



## A taxonomic and phylogenetic re-appraisal of the genus *Curvularia* (Pleosporaceae): human and plant pathogens

DIMUTHU S. MANAMGODA<sup>1,2,3</sup>, AMY Y. ROSSMAN<sup>3</sup>, LISA A. CASTLEBURY<sup>3</sup>, EKACHAI CHUKEATIROTE<sup>4</sup> & KEVIN D. HYDE<sup>1,2,4\*</sup>

<sup>1</sup>Key Laboratory for Plant Biodiversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming, 650201 Yunnan, China.

<sup>2</sup>World Agro-forestry Centre, East and Central Asia, Kunming 650201, China.

<sup>3</sup>Systematic Mycology and Microbiology Laboratory, United States Department of Agriculture, Agricultural Research Service, Beltsville, Maryland, 20705 USA.

<sup>4</sup>Institute of Excellence in Fungal Research, School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand.

### Abstract

*Curvularia* is an important genus whose species are widely distributed phytopathogens as well as opportunistic pathogens on human and animals. The purpose of this study is to re-evaluate the phylogenetic relationships of the species in the genus *Curvularia* using ITS (nuclear ribosomal internal transcribed spacer), GPDH (glyceraldehyde-3-phosphate dehydrogenase) and TEF (translation elongation factor) gene regions and to provide modern descriptions and illustrations of *Curvularia australis*, *Curvularia buchloës*, *C. cymbopogonis*, *C. hawaiiensis*, *C. neoindica*, *C. neergaardii*, *C. nicotiae*, *C. nodulosa*, *C. ryleyi*, and *C. subpapendorffii* which lack recent descriptions with details of host and distribution. A multi-gene phylogenetic tree based on ITS, GPDH and TEF gene regions is used to define species of a fresh collections obtained from various hosts and geographic locations in the world. Both human and plant associated species of *Curvularia* are included in the phylogenetic analysis. Some species that have previously been described from humans are herein reported from plant material as pathogens or saprobes and *vice versa*. Novel host associations are reported for *C. asianensis*, *C. borrierae*, *C. hominis*, *C. muehlenbeckiae*, *C. trifolii* and *C. verruculosa*.

**Key words:** Dothideomycetes, Keratitis, Morphology, Opportunistic infections, Pleosporales

### Introduction

The genus *Curvularia* is comprised species associated with plant and human as pathogens worldwide (Sivanesan 1987; Manamgoda *et al.* 2012 a, b, da Cunha *et al.* 2013, Hyde *et al.* 2014). In addition to a host association with living organisms, including humans and plants, these species are reported from the air (Rangaswamy *et al.* 2013, de Aldana *et al.* 2013), fresh water (Verma *et al.* 2013) and soil (Manamgoda *et al.* 2011). Currently there are 133 species of *Curvularia* are listed in *Index Fungorum* (accessed on 05th April 2015). Although a recent phylogenetic assessment of the *Bipolaris-Cochliobolus-Curvularia* complex (Manamgoda *et al.* 2012a) and a subsequent monographic treatment of the genus *Bipolaris* (Manamgoda *et al.* 2014) are available, a detailed revision of the genus *Curvularia* has not been provided. *Curvularia sensu* Manamgoda is now considered as a well-characterized genus that is distinct from *Bipolaris* and supported by robust generic boundaries inferred by molecular data (da Cunha *et al.* 2013, Hyde *et al.* 2014, Madrid *et al.* 2014, Tan *et al.* 2014).

The key morphological characteristics of the asexual morphs of *Curvularia* are the curved conidia with hyaline apical cells having two or three central darkened cells, one of which is enlarged and contributes to the curvature (Shoemaker 1959). The sexual morph comprises black, globose ascomata, bitunicate, and cylindrical asci with filiform, hyaline ascospores, which are loosely arranged into a helix or in parallel. The sexual morph is not generally found in nature although it may be produced in culture under experimental conditions (Nelson 1964).

Species of *Curvularia* can be found in nature as endophytes (Tadych *et al.* 2012, Gautam *et al.* 2013, Jena & Tayung 2013), epiphytes (Diaz & Oyama 2007), saprophytes (Manamgoda *et al.* 2012b) and pathogens (Akter *et*