



Phylogenetic placement of a new species of *Corynesporopsis* from dead acacia wood indicates occurrence of tretic conidiogenesis within Xylariales

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Abstract

A new species of *Corynesporopsis* from rotting wood of *Acacia confusa* differs from similar species with one-septate conidia by comparatively short conidiophores and conidia and deeper brown pigmentation of conidiogenous cells than of more proximal cells of the conidiophore. Morphology in culture differs from that *in situ* mainly by hyaline vegetative hyphae and branched conidiophores. A phylogenetic analysis including a species of *Corynesporopsis* indicates a close relationship to Xylariales and the occurrence of tretic conidiogenesis in this order. *Corynesporopsis quercicola* is a new record for Taiwan.

Key words: Ascomycota, *Bispora betulina*, hyphomycetes, saprobic fungi

Introduction

The hyphomycetous genus *Corynesporopsis* was proposed based on *C. quercicola* by Kirk (1981a). The main features are unbranched chains of septate pigmented conidia arising from terminal, integrated monotretic conidiogenous cells of mostly simple, cylindrical, pigmented conidiophores. Castañeda Ruiz *et al.* (2011) provided a key to the known ten species. Two further species were added by Ma *et al.* (2012) and Xia *et al.* (2013). The species are known from dead parts of plants and considered saprobic. Hitherto only a single species has been cultivated (Castañeda Ruiz *et al.* 2011). A molecular phylogenetic evaluation has not been undertaken, since no species is represented by a DNA sequence in GenBank. A sexual morph relationship has hitherto not been indicated neither by cultivation, observation of conidiophores connected to ascomata, or molecular phylogenetic analysis so that it is even unclear whether *Corynesporopsis* species belong to Asco- or Basidiomycota.

The area of natural distribution of *Acacia confusa* Merr. (*Fabaceae*) is southern Taiwan and the Philippines. The plant is quite stress-resistant and used for stabilizing soil and historically also for producing charcoal. Under the Japanese rule in Taiwan, the tree was, therefore, planted artificially at low elevations throughout Taiwan and has become and still remains one of the most common trees of the woody flora of the island (Kuo 2001). The species is considered a pioneer tree with a comparatively short life-span (Kuo 2001). Several species of wood-rotting fungi are, therefore, often found on dead stems, mainly Basidiomycota like *Amauroderma exile* (Berk.) Torrend, *Ganoderma* spp., *Loweoporus tephroporus* (Mont.) Ryvarden, *Postia caesia* (Schrad.) P. Karst., and *Schizophyllum commune* Fr. (Fu & Chang 2009). At later stages of wood-rot caused by these Basidiomycota and termites, we found a species of *Corynesporopsis* which is described in this study.

Materials and methods

A portion of dead wood of a stump of *Acacia confusa* collected in October 2013 on the campus of National Central University, Jhongli City, in northern Taiwan was kept under moist-chamber condition in a plastic bag at room temperature for 7–10 days, before the fungus on the wood was examined. The characterization of the species is mainly based on this collection. Two other wood samples of dead *A. confusa* were collected from another stem at the same place as well as in a neighboring city and examined within two days after collection. Samples of rotting wood were collected

supported (Nonaka *et al.* 2013). Another clade composed of species of *Lopadostoma* and *Creosphaeria sassafras* was well supported outside the strongly supported clades of *Xylariaceae* (species of *Anthostomella*, *Barrmaelia*, *Daldinia*, *Hypoxyton*, and *Xylaria*) and *Diatrypaceae*. Several other genera within the Xylariales without family affiliations or “*Xylariaceae s. lat.*” were also recorded by Jaklitsch & Voglmayr (2012). Such data indicate that new families need to be proposed in the Xylariales. Although other genes appear to allow better resolution than ribosomal DNA, too few sequences are available for this analysis (Pinnoi *et al.* 2010, Jaklitsch *et al.* 2014) which is not the scope of our study.

In addition to sequencing and analyzing protein genes (Mirabolfathy *et al.* 2013), asexual morphs will play important roles for defining such families, as it is already the case within the *Xylariaceae* (Stadler 2011, Stadler *et al.* 2013). Hitherto, no asexual stage with tretic conidiogenesis typical of *Corynesporopsis* has been recorded for the Xylariales and confirms the need of further collection, cultivation, morphological and molecular study of asexual and sexual stages of the Xylariales (Stadler 2011, Jaklitsch & Voglmayr 2012). Because of culture contamination, the type species, *C. quercicola*, could not be included. In the Xylariales, conidiogenesis is predominantly sympodial as it was exemplarily illustrated by Ju & Rogers (2001), and exceptionally annellidic (Seifert *et al.* 2011, Stadler 2011). Tretic conidiogenesis has been recorded for Asterinales, Capnodiales, Chaetosphaeriales, Diaporthales, Helotiales, Pleosporales, and other Pezizomycotina hitherto not assigned to an order (Shenoy *et al.* 2010, Seifert *et al.* 2011).

As Morgan-Jones *et al.* (1987) pointed out in discussing the distinction between *Bispora* and *Corynesporopsis*, in addition or instead of tretic conidiogenesis, a blastic one might also occur, since the base of conidia can be truncate in some species assigned to genera defined by tretic conidiogenesis. Alternatively to a blastic conidiogenesis, a broadly truncate conidium base could be explained by an additional change of the conidium morphology during maturation after a tretic development and dehiscence from the conidiophore. Species with clearly truncate conidiogenous loci and hila, such as *C. liquidambaris* Jian Ma & X.G. Zhang, and the similar species *Heteroconium ponapense* Matsush., which also have broad darkened septa in the conidiophores and conidia (Matsushima 1983, Ma *et al.* 2012) share high similarity with *Bispora*, but hitherto no ITS or LSU rDNA sequences are available for those species as well as for identified *Bispora* species. Since in these and other similar genera quite simple conidiophores and catenate conidia are probably polyphyletic characters, DNA analyses are needed for evaluating the phylogenetic significance of characteristics of conidiogenesis and broad dark septa in the conidiophores, before meaningful new generic arrangements could be done.

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