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Hidden diversity of myxomycetes: problems and perspectives

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Motivation and Aim: Myxomycetes (= Myxogastria, plasmodial slime molds) represent a monophyletic group of free-living amoeboid protists within the supergroup Amoebozoa that are characterized by a unique life cycle with an alternation of uninucleate myxamoebae/swarm cells, multinucleate plasmodia and fruiting bodies (sporocarps) filled with airborne spores. Since Linnean times about 1000 species were validly described within five orders based almost exclusively on morphological characters of the sporocarps. However, DNA sequence-based studies revealed a paraphyly of many taxonomical groups within the class as well as an unexpected extent of hidden diversity. The direction of further research in the field of myxomycete taxonomy and diversity studies using modern approaches should be outlined.
Results and discussion: In recent years, a number of molecular phylogenetic studies revealed two problems of the morphological approach. 1. The long established five-order system does not reflect correctly the phylogenetic relationships within the class. This could be solved by creating a system based on the analysis of multiple gene markers, e. g. transcriptomic or genomic data. At the moment, transcriptomic data are available for only four myxomycetes species and genomic data for one. 2. Many morphospecies seem to comprise several, reproductively isolated, biospecies; others are even paraphyletic [1]. Application of DNA barcoding [2] and 18S amplicon metagenomics [3] provided evidence that diversity assessments based on morphological determination of sporocarps underestimate the diversity of the group. The presence of phylogenetic clades consisting of OTUs not matching to any known species, as well as several reports of myxamoebal strains with unknown species identity isolated from unusual habitats lend evidence for a significant, yet undescribed diversity of myxomycetes which presumably never or rarely form sporocarps. However, the incompleteness of the currently existing database of reference sequences does not allow us to distinguish such species reliably.
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