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T6PP069:

Identification of genomic regions and candidate genes for nutritional traits in groundnut

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Malnutrition is a major challenge globally and groundnut is highly nutritious self-pollinated legume crop blessed with ample genomic resources including routine deployment of genomic-assisted breeding. In order to identify genomic regions and candidate genes for iron (Fe), zinc (Zn), protein and oil content, we have performed genome wide association study (GWAS) (diverse 184 accessions). GWAS analysis using 58K high density SNP array genotyping data and two seasons of phenotyping data identified 12 MTAs (marker-trait associations) for Fe, 45 MTAs for Zn, 21 MTAs for protein and 13 MTAs for oil content. Interestingly, the MTA (Ah03_ 42618206) and MTA (Ah03_23761976) were found common for both season for protein and oil respectively. Additionally, we have performed genetic mapping using recombinant inbred population (ICGV 00440 × ICGV 06040; 218 lines). Genetic mapping and quantitative trait locus (QTL) analysis (474 mapped SNP loci; 1536.33 cM) using two seasons phenotypic data and genotypic data with 5K mid-density assay identified six main-effect QTLs for Fe content with phenotypic variation explained (PVE) ranging from 7.3% (*qFe-Ah11*) to 30.0% (*qFe-Ah14*). Similarly, five main effect QTLs were identified for Zn content with PVE ranging from 5.6% (*qZn-Ah11*) to 32.8% (*qZn-Ah08*). Interestingly, we found three co-localized QTLs (*qFe-Ah01, qZn-Ah03 and qFe-Ah11*) for Fe and Zn content. Consequently, Ah03, Ah04 and Ah07 genomic regions were found common for Fe and Ah01, Ah03, Ah11 and Ah13 were found common for Zn through genetic and association mapping. These genomic regions harboured key candidate genes such as, *ZIP transporter*, *bZIP transcription factor*, *vacuolar iron transporter, protein kinase superfamily protein and acyl carrier protein* etc. for Fe, Zn, protein and oil. These results may further facilitate fine mapping and haplotype analysis for high Fe, Zn, protein and oil in groundnut.

T6PP070:

Dryland legumes genetic resources for breeding crops adapting to climate change

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Global climate change combined with population growth is imposing huge pressure on increasing crop productivity. Crops having climate-smart adaptation together with better nutritional quality supports sustainable agriculture and nutritional security. Dryland legumes such as chickpea, pigeonpea, and groundnut are climate-smart crops with enormous agronomic features and nutritional quality, which offer myriad of benefits for sustainable production systems. In addition, growing these crops enhances soil fertility through fixing atmospheric nitrogen. Globally, over 268,000 germplasm accessions of three dryland legumes, chickpea (>98,700), pigeonpea (>40,800), and groundnut (>129,000) are conserved in the ex-situ genebanks. ICRISAT Genebank conserves the largest collections of chickpea (20,993 from 61 countries), pigeonpea (13,787 from 74 countries), and groundnut (15,896 from 92 countries) and distributed over 822,709 seed samples of these crops globally. These collections comprise of landraces (68.73%), breeding/advanced materials (4.34%) and wild and weedy relatives (3.11%). Germplasm diversity subsets such as core (10% of the entire collection) and mini core (10% of the core) have been established and evaluated extensively, which resulted in the identification of promising sources for agronomic and grain quality traits, and for tolerance to biotic and abiotic stress. Evaluation of the chickpea mini core consisting of 211 accessions was carried out for morphological, physical, and hydration traits, and promising sources have been identified for biotic and abiotic stress. Similarly, the evaluation of groundnut and pigeonpea mini core collections resulted in the identification of multiple resistance and nutritionally dense germplasm for use in crop improvement. A recent study on grain nutrient variability revealed a large potential of pigeonpea for protein (23.35–29.50%) and calcium (353.71–877.66 mg/kg in seed coat) besides other nutrients. Exploiting these trait-specific germplasm sources in crop improvement holds the key to addressing the food and nutritional security of smallholder farmers in a changing climate scenario.