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Genetic Diversity Analysis in Triticum Aestivum Using Microsatellite Markers

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Abstract : In the present study, the simple sequence repeat(SSR) markers have been used in analysis of genetic diversity of 37 genotypes of Triticum aestivum. The DNA was extracted using cTAB method. The DNA was quantified using the fluorimeter. The annealing temperatures for 27 primer pairs were standardized using gradient PCR, out of which 16 primers gave satisfactory amplification at temperature ranging from 50-62^0 C. Out of 16 polymorphic SSR markers only 10 SSR primer pairs were used in the study generating 34 reproducible amplicons among 37 genotypes out of which 30 were polymorphic. Primer pairs Xgwm533, Xgwm 160, Xgwm 408, Xgwm 120, Xgwm 186, Xgwm 261 produced maximum percent of polymorphic bands (100%). The bands ranged on an average of 3.4 bands per primer. The genetic relationship was determined using Jaccard pair wise similarity co-efficient and UPGMA cluster analysis with NTSYS Pc.2 software. The values of similarity index range from 0-1. The similarity coefficient ranged from 0.13 to 0.97. A minimum genetic similarity (0.13) was observed between VL 804 and HPW 288, meaning they are only 13% similar. More number of available SSR markers can be useful for supporting the genetic diversity analysis in the above wheat genotypes.

Keywords : wheat, genetic diversity, microsatellite, polymorphism
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