



Towards a natural classification of Dothideomycetes 7: The genera *Allosoma*, *Austropleospora*, *Dangeardiella*, *Griggsia* and *Karschia* (Dothideomycetes *incertae sedis*)

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Abstract

This is the seventh of a series of papers in which we report on re-examination of herbarium types of Dothideomycetes genera, *incertae sedis*. By examining and re-describing the generic types which are not previously illustrated or are poorly described, we attempt to propose their familial and higher placement according to the morphology based on modern taxonomic concepts. In this paper the type specimens of *Allosoma*, *Austropleospora*, *Dangeardiella*, *Griggsia* and *Karschia* were re-examined and are illustrated. An overview of the history and descriptions and illustrations of these genera are provided. Based on morphological similarities, *Allosoma* is placed in Englerulaceae, while *Austropleospora* and *Karschia* are transferred to Pleosporaceae, and Lichenotheliaceae, respectively. *Dangeardiella* is classified in Pleosporales, genera *incertae sedis*, while *Griggsia* is placed in Sordariomycetes, genera *incertae sedis* as it is not typical of any existing family of Dothideomycetes as it has unitunicate asci. Recollection, epitypification and multi-gene molecular analyses are needed for all type species of these genera in order to resolve their familial status. By illustrating and redescribing the type species, we expect to stimulate interest for these fungi to be recollected, sequenced and placed in a natural taxonomic framework in the Ascomycota.

Key words: Ascomycota, Dothideomycetes, Englerulaceae, Lichenotheliaceae, Pleosporaceae, morphology

Introduction

Dothideomycetes, the most diverse class in the Phylum Ascomycota include saprobes, phytopathogens, endophytes, epiphytes, fungicolous, lichenized, or lichenicolous fungi that occur in terrestrial, freshwater and marine habitats (Kirk *et al.* 2008, Hyde *et al.* 2013). Lumbsch & Huhndorf (2010) included two subclasses as well as numerous families under eleven orders within the Dothideomycetes and 34 unclassified families with over 175 genera in Dothideomycetes *incertae sedis*. Hyde *et al.* (2013) accepted 22 orders and 105 families within the Dothideomycetes and included 26 families under Dothideomycetes *incertae sedis*.

We are studying the genera placed in Dothideomycetes, genera *incertae sedis* (Ariyawansa *et al.* 2013, Ariyawansa *et al.* 2014, Dai *et al.* 2014b, Li *et al.* 2014, Tian *et al.* 2014, Thambugala *et al.* 2014). These genera have generally been poorly described, often not previously illustrated and are poorly known. In order to stimulate interest in recollection and sequencing of these genera we have re-examined, illustrated and re-described the types. In this study we treat the poorly known genera *Allosoma*, *Austropleospora*, *Dangeardiella*, *Griggsia* and *Karschia* and place them in a natural taxonomic framework in the Ascomycota. *Allosoma* is placed in Englerulaceae, while *Austropleospora* and *Karschia* are transferred to Pleosporaceae and Lichenotheliaceae respectively. *Dangeardiella* is classified in Pleosporales, genera *incertae sedis*, while *Griggsia* is included in Sordariomycetes *incertae sedis* as it is not typical of any existing family of Dothideomycetes due to its unitunicate asci.

Material examined:—PUERTO RICO. Maricao: Alto de Bandera, on *Cyathea arborea* (Cyatheaceae). 14 & 19 July 1915. F.L. Stevens. No. 8276 and 8794. (NY 01102841!, holotype).

Notes:—*Griggsia* was introduced by Stevens & Dalbey (1919) as a monotypic genus and is typified by *Griggsia cyathea*. It is characterized by superficial ascomata, filamentous, unbranched, septate, pseudoparaphyses, unitunicate, broadly obovoid ascii and broadly oval, hyaline, 1-celled ascospores. Lumbsch & Huhndorf (2010) included this genus under Dothideomycetes, genera *incertae sedis*. *Griggsia* should be excluded from Dothideomycetes because ascii are unitunicate (Schoch *et al.* 2006, Hyde *et al.* 2013). Therefore we place *Griggsia* in Sordariomycetes *incertae sedis* pending molecular investigation. The species needs recollecting, sequencing and epitypifying in order to clarify the familial status.

Acknowledgments

We thank the Directors and Curators of BRIP, GZU, NY and S herbaria for the loan of specimens in their keeping. The Mushroom Research Foundation, Chiang Rai, Thailand and Guizhou Key Laboratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Xiaohe District, Guiyang City, Guizhou Province, People's Republic of China are acknowledged for providing postgraduate scholarship support to Kasun M. Thambugala. The authors gratefully acknowledge MFLU grant (56101020032) for supporting studies on Dothideomycetes.

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