

cleaving Platyhelminthes such as the polyclads. If acoel 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

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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 Palearctic 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

BAGUÑA, 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.