

## INTER SIMPLE SEQUENCE REPEATS (ISSR) GENETIC DIVERGENCE AND VARIETAL IDENTIFICATION OF BANANAS IN PAKISTAN

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### ABSTRACT

Banana is regarded as a major cash crop in some areas of Pakistan but there is a lack of information on genetic diversity among varieties locally cultivated. It is quite important to find duplication in banana varieties because of the narrow genetic base present in case of banana. Environment greatly affects the phenotypic expression and makes it difficult to differentiate among the cultivars on morphological basis. DNA markers based techniques have been used to rapidly identify varieties. We used Inter Simple Sequence Repeats (ISSR) markers to identify banana cultivars and to investigate the genetic variation in 14 local banana varieties grown in Pakistan. Out of forty-five primers used, forty primers showed reproducible results and produced 109 polymorphic bands, which accounted for 44.57% polymorphism. The ISSR markers UBC-835 and UBC-834 detected the highest level of polymorphism in banana varieties (86-88%) while UBC-857 detected the lowest (46%) polymorphic. The size of amplified PCR product ranged between 100-1500 bp. Pairwise Jaccard's similarity co-efficient values were calculated in NTSYS-PC version 2.1. The similarity co-efficient ranged between 0.56 - 0.88. Multivariate analysis divided 14 banana varieties into two distinct groups A and B, and further divided into subgroups, clusters and sub-clusters. This study indicated that at molecular level, the varieties in group-A were 66% similar. The varieties in group-B were 88% similar. Nei's genetic diversity, PCA analysis and minimum spanning tree depicted Fenjiao, Dajiao and NIGAB 2 was found to be most diverge as compared to all members of the three populations. Out of 14 varieties used, eleven varieties were uniquely identified by 54 polymorphic ISSR bands of different sizes. Some varieties like NIGAB-1 and NIGAB-2 were uniquely identified only with one band while others were tagged by multiple unique bands.

Keywords: Genetic diversity, ISSR, Varieties identification, Cluster Analysis