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Taxonomy and epidemiology of *Mucor irregularis*, agent of chronic cutaneous mucormycosis

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view table of contents

next article

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Suggestions

Mucormycosis usually presents as a progressive infection with significant angio-invasion. Mucormycosis due to *Mucor irregularis* (formerly *Rhizomucor variabilis* var. *variabilis*), however, is exceptional in causing chronic cutaneous infection in immunocompetent humans, ultimately leading to severe morbidity if left untreated. More than 90 % of the cases known to date were reported from Asia, mainly from China. The nearest neighbour of *M. irregularis* is the saprobic species *M. hiemalis*. The aim of this study was to evaluate the taxonomic position, epidemiology, and intra- and inter-species diversity of *M. irregularis* based on 21 strains (clinical n = 17) by multilocus analysis using ITS, LSU, *RPB1* and *RPB2* genes, compared to results of cluster analysis with amplified fragment length polymorphism (AFLP) data. By combining MLST and AFLP analyses, *M. irregularis* was found to be monophyletic with high bootstrap support, and consisted of five subgroups, which were not concordant in all partitions. It was thus confirmed that *M. irregularis* is a single species at 96.1–100 % ITS similarity and low recombination rates between populations. Some geographic structuring was noted with some localised populations, which may be explained by limited air-dispersal. The natural habitat of the species is likely to be in soil and decomposing plant material.

Keywords: BIODIVERSITY; CHRONIC CUTANEOUS INFECTION; EPIDEMIOLOGY; MUCOR HIEMALIS; MUCOR IRREGULARIS; MUCORMYCOSIS; TAXONOMY

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