



Identification of phytopathogens from a taxonomic view, an example of Cryphonectriaceae

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Introduction

Plant diseases cause lots of losses worldwide, and pathogens identification is essential during diseases studies. Traditional identification of phytopathogens mainly relied on host information and pathogen morphological characteristics, which limited the discovery of similar pathogens on the same hosts. Recently, the application of phylogenetics to plant pathology greatly promotes the discovery of larvaceous fungi. For example, novel genera in Cryphonectriaceae were described as phytopathogens continuously in the past two decades.

Cryphonectriaceae is a worldwide fungal family, with most members pathogenic to Myrtiflorae and Fagaceae plants. This family was established in 2006, basing on *Endothia-Cryphonetria* complex, *Amphilogia*, *Chrysosporthe* and *Rostraureum* (Gryzenhout *et al.*, 2006). Further studies increased 17 genera in this family depended on DNA sequence data, supported by morphological evidence.

Original genera of Cryphonectriaceae were combined by orange stromata and purple reaction in 3% KOH, which differed from the other families in Diaporthales. Subsequent genera were newly described or transferred from imperfect fungi depending on phylogenetic relationships.

Aurantiosacculus was firstly proposed as a pathogenic genus of eucalyptus leaf diseases, recognized by the properties of bright orange conidiomata and sigmoid conidia (Dyko and Sutton, 1979). Orange conidiomata is consistent with Cryphonectriaceae features, while sigmoid conidia are unique among Cryphonectriaceae members whereas purple reaction in KOH is mystery. DNA sequence evidence demonstrated this genus as a member of Cryphonectriaceae (Crous *et al.*, 2012).

Chrysomorbus is newly described based only on asexual states from *Lagerstroemia speciosa*, which is an ornamental plant in Myrtiflorae.

Species differentiation of asexual states in Cryphonectriaceae was not obvious, the same as genera. *Chrysomorbus* is classified in Cryphonectriaceae and proposed as a novel genus supported by DNA sequence data (Chen *et al.*, 2018).

During traditional pathogens identification, host information was important to identify the species rank, which led to doubtful results of similar asexual states on related hosts.

Asexual state of *Cryphonectria* and *Endothia* on Fagaceae hosts shared similar morphological characteristics, including orange pycnidium, hyaline, fusoid to oval conidia. Cryphonectriaceae pathogens causing canker disease to Fagaceae plants including commercial chestnut and oak plantation were not easy to identify. Internal transcribed spacer (ITS) regions could separate these pathogens well (Fig. 1).

References

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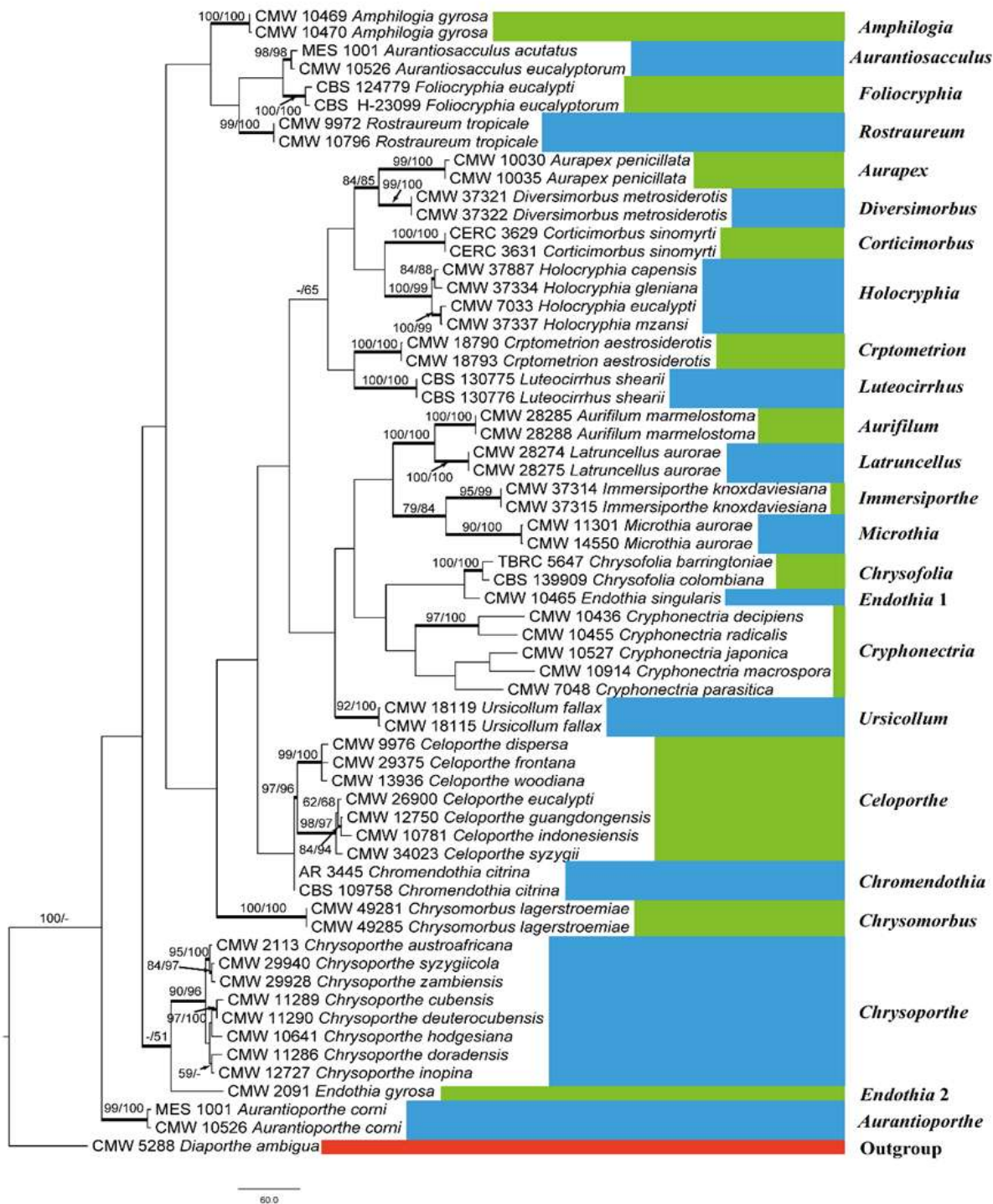


Fig. 1. Phylogram of LSU, ITS, TUB1 and TUB2 regions based on MP, ML and Bayesian analysis. Values above the branches indicate maximum parsimony bootstrap (MP BP $\geq 50\%$) and maximum likelihood bootstrap (ML BP $\geq 50\%$). Thickened branches represent posterior probabilities above 0.90 from BI. Scale bar = 60 nucleotide substitutions.