

SL304

Interpretation of Random Amplified Polymorphic DNA Markers in *Hypoxylon truncatum*

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Genetic variation within and among six populations of *Hypoxylon truncatum* was assessed by characterizing random amplified polymorphic DNA markers: one population from Louisiana, one from Mississippi, one from southern Illinois, two from central Illinois, and one from northern Illinois. Nine isolates from each population were characterized. Results were analyzed phenetically. With 18 randomly chosen 10-mer primers, genetic variation was assessed among isolates from a single stroma, and among isolates from different stromata from the same collection. Twenty arbitrarily chosen 10-mer primers were used to assess genetic variation among 54 isolates (nine from each of the six populations) and a 99 character by 54 isolate matrix was generated. Phenetic analysis separated the 54 isolates into two genetically distinct groups that corresponded with different stromatal type. The results of the present study suggest that stromatal type is a significant taxonomic character in *H. truncatum*-like fungi and that the two forms of stromata in *H. truncatum sensu* Miller are indicative of distinct species. Phenogram branching patterns did not correspond with geographically distant populations. Gene flow between these populations may be responsible for this finding.