

An individual look at the oxymonad *Streblomastix strix* and its bacterial symbionts using single cell genomics

S. C. Treitli¹, M. Kolisko², P. Keeling³, V. Hampl¹

1. Charles University, Faculty of Science, Department of Parasitology, Prague, Czech Republic.

2. Biology Centre, Institute of Parasitology, Czech Academy of Sciences, České Budějovice

3. Department of Botany, University of British Columbia, Vancouver, British Columbia, Canada

Oxymonads are a group of protists which live as intestinal endosymbionts in the gut of insects and vertebrates. Most of their representatives are found in termites and wood feeding cockroaches where they are closely associated with prokaryotes located inside or on the surface of their cells. However, most of oxymonads cannot be cultured in vitro, which makes it difficult to study the relationship between oxymonads and their bacterial symbionts. Our work is focused on the oxymonad *Streblomastix strix* which lives in the gut of the termite *Zootermopsis angusticolis*. This oxymonad is highly adapted to harbor bacterial symbionts by enlargement of its surface area. Using single cell picking and whole genome amplification, we managed to amplify the DNA of *Streblomastix strix* and its bacterial symbionts and we sequenced it using next generation sequencing. Our preliminary results show the presence of 14 Bacteroidetes SSU sequences, one SSU from genus *Endomicrobium* and five other SSU sequences from other bacteria. Using FISH, we managed to confirm that all Bacteroidetes SSU sequences originate from symbiotic bacteria of *Streblomastix strix*. Our preliminary annotation of the Bacteroidetes metagenome shows that the symbiotic bacteria possess enzymes involved in nitrogen fixation and cellulose degradation, both metabolic pathways being very important for survival in the gut of the termites.