

## Taxonomy and phylogeny of *Diaporthe* associated with dieback diseases in China

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**Purpose:** *Diaporthe* species have often been reported as important plant pathogens, saprobes, and endophytes on a wide range of plant hosts. Although several *Diaporthe* species have been recorded in China, little is known about species able to infect forest trees. The primary aim of the present study was thus to clarify the taxonomy and phylogeny of a large collection of *Diaporthe* species associated with dieback diseases in China.

**Methods:** The current results emphasized on 38 species from 104 representative isolates involving 22 host genera using comparisons of DNA sequence data for the nuclear ribosomal internal transcribed spacer (ITS), calmodulin (cal), histone H3 (his3), partial translation elongation factor-1 $\alpha$  (tef1) and  $\beta$ -tubulin (tub2) gene regions as well as their morphological features.

**Results and conclusions:** Thirty-one novel taxa are introduced and *Diaporthe eres* was found as the most common species associated with diversity hosts. The current study improves the understanding of species causing diebacks on ecological and economic forest trees and provides useful information for the effective disease management of these hosts in China.