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Sanghuangporus pilatii, a new combination, revealed as European relative of Asian medicinal fungi

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Phellinus pilatii Černý (1968: 2) was first described from the southern part of Czechoslovakia (now southeastern Czech Republic in the South Moravia region). The species grows on both the living trees and dead wood of *Populus alba* and *P.* × *canescens*, and is characterized by an imperfect stage that produces chlamydospores on scars left by fallen branches on living trees. Basidiomes later develop in the same place as (or on top of) the asexual structures, in tree cavities and on fallen dead trees. The species is distributed throughout south and southeast Europe and warmer parts of Central Europe. The species has been recorded in southeastern Czech Republic, southern Slovakia, Hungary, Italy, Bulgaria, Italy, Romania, countries of the former Yugoslavia and the European part of Turkey (Bernicchia 1995, Denchev and Assyov 2010, Černý 1968, Doğan *et al*. 2005, Ryvarden and Gilbertson 1994).

This species has perennial, hard basidiomes with a dimitic hyphal system typical for *Phellinus* Quél. (Quélet 1886: 172) but differs from the species of the genus because of its colored basidiospores, which resemble those of *Fulvifomes* Murrill (1914: 49), *Fomitiporella* Murrill (1907: 12) or *Inonotus* P. Karst. (Karsten 1879: 39). However, *Inonotus* is characterized by a monomitic hyphal system and annual, usually soft basidiomes. Fiasson and Niemelä (1984) placed the species in *Porodaedalea* Murrill (1905: 367), but this genus grows exclusively on conifers and has a different basidiome morphology (e.g. concentrically sulcate pileus surface with zones). To address the confusion around *P. pilatii*, I conducted a DNA sequence study to elucidate the position of this species within the Hymenochaetales.

Macroscopic descriptions of examined specimens are based on dried basidiocarps. Color abbreviations follow the guidelines established by Kornerup and Wanscher (1983), and herbarium abbreviations follow Thiers (2015). Microscopic features were described from dried material mounted in 5% KOH, Melzer's reagent and cotton blue using an Olympus BX-50 light microscope (Tokyo, Japan) with a magnification of 1000× and Motic Images Plus 2.0 (Hong Kong, China) software.

To present the size range of the basidiospores, 5% of the measurements were excluded from each end of the range and are given in parentheses. For basidiospores, the factors E (quotient of length and width in any one spore) and Q (mean of E-values of a single specimen) are used.

DNA was extracted from dried basidiocarps using the DNEasy Plant Mini Kit (Qiagen) and the PowerSoil DNA Isolation Kit (MoBio). DNA fragments encompassing the internal transcribed spacer (ITS) and large subunit (LSU) regions of nuclear ribosomal RNA gene were amplified as previously described (Tomšovský 2012).

Amplified DNA was purified and sequenced by Macrogen (Korea). All newly generated sequences were deposited in GenBank (http://www.ncbi.nlm.nih.gov/). For sequence numbers, see FIGURES 1−2 and the list of Materials studied.

The LSU and ITS sequence datasets were enriched with previously published sequences of Hymenochaetales (Wagner & Fischer 2002, Vlasák *et al*. 2013, Zhou *et al*. 2014, Zhou *et al*. 2015).

The Bayesian analyses were run in MrBayes 3.2.6 (Huelsenbeck & Ronquist 2003). Likelihood settings from the best-fit model (TrN+I+G = LSU dataset; HKY+I+G = ITS dataset) were selected using the Bayesian information criteria in jModelTest2 (Darriba *et al*. 2012). The four chains were run for 10 million generations. One million generations were discarded as burn-in. Sampling frequency was set to every 100th generation. Additional phylogenetic analyses of both datasets were carried out in PHYML, which estimated the maximum likelihood phylogenies and were processed on the server Phylogeny.fr (Dereeper *et al*. 2008) using the "A la Carte" mode. Bootstrap branch support values (BPs) were estimated in PHYML using the maximum likelihood criteria and 100 replicates.

The LSU dataset of 33 sequences included a total of 596 positions; among these positions, 420 were constant and 55 were variable. The ITS dataset of 31 sequences included 963 positions (521 constant and 123 variable). The Genbank accession numbers of the new sequences are KT428764-KT428766.

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