

Results

1. We sequenced SSU rDNA of *Protoopalina intestinalis*, representative of opalinids, and *Karotomorpha*, a proteromonadid with hitherto no molecular data available. Analyses of these data confirmed close affinity of the two families and also the paraphyly of proteromonadids – the resulting topology was (Proteromonas + (Karotomorpha + Protoopalina)). Slopalinids belonged within stramenopiles in our analyses.
2. In our analyses, the genus *Blastocystis*, genetically quite variable, formed a sister group of slopalinids within the group of Stramenopila.
3. We sequenced SSU rDNA of two *Chilomastix* isolates. The sequences differed substantially in length and composition, but formed a monophylum in resulting phylogenetic trees. Surprisingly, *Retortamonas* was not reconstructed as a sister group of *Chilomastix*, but the two genera formed a paraphyletic group from which the diplomonads evolved (with *Retortamonas* closer to diplomonads). This result implies that the ancestor of diplomonads (including enteromonads) was retortamonadid-like.
4. We sequenced and analysed SSU rDNA of two morphologically well defined amoebae, *Mayorella gemmifera* and *Saccamoeba limax*. We have found that another sequence ascribed to *S. limax* and used in some analyses probably originates from a

misidentified organism.

5. We have programmed the program SlowFaster. It is a unique user-friendly tool leading a user step-by-step through the whole process of slow-fast analysis. We believe that this tool will allow other authors to better exploit their datasets.

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