Characterization of Malaysian Trichoderma isolates using random amplified microsatellites (RAMS)

Abstract

Trichoderma species are commercially applied as biocontrol agents against numerous plant pathogenic fungi due to their production of antifungal metabolites, competition for nutrients and space, and mycoparasitism. However, currently the identification of Trichoderma species from throughout the world based on micro-morphological descriptions is tedious and prone to error. The correct identification of Trichoderma species is important as several traits are species-specific. The Random Amplified Microsatellites (RAMS) analysis done using five primers in this study showed different degrees of the genetic similarity among 42 isolates of this genus. The genetic similarity values were found to be in the range of 12.50-85.11% based on a total of 76 bands scored in the Trichoderma isolates. Of these 76 bands, 96.05% were polymorphic, 3.95% were monomorphic and 16% were exclusive bands. Two bands (250 bp and 200 bp) produced by primer LR-5 and one band (250 bp) by primer P1A were present in all the Trichoderma isolates collected from healthy and infected oil palm plantation soils. Cluster analysis based on UPGMA of the RAMS marker data showed that T. harzianum, T. virens and T. longibrachiatum isolates were grouped into different clades and lineages. In this study we found that although T. aureoviride isolates were morphologically different when compared to T. harzianum isolates, the UPGMA cluster analysis showed that the majority isolates of T. aureoviride (seven from nine) were closely related to the isolates of T. harzianum.