

4th International Conference on Plant Science and Agriculture

March 09, 2022 | Webinar

Genome wide association analysis to enhance seed and nutrition quality traits in pigeonpea

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Pigeonpea is an important legume crop with high protein content and nutritional attributes for more than a billion-people living in South Asia. Ever-increasing pigeonpea consumption as a major source of protein necessitates the improvement of varieties for more efficient production. The nutritional value enrichment of pigeonpea is very much essential to reduce malnutrition of developing countries in the post green revolution era. To utilize its potential, a coordinated and comprehensive evaluation of germplasm is required. Identification of potential genes/alleles governing complex traits of seed quality and nutritional content such as seed weight, seed colour, total protein content (TPC), amino acid and resistance starch are essential in marker-assisted breeding for quality trait improvement of pigeonpea. The current gain in knowledge on the seed quality and nutritional value related genes and QTLs will help into develop desired genotypes for the humankind. The availability of gene-based markers and advanced tool will assist breeders to accumulate specific alleles of genes known to play a role in nutritional grain quality traits in pigeonpea. Therefore, the present study on the profiling for the first-time to understand these complex genetic architectures of qualitative and quantitative traits in pigeonpea. For GWAS (genome-wide association study), high-throughput genotyping information of 62K SNP “CcSNPnks” genic chip genome-based SNPs discovered from 45 diverse varieties of pigeonpea utilized. The chip comprises total 62,053 SNPs from 9629 genes

belonging to five different categories, including 4314 single-copy genes unique to pigeonpea, 4328 single-copy genes conserved between soybean and pigeonpea, 156 homologs of agronomically important cloned genes, 746 disease resistance and defense response genes and 85 multi-copy genes of pigeonpea. Our analysis revealed that the average protein content carrying genotypes are DG(RG)45, AKPR -324, MC-99, UP-73 and BRG-2 (16.8, 19.3, 21.5, 24.7, 30.3 gm). This led to identification of most effective genomic loci (genes) associated with seed quality and nutritional content in pigeonpea from diverse sets of wild and cultivated genetic backgrounds. The informative functionally relevant molecular tags scaled down essentially have potential to accelerate marker assisted genetic improvement by developing seed quality and nutritionally rich pigeonpea cultivars.

Speaker Biography

Nisha Singh is working as an assistant professor (bioinformatics), department of bioinformatics, COABT, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana and DST-INSPIRE faculty at ICAR-National institute for plant biotechnology, New Delhi, India. She has completed her PhD in plant genomics from ICAR-NIPB, New Delhi, India and postdoctoral studies from Cornell University, Ithaca, New York, USA. She has rich expertise in crop genomics, proteomics and bioinformatics and well recognized national and international level. She has published more than 50 papers in reputed international journals and has been serving as an editorial board member and reviewer of reputed journals.

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