

**Charles University, Faculty of Science**  
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Abstract (en)



Analysis of the genome of a free-living amoeba *Mastigamoeba balamuthi* and its comparison with  
pathogenic *Entamoeba histolytica*

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## Abstract

Examination and comparison of organisms have been tremendously important for the study of life's history on earth. The progress of our understanding of the genetic basis of heredity and the recent boom of sequencing technologies allows us to continue in this exciting field of research from the perspective of genes and genomes. In this work, I focus on the study of an anaerobic amoeba *Mastigamoeba balamuthi*, which is related to an important human pathogen *Entamoeba histolytica*. Comparative analysis allows us to draw some conclusions about the nature of the common ancestor of *Mastigamoeba* and *E. histolytica*, how it adapted to the anaerobic lifestyle, and about the way the *Entamoeba* lineage evolved to become a successful parasite. Surprisingly we also noticed that besides hydrogenosomes (hydrogen-producing organelles related to mitochondria), *M. balamuthi* also harbors peroxisomes – organelles thought to be absent in anaerobic organisms. This finding motivated us to inquire more about peroxisomes in other eukaryotic lineages. We found out that there is a reduced set of peroxisomal markers in certain *Entamoeba* species. Moreover, we showed that peroxisomes were independently lost in several lineages of parasitic helminths and a free-living tunicate *Oikopleura dioica*.