Abstrac

Studying gene diversity of mango types using transposon elements in southern IRAN Genetic resources are base foundation in plant breeding they provide gene storage for breeding with desirable properties and in order to utilize gene types we need to accurately identify them . for this purpose we analyzed gene diversity among 30 gene types in southern IRAN using 15 molecule indicators based on transposon elements. studied gene types were varieties gathered from 5 regions in southern IRAN they were kept at -70 c before any experiment . we analyzed 30 gene types with 15 transposon primer solitary and combinatory then load the PCR products on AGARES gel which resulted in only 11 primer showing visible band . presence or lack of presence of band was rated on zero or one base and visible polygons catalyzed by multi-variant methods . results of such primers demonstrated that with using PCR reaction 66 measurable DNA were duplicated which 66 bands equal to 100 percent of bands were polygons . average duplicated band of every prime combination were 6 numbers . cluster analysis based on UPGMA method and JACCARD similarity coefficient was performed which numbers at similarity coefficient of 0.38 divided into 4 category . results of molecular variance analysis demonstrated that at the statistical level of 0.01 there is significant difference between different regions gene types . in other words categorization was done correctly based on this data 67% of total diversity is in population and 33% is intra-population . in catalyzing to basic parameters the first 6 parameters explained 81 percent of all changes . first second and third parameters respectively explained 24 17 and 14 percent of variation . LTR1 & LTR2 and LTR1 & LTR3 respectively formed the most polygons band with 12 and 7 bands which can prove useful in identifying mango gene types and genetic analysis.

Keywords: mango - transposon - gene - diversity - IRAP



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