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MYCOSCIENCE

ISSN 1340-3540 (print), 1618-2545 (online)

journal homepage: www.elsevier.com/locate/myc

Short communication

Penicillium chroogomphum, a new species in *Penicillium* section *Ramosa* isolated from fruiting bodies of *Chroogomphus rutilus* in China

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ARTICLE INFO

Article history:
Received 18 March 2015
Received in revised form
4 September 2015
Accepted 7 September 2015
Available online 10 November 2015

Keywords:
benA
cmd
ITS
Phylogeny
Taxonomy

ABSTRACT

During tissue culture from fruiting bodies of *Chroogomphus rutilus*, two *Penicillium* sp. strains were isolated that could not be assigned to any described species based on morphological and molecular phylogenetic analysis. Multigene phylogenetic analyses with the nuclear ribosomal internal transcribed spacer (ITS) region, β-tubulin (*benA*) and calmodulin (*cmd*) genes, as well as morphological analyses revealed that these isolates were in the *Penicillium* section *Ramosa*. These isolates were closely related to *P. lenticrescens* and *P. soppii* in terms of multigene phylogeny, but their colonies and micro-morphological characters differed from these closest related species. We consider that these isolates constitute a new species in the genus *Penicillium* section *Ramosa* and propose the name *P. chroogomphum*.

Taxa belonging to the genus *Penicillium* Link occur in a diverse range of habitats such as soil, air, water and indoor environments (Visagie et al. 2009, 2014b; Sang et al. 2013). They play various roles in natural ecosystems and are very important to the biotechnology and food industry (Yamazaki et al. 2010; Bernaldez et al. 2013; Alvarenga et al. 2014; Cakmakci et al. 2014; Santini et al. 2014; Ribeiro Correa et al. 2015; Xiao et al. 2015). *Penicillium* spp. are characterised by their branched or simple hyaline brush-like conidiophores (Visagie et al. 2009). Identification and nomenclature of the genus *Penicillium* have been studied since Link (1809). To date, the genus currently contains 359 accepted species divided among 25 sections (Visagie et al. 2014b; You et al. 2014; Park et al. 2015; Perrone et al. 2015; Peterson et al. 2015).

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http://dx.doi.org/10.1016/j.myc.2015.09.001

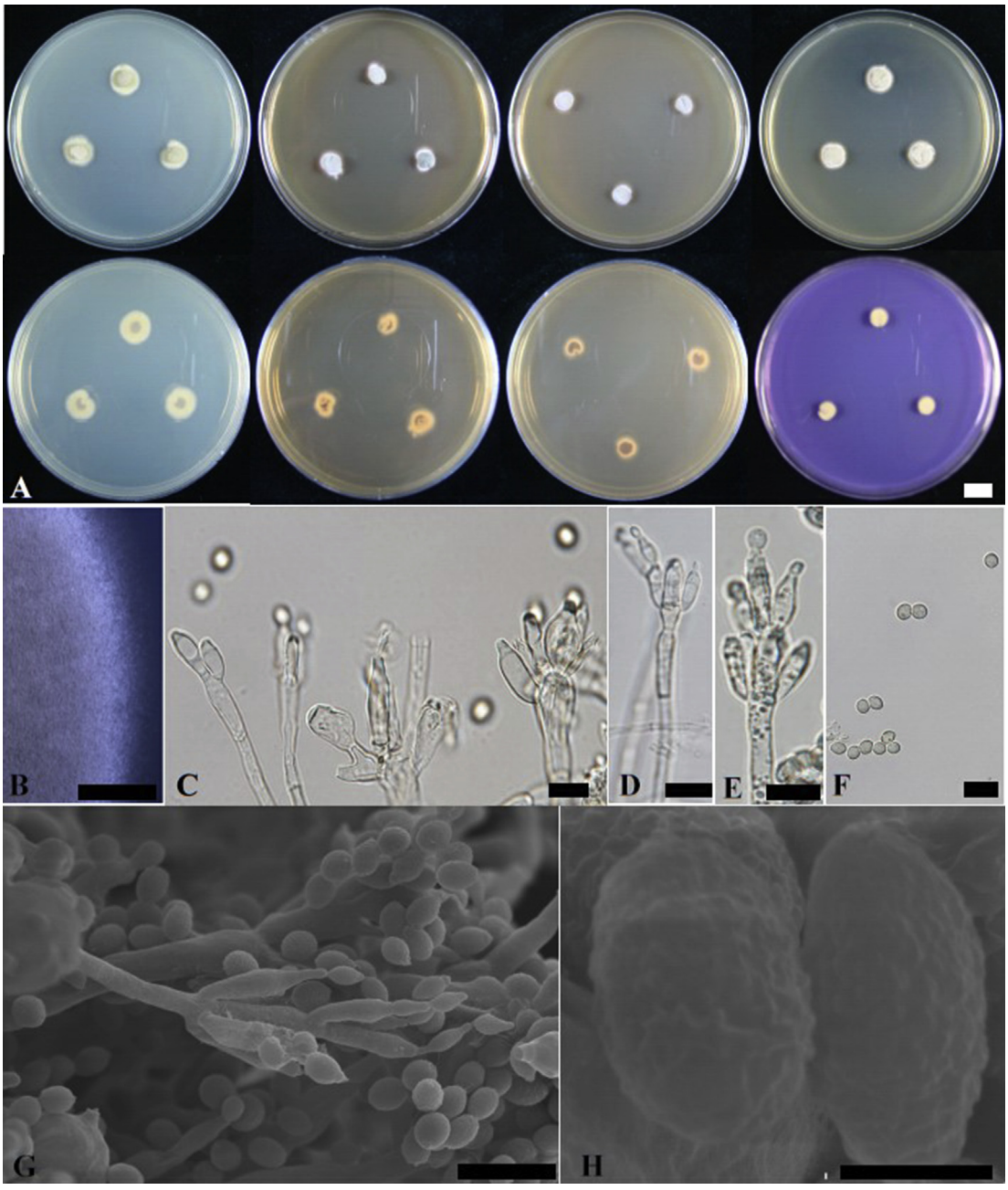

Fig. 1 – *Penicilium chroogomphum* CBS 136204^T. A: Colonies: top row left to right, obverse CYA, YES, DG18 and MEA; bottom row left to right, reverse CYA, reverse YES, reverse DG18 and obverse CREA; B: Colony texture on PDA after 20 d; C–E: Conidiophores under light microscope; F: Conidia under light microscope; G: Conidiophores under SEM; H: Conidia under SEM; *Bars*: A, B 1 cm; C–G 20 μm; H 3 μm.

Phylogenetic analyses of *Penicillium* spp. has been based on numerous genes, such as rRNA internal transcribed spacer (ITS), D1/D2 region of large subunit (LSU), β-tubulin (*benA*), calmodulin (*cmd*), cytochrome C oxidase subunit 1 (*cox1*), translation elongation factor 1-α (*tef1-α*), and DNA-directed RNA polymerase II subunit (*rpb2*) genes (Frisvad et al. 2006; Visagie et al. 2009, 2014a; Houbraken et al. 2011; Davolos et al. 2012; Sang et al. 2013; Wang and Wang 2013; Wang et al. 2014; Park et al. 2015). Visagie et al. (2014b) suggested ITS as the DNA barcoding for identification of *Penicillium* sp. and *benA* gene as the secondary marker. The well-established phylogeny of *Penicillium* section *Ramosa* by Visagie et al. (2014a) used combined ITS, *benA* and *cmd* gene sequences and has provided us with a background for molecular identification of our new isolates.

During tissue culture from fruiting bodies of *Chroogomphus rutilus* (Schaeff.) O.K. Mill., two *Penicillium* sp. isolates were obtained that could not be assigned to any described species. The present study was initiated to assess the placement of these isolates within the genus *Penicillium* based on molecular phylogenetic analyses as well as morphological characters.