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Abstract Book

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T6PP025:

Characterizing mapping population parents for fodder quality and biomass related traits in pearl millet

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Pearl millet is one of the most important crops that provide food, fodder, feed, and fuel to millions of poor families and their livestock. The objective of this study was to identify the best pair of mapping population and assessment of variability for fodder traits. A total of 45 parents representing 23 mapping populations were used for characterization in a two-replication alpha lattice design during summer 2019. Pairwise t-test analysis reported significant differences for targeted traits. Mapping population with significant contrast was identified (Jakhrana S8-28-2-P4 × RIB 335/74-P1). In variability analysis, In-vitro Organic Matter Digestibility (IVOMD) ranged from 54-72.22%, acid detergent fiber (28.6-52.3%), neutral detergent fiber (60-75.2%), metabolizable energy (5.81-9.67MJ/Kg) and crude protein (7.11-14.2 g/kg). The range for biomass-related traits, total Biomass (TB) (70-859q/ha), total leaf weight (43-134), total stem weight (65-156), 50% flowering (36-119 days) and number of tillers (2.9-12.59), plant height (48.43-186cm), leaf length (18.72-65cm), leaf breadth (1.6-4.32cm) and stem girth (6.15-17.73mm), leaf stem ratio (0.27-2.06) was reported. Top five lines identified for IVOMD were (ICMB841)-P3-P4, ICMB95333-P5, LGD-1-B-10, ICMB-89111-P2 and RIB335/74-P1, while for TB, top five genotypes were P1449-2-P1, IP18293, H77/833-2-P10(P5), ICMP451-P6 and ICMS8511-S1-17-2-1-1-B-P03. The significant differences between pairs would be further used for crop improvement purpose such as the mapping of QTLs/alleles for fodder traits. Furthermore, genotype differences reveal diverse genetic make-up of cultivars, which could be valuable in identifying superior gene combinations for key traits along with application in heterosis breeding.

T6PP026:

Advances in finger millet genomics research at ICRISAT

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Genomic resources and molecular markers play an important role in designing novel breeding programs to accelerate genetic gains in crops. Next generation sequencing (NGS) and genotyping technologies have impacted enormously in the crop improvement process. Genomics approaches such as association studies, QTL analysis, multi-omics etc. provided opportunities to study genetic variation and identify useful alleles in genome for use in molecular breeding. Several genomics resources have been generated and successfully deployed in different crops resulting in improved lines/ developed cultivars. However, these success stories have been largely restricted to major cereal/ legumes and is time to generate genomics resources for utilization in other minor food crops including millets. Finger millet [*Eleusine coracana* (L.) Gaertn.], a climate-resilient nutrient-dense crop among the six small millets has been recently added in research portfolio of the ICRISAT as one of its mandate crops. Currently, the genebank at ICRISAT conserves nearly 7,500 finger millet germplasm accessions. Towards development of genomics resources, ICRISAT in collaboration with several national and international partners have initiated research in this direction to dissect and understand biological mechanisms of complex traits for finger millet improvement. For instance, whole genome re-sequencing of 172 lines resulted in identification of 65,04,522 SNP markers. Data analysis revealed classification of identified SNPs into A and B genomes, chromosome-wise distribution, SNP density, transitions and transversions. Utilizing high quality non-redundant SNPs, precise and cost-effective SNP genotyping assays like Quality Control (QC; 48 SNPs) and Mid-density SNP array (3000 SNPs) panels were developed for deploying in finger millet breeding programs. These SNP panels are being used for hybridity testing, fingerprinting of the released varieties as well as assessing their adoption in addition to genetics and breeding applications. In another study, genome wide association studies have provided significant marker-trait associations and candidate genes for nutritional traits in finger millet. Efforts are underway to dissect the genetic basis of blast resistance mechanism through QTL mapping and RNA-seq approaches. All these genomic resources along with the above-mentioned approaches will be used for strengthening the finger millet breeding.