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Screening of different soybean genotypes for seed longevity traits through molecular markers

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Molecular genetic markers have brought phenomenal changes in the area of plant biotechnology by their ability to produce unique DNA profiles in various crops. DNA markers have become fundamental tools for research involving soybean improvement programs. Availability of molecular marker technology has made possible the genetic dissection and characterization of many quantitatively inherited seed quality traits in soybean. The present study employed microsatellites or simple sequence repeat (SSR) markers to assess genetic polymorphism. With the development and public release of SSR primers, SSR markers have become available on molecular soybean linkage group. Molecular markers tightly linked to desired genes are a valuable tool to detect genotypes of interest, saving time and resources. In the present investigation, six soybean genotypes viz., Kalitur, Birsa soya, JS-9305, JS-335, JS-71-05 and Co-1 were subjected to SSR marker analysis to screen the genotypes for seed longevity. Out of 14 primers viz., Satt285, Satt434, Satt538, Satt600, Satt598, Satt281, Satt658, Satt187, Satt310, Satt472, Satt459, Satt489, Satt316 and Satt288 screened for seed longevity, the primer Satt 285, Satt 316, Satt 434 and Satt 281 gave distinct banding pattern. They produced an amplicon size range from 184 bp for those genotypes which are having poor seed longevity across the genotypes and the same loci produced amplicon size range up to 235 bp for those genotypes having good seed longevity. This distinct banding pattern for the good and poor seed longevity genotypes gave a clear cut differentiation between the two extremes of seed longevity at the molecular level. A dendrogram based on UPGMA analysis grouped the six genotypes into three clusters, There was clear clustering of the six genotypes in 3 major clusters, which were grouped as good and poor seed longevity based on molecular data, where cluster I included the genotypes Kalitur, Birsa soya, and JS-9305 with good seed longevity. However, cluster III included genotype JS-71-05 with poor seed longevity.