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## Phylogenetic re-assessment of the genus *Curvularia*

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The fungal genus *Curvularia* (Dothideomycetes, Pleosporales) consists of important pathogens, which cause devastating diseases globally on plants and human beings. Recently, the generic limit was re-defined and as a result, some of the species previously placed in the sister genus *Bipolaris* now belong to the genus *Curvularia* based on morphological and molecular data. Large number of novel *Curvularia* species have been introduced following the re-assessment of generic limits since the year 2012. However, 32 species of *Curvularia* described within last six years following the first assessment were not included in a recent phylogenetic analysis. Therefore, the major objective of this study was to incorporate the recently described *Curvularia* species in an up-to-date phylogeny. During the current study, we inferred phylogenetic trees of single loci of ribosomal Internal Transcribed Spacer region (ITS), partial Glyceraldehyde 3-Phosphate Dehydrogenase (GPDH), 28S ribosomal Large Sub-Unit (LSU), Translation Elongation Factor 1- $\alpha$  (TEF) and RNA Polymerase-2 (RPB2). In total, 104 species of *Curvularia* and several closely related taxa of the allied genera obtained from GenBank were analyzed using PAUP v.4.0b10 for the Maximum Parsimony (MP) and RAxML v.7.4.2 Black Box in the CIPRES Science Gateway platform for the Maximum Likelihood (ML) methods. Data set consisted of 57 ex-type cultures and their available DNA sequences. Single gene trees of all five loci were compared for their congruency and multi-gene phylogenetic analysis was carried out using ML method. To determine most suitable loci for species level phylogenetic inference of closely related species within *Curvularia*, ITS, GPDH, TEF and LSU were employed with the Phylogenetic Informativeness (PI) profiling test implemented in the online program PhyDesign. The concatenated DNA sequence alignment consisted of 2668 constant characters, 183 characters were variable and parsimony uninformative and 653 were parsimony informative. The final Likelihood value was -25783.8. About 78 species incorporated in the phylogenetic analysis were well resolved based on combined analysis. According to the PhyDesign analysis, the GPDH gene region was the highest informative in species level phylogeny whereas LSU loci found to be the least informative. Resulted tree is the most up-to-date phylogenetic tree available for the genus *Curvularia* which is the backbone for phylogenetic placement and identification of other *Curvularia* species isolated from Sri Lanka and elsewhere.

**Keywords:** Backbone tree, *Curvularia*, pathogens, phylogenetic informativeness

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