

## Two chytrid-like parasites form a novel divergent fungal clade.

S.A. Karpov<sup>1,2</sup>, P. López-García<sup>3</sup>, M.A. Mamkaeva<sup>2</sup>, V.I. Klimov<sup>2</sup>, A.E. Vishnyakov<sup>2</sup>, V.S. Tsvetkova<sup>2</sup>, and D. Moreira<sup>3</sup>

1. Zoological Institute, Russian Academy of Sciences, St. Petersburg 199034, Russian Federation

2. St. Petersburg State University, St. Petersburg 199034, Russian Federation

3. Unité d'Ecologie, Systématique et Evolution, CNRS 8079, Université Paris-Sud, 91400 Orsay, France

Molecular phylogenetic analyses of parasitic chytridiomycetes in addition to classically well-studied fungal lineages is expanding the diversity of poorly known lineages of zoosporic fungi. Interestingly, some novel zoosporic fungi studied occupy surprisingly late-branching positions in the fungal tree, as is the case of *Olpidium* (Sekimoto et al., BMC Evol Biol 2011). Here, we describe molecular phylogeny and ultrastructure of *Amoeboradix gromovi* and *Sanchytrium tribonematis* (Sanchytriaceae) – two chytrid-like parasites of the yellow-green alga *Tribonema gayanum* unusually endowed with amoeboid zoospores with highly reduced flagellum (pseudocilium). Morphological features of both species observed by light microscope recall previous descriptions of typical chytrid *Rhizophyidium anatropum*. Remarkably, the zoospore ultrastructure exhibits one of the longest kinetosomes known in eukaryotes, yet being highly reduced, being only composed of microtubular singlets or doublets. Molecular phylogenetic analyses of 18S+28S rRNA concatenated genes obtained from infected cultures, single-picked zoospores and sporangia of *Amoeboradix* and *Sanchytrium* revealed their close relationship to each other, forming a robust monophyletic clade. However, this cluster does not group with any known zoosporic fungi and is very divergent, branching, albeit with low support, in a basal position with respect to Glomeromycota and Dikarya. Therefore, the *Amoeboradix-Sanchytrium* clade represents a new fungal lineage. Future multi-gene analyses from genome or transcriptome sequences should help to find a fungal home for the family Sanchytriaceae, which remains *incertae sedis* within Fungi.