

Level in allozyme variations of Malaysian isolates of *Trichoderma harzianum* and its taxonomic implications

Abstract

Electrophoretic variation of nine allozyme systems encoded by 14 gene loci were studied on 47 isolates from 3 species of *Trichoderma* namely, *T. harzianum*, *T. aureoviride* and *T. longibrachiatum*. Polyacrylamide gel electrophoresis was used to investigate the taxonomic circumscription of *T. harzianum* populations and to evaluate the levels of genetic variations and the population structure. The level of genetic variations in *T. harzianum* populations were moderately high ($P = 57.10\%$, $A = 0.7857$, $A_p = 0.60714$ and $HE = 0.1542$) compared to *T. aureoviride* and *T. longibrachiatum*. The genetic variation attributable to differences among populations was 7.857% . The mean gene flow among populations was $N_m = 1.3351$. Genetic identities (I) ranged from 0.9397 to 0.9642 with a mean of 0.94846 . Outcrossing rates based on fixation indices average (t) was 0.2334 . Nevertheless, the alleles for α -EST-b showed a very low frequency of 0.0400 . The polymorphic locus of MDH1 was of the fast allele of *T. harzianum*, MD1-a, was prevalent in *T. aureoviride* and *T. longibrachiatum* populations. Using a UPGMA cluster analysis, *T. harzianum* and *T. longibrachiatum* populations were totally separated in these cluster except *T. aureoviride* populations. *Trichoderma harzianum* populations found high levels of genetic variations comparing with others populations of *Trichoderma* species