Knufia aspidiotus sp. nov., a new black yeast from scale insects

FAN HE¹,², BIN LIN¹,², JING-ZU SUN² & XING-ZHONG LIU¹,²*
¹School of Life Sciences, University of Science and Technology of China, Hefei 230026, Anhui Province, P. R. China
²State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, P. R. China
*email: liuxz@im.ac.cn
#These authors contributed equally to this work.

Abstract

Three ascomycetes, isolated from the body cavity of the scale insect, Aspidiotus sp., collected in Song Mountain, Yanqing, Beijing, China, were identified to be a new species of Knufia. Knufia aspidiotus sp. nov. is introduced in this paper. The species is characterized by slow-growing, dematiaceous and blastic, endogenous conidia in undifferentiated hyphae, as well as darkly pigmented, enlarged multicellular bodies, and is similar to other Knufia species in morphology. Phylogenetic analyses, based on the small ribosomal subunit (SSU) gene and internal transcribed spacer (ITS) region, indicated that Knufia aspidiotus was related to, but clearly distant from other sequenced species in Knufia.

Key words: new species, morphology, phylogeny, taxonomy

Introduction


The diagnostic features of Knufia, based on the morphology of type species, K. cryptophialidica, are the formation of black, slow-growing colonies and production of conidia from undifferentiated, holoblastic, conidiogenous cells on the hyphae, as well as from phialides (Hutchison et al. 1995). After studying four strains of K. cryptophialidica (including the ex-type strain), Tsuneda and Currah (2005), however, concluded that phialidic conidia production was not a constant character. Only the ex-type culture formed phialides, while K. endospora lacked phialidic conidiogenesis (Tsuneda et al. 2004, 2011). Comparison of morphological characters of Knufia species in culture indicate (1) slow-growing, black colonies; (2) blastic, and endogenous conidia in undifferentiated hyphae or multicellular bodies; and (3) darkly pigmented, enlarged multicellular bodies are reliable characteristics to differentiate species (Tsuneda et al. 2004, 2005, 2011).

Molecular analyses have recently been applied to the taxonomy and phylogeny of black yeasts (Halici et al. 2010, Nelsen et al. 2011, Feng et al. 2012, Lawrey et al. 2012, Chomnunti et al. 2013). This is because black yeasts are notoriously difficult to identify by morphology alone, due to their lack of significant differentiation, their pleomorphic growth, and their variable modes of conidiogenesis (Untereiner et al. 1995, Sterflinger 2006). The large and small ribosomal subunit sequences (LSU and SSU) are suitable for placement
References

http://dx.doi.org/10.1016/j.micron.2004.09.004


http://dx.doi.org/10.3852/11-066

http://dx.doi.org/10.1007/s13225-012-0194-5


http://dx.doi.org/10.1007/s13225-012-0194-5


http://dx.doi.org/10.3114/sim.2008.61.11

http://dx.doi.org/10.1007/s13225-009-0033-y


http://dx.doi.org/10.3732/ajb.94.9.1515

http://dx.doi.org/10.2307/3760868

http://dx.doi.org/10.1093/nar/gki198

http://dx.doi.org/10.1007/s13225-012-0166-9

http://dx.doi.org/10.1007/s13225-012-0166-9

http://dx.doi.org/10.1007/s13225-012-0166-9

http://dx.doi.org/10.1007/s13225-012-0166-9


http://dx.doi.org/10.1007/s13225-011-0144-7


http://dx.doi.org/10.1371/journal.pone.0063547


http://dx.doi.org/10.3767/003158508X371379


http://dx.doi.org/10.1111/j.1439-0507.2011.02055.x


http://dx.doi.org/10.1007/s13225-013-0234-9


http://dx.doi.org/10.1023/A:1000570429688


http://dx.doi.org/10.1139/B05-029


http://dx.doi.org/10.1139/B11-041


http://dx.doi.org/10.1007/s13225-011-0097-x


http://dx.doi.org/10.1007/s13225-013-0246-5


http://dx.doi.org/10.1023/A:1000157803954