

Species Limits in *Curvularia*: Updated Backbone Phylogeny and Fresh Collections from Sri Lanka

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The genus *Curvularia* comprises of fungal species frequently encountered as saprophytes, endophytes and pathogens. Both living and dead weeds as well as crops are well known for the survival and completion of life cycles of *Curvularia* in nature. Molecular phylogenetic assessments are leading to precise identification of species in this genus from closely related taxa since morphological identification alone is often insufficient for species discrimination. Updated molecular phylogeny with all the existing *Curvularia* species is essential in order to infer phylogenetic relationships for freshly collected strains. The major objective of this study is to assess the evolutionary relationships of species of *Curvularia* collected from Poaceous crops and related weed hosts in Sri Lanka incorporating them in an updated backbone phylogeny with all of the available ex-type *Curvularia* sequences. Fresh collections were made from selected Poaceous weeds, rice and maize crops and morphological characters were assessed based on microscopic imaging and culture based studies. An updated backbone phylogenetic tree was constructed based on ribosomal Internal Transcribed Spacer region and partial Glyceraldehyde 3-Phosphate Dehydrogenase using maximum parsimony, was used to place the fresh collections within the genus. In addition, Phylogenetic Informativeness (PI) profiling test was performed to evaluate the informativeness of loci at species level phylogenetic discrimination. The PI profiling proved that the GPDH is the highest informative locus among the loci compared for this genus. The fresh collections of *Curvularia* from local study sites which were incorporated in the current phylogeny were grouped within several different clades such as *geniculata*-clade, *hominis*-clade and *lunata*-clade, emphasizing the existence of diverse array of species among fresh collections. Therefore, it is vital to collect more samples from both crops and weed residues in order to establish impact on these pathogens on crops and to understand their host range and shifting patterns of life modes.

Keywords: Fungi, Pathogen, Phylogenetic informativeness, *Curvularia* spp.

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