



Taxonomy and phylogeny of *Cercospora* spp. from Northern Thailand

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Abstract

The genus *Cercospora* represents a group of important plant pathogenic fungi with a wide geographic distribution, being commonly associated with leaf spots on a broad range of plant hosts. The goal of the present study was to conduct a morphological and molecular phylogenetic analysis of the *Cercospora* spp. occurring on various plants growing in Northern Thailand, an area with a tropical savannah climate, and a rich diversity of vascular plants. Sixty *Cercospora* isolates were collected from 29 host species (representing 16 plant families). Partial nucleotide sequence data for two gene loci (ITS and *cmdA*), were generated for all isolates. Results from this study indicate that members of the genus *Cercospora* vary regarding host specificity, with some taxa having wide host ranges, and others being host-specific. Based on cultural, morphological and phylogenetic data, four new species of *Cercospora* could be identified: *C. glycinicola* (from *Glycine max*), *C. cyperacearum* and *C. cyperina* (from *Cyperus alternifolius*), and *C. musigena* (from *Musa* sp.). The most common *Cercospora* sp. found in Northern Thailand was *C. cf. malloti*, which occurred on a wide host range. Several collections could not be resolved to species level due to the lack of reference cultures and DNA data for morphologically similar species. Further collections from other countries are needed to help resolve the taxonomy of some species complexes occurring on various plant hosts in Thailand.

Key words: biodiversity, cercosporoid hyphomycetes, Mycosphaerellaceae, phylogeny

Introduction

Species of *Cercospora* (Mycosphaerellaceae, Capnodiales) commonly occur associated with leaf and fruit spots on a range of cultivated and wild plants worldwide (Crous & Braun 2003, Groenewald *et al.* 2013, Amaradasa *et al.* 2014, Bakhshi *et al.* 2015b). To date there have been several studies focused on these fungi in Thailand, and more than 500 cercosporoid species have been identified (Giatgong 1980, Sontirat *et al.* 1980, Petcharat & Kanjanamaneesathian 1989, Braun *et al.* 2006, Meeboon *et al.* 2007a, 2007b, 2007c, 2008, Nakashima *et al.* 2007, Phengsintham *et al.* 2013). However, almost all these studies have thus far relied exclusively on morphological data, and very few records are supported by cultures and DNA data. The first application of DNA phylogenetic analysis (ITS) to distinguish *Cercospora* species from Thailand was published by To-anun *et al.* (2010, 2011). In other studies multi-locus DNA data proved highly effective to distinguish among species of cercosporoid fungi (Groenewald *et al.* 2013, Crous *et al.* 2013, Bakhshi *et al.* 2015a, 2015b). The same approach also proved successful to study other, related, cercosporoid genera from Thailand (Hunter *et al.* 2006, Cheewangkoon *et al.* 2008). To date, however, most cercosporoid records from Thailand cannot be substantiated based on a lack of cultures and DNA data. The main objective of the present study was therefore to confirm the identification of different *Cercospora* spp. associated with various plant diseases from Northern Thailand, and to resolve their taxonomy and DNA phylogeny.