

Morphological and physiological characterisation and multigene phylogeny of the zygomycetous fungal order Mortierellales

Tamás Petkovits

Department of Microbiology, University of Szeged, Szeged, Hungary

Mortierellales is one of the largest groups of Zygomycota. These fungi have practical importance as producers of polyunsaturated fatty acids, such as arachidonic acid, and as biotransforming agents of different organic compounds used in the pharmacological and chemical industries. Understanding the evolution of Mortierellales including the origin and evolutionary role of their enzymes may increase the biotechnological relevance of these fungi. Originally, this group was considered as a family of the order Mucorales. In the recent past, phylogeny of Zygomycetes had been analysed in detail revealing the need of the establishment of the new order Mortierellales. However, these works focused mainly on the Mucorales and the phylogenetic relationships within the Mortierellales remained unresolved. Molecular phylogenetic data suggest that the presently accepted, morphology-based taxonomy of the order is highly unnatural.

We inferred phylogenetic relationships of the Mortierellales using a combined matrix of nrITS, 5.8S, nrLSU, nrSSU, EF1- α and RPB1 sequences from 106 strains of *Mortierella*- and related taxa. PCR was carried out and the questioned sequences defined. Sequences were aligned by using the softwares MUSCLE and Probalign. The phylogenetic analyses were made by using Maximum Likelihood and Bayesian estimation. Phylogenetic trees were calculated on the strength of the sequences of each ribosomal subunit on its own and on a fourth, combined, large alignment including all of them. Results suggest that the genus *Mortierella* is paraphyletic and includes the genera *Gamsiella*, *Dissophora* and *Lobosporangium*. The relationships between the larger groups of the genus *Mortierella* also became clearer, as we found that *M. verticillata* and *M. humilis* are closely related to each other. The same conclusion goes to *M. gamsii* and *M. hyalina*. It seems that *G. multidivariata* and *M. mutabilis* are in close relationship not only on a phylogenetic but also on morphological basis.

Morphological investigations were carried out using both light- and scanning electron microscopic techniques. Our goal was to reveal the fine structure of the observed characters, such as branching of the sporangiophores, ornaments of the sporangia and the mycelial structure. We found that phenotypic traits of these fungi strongly depend on the culturing conditions. We also investigated the carbon source utilization patterns of the fungi by using 67 different carbon sources. This research showed that delimitation of the species is difficult by using only morphological and/or physiological characters but merged with the phylogenetic results they improve the understanding of the relationships within this fungal group.

The research was supported by the international cooperation grant of DFG and OTKA (OTKA NN75255).

Supervisor: Tamás Papp
E-mail: pettam@gmail.com

Relationship between reactive oxygen (ROS) and reactive nitrogen species (RNS) and auxin in *Arabidopsis* development under copper excess

Andrea Pető

Department of Plant Biology, University of Szeged, Szeged, Hungary

Copper (Cu^{2+}) is an essential microelement but its excess influences the shoot and root architecture of plants. This heavy metal induces ROS production leading to oxidative stress condition. Moreover, alterations of nitric oxide (NO) levels can also be detected, which plays a role e.g. in cell death induction. Based on these, the aim of this study was to investigate the morphological and physiological responses and the possible relationship between ROS and RNS during short-term (7-day-long) and longer (17-day-old) copper exposure in the root tips of *Arabidopsis* using microscopic methods.

For the experiments (*Col-0*, WT), NO-overproducer (*nox1*), NO-deficient mutants (*nialnia2*, *nialnia2noa1-2*) and the S-nitrosogluthione reductase (GSNOR)-deficient *gsnor1-3* plants were used. Also *Arabidopsis* plants with low (*vtc2-1* and *vtc2-3*) and high ascorbate content (*miox4*) were treated with 0, 5, 25 and 50 μM CuSO_4 .

During short-term treatments, Cu^{2+} at a concentration of 50 μM resulted in a large reduction in cotyledon area and hypocotyl and primary root lengths, accompanied by an increase in auxin levels. In cotyledons, a low Cu^{2+} concentration promoted NO accumulation, which was arrested by nitric oxide synthase or nitrate reductase inhibitors. The 5 μM Cu^{2+} -induced NO synthesis was not detectable in *nialnia2* or *nialnia2noa1-2* plants. In roots, Cu^{2+} caused a decrease of the NO level, which was not associated with superoxide and peroxynitrite formation. Inhibition of auxin transport resulted in an increase in NO levels, while exogenous application of an NO donor reduced the auxin-dependent DR5::GUS expression. The elongation processes of *nox1* were not sensitive to Cu^{2+} , but NO-deficient plants showed diverse growth responses.

Copper excess caused the inhibition of stem and root growth of 17-day-old *Arabidopsis*, during which cell elongation, division and expansion were also modified. The symptoms of stress induced morphogenic response (SIMR) were found in the root system of 25 μM