

Allozyme variations 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 $H = 0.1542$) 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 $Nm = 1.3351$. 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 -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. *T. harzianum* presents high levels of genetic diversity compared with other *Trichoderma* species.

Keyword: *Trichoderma*; Polyacrylamide gel electrophoresis; Allozymes; Genetic variations; Identification of fungi