Biodiversity of Coastal Marine Ecosystems

Pattern and Process - A Euroconference

Carlo H.R. Heip, Herman Hummel, Pim H. van Avesaath

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Editors:
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Corinth Greece 05 - 10 May 2001

Euroconference 2001-169
organised by
ESF (European Science Foundation)

in association with
MARS (Marine Research Stations Network)
BIOMARE (EC Concerted Action EVR1-CT2000-20002)

Supported by EC, Research DG,
Human Potential Programme, High-Level Scientific Conferences
Contract HPCF-CT-2000-00223

With co-sponsoring from UNESCO Venice Office

Chair: Carlo Heip - NL, Netherlands Institute of Ecology, Yerseke, NL
Vice-chair: Richard Warwick - UK, Plymouth Marine Laboratory, Plymouth, UK

Topics:

1. General patterns in marine biodiversity
2. Patterns of coastal marine biodiversity in major groups
3. Patterns of biodiversity in different habitats
4. The human factor
5. Methodology, European Co-operation, End Users

First published in 2003

ISBN 90-74638-16-3

Printed by ADZ
Vlissingen
the Netherlands

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Scientific/technological objectives and Content

Carlo Heip

The objective of the conference was to inventory, summarise and generalise the scientific knowledge on the structure and function of marine biodiversity in coastal marine areas of Europe. Now that the Rio Convention has been ratified by nearly all European countries, and by the European Union, it becomes clear that the knowledge required to cover the obligations of the convention is simply not available, even in Europe where the seas have been explored since hundreds of years and taxonomic and general ecological knowledge is well advanced when compared to other areas of the world.

Despite the broad definition of biodiversity adopted in Rio, covering variation in genes, species and habitats, biodiversity has for some time been associated with species and taxonomy only. Several efforts are presently underway to inventory Europe's flora and fauna. These have shown that a lot remains to be discovered, even in Europe, for example microbial diversity, diversity in cryptic habitats like submarine caves, symbionts and parasites, viruses and fungi etc etc.. Perhaps more important is that the ecological role of biodiversity has hardly been addressed at all. The relationships between the three components of biodiversity, genetic, species and habitat diversity have hardly been explored and the role of biodiversity in marine ecosystem functioning is still largely unknown. Marine research has borrowed its concepts and paradigms from terrestrial biodiversity studies and there is no substantial body of knowledge on the subject. Adequate assessment of the risks to marine systems due to species or habitat loss or to accidental species introductions is therefore at present impossible.

The EURESCO meeting aimed at increasing relevant knowledge by a stepwise approach in which first an inventory is made of what is known on the three aspects of biodiversity (genes, species, habitat) in shallow coastal areas. From such inventories comparisons and generalisations are possible and the relevant questions and research priorities to understand what causes the observed patterns can be formulated. The meeting also addressed the urgent and important problem of biodiversity assessment using rapid (molecular techniques, functional species, remote sensing) but reliable technology.
In a second meeting, that will be prepared over the next two years, the emphasis will be on functional studies that try to understand the role of biodiversity in biogeochemical cycles, ecosystem productivity and food web structure.

The Marine Biodiversity Conference brought together the widely separated marine biodiversity research projects that have been started in many countries as a consequence of the Rio Convention, and focussed on the large-scale and the long-term changes and on the problems in monitoring and surveying biodiversity.

Acknowledgements

This publication is based on the presentations made at the European Research Conference (EURESCO) on "Biodiversity of Coastal Marine Ecosystems: Pattern and Process – A Euroconference", Corinth, Greece, 5-10 May 2001, organised by the European Science Foundation and supported by the European Commission, Research DG, Human Potential Programme, High Level Scientific Conferences, Contract HPCF-CT-2000-00223. This information is the sole responsibility of the authors and does not reflect the ESF or Community's opinion. The ESF and the Community are not responsible for any use that might be made of data appearing in this publication.

The co-sponsoring by the UNESCO Venice Office - Regional Office for Science and Technology for Europe (UVO-ROSTE) - is acknowledged, whereby especially the participation of young scientists, experts and representatives from Central and East European countries was facilitated.

Patterns of coastal marine biodiversity in major groups

Chaired by
Jeanine Olsen
Marina Montresor

Microbial (and viral) diversity: general patterns in marine and coastal environments

Patterns of coastal marine biodiversity in major groups

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Advances in molecular approaches to characterize pure cultures and microbial communities (e.g., marine snow, biofilms, symbionts, low-diversity habitats) have markedly improved our knowledge about microbial diversity. Sequencing of genes, in-situ hybridisation of fluorescent probes (FISH) to functional and rRNA genes, FISH in combination with microautoradiography as well as flow cytometry and cell sorting followed by molecular and activity measurement are only the most prominent techniques. Despite this progress, difficulties arise when selected data on individual environments are used for generalization and to generate common patterns from results of studies performed on the characterization of isolated microorganisms. The estimated number of prokaryotic cells in the marine environment is around 2.9 x 10^{28} (open ocean – 1.2 x 10^{28}, oceanic sediment, top 10 cm – 1.7 x 10^{28}) (Whitman et a., Proc. Natl. Acad. Sci. USA 95, 6578-6583, 1998) and the number of viruses in the open ocean (10^{3}-10^{6} ml^{-1}) are reported to exceed that of prokaryotes 5- to 10-fold (estimates for fungi and yeasts were not considered here). On the basis of these figures and supported by molecular data on prokaryotes it can thus be assumed that the various sites in which microorganisms thrive (to name a few: water column, deep sea, sediment, marine snow, sea foam, eukaryotic cells [commensales, parasites, symbionts], river plumes, estuarines, man made material) are full of unidentified taxa, varying in numbers and phylogenetic identity, many of which form consortia of mainly unidentified complexity. Neither the identity of individual prokaryotic taxa, nor the compositions of community structures have been elucidated in sufficient depth to explain their function at a higher trophic level.

The assessment of phylogenetic diversity is further complicated: (i) about 5000 prokaryotic species have been validly described, including only a few hundred from the marine environment; though molecular data are available for all of them the reference database is small. (ii) the majority of cells observed under the microscope or assessed by the presence of phylotaxa in clone libraries of environmental DNA cannot be cultured in the laboratory. (iii) even if cultured, reliable methods for rapidly assessing genomic differences on a large number of isolates are lacking and strains with superficial similarity are judged to be identical and thus discarded. (iv) the number of clones analysed from these clone libraries is small (only 3-10% of total cells ml^{-1} seawater), most likely ignoring rare taxa. (v) in coastal and river plumes waters and sediments marine communities are intermixed with terrestrial organisms, detected mainly by the presence of Gram-positive bacteria, e.g. bacilli and actinobacteria.

As the physiological properties can only be assessed meaningfully for cultured strains, the assessment of functional diversity is restricted by (i) the uncertainty whether physiological properties determined in the laboratory are those actually expressed in situ; the physiological diversity of strains of a described prokaryotic species may be significantly larger that that expressed by the type strain and (ii) the inability to conclude on metabolic traits from taxa represented only by their sequence of ribosomal DNA.

Despite these obstacles certain pattern do emerge from studies on cultured and as yet uncultured prokaryotes. The latter studies, introduced 10 years ago, include, among others, the coasts and open waters of the Atlantic and Pacific Oceans, the North Sea, Mediterranean Sea, Arctic Sea and Antarctic Sea. Ribosomal DNA sequences indicate that the majority of phylotaxa belong to very few main lineages of the domains Archaea and Bacteria (for restrictions see above).

Two groups (marine groups I and II) have been identified to belong to the Archaea. Group I belong to the *Crenarchaeota*, mainly consisting of thermophilic and acidophilic organisms. Group II branches within the radiation of *Euryarchaeota*, containing methanogens, halophiles and *Thermoplasma*. Both groups are remotely related from their nearest cultured taxon which does not allow to speculated on the metabolism of these phylotaxa. Their origin is as undetermined as their function.

Phylotaxa of the domain Bacteria fall into the species-rich main lineages of cyanobacteria (*Prochlorococcus*, *Synechococcus*), *Cytophaga-Flavobacterium* and *Proteobacteria.* Planctomycetes (predominant in marine snow), verrucomicrobia, nitrate-oxidizers, spirochaeta and other taxa are found occasionally. The vast majority

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of phylotaxa of the open oceans identified as yet are members of the α- and γ-subclasses of *Proteobacteria* to which also the majority of cultured marine species belong. It is therefore not surprising to find as yet uncultured organisms genomically closely related to described species, e.g., of the genera *Caulobacter, Sulfitobacter, Roseobacter* and *Marinosulfonas* (α-subclass) and *Alteromonas, Pseudoalteromonas, Vibrio, Shewanella,* and *Marinobacter* (γ-subclass). Rarely, however, are these phylotaxa, as well as cultured organisms from the same environment, genomically identical to described species. This is especially evident, when a large number of 16S rDNA clones are available for phylogenetic analysis (e.g., *Alteromonas macloedii*). The majority of clone sequences from the marine environment are indicative of novel taxa, mostly representing novel species, genera and families but even novel deep branching lineages. The function of members of the α- and γ- subclasses of *Proteobacteria* have not been assessed in detail. As hypothesized (Zavarzin et al., Can. J. Microbiol. 37, 1-6, 1991) members of the former taxon are oriented towards substances diffusing from organic decomposition in the aerobic zone, while many members of the latter taxon are facultatively anaerobic and fermentative as well as aerobes involved in the breakdown of polysaccharides produced by primary producers.

Another major source of diversity is the eukaryote-prokaryote relationship of which mainly the symbiosis has revealed a surprising range of hitherto uncultivated bacteria. Most of these organisms found in tube worms, gills of mussels, clams, oligochaeta and fish originate from within the γ-subclass of *Proteobacteria* but symbionts are also found in the α- and δ-subclasses).

The experience of the past 10 years, including the notion of pitfalls included in each newly developed technique, guide us to changes in the assessment of microbial diversity (the following is by no means a complete listing). The mere assessment of diversity must be replaced by a strategy in which phylogenetic and functional diversity are linked with population genetics, allowing assessment of horizontal and lateral gene transfer and interactions between strains in space and time. Here, mechanisms leading to stable eukaryote-prokaryote interactions appear of special interest. Application of microautoradiography, three-dimensional resolution of community partners, FISH hybridisation and novel non-invasive techniques will play an increasingly important role. Results of meta-genome and whole genome sequencing of key strains of the marine environment will guide us to the identification of key genes to be targeted by high throughput assays such as DNA arrays or DNA chips. High-throughput sorting analyses and molecular tools are to be developed to eliminate genomically and phenotypically highly similar strains, which are the consequence of extensive screening regimes. Fourier-transformed infrared spectroscopy and automated DNA-pattern generating methods are already in place and should be miniaturized. This, in the end, will facilitate at-site analysis without effecting sample processing. Innovative isolation techniques should be developed for those phylotaxa recognized to be dominant in a given sample. Though environmental clone libraries and expression libraries are already commercialised, long-term preservation of novel taxa are prerequisite for future studies on gene expression. The establishment of biological resource centres (cultures and parts thereof) and networking between material and information are mandatory for efficient research.

Discussion

The gigantic number of bacterial cells is beyond imagination. Even if calculations on prokaryotic cell numbers are out by several orders of magnitude, there are still 109 more cells in the sea than stars in the milky way.

The majority of gram-positive bacteria found in marine sediments are of terrestrial origin. They appear well adapted to survive adverse conditions in soil and few only are adjusted to the marine environment. As judged from the branching point in the16S ribosomal DNA tree, gram-positives evolved later in evolution than many of the gram-negative bacterial phyla. One could argue that the ancestor of the gram-positives (and cyanobacteria) was a descendent of certain gram-negative bacteria that explored the the terrestrial environment, about 2.0-1.5 billion years ago.

The definition of the taxon "species" is a complex and could not be discussed in detail during the discussion. In summary,the present concept is pragmatic, artificial and arbitrary, based on the assumption that strains with similar genomic and phenotypic properties are recognizable units that represent biological entities. Based upon the assumption that, whenever investigated, each eukaryotic species contains at least one new prokaryotic species (symbionts, commensals), the numbers of prokaryotes are at least as high as the number of eukaryotic species. One could also speculate that the number of viral species doubles this number as it is not unlikely that a new virus species is found in each eukaryotic and prokaryotic species.

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Diversity of prokaryotes: Water column versus sediments

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The interest to understand microbial diversity, and the structure and function of their communities in natural ecosystems has increased in parallel to the development of molecular techniques applied to microbial ecology. Research in this field has given unexpected results like the realisation that our knowledge about the real microbial diversity is extremely sparse. Altogether, the total prokaryotic abundance in the biosphere has been calculated to be over 10^{30} cells, and some calculations also indicate that the number of prokaryotic species should then be much higher than 10^{7} (Whitman et al., 1998). To the present we have characterised around 5000 different species which might represent less than 0.01% of the total harboured in the biosphere. The main reason for this lack of knowledge about the real prokaryotic diversity is that to the date it is still necessary to culture the organisms in the laboratory in order to characterise them (Rosselló-Mora and Amann, 2000), and most of the microorganisms refuse to be cultured in the laboratory. This is especially true for marine environments where microbial diversity research has suffered a delay in respect to other environments.

Because of the large dimensions of the marine environment on the Earth, marine prokaryotic communities play an essential role in the biogeochemical cycling of matter and energy in the biosphere, specially those benthonic where the complete mineralization of the organic matter is undergone (Thamdrup et al., 2000). The current knowledge on marine microbial ecosystems is biased towards the planktonic systems, and less is known about benthonic marine microbial communities. However, a common trait among both systems is that they are extremely complex and no generalisations can be done. Indeed, the diversity observed in such environments are less dependent on the geographical situation, but on seasonal changes of physico-chemical and biological parameters. Molecular techniques like fluorescence in situ hybridisation (FISH) show that the metabolic state of such communities is reflected by the amount and type of prokaryotic cells containing high amounts of rRNA, and both are dependent on the quality and quantity of available substrates and nutrients.

The water column is dominated mainly by aerobic gramnegative prokaryotes whose identity is only known after clone library screening and sequencing. The most dominant planktonic organisms have never been isolated in pure culture. Cyanobacteria are the most common prokaryotic primary producers, whereas Cytophaga-Flavobacterium-Bacteroides (CFB) alternate their predominance with members of the a-subclass of Proteobacteria, and both are the most common secondary producers. One of the most important advances in molecular ecology of microorganisms has been the observation that Archaea is as well represented in such mesophilic and aerobic environments. In spite of the advances, not very much is known about their function in the environment.

On the other hand, marine sediments are mostly anaerobic, and thus dominated by a wide range of dissimilatory reducers of electron acceptors that superimpose in a vertical stratification. Molecular techniques combined with biogeochemical process measurements have shown that sulphate reducers are the most common mineralizers in marine sediments, whereas members of the CFB might undergo fermentation (Rosselló-Mora et al., 2000). Somehow, CFB rule the prokaryotic population dynamics in euthrophic systems (Llobet-Brossa et al., 1998).

We are entering in a new era of microbial molecular ecology. In the rush of the Genome research, and the sequencing potential of the new machines it seems possible to analyse the genome sequence of environmentally important uncultured microorganisms. Immediate future perspectives in marine environments are focused in to the cloning and sequencing of genomes present in the environment. It is possible that with this approach we will have a much better understanding of the role of marine prokaryotes in their environment, as well as their isolation in pure culture might be feasible.

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Patterns of coastal marine biodiversity in major groups

Diversity of phytoplankton

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Phytoplankton is characterized by phylogenetic diversity coupled with species paucity: at least 10 lineages are represented some with less than a 100 known species, others with several 1,000. In contrast, land plants are represented by about 250,000 species but all from only one lineage. The relationship between form and function in land plants is well known and species diversity can be related to spatial heterogeneity of the physical environment. In contrast the much wider range of shapes in phytoplankton is yet unexplained. The co-ocurrence of many species in the same water column is traditionally related to mechanisms of resource acquisition (affinity to certain nutrients or light regimes), hence competition is widely regarded as the key factor shaping species composition and succession. Since most phytoplankton cells are eaten before they can complete their life cycle, I argue that agents of mortality (i.e. debilitators and killers: pathogens, parasites, predators) play a greater role in shaping plankton form and function than resource acquisition and that the defence mechanisms and the evolution of a „pelagic arms race“ have significant impact on productivity, food web structure and hence also biogeochemical cycles in the oceans.

Discussion

The breaking process of long chain forming diatoms cannot be explained at the moment. Probably the dead cells play a role in this process. It was suggested to make a model to study this process.

There have been various extinction events in diatoms. There are records of extinctions without any apparent, environmental causes: species appear and then they are gone. This is something that has to be studied in more detail.

The form-function theory and study could be supplemented with the comparison between the marine and freshwater environment. The basics are the same. However, the shells of freshwater diatoms are much thicker than those of marine species. We do not understand yet completely why the chlorophytes are so important in lakes compared to the ocean.

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The role of cysts and spores in maintaining diversity of coastal phytoplankton

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Cysts, spores, akinetes, statospores, resting cells, are different names to define peculiar stages in the life cycle of many phytoplanktonic organisms (i.e. diatoms, dinoflagellates, cyanobacteria, chrysophyceans, raphidophyceans). All these stages share ultrastructural and physiological features that differentiate them from the corresponding motile stages. Their cytoplasm is packed with reserve materials, chloroplasts are shrunken and metabolic rate is extremely low. Cell walls are thick: diatom and chrysophycean spores are surrounded by a tough layer of biogenic silica, many dinoflagellate cysts have sporopollenine-like material or a calcium carbonate covering, other cysts present mucous coatings.

These stages represent a 'temporary stop' in the life history of the planktonic population and can thus be defined as 'resting stages', as opposed to 'growth stages' which are the cells undergoing vegetative division and thus responsible for the biomass increase of the population. The morphological and physiological characters of resting stages suggest defence against extreme environmental conditions or attacks of external killers i.e. predators, viruses, parasites. Phytoplankton taxa capable of producing resting stages can thus allocate a fraction of their biomass in highly differentiated cells that are capable of surviving in the sediments or in deeper layers of the water column. The ecological role of these cells can be compared to that of 'seed beds' in higher plants: they represent a storage of material for the inoculum of a subsequent growth phase of the planktonic population, once environmental conditions become suitable for vegetative growth. Resting stages undergo either true dormancy or quiescence periods of variable lengths, which can be regulated by internal clocks and modulated by external environmental cues. Dinoflagellate cysts, diatom spores and resting cells can remain viable for many years in the sediments, thus representing a long-term reserve of the planktonic populations over the years.

Coastal phytoplankton research has mainly concentrated on measuring physico-chemical properties of the environment in relation to productivity, but few dedicated autecological studies have been carried out and the life cycles of only a limited number of species have been resolved so far. Biological information on the different life strategies of phytoplankton species is an invaluable requisite for the comprehension of successional and distributional patterns of marine species. Recently, increased attention on the importance of these studies has been drawn due to need of understanding Harmful Algal Bloom (HAB) dynamics. Such blooms represent a serious thread to human health and national economies. Many harmful or toxic species (i.e. cyanobacteria, dinoflagellates, raphidophyceans) turned out to produce resting stages which are currently being distributed world-wide by anthropic activities such as translocation of shellfish and ballast water discharge. Mapping of cyst beds extension, knowledge of the factors that induce the production of resting stages, their survival capabilities, and their germination timing represent key data for the understanding of HAB events.

Continental shelves, together with inshore freshwater bodies, show the highest diversity of taxa with resting/survival stages, as compared to the open oceanic waters. This is also true for several micro- and meso-zooplanktonic taxa such as Copepods, Cladocerans, Rotifers, and Tintinnids. Different environments thus select specific life cycle types. Coastal marine waters and inland freshwater systems share relatively shallow bottoms, which fostered the evolution of meroplanktonic life strategies that include benthic resting stages. Coastal environments are characterized by a high temporal and spatial variability in their hydrographic features due to their specific topography and the intensity and extension of, for example, coastal currents, frontal systems, estuaries, tidal mixing and upwelling. Such high hydrographical diversity is reflected by high species diversity and successional patterns. However, the knowledge of the different life strategies of phytoplanktonic species that are superimposed on the physical scale can significantly help in understanding successional patterns in different areas.

Phytoplankton resting stages are generally interpreted as a dispersal mechanisms, however they can also be seen as anchoring systems to hold planktonic populations in a specific area and limit their dispersal in open oceanic watrs. The sticky mucous covering and branched ornamentations on the walls of resting stages can help in binding resting stages to the sediment and providing protection against grazing by benthic predators. Resting stages thus contribute in maintaining diversity of coastal marine phytoplankton through their capacity of acting both as dispersal and as space-holding stages, coupled with their propensity to survive for prolonged times.

Examples of the tight gearing between recurrent hydrographical events and planktonic organisms life cycles features are provided by upwelling systems. In these areas intense diatom blooms, mainly constituted by spore-forming diatoms occur as a consequence of the increased nutrient concentration. Spores are formed towards the end of the bloom, they sink on surface sediments or at the pycnocline in offshore waters from which they are resuspended by a subsequent upwelling event (Garrison 1981).

Another example is provided by freshwater bodies, where recurrent timing of planktonic stages in the water column can be explained by the production of resting stages that sink on the bottom and undergo a period of dormancy. The length of dormancy is different among species, and is followed by a quiescent period that can be interrupted only within specific temperature windows. Germination thus occurs only over a relatively limited time interval and provides the inoculum of vegetative stages in the water column (Rengefors & Anderson 1998). Similar studies, carried out in the northern Baltic Sea, provided the explanation for the onset of spring dinoflagellate blooms in the area. The two dominant species are cyst-formers that start to germinate and build up the motile population already under the ice cover in winter. Cells are adapted to low temperatures and poor light conditions and are thus able to maintain an inoculum population under the harsh winter conditions. This early and relatively abundant seeding probably favors dinoflagellates over diatoms, which are generally responsible of the early spring blooms in coastal areas (Kremp & Anderson 2000).

In coastal waters of the Mediterranean Sea dinoflagellate cyst fluxes have been quantified over the annual cycle and different cyst production patterns have been observed. Some species form cysts almost uninterruptedly during the annual cycle, whereas others only produce cysts over a narrower time window, during summer or early autumn (Montresor *et al.* 1998). Calcareous cysts are the most abundant morphotypes in the area and laboratory experiments demonstrated that also closely related species can have dormancy periods of markedly different lengths. Moreover, short daylength conditions can notably augment cyst production in some of these species (Sgrosso *et al.* 2001). These findings agree with sediment trap records showing calcareous cyst production peaks at the beginning of autumn.

I outlined some of the major characters of marine phytoplankton resting stages and presented some examples of the valuable ecological information that can be gained by studies of phytoplankton life cycles. Many questions still deserve interdisciplinary research. They range from taxonomic studies needed to identify the many unknow relationships between vegetative cells and their corresponding resting stages, to the comprehension of the physiological and molecular mechanisms that regulate the shift from resting to growth phase. Both classical and advanced technologies are now available and the study of phytoplankton life cycles should represent a challenge for a better understanding of coastal aquatic ecosystems.

Discussion

It is not yet explored whether encystment is entirely induced by environment, physical factors, internal clocks, defence towards predators or by exudates produced by competitors. Yet this is very interesting to study.

It is difficult to say whether the diversity of the spores/cysts is the same as that of the planktonic stages. Differences in morphology between the motile stages and the resting stages have been studied only for a limited number of species, but there is not a one to one correspondence. You have different planktonic species, which form the same morpho-type of cysts. But also the other way around is known: there are morphologically similar and phylogenetically closely related species that produce

different cysts. The crucial point is the understanding of the adaptive significance of the different morphologies, for both motile cells and cysts.
Cysts were presented as a way to maintain biodiversity. On the other hand, cysts can introduce invaders from different areas. In terms of biodiversity the introduced species can cause costs for the maintenance of biodiversity. Marina Montresor did not see this as a cost for the marine environment. At some times you can have problems: a newly introduced species can form massive blooms and overgrow the resident species, but over short time a new equilibrium is reached. Once more, species capable of forming resting stages, which can survive for decades in the sediments, constitute a biodiversity reservoir for coastal environments.

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Patterns of coastal marine biodiversity in major groups

Diversity of symbiosis in marine invertebrates

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Symbioses are defined as the living together of two or more differently named organisms. Such associations bring a new dimension to the term biodiversity, as their study involves describing the variety of the individual partners within the association as well as the diversity of the symbiotic associations as a whole.

Symbioses between bacteria and eukaryotes are widespread in the marine environment and their diversity is a demonstration of their plasticity and evolutionary success. Symbiotic associations between chemoautotrophic, sulfide-oxidizing bacteria and marine invertebrates were first discovered at hydrothermal vents in the deep sea but are now known to be common in sulfide-rich coastal marine sediments. One of the most numerous and diverse chemoautotrophic host groups in shallow water sediments are tubificid oligochaetes. In these worms, the associations range from a loose ectosymbiosis to an established endosymbiosis and correspondingly, from a fully developed gut to a gutless condition exists. The symbiotic associations between gutless oligochaetes and their endosymbiotic bacteria are obligate, and the hosts lack mouth, gut, anus, and nephridia (kidney-like organs). More than 100 gutless oligochaete species have been described that occur worldwide in different environments that range from coral reef sediments to intertidal sand flats. Using both classical and molecular techniques, we have begun to unravel the biodiversity of both the hosts and their symbionts, to gain a better understanding of the biodiversity and biogeography of these symbiotic associations.

We have now examined host species from Australia, Bermuda, the Bahamas, and the Mediterranean. In the gutless oligochaetes, the primary endosymbionts are chemoautotrophic sulfide-oxidizers (Krieger et al. 2000) that belong to the gamma subclass of the Proteobacteria and cluster with other previously described chemoautotrophic symbionts. The oligochaete endosymbionts are remarkably closely related to the ectosymbionts of nematodes, despite the fact that these two host groups are not related to each other. In many sediments, symbiotic oligochaetes and nematodes co-occur and we are currently investigating whether the biogeography of these hosts is mirrored in their phylogeny.

In contrast to many other marine hosts that generally harbor only a single symbiont species, gutless oligochaetes have established stable associations with multiple symbiont species. In addition to their primary symbionts these worms harbor a diverse assemblage of secondary symbionts, belonging to the alpha or delta subclass of the Proteobacteria, and the spirochetes (Dubilier et al. 1999). The phylogenetic diversity of the secondary symbionts implies a remarkable physiological diversity of these bacteria with unique, as yet unknown symbiotic interactions. Indeed, in one oligochaete host, we discovered a novel type of endosymbiotic syntrophy (Dubilier et al. 2001). In this worm, the secondary symbiont is a sulfate reducer that produces sulfide as a metabolic endproduct. This internally produced sulfide can be used by the primary, sulfide-oxidizing symbionts for the autotrophic fixation of CO_2. The acquisition of this internal sulfide source may have enabled these hosts to colonize the sulfide-poor sediments in which they occur, thus extending their geographic distribution.

Discussion

Some scientists found symbionts in echinoderms that were sulphate reducers, but were not able to detect any primary producers. This was considered curious because it would mean that this type of symbiosis could not work. An explanation for this may be that the research was based on clone libraries. This technique is considered not adequate for such studies because the technique does not show that the sequences that are found really occur in the host. Sulphate reducers are fairly often found in the guts (but it is not sure what they are doing there). Furthermore contamination is also possible, even when high numbers were found. It is a common problem with 16 S libraries.

The simplest way to detect the symbiont associations is with electron microscopy.

At Elba in the Mediterranean, the worms with their sulfate-reducing symbionts occur in front of seagrass meadows in coarse-grained sediments with a high advective transport of plankton. These sediments are very coarse and probably oxygen can penetrate very deep into the sediment. It is possible that many free-living sulphate-reducing bacteria occur in these sediments. It was hypothesized that the transport of oxygen through the sediment and the advective transport will enable substances from the water column to be pushed into the sediment, creating a suitable substrate for the sulphate-reducing symbionts. The worms can migrate between deeper sulphidic sediments and the higher oxygenated sediments.

In some coastal regions you see a similar process caused by the movement of the pycnocline. The sediment pore water gets flushed by the movement of the pycnocline by density displacement when the pycnocline is situated on the sediment. If the pycnocline rises, it flushes the pore water resulting in an input of nutrients. There is a continuous oscillation in nutrient content of the pore-water.

Symbiotic associations can be established by co-evolution or convergent evolution. All the primary symbionts have a common ancestor, and it is possible that co-evolution between the hosts and their primary symbionts occured. In contrast, the phylogenetic diversity of the secondary symbionts is high, indicating that these associations were established in convergent evolution.

The symbionts are probably transmitted from one generation to the next. The unfertilised eggs do not have bacterial symbionts. The egg is not in a cocoon like other marine oligochaetes. The egg is deposited in the sediment without a cocoon. The egg has to move a few segments along the body of the worm to the spermatheca to get fertilised. As the egg comes out of the adult worm there iare two genital pads on the ventral side of the worm that are full of bacteria: both the primary and the secondary symbionts. As the egg comes out, there seem to be tears in these genital pads. As soon as the egg is outside of the worm, it is covered with a thin mucus laver. In between the egg and this mucus layer, bacterial morphotypes that look like the primary and secondary symbionts are visible. At a later stage you see organelles inside the fertilised eggs. It is not yet clear whether these are mitochondria or bacteria. Hybridisation techniques at the electron microscopic level are being used to resolve this. It is possible that the transmission of the primary symbionts occurs from generation to generation.

It is possible that the secondary symbionts are transmitted similarly. However, there appears to be a leaky inheritance. It seems that the eggs are continuously taking up new bacteria from the environment as they are deposited into the sediment. This could explain the phylogenetic diversity of the secondary symbiont .It would be an interesting study to look at different stages of the egg, because we expect to find different bacteria attached to it. If the secondary symbionts also occur in a free-living stage, they should be culturable. Until now attempts to do this have failed, but that does not mean anything.It can take a long time to succeed in culturing a microorganism.

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Molecular genetics in benthic macrophyte diversity research

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Biodiversity continues to be a major focus of international research agendas. The population level is one of the most attractive because it is at this level that contemporary ecological processes act and it is here that population genetics theory can be utilized to it fullest extent to describe and to test hypotheses about population differentiation, adaptation and speciation. With respect to conservation of biodiversity, it is of interest to know how extensive benthic seaweed populations are, where their boundaries occur, how genetically diverse (or depauperate) they are and what this means for determining "biodiversity hotspots. In this talk I will present two examples from our laboratory in which genetic methods have been applied to investigate some of the above questions in marine macrophytes.

Ascophyllum nodosum is dominant seaweed along many rocky intertidal shores throughout the North Atlantic. Next to the kelps, fucalean taxa such as *Ascophyllum* are the largest macrophytes and provide important habitat for invertebrates. Genetic structure was investigated over a range of scales throughout the North Atlantic basin. The analysis is based on six polymorphic microsatellite loci and >1000 individuals. Strong genetic structure at small spatial scale was found and is consistent with demographic models based on long-lived individuals, low recruitment and many sib matings. At large spatial scales only weak population differentiation was found. This is consistent with recent recolonization of the North Atlantic following the last glacial maximum. Demographic modeling in *Ascophyllum* reveal that survival and not recruitment are key key, that generation times in the Brittany area are about 60 yrs and individual genets may by >200 years old. High allelic diversity in the Brittany area suggests that it is an archival hotspot of biodiversity in western Europe.

The seagrass *Zostera marina* is also found throughout European coastal seas. Because seagrasses have a rhizomatous growth form of genets and many ramets, the first task at hand is to determine the genetic individual. Characterization of clonal diversity and overall bed architecture from the genetic perspective can be done using high-resolution microsatellite loci, which have been developed for *Z. marina*. The range of diversity so far detected ranges from ancient monoclonal meadows in the Central Baltic to highly diverse meadows in the Western Baltic and North Seas. Knowledge about the local diversity and architecture of beds provides invaluable information about past habitat fragmentation as well as present stability. Seagrass ecosystems are highly vulnerable and are difficult to recover once lost. Although regional populations of *Z. marina* are connected by gene flow, significant population differentiation was detectable at scale of 50 km and up.

The opportunities for utilizing benthic macrophytes as biodiversity monitors along the proposed BIOMARE transects is excellent. Standardized protocols for sampling and genetic assays have already been developed and would be easy to implement in a genetic monitor program.

Discussion

Steve Hawkins visited the Azores some years ago and found some drifting thalli of *Sargassum* and *Ascophyllum* that most probably came from the US. Crossing the Atlantic was apparently no problem for these seaweeds. Genetic studies using microsatellite loci by Jeanine Olsen, Per Åberg and colleagues now confirm that long-distance dispersal "happens"—and we can trace it. Using the seaweed *Ascophyllum nodosum* and the seagrass *Zostera marina* as examples, Jeanine Olsen illustrated how high resolution genetic markers can be used in conjunction with demographic modelling to explore a myriad of biodiversity questions at the population level. For example, how much diversity is there in a particular species, how is it distributed geographically, where are the European hotspots, where are the vulnerable edge zones where populations are at risk, how do life histories affect persistence and recovery of local populations in the face of habitat fragementation, catastrophic impact or gradual climate change?

Turning first to *Ascophyllum*, demographic studies (which utilized matrix modelling) in western Sweden, Isle of Man and Brittany showed that *Ascophyllum* is a very long-lived seaweed. Ten to twenty year old individuals have been empirically documented by many workers, whereas the new results suggest that genetic individuals are often >200 years old—an age not previously considered for marine macrophytes. The same is also true for some seagrasses. This means that we need to rethink our timeframes. Many sea "weeds" should be thought of as marine "trees". Genetic and demographic studies also revealed that recruitment is poor in *Ascophyllum* with very slow recovery rates if plants are entirely removed from the substrate. This means that long-lived fucoids, which provide dominant structure along rocky intertidal shores will have difficulty in recovering in the event of habitat fragmentation or other catastrophic impacts. Some of the populations in Brittany, for example, may actually reflect original recolonization following the retractions of ice some 10,000 years ago. A phylogeographic survey of *Ascophyllum* further revealed that the Brittany peninsula harbors the highest allelic diversity, which is consistent with refugial areas that existed during the last glacial maximum (LGM). Given these results, it was suggested that the Brittany area be recognized as a node of high marine biodiversity in western Europe. Although perhaps a bit premature, the idea is good. The degree to which Brittany holds as a biodiversity node for other benthic species is likely to be related to the nature of the life history and temperature tolerances that would have been affected during previous climatic shifts in sea surface temperature. In other words, by identifying a core group of benthic species with different temperature boundaries, the possibilities of establishing indicators of climate change are quite good.

Turning next to seagrasses, they too are important indicators of changes in biodiversity. Though we analyze at the level of populations, in fact we are also monitoring at the level of the ecosystem—a special aspect of seagrasses. Genetic markers, again come to the rescue. In the case of *Zostera marina*, the genet-ramet structure makes it virtually impossible to separate individuals in the sea of leaf shoots that form a meadow. We asked the question, "What is a genetic individual?" Excavation of rhizomes is no guarantee because connections are easily broken over the years. Only by the use of high resolution, multi-locus genotypes can absolute identification be determined. In this way, the contribution of clonal propagation to population structure of a meadow can be mapped. Results from work by Thorsten Reusch, a former post-doc in the Groningen lab, indicate a variety of meadow architectures. These ranged from giant monoclonal meadows in the central Baltic to highly diverse, multiclonal meadows with varying degrees of monoclonal patchiness embedded at different scales in the western Baltic and North Seas. Genetic characterization of local meadows in this way can provide profound insights on such diverse processeses as meadow age, past habitat fragmentation and current genetic diversity, as well as possible inbreeding depression and forecasting of ecosystem health. Because there is no such thing as a "typical" seagrass meadow, we can actually exploit the lack of generalization to set criteria for measuring local to regional change in response to whatever variable we choose.

Zostera marina occurs throughout the North Atlantic and along all of the proposed BIOMARE transects. Many scales could be investigated in a coordinated manner because the necessary genetic markers have been developed and uniform assay protocols have already been put in place. The same is true for *Ascophyllum* and *Fucus serratus*, both of which occupy slightly different postions in the inter- and subtidal zones.

In conclusion, this presentation clearly demonstrated the power of the molecular ecology approach in biodiversity research at the population level. Fucoid seaweeds and seagrasses are clear candidates for long-term monitoring as well as forecasting of changes along European coastlines. The BIOMARE infrastructure will make this relatively painless.

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Diversity of zooplankton

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Biodiversity, as defined in the Biodiversity Convention, is the variety of the natural world at all levels of biological organisation (genetic, populations, community, landscape) and over all spatial and temporal scales. This is a very fuzzy concept, so it has to be made quite clear as to exactly what aspect is being discussed. I mostly address the factors influencing species richness – i.e. the inventory of species that may occur in the plankton, but inevitably also allude to the processes affecting dominance.

Scale and pattern both in time and in space is of fundamental importance (Ormond *et al.* 1997). Not only does our perception of the natural world change with scale, but also the relative importance of the factors influencing the patterns change radically. So a necessary basic requirement is to ensure that our scales of observation are tuned to appropriate scales of the pattern and/or process being studied. Temporal scales can be roughly subdivided into long-, medium- and short-term. Long-term scales (say $>10^4$y) range through evolution, geological changes to coastal habitats (e.g. the fluctuations of sea-level during the glaciations), and vicariance events (e.g. the drying up of the Mediterranean and the opening and re-closure of the Panama Isthmus), and affects the subset of the global species inventory that occurs in any locality. Medium-term changes (say $\sim10^4$ to 10^2y) tend to be dominant in controlling dispersal mechanisms, and short-term change (say 10^{-3} to 10^2y) in the control of persistence (maintenance) of the species assemblages we observe (Figure 1) There are many cyclic and acyclic changes in the physical, chemical and biological environments that are familiar and relatively well understood phenomena (tides, wind patterns, weather patterns), but there are many others which have only recently been recognised and are still poorly understood (e.g. climate regime shifts, ENSO and NAO fluctuations). In addition, there are major catastrophic events such as major seismic or volcanic events, abnormal weather patterns, which can also disrupt “normal” biological patterns and processes, sometimes irreversibly. The impacts of some anthropogenic activity such as the building of sea-level canals between disparate seas, the interception of freshwater outflows, direct or accidental introduction of non-native species may have impacts analogous to such “events”. It is of fundamental importance that we understand the interrelatedness of ecological processes (for example land-use in the coastal region, the building of dams for irrigation and coastal engineering can have major impacts on inshore plankton through changing hydrographic regimes, affecting nutrients cycles, and altering biological interactions). We tend to ignore the fact that the natural world is so “joined up” particularly when trying to attribute causality.

We perceive the planktonic world through our sampling methods and protocols. These give us a very limited (and not necessarily either matching or relevant) series windows on to the full spectrum of variability. For example, it can be demonstrated that simply changing sample size, our perception of distributional patterns can be drastically modified. There are well-established time/space relationships in many physical processes, and inappropriately scaled sampling regime may blind us to the significance of ecological responses to hydrodynamic forcing. Strong biases are introduced by the fishing efficiencies of nets (species richness varies strikingly with mesh size), the need to subsample, and subjectivity in what analysts are aware of and can recognise in samples (should eggs be identified and enumerated?).

Neritic plankton is very different in character from oceanic plankton in its diversity and composition. Transects sampled across continental shelves show that open ocean plankton assemblages are *locally* richer in species than their neritic counterparts (note I use assemblage as a term to describe what co-occurs, whereas community suggests an ecologically functional unit, and, as discussed below, all that is caught in a net is often not in the same functional unit). However, global inventories of neritic taxa are very much larger than oceanic species (so can we expect there to be any relationship between local and global species richness?). Coastal environments are far more finely structured physical, geographical and chemically, because of the complex and intimate interactions between the seabed structure (bathymetry, geology and “weather”) ties the composition of neritic plankton assemblages far more tightly to locality than is seen in open ocean plankton.

Patterns of coastal marine biodiversity in major groups

The neritic plankton assemblages consist of:- a. holoplankton species that are planktonic throughout there life-cycle (they occur year-round in the plankton, although at high latitudes some may over-winter as eggs or resting stages on the sea-bed); b. meroplankton, the larval stages of benthic species (often difficult to identify with any precision), which can make up >50% of net samples, and are highly seasonal in occurrence and composition and are derived from the diverse local benthic and littoral assemblages; c. immigrants advected in from oceanic water; d. immigrants from freshwater; e. non-native introduction; f. benthic species thrown into suspension by storms and strong waves action. Should every taxon sampled be included in estimates of diversity? While it does not seem logical to include them all, especially those that play little or no part in pelagic prosesses, no attempts have been made to develop criteria for the inclusion or omission of meroplanktonic species.

Thus factors that influence the composition of the species inventory include:- geological history of tectonic movements and sea-level fluctuations (isolation, dispersion), evolutionary history of extinctions, radiations, larval evolution, and changes in dispersion and geneflow.

Factors influencing maintenance mechanisms include: - Geographical factors (latitude, coastal morphology, exposure to wind and current, bottom type, riverine discharges, climate); hydrodynamics (currents, tides) productivity (nutrient regimes, organic supplies local and imported, sediment loads, vertical mixing and stratification, seasonality etc); biotic processes and feedbacks (ecosystem structure, food-web structure, interspecific competition, invasions, local and global extinctions). All of which are influenced to a lesser or greater extent by local anthropogenic impacts resulting from exploitation (living and non-living resources, recreation), pollution, eutrophication, coastal engineering and protection, land-use, and water management. Perhaps of most concern long-term are the global impacts that are the products of the burgeoning human population and resource exploitation, such as global warming, excessive fixation of atmospheric nitrogen and the occupation of coastal fringes.

The prediction of future changes in population structural and ecological diversity will be essential if the effectiveness (and cost effectiveness) of environmental management of coastal waters is to be optimised. For this a key requirement is to develop means of discriminating between variability that is "natural" and that which is anthropogenically driven, and this should be a target for future studies of coastal plankton.

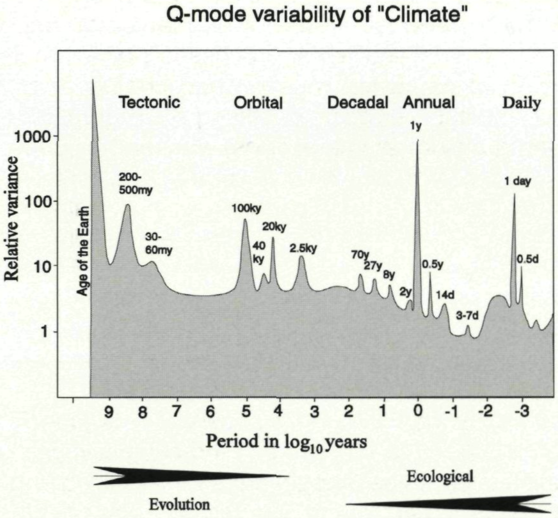
Q-mode variability of "Climate"

Figure 1. Relative variance of 'climate' over the full spectrum of time scale experienced by life on Earth, driven by tectonic shifts on ocean basins and the arrangements of continents, to planetary oscillations to climate fluctuations.

The longer-term oscillations have had major impact on evolution and speciation patterns, but these are also overlain by cataclysmic events leading to mass extinctions. It is the shorter-term events that influence the maintenance of assemblages. Least understood are the medium decadal and centurial fluctuations in climate (based on Mitchell, 1976).

Discussion

Taking into account inter annual variability and resting stages, what kind of intervals you must take to monitor the status of plankton diversity?

There is no simple answer to this question. You need a lot of understanding about the area you work in. You need information about circulation patterns, plumes, runoffs, etc.

There is no right answer because inevitably you run into these problems of selectivity of the way you are looking at these systems. If you are not actually sampling at the right sort of time and space frame then your answer could be entirely misleading.
The continuous plankton recorder is adequate for the collection of time series and is very suitable for the monitoring of changes. The spatial scale considered is large enough. However the samples are not suitable to study what is actually there in terms of the species inventory.

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Ciliate Microzooplankton, An Example of Congruence of Local and Regional Diversity

Patterns of coastal marine biodiversity in major groups

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Microzooplankton occupy a key position in planktonic food webs, linking algal and bacterial production to higher trophic levels and among the microzooplankton, ciliate protists often dominate. Tintinnids, characterized by the possession of species-specific loricas or shells, are a ubiquitous component of marine ciliate communities. Among sea microbes, tintinnids are unique because they are both quantitatively important in food chain dynamics and a group in which species identifications are based largely on gross morphology of the lorica. In contrast with most microbial groups, identifications can be made using the relatively low tech method of light microscopy and the exploitation of comparative data gathered over the past 100 years is possible. I examined species and morphological diversity of tintinnids in 2 systems, the Mediterranean Sea and the Chesapeake Bay to compare tintinnid diversity patterns with those of other taxa. Mediterranean samples were used to investigate relationships between resources and diversity over a large spatial scale. Correspondence of tintinnids with typical estuarine diversity patterns was examined in Chesapeake Bay tintinnids.

In the Mediterranean Sea, a longitudinal gradient of chlorophyll concentrations and primary production is found, rather than the latitudinal gradient of the world ocean. Samples from oceanographic campaigns in June and September were employed to compare diversity of tintinnids to availability of food resources in the form of chlorophyll stocks or primary production. June samples, gathered in 1992 and 1996 (see Dolan 2000), showed a distinct gradient of increasing diversity from west to east corresponding to reductions in chlorophyll stocks and a deepening of the chlorophyll maximum layer. The gradient of taxonomic diversity (numbers of species, genera, and values of H') corresponded roughly with morphological diversity, in the form of SD's of lorica length but not oral diameter. The lack of relationship between taxonomic diversity and the variance of oral diameters lent little support to the idea that taxonomic diversity was linked to resource or feeding diversity. However, there was little data available on the composition the phytoplankton. Thus, while a longitudinal trend was found, analogous to the latitudinal diversity gradient found among many groups in the world ocean, the mechanism was obscure.

In September 1999 a campaign which sampled waters from the Moroccan upwelling system to the eastern basin of the Mediterranean provided samples for tintinnid studies as well as detailed phytoplankton pigment data. The September pattern of tintinnid diversity differed considerably from that based on June samples. While chlorophyll and primary production again declined from west to east, tintinnid diversity increased from west to east but reached a plateau in the central basin. Morphological diversity, as H' values for size-classes of oral diameters and lorica lengths, paralleled taxonomic diversity. Phytoplankton accessory pigment data permitted division of the chlorophyll crop into 3 size-fractions, pico, nano and micro-chlorophyll (see Vidussi et al. 2001). Considering each size-fraction as a separate species allows calculation of a crude index of phytoplankton 'size-diversity' (chlorophyll-size H'). This metric of tintinnid food-resource diversity was correlated with tintinnid taxonomic and morphological diversity. Along a large geographic gradient (e.g., 10°W -> 25°E) taxonomic diversity can be linked to morphological diversity which can in turn be associated with food resource diversity (Figure 1).

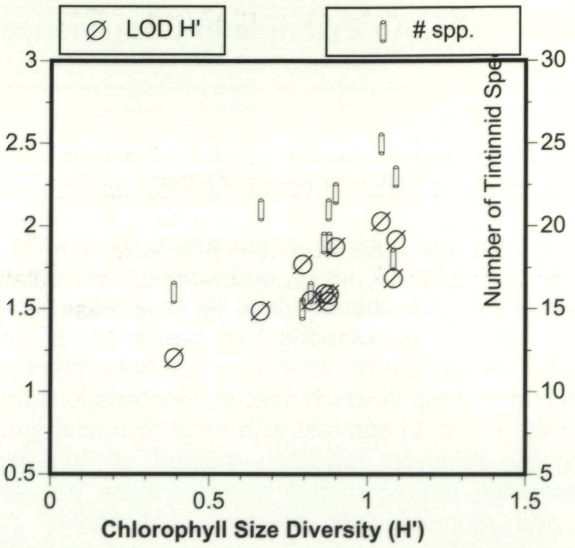

Figure 1. The relationship between resource diversity (size-class diversity of the chlorophyll crop) and tintinnid morphological and taxonomic diversity in terms of oral diameters (LOD) or numbers of species (# spp).

On a smaller spatial scale, a direct comparison of tintinnid diversity with patterns reported for other groups was made in the Chesapeake Bay, a large, eutrophic, coastal plain estuary. Estuaries are typically described as low-diversity environments in which for a given group, biomass decreases and diversity increases with salinity. Tintinnid diversity appeared unrelated to salinity and population density. Diversity was remarkably high, comparable to that of the oligotrophic eastern Mediterranean but along a spatial gradient of 10^1 km, no clear trends were evident, in contrast to the patterns found in the Mediterranean at a scale of 10^2 km.

The similarity of average values of diversity metrics in 2 very distinct systems whose only obvious common characteristic is latitude (both range from about 37°N – 40°N) prompted an examination of latitudinal trends using easily available literature reports giving numbers of species found at single points and single times (regardless of sampling method); maximum species numbers were chosen when a range was reported. The results (Figure 2) suggested that over a global scale a clear gradient was apparent with latitude a better predictor of species abundance than type of environment (e.g., estuary vs. oligotrophic marine), over very large geographic scales (10^3 km).

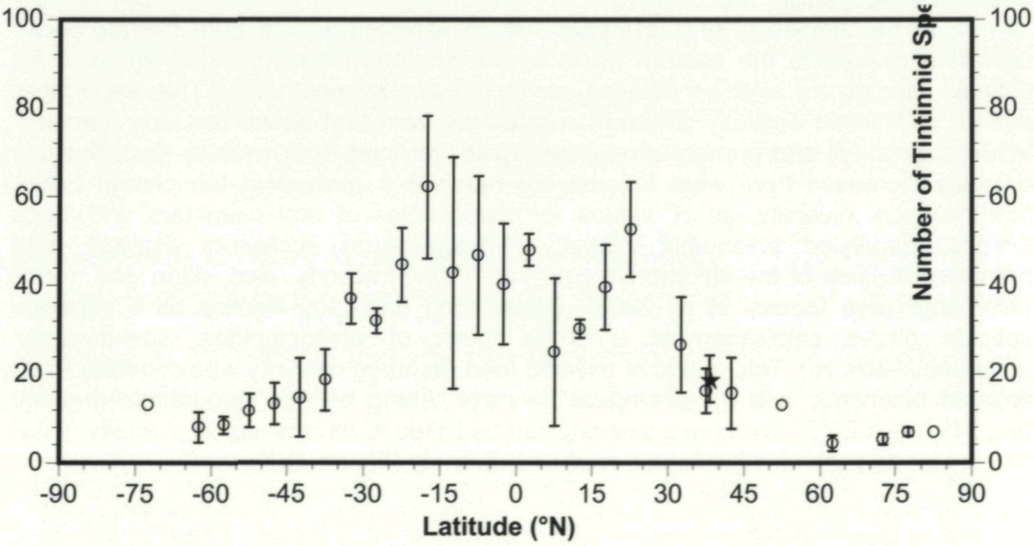

Figure 2. Latitudinal trends in tintinnid species abundance, based on literature reports. Maximum species abundance for individual locations (n = 168) were averaged (±sd) within sets of 5° of latitude and were plotted against the mid-points of the 5° bands. Regression relationships are for the southern latitude estimates (n = 13), $r^2 = 0.75$, $x = 0.703 * lat + 0.531$ and for the northern latitudes (n = 13): $r^2 = 0.70$, $x = -0.50 * lat + 0.452$.

Over small spatial scales (10^1 km) diversity can appear unrelated to either physical conditions of the water column (e.g., turbulence) or biological (e.g., chlorophyll concentrations). Over large spatial scales (10^2 km), patterns emerge as water column conditions shift dramatically. However, over very large spatial scales (10^3 km) local diversity appears to reflect regional diversity, which may in turn be governed by such factors as temperature constraints on geographic ranges of individual species.

Acknowledgements. This research was funded in part by NTAP (contract EVK3-CT-2000-00022) of the EU RTD program "Environment & Sustainable Development", Eloise project cluster and the CNRS through PROSOPE (JGOFS-France).

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Patterns of biodiversity in different habitats

Chaired by
Richard Warwick
Karsten Reise
Victor Smetacek

Patterns of biodiversity in different habitats

Animal diversity in shallow water sediments

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It is generally believed that species richness increases with depth to a maximum at around 2,000m. This paradigm was based on data collected in the late 1950's and early 1960's. Recent data however, show that the 1960's data are not representative and thus the paradigms need re-examination. The basic problem is that the data are taken on ecological scales and yet they are used to answer evolutionary questions. Data representing appropriate evolutionary spatial scales have been collected from coastal areas and show that species richness may be as high as the highest recorded in the deep-sea. Whilst this suggests that the cline of increasing diversity from shallow to deep-sea does not exist, the database for the deep sea is not yet sufficient to draw such a conclusion. It seems likely that local species richness is linearly related to regional species richness. This implies that it is the regional species pool that determines local richness rather than local scale biological interactions, which have been intensively studied.

Research priority should be given to assessment of the spatial scales and dynamics of species richness from local patches to assemblages habitats and landscapes, especially in coastal areas where the threats to biodiversity are greatest. New technologies are available, such as side-scan sonar, acoustics, and under-water digital video cameras but as yet have been relatively little used. Rapid-assessment techniques and surrogates for complete species inventories also are key areas for study as are studies of the relationship between species richness and functional processes. Finally, better data on the economic value of intact coastal systems are needed so that evaluations of the balance between the needs for conservation and exploitation can be made on a more rational basis than is used today. The long-term protection of the biodiversity that we have is likely to be more economically valuable than short-term exploitation.

Discussion

Q: In one of the presented theories it was hypothesised that the regional species pool is the primary determinant of local species richness. However, local species richness is determined not only by random selection of the regional species pool but also by ecological processes that modify the local pattern.
A: Agreed. However, at local scales disturbance, whether caused by physical processes, competitive interactions, or predation, creates available space. The space is then colonised by species from the regional species pool. Thus although predation and competition are important processes the large numbers of species found in local samples are comprised mainly of species occurring at low abundances, which are derived from the regional pool. Hence regional species richness is extremely important. Another neglected aspect that is really important but missing in studies of marine species richness is the geographical range of species. Our studies suggest that ranges are narrow, but how this aspect relates to defining regional richness in coastal areas has not been studied.

Q: Another major point is that species identity is often not considered. We only count numbers of species present.
A: From an ecological point of view it is more interesting, and important, to focus on the composition of communities, which species are present, what they are doing, and how important individual species are in the functioning of the system.

Q: In the relationship between temperature and energy and species richness, is energy expressed as an input like carbon, or Joules?
A: On global scale solar energy input does not correlate well with marine productivity. So equating energy to temperature to productivity to evapo-transpiration seems to be stretching the argument.

A: Wright's hypothesis is simply to use energy as a substitute for area in the species : area relationship. For terrestrial systems energy input has been replaced by evapotranspiration and this gives excellent fits to data on terrestrial plants. Thus it is not area that controls species richness but something related to area. The marine data on species richness of gastropod snails shows that richness is correlated with Sea Surface Temperature? Does the relationship fit for other taxa and other areas? What is the mechanism that explains this relationship? Not all tropical areas have equally high species richness so temperature would not appear to be the most obvious correlate with richness. More studies are urgently needed.

Thermal ecotypes in a tropical to warm-temperate marine macrophyte: Analysis of the physiological background of ecotypic differentiation

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The green macrophyte Valonia utricularis has a world wide tropical to warm-temperate distribution, occurring also in the Mediterranean. It extends in the northeast Atlantic to the coast of Portugal (39ºN, annual temperatures: 13-17ºC), while the northern distribution limit in the northwest Pacific is much further south (26ºN, annual temperatures: 21-29ºC). Annual temperature ranges in tropical localities are between 25 and 28ºC, but are broader and lower in warm-temperate localities of the western Mediterranean (13-24ºC). A data set of thermal traits (survival ranges, temperature requirements for growth and reproduction) of 13 isolates of V. utricularis was obtained and a detailed biogeographical analysis was made on the importance of physiological constraints, trade-offs and local selection pressure for the development of temperature ecotypes. Growth and survival ranges of the Atlantic/Mediterranean compared to the Indo-west Pacific isolates were shifted to lower temperatures, accompanied by parallel, though smaller shifts at high temperatures. The former group sporulated at 18-20ºC, while the latter does so at 28-30ºC. Thus, the isolates of V. utricularis could be assigned to two thermal ecotypes: to a more cold-tolerant eurythermal northeast Atlantic/Mediterranean and to a more cold-sensitive stenothermal Indo-west Pacific type.

The physiological background of the ecotypic differentiation was studied in 9 isolates in the second part of the project using in vivo chlorophyll a fluorescence measurements to assess temperature effects on photosynthetic performance. Relative susceptibility to chilling-induced photoinhibition and its recovery was studied by following the maximal quantum efficiency of photosystem II (Fv/Fm) as a measure of photoinhibition. Two different types of photoinhibition can be distinguished by their different relaxation times: a protective down-regulation and damage to photosystem II reaction center proteins. We could demonstrate that the Atlantic/Mediterranean isolates were relatively less susceptible to the applied cold stress of 5ºC, since more than 80% of the inhibition could be attributed to dynamic down-regulation of photosystem II. The Indian Ocean isolates were predominantly damaged and the northwest Pacific isolates had an in-between position.

Short-term temperature response of photosynthetic performance was examined by measuring the effective quantum yield of photosystem II (ΦPSII) between 5 and 35ºC. Also light-response curves were recorded at sub-optimal, optimal and supra-optimal temperatures. Plants were grown under optimal (25ºC) and sub-optimal temperature conditions (where they reach 30% of their maximal relative growth rate) in order to assess their capacity for low temperature acclimation. We could show that the Atlantic/Mediterranean isolates had lower temperature optima of photosynthesis (18-20ºC versus 25-30ºC) and possessed additionally a high capacity for acclimation to sub-optimal growth temperatures which was lacking in the Indo-west Pacific isolates (see Fig.).

The obtained physiological results mirror the ecotypic differentiation described with respect to growth and survival. The results can be interpreted as an adaptation of the northeast Atlantic/Mediterranean isolates to lower winter temperatures but also to broader annual temperature ranges at the warm-temperate locations. In contrast, low temperature tolerance and acclimation responses of the true tropical Indian Ocean isolates are rather limited which is in accordance with constant, high local temperatures.

Phylogenetic and distributional evidence suggests a tropical origin of the genus Valonia with subsequent extensions of ranges into warm-temperate waters. Pleistocene glaciations (18,000 years BP), which acted differently at the northeastern Atlantic and northwestern Pacific coasts, are presumably responsible for cold-adaptation taking place in the Atlantic and not in the Pacific populations. First of all were the temperature shifts more severe in the Atlantic than in the Pacific. We hypothesize that temperature stress in isolation is particularly responsible for the cold adaptation of the Atlantic populations. Even though possible refuges existed in both oceans (Atlantic: eastern Mediterranean and Cape Verde Islands; Pacific: Indian Ocean), cold sensitive populations trapped in the eastern Mediterranean were subjected to low temperature stress and could have developed adaptations to low temperatures under reduced gene flow.

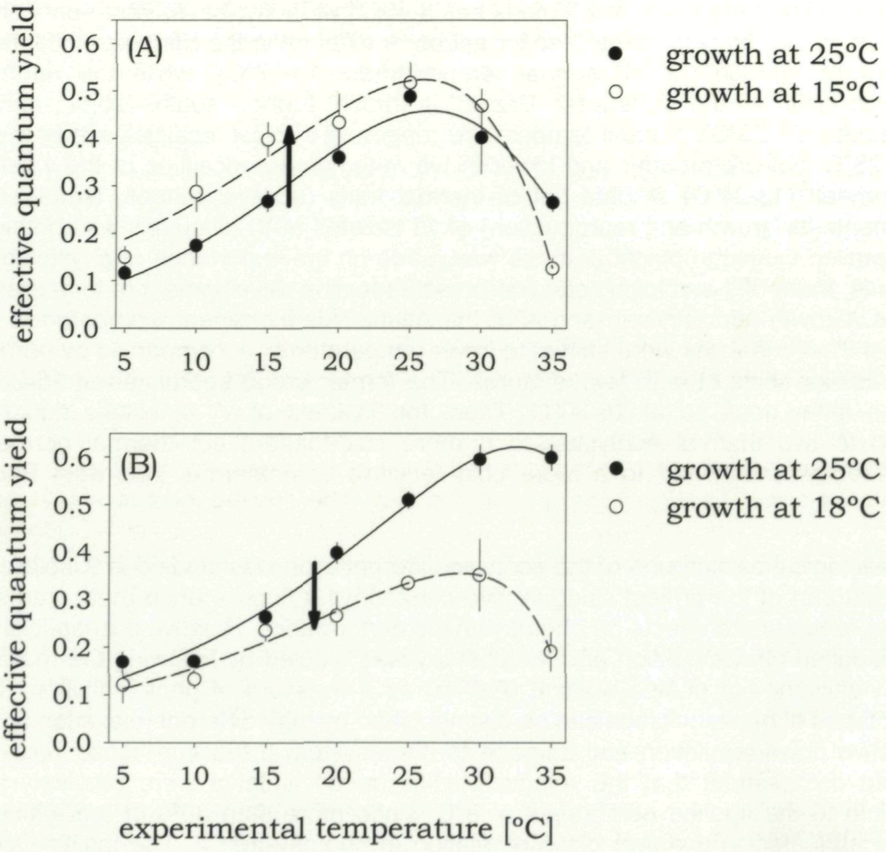

Figure 2: Short-term temperature response of effective quantum yield (ΦPSII) of (A) a Mediterranean and (B) an Indian Ocean isolate. Experimental data and fitted curves are shown for plants grown at optimal (filled circles, solid line) and at sub-optimal temperature (open circles, dashed line). Data represent average and standard deviation of n=3 measurements. Arrows indicate presence or absence of acclimation potential.

Diversity of benthic copepods in a dynamic but intensively exploited marine environment

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Harpacticoid copepods of subtidal sandbanks on the Belgian Continental Shelf are investigated in order to find ecological indicators for monitoring purposes and to indicate vulnerable and threatened habitats. Four ecotypes exist among harpacticoid copepods: big epibenthic and endobenthic species, tiny interstitial species and a few free swimming species. Density, diversity and community structure of harpacticoid copepods were analysed on the Kwintebank, a linear subtidal sandbank in the Belgian coastal waters. It is a high-energy environment, subject to very strong tidal currents, which run parallel to the long axis of the sandbank (Willems et al., 1982). The northern landscape of the sandbank is characterised by big sand waves, with coarse sands at the tops and finer sediments in the depressions, creating a very divers and dynamic biotope for meiofaunal organisms. The southern part consists of a flat plateau of fine sands. These morphological characteristics (Fig.1) and granulometric gradient are a result of the local tidal current patterns, mainly the flood stream. Because of its location near the coast, the appropriate grain size of the sand and the low lime content, more than 95% of the sand extraction on the Belgian Continental Shelf occurs on the Kwintebank, being concentrated at the northwestern tip and in the centre of the bank. The extraction activities impact bottom habitat structure and diversity by coarsening and homogenising the sediment and cause a strong erosion process. The communities of sandbanks in areas with a high amount of exposure are adapted to continuous changing conditions, but these disruptive and widespread human-induced physical disturbances may decrease community complexity and increase the abundance of opportunistic species.

Samples were taken in 1997 with a Reineck box corer and included 10 stations on the bank and 2 in the gullies next to the bank. 80 copepod species were recorded, of which 38 % were new to science. Diversity was highest in the most dynamic northern part of the sandbank and decreased to the south. Three major copepod communities were distinguished on the bank. Their occur-rence was related to the linear gradient from fine sands in the south to coarser sands in the north. A fourth community was found in the gullies next to the bank and in one station positioned in the centre of the bank (Fig.1). This station was characterised by a very low density and diversity although the sediment composition of this station was comparable to other bank stations. In this area sand extraction activities caused a coarsening of the sediment and an increase in depth. Over the entire sandbank analogies were found in the occurrence of erosion and extraction areas and the distribution of harpacticoid communities (Fig.1). Sand extraction activities can result in direct and indirect effects on harpacticoid communities. Direct changes can result from physical stress while habitat modification through changes in sedimentation pattern and sediment com-position cause indirect changes (Fig. 2). In the most intensively exploited stations a significantly higher density of juveniles and the occurrence of harpacticoid species typical of physically stressed environments were found. Both observations are directly related to sand extraction intensity. The results of 1997 were compared with copepod species distribution data collected in 1978 (Claeys, 1979), prior to intensive sand extraction. The harpacticoid community structure of the southern part of the bank was still comparable after 20 years and hence stable in time. In the northern part diversity remained high but the abundance of big epi- and endobenthic species decreased and species composition altered in favour of interstitial species, which are able to hide deeper into the sediment. In the centre of the bank diversity decreased: a shift was recorded from a species rich northern community to a southern community (less species, high dominance of Paraleptastacus espinulatus, Leptastacus laticaudatus s. str. and Kliopsyllus constrictus s. str.) as a result of changes in sediment characteristics. A geomorphological survey of the last six years indicated an unnatural increase of depth of 5 m in this area (Fund for Sand Extraction, unpublished data). Due to sand extraction depth increased, sand waves were flattened and a depression was formed in this area, located near to the station with the very low density and diversity (Fig. 1). The altered sediment composition may be the result of an accretion of fine sediments, as a consequence of changed current patterns in the depression. The shift in community structure can be considered as an indirect effect of sand extraction (Fig. 1 & 2).

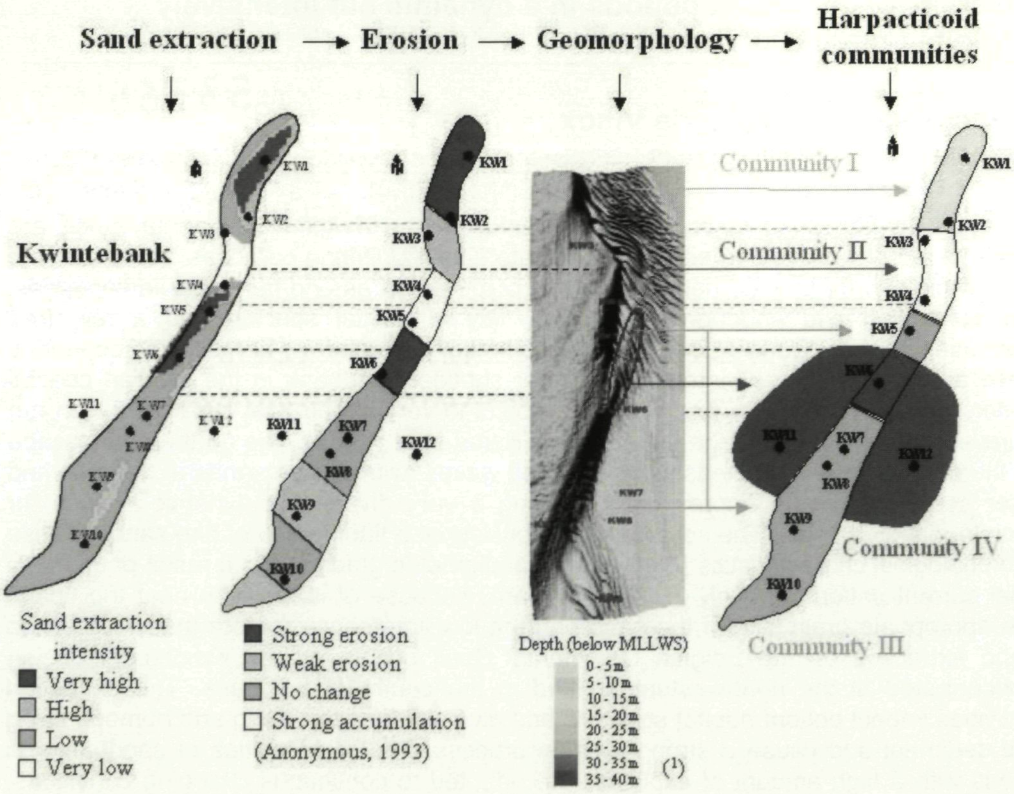

Figure 1. (1) Multibeam recording: Geological Survey of Belgium - Continental Shelf Team + Research Unit for Marine and Coastal Geomorphology, University of Gent.

The extension of the present depression due to sand extraction can become quite problematic, if these human-induced physical disturbances may cause a continuing erosion and im-poverishment. Spreading the extraction activities over the different sandbanks in the concession zone will help decreasing the disturbance frequency and intensity.

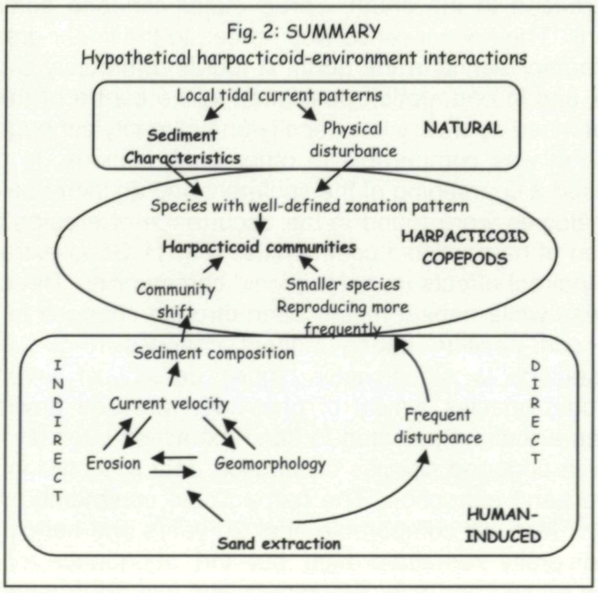

Figure 2. Hypothetical harpacticoid-environment interactions

Discussion

Harpacticoid copepods can be important in the alimentary diet of mysids, juvenile flatfishes and especially of non-commercially fish species like gobies. The epipsammic forms can make up to 70 % of the stomach content of a goby but interstitial species are usually not found in the stomachs. But some American demersal fishes do use interstitial species as an important food source. Harpacticoids have a high nutritional value and the various life cycle stages bridge a gap in the size spectrum of available food. The decline in endo- and epibenthic species can limit the food availability for demersal fishes.

The life cycle of the small interstitial species lasts from some weeks up to a few months. The larger epi -and endobenthic organisms are living up to one year.

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Patterns of biodiversity in different habitats

Setting patterns of diversity in marine sediment communities: The importance of bioturbation

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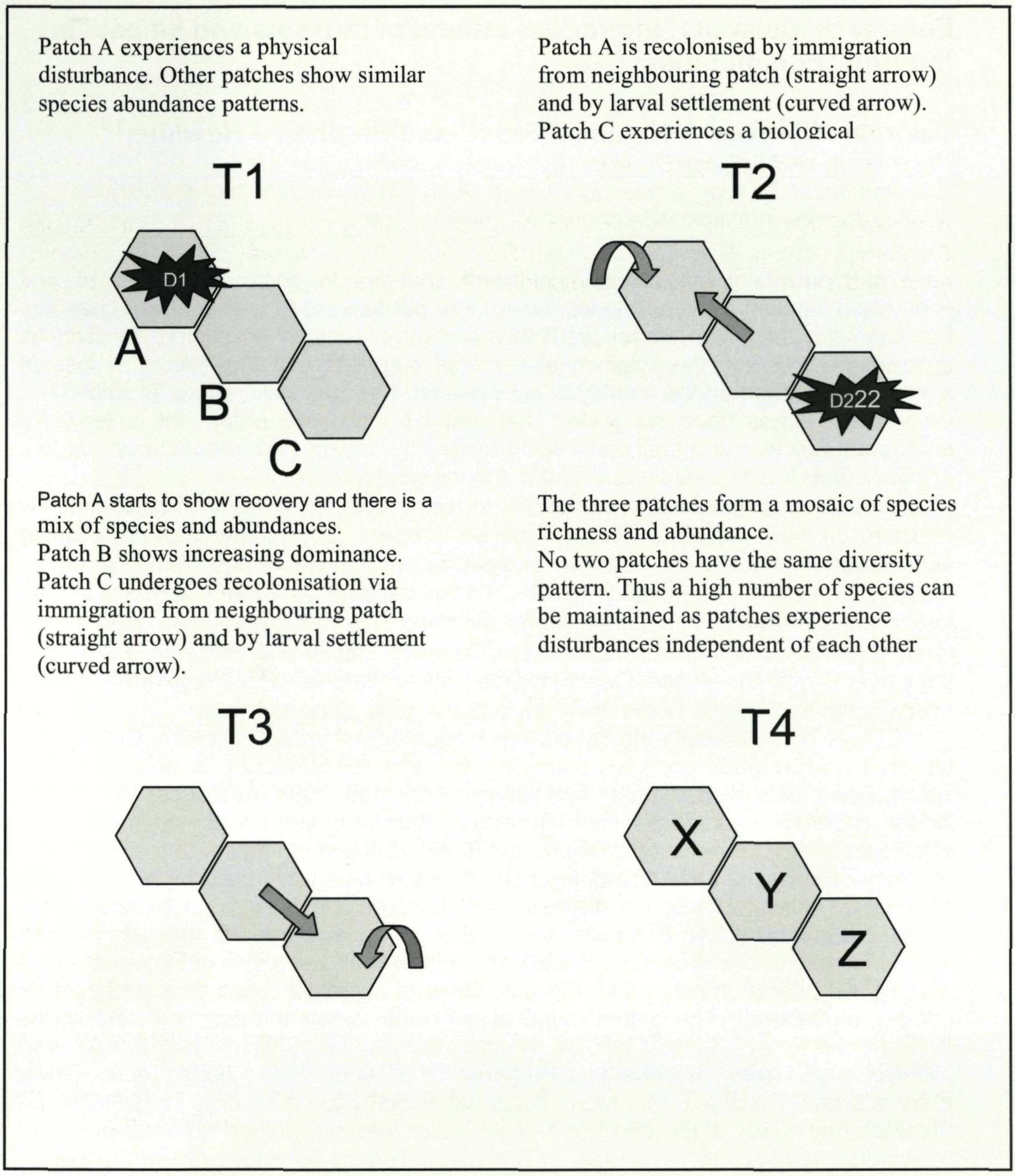
A series of manipulative experiments was conducted in the mesocosm at the Marine Research Station Solbergstrand (MRSS) near Oslo, Norway. The experiments examined the effects of physical disturbance, as a consequence of bioturbation, and organic enrichment both independently and in combination on a typical macrobenthic infaunal community of muddy-sand. Sediment, together with associated fauna, was transplanted into the mesocosm from Bjørnhordenbukta, a small sheltered bay near the MRSS. To investigate the effect of disturbance intensity and type on benthic infaunal diversity and community structure, bioturbating species with contrasting feeding strategies and mobilities were added, at a number of densities, to areas of caged sediment. Results demonstrated that changes in the diversity and structure of an infaunal community were dependent on the intensity at which the sediment was disturbed as well as the mechanism by which this disturbance was generated. In areas containing low densities of bulldozing bioturbators (*Brissopsis lyrifera* and *Nuculoma tenuis*), diversity was higher than in areas with no bioturbators and areas with high bioturbator densities. The effects of these bulldozing bioturbators on macrobenthic diversity and community structure were shown to differ from those of other types of bioturbating species (*Calocaris macandreae* and *Abra alba*). Using a "spatial-temporal mosaic model" (Figure 1) as suggested in a paper by Grassle & Morse-Porteous (1987) it is possible to understand the dynamics within which bioturbation is operating by visualising a spatially structured framework of patches creating a mosaic of different assemblages. Patches are created as different types of disturbances are followed by lateral immigration and larval recruitment. We believe that bioturbation may be considered as an important patch forming process within such a model. In a multi-factorial experiment, the effect of physical disturbance on macrobenthic communities was shown to interact with the effect of organic enrichment, both synergistically and antagonistically. These experiments demonstrated support for two aspects of non-equilibrium diversity theory, the Intermediate Disturbance Hypothesis and the Dynamic Equilibrium Model.

It was concluded that patchiness in the density and distribution of different types of bioturbators played an important rôle in creating heterogeneity and maintaining diversity in benthic communities. Additionally, the creation of heterogeneity by bioturbation may be exacerbated by variations in the supply of organic material.



Patch A experiences a physical disturbance. Other patches show similar species abundance patterns.

Patch A is recolonised by immigration from neighbouring patch (straight arrow) and by larval settlement (curved arrow). Patch C experiences a biological

Patch A starts to show recovery and there is a mix of species and abundances. Patch B shows increasing dominance. Patch C undergoes recolonisation via immigration from neighbouring patch (straight arrow) and by larval settlement (curved arrow).

The three patches form a mosaic of species richness and abundance. No two patches have the same diversity pattern. Thus a high number of species can be maintained as patches experience disturbances independent of each other

Figure 1. Summary of the Grassle & Morse-Porteous' "Spatio-Temporal Mosaic" theory (1987).

Patterns of biodiversity in different habitats

Loss of biodiversity: interactive effects of mussels and limpets in intertidal communities

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Loss of biodiversity may cause significant changes to community structure and ecosystem function. Several models have been put forward to predict these changes. For example, the ‘rivet’ model predicts a steady change in ecosystem function as species are lost and the ‘idiosyncratic’ model suggests that the effects of loss of species will depend on the identity of species lost (Lawton, 1994. *Oikos* 71: 367-374). Conversely, it has been suggested that many species are redundant in terms of ecosystem function and their loss would have little impact (the ‘redundancy’ model). These models have rarely been tested in marine environments.

Limpets and mussels are thought to be important in controlling community structure on wave-exposed shores in the UK: limpets as keystone grazers, reducing algal cover; mussels as ecosystem engineers, providing a refuge from grazing for algae and habitat for many other species. To test hypotheses about the effects of their loss, limpets and/or mussels were removed from experimental plots (with unmanipulated controls) on two shores in Cornwall: Harlyn and Polzeath. Plots were 0.5 x 0.5 m (n = 8). Mussels were scraped away; limpets were removed manually every month from the plot itself and from a ‘buffer zone’ surrounding it.

Effects on community structure were evaluated using Multi-Dimensional Scaling (in the PRIMER package, www.primer-e.com) and NP-MANOVA, a new technique which allows tests of multivariate interactions (Anderson, 2001. *Aust. Ecol.* 26: 32-46). At one site there was a significant interaction. Removing limpets at Harlyn caused a significant shift in community structure, but in the absence of limpets, the presence or absence of mussels made little difference. Where limpets were present, however, the removal of mussels caused a dramatic shift towards a different and more spatially variable community. At Polzeath, the presence or absence of mussels caused significant differences in community structure. Limpets played a less important role.

To test effects on ecosystem function, cover of algae was used as a surrogate for primary productivity. The natural algal assemblage varied through time and at the different sites. At Harlyn, fucoids (*Fucus spiralis* and *Fucus vesiculosus* var. *evesiculosus*) were abundant throughout the year and ephemerals (*Ulva*, *Enteromorpha*, *Porphyra*, etc.) contributed significantly to cover only in the summer. Polzeath had fewer algae and most of its cover was due to the summer bloom of ephemerals (particularly *Porphyra*). At Harlyn, the limpets (keystone grazers) played a major role in controlling algae, but their effects were mediated by the presence of mussels. Other grazers were not able to fulfil their role and algae grew in plots from which they had been removed. At Polzeath, on the other hand, mussels (ecosystem engineers) were far more important. In places without mussels, the effects of limpets were negligible. *Porphyra* tended to grow on mussels regardless of the presence or absence of limpets.

In summary, the experiment provided support for the idiosyncratic model in that the loss of each of the species caused different effects. However, many of the effects were interactive, i.e. depended not just on which species was lost, but on which combination of species was lost. Effects of loss of species also varied from site to site and apparently depended on the composition of the local community. Interactive and spatially variable effects have not been demonstrated in this context before. These findings represent a valuable contribution from a marine habitat to the debate on the effect of loss of species from ecosystems.

Research funded by the Natural Environment Research Council

Discussion

Factors likely to influence mussel populations include predation (e.g. by dogwhelks), recruitment, disturbance by storms (perhaps mediated by epiphyte loads).

The experiment was towards testing the effect of losing individual species and checking the biodiversity piece by piece. Other organisms like littorinids were not removed. An extension will be to look at manipulation of the assemblage of gastropods in different combinations.

Comparison Characteristic of the Halacaridae Fauna from the Black and Mediterranean Seas

Patterns of biodiversity in different habitats

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Halacarids belong to the permanent component of meiobenthos and live in different environmental conditions. They live on different substrata - algae, barnacles, mussels, hydrozoan- and bryozoan- colonies, etc. and are absent or rare on a silty sediments and in oxygen-free habitats or in areas regularly defaunated due to heavy pollution. Their input into the quantitative composition of the meiobenthos is minor, but sometimes they can occur in very high numbers, equaling 60-90% of the total meiofauna. At present time about 900 (36 genera) halacarid species have been described from all over the world, they are preliminary marine but about 60 species have specialized to live in freshwaters (Bartsch, 1989).

Investigation of the halacarids fauna of the Black Sea started rather late, in the beginning of the 20th century. Bulgarian scientist G. Chichkoff published first records about marine mites of the Black Sea in 1907; for the Mediterranean Sea, in 1888-1901, were already published works of E.L. Trouessart about Halacaridae fauna near the French coast.

Odessa Branch of the Institute of Biology of Southern Seas (IBSS) caries out works on meiobenthos since 1973. First studies were dedicated to the meiofauna community of Odessa Bay, some nearby limans and the northwestern part of the Black Sea. Halacaridae species diversity was studied only during 1974-1979. From 1994 we started investigation of marine mites inhabiting different biotops of the northwestern part of the Black Sea. Our results showed changers in species composition and in density of marine mites settlements during the last 15 years. It is connected with the changers of the environmental conditions - anthropogenic eutrophication processes in the Black Sea. Marine mites exhibit high sensitivity to anthropogenic inputs that makes them an excellent bioindicator of habitat pollution. They are abundant and present big species diversity in good environmental conditions. At present time fauna of the marine mites of the Black Sea estimates about 53 species, belonging to 14 genera, while in the Mediterranean Sea lives 85 species belonging to 16 genera (Table). According to published records, 33 species of Halacaridae were found along the Ukrainian coast of the Black Sea (Vorobyova, 1999; Gelmboldt, 2001). In comparison with the Mediterranean fauna, the halacarid fauna in the Black Sea is reduced (because mariner mites evolved from the semiaquatic prostigmatid ancestors that colonized the seashores and only later have colonized the freshwater realm). Not all Mediterranean species are able to adapt and become naturalized in the Black Sea; some of them are prevented from doing so by low water salinity (mean surface salinity is 17-18 ‰ due to the inflow of the continental waters), some by low water temperatures during the winter and others by lack of suitable deep-water habitats because of the presence of hydrogen sulphide. So fare from the 53 Black Sea species 11 species are recorded only from this basin, 10 species also occur in the Mediterranean Sea they belong to the Mediterranean settlers which entered the Black Sea waters via Bosphorus approximately 5-6 000 years ago and got adapted to the new conditions. 5 species that inhabit Black Sea are also found in Atlantic region. They belong to the thermophobic species originating form the cold seas, in literature they are referred as “Boreal-Atlantic relicts”. It is difficult to be certain when and how these cold-water species were introduced into the Black Sea. They may have entered through the river systems during the time of the Neoeuxinian Lake (that existed since 20,000 to 7 000 years ago), or at a later date during the early stages of the formation of the Bosphorus, when the Mediterranean Sea was colder than it is today.

Of the 85 marine halacarid species recorded from the Mediterranean, 35 are recorded only from this sea, while 31 species are also present in Atlantic.

The most species that inhabit the Black sea are ubiquists - they are able to survive in the waters with the wide salinity range from 16-18% in the near shore regions up to the 25% as in the limans.

In future we can forecast that further investigations will result in new records or even species from that regions of the Black Sea so the list of species will be increased.

However, it is unlikely to result in recovery of as many species as are known for the Mediterranean Sea.

Number of halacarid species recorded from the Mediterranean and the Black Seas

Genera	Mediterranean Sea*	Black Sea **
Actacarus	2	4
Acarohelopodia	3	1
Acaromantis	2	0
Agaue	3	1
Agauopsis	6	4
Anomalohalacarus	6	0
Arhodeoporus	3	1
Caspihalacarus	0	2
Coloboceras	2	0
Copidognathus	28	17
Copidognathides	0	1
Halacarellus	3	9
Isobactrus	2	2
Lohmannella	4	1
Rhombognathus	10	7
Rhombognathides	0	1
Scaptognathus	4	0
Simognathus	2	0
Thalassarachna	5	1/ 3
Total	85	53

*- Bartsch, 1989; European Register of marine species (from the web site)

** - Vorobyova, 1999; Gelmboldt, 2001 and unpublished records

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Patterns of biodiversity
in different habitats

Temporal variations and succession of sublittoral rocky bottom biota in the arctic Kongsfjord using underwater photographs and image analysis

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Temporal variations and succession of a macrobenthic community from a rocky bottom locality in the Arctic Kongsfjorden at Svalbard was investigated by analysis of long time series of photographs of permanently marked underwater areas. This photographic monitoring is probably the longest time-series of rocky bottom biota from arctic areas, with pictures taken annually (July-September) from 1980.

Underwater photography is a useful “non-destructive” method for obtaining information of conspicuous epifaunal organisms. Photographs of permanently marked areas through long time-periods give opportunity to study population dynamics (settlement, age, mortality), individual growth, productivity, competition for space, predation and community succession.

Many high latitude fjords, such as Kongsfjorden on Svalbard, are heavily influenced by glacial discharges of cold water, glacial ice and sediments. There are also strong seasonal fluctuations in light, sea-ice cover, freshwater inflow, surface salinities and sediment input. These environmental factors have major impacts on the composition and temporal variations of benthic communities.

The photographed areas (ten ¼ m^2 squares) are marked on the rock bottom and re-found each year using landmarks and GPS- positions. The studied area is located on horizontal bottom at 15 m depth near Kvadehuken (Position: 78° 58,6’ N, 11° 30,1’ E) in the outer part of Kongsfjorden. At the start of the monitoring project in 1980, all organisms from half of the investigated area were removed, with the aim to study succession of cleaned areas. The other part remained undisturbed and is regarded as a control for the natural development.

The marked areas are photographed using a Hasselblad SWC fitted with correction lenses in a Hasselblad underwater housing. The technique is based upon stereo-photographs and was developed by Tomas Lundälv at the Kristineberg Marinebiological Station (Sweden). Positive Ectachrome 200 was used throughout the study. A flat bed scanner (Saphir ultra 2-Linotype Hell) and the software package "Lino color", version 6.0.5. was used to perform the scanning process of the photographed pictures.

Digital image analysis and processing was carried out using Adobe Photoshop/ Macintosh with the “Fovea pro”- image analysis plug-in toolkit. Special effort was paid to find a suitable and efficient method to retrieve quantitative data of conspicuous macrobenthic solitary (e.g. sea-anemones and sea urchins) and colonial invertebrates (e.g. colonial ascidians and bryozoans) and algae. The application of “Action”- files in Adobe Photoshop was an efficient tool to a rapid image analyse process, thus a larger amount of data could be achieved. After image corrections of light and colour, the organisms were individually selected by using “magic wand tool” or by their special colour range (colonial organisms) and placed on separate image layers. Data of abundance and the covered area could be retrieved using the measuring filter toolkit. For this reason, a unique colour code in RGB was assigned to each species, in order to identify it in the subsequent data file.

During the analysis, 19 species/taxa and typical bottom features such as cover of sediments were treated. The most abundant solitary organism was the actinian *Urticina eques*. The densities ranged from 50- 300 ind m^{-2} , the relative covered area ranged from 5- 12% during the period of investigation. The cleaned area revealed values comparable to the reference area from a period of 6-8 years after the starting point; thus this period is regarded as a natural recovery time for this species. In the beginning of the nineties, a drastically decline of the population was observed, which seems to be a negative correlation to the extended cover of brown algae (Fig. 1).

The sea urchin *Strongylocentrotus droebachiensis* was recorded in high densities (20- 40 ind m^{-2}), which induces a heavy predation pressure on the locality. It is thus referred as a keystone species in the area. A positive correlation to the occurrence of brown-algae as a major food resource of sea urchins was observed (Fig. 1).

Patterns of biodiversity in different habitats

Brown algae and calcareous algae were covering large areas. Brown algae showed increased densities from the beginning of the nineties. Nevertheless huge variations are observed during the monitoring period, which could be connected to variations in ice cover during the photosynthetic active period.

The project is part of the program "Arctic Light and Heath" supported by the Norwegian Research Council.

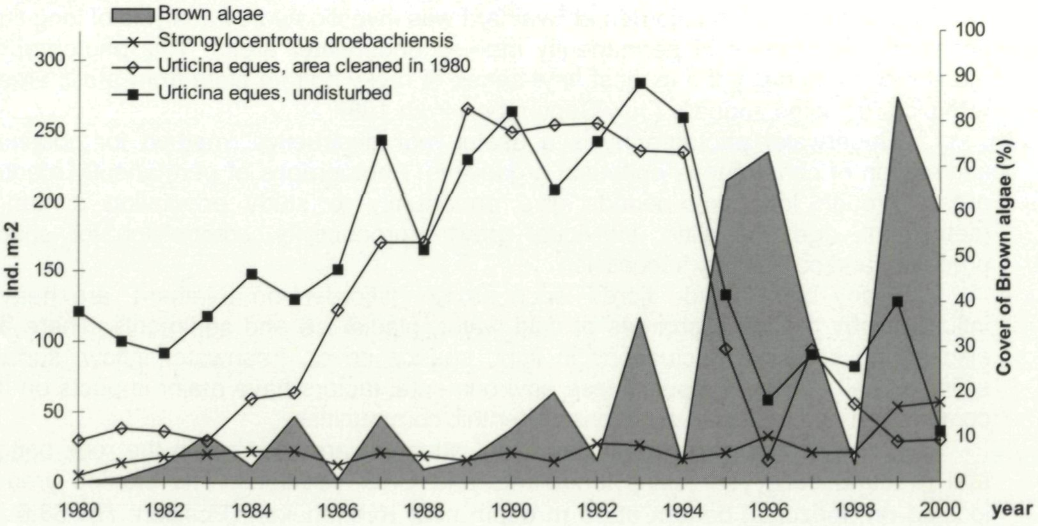

Figure1. Variation of brown algae, the sea-urchin Strongylocentrotus droebachiensis and the sea-anemone Urticina eques at 15 m depth, Kvadehuken, Kongsfjord.

Zoobenthic diversity in the Black Sea - constraints in relation to natural and anthropogenic factors

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The Black Sea represents a unique environment in that it is a relatively small, deep, inland basin, which is connected by a shallow water passage, the Bosphorous Strait, to the Mediterranean. The restricted water exchange with the Sea of Marmara and the relatively large amount of river discharges are the two principal contributing factors for its comparatively low salinity and the formation of permanent halocline that prevents the vertical transfer of energy and substances. Therefore, the Black Sea forms a semi-stagnant basin with anoxic conditions below 150-200 m water depth.

Among natural environmental factors, low salinity and anoxia in almost 90 % of basin's volume constitute the two major limitations to benthic fauna diversity.

Decreased diversity in the Black Sea due to low salinity is evidenced both in the number of species and in the number of higher taxonomic groups - families, orders, classes and phyla. Many taxa, otherwise diverse in the World Ocean, have only a few representatives in the Black Sea (Porifera, Anthozoa, Echinodermata, Bryozoa, Phoronida) and others are entirely absent (Sipunculida, Cephalopoda, Brachiopoda). The dependence of benthic species diversity on the salinity is related to the lack of osmoregulation mechanisms in the majority of the invertebrates. Being stenohaline, many marine species can not settle in the Black Sea, which is characterised by low and wide-ranging salinity.

Permanent anoxia below 150-200 m depth results in a decrease of habitat diversity, which has negative implications for the species diversity. Indeed, certain groups of animals attain their greatest diversity in the deep-sea; others are exclusively deep-water inhabitants, therefore represented by few or none species in the Black Sea (Echiura, Vestimenifera, Pogonophora, Enteropneusta, Crinopidea).

Generally, it has been established that the species diversity of the Black Sea zoobenthos is approximately three - five times lower compared with that of the Mediterranean.

During the recent decades, dramatic changes have occurred in the Black Sea ecosystem under the impact of anthropogenic factors. Being a practically enclosed catchment basin of the rivers draining half of Europe and parts of Asia, the Black Sea is very sensitive to cultural eutrophication, which is identified as a key ecological issue. Studies on the Black Sea macrofauna have exhibited that the level of disturbance due to eutrophication is adequately reflected in the qualitative composition and quantitative structure of zoobenthic communities. Decrease of species diversity, shift of numerical dominance from molluscs to polychaetes, change in species composition with sensitive groups (Crustacea) decline and introduction of better-adapted euribiotic invaders (Mollusca) are among the secondary effects of eutriphication with respect to bottom macrofauna. These effects have been appropriately employed for bioindication of the level of environmental stress.

Recently, the Black Sea ecosystem has entered a phase of relaxation regarding the eutrophication pressure. The first signs of recovery have been displayed by the pelagic communities, while zoobenthic communities have manifested slower response with still uncertain indications of rehabilitation.

During the last decade bottom trawling became a widespread practice along the Bulgarian Black Sea coast and raised a significant environmental concern. Studies addressing the problem gave some preliminary assessments of bottom trawling impact on the benthic communities - disruption of mussel beds, decline in some valuable invertebrates populations, general diversity decrease in the impacted areas. The effects of bottom trawling on the seabed have been recognised world-wide as a major threat to biological diversity and economic sustainability. This issue needs a special attention and further investigations in the Black Sea region due to the basin's inherent ecological vulnerability.

Methodology, European Co-operation, End Users

Chaired by
John Gray
Frederick Grassle

53386

Rapid assessment of seabed biodiversity: lower taxonomic resolution and indicator groups as surrogates for species level identification

Methodology, European Co-operation, End Users

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The seafloor is the largest habitat on earth. The size of the seabed and the number of species expected to live in this habitat makes the assessment of seabed biodiversity a daunting task. For the marine environment, there is an additional complicating factor; most of the data sets used and methods developed for biodiversity studies are based on terrestrial systems and many principles developed for terrestrial habitats may be inappropriate for marine habitats. Hence, there is a greater need than ever to describe and understand marine biodiversity through approaches that address patterns, processes and pragmatic approaches to management.

The main challenge to benthic ecologists in relation to biodiversity is the enormous size and heterogeneity of benthic habitats, and the great number of species they contain. For example, in Norway the coast stretches from 57-71° N, a distance of more than 1 500 km. A compilation of registered benthic organisms now contains almost 4000 macrobenthic species from a limited study area. In general, most marine areas are poorly sampled and we have only spotty coverage based on point samples, normally grab samples. Detailed investigations for such huge areas are impossible. Even if large numbers of samples are collected, processing is very expensive and time consuming and taxonomic literature and expertise are limited. Therefore, at present there is a large difference between the spatial scales on which marine biodiversity mapping is possible and the scales at which management decisions need to be made. The size of the areas to be investigated and the above mentioned constraints underline the need for appropriate rapid assessment methods by which marine biodiversity can be investigated.

Rapid assessment techniques are alternative methods to traditional, full species determination, and are used in order to assess major components of biodiversity. Rapid assessment most often implies the use of surrogates. Surrogates are used as proxies for species level identifications; they are quantities that correlate strongly with species richness and community patterns, but are easier to obtain. There are two major groups of rapid assessment techniques used in benthic investigations: 1) the use of taxonomic levels other than species (e.g. family level identification), indicator taxa, functional groups and environmental variables; 2) use of REMOTS (remote sensing techniques) like acoustic sediment classification methods (e.g. Roxann, QTC), side-scan sonars, sediment profiling images (SPIs), still- and video images from ROVs.

In biodiversity investigations both the number of organisms and patterns are important, and therefore both univariate (e.g. number of species) and multivariate (community level) analyses are relevant in biodiversity studies. In order to reveal species diversity patterns and gain an adequate understanding of biodiversity, the use of surrogates has been recommended. In soft-sediment systems, surrogates for biodiversity are essential and must become the norm in comprehensive surveys.

Benthic invertebrates are the major non-microbial component of marine biodiversity. In marine sediments, the macrofauna (organisms retained on a 0.3 - 1mm sieve) usually dominate the biomass and include key taxa such as polychaetes, molluscs, crustaceans, echinoderms and numerous other phyla.

I will present results using two of the methods in the first group of techniques listed above, lower taxonomic resolution and indicator groups, to explore the potential of these surrogates for species level information. The results shown are based on investigations of existing data sets where the benthic macrofauna already have been identified to the species level. Hence the answer book is already present, and the degree of loss of information by using these two rapid techniques (surrogates) can be compared and estimated. The datasets used are from Norwegian offshore oil monitoring, a larger compilation of marine organisms along the Norwegian coast, from the Oslofjord, and from the Irish Sea.

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There was an obvious relationship between the number of species (species richness) and the number of genera and families within the datasets, and correlations between species richness and higher level taxa were high (r>0.90). Also, the multivariate patterns were very similar for these three taxonomic levels (r>0.80), which clearly indicate that benthic investigations at the level of genus or family will be acceptable as a surrogate for species level studies. The time needed to identify organisms to the level of family has been shown in several studies to be about 50% of that required for species level identification.

Polychaetes are often numerically dominant in benthic assemblages, both with regard to number of species and their abundance and may therefore be good indicators of species richness and community patterns in benthic invertebrate assemblages. Polychaetes are also well suited as indicators of environmental disturbance since this group contain both sensitive and tolerant species and are found along the whole gradient from pristine to heavily disturbed areas. Species richness was calculated for the 12 largest polychaete orders in the dataset from the Norwegian coast, and those that showed highest correlations to species level data were investigated further for their potential as indicator groups. Four orders showed high correlations with species richness (orders Phyllodocida, Spionida, Capitellida and Terebellida). Capitellida was excluded as a good indicator group since it contains too many species, while Phyllodocida and Spionida were excluded due to small body size and complicated taxonomy. The order Terebellida contains mainly larger organisms that are easier to identify than smaller taxa. Based on ratios between number of Terebellida and number of remaining polychaetes, all the four datasets showed that the polychaete order Terebellida was a good indicator for polychaete species richness and to a lesser degree to species richness in the entire benthic assemblage. Multivariate analyses also demonstrated that the Terebellida mirrored community patterns well. The Terebellida, therefore, have the potential of being a good indicator group for benthic species richness.

In conclusion, we are at present in a preliminary stage of investigations of rapid assessment methods in benthic studies. Already existing data are often suitable to test the application and performance of rapid assessment techniques and should be used for this purpose. Both univariate (e.g. species richness) and multivariate (e.g. multidimensional scaling, MDS) should be used to investigate the application of surrogates in benthic studies. The use of surrogates such as lower taxonomic resolution and indicator groups should be combined with results from REMOTs (remote sensing techniques) like acoustic sediment classification, side-scan sonar images, sediment profiling images and video images. There is an urgent need for further tests of surrogates for benthic biodiversity from different habitats, geographical areas and scales before recommendations for the most suitable rapid assessment methods can be given.

Discussion

It has been demonstrated that the approach works fairly well for higher taxonomic levels for very diverse systems. It is not yet known whether the system can cope with other habitats of less diverse systems. Data from disturbed areas with low diversity (low number of species) have been used also, but the possible use of higher taxonomic levels or indicator groups in environments with very few species has not yet been tested.

Normally it is possible to use polychaetes because they are very abundant. The polychaetes is a group that has adapted to a very large range of habitats. In relation to disturbance there should be high potentials in the above methods.

The quality of the dataset (sampling intensity) and the intensity of the sampling in the different regions have an impact on the results.

Principal Component Analyses (PCA) is a group of multivariate techniques that is not adequate for species data. Multidimensional scaling (MDS) was used for the multivariate approach. If you want to study only environmental variables , than PCA is a suitable method.

An important question remains: are the correlations that were found real or not? Definitely they are real. The biological explanations for this are not yet studied. The good correlations are probably related also to taxonomic hierarchy. In a lot of marine data the species to genus / families ratios are very low. This very low species-genus and species-family ratio results in good correlations. The situation is often different for terrestrial datasets.

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Relatedness of species: A neglected aspect of biodiversity

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At the organismal level, the most widely used biodiversity measures are those based on the number of species present, perhaps adjusted for the number of individuals sampled. These may be of value as comparative biodiversity measures in situations where sampling methods, sample sizes and habitat types are carefully controlled, as might be the case in a local environmental impact study, but are of doubtful utility for more diffusely collected data on wider spatial and longer temporal scales. The dependence of richness measures, such as the simple observed number of species, on the sampling effort is one of the most fundamental difficulties in any field assessment of diversity, particularly in marine environments where one is rarely at the asymptote of the species-area relationship.

Species diversity, based on evenness and richness properties, seems in some way to be homeostatic, except at high levels of disturbance, and may not be a reliable measure of important changes in biodiversity. For example, in the North Sea there are indications that certain major taxa are decreasing at the expense of others in response to both natural variability and anthropogenic pressures which indicates a major change in biodiversity but may not be detectable as a net change in species diversity. If we continue to use these traditional indices for monitoring purposes, changes in biodiversity may go undetected until a very advanced stage of environmental degradation is reached.

"A measure of the biodiversity of a site ought ideally to say something about how different the inhabitants are from each other" (Harper & Hawksworth 1994). Simply to say whether or not they belong to the same species is clearly insufficient. Taxonomic distinctness indices are properties of an assemblage and measure features of its overall taxonomic spread. Average taxonomic distinctness (Δ^+) is a measure of the degree to which the species are related taxonomically to each other, and is the average path length between every pair of species traced through a taxonomic tree. The degree to which certain taxa from the regional species pool are over- or under-represented is another biodiversity attribute of ecological relevance. This is reflected in *variability* of the full set of pairwise distinctness weights making up the average, termed variation in taxonomic distinctness (Λ^+). Both measures have the distinct advantage of being unbiased by sample size.

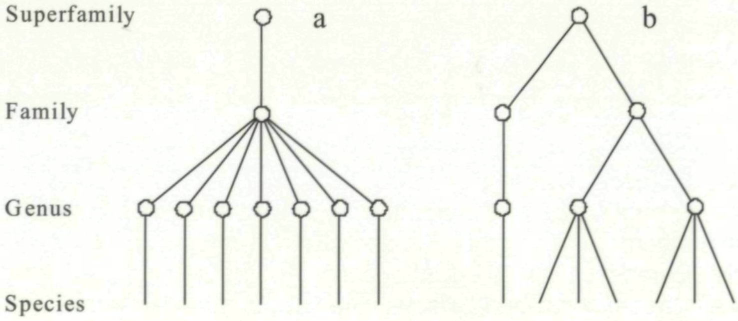

Figure 1. Two hypothetical taxonomic trees showing the taxonomic relationships between 7 species

If the three step lengths between the four taxonomic levels are each 33.33, the value for average taxonomic distinctness (Δ^+) in both cases is 66.67. However, the variation in taxonomic distinctness (Λ^+) is higher in b (634.9) than in a, where it is zero.

For Δ^+ and Λ^+ a simple permutation test of the hypothesis that the assemblage has a taxonomic structure that is representative of the full biodiversity of the regional species pool can be constructed. Say the local assemblage comprises *m* species, then the measured values of Δ^+ and Λ^+ can be compared with the range of values from, perhaps, 1000 random selections of *m* species from the potential regional source pool of species. If the measured value falls outside the 95% probability limits of this null distribution, then statistically it cannot be considered representative of the full list. If the values fall within these limits then the assemblage is not significantly different in

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taxonomic structure than the regional pool, at least in terms of these summary criteria. Results of this type can be visualised as histograms for the simulated null distribution, with an indication of the comparative position of the measured value. Alternatively, local distinctness measures can be plotted on a "confidence funnel" consisting of the 95% confidence intervals of distinctness values for subsets of different numbers of species randomly selected from the regional pool, or both Δ^+ and Λ^+ can be compared on biplots, in which case the 95% confidence intervals from the regional pool become ellipses.

These measures are beginning to find application in broad scale geographical comparisons of biodiversity, in environmental impact assessment, and in evaluation of surrogates for biodiversity estimation (see References), and also for predicting the effect of long term (e.g. climate) change on biodiversity. Examples of these applications, using macrobenthos, freeliving nematode, fish and mollusc assemblages are provided.

Discussion

It is possible to use the same approach to create a measure of functional diversity, for example feeding behaviour, but also other functions are possible. Any classification of species that has a hierarchical structure is potentially amenable, but it is unlikely that functional classifications would have as many hierarchical levels as long taxonomic tress.

There is a lot of subjectivity/ arbitrary in some taxonomic classifications. Ideally we should be using phylogenetic cladograms, but at the moment there is not an overview for the whole of the animal kingdom. Therefore we have to be more pragmatic and use the traditional Linnean classifications of the group of organisms we are dealing with.

In plots of the average versus the variation in taxonomic distinctness, in some cases they appear to be negatively or positively correlated and in other cases there is no correlation. The reasons for this are not known at the moment. This is something that will be pursued. It says something about how these groups of organisms are structured.

There is a problem in the definition of the regional species pool. It is easy to establish for the British Isles, for example, but it is more difficult for e.g. the Norwegian coastal region. Ideally the pool should include any species that could potentially occur in the habitat or region under consideration, but often a more pragmatic approach is to evaluate individual stations or areas in a survey against a master list of all species found in the survey. It is important to appreciate that it is the *structure* of the species pool against which individual samples or sites are evaluated, and it is not necessary for the species present at a station to be a proper subset of the master list.

A number of studies suggest that the border of the real regional species pool from Northern Europe is the shelf outline. The scale of regional pool depends on the scale of the processes that you are interested in. If you define the regional pool as all the species on the continental shelf, you are combining biogeographic processes and local ecological processes. However, the extension of the regional pool would make the application of the techniques much more difficult because the species pool would become very large.

The changes that took place in the benthos of the North Sea during the 1987 'regime shift' were very subtle, but invloved a clear step change in average taxonomic distinctness, i.e. the species became more closely related to each other. The changes were far reaching and affected the whole ecosystem including the benthos, plankton and fish. The cause of the changes is under debate.

The use of approaches based on species richness and evenness, e.g. Shannon diversity (H') are only applicable for relatively small controlled studies that are comparable with each other. The strength of the presented metrics is that they can be used for large geographic areas when you really do not have strictly comparable data data in terms of sampling effort or methodology. In such large areas you do not know what the abundance data are; you only have species lists.

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Diversity of habitats and species at sedimentary shorelines: Restoring losses by nourishing sand

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Where the sea meets the land, parallel strips of habitats occur across steep gradients. At sedimentary shores, the transition zone from marine to terrestrial species assemblages is highly dynamic. It is mainly located between neap and spring tide levels or between the water levels occurring during onshore and offshore winds at tidal and non-tidal coasts, respectively. The diversity of habitats across and along shorelines is high at intermediate conditions, and low at the exposed beaches as well as at the very sheltered, almost plain marshes. Close to mean high water level, the marine macrobenthos as well as the vascular plants exhibit strong species dominance, the latter often occurring in monospecific stands. This low alpha-diversity is partly compensated by a higher beta-diversity due to the morphological variety of shorelines. On the other hand, small organisms like the aquatic meiofauna exhibit high diversity and species richness up to spring tide level. In vegetated marshes the habitat is shared with a diverse terrestrial arthropod fauna. Shorebirds congregate in conspicuous numbers at this ecotone. A gradual transition zone constitutes an effective filter for effluents from the land and functions as a buffer against flooding from the sea.

As human populations increasingly concentrate at the edges of the sea and as sea level rise (SLR) is likely to continue and accelerate, sedimentary shores become squeezed and transformed. Depending on the local supply of sediment, tidal flats, salt marshes or mangroves may adjust to SLR by accumulating deposits but still recede at their seaward edge. Generally, sediment supply is limited at islands but may be sufficient at mainland shores. A landward shift of shorelines in response to SLR is rarely possible any more. On a world-wide scale, coastal marshes have been drained, filled, diked, flooded with freshwater, converted into salinas, impounded for shrimp culture, subjected to measures of mosquito control, and used for agricultural, industrial or urban development. More and more sedimentary shorelines are defended with boulders, asphalt or concrete to prevent erosion. However, with these measures of coastal conversion and protection, the biota specific to the transitional zone between the marine and terrestrial environment become eliminated. As a further consequence, coastal waters seaward of converted marshes become more turbid, and large areas of seagrass may succumb for lack of light.

As a remedial action, a managed shoreline retreat would be a logical step in the face of SLR. However, intensive use, human crowding and highly developed infrastructures at most of the coasts do not offer much room to move landwards, particularly not on islands. As an alternative, it is suggested to artificially supply sand from the bottom of the sea to sheltered shorelines which have been armoured with defensive structures like stonewalls and groines. At most sheltered shores, the longevity of artificial deposits of sand will be in the order of several decades. This is sufficient time for the natural colonization by shoreline biota. Sand should not simply be dumped onto the shore to provide a beach. It is ecologically more rewarding, to generate sandy spits, chains or clusters of islets or sand bars. In their shelter, mudflats and saltmarsh vegetation may develop. A semicircular arrangement of a sand ridge in front of a seawall may enclose stagnant and temporary brackish water with a marine overwash during storm tides. Islets may offer breeding sites for coastal birds safe from mammalian predators.

Sand nourishing operations at converted and defended sheltered shorelines have multiple advantages. They appease the hunger for sand at erosive shorelines and dissipate wave energy. They restore dynamic shoreline habitats with the associated biota which otherwise would be lost. Finally, shoreline aesthetics will improve and this in turn may increase the touristic reputation and quality of coastal life.

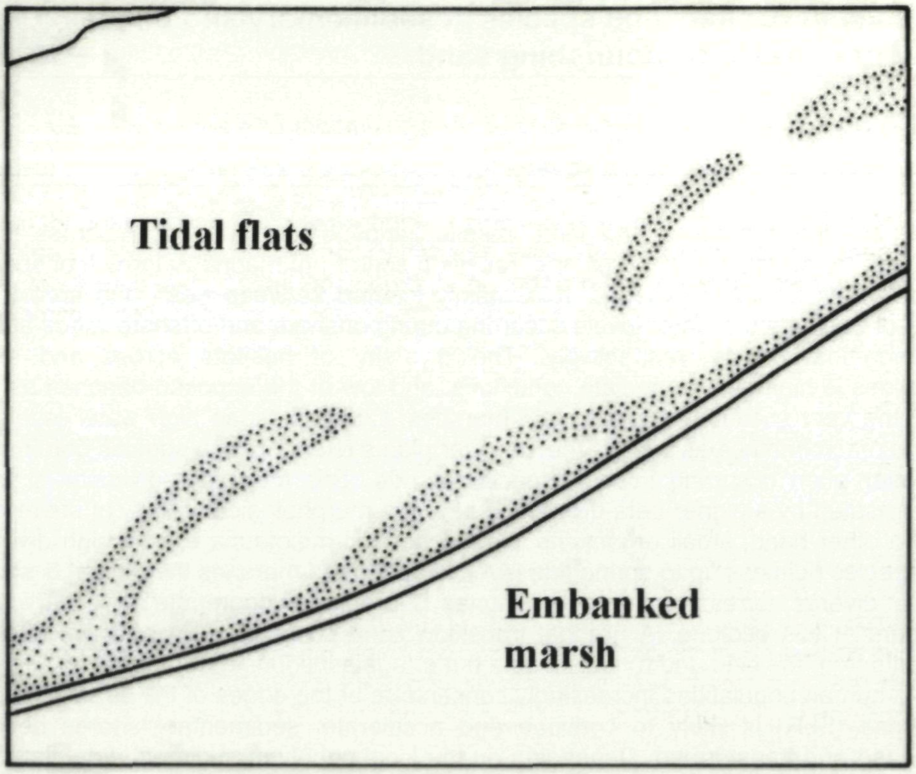

Figure 1. Sketch of artificially added sand deposits (dotted) in front of a dike.

Sketch for the design of artificially added sand deposits (dotted) in front of a dike to restore dynamic and diverse shoreline habitats. It is expected that mud accumulates in the shelter of sand bars and spits, plant succession proceeds on the deposits, and birds establish breeding colonies.

Biodiversity data

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Understanding and predicting the patterns of biodiversity and species abundances in the oceans, particularly on large scales, generally requires the integration of data from multiple sources. Data on the distribution of organisms must be related to physical, chemical, geological, and anthropological information, and can itself come from multiple studies. Recent advances in computing power, internet connectivity, and data management tools have created new ways to share and analyse data. Efforts such as SeamountsOnline (http://seamounts.sdsc.edu) and the Ocean Biogeographic Information System (http://www.iobis.org) are applying these tools to create integrated web-based resources for accessing and integrating marine biodiversity data.

The SeamountsOnline project, funded by the US National Science Foundation, focuses on seamount habitats. Seamounts are areas of elevation in the ocean floor; underwater "mountains" that do not break the water's surface. Numbering in the tens of thousands and found in all ocean basins, they are biologically important both as commercial fishing grounds and as areas with high biodiversity and endemism. Like terrestrial islands, seamounts may play an important role in the origin of new species and the geographic dispersal of species. SeamountsOnline has the following main goals:

- To gather published and unpublished data documenting the distribution of species on seamounts
- To integrate these data into a searchable relational database, including information on data collection methods, authorities, precision and uncertainty, etc.
- To collect global-scale coverages of environmental information relevant to understanding patterns in marine distributions: e.g., depth, temperature, productivity, distance from like habitat, etc.
- To provide the above data resources freely to researchers and managers through an online interface for searching, downloading, visualizing and analyzing data.

A related goal of the SeamountsOnline project is to assess and compare several statistical approaches for relating environmental factors to the distributions of species, community types, or levels of diversity. Two new "machine learning" tools developed by David Stockwell at the San Diego Supercomputer Center and available online at http://biodi.sdsc.edu will be compared to more traditional multivariate techniques using data within the SeamountsOnline system. For more information, to get on a mailing list for updates, or to discuss sources of seamount data please contact Karen Stocks (kstocks@sdsc.edu).

At present, the data content of SeamountsOnline can be accessed two ways: through the data search interface at seamounts.sdsc.edu, and through the distributed data center of the Ocean Biogeographic Information System (OBIS). OBIS is the information component of the Census of Marine Life, an international science program to assess and explain the diversity, distribution, and abundance of life in the oceans. Traditionally, a major barrier to collaboration among scientists has been the segregation of information and technological skills within different disciplines. Valuable data resources lie within discipline-specific journals and in the unpublished holdings of specialists or institutions. Many of these are in incompatible formats, underdocumented, or not in electronic format at all. OBIS seeks to foster collaborative and integrative research by creating a world-wide, inter-networked, interoperating system for biogeographic information. Component databases will cover global ocean geospatial survey data, synoptic ocean environment data, and species-specific systematics, genetics, and life-history data. The system of databases will be accessible through an OBIS web portal, which will provide tools for searching and integrating across the distributed databases for retrieving, mapping, and analyzing data. OBIS, guided by an international steering committee, will seek to interact synergistically with existing programs such as FishBase, GenBank, the Global Ocean Observing System, ETI, Gaia 21, ITIS, and Species2000. It is a Global Biodiversity Information Facility Associate Member.

A second goal of the OBIS federation is to facilitate future collaborations and interoperability within marine biogeographic research. OBIS will assess and promote standards for data storage, documentation, and transfer. It will provide tools, such as flexible relational database models, to facilitate data management within the research community.

The informatics infrastructure for OBIS is being developed at the U.S. OBIS Secretariat at Rutgers University by Yunqing (Phoebe) Zhang and Fred Grassle under a grant from the U.S. National Science Foundation. To initiate the development of data resources, the U.S. National Ocean Partnership Program together with the Sloan Foundation has funded eight projects covering datasets on cephalopods, hexacorals, Indo-Pacific marine mollusks, genetic sequences of calanoid copepods and euphausiids, zooplankton of the subtropical Atlantic, a checklist of fish species, and the ecosystem of the Gulf of Maine (see http://core.cast.msstate.edu/censobis1.html for details). As of press time, OBIS' distributed Data Center was providing access to over 400,000 georeferenced species records from the component datasets: Biogeoinformatics of Hexacorals, CephBase, FishBase, FishNet, BATS Zooplankton, Indo-Pacific Marine Mollusc Database, SeamountsOnline and ZooGene.

Discussion

Question: How do you handle the fact that many areas of the ocean are undersampled, and this gives a very incomplete picture of many species' ranges?
Answer: In order to correctly interpret a map of the locations where a species has been found, it is important to know whether the regions where it has not been found represent true absences or areas that have not been sampled. SeamountsOnline is addressing this problem by including sampling information when available. For each seamount, users will be able to access both the list of species that have been observed there and a description of all samples that have been recorded there, including the sampling method used and the taxa that were considered. In this way users can decide for themselves which areas are likely absences and which represent gaps in the data. Unfortunately, sampling information is often not preserved in data publications, particularly in the taxonomic literature, resulting in uncertainties.

Question: Can the databases you have discussed be used for examining changes over time?
Answer: While the core information in both databases is an observation of a particular species at a particular location, additional information is also recorded about who made the observation and how. Date of sampling is one of the variables included, so that time series can be constructed if the data are available to support it.

Question: Is OBIS interacting with the ETI group in Amsterdam and with other biodiversity information groups?
Answer: Yes, the project is in communication with the Expert Center for Taxonomic Information about how the projects might interact. While ETI does have large marine databases, they distribute data through CDs and not through a web site and we are still exploring how the two groups might work together. We have also become an Associate Member in the Global Biodiversity Information Facility and are actively exploring links with other data centres.

Question: What incentives do researchers have to share their data?
Answer: Users of the data will be required to cite the original data source, providing credit to the data provider. We can keep statistics on how often data are accessed, giving data providers a way to justify their work. OBIS will also make data analysis and visualization tools available to use on data in the system. Data owners will always be able to control how their data are viewed and represented in the system, and will be able to block access to sensitive or incomplete parts of their data. Hopefully the project will make scientists enthusiastic by showing the advances that can be made once data from many sources are brought together, and many will join the initiative.

Remote sensing of biodiversity

Methodology, European
Co-operation,
End Users

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Maintenance of biodiversity is recognised to be one of the most important challenges for the 21st century but research is required to develop new methodologies to establish appropriate scales of diversity in natural ecosystems. In the last 5 years, satellite remote sensing has proved to be a useful tool, particularly in the study of terrestrial biodiversity. This mostly relates to the determination of habitat type as well as giving useful information on major plant species. It is widely recognised that satellite remote sensing is an increasingly valuable tool in tracking changes in terrestrial ecosystems in response to climate change. The advantages of remote sensing are clear. Satellite images cover very large areas of the global surface and different biotopes can be readily distinguished. With a large archive of images, it has been possible to establish temporal changes and, for example, to quantify land-use change over time scales of a decade or so. A recent example is the work of Peralta and Mather (2000) who used satellite imagery to determine the extent of deforestation in the Amazonian rainforest.

In contrast to terrestrial ecology, remote sensing has yet to make a significant impact on studies of marine biodiversity. Remote sensing techniques have been applied to estuaries and coastal zones but the research has largely focussed on topographic studies, such as mapping of sandbank movement and estuarine fronts (Cracknell, (1999). One successful estuarine study used aircraft remote sensing to determine intertidal biotopes in the Humber estuary. Thomson et al. (1998) used the Compact Airborne Spectrographic Imager (CASI) to map intertidal and salt marsh biota and to determine seasonal changes in salt marsh vegetation.

However, there have been very few papers on marine biodiversity which have used satellite remote sensing. This may be partly due to fundamental differences in marine and terrestrial ecosystems – low biomass, high turnover systems in the sea and high biomass, low turnover on land – but also through lack of research tools and appropriate methodologies.

Two habitats in the marine environment are accessible to satellite and aircraft remote sensing – the surface of the water column and intertidal sediments. Ocean colour sensors, such as SeaWiFS, have proved invaluable in mapping photosynthetic pigment distributions in the sea and recently these data have been used to estimate primary production rates on regional and global scales (Behrenfeld, et al., 2001). These estimates depend on the accurate estimation of chlorophyll — the major pigment involved in the harvesting of light for photosynthesis. Since chlorophyll is ubiquitous in all photosynthetic organisms, it cannot be used directly in studies of phytoplankton diversity. However, other accessory pigments are characteristic of different phytoplankton taxa and are accessible to quantification from ocean colour sensors. Current research effort aims to determine if the latest generation of ocean colour satellites have sufficient resolution to determine the dominant phytoplankton groups present in natural phytoplankton assemblages.

The ability to detect different phytoplankton taxa from space could be of particular relevance to the problem of harmful algal blooms, which are an increasing world-wide problem in coastal seas. However, it is likely that new approaches will also be required which will enable integration of remote sensing data with knowledge from ship-based measurements. An example of knowledge integration comes from oligotrophic oceans which are dominated by very small phytoplankton cells. These picophytoplankton are cyanobacteria or prochlorophytes and rarely develop high biomass. Therefore, it should be possible to develop a knowledge-based system that gives a probability of certain events; e.g. if high chlorophyll concentrations appear in oligotrophic regions, it is likely that a localised increase in nutrient supply has allowed the development of larger phytoplankton cells. So information on phytoplankton diversity may be gained by merging remote sensing data with knowledge of ecosystem responses.

Other aspects of diversity may also be amenable to remote sensing. For example, algorithms have been published (Casamayor et al., 1999) which relate bacterial biomass and production to temperature and chlorophyll concentration — 2 parameters accessible to remote sensing. Zooplankton species and abundance may be related to the presence of specific phytoplankton taxa. Again using the example of picoplankton, it is known that mesozooplankton grazing on these cells is very inefficient; so mesozooplankton are not abundant in regions which are dominated by picoplankton. This knowledge can be used to scale the likely geographic distribution of mesozooplankton on a global scale, based on dominant phytoplankton taxa in different marine provinces.

There is great potential to utilise a knowledge-based system to access the information which is increasingly available from satellite remote sensing in relation to marine biodiversity studies of coastal, shelf and deep seas. Although, the latest generation of satellites has spatial resolutions which could be useful in studies of the intertidal (i.e. 10s of metres), aircraft-based sensors probably offer more immediately useful information. Macroalgae and benthic microalgae can be quantified from remotely-sensed pigment distributions. Pigment complement could also indicate plant type and could be developed to determine, for example, the distribution of nuisance macroalgae, such as *Enteromorpha* species which are colonising coastal zones experiencing eutrophication.

As with water column studies, it should be possible to integrate information that can be derived from remote sensing with existing knowledge on, for example, benthic fauna. Substratum and sediment type determine the benthic flora and fauna which will be present. Animal communities which live in sediments or on the surface of intertidal substrata can be characterised on the basis of habitat – sediment type, level of primary production, sediment erosion, water scour etc – all features which can be determined by remote sensing.

Therefore, by combining knowledge from field data with remote sensing, I believe that there is considerable potential to develop novel approaches that will determine biodiversity-relevant measurements on large spatial and temporal scales in coastal seas.

Discussion

The major controlling factor of productivity appeared to be the chlorophyll concentration. Other factors such as nutrients, light, subsurface chlorophyll maxima, etc. appeared not important. There are geographical differences in the chlorophyll / production relation that was shown which are not understood. It could be that are latitudinal differences in the efficiency with which light is used and this may have an effect. Nevertheless, chlorophyll concentration appears to be the major factor that determines the level of productivity.

In recent years, remote sensing aircraft have been used very successful to monitor intertidal areas. Remote sensing photographs in true colours are used and this may be an advantage: red algae are red, green algae are green and brown algae are brown. However the colour scanners have several hundreds of wave bands and they give much more information than colour photographs. They record very subtle differences in pigment concentration and composition and have the advantage is that you can quantify the data. Hence it is possible to get an estimate of the biomass.

In coastal areas, coloured dissolved organic matter and suspended organic matter have a similar absorption spectrum to chlorophyll. In estuaries and near-coastal regions, it is difficult to estimate chlorophyll concentration because of the absorption of light by organic matter. The Plymouth Marine Laboratory is developing models to compensate for this by subtracting the influence of coloured dissolved organic matter and get a much better estimate of chlorophyll concentration.

Seagrass beds ought to be accessible for remote sensing. Seagrasses usually influence the optical properties of overlying seawater so should be quantifiable, especially from aircraft. But it depends on water clarity. There is potential to develop remote sensing to map seagrasses and kelp beds.

Another remote sensing method, in this case deployed on ships, that is being developed is acoustic techniques. Researchers are using these techniques to look at predator prey relationships between zooplankton. It is possible to see how the predators avoid each other at the individual level. The method also has potential for mapping sediments and kelp beds.

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Methodology, European
Co-operation,
End Users

Role of on-line species information systems in taxonomy and biodiversity

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The importance of species names

Species are the most practical and widely applicable measure ("international currency") of biodiversity, and the only one with a well-established standardised code of nomenclature. The presence and absence of species in check-lists can be tools for biodiversity assessment, nature conservation management, pollution monitoring and assessment, and taken over time provide measures of ecosystem change (colonisation theory, community equilibrium, etc.). The Convention on Biological Diversity defines biodiversity as the variation within species, between species, and of ecosystems. The species concept is clearly central to all these approaches. For example, geographically isolated populations, and differences within a species whether ecological, physiological, or morphological all provide measures of within species biodiversity. The species concept itself defines variation between species, and assemblages of species characterise the state of ecosystems. More recently, the relatedness of species is being developed to provide a 'phylogenetic' measure of biodiversity that recognises the evolutionary history of species. In this, samples of equal number of species but more families or phyla are regarded as having greater biodiversity.

However, there are problems in using species lists. Firstly, lists may exclude species because: undiscovered species may be given the name of a known relative; and observers may fail to correctly recognise a species. Secondly, species may be given the wrong name because of: inadequate identification guides; insufficient taxonomic training; unknown literature; and errors and oversights by the identifying person. These problems generally result in underestimates of species richness.

Benefits of the internet

Imagine the time saved by taxonomists and increased accuracy of people identifying species, if they could search accurate information on (a) correct (and incorrect) species names, (b) species habitat and ecology, (c) distribution, (d) identifying features, within minutes on the internet. Instead of spending hours seeking out rare publications and studying (or overlooking) them, scientists would rapidly be able to give a correct name to observed specimens, or describe it as a new species. Once described, knowledge of the new species would be rapidly available through the Internet, minimizing the likelihood of others wasting their time describing the species under a different name. This rapid access to quality-controlled information would allow easy entry of young scientists, students and amateurs into the field of study. On-line polychotomous visual identification keys will make identification easier and allow for decreased training periods for taxonomists. I suggest that the construction of on-line species information systems will be excellent value-for-money in overcoming the taxonomic impediment to describing biodiversity. In addition, such information systems are in any case required for effective research and management of marine biodiversity (both within species, between species, and of ecosystems). Correct names and species identifications (i.e. taxonomy) are the basis for quality control in biodiversity research and management.

On-line species information systems

The establishment of a globally accessible database of all species names has begun. Species 2000 (www.sp2000.org) is a federation of databases with species names and synonyms that are (or soon will be) available on-line for all world taxa. The North American Integrated Taxonomic Information System is a similar all-taxon initiative (www.itis.org) with a centralised database at its core. For marine species the most comprehensive regional all-taxon list of species is the European Register of Marine Species (ERMS). A global list of marine species that contributed to ERMS is the UNESCO Register of Marine Organisms (URMO) (http: //www2.eti.uva.nl/database/urmo/default.html). All of these initiatives are working closely together to avoid overlap and so achieve a world list as soon as possible.

Methodology, European Co-operation, End Users

The species lists are only the first step in a full information system. They need to be linked to information on 'other names', geographical distribution, ecology, identification, and management importance (e.g. social, commercial, conservation). The lists and their associated information are most effectively edited by the taxonomic experts. The compilation of species lists not only produces a useful list, but also has added benefits in networking specialists, and developing working relationships amongst experts that enable additional projects to be developed and funded.

The first step in compiling such information systems is a 'dictionary' of species names. The European Register of Marine Species (a project funded under the European Commission MAST research programme), compiled the first list of species in Europe's seas. This project produced a list of 28,000 species in two years on a budget of 385,000 Euro. It involved a partnership of 22 organizations, 170 contributing scientists, and links with 42 other organizations. The lists were published on the world wide web (erms.biol.soton.ac.uk) and as a book. The project also identified over 600 experts from 37 countries in the identification of marine species that occur in Europe, and their age structure did not suggest that taxonomists were all retiring into extinction. However, coverage of expertise was very uneven, with fewer experts for the most species rich taxa. An analysis of the 840 available identification guides showed that most series were out of date, and that there were fewer guides where there were most species, namely for the Mediterranean and southern parts of the European Atlantic ocean. Other impediments to information availability were that few museums had the resources to enter data from their collections into databases; thus awareness of what information they had was very limited.

ERMS directly contributed to the successful launch of Fauna Europaea, a project that will list all terrestrial and freshwater fauna in Europe (www.faunaeur.org). A parallel project aims to revise the already published Flora Europaea into an on-line database on all land plants in Europe (Euro+Med Plantbase). The database of experts established by ERMS is being built upon by the BIOMARE marine biodiversity research network (www.biomareweb.org). Comparable initiatives are being launched elsewhere in the world, such as the Centre of Marine Biodiversity (www.marinebiodiversity.ca) in Atlantic Canada. The ERMS list is now being converted into an on-line relational database.

The Census of Marine Life (coml.org) aims to produce a census of all species in the world oceans from the past, present and future. Its dataserver is the Ocean Biogeographic Information system (iobis.org) which brings together data both through linking federated databases, and/or archiving data in a central database; and then provides on-line sets of environmental data and analytical (e.g. GIS, statistical) tools for users. For example, the gulf of Maine Biogeographic Information system (GMBIS) brings together data from fishery cruises and museum collections into an on-line GIS. OBIS is an associate member of the Global Biodiversity Information Facility (GBIF, www.gbif.org) and the leading marine data provider to GBIF. The next few years will see ERMS developing into an on-line atlas that will contribute to OBIS and GBIF, and so enable analysis of data beyond the European scale.

All of the above mentioned projects and initiatives are committed to making information on marine species freely available through the internet. Only people and organizations willing to make their data available in this way can participate in these initiatives. The internet provides a new outlet for rapid publication that can be as quality controlled as any other publication. Good science demands such rapid publication. Unlike conventional libraries, there are no permanent archives of electronic data, but these are being developed (e.g. OBIS). It should become a requirement of 'good practice' in biodiversity research to lodge data into on-line databases, just as it is to lodge type specimens of a new species into a museum. The internet is becoming a critical tool in taxonomy, primarily by facilitating the rapid communication and publication of species information. It also enables ecologists and environmental managers to have more rapid access to quality data. Increased automation of data retrieval and analysis through new on-line software tools will provide an added level of service to educators, researchers and environmental mangers. With this, the demand for skilled taxonomists will increase rather than decrease because of the need for quality control of the underlying biodiversity data.

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How does aggregation of macrobenthic data to taxonomic levels higher than species correspond to functional type groupings

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Traditional monitoring surveys of macrobenthic community structure at the species level are expensive time-consuming exercises that require a level of taxonomic expertise. It is well established that aggregation of macrobenthic data to family level, while decreasing the cost and duration of monitoring efforts, results in no significant loss of resolution in detecting disturbance in coastal communities. Expected loss of ecosystem function associated with predicted decreases in biodiversity has recently stimulated interest in functional redundancy in communities. Discrete functional type classifications have been criticised as inadequately representing the potential number of ecological roles performed by species. The correlation between various taxonomic levels and functional type (classified according to bioturbation potential) was investigated using univariate (number of taxa, diversity, richness, evenness and Warwick's statistic) and multivariate data analysis. Time series data, incorporating a major storm disturbance, both from a stable, high diversity, *Amphiura* community and a frequently disturbed, low diversity, *Abra* community were analysed. At both stations univariate analyses revealed strong positive correlations between species, family and functional type, while higher taxonomic levels were less strongly correlated with these three. The less diverse station showed higher correlation between species and functional type. Higher agglomerative clustering produced temporal groupings for functional type that closely resembled those of species and family level, particularly at the less diverse site. However, multivariate analyses correlated each taxonomic level most strongly with that nearest to it. At the more diverse station functional type was not significantly correlated with any taxonomic level, while at the less diverse station it was significantly, but not strongly, correlated with species, family, phylum and class in that order. Lesser correlation between species and functional type is attributed to a greater degree of functional redundancy, and to a greater frequency of individuals of the same species occupying different size classes, at the more diverse site. Aggregation of faunal data to functional type level allows change in community structure to be discriminated, but is more expensive than species based analysis if samples must first be identified to species level. Family level analyses may be a more cost efficient alternative that can reflect the multiplicity of ecological roles played by species, rather than focussing on one discrete function.

The human factor

Chaired by
Mark Costello

Biodiversity and conservation (new approaches for protecting seabed wildlife)

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Human activities have altered patterns of coastal marine biodiversity – in some cases forever. However, many parts of the marine environment are in near pristine condition and only two marine species can definitely be identified as made extinct by humans in the north-east Atlantic: Steller's sea cow and the great auk. Humans are, like fish, birds and other mammals, a natural part of the ecosystem. However, the ability of humans to adversely affect biodiversity is far in excess of what might be considered normal for a single species. In many cases, our activities adversely affect the very features that we cherish – whether for commercial, resource utilization, scientific research or recreational reasons. In this presentation, I will explore how our increasing knowledge of biodiversity and of the impacts of human activities can be used for management of human activities. I will furthermore promote a view that an overall 'duty of care' exists throughout the marine environment and that marine protected areas may have a small and often ineffective role in contributing to what should be overarching measures of good stewardship.

The presentation that I gave at the biodiversity conference in London in 1996 (Hiscock 1997) followed mainly what might be considered 'traditional' lines. It particularly described ways of structuring information to apply criteria that identified potential marine protected areas. Since 1997, we have moved forward significantly in our ability to structure and disseminate information so that we can now look at scientifically based decision making across the whole marine environment. We now have frameworks in place or coming into place that identify biotopes in a comprehensive way (the BioMar Britain and Ireland biotopes classification and now a Europe-wide classification under the European Union Nature Information System - EUNIS) (http://www.mnhn.fr/ctn/products/eunishabuk.html). These frameworks allow us to compare 'like-with-like' to identify best or most representative examples. We are accessing survey data more effectively and comprehensively, largely through a more open view of access but also because computers can hold much larger databases (for example, see www.searchnbn.net). Access to survey information often means that we do not need to undertake new survey work although getting new scientists to ask whether something has already been done seems to be asking a lot. We do not yet, except in perhaps a very small number of mammals and some commercial fish populations, have the information to identify critically declining species but we can more-and-more identify which species and biotopes are rare or scarce (see, for instance, Sanderson 1996). Finally, we can use substantial literature sources to identify the likely sensitivity and recoverability of species and biotopes to different human activities through a knowledge of the environmental factors those activities influence. Structuring that information is not easy but has been undertaken by scientists developing biology and sensitivity key information for the Marine Life Information Network (*MarLIN*) programme (see www.marlin.ac.uk).

There are significant issues to address in marine wildlife protection and management. They include understanding the impact of non-native species and the effects of climate change. We also have to advise politicians and do the best that we can to achieve the imperatives they identify in directives, conventions and statutes. These imperatives often include maintenance of biodiversity or seek to use biodiversity measures or indicators as a way of assessing 'ecological quality' and 'ecological quality objectives'. Converting such political actions into scientifically sound measures may be very difficult.

'Conservation' is an active process that involves regulating human activities, often including manipulating natural processes, to maintain the diversity of life on this planet. In many situations 'protection' would be a better term to use as many marine habitats and communities are in a near pristine condition but need to be protected from certain human activities or inputs.

The human factor

What really matters in taking action to conserve biodiversity is having good information and using it in a structured scientifically sound manner.

However, the motivation for protecting marine biodiversity is, in the end, going to be a selfish one. Harmful or perceived harmful practices often only stop because of public pressure especially through market forces. But humans will protect what we value – the more that we celebrate and cherish the variety of life on this planet, the more easy it is going to be to sustain its diversity of content for ever.

Enjoy the diversity of marine life and share your enjoyment with others.

Discussion

Some of the species that were presented as rare in Britainare rare because they are at the northern limits of their distribution range. In a more European wide context, the species do not require conservation action: the species are rare in Britain but abundant in Europe. However, these species are important because they are part of the biodiversity that is part of Britain. Whether they are at their northern limits or southern limits of limits of their range it does not matter. Britain is considered a particular region because of the separation from the continental Europe.

Some participants suggested that it is not possible to combine the roles of scientist and conservationist. In some cases there is a conflict between conservation and otherinterests, such as fisheries. The conservationscientist mayhave a bias against fisheries and in favour of protection.

Keith Hiscock disagreed and indicated that it is important to differentiate between using an objective scientific approach to minimize adverse effects of human activities and the campaigning approach of some NGO's.

It is also up to the scientist to present their information in an understandable way if decision makers are to be influenced to make scientifically-based decisions.

The point was made from the audience that, in the Netherlands, there are substantial debates on fishing and protected areas. Some scientists say very clearly that there are data showing that fishing causes damage. If they suggest removing fisheries from an area, this will bring them into a position where politicians not longer believe them because they become connected to the 'camp' of the campaigners. Scientists who are involved in discussion about what is the best thing to do with regard to environmental protection may find that, for instance, after two years of scientific discussion their conclusions can be reversed in five days because of public pressure (for instance, disposal of Brent Spar).

There seems to be a conflict between politics / policymaking and marine biodiversity research. Conservation of biodiversity needs to be raised up the agenda. Two examples:

1. Because of the Bathing Water Directives, a lot of local authorities in Britain clean up their seaweed from the strand line. As a result they reduce the biodiversity of the beaches and they increase the erosion. But this Directive from Europe drives them to clear away the seaweed otherwise they do not get their Blue Flag bathing beaches.
2. If you read the Quality Status Reports of OSPAR (OSPAR is about as political as you can get in this sort of decision making) every single one of the regional reports comes to the conclusion that the biggest threat to the marine environment (not just to biodiversity) is fishing. But fishing is not within the 'competence' of OSPAR. The OSPAR initiative [Annex V of the Convention] does not carry the weight to put scientifically objective conclusions into decision-making. Even when science shows an adverse effect (for instance unsustainable fishing) there is a socio-economic problem in taking action: the potential for unemployment in the fishing industry. Fishermen in many places are beginning to realise that, unless they take action themselves, their resource will be diminished. It is only where local fishermen have active control over measures taken that they are willing to take action.

It is a pity that it takes painfully long for politicians to decide what is quite obvious and for which we can see solutions. There are win-win solutions in terms of fisheries and conservation, but it is still not possible to implement changes or to implement them quickly enough to achieve those solutions.

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Impact of fish farming on marine biodiversity

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Fish farming interferes directly or indirectly with different biogeochemical processes in the marine environment, involving impacts at varying spatial and temporal scales. It is a rapidly expanding industry with high potential for further expansion and therefore, has the potential for large-scale effects. It takes place mainly in the coastal zone where biodiversity is high and human pressures are increasing and complex. In this context, fish farming is a very good example for analysing human impacts on marine biodiversity.

During the last few years, it has been shown that effects of fish farming on marine sediments may range from very significant to relatively negligible, depending on sediment type and the local water currents. However, the zone of the seabed affected rarely exceeds 20-30 m from the edge of the cages (Karakassis et al. 1998, 2000). The recovery of the impacted zone is occasionally delayed due to secondary disturbance (Karakassis et al. 1999). Although cage farming results in considerable nutrient release into the water column (in particular NH4 and PO4 ions), it was proven to be difficult to identify signs of eutrophication in the water column close to fish farming facilities (Pitta et al. 1999).

All the above effects are related to small spatial scales and occasionally might be related to a local decrease in diversity. However, diversity indices, dominance and equitability (the "ecodiversity" according to Margalef 1997) do not tell us a lot about biodiversity and therefore the two terms should not be used as synonyms. A local decrease in (eco-) diversity does not necessarily imply an irreversible decrease of the repository of genotypes which is the actual richness of "nature's dictionary" (Margalef 1997). Fish farming, like other human activities, may cause significant risks for biodiversity only when the effects become "climatic" i.e. when they become so persistent in time and so extended in space that no organism can escape their influence, or when the scales of recovery processes are longer that those required for the impact to get established. The ecological processes which are likely to be affected are those with spatio-temporal scales overlapping with the scales of impact. A human action causes risks for biodiversity when:

- the damaged ecosystem constitutes the habitat of an endangered species
- the damaged ecosystem is a nursery ground for species affecting the ecology of a broad marine area
- the damaged ecosystem is a rare and region-specific habitat
- the damaged ecosystem is impaired, to that an extent that its loss is irreversible on a human time scale

Calculations of the mass balances for fish farming in the Mediterranean have showed that the effect of nutrients released from fish farming may cause at the long term less than 1% increase in nutrient concentrations whereas the overall anthropogenic effects are likely to cause a 30% increase in 30 years. This type of change is very likely to alter ecological processes affecting biodiversity of the world's most oligotrophic Sea.

Naylor et al. (2000) have expressed concerns on indirect effects of fish farming on wild stocks through increasing demand for fish meal. However, ongoing research projects have provided indications on mesoscale increase of wild fish biomass in areas of increased fish farming production.

A series of recently started EU funded projects are designed to address the issue of effects of fish farming on marine biodiversity at different spatial scales involving interdisciplinary surveys in the Mediterranean and other European marine coastal areas.

Discussion

It is interesting to look also at fermentation products in the soil. The accumulation of organic matter allows this process, and the sulphide concentration is not so high.

There is no work done yet on the effects of antibiotics on the microbial communities in the sediment. Studies carried out in Norway showed that antibiotics have a large effect on microbial communities.

The fishmeal for the mariculture is being imported from high productivity areas (small pelagic stocks from upwelling areas).

The collection of fishmeal has an impact on the North Sea. Several million tons of small fish are caught by industrial fisheries and goes into fish food to the aquaculture. A study carried out in a bay in Canada showed that aquaculture impacted an entire bay in a gradient (farm field effect). It is not expected that the farm field effect will be detectable at a large scale such as the Atlantic or the Mediterranean, but there should be something in between that might be the case.

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The use of new tools to integrate Tourism into sustainable management of coastal areas.

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The conservation of Biodiversity became a priority issue in the political agendas of nations since the Rio Conference in 1992. However, as it has been pointed out recently, Biodiversity issues need to go beyond the creation of protected areas and conservation agencies. Given its cross-sectional linkages with almost all aspects of human life, Biodiversity cannot be conserved through the artificial exclusion of economic forces that are finally its main causes of change. The integration of human activities into the functioning of these ecosystems is crucial in the efforts to conserve and sustainably manage Biodiversity.

In North-western Mediterranean coastal areas, Tourism is the main human-based economic activity. Spain, undeniably one of world's tourist powers, is ranking third in terms of the number of visitors, hosting over 45 million tourist every year. The tourist sector, with annual revenues exceeding 27 million EUROS, represents 10.6% of the country's GDP and serves to finance 154% of its trade deficit. The greater part of the tourist industry is concentrated along the Mediterranean seaboard. Catalunya with 18 million visitors per year is leading the number of visitors in Spain and the Costa Brava (220 Km coastline) accounts for 30% of those tourists (around 7 million year visitors). Since Tourism and Recreation can threaten the environment if not well managed, and at the same time be affected by the environment, there is an urgent need today for a better understanding of regional environmental change processes as a consequence of such human intervention. In 1999, we started a research project focused in the search for the best possible protocols to assure an Environmental Sustainable Tourism Development in the Costa Brava. Using a P-S-I-R methodology, the main goals of this project were: a) to fully assess the environmental implications of mass tourism in the area searching for actions to balance economic growth development and the maintenance of Biodiversity and Ecosystem Health, and b) to ensure the participation of local communities in the process of creating measures to conserve regional Biodiversity.

Previous a detailed compilation of published scientific and technical information in a Microsoft Access data base, and the records of environmental data coming from very different sources, the development of decision support tools for sustainable regional development based on multicriteria analysis and a holistic, system-oriented approach has been one of the outputs of this research. These tools have been analyzed in a pilot plan developed in the region of La Selva Marítima (Southern Costa Brava), municipalities of Blanes, Lloret de Mar, and Tossa de Mar. We are using three basic tools:

A) Information-based instruments: development of an environmental indicator-based report

Three types of environmental indicators have been analysed: a) sectorial management performance indicators that shows the introduction of Environmental management concepts in the companies of the different tourist sectors as well as the evaluation of the efforts made by the different agents in the implementation of environmental management commitments, b) territorial indicators of environmental management targeted to the different points of the P-S-I-R chain related to coastal ecosystems, and c) territorial indicators of environmental condition, measuring the system's stresses and associated conditions in time.

B) Information-based instruments: the application of GIS to coastal management.

We have introduced the exhaustive information generated during the output of the project (environmental management, land-use occupation, spatial planning, geographic data, infrastructures, ecosystem cartography…) in the GIS environment. The programs, techniques, and procedures of the GIS methodology will be used for spatial analysis, Biodiversity assessment, and evaluation, as well as to display the future scenarios predicted.

C) Information-based instruments: a quantitative method to detect Biodiversity regional change, the AMOEBA approach

We use the AMOEBA concept (Ten Brink et al., 1991) to propose a model to follow the evolution of the ecosystem environmental condition in the area. The AMOEBA concept is based on the selection of species as key target variables to evaluate the human impact on Coastal Biodiversity. To select key species we use an adaptation of the Leopold matrix to establish links between impact producers and impact receivers.

Acknowledgements

This research was supported by the R+D National Plan with FEDER Funds (2FD97-0489). The research is done in cooperation with the Economy Department of the University of Girona, the Business Administration School of ESADE, and the Patronato of Turismo Costa Brava-Girona, and with the support of the Autonomous Government of Catalonia.

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Synthesis

There is such a huge range of scientific disciplines involved in the study of marine biodiversity that it is not possible to make any kind of synthesis of the situation at the present time. I summarised the nature of this complexity of biodiversity studies to see where we stand. It seems to me that biodiversity really has two major axes.

Size.

We are studying organisms through the size of viruses, through bacteria, protozoans, benthos meiofauna, macrofauna, megafauna, with equivalents in the plankton and the plant kingdom, through the largest organisms such as whales or giant kelps.

Level of organization.

We are studying a range of different levels of organization for each of these groups: individuals, genes, population, species community habitats and landscape.

With a huge variety of techniques are used to study the biodiversity at these different levels of biological organization: from molecular methods, genetic studies through to satellite imaginary or landscape scale studies.

For each of the individual cells of this matrix we need to ask a number of important questions about biodiversity:

- How many distinct units are present?
- What are the spatial and temporal patterns?
- What are the drivers of biodiversity?
- How is biodiversity originated?
- How is biodiversity maintained?
- What are the threats to biodiversity in each cell?
- How we might conserve and restore biodiversity.
- What role these various components play in the ecosystem functioning?

This involves a huge range of disciplines from biological, physical, chemical studies.

Most of the papers presented here and most of the posters that we have seen so far address to one or more of these questions in one single cell of this large matrix.

There are questions that we need to address that involve interactions within this matrix: horizontal interactions and vertical interactions, e.g.

- To what extent the biodiversity of smaller affect the biodiversity of larger organisms?
- To what extent the biodiversity of larger organisms in turn affect the biodiversity of smaller organisms?

This works in both directions of the axis. We can consider interaction at the vertical axis also:

- To what extents are there trade-offs between genetic diversity and species diversity?

These are questions we have not demonstrated to be addressed yet. We focused more on the answering of the questions within the individual cells of the matrix.

Then there are bigger questions that involve the whole matrix.

- How are food web structure and biodiversity related?
- To what extent is the nature of biodiversity fractal or not?

The key question really than is:

- To answer these questions about biodiversity do we really need to know exactly what is going on in each of these individual cells or are there top-down approaches to answer these big questions?

There is no doubt that the ease of study and the confidence that we have in the information available probably increases as we move from the small size to the larger size scale. We really have little information on how many organisms there are in the oceans. But we do know a lot of the whales.

Discussion

Within each cell of the presented matrix, specialists know what to do next. Talking about future needs and directions, the big picture is the integration between the different cells of that matrix and right now the funding structures are starting to encourage the interdisciplinary research. But that needs to be increased further. Also

we need to think about how all these different disciplines add, and are related to each other. We need to do some sort of research to make these connections clear.
All of us can function in a cell with our individual research whatever that may be; the opportunity is coming to a BIOMARE like transect idea in a European effort. Looking at latitudinal gradients, sea surface temperature gradients or something else and trying to link a series of questions together that haven been condemned from multiple labs addressing to questions within the cells.
Such an approach is possible for similar systems but becomes more difficult with several different systems.

Large scale surveys are expensive. There will be funding problems. Agreement on a kind of protocol for the standard of sampling is necessary. When we are looking at large scale spatial range it might be worth wile to standardize the sampling method because then you can compare. This requires coordination.

One of the key questions in marine biodiversity research was considered the way in which ecosystems are integrated. Questions like: does a whale care about bacteria and do bacteria care about whales? One way to attack this is to look at the relationship of life histories. Somewhere within the already present information there is a lot of important information about how life history characteristics interact. Hints were given in the talks of various people, but it remain statements. We are not addressing to the question: 'So what?'

Although it is important to know what we are talking about and what we are trying to measure, moving into a discussion about defining our terms more carefully is not going to help the problem. The world is moving on and decisions are being made about what to conserve and were to go. We have to move with what we have.

We are very skilled in the descriptive phase and that is surprising because the red book lists all the questions and hypothesis on long term. It is very difficult to raise funds for pure descriptive research, unless for very distinct groups. Should we think more about hypothesis testing? However, both aspects are part of integral scientific methods. You have to have descriptive studies to determine what the patterns of biodiversity are and than hypothesis are developed and tested to explain these patterns. It is not possible to see the one loose from the other. A balance should be achieved between descriptive and hypothesis driven science, which is not hierarchical. For political reasons (fund raising)

We do know a lot at the moment but we are happily to sit in our own cell. There needs to be a putting together of what we already have been found. Scientists should be encouraged to bring together their knowledge in databases. There should be more basic biological data incorporated in more sophisticated ecological models. Other disciplines should be included as well: chemists, physicists, etc. Remains the question about how that kind of work gets funded in future.
In general, models are either putting more taxonomic resolution at the top end or at the bottom end. What was considered new of the presentations had to do with the bottom end. We need to think about the biodiversity of primary productivity, and raise issues that relates to the some larger productivity models such as the productivity of seagrasses, the distribution of macro algae, chemosynthesis and the consequences of the parents of primary productivity.
Because of the complexity of the ecosystem, it is difficult to predict the consequences of any particular change in one part of the system.
Will ecological modelers be able to bring in that kind of level of diversity? Ecological modeling is still in the stage of having one box for phytoplankton and one box for predators. They are all very valid and important but it is a long way from the source of discussions that are going on here today. It is important to bring the two together and in doing that we will understand better the relation between the function of ecosystems and the impact on biodiversity.
For the development of models it is obvious that we need more dependent variables. There has to be more complexity in the system. Important knowledge that is missing at the moment is information about what enables marine ecosystems to repeat itself. Some basic research is still needed.

It is important not to consider a narrow definition of modeling. It is possible to use modeling in a wider context like the roles of life histories. In general modeling should become an integral part of marine biodiversity research.

Scientific Highlights

The fundamental physical unit of biology and therefore of ecology is the individual organism. In ecology attention is nearly always focused on the population or community, and ecologists every now and then have to be reminded of the fact that populations are conceptual units that cannot be observed and therefore not studied in a physical sense. Only individual organisms can.

The concept of biodiversity brings us back to this reality. When we observe or sample the coastal seas, we are dealing with viruses smaller than 0,1 µm and with whales of 30 m length, organisms with sizes spanning nine orders of magnitude, or nearly the difference between a salt grain and the moon. Moreover, their number is simply huge. It is estimated that around 1,1 x 10^{29} prokaryotic cells inhabit the open oceans, more than all the stars in the universe together and there are close to ten times as much viruses.

How to deal with all this complexity? The central concept of species as clusters of similar (but not identical) organisms breaks down when we have to deal with the microbes. When microbiology started, its taxonomy followed the Linnean approach, but added the additional complication that names could only be given to cultivable species. It is now recognized that only about 5-6 genera from the marine environment can be cultured, and about 4000 species of marine bacteria have been described (besides 4000 species of marine viruses and 10,000 species of marine fungi). By using the modern molecular techniques it is now clear that this leaves out about 95 % of the existing genetic variability. Rossello-Mora from the University of the Balearic Islands showed that this also leaves out a large part of ecosystem metabolism, which can not be linked to bacterial numbers for the moment, although some progress is being made but many mysteries remain as well, such as the abundance of Cytofaga strains in anaerobic layers.

So, not only do we not know the names of the bugs, we do not know what they do either, as was demonstrated by the very recent discovery of two groups of Archaea that occur everywhere in the oceans but whose function is unknown. This lack of knowledge may be worrying but even more worrying is that nobody seems to do anything about it. Funding is difficult to obtain, as the outcome is predictable (everything is new) and therefore very few attempts are made to find new culture methods. Perhaps more interest will come now that pathogenic Vibrio's have been found at low salinities in marine sediments. There is also the potential transfer of marine viruses to man when algae are used as fodder for animals, a situation not dissimilar to the practices that lead to BSE crisis in Europe.

There are about 500,000 species described from the world's seas and oceans. In Europe there is now a quite precise figure of 29,000 marine plants and animals. This may appear a small number compared with the millions of terrestrial organisms. Yet, many undescribed species remain. New marine viruses are described at a rate of about 120 new species per year, fungi are not rare in the marine environment, as many textbooks state, but most were described in the sixties and interest has somewhat ceased since. It is clear that many species still await discovery and scientific description. But how many? That is still hard to say, and estimates go from 1 to 10 million and even more for the deep sea. Shallow waters are of course better studied, but most ecologists and taxonomists live in the north in temperate climates and some surveys show that perhaps 50 to 90 % of all species even in shallow water are as yet undescribed. The problem was not discussed in detail at the conference, but the feeling was that the total number of marine species will in the end prove to be similar to the total number of species on the land. Diversity at the higher taxonomic level is considerably higher in the oceans, since a large number of animal phyla are exclusive for the seas whereas only one is exclusive for the land.

The use of species as the units to describe and understand biological complexity requires to a certain extent that at least the common species in certain habitats are known and can be identified. The problem of disappearing taxonomic expertise has been mentioned many times over the last decade and it is true that there are few remaining specialists for some of the more 'obscure' plant and animal groups. As a whole the situation of taxonomy was not considered to be particularly worse than that of marine ecology, but it was also recognized that a large problem exists because of the lack of good identification guides. Most of these guides are very old and deal with regional areas. They should be updated and made available in electronic form. Identification must also be aided by imaging and computing tools.

Another way to aggregate the characteristics of individuals is to look at their ecological function. In the past few years the concept of ecosystem engineers has gained a lot of attention. Some of these ecosystem engineers are also keystone species, species that determine to a large extent the functioning of an ecosystem. Examples of such species are mussels or oysters that form reefs in soft sediments and filter an enormous quantity of water. In this case ecosystem functioning is to a large extent linked with the characteristics of a single species. Similarly, species can be grouped together when they perform similar roles in the ecosystem. This is particularly useful and even essential for ecological modeling that cannot proceed over a certain restricted number of state variables. Another example are primary producers with different pigments that can even be monitored through remote sensing from planes or satellites.

As already mentioned, species contain collections of very similar DNA (and/or RNA) and fingerprinting techniques are now widely applied in order to detect their identity, their genetic characteristics and relationships. In this way the very powerful theories of population genetics and demography can be applied and dispersal and genetic origin retraced. The brown seaweed Ascophyllum nodosum has been studied in this way by the team of Jeannine Olsen from Groningen University in the Netherlands. After the last ice age this species was probably restricted to a few areas in Spain. After the retreat it rapidly recolonized the northern Atlantic up till the east coast of the United States. Dispersal by dislodged thalli is very rapid and observations of floating plants near the Azores show that they probably can cross the Atlantic. The zygotes however only move a few meters away from the mother plant. Amazingly, the generation time of this species is around 60 years and the basal genets may be more than 300 years old and that makes the species particularly vulnerable to human destruction. Another amazing claim made by this research group is the discovery of a single clone of Zostera marine in Finland which appears to cover a surface of 7000 m^2 and might be over 1600 years old.

The very powerful genetic techniques now at our disposal not only permit to get detailed information on the genetic relationships between individual plants and animals but also to get an informed estimate of the total amount of genes (alleles) within species or in an area on the whole and their rate of dispersal. In this way the concept of biodiversity hotspots, that has recently attracted a great deal of attention in the terrestrial biosphere, may now be applied to marine systems. For Ascophyllum it was shown that Britanny in France is such a biodiversity hotspot and we can only hope that a concerted action will bring into focus many more of such areas in Europe for plants such as seagrasses, kelps and fucoid seaweeds.

Plants and animals not only contain their own genes but also many foreign ones, either within their own genetic material or as foreign DNA, cells or organisms included within their own. This can complicate genetic analysis but it also provides many fascinating examples of interactions between individuals (and hence species). At the conference an example of this was given by Nicole Dubilier from the Max Planck Institute of Marine Microbiology in Bremen. In many coastal areas of the world marine invertebrates live in symbiosis with sulfide-oxidizing bacteria that provide food for their hosts. Such chemoautotrophic symbioses are very widespread in nature and two of the most diverse host groups that are being studied by researchers in Austria and Germany are oligochaete and nematode worms. The oligochaete hosts do not have a mouth or gut and always contain at least two kinds of bacteria in their body wall. These are called primary and secondary symbionts and have not yet been cultivated. Using molecular techniques, Nicole Dubilier and colleagues have shown that the primary symbionts are always sulfide-oxdizing bacteria while the secondary symbionts vary from host to host.

The role of the secondary symbiont is now understood in an oligochaete that occurs in the Mediterranean: it is a sulfate reducer that produces internal sulfide for the primary sulfide-oxidizing symbiont. This internal symbiotic sulfur cycle explains how these hosts can survive in sediments with little or no sulfide.

Of course, the archetypical symbiotic units are the organelles of plants and animals. These organelles maintain some of their ancient DNA and can therefore be dated. Linda Medlin of the Alfred Wegener Institute in Bremerhaven told the conference that all dated phytoplankton species date from the Trias or later and are at most 255 My old. This coincides with the largest known mass extinction event in the history of the earth. The molecular identification techniques developed by her and her colleagues have also allowed the detection of three new algal classes (comparable to birds and mammals in the vertebrates) in the last ten years. In this field as well, problems of identification and cultivation remain huge. Even within the life cycle of a single species, the haploid and diploid phase of coccolithophorids have been described as different species. Some phytoplankton species produce cysts, which can be zygotes (dinoflagellates) or resting stages (diatoms), and which survive for more than one year in sediments. They may serve as the most important vehicles for survival and transport.

These techniques also allow to make a distinction between different clones, and it has been demonstrated by Medlin and co-workers that the strains of Alexandrium >>>> in the Orkney islands are the toxic ones from the United States rather than the innocent strains occurring normally in the North Sea. This brings us to another hotly debated issue, the presence of cosmopolitan species perceived to be much more common in marine than in terrestrial environments. There are only 86 species of euphausiids worldwide. Very famous in this respect are benthic ciliates of which Tom Fenchel from Denmark said long ago that all species are everywhere. Classical morphological studies indeed often do not allow distinction between organisms from different parts of the world. Under stressed conditions, such as heavy organic loading, the total genetic diversity and the number of species declines, but those species that remain often get engaged in speciation with the creation of cryptic or sibling species that only differ in minute details of morphology or physiology. John Dolan, from the Observatoire Oceanologique of Villefranche, showed that the tintinnids (small ciliates that live in tubes called lorica's) from the Eastern Mediterranean are very similar to those found in Chesapeake Bay, two marine environments that can hardly be more different. So there is some proof for the concept, but it remains to be seen when other than morphological criteria are applied whether this still holds.

Marine ecology has borrowed most of its concepts from terrestrial ecology but not only has to deal with very different organisms but also very different scales of space and time. The issue of why marine organisms are different was discussed by Victor Smetacek from the Alfred Wegener Institute in Bremerhaven, who showed that most phytoplankton dies because it is killed, by viruses, by bacteria and parasitoids, and that consequently many morphological features of phytoplankton can be interpreted as resulting from selection of defences against grazing. The issue of scale has been repeatedly discussed during the conference. Depending on scale the driving forces for biodiversity change become different, from geological, over evolutionary to ecological. Spatial scales have very important implications for the number of individuals and thus species that is detected. This problem is only too apparent in the large number of metrics that have been proposed to quantify biodiversity and that John Gray and Fredo Olsgard from Oslo University discussed. Many of them depend on an estimate of abundance and/or species richness from samples that cover only a minute part of the area they are supposed to represent. It has been estimated that our knowledge of the deep sea benthos is based on an area sampled smaller than a football field. Such metrics are widely used in evaluating the environmental impact of such diverse effects as oil and gas exploitation in Norway and aquaculture in Greece. They are very labor intensive and therefore costly and a search for surrogate or rapid assessment methods is of great economic interest. One possibility is to restrict the taxonomic analysis to levels higher than the species and it was shown several times at the conference that this does not necessarily lead to a substantial loss of information. On the other hand, a different class of indices was presented by Richard Warwick from the Plymouth Marine Laboratory, and those indices are based on using the taxonomic classification of the specimens.

Monitoring of marine biodiversity, like almost any monitoring, is only useful when it is done over sufficiently long periods of time. As an example, Stephen Hawkins from the MBA in Plymouth showed how the coastal communities in Cornwall continued to change for 10-15 years after the Torrey Canyon oil spill. Technological advances in monitoring biodiversity have been few in the past number of years, but there have been some. Remote sensing of biodiversity is still in its infancy, but Ian Joint from the Plymouth Marine Laboratory showed that plant pigments can and in the future will undoubtedly be used as tracers of changes, even in the coastal environment. In major monitoring projects an instrument called a Sediment Profiler has been used that is basically a camera able to photograph sediment profiles in situ. From such profiles a number of characteristics such as the depth of the oxidized layer, the present of animal tubes or burrows and the grain size of the sediments can be obtained. In principle the whole procedure could be automatic allowing a rapid assessment of the biogeochemical status of marine sediments. This has been applied already in aquaculture research in Greece, as was shown by Ioannis Karakassis from the Institute of Marine Biology in Crete. Fish farming effects could be important if the introduced nutrients increased significantly concentrations in seawater and particularly of the limiting nutrient. It has been shown that introduced nutrients from fish farms are unlikely to increase nutrients more than 1% in the Mediterranean although other human activities are likely to lead in a rise of nutrient levels of about 30 % in a period of thirty years. Fish farms however, are likely to cause significant increase at local scales thereby affecting the trophic status and the biodiversity.

The impact of fisheries on marine sediments is a highly controversial issue in Europe. In the Dutch Wadden Sea some scientists claim that the extensive mechanical harvesting of cockles leads to long-term changes in sediments system wide. Wim Wolff, from Groningen University in the Netherlands, showed that about 50 species have gone extinct in the Wadden Sea in historical (and pre-historical) times, including such exotics as the Grey Whale. Of these 50 extinctions, about 25 are due to human exploitation and they concern large species; about 17 have disappeared beccause of habitat loss, and these are mainly small species. Pollution only accounted for 3 extinctions. Local mass extinctions may be on the increase; Jean-Pierre Feral from the Banyuls Oceanological Observatory documented a severe mass mortality in the Western Mediterrenean where in 1999 water temperatures were above 23-24 C for several months.

The Euroconference also brought about very lively discussions on the problems of applying biodiversity science to the problems of managing the coastal environment. The legal framework for biodiversity is the Rio Convention and its marine part the Djakarta Mandate. Most European countries have legal obligations within this framework. In Europe the European Environment Agency is now involved in implementing action concerning biodiversity for Europe's waters. For the EU countries, the protection of the marine environment is only starting, but the legal framework is there (EU Habitat Directive and to a certain extent the new EU Water Directive),. Nationally, in some countries, such as the UK, a large effort of structuring marine conservation has already been undertaken, as was explained by Keith Hiscock from the MBA. Finally, although the international framework is there, the implementation still needs a lot of intention. There are problems of organising the science, both within Europe and globally. Networks such as MARS (European Research Stations Network) and NAML (Assocation of North America Marine Laboratories) are now starting to link, also in support of the DIVERSITAS programme. There are problems of data availability, and some recent projects such as OBIS (the Ocean Biodiversity Information System) presented by Karen Stocks from Scripps, USA, MarLin (the Marine Life Information Network for Britain and Ireland) presented by Keith Hiscock and their link to planned GBIS (Global Biodiversity Information System) will all require efforts from the scientific community in the next years to come.

Carlo Heip

Biodiversity of continental shelf soft-sediment macrobenthos communities

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Soft-sediment macrobenthos data from two large areas at the Norwegian continental shelf (Area 1: 61° N, Area 2: 56-57° N) were used to examine distributions of species, community structure and differences, and how different measures of biodiversity are related to environmental variability. In Area 1 (35 sites, sampling scale 45 x 60 km) depth ranged from 115 to 331 m, and there was considerable variation in sediment characteristics. 22 out of 35 sites had more than 100 species, and the total species richness was 508. In Area 2 (16 sites, 70 x 130 km) depth (about 70 m) and sediment characteristics were remarkably uniform. The highest local species richness in Area 2 was 81, and the total number of species was 175. The distribution of species varied between the four dominant taxonomic groups, the polychaetes, crustaceans, molluscs and echinoderms. Polychaetes were the most common group and had the highest proportion of widespread species, whereas crustaceans were more restricted in their distributions than the other groups. Whittaker's beta diversity measure (β_W, extent of change in species composition among sites) was highest for those groups with the highest proportion of restricted-range species. Within taxonomic groups, beta diversity (β_W) increased with environmental dissimilarity between sites. The number of shared species, the complementarity (biotic distinctness), and the Bray-Curtis similarity between all pairwise combinations of sites also showed that beta diversity was highest in Area 1. Thus, alpha, beta and gamma diversity increased with environmental variability. Change in environment, notably depth followed by median grain size, had stronger effect on beta diversity, especially Bray-Curtis similarity, than spatial distance between sites in Area 1. In Area 2 neither the number of shared species nor the complementarity was linked to spatial distance, but the Bray-Curtis similarity was a function of spatial arrangement. The abstract concept of biodiversity as the 'variety of life' cannot be encapsulated by a single measure. Distributions of species and community differences should be taken into account in addition to species diversity when measuring marine biodiversity and planning conservation areas, and more than one taxonomic group should be studied in a system.

Comparitive characteristics of the Halacaridae fauna from the Black and Mediterranean Seas

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Halacarids belong to the permanent component of meiobenthos and live in different environmental conditions. They live on different substrata - algae, barnacles, mussels, hydrozoan- and bryozoan- colonies, etc. and are absent or rare on a silty sediments and in oxygen-free habitats or in areas regularly defaunated due to heavy pollution. Their input into the quantitative composition of the meiobenthos is minor, but sometimes they can occur in very high numbers, equaling 60-90% of the total meiofauna. At present time about 900 (36 genera) halacarid species have been described from all over the world, they are preliminary marine but about 60 species have specialized to live in freshwaters.

Investigation of the halacarids fauna of the Black Sea started rather late, in the beginning of the 20th century. Bulgarian scientist G. Chichkoff published first records about marine mites of the Black Sea in 1907; for the Mediterranean Sea, in 1888-1901, were already published works of E.L. Trouessart about Halacaridae fauna near the French coast.

Odessa Branch of the Institute of Biology of Southern Seas (IBSS) caries out works on meiobenthos since 1973. First studies were dedicated to the meiofauna community of Odessa Bay, some nearby limans and the northwestern part of the Black Sea. Halacaridae species diversity was studied only during 1974-1979. From 1994 we started investigation of marine mites inhabiting different biotops of the northwestern part of the Black Sea. Our results showed changers in species composition and in density of marine mites settlements during the last 15 years. It is connected with the changers of the environmental conditions - anthropogenic eutrophication processes in the Black Sea. Marine mites exhibit high sensitivity to anthropogenic inputs that makes them an excellent sentinel of habitat pollution. They are abundant and present big species diversity in good environmental conditions.

At present time fauna of the marine mites of the Black Sea estimates about 53 species, belonging to 14 genera, while in the Mediterranean Sea lives 85 species belonging to 18 genera. According to published records, 33 species of Halacaridae were found along the Ukrainian coast of the Black Sea. On the basis of the literature data and personnel investigation will be given a comparison characteristic of the marine mites fauna of the Mediterranean and the Black Sea with the mentioning of their differences and similarities.

Oligotrophic bacterial communities versus communities adapted to eutrophic conditions as criterion for evaluating the anthropogenic influence on marine areas

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The need of monitoring impacted marine areas is a tool for developing fast and reproducible analytical strategies. Bacteria are quick answering to the environmental changes, an, therefore, they have already been used as indicators for several kind of human activities. Here we propose the analysis of the mean structure of bacterial communities based on the trophic characteristics of the dominant bacterial populations for evaluating the anthropic impact on the natural organic pool. For such purpose seawater samples have been collected in three different areas of the South-western Mediterranean Sea, representative of coastal (CS1), gulf (CS2) and pelagic marine environments (P3). The samples have been analysed by fluorescence *in situ* hybridisation (FISH) with classical 16S rRNA targeting oligonucleotide probes specific for different bacterial taxa, and by means of the extinction dilution technique followed by the 16S rDNA-based taxonomic characterisation of the most diluted samples. Bacterial taxa of classical terrestrial origin, adapted to carbon-rich conditions, predominated in the coastal samples (CS1 and CS2), whereas the pelagic sample was mainly characterised by unculturable marine species. Subculturing the most diluted P3 samples on an organic rich medium was allowing the growth of bacteria adapted to eutrophic conditions that were not retrieved by direct analysis of the source dilution. These bacteria could represent starved forms of *r*-strategist species able to bloom after an organic input.

Importance of habitat diversity for initial settlement and adult distribution of *Macoma balthica*

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Most benthic communities are characterised by a heterogeneous distribution of adults over large spatial scales. The distribution of bivalves such as *Macoma balthica* in intertidal areas is the result of a combination of local differences in primary settlement of pelagic larvae and post-settlement processes such as mortality and migration (Bouma, in press). A suitable habitat for adults does not necessarily make a suitable settlement site for their larvae. Local hydrodynamics are an important factor for both life stages. Adult *Macomas* need a current strong enough to ensure sufficient food supply, but very strong flow can also inhibit feeding. Flow patterns also dominate settlement patterns of pelagic larvae. The questions addressed in this experiment were: How do local habitat parameters such as current velocity affect primary larval settlement? How do adult distribution patterns relate to current velocity, and how do the two compare?

Primary settlement of *Macoma* larvae and larval mimics (polystyrene spheres) was studied in a flume reproducing realistic flow-velocities. Settlement of both *Macoma* larvae and mimics increased significantly with current velocity. Shear stress □ increased with increasing free stream velocity, but stayed below critical resuspension values. Bouma *et al.* (in press) showed a correlation with bed level height for small recruits which becomes weaker with increasing size. Bed level height corresponds with maximum current velocity at an intertidal flat. Based on the Flume results and Bouma we hypothesise that small primary settlers are largely influenced by local current velocities which causes settlement to increase with current velocity below the critical resuspension threshold. Above this threshold settlement may decrease with current velocity.
A response curve from model calculations (logistic regression)(Ysebaert *et al.*, in press) calculating the probability of occurrence of adult *Macoma* in relation to maximum ebb current velocity in the Schelde estuary was used to estimate predicted settlement of larvae in an optimal habitat for adults. The observed settlement values in the experiments show a more pronounced effect of flow velocity than the model predictions at the flow velocities used in the settlement experiment (0.05 m s^{-1} ; 0.15 m s^{-1}).

Primary settlement of pelagic larvae is largely controlled by hydrodynamic factors. Distribution patterns of newly settled *Macomas* do not resemble adult distributions. Post-settlement processes such as migration, secondary settlement, either passive or active, and mortality (due to predation, food availability, competition) seem to be important factors determining adult distributions.

A habitat with a large variety of flow conditions, suitable for settling larvae, juvenile and adult *Macoma* would be needed to sustain a healthy population. A diverse area is needed to successfully complete the stages from settler to adult.

Anchialine caves: Hot-spots of ancient biodiversity at the ocean rim

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Anchialine caves (karstic voids or lava tubes flooded by stagnant sea water) represent by their unaccessibility and the important faunistic discoveries they are delivering, one of the last frontiers to resolve the Planet's Biodiversity. Odd cave-adapted creatures, including an entire class (Remipedia) and four different orders of crustaceans (Thermosbaenacea, Mictacea, Bochusacea and Platycopioida), as well as many other taxa of lower rank (family, genus) are exclussive of these still, often oligoxic, salty groundwaters. Many of these animals could be considered as phylogenetic relics, helping to ellucidate the relationships between various groups of crustaceans: they express ancestral or intermediate character states whose existence were already advanced or assumed elsewhere. In addition, most belong to strictly subterranean lineages whose current distribution patterns fit perfectly into the areas covered by late Mesozoic seas.This fact, combined with their extremely reduced potential for dispersal, point to vicariance by plate tectonics as the driving force for their current distributions.

The peri-Mediterranean area is a privileged region for the study of anchialine Biology, and is shedding light on the evolution of marine biodiversity in this basin. This poster reviews the main anchialine stations in the region, show some of the most stricking global distribution patterns displayed by anchialine lineages with Mediterranean representatives, and also which are the main Conservation threats for these peculiar habitats, frequently placed beneath holiday resorts.

Understanding marine species patterns across spatial scales

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Range sizes have been used as an important species characteristic that has implications for extinction probabilities. In marine systems, range sizes may be difficult to estimate and inferences about species ranges can be confounded following introductions associated with shipping. An alternative approach is to consider distribution patterns within species ranges. Initial results suggest fundamental differences in the distribution patterns of species with different reproductive strategies. These patterns are reflected in species richness at a number of scales.

On the Black Sea plankton diversity in relation to some aspects of anthropogenic impact

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As a result by intensive human activity, during the last two decades the Black Sea ecosystem has been identified by the international scientific community in ecological degradation (Mee L., 1992). The anthropogenic eutrophication and the outburst of the exotic ctenophore Mnemiopsis leidyi are already considered as key ecological problems for the Black Sea ecosystem health, induced in the 80ies-early 90ies expansion of phytoplankton blooms, reducing the zooplankton diversity, sharp decline of the commercial fish stock and dramatic changes in pelagic community structure (Kamburska et al., 1999, Moncheva et al., 2000). According to GESAMP (1995), biodiversity changes can be used as biological indicator for the stressed ecosystem.

The present paper is a comprehensive overview (inventory) of the phytoplankton and zooplankton species diversity during the different phases of the Black Sea ecosystem evolution, depending on the anthropogenic eutrophication and *M. leid*yi explosion. In order to measure the biological response to these aspects of anthropogenic impact, phyto-mesozooplankton interaction pattern (ecological ratios) are also discussed. The study is based on the long-term spring/summer monitoring data from the stations along the Bulgarian Black Sea coast. The data were processed applying statistical analyses.

The results reveal significant alterations in phytoplankton and zooplankton taxonomic composition during the different periods. Initially the Black Sea ecosystem evolution has been subdivided into different phases: pristine period (50-70ies); period of intensive eutrophication (70-80ies), superimposed in the late

80ies to the effect of *M. leidyi* expansion; and recent period of relative improvement of the ecological state (90ies). Phytoplankton and zooplankton communities manifest parallel structural changes in terms of major taxonomic groups during the different phases. In the period of intensive eutrophication (70-80ies) the inversion in the dominance of their major taxonomic groups were evident. The opportunistic dinoflagellates overdominating the diatoms and the phytoplankton blooms becoming a recurrent phenomena. The diversity and biomass dynamic of Copepods (dominant for the Black Sea ecosystem zooplankton group) decreased substantially. During the 80ies-mid90ies, species such as *Centropages kroyeri*, *Oithona nana* were rare, while *Anomalocera pattersoni* and *Pontella mediterranea* were absent. On the contrary the heterotrophic dinofllagellate *Noctiluca scintillans* became dominant with frequent and massive blooms. Furthermore, the expansion of the newcomer *M. leidyi* in the late 80ies, substantially contributed to the decreasing of the zooplankton diversity and maintenance of the fodder zooplankton biomass at a critical low level. During the 90ies, the Black Sea ecosystem emerged from the state of critical ecological instability into a phase of relative recovery, due to the relaxation of anthropogenic pressure, not ignoring the possible impact of the global climatic changes too. In contrast to the 80ies the Bacillariophyceae: Dinophyceae and Copepoda: Cladocera biomass ratios increased in favour of diatoms, respectively of Copepods similar to the early 70ies. Typical for the pristine period copepod species (*C. kroeyri, A. pattersoni*) were recorded in visible concentrations at the end of 90ies along the Bulgarian Black Sea coast. Recently naturalised exotic ctenophore *Beroe ovata*, as the only predator of *M. leidyi* in Black Sea most likely also contributes to the current zooplankton taxonomic structure changes, but also provides argument for instability of the Black Sea biodiversity.

At the same time the increased zooplankton diversity in 1998-2000 (in terms of Copepods, Cladocerans, Ctenophores species) was accompanying by total zooplankton abundance and biomass at lower level than in 1995-1997. The total zooplankton biomass in summer 2000 was twice lower in comparison to 1999 and 7 times fold than in 1998 at 3 miles at Cape Galata (Kamburska, in preparation). Furthermore, in 2000 along the Bulgarian Black Sea coast were recorded tumour-like anomalies on young copepods, alarming for possible natural enemy, parasites, or indicate the emergence of a global phenomenon with a common etiology (Vanderploeg, 1996), not ignoring the possible impact of global climatic changes too.

The increased zooplankton diversity in the recent period provide more evidences to claim the relative improvement of the ecosystem. Nevertheless, the extremely low parameters (abundance, biomass) and the observed tumour-like abnormalities on copepods in the last 2-3 years put the question for other factors besides the anthropogenic eutrophication and *M. leidyi*'s invasion impact on the biodiversity.

Impact of fisheries on diversity of demersal fish communities

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The reductions of catch rates and mean size of individuals is well documented in world fisheries (Pitcher 1996). Consequently, new approaches to the study of exploited populations have been suggested, including the study of the fish assemblage structure in relation to environmental variables, and the characterization of seasonal changes to improve management practices. Despite this progress, basic descriptions of demersal fish faunas comprising both commercially exploited species as well as non-targeted components are not yet widely available for many coastal and offshore regions, although their value with respect to understanding possible fishing effects may be high (Rogers et al. 1999). As pointed out by Caddy and Sharp (1988) this type of study is a necessary step towards understanding the dynamics of multispecies stocks. Such work can then be extended to descriptive community dynamics to find general patterns, which may be associated with particular environmental conditions and fishing effort.

The spatial structure and seasonal changes of the demersal fish assemblages on the continental shelf (20-200 m) and upper slope (200-500 m) in the Northern Aegean Thracian and Ionian Seas (N. E. Mediterranean, Greece), where demersal fish are heavily exploited as principal targets or as by-catch, were analysed. Seasonal experimental trawl surveys were carried out from summer 1983 to autumn 1993 during which a total of 179 fish species were caught. Different statistics (i.e. classification and ordination methods, aggregate indicators of ecosystem status and diversity indices) were applied to the species abundance matrix, to investigate the spatial structure, diversity patterns and the main faunistic assemblages in the of the demersal fish communities.

The analysis of 717 bottom trawls revealed that, in general, species diversity, richness and evenness decreased with water depth, with the largest values at depths < 100 m, whereas dominance increased with depth, with its maximum at depths > 200 m. The effect of depth on the diversity patterns observed were always significant, while seasonal trends were similar with those described for the overall diversity characteristics in each area. Different demersal fish communities were found on the shelf and the upper slope. However, since most species had a wide distribution range these differences were rather quantitative than qualitative, at least with regard to the distribution of the characteristic species in the sampled stations.

The results indicated that although spatial changes in abundance could be detected, temporal changes were not obvious. Environmental variability and overexploitation, as well as differences in species' life-history strategies, have both influenced the structure of the demersal fish assemblages found along the depth gradient studied. The organization of the demersal fish assemblages analysed was determined to a great extent by an unidirectional trend induced by the fishery, the particular bottom topography and the oceanographic characteristics of the study areas.

Species richness and temporal stability in natural macroalgal communities

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Are species-rich communities more temporally stable than species-poor communities? To address that question we studied 120 macroalgal communities every year in nine years in three districts in Danish waters. Variation in species number and turnover of species from year to year declined significantly with increasing species richness. Species within form-functional groups tended to make up at fixed proportion of the species-rich communities and the year-to-year variation in their abundance declined with increasing species richness. Also, the year-to-year variation in abundance of many species declined in species-rich communities. Communities within the three districts followed the same stability patterns although the three districts are very different in terms of environmental stress and variability. The overall conclusion is that species richness increases the stability of macroalgal communities.

Revising the taxonomic composition and distribution of Fucophyceae of the Black Sea.

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The intensification of marine floristic studies is owing to the global concern for biodiversity conservation and the necessity to solve synecological problems (gene pool maintenance, population sustainability, ecosystem and landscape diversity stabilization). These tasks are is special significance to the Black Sea in which bottom vegetation generally occupies narrow (0 -20 m) stretch on the shelf and determines the condition and functioning of coastal ecosystems.

Though the marine flora has been well studied, only recently the check-list of brown algae has been compiled taking into account the taxonomic and nomenclature changes based on literature and original data available. As a result, comparison can now be made between local and regional flora of the Mediterranean; the analysis of the distribution of Fucophyceae in 5 Black Sea areas (Ukraine, Russia and Georgia, Turkey, Romania and Bulgaria) has been made (table1).

Table 1. Taxonomic composition of Fucophyceae in different areas of the Black Sea

Floristic region, coastal zone	The number of orders	The number of families	The number of genera
Ukraine	10	23	40
Russia and Georgia	9	19	32
Bulgaria	9	15	24
Romania	8	13	22
Turkey	8	14	18

Brown algae comprise 76 species (90 intraspecific taxa), representing 10 orders, 24 families and 44 genera. Orders Dictyosiphonales, Ectocarpales and Chordariales have the greatest species richness (table 2).

Table 2. The taxonomic composition and the number of taxa of Fucophyceae in the Black Sea

The order	The number of families	The number of genera	The number of species
Ectocarpales	2 / 8,3	9 / 20,5	18 / 23,7
Chordariales	5 / 20,8	12 / 27,3	20 / 26,3
Sporochnales	1 / 4,2	1 / 2,3	1 / 1,3
Desmarestiales	1 / 4,2	1 / 2,3	1 / 1,3
Dictyosiphonales	6 / 25,0	8 / 18,2	11 / 14,5
Scytosiphonales	1 / 4,2	2 / 4,5	2 / 2,6

Cutleriales	1 / 4,2	2 / 4,5	3 / 3,9
Sphacelariales	4 / 16,6	4 / 9,0	6 / 7,9
Dictyotales	1 / 4,2	3 / 6,9	6 / 7,9
Fucales	2 / 8,3	2 / 4,5	8 / 10,5
Total:	24	44	76

* beyond the boundary – %.

The number of species and intraspecific taxa is the largest in the genera *Cystoseira* (11) and *Ectocarpus* (10). New for the flora are 10 species described in the coastal water of Turkey (5), Ukraine (2), Romania (2) and Bulgaria (1): *Cutleria chilosa* (Falkenb.) Silva,*Cystoseira compressa* (Esper) Gerloff *et* Nizamuddin,*C. corniculata* (Wulf.) Zanard., *C. schiffneri* Hamel, *Desmarestia viridis* O.F. Müll., *Ectocarpus caspicus* Henckel, *Leathesia mucosa* J. Feldm, *Protectocarpus speciosus* (Böerg.) Kornm., *Sargassum acinarium* (L.) C. Ag., *S. hornschuchii* C. Ag.

The flora of brown algae includes 6 species not occurring in any of 15 Mediterranean localities: *Pseudolithoderma extensum*, *Elachista scutulata*, *Myrionema balticum*, *Dictyosiphon chordaria*, *Punctaria plantaguinea* and *Cystoseira barbata* var. *barbata* f. *flaccida*. Some of them are autochthonous and have been occurring since the Ice Age. However, allochthonous species of the Atlantic origin are generally prevailing in the flora.

Fucophyceae have the number of genera and species 2-3 times as less as Mediterranean ones that is primarily due to the isolated situation, the salinity and temperature regime of the Black Sea (tabl.3). The highest species diversity was found in the coastal zone of Ukraine and Russia (65 and 51 species); in coastal waters of Turkey, Romania and Bulgaria it reduces to 25, 31 and 36 species correspondingly.

In recent years the flora of brown algae substantially changed. *Stilophora tuberculosa*, *Arthrocladia villosa, Striaria attenuata, Spermatochnus paradoxus* formerly described as associated have not been found near the coast of Ukraine and Russia. Near the Anatolian coast 3 new species of the genus *Cystoseira* and 2 of the genus *Sargassum* appeared; the fact they grow together characterizes the zone as transitional from boreal to tropical. Apparently, the global climatic warming would involve enlargement the phytogeographical and species composition of Black Sea brown algae owing to immigration of new thermophilous species. The probability of such findings is especially high along the Caucasian and Turkish shoreline because of the direction of the main Black Sea current and the local environment similar to the adjoining Mediterranean areas.

Table 3. Fucophyceae in the Black Sea and in the Mediterranean

Taxa, number	The Black Sea	The Mediterranean
Specie	76	224
Genera	44	89
Family	24	30
Order	10	12
Ns/Ng	1,72	2,51
Ns/Nf	3,17	7,46
Ng/Nf	1,83	2,97

Ns/Ng – ratio between the number of species and the number of genera, Ns/Nf – species number and family number, Ng/Nf – genus to family number.

Ecology of the phytoplankton blooms in the coastal Adriatic waters

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Eutrophication of the marine ecosystem is an increasing problem all over the world. The first sign of eutrophication is increase of the phytoplankton biomass and decrease of the phytoplankton diversity. In Adriatic coastal waters prevail diatom species, but due to eutrophication, calm and warm weather in some semi-closed bays occur dinoflagellate blooms. Since 1980 in the Kaštela Bay red tide due to *Lingulodinium polyedra* has been observed regularly every year. In summer 1992 red tide bloom of *Alexandrium minutum* occurred instead bloom of *L. polyedra* what caused significantly lower bottom temperature than the average of 42 years monthly measurement.

The bloom of *P. minimum* is recorded in summer 1983 in Šibenik Bay and it occurs every summer after that. This area is very eutrophicated due the river Krka discharge and human activity. P. minimum favors low salinity and temperature up to 20 ^{0}C. Another factor that has made an important contribution to the start and maintenance of the *P. minimum* red tides is the previous blooms of the other phytoplankton species. In 1998

the bloom of *P. minimum* (10^6 cells L^{-1}) was associated to high abundance of *Leptocylindrus danicus* (3 x 10^6 cells L^{-1}) and was preceded by a dense *Skeletonema costatum* population (3 x 10^6 cells L^{-1}).
Research on Dinophysis species increased greatly after they were linked to a new type of shellfish poisoning named "Diarrhetic Shellfish Poisoning" DSP. In the Adriatic water we recorded *D. sacculus, D. caudata, D. tripos, D. acuminata* and *D. fortii.* All these species is the most abundant in the warm period with highest concentration of $10^3 - 10^4$ cells L^{-1}. High concentrations of *D. fortii* occurred with dense population of diatom *Skeletonema costatum* in Lim Bay at 23 ^{0}C sea temperature and salinity 37 psu. During this bloom, mouse bioassay showed presence of DSP-toxins in the shellfish. *D. caudata* is the most common in coastal waters all year long.

Microbial diversity in nutrient manipulated mesocosms

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Genetic analysis of natural communities has revealed an enormous diversity that could not be recovered by classical cultural approaches. With the introduction of methods such as denaturant gradient gel electrophoresis (DGGE) and fluorescent in situ hybridization (FISH) it has become possible to study diversity in the bacterioplankton communities at a level of resolution not previously attainable. These fingerprinting techniques are rapid and straightforward and data collection with such methods is also relatively efficient. Therefore with the use of these techniques it is feasible to study diversity changes in experimental situations where many samples are often required as with micro- and mesocosms experiments. Changes in natural bacterial and viral assemblages were studied in seawater mesocosms manipulated with inorganic (nitrate + phosphate) and inorganic + organic (glucose) nutrient additions. As inferred from the gel band-patterns obtained by denaturant gradient gel electrophoresis (DGGE) only moderate changes within the bacterial community took place when mineral nutrients were added alone. Supplementing the mineral nutrients with glucose in excess of what the bacteria could consume led, however, to major changes in band patterns. Based on fluorescence in-situ hybridisation (FISH), the major response was an increase in the population of γ-proteobacteria with a smaller response in α-proteobacteria. Sequencing of bands from the DGGE-gels indicated a distinct shift in the dominating populations due to the different manipulations and that glucose+mineral nutrient led to a vibrio-dominated bacterial community. Correspondence between a large-celled bacterial morphotype and DGGE-gel bands dominating in glucose-amended mesocosms was established by a FISH-probe constructed from band sequence information identifying the species as phylogenetically affiliated to *Vibrio splendidus.* The results from this study shows that supplementing balanced nitrate;phosphate additions with glucose had a major effect on bacterial production and on the community composition as measured with FISH and DGGE. We suggest that the feature allowing bacteria to become dominant after glucose addition is a high ability to compete for the limiting mineral nutrient under energy and carbon replete conditions, rather than any excellence in competing for glucose.

Ecological and evolutionary diversity of macroalgae: examples from the fucoids

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The variety of ecological processes and functions of marine macroalgae is an important component of macroalgal biodiversity. It is now widely recognised that important biodiversity units range from a broad taxonomic scale (e.g., ancient and evolutionarily distant taxa) to a genetic scale (e.g., within-species diversity). Not so well recognised is the importance of closely related species complexes which are still undergoing processes of rapid evolution. The genus *Fucus* is one such example: it has recently radiated into an ill-defined number of species that are very closely related and hard to distinguish. These often differ only in particular ecological characteristics that are under strong selective pressure, such as resistance to abiotic stress and reproductive success, including how successful external fertilisation is in monoecious versus dioecious species and survival of recruits following settlement. Reproductive system and selection are reflected into population genetic structure. Our research focuses on these questions, aiming at identifying stress-driven evolution, reproductive success in monoecious versus dioecious species, and the genetic structure of populations near their southern limits of distribution on the Iberian coasts versus continuous populations further North in Europe. Such boundary populations experience strong selective pressures and are likely to diverge from neighboring populations. This research will provide a basis for conservation of the marine biodiversity of the Lusitania province, in particular for populations at the boundary of the species' distributions, which are often particularly sensitive to environmental threats. The effects of short-term

perturbations or long-term environmental shifts (e.g., climate change) on ecosystem functioning are likely to be magnified on these biogeographic boundary zones. In addition, rapidly radiating species such as within the genus *Fucus* are important biodiversity units undergoing rapid evolution and are therefore important for conservation of biodiversity as a dynamic process.

Blank spaces in the knowledge of coastal marine biodiversity

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Investigation – understanding – risk prediction – conservation – these are steps towards biodiversity conservation. The crucial point of this way is understanding of biodiversity as an integrated versatile system with a complex hierarchy; it is this system that sustains efficient functioning of our biosphere.

Have we got this understanding, and can we adequately identify and quantitatively assess principal characteristics of the integrated biodiversity system? Have we gained sufficient knowledge about the entire variety of types describing land and water areas and all groups of organisms?

The answer is “no” rather than “yes”.

There are multiple blank spots both in theory and in practice of studying biodiversity. In this connection let us consider a few problems without trying to find an immediate answer to them.

Biodiversity system and exotic species.

More than 40 alien species have become common in the Black Sea (Shadrin, 2000), adding to the list of Black Sea species. Does it imply that biodiversity has increased on some level? On the global scale the similarity between species structure of different water bodies is growing; however the unification does not foster total biodiversity. Then how should biodiversity on a local scale be treated? Let us address the case of *Acartia tonsa* (Copepoda), a species brought into Sevastopol Bay (Black Sea) by accident (Shadrin, Gubanova, Popova, 1999) (see figer I).

The question is whether introduced aliens contribute to greater biodiversity in coastal zones. The answer depends on the scale used in assessment of the estimated using fractal but not additive units.

In normally functioning ecosystems biodiversity found at different levels is mutually additive in quantitative aspect. Our study on Copepods clearly show that at sites where genetic diversity is high, physiological variability of the copepods in populations decreases, and vice versa (Evstigneev, Shadrin, 1994); where species diversity is high in a taxocene polymorphism is only faintly manifested in the populations (Shadrin, Popova, 1992). Then how should total biodiversity of an ecosystem be integrally characterized?

With growing environmental pollution, the diversity is decreasing on every levels of organization of the Copepoda taxocene (Shadrin, Popova, 1994; others). Will the supplementarity of diversity sustain during these changes?

In that way should we quantitatively characterize the decline of the integrated diversity?

Sea – land contact zone with the adjoining water bodies: A main blank space.

Is it possible to conserve coastal marine biodiversity without appreciating and protecting this special zone? Coastline zone is a crossroad of the terrestrial and marine food chains; it also combines as well as rivers the seas and their watershed into integrated system (Shadrin, 1998). Pertiment data, though very fragmentary, suggest that the zone is remarkable for its high biodiversity and unique environmental processes.

For example, in phytoplankton of the Odessa Bay (Black Sea) there are 86 species of Bacillariophyta, while at a site of the bay’s supralittoral, only in one biotope (psammon) the number of species of Bacillariophyta is as large as 157 (Gerasimyuk, Tarasova, 2000; Belenkova, 2000). The diversity of biotopes as well as microbiotopes is very rich over coastline (Supralittoral).

And Backalskaya spit (about 25 sq. km) with its different lakes demonstrates such diversity.

Summer measured at a series of sites salinity estimates varied there from 16 to 300%, temperature from 25 to 50°C, pH from 6 to 10. Photographs taken in March 2001 prove the rich diversity of biotopes. Biodiversity is high, too but recently is under our study. One more unique phenomenon here are communities of relict cyanobacterial biofilms (mats); their diversity and ecological significance are poorly known by now and need further studying.

The main difficulty encountered in developing understanding about importance of biodiversity and its conservation is the lack of common vision of the subject, relevant goals, objectives and methods among scientists, politicians, economists and general public!

This difficulty can only be overcome if polylogical mentality replaces monological; but this problem refers to philosophy and social psychology rather than to ecology.

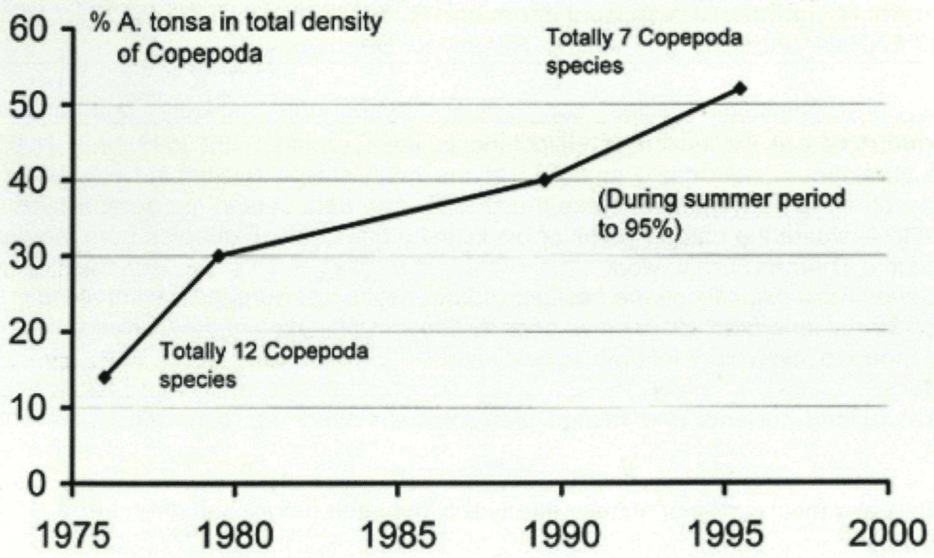

Figure 1. Long-term changes of average year % of Acartia tonsa in Copepoda taxocene (the Sevastopol Bay)

Biological invasions in coastal marine habitats: a population genetics approach

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The purpose of this contribution is twofold. First, a short overview of the importance of biological invasions for biodiversity in coastal marine environments will be given. Then somme issues that may be solved by using population genetics appraoches will be presented.

The introduction of a new species within an habitat may abruptly modify the interactions among indigeneous species and the stability of the whole ecosystem. Biological invasions are one of the majors threats for marine biodiversity in coastal environments. Deliberate or accidental introductions of new species in marine habitats are tightly linked to human activities as shipping or mariculture. Indeed the rate and volume of trade has been increasing since the beginning of the 20th century. Likewise, an increasing rate of marine biological invasions has been recorded.

Regarding the invasion of an area by a foreign species, numerous conceptual frameworks and methodological outlines have been developed (demography, spatial ecology, theoretical modeling). Interestingly, population genetics methods have not been fully exploited. However, population genetics approaches provide powerful tools to trace back historical processes, monitor dispersal, and assess some parameters of the reproductive systems. Such methods are of particular values when direct monitoring of individuals are difficult to carry out. moreover, recent statistical developments provide the opportunity to study newly founded populations and to elucidate recent gene flow.

As invasive species are serious threats for coastal marine biodiversity, it is crucial to determine the pathways by which the invasions occured as well as the dynamics of the species in the new territories (colonization, dispersal, population stability). Molecular ecology and population biology are helpful to determine the conditions by which the establishment and dispersal of the invasive species in marine coastal habitats are successful.

The questions adressed are (i) what are the main steps of the invasion history and the major introduction pathways? (ii) what are the critical stages that contribute to dispersal ability? (iii) what are the dynamics and the recruitment patterns? To what extent can the patterns observed be associated to specific life history traits? (iv) Did life history traits, population dynamics and species diversity be altered during the colonization process when compared to the native area?

The Helgoland biological and oceanographic time series

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Since the nineteen-sixties, phytoplankton species composition, temperature, salinity and nutrient concentrations have been monitored at the Island of Helgoland in the German Bight (54° 11,3´ N 07° 54,0´E). This involves both continuous (work-daily) sampling at the main station (Helgoland Reede) and three monthly sampling transects. It is now timely to place these long-term data sets in the perspectives of global and local change and to evaluate the data in terms of biodiversity questions. Examples from the data set are presented and placed in a Thematic Framework.
When the Helgoland Time-Series were established the background questions justifying them went along the lines of obtaining a data base for the long term observation of potential eutrophication in the German Bight.
The basis has now been extended to involve the following questions:

1) Global Warming questions
   (changes in temperature and currents and related planktonic transport e.g. occurrence of warm-water species).
2) Local change questions
   (change in Elbe outflow and local currents, nutrient inputs e.g. the latter before and after the reunification).
3) Seasonality of plankton
   (the data will be used to provide a baseline on planktonic succession and phytoplankton-zooplankton interactions).
4) Occurance of toxic algae
   (the data will be used to provide information on the occurrence of toxic algae).
5) Ecological organism interactions
   (the relevance of specific organisms in particular ecological questions such as the induction of morph in algae).

Each of these topics is directly related to questions of changes in Biodiversity and the induction and consequences thereof. The long-term data sets will serve as a basis for investigations into these topics.

Examples from the data set
Nutrients: An example of the nitrate concentrations at the Helgoland site is given in figure 1 below. Phosphate concentrations are given in figure 2. When comparing the values with those of salinity given in figure 3 it is clear that the input of freshwater (from the Elbe) also carried nutrients into the German Bight and that now that in recent years the nutrient loading of the Elbe is less the nutrient values of the German Bight are also getting lower.
Specific topic example: Has there been a change in wind regime and what are the Consequences.
One of the questions which needs to be answered is whether the wind direction E to NE has decreased over the last 20 years, if so is this mirrored by the Phytoplankton, e.g. do we find less benthic species form the Northern Wadden Sea in the water column. From the wind directions we have seen that there has been an increase in the wind sector SSE-WNW. If one were to look at such benthic-pelagic algae as *Paralia sulcata* (Figure 4) or *Odontella aurita* versus the occurence of a ubiquitous planktonic species *Euchampia zoodiacus* it should be possible to determine whether wind has an effect on the abundance of benthic algae in the phytoplankton. This is one of our current goals. The ecological consequences of this in terms of benthic-pelagic coupling are being evaluated in experiments.

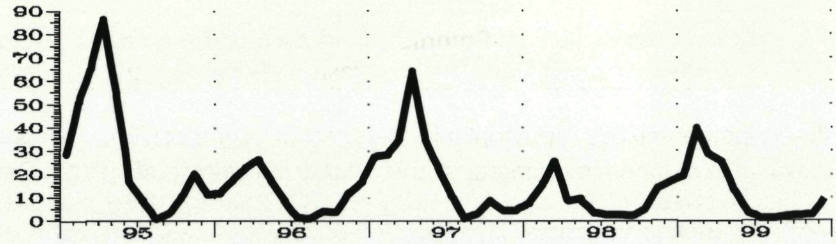


Figure 1
Monthly medians of Nitrateμmol.l^{-1}

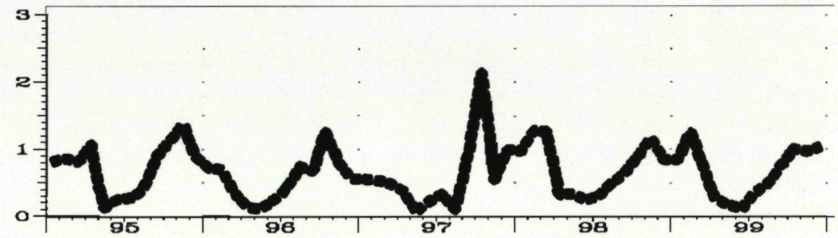


Figure 2
Monthly medians of Phosphate μmol.l^{-1}

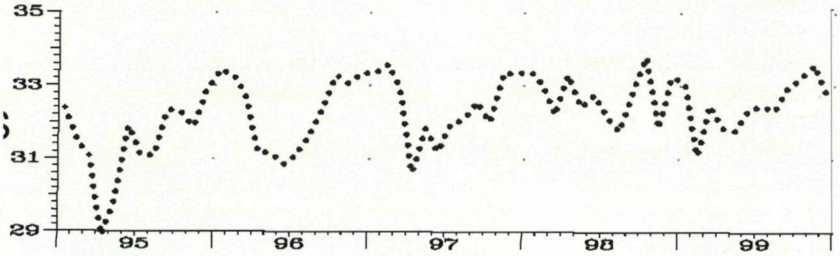
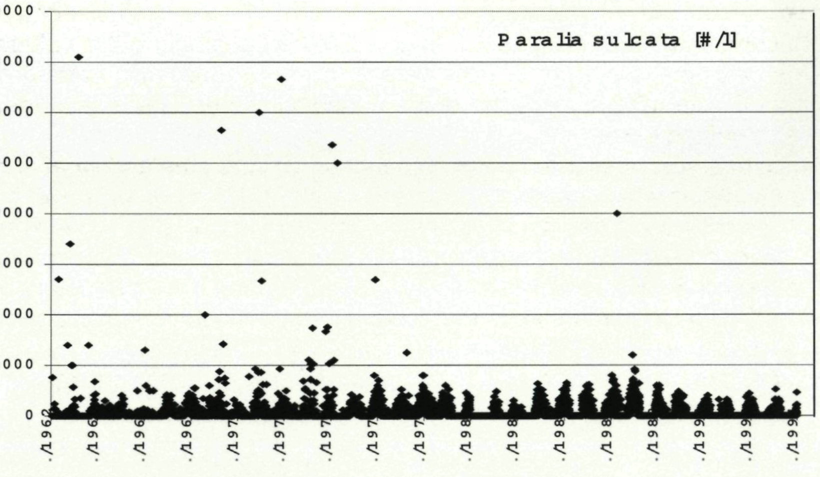


Figure 3
Monthly medians of Salinity.

Figure 4
Occurrence of *Paralia sulcata*



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