Dissertation Title	Molecular phylogeny and taxonomy of Plant pathogenic genera *Diaporthe* (*Phomopsis*) and *Colletotrichum*
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ABSTRACT

The genus *Diaporthe* (*Phomopsis*) is an important genus of phytopathogenic fungi with a worldwide distribution. Cryptic diversification, phenotypic plasticity and extensive host associations have complicated accurate species identification in the genus. In this study, the phylogenetic species recognition of *Diaporthe* is re-evaluated with worldwide collections with special reference to the significant phytopathogens on crops, ornamentals and forest trees and species complexes.

The Genealogical Concordance Phylogenetic Species Recognition (GCPSR) was applied to resolve the species limits with four gene phylogenetic analysis of ITS (nuclear ribosomal internal transcribed spacer), EF1-α (translation elongation factor 1-α), TUB (β tubulin) and CAL (calmodulin). The four gene combined phylogeny was used to define novel taxa from Thailand including *D. ptercarpicola*, *D. siamensis* and *D. thunbergii*. The species of *Diaporthe* associated with melanose and stem end rot of Citrus were re-defined, implementing the combined analysis of ITS, EF1-α, TUB, CAL and ACT (actin) genes and Genealogical Sorting Index methods.

Diaporthe citri, *D. cytosporella*, *D. foeniculina* and *D. rudis*, are epitypified with clarification of nomenclature and taxonomy.

The *Diaporthe sojae* species complex associated with soybean, cucurbits, and other herbaceous hosts were resolved based on five gene analysis including ITS, EF1-α, TUB, CAL and HIS (histone-3) genes. The seed decay pathogen *D. longicolla* was distinguished from the pod and stem blight pathogen *Diaporthe sojae*. The Lima bean pathogen *D. phaseolorum*, other herbaceous crop pathogens including *D. arctii*, *D. batatas* and *D. cucurbitae* were resolved with epitypes designated with the introduction of a new species *D. ueckerae* from cucurbits in USA.

The generic type species *Diaporthe eres* was redefined with the strict application of genealogical concordance and non-discordance criteria in conjunction with morphology with the epitypification of six phylogenetic species within the complex. Eight molecular markers including ACT, Apn2 (DNA-lyase), CAL, EF1-α, Fg1093 (ribosomal protein L37), HIS, ITS and TUB were used in the phylogenetic analyses and testing the informativeness. The caution is warranted using the ITS sequence data within the cryptic species complexes, and EF1-α is proved to be the best single marker to resolve the species. The utility of EF1-α, Apn2, HIS and ACT genes are found to be superior to the other genes used with reference to the phylogenetic informativeness. New primers were designed and made available for the amplification of Apn2, ACT and CAL genes within *Diaporthe*. Guidelines for the identification and description of new species are provided with the discussions on insights in to the evolution and the pattern of speciation within the genus.

A molecular phylogenetic analysis of anthracnose pathogens of tropical fruits was performed, with fresh collection of economic and wild fruits in northern Thailand. The species within *Colletotrichum gloesporioides* species complex were found to be the dominant among anthracnose pathogens. A six gene combined phylogeny of ITS, ACT, TUB, CAL, GPDH (glyceraldehyde-3-phosphate

dehydrogenase), GS (glutamine synthetase) was used to resolve the *C. gloesporioides* species complex with the description of the new species, *C. syzygicola*. In general, this thesis provides a comprehensive account in terms of utility of molecular data to resolve plant pathogenic species complexes in fungi. A number of economically important species of common plant pathogenic genera, *Diaporthe* and *Colletotrichum* were re-defined with accurate phylogenetic placement, morphology and insights in to the speciation and evolution.

Keywords: Canker / Diaporthales / DNA-lyase / Endophytes / Epitypification / Evolution / Gene discordance / Genealogical sorting index / Melanose / New primers / Phylogenetic informativeness / Soybean seed decay / Speciation / Species complex / Tropical fruit pathogens