D L Savithramma et al., J Proteomics Bioinform 2016, 9:12(Suppl)
http://dx.doi.org/10.4172/0974-276X.C1.094

Development and characterization of newly developed genomic SSR markers in Mung bean (*Vigna radiate* (L.) Wilczek)

D L Savithramma and C K Divya Ramakrishnan
University of Agricultural Science, India

Simple sequence repeat (SSR) markers are a major molecular tool for genetic and genomic research that have been extensively developed and used in major crops. However, few are available in mungbean (*Vigna radiate* (L) Wilczek), an economically important protein rich (22-24%) edible food legume of South and Southeast Asia. Mung bean is a self-pollinating diploid grain legume with the genome size of 560 Mb. Therefore, the application of molecular markers can play key role in direct improvement of mung bean. Development and use of molecular markers in the species are limited. The major objective of this study was development for a set of simple sequence repeat (SSR) markers based on construction of SSR-enriched genomic DNA libraries, sequencing, and validation of designed primers. Mungbean genotypes Chinamung and BL 849 were used to isolate DNA for constructing SSR-enriched genomic libraries. More than 200 positive clones were purified and they were sequenced using vector specific primer. Quality of all DNA sequences was analyzed. After trimming off the vector sequences, all the sequences were placed in a fasta file for further analysis with the CAP3 program to categorize the sequences into contiguous sequences (contigs) and singletons(non repeating). The two categories of sequences were run separately with the SSR Locator program for SSR detection and primer designing. The parameters for the primer design were given as amplicon size in 140–350 bp, primer length of 18–22 bases with 20 as the optimum, annealing temperature of 55–61°C with an optimum of 59°C, GC clamp 0, G/C content 45–50%, start and end point automatic scan and end stability at 250. A total of 40 primer pairs were designed from the microsatellite-containing sequences. Newly synthesized 40 mung bean SSR primers were used for genetic diversity studies with 24 genotypes and dendrogram was constructed. Out of 40 designed primer pairs 26 primer pairs were found to amplify bands of the expected sizes while eleven primers failed to amplify and three primers produced monomorphic bands. The overall size of the amplified product varied from 110 to 400 bp. The coefficient of genetic dissimilarity ranged from 0.159 to 0.536. Pair-wise estimates of dissimilarity ranged from 0.14 to 0.90 and the average dissimilarity among all 24 genotypes was 0.365. Two genotypes LM 192 and IC325738 were the closest related genotypes with the lowest dissimilarity index of 0.159. The highest dissimilarity (0.536) was observed between genotypes WBM and SML 348. The SSR markers developed in the study are highly valuable for molecular and traditional breeding research.

Biography

D L Savithramma has completed her PhD from University of Agricultural Sciences, Bangalore, India and Postdoctoral studies as a Biotechnology National Associate from Indian Institute Science, Bangalore, India. She is a Professor of Genetics and Plant Breeding at University of Agricultural Sciences, Bangalore, India, one of the premier Agricultural Universities in India. She has published more than 70 papers in reputed journals and has released seven varieties in vegetable cowpea, seed cowpea, peanut and *Chrysanthemum*.

nesarns@gmail.com

Notes: