

Plant Genomics

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Translating advances in pearl millet genomics to farmer preferred cultivars

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Pearl millet is one of the most climate resilient cereals. It is grown in marginal and dry areas of the world with poor soil fertility, low moisture holding capacity in subsistence agriculture. It forms critical food, nutrition and livelihood support for the millions of poor living in Africa, Asia and other parts of the world. Pearl millet is one of the cereals which received poor attention towards generation of genetic and genomic resources in the past. However, lately a lot of efforts have been made in trait discovery, mapping and deployment of some key traits. One successful example is HHB 67 Improved, which is the first marker-assisted breeding product in India and is grown in more than 750,000 ha every year. In pearl millet more than 20 pairs of mapping population have been generated, segregating for an array of traits of economic interest. In addition, a world association mapping panel called PMiGAP, chromosome segment substitution lines (CSSLs), TILLING population have been developed. Recently, at ICRISAT the whole genome sequencing of a pearl millet reference line Tift23D2B1P1-P5 has been completed, along with re-sequencing of about 1,000 accessions consisting of wild and cultivated germplasm and breeding lines. By virtue of available genetic maps, QTL locations and effects, the pearl millet community is strongly placed for mining genes and gene networks for an array of traits. The genome sequence will help us utilize various reverse genetics tools, carry out genome-wide association studies (GWAS), genomic selection (GS) leading to efficient cultivar development.

Biography

Rakesh K Srivastava has obtained his PhD from the Indian Agricultural Research Institute (IARI) New Delhi, India. He currently leads the pearl millet genomics team at ICRISAT, India. He is extensively involved in generation of various genetic and genomic resources, mining, mapping and deployment of QTLs/genes for various biotic, abiotic, grain and fodder quality traits in collaboration with the National Agricultural Research System (NARS) in pearl millet. He has contributed significantly towards the international whole genome sequencing for pearl millet involving world reference germplasm and entire association mapping panel. He is actively involved in various capacity building programs for NARS.

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