

## Abstract

Ciliates are the most diversified protists in suboxic and anoxic habitats where they often form symbioses with prokaryotes. Although the diversity of anaerobic ciliates has been overlooked for a long time, anaerobic representatives can be found in most ciliate classes. This study focuses on anaerobic ciliates from the subclass Scuticociliatia, a neglected lineage, which belongs to the species-rich class Oligohymenophorea. One of the main outcomes resulting from this study is the discovery of a novel anaerobic clade of ciliates, from which only one species has been described molecularly to date. We have shown that the clade represents a diversified lineage, likely a new order. Thanks to the sampling of many freshwater and marine anoxic sediments, we have established the largest culture collection of anaerobic scuticociliates in the world. This has enabled us to determine the 18S rRNA gene sequences of 55 cultured anaerobic scuticociliates and to study their morphology both *in-vivo* and using various silver-impregnation methods. Besides, we applied transmission and scanning electron microscopy techniques to study the ultrastructure of both ciliates and symbionts. To identify the symbionts, we also employed other methods including microbiome sequencing and fluorescence *in-situ* hybridization. Since all the studied representatives of the new clade host prokaryotic symbionts, we conclude that symbioses of anaerobic ciliates and prokaryotes are a common life strategy in the extreme conditions of freshwater and marine anoxic sediments. A preliminary analysis of the transcriptome of a marine scuticociliate gave us the very first insights into energetic metabolism of marine anaerobic representative from the subclass Scuticociliatia.

Key words: anaerobic ciliates, diversity, microbiome, Scuticociliatia, symbioses with prokaryotes, transcriptome