

Abstract

The aim of this study was to investigate the genetic polymorphism among Sistan grapevines using retrotransposon-based molecular markers. Leaf samples were collected from the genotypes in the Zahak Research Station and maintained at -70°C. Thirty-three genotypes were analyzed using five pair single forward or reverse retrotransposon-based primers, together with paired primers. PCR products were examined by agarose gel electrophoresis. Presence or absence of PCR products were scored and analyzed using multivariate methods. Polymorphism information content values were quite fluctuating except for one cultivar, varying from 0.434 and 0.312. Cluster analysis was performed using UPGMA method and Jaccard's similarity coefficient and cultivars were divided into 13 main groups in 0.54 similarity coefficient. Principal component analysis indicated three components explaining 67% of the variation among the studied population. The first three components justified 44%, 7.6% and 5% of the total variations respectively. Mantel test indicated $r=0.77$ for the correlation between the similarity matrix and cophentic coefficient. Except for a few genotypes, no correlation was observed between polymorphism and geographic distribution of the cultivars. The results were compared with former studies using different molecular markers and the feasibility of the retrotransposon-based markers for cultivar DNA fingerprinting was discussed.

Key words: Grapevine, *Vitis*, retrotransposon, inter retrotransposon amplification polymorphism, biodiversity.



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