of taxonomists to use these tools.
- BIS cannot exist without data. New research results are still needed to fully employ all possibilities of BIS. Data already available in a BIS may point out research topics of first interest.

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APPENDIX – PUBLICATION LIST TIM DEPREZ (AS ON JUNE-2006)

1. A1 publications

Deprez, T.; Wooldridge, T.; Mees, J. (2000). A new species of Gastrosaccus (Crustacea, Mysidacea) from Algoa Bay (South Africa). Hydrobiologia 441: 141-148.

Deprez, T.; Wooldridge, T.; Mees, J. (2001). Idiomysis mozambicus, a new mysid species (Crustacea: Mysidacea) from Mozambique. Hydrobiologia 459(1-3): 47-49.

Remerie, T.; Bulckaen, B.; Calderon, J.; Deprez, T.; Mees, J.; Vanfleteren, J.; Vanreusel, A.; Vierstraete, A.; Vincx, M.; Wittmann, K.J.; Wooldridge, T. (2004). Phylogenetic relationships within the Mysidae (Crustacea, Peracarida, Mysida) based on nuclear 18S ribosomal RNA sequences. Molecular Phylogenetics and Evolution 32(3): 770-777.

Deprez T., Steyaert M., Speybroeck J., Raes M., Vanaverbeke J., Merckx B., Vincx M. NeMysKey, a concept for documented polytomous identification keys (Submitted to Biodiversity Informatics)

Deprez, T.; Merckx B. A review of the genus Siriella (Mysida, Peracarida) (IN PREP.)

Deprez, T.; Jocqué M. A review of the genus Anchialina (Mysida, Peracarida) (IN PREP.)

Others

Deprez, T.; Vanden Berghe, E.; Vincx, M. (2004). NeMys: a multidisciplinary biological information system, in: Vanden Berghe, E. et al. (Ed.) (2004). Proceedings 'The Colour of Ocean Data': international symposium on oceanographic data and information management with special attention to biological data Brussels, Belgium, November 25-27, 2002. IOC Workshop Report, 188: pp. 57-63.

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Degraer S., Wittoeck J., Appeltans W., Cooreman K., Deprez T., Hillewaert H., Hostens K., Mees J., Vanden Berghe E. & Vincx M. (2006). The macrobenthos atlas of the Belgian part of the North Sea. Belgian Science Policy. D/2005/1191/3. ISBN 90-810081-6-1. 164 pp.