

Abstract

A reappraisal of the phylogenetic integrity of bitunicate ascomycete fungi belonging to or previously affiliated with the Hysteriaceae, Mytiliniaceae, Gloniaceae and Patellariaceae is presented, based on an analysis of 121 isolates and four nuclear genes, the ribosomal large and small subunits, transcription elongation factor 1 and the second largest RNA polymerase II subunit. A geographically diverse and high density taxon sampling strategy was employed, including multiple isolates/species from the following genera: *Anteaglonium* (6/4), *Encephalographa* (1/1), *Farlowiella* (3/1), *Gloniopsis* (8/4), *Glonium* (4/2), *Hysterium* (12/5), *Hysterobrevium* (14/3), *Hysterographium* (2/1), *Hysteropatella* (2/2), *Lophium* (4/2), *Mytilinidion* (13/10), *Oedohysterium* (5/3), *Ostreichnion* (2/2), *Patellaria* (1/1), *Psiloglonium* (11/3), *Quasiconcha* (1/1), *Rhytidhysterium* (8/3), and 24 outgroup taxa. Sequence data indicate that although the Hysteriales are closely related to the Pleosporales, sufficient branch support exists for their separation into separate orders within the Pleosporomycetidae. The Mytilinidiales are more distantly related within the subclass and show a close association with the Gloniaceae. Although there are examples of concordance between morphological and molecular data, these are few. Molecular data instead support the premise of a large number of convergent evolutionary lineages, which do not correspond to previously held assumptions of synapomorphy relating to spore morphology. Thus, within the Hysteriaceae, the genera *Gloniopsis*, *Glonium*, *Hysterium* and *Hysterographium* are highly polyphyletic. This necessitated the transfer of two species of *Hysterium* to *Oedohysterium* gen. nov. (*Od. insidens* comb. nov. and *Od. sinense* comb. nov.), the description of a new species, *Hysterium barrianum* sp. nov., and the transfer of two species of *Gloniopsis* to *Hysterobrevium* gen. nov. (*Hb. smilacis* comb. nov. and *Hb. constrictum* comb. nov.). While *Hysterographium*, with the type *Hg. fraxini*, is removed from the Hysteriaceae, some of its species remain within the family, transferred here to *Oedohysterium* (*Od. pulchrum* comb. nov.), *Hysterobrevium* (*Hb. morici* comb. nov.) and *Gloniopsis* (*Gp. subrugosum* comb. nov.); the latter genus, in addition to the type, *Gp. praelonga*, with two new species, *Gp. arciformis* sp. nov. and *Gp. kenyensis* sp. nov. The genus *Glonium* is now divided into *Anteaglonium* (Pleosporales), *Glonium* (Gloniaceae), and *Psiloglonium* (Hysteriaceae). The hysterothecium has evolved convergently no less than five times within the Pleosporomycetidae (e.g., *Anteaglonium*, *Farlowiella*, *Glonium*, *Hysterographium* and the Hysteriaceae). Similarly, thin-walled mytilinidioid (e.g., *Ostreichnion*) and patellarioid (e.g., *Rhytidhysterium*) genera,

previously in the Mytiliniaceae and Patellariaceae, respectively, transferred here to the Hysteriaceae, have also evolved at least twice within the subclass. As such, character states traditionally considered to represent synapomorphies among these fungi, whether they relate to spore septation or the ascomata, in fact, represent symplesiomorphies, and most likely have arisen multiple times through convergent evolutionary processes in response to common selective