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A polyphasic approach to characterise two novel species of *Phoma* (*Didymellaceae*) from China

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Abstract

Phoma odoratissimi sp. nov. on *Viburnum odoratissimum* and *Syringa oblate*, and *Phoma segeticola* sp. nov. on *Cirsium segetum* from China are introduced and described, employing a polyphasic approach characterising morphological characteristics, host association and phylogeny. Both species are the first records of *Phoma* species on their respective hosts. Multilocus phylogenetic tree was inferred using combined sequences of the internal transcribed spacer regions 1 & 2 and 5.8S nrDNA (ITS), and partial large subunit 28S nrDNA region (LSU), β-tubulin (TUB) region and RNA polymerase II (RPB2) region. The two new species clustered in two separate and distinct lineages, and are distinct from their allied species.

Key words: Karst, morphology, plant pathogen, phylogeny, taxonomy

INTRODUCTION

The coelomycetous genus *Phoma* Sacc. emend. Boerema & G.J. Bollen is omnipresent in the environments and consists of pathogens, opportunists and several saprobic species from a wide range of substrates (Aveskamp *et al.* 2008, de Gruyter *et al.* 2009). The majority of *Phoma* species are plant pathogens causing mainly leaf and stem spots on land plants (Aveskamp *et al.* 2010), e.g. *P. destructiva* Plowr. as the agent of tomato leaf and stem blight (Boerema *et al*. 2004), *P. medicaginis* Malbr. & Roum. varieties and *P. sclerotioides* Preuss ex Sacc. respectively as the agents of black stem and brown root rot of alfalfa (Wunsch & Bergstrom 2011). These plant diseases associated with the genus *Phoma* had lead to significant economic losses (Aveskamp *et al.* 2008). Furthermore, some pathogens with quarantine significance might cause biosecurity issues in trades (Aveskamp *et al.* 2008), such as *P. bellidis* Neerg., *P. clematidina* (Thüm.) Boerema and *P. eupyrena* Sacc. listed as quarantine organisms of the European Plant Protection Organization (EPPO, www.eppt.eppo.org). Several species have also been recognized as endophytic, fungicolous and lichenicolous, as well as pathogens of human and animals (Aveskamp *et al.* 2008, 2010). For example, some *Phoma* spp. are endophytes associated with different plants, such as *Melia azedarach* L. (Zhang *et al.* 2012) and *Arisaema erubescens* (Wall.) Schott (Wang *et al.* 2012); some species were isolated from other fungi like *Hypoxylon* Bull. (Che *et al.* 2002); *P. fuliginosa* M.S. Cole & D. Hawksw. and *P. cladoniicola* Diederich, Kocourk. & Etayo were discovered from lichen (Hawksworth *et al.* 2004, Diederich *et al.* 2007); *P. cruis-hominis* Punith. was reported as human pathogen (Punithalingam 1979), and *P. herbarum* can cause diseases in fish (Ross *et al.* 1975, Faisal *et al.* 2007) and cattle (Costa *et al.* 1993).

The genus *Phoma* was established by Saccardo (Saccardo 1880), and later revised by Boerema and Bollen (Boerema & Bollen 1975). By far, more than 3000 *Phoma* epithets have been recorded in MycoBank (Crous *et al.* 2004), and admittedly the traditional host association based nomenclature led to this number (Aveskamp *et al.* 2008, 2010). Two hundred and twenty three taxa have been accepted in the genus but subdivided into nine sections based on morphological characters (Boerema *et al.* 2004). However, the delimitation of sections was somewhat ambiguous, and the classification did not reflect the evolutionary relationships (de Gruyter *et al.* 2012). Molecular phylogenetic studies performed by de Gruyter *et al.* (2009, 2010, 2012) and Aveskamp *et al.* (2010) revealed that *Phoma* was highly het-

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