Phytotaxa 177 (3): 183–187
www.mapress.com/phytotaxa/

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

http://dx.doi.org/10.11646/phytotaxa.177.3.7

Notes on the taxonomic positions of some Hymenochaetaceae (Basidiomycota) species with colored basidiospores

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Hymenochaetaceae, belonging to Hymenochaetales and accommodating around 500 species, is one of the largest families in Basidiomycota (Kirk *et al.* 2008). Traditionally, poroid species in Hymenochaetaceae are mainly placed in *Inonotus* P. Karst. *sensu lato* and *Phellinus* Quél. *sensu lato*. To make a more natural taxonomic system, some small genera were segregated from the two large genera, and support for most of them was confirmed by later phylogenetic evidence (Wagner & Fischer 2002). Of the currently accepted genera, *Fomitiporella* Murrill, *Fulvifomes* Murrill and *Phylloporia* Murrill have species bearing non-stipitate basidiomes, no setae and colored basidiospores (Zhou & Dai 2012, Zhou 2014a, b). Several species in *Inonotus sensu stricto* also have these features. Therefore, it is hard to decide in which genus certain species should belong, based solely on morphological features. For this work, I performed phylogenetic analyses from nLSU and ITS sequences to explore the phylogenetic relationships of some species as discussed above, including *Inonotus tenuissimus* H.Y. Yu, C.L. Zhao & Y.C. Dai, *Fomitiporella caryophylli* (Racib.) T. Wagner & M. Fisch., *Fulvifomes chinensis* (Pilát) Y.C. Dai, *Fulvifomes inermis* (Ellis & Everh.) Y.C. Dai and *Phylloporia resupinata* Douanla-Meli & Ryvarden. Their taxonomic positions at generic level were also discussed considering morphology.

The studied specimens (see below for their details) are deposited in the herbarium of the Institute of Applied Ecology, Chinese Academy of Sciences (IFP). Phire® Plant Direct PCR Kit was used to amplify the nLSU and ITS regions from herbarium specimens with primer pairs LR0R & LR7 (Vilgalys & Hester 1990) and ITS5 & ITS4 (White *et al.* 1990), respectively, according to the manufacturer's instructions. The PCR procedure was as follows: initial denaturation at 98 C for 5 min, followed by 39 cycles at 98 C for 5 s, 48 C (for nLSU region)/59 C (for ITS region) for 5 s and 72 C for 5 s, and a final extension of 72 C for 10 min. Successful amplicons were sequenced in Beijing Genomics Institute, China with primers LR0R, LR7, LR3 and LR3R (Vilgalys & Hester 1990) for nLSU sequences and ITS5 and ITS4 for ITS sequences. The newly generated sequences were deposited at GenBank (http://www.ncbi.nlm.nih.gov; Figs 1, 2). In addition to these newly generated sequences, other morphologically and taxonomically related sequences retrieved from GenBank (Figs. 1, 2) were also used for phylogenetic analyses. *Phellinus laevigatus* (P. Karst.) Bourdot & Galzin and *P. populicola* Niemelä were selected as outgroup (Wagner & Fischer 2002). The nLSU and ITS datasets were aligned using MAFFT 7 online (http://mafft.cbrc.jp/alignment/server/; Katoh & Standley 2013) with Q-INS-i option (Katoh & Toh 2008). Both resulting alignments were used to construct phylogenetic trees with maximum likelihood (ML) and maximum parsimony (MP) criteria. ML analysis was performed using raxmlGUI 1.2 (Stamatakis 2006, Silvestro & Michalak 2012) with GTR + I + G model estimated as the best-fit evolutionary model by jModelTest (Guindon & Gascuel 2003, Posada 2008) and auto FC option (Pattengale *et al.* 2010) in bootstrap (BS) replicates. MP trees were conducted using PAUP* 4.0b10 (Swofford 2002) with heuristic search and 1000 BS replicates. All characters were equally weighted with gaps as missing data. Other parameters were set as follows: starting tree obtained via stepwise addition, tree-bisection-reconnection branch swapping, steepest descent option not in effect, and 'MULTREES' option in effect.

A total of 11 nLSU and 6 ITS sequences were newly generated. The nLSU dataset with 42 sequences resulted in an alignment of 912 characters, of which 648 are constant, 95 parsimony-uninformative and 169 parsimony-informative. The BS search for ML analysis stopped after 300 replicates. MP analysis generated 131 equally most parsimonious trees of 652 steps (CI = 0.505 and RI = 0.687). The tree from nLSU dataset (Fig. 1) showed that none of the five species mentioned above was nested within the generic clade with high statistical support as they were supposed to be, and no known genus with similar morphology to the five species could accommodate them. In addition, *Fomitiporella caryophylli* and *Fulvifomes inermis* clustered together in a single lineage.

Accepted by Genevieve Gates: 1 Aug. 2014; published: 29 Aug. 2014

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Acknowledgements

The research was financed by the National Natural Science Foundation of China (Project No. 31200015) and the Youth Fund for Creative Research Groups, Institute of Applied Ecology, Chinese Academy of Sciences.

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