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Development of High Density Linkage Map of Pigeonpea (Cajanus cajan (L.) Millsp.) using 62K SNP Chip
Sangeeta Singh¹, Ajay Kumar Mahato¹, Ranjeet S Raje², Vandna Rai¹, Tilak R. Sharma¹ and Nagendra K. Singh¹
(1) ICAR National Research Centre on Plant Biotechnology, New Delhi, India
(2) Division of Genetics, Indian Agricultural Research Institute, New Delhi, India

Pigeonpea (Cajanus cajan L.) is the second most important pulse crop and one of the most important sources of dietary protein in India. The major constraints for pigeonpea productivity are inadequate availability of seeds of improved varieties, and a range of biotic and abiotic stresses. Draft sequence of the pigeon pea is already available but we need to develop high quality reference sequence of each of the eleven pigeonpea chromosomes to facilitate gene discovery and molecular breeding. In pigeonpea, earlier a very small number of SSRs was available and the level of polymorphisms is low. Thus, to have a sufficient coverage of the genome more SNP markers are required. SNPs are the most abundant DNA markers in the plant genomes, have tremendous applications in creating high density map, tagging of economical important genes, genotyping and evolution among the plant genetics. We have developed genic SNP genotyping chip under Indo-Swiss Collaboration in Biotechnology (ISCB) for genetic as well as molecular breeding applications in pigeonpea. The chip incorporates 62K SNPs from five categories of genes. The chip was validated successfully in the wetlab using GeneTitan on 96 variety and 96 RILs population of pigeonpea. SNP genotypes were called using the Axiom Analysis Suite software. High-performing SNPs with a DQC of >0.85 and average call rates of >95.0% were used for analyses. A High density SNP linkage map was constructed using JoinMap v4.1 Software. Availability of high-density linkage map will help better anchoring of the pigeon pea genome to its chromosomes and mapping of genes and QTLs for useful agronomic traits.

Session Selection: Genome Mapping, Tagging & Characterization: Legumes, Soybeans, Common Beans
Submitter's / presenter's email address: sangeeta10mar@gmail.com