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Phylogenetic reassessment of the *Chaetomium globosum* species complex

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Abstract



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Chaetomium globosum, the type species of the genus, is ubiquitous, occurring on a wide variety of substrates, in air and in marine environments. This species is recognised as a cellulolytic and/or endophytic fungus. It is also known as a source of secondary metabolites with various biological activities, having great potential in the agricultural, medicinal and industrial fields. On the negative side, *C. globosum* has been reported as an air contaminant causing adverse health effects and as causal agent of human fungal infections. However, the taxonomic status of *C. globosum* is still poorly understood. The contemporary species concept for this fungus includes a broadly defined morphological diversity as well as a large number of synonymies with limited phylogenetic evidence. The aim of this study is, therefore, to resolve the phylogenetic limits of *C. globosum* s.str. and related species. Screening of isolates in the collections of the CBS-KNAW Fungal Biodiversity Centre (The Netherlands) and the China General Microbiological Culture Collection Centre (China) resulted in recognising 80 representative isolates of the *C. globosum* species complex. Thirty-six species are identified based on phylogenetic inference of six loci, supported by typical morphological characters, mainly ascospore shape. Of these, 12 species are newly described here. Additionally, *C. cruentum*, *C. mollipilium*, *C. rectum*, *C. subterraneum* and two varieties of *C. globosum* are synonymised under *C. globosum* s.str., and six species are resurrected, i.e. *C. angustispirale*, *C. coarctatum*, *C. cochliodes*, *C. olivaceum*, *C. spiculipilium* and *C. subglobosum*. *Chaetomium ascotrichoides* is segregated from *C. madrasense* and the genus name *Chaetomidium* is rejected. Five species, including *C. globosum* s.str., are typified here to stabilise their taxonomic status. A further evaluation of the six loci used in this study as potential barcodes indicated that the 28S large subunit (LSU) nrDNA and the internal transcribed spacer regions and intervening 5.8S nrRNA (ITS) gene regions were unreliable to resolve species, whereas β -tubulin (*tub2*) and RNA polymerase II second largest subunit (*rpb2*) showed the greatest promise as DNA barcodes for differentiating *Chaetomium* species. This study provides a starting point to establish a more robust classification system for *Chaetomium* and for the *Chaetomiaceae*.

Keywords: DNA BARCODE; EPITYPIFICATION; MULTI-GENE PHYLOGENY; SPECIES COMPLEX; SYSTEMATICS

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