Abstract

Ciliates (Ciliata) are single-celled eukaryotic organisms belonging to the large group Alveolata. Ciliates are classified to eleven classes. Anaerobic/microaerophilic representatives belong to classes Armophorea, Litostomatea, Plagiopylea, Oligohymenophorea, and Prostomatea. The mitochondrion of the anaerobic ciliates has been tranformed to hydrogenosome. The anaerobic ciliates are characteristic for the presence of methanogenic symbionts in the cytoplasm near hydrogenosomes. Anaerobic flagellates are free-living or they live as commensals, mutualists or parasites in the digestive tract of animals including humans.

The true diversity of anaerobic ciliates is still not fully understood. The reason is that only sequences of described ciliate species are usually included into phylogenetic analyses. However, many environmental sequences representing considerable part of known molecular diversity of ciliates have been published as well. The aim of this work was to obtain and analyze sequence data of anaerobic free-living ciliates. We have determined SSU rDNA sequences of 32 different freshwater and marine strains of ciliates. Phylogenetic analyses showed that the strains belonged mostly to the classes Armophorea, Plagiopylea and Oligohymenophorea. The strain LIVADIAN belonged, together with genera *Paraspathidium, Askenasia, Urotricha, Cryptocaryon*, and several environmental sequences, to the class Prostomatea. Our data also suggested that the Plagiopylea likely belongs to the class Prostomatea as well, instead of representing an independent ciliate class.

Key words: anaerobiosis; Armophorea; ciliates; hydrogenosome; methanogenic symbionts; Oligohymenophorea, Plagiopylea, Prostomatea, SSU rDNA