

Abstract:

Objective: To examine the distribution of dispersed repetitive DNA (Enterobacterial Repetitive Intergenic Consensus (ERIC), BOX, and Repetitive Extragenic Palindromic (REP) sequences in the genome of *Exserohilum turcicum* using conserved primers. Methodology and results: DNA amplification was done using standard PCR procedures and the resultant PCR products analyzed by agarose and polyacrylamide gel electrophoresis. The different markers produced characteristic banding patterns and the similarity matrices from binary banding data was derived with the similarity for qualitative data program (SIMQUAL). Cluster analysis showed close genetic similarities between Kenyan, German and Austrian isolates of *E. turcicum*. The average gene diversity from BOX sequences was 0.28 whereas for ERIC and REP sequences, it was 0.14 and 0.05, respectively. Conclusion and application of findings: The study showed that discrimination of closely related strains can be achieved using REP, BOX and ERIC PCR fingerprinting. We recommend these markers as a rapid tool for the genetic characterization of large populations of *E. turcicum*.