

# **Phylogenomic analysis of SAL super-group (Ciliophora), including novel marine lineages of anaerobic ciliates, which host prokaryotic symbionts**

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Ciliates are among the most studied protists and are well known for their ability to penetrate into a variety of environments, including extreme ones, such as hypoxic and anoxic sediments, and for their ability to form various symbiotic relationships. Yet, their true diversity is still far from fully described and much remains unknown about the nature of their symbioses, particularly within the anaerobic lineages. Here, we present phylogenomic analyses of anaerobic ciliates within the SAL group (Spirotrichea, Armophorea, and Litostomatea), including two deep novel lineages of marine ciliates that we have discovered. We have sequenced a transcriptome of one species of the novel lineage and a metagenome of one species from the second novel lineage, as well as four metagenomes of species of Metopida, two of which may represent novel species. We have performed pilot studies on the energy metabolism and characterization of metabolic pathways from the transcriptome. In addition, we studied the MROs (mitochondrion related organelles) present in these organisms and found that the MROs of several studied lineages appear to have a genome. Interestingly, most of the studied taxa host various ecto- and endosymbionts that persist in our long-term ciliate cultures. Using autofluorescence, FISH and CARD – FISH methods, we discovered that at least some of the endosymbionts are methanogenic Archaea, while others host sulphate-reducing deltaproteobacteria on their cell surface.