

Merging molecular phylogeny and classical taxonomy of tintinnid ciliates

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In recent years, the amount of new environmental sequences of eukaryotic marker genes, particularly 18S rRNA genes, is increasing exponentially to the detriment of more classical studies. However, it is often impossible to associate those sequences to described protist species. Coupling molecular and morphological identification of species is now critical to study efficiently the ecology and evolution of planktonic protists. Among microzooplankton, the tintinnid ciliates are an ecologically important compartment. They form a monophyletic, taxon-rich order, the members of which are characterized morphologically by the possession of an external secreted shell, the lorica. The molecular information available for different species described by classical morphology is relatively scarce and the phylogenetic relationships between species within the order a matter of debate. In the present study, we amplified and sequenced, from individual cells, the 18S rRNA genes for 28 morphologically distinct species representative of the Tintinnida families. Among these, the 18S rDNA sequences of 15 species are new for the GenBank database: *Amphorides amphora*, *A. quadrilineata*, *Steenstrupiella* sp., *Canthariella* sp., *Eutintinnus* sp., *Dadayiella ganymedes*, *Xystonella longicauda*, *Climacocylis scalaria*, *Rhabdonella armor*, *R. spiralis*, *Cyttarocylis cassis*, *Petalotricha ampulla*, *Undella marsupialis*, *U. magna*, *U. clarapedei*, *Codonellopsis orthoceras*, *Codonella aspera*, *Dictyocysta lepida*. Our molecular phylogenetic analyses of the Tintinnida with this enriched taxon-sampling allow us to propose some changes in the taxonomy of this group and, more generally, to discuss the importance of molecular data from a microevolutionary perspective.