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DNA barcoding in *Mucorales*: an inventory of biodiversity

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Abstract



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The order *Mucorales* comprises predominantly fast-growing saprotrophic fungi, some of which are used for the fermentation of foodstuffs but it also includes species known to cause infections in patients with severe immune or metabolic impairments. To inventory biodiversity in *Mucorales* ITS barcodes of 668 strains in 203 taxa were generated covering more than two thirds of the recognised species. Using the ITS sequences, Molecular Operational Taxonomic Units were defined by a similarity threshold of 99 %. An LSU sequence was generated for each unit as well. Analysis of the LSU sequences revealed that conventional phenotypic classifications of the *Mucoraceae* are highly artificial. The LSU- and ITS-based trees suggest that characters, such as rhizoids and sporangia, traditionally used in mucoralean taxonomy are plesiomorphic traits. The ITS region turned out to be an appropriate barcoding marker in *Mucorales*. It could be sequenced directly in 82 % of the strains and its variability was sufficient to resolve most of the morphospecies. Molecular identification turned out to be problematic only for the species complexes of *Mucor circinelloides*, *M. flavus*, *M. piriformis* and *Zygorhynchus moelleri*. As many as 12 possibly undescribed species were detected. Intraspecific variability differed widely among mucoralean species ranging from 0 % in *Backusella circina* to 13.3 % in *Cunninghamella echinulata*. A high proportion of clinical strains was included for molecular identification. Clinical isolates of *Cunninghamella elegans* were identified molecularly for the first time. As a result of the phylogenetic analyses several taxonomic and nomenclatural changes became necessary. The genus *Backusella* was emended to include all species with transitorily recurved sporangiophores. Since this matched molecular data all *Mucor* species possessing this character were transferred to *Backusella*. The genus *Zygorhynchus* was shown to be polyphyletic based on ITS and LSU data. Consequently, *Zygorhynchus* was abandoned and all species were reclassified in *Mucor*. Our phylogenetic analyses showed, furthermore, that all non-thermophilic *Rhizomucor* species belong to *Mucor*. Accordingly, *Rhizomucor endophyticus* was transferred to *Mucor* and *Rhizomucor chlamydosporus* was synonymised with *Mucor indicus*. Lecto-, epi- or neotypes were designated for several taxa.

Keywords: BACKUSELLA; BIODIVERSITY; CLINICAL RELEVANCE; DNA BARCODING; INTRASPECIFIC VARIABILITY; ITS; LSU; MUCOR; MUCORALES; NOMENCLATURE; RHIZOMUCOR; TAXONOMY; ZYGORHYNCHUS

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