Molecular phylogeny reveals novel evolutionary lineages of *Curvularia* from Sri Lanka

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Abstract

The genus *Curvularia* comprises phytopathogenic fungi causing diseases on cereals and grasses. The species of *Curvularia* can be also found as endophytes or saprobes on dead material of plant hosts and are known to be opportunistic human pathogens on immunocompromised patients. The *Curvularia* species that cause diseases on staple crops, wild relatives and weeds in Sri Lanka are poorly known. Insufficient data on identifications of emerging fungal diseases can be a threat on both commercial cultivations as well as small scale farmlands. Therefore an assessment of *Curvularia* species associated with cereal crops, their relatives and weeds is vital, regarding crop and fiber security of the country. The major objective of this study was to collect *Curvularia* spp. from cereal crops, their wild relatives and weeds in Sri Lanka, to accurately identify them and to establish their evolutionary relationships. Fresh collections of about 20 isolates of *Curvularia* were used in this study collected from thirteen different locations across four provinces. Fungi were isolated and morphological characters were assessed based on digital imaging. Molecular phylogenetic analyses were performed for the fresh collections from this study along with available ex-type species for ITS and GPDH loci. The combined analysis revealed that the common occurrence of *C. affinis*, *C. geniculata* and *C. dactyloctenicola* from different hosts. At least five species were distinct from known species based on current phylogeny and considered to be potentially novel lineages within the genus. Therefore, the results suggest an unexpected diversity within limited geographic region of the Island.