ABSTRACTS

Nemertodermatida, a basal bilaterian group

Ulf Jondelius[1], Iñaki Ruiz-Trillo[2], Jaume Baguña[2] and Marta Riutort[2]

[1] **Evolutionary Biology Centre, Uppsala University, Norbyvägen 18D 752 36 Uppsala, Sweden**
[2] **Departament de Genètica, Universitat de Barcelona, Diagonal 645, 08028 Barcelona, Spain**

The taxon Nemertodermatida was originally classified within the Acoela, but was later separated from the acoels on account of their distinct intestinal lumen. More recently Nemertodermatida was hypothesised as the sister group of the Acoela in the taxon Acoelomorpha owing to similarities in epidermal ciliary systems in the two groups. However, in the first analyses of ribosomal DNA the nemertodermatid *Nemertinoides elongatus* grouped with members of the Rhabditophora and not with acoels.

We sequenced 18S rDNA from four Nemertodermatida and used parsimony analysis and parsimony jack-knifing of nucleotide and nucleotide triplet sequences to generate a hypothesis of the phylogeny of the Nemertodermatida. A secondary structure alignment and five multiple alignments with different gap opening penalties (ClustalW) were evaluated, all yielding similar results. The Nemertodermatida group basally in the bilaterian clade separate from the Acoela in our most parsimonious trees. The same results were obtained when the data set was analysed with maximum likelihood methods.

Branch support is low for the basal clades of the Bilateria in 18S rDNA. When Acoela were excluded from the data set, there was jack-knife support for the Nemertodermatida as the basal bilaterian clade. When the Nemertodermatida were excluded and Acoela left in the dataset, the Acoela was supported as the sister group of other bilaterians. With both Acoela and Nemertodermatida present, support for a basal bilaterian clade was absent.

The sequence labelled *Nemertinoides elongatus* (Genbank Acc no U70083) grouped with Rhabditophora (separately from the Nemertodermatida) also in our analyses. This indicates that the sequence is derived not from a member of the Nemertodermatida, but from a species of the Rhabditophora.

Results can be found in

Ruiz-Trillo, I., M. Riutort, D.T.J. Littlewood, E.A. Herniou & J. Baguñà (1999) Acoel flatworms: earliest extant bilaterian metazoans, not members of Platyhelminthes. *Science*, 283: 1919-1923.

The development of *Neochildia fusca* supports the position of the acoels as basal bilaterians

Barbara C. Boyer, Jonathan Q. Henry and Mark Q. Martindale

The Marine Biological Laboratory, Woods Hole, MA, USA

The phylogenetic position of the acoel flatworms has long been controversial. They have traditionally been placed within the Platyhelminthes, either at the base of the metazoan tree or in the Lophotrochozoa. However, recent evidence suggests that they belong in a separate phylum of basal, direct-developing triploblastic metazoans (*Science* 283: 1919-1923). Acoel embryos exhibit a unique form of development that previously has been related to that found in polyclad turbellarians and coelomate spiralians, which display typical quartet spiral cleavage. Because developmental characteristics can provide evidence of relationships among metazoan groups, we used modern lineage tracers to generate the cell lineage of the acoel *Neochildia fusca*. Cleavage occurs in a duet pattern in which the second cleavage plane is leiotropically oblique relative to the animal vegetal axis. At the four-cell stage, the plane of first cleavage corresponds to the plane of bilateral symmetry, and subsequent cleavages are symmetrical across the sagittal plane. The first three micromere duets generate only ectodermal derivatives; there is no ectomesoderm. Both third duet macromeres produce the endomesoderm, including the complex musculature, as well as the peripheral and central parenchymas. The cleavage pattern, cell lineage, and mesodermal origins of *N. fusca* share little similarity with those of other metazoans, including the quartet-

cleaving Platyhelminthes such as the polyclads. If acoels flatworms belong to the lophotrochozoan clade, their development appears to represent a degenerate condition related to the abandonment of larval development.

Alternatively, however, we suggest that the acoel developmental program may be related to that of ancestral bilaterians, which were represented by small direct-developing, acoelomate animals exhibiting a form of bilateral (or biradial) cleavage, with mesodermal tissues arising solely from endodermal lineages.

Results can be found in

BOYER, B.C., J.Q. HENRY & M.Q. MARTINDALE (1996). Modified spiral cleavage: The duet pattern and early blastomere fates in the acoel turbellarian *Neochildia fusca*. *Biol. Bull.*, 191: 285-286.

HENRY, J.Q., M.Q. MARTINDALE & B.C. BOYER (2000). The unique developmental program of the acoel flatworm *Neochildia fusca*. *Dev. Biol.*, 220: 285-295.

Molecular markers for taxonomic identification and phylogeny of species of the genus *Dugesia* in the western Mediterranean

Jaume Baguñà, Salvador Carranza and Marta Riutort

Departament de Genètica, Facultat de Biologia, Universitat de Barcelona, Diagonal 645, 08028 Barcelona, Spain.

The genus *Dugesia* (Gérard, 1850) comprises up to 70 described species, formerly included within the so-called species group or species complex *Dugesia gonocephala sensu lato* (s.l.), widely distributed in Africa and the Paleartic and Oriental regions. In the western Mediterranean, eight species of *Dugesia* have so far been reported. In this area, however, fissiparous populations clearly outnumber conspecific sexual populations. Because in *Dugesia* most species (the exceptions being *Dugesia hepta* and *Dugesia sicula*) have karyotypes that are a multiple of a basic haploid number of eight with almost identical karyograms, and because polyploidies, aneuploidies and the presence of B-chromosomes have been frequently reported, karyotypic analyses are of little help to assign fissiparous populations to their sexual counterparts. In addition the phylogenetic relationships between these species are still far from clear.

Here, we review the recent application of molecular markers that identify species or groups of species and that lead to a tentative new phylogeny for the species studied. In particular, we discuss results using sequences of the internal transcribed spacer region (ITS-1) of ribosomal DNA, the presence/absence of a family of long interspersed repeated elements (De1) first isolated in *Dugesia etrusca* (BATISTONI et al, 1999) and restriction pattern analysis of rDNA (BATISTONI et al, 1999). Main results were: 1) ITS-1 sequences and De1 contribute useful qualitative markers to identify single species or groups of species; 2) distance and parsimony analyses drawn from ITS-1 sequences show two main phylogenetic assemblages within the species studied, with a good internal resolution; and 3) all asexual populations were unambiguously assigned to particular sexual species.

These results show the usefulness of a molecular approach to taxonomy and phylogeny and the need to make congruent morphologically-based and molecularly-based taxonomies and phylogenies.

Results can be found in

BAGUÑÀ, J., S. CARRANZA, M. PALA, C. RIBERA, G. GIRIBET, M.A. ARNEDO, M. RIBAS & M. RIUTORT (1999). From morphology and karyology to molecules. New methods for taxonomical identification of asexual populations of freshwater planarians. A tribute to Professor Mario Benazzi. *Ital. J. Zool.*, 66: 207-214.

BATISTONI, R., L. ROSSI, A. SALVETTI & P. DERI (1999). A molecular cytogenetic comparison of planarians from the *'Dugesia gonocephala* group' (Platyhelminthes, Tricladida). *Ital. J. Zool.*, 66: 239-244.