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Abstract Book



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T6PP045:

Millets germplasm resources to breed climate-resilient cultivars for sustainable agri-food systems in the drylands

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With dryland food supply being challenged by climate variabilities, the world may be leaning towards a global food crisis. This will effect largely the poor and the smallholder farmers because of low crop and livestock productivity, income and nutrition. Drylands occupy about 41% of the global land. Millets with C₄ photosynthetic mechanism are the potential crops which can drive drylands towards climate resilience and sustainability because of higher productivity with minimal input, adapting to diverse ecologies and the grains are more nutritious than the major cereals. The ICRISAT Genebank conserves global collections of millets including sorghum (42799), pearl millet (24633), finger millet (7519), foxtail millet (1542), proso millet (849), barnyard millet (749), Kodo millet (665) and little millet (473), and distributed over 776,000 seed samples of these crops globally. Extensive evaluation of germplasm and diversity subsets such as core and mini-core collection resulted in the identification of trait-specific sources for breeding climate-resilient and nutrient-dense crops. The key trait-specific sources identified in sorghum include drought, low-temperature stress tolerance, photoperiod and temperature insensitivity, grain nutrients, fodder quality, and several insect pests and diseases resistance; in pearl millet for early maturity, fodder yield and quality, drought, salinity and heat stress tolerance, and resistance to downy mildew, rust and blast; finger millet and foxtail millet for drought and salinity tolerance, resistance to blast and high grain nutrients; and proso millet, kodo millet, little millet and barnyard millet for yield, and grain nutrients. ICRISAT is working towards large-scale high-throughput phenotypic and genomic characterization and trait discovery to support breeding climate-resilient nutrient-dense cultivars in millets for increasing productivity and resilience in the drylands. Researchers can obtain seed samples of millets germplasm from the ICRISAT genebank (<http://genebank.icrisat.org/>) following the Standard Material Transfer Agreement.

T6PP046:

Haplotype mining for EPSPS and ALS herbicide resistance genes in diverse sequenced panel of 401 pigeonpea lines

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Weeds are among the difficult-to-control biotic stresses that have continually disrupted crops, resulting in low grain yield including pigeonpea. Finding genetic solution for weed control is more resource saving and ecofriendly in view of huge genetic diversity in pigeonpea germplasm. In this context, the whole genome sequencing on 401 diverse pigeonpea with average $\geq 10X$ coverage sequencing data and genome mapping of 99.18%, along with the improved version of Asha reference genome was used. SNP calling identified 21,404,811 SNPs and InDels 5,542,227, which was reduced to 8,33,756 SNPs on applying filter of maf 2% and missing call <20%. Two candidate genes *EPSPS* (*5-enolpyruvylshikimate-3-phosphate synthase*) and *ALS* (*Acetolactate synthase*), which are reported for its high herbicides resistance levels in crops were analyzed for sequence variation in this diverse panel. These genes were searched in annotation file of newly developed reference genome of pigeonpea and its similarity at complete sequence and domain level was confirmed using blastn, blastx and HMMer programs. As a result, four haplotypes for one copy of *EPSPS* gene located on chromosome 1, and 30 haplotypes for two gene copies of *ALS* genes located on chromosome 9 were identified. Thirty-three variants were identified for *ALS* gene, 6 missense (Cc_v2.0_22271) and 22 intronic variants (Cc_v2.0_22275 and Cc_v2.0_22271). *EPSPS* (Cc_v2.0_02093) have one 3'UTR and three intronic variants. To validate the results, the selective lines would be phenotyped for herbicide tolerance for trait confirmation and potential use in breeding herbicide tolerant pigeonpea lines. This also opens up opportunities for identifying natural variation in other related crop species such as chickpea and groundnut.