

Oxymonads are a group of heterotrophic flagellates living in low oxygen environment. These protists inhabit mainly the gut of xylophagous insects (cockroaches, termites), with an exception of the genus *Monocercomonoides*, which was described from the intestinal contents of many vertebrates. On the basis of molecular data, Oxymonadida are classified into the supergroup Excavata (Cavalier-Smith, 2002; Simpson et al., 2006, Hampl et al. 2009).

This thesis was focused on the diversity of genus *Monocecomonoides* from the morphologically simplest family *Polymastigidae*. The main goal of our work was to gather sequence data from strains isolated from a wide spectrum of hosts. We have obtained 26 partial sequences of the gene for the SSU rDNA in total, of which two belonged to another oxymonad, apparently genus *Oxymonas*. Our phylogenetic analysis indicated that the representatives of the genus *Monocercomonoides* form one group, however with a low bootstrap support.

On the basis of published data about the presence of non-canonical genetic code in some oxymonads (Keeling and Leander, 2003; de Koning et al., 2008), we decided to explore this rare phenomenon in representatives of the genus *Monocercomonoides*. For this part of the study we gathered 9 partial sequences of α -tubulin gene. In these sequences we have not observed the use of non-canonical genetic code.