IDT9-077 | Towards defining heterotic pools for accelerating hybrid breeding in pigeonpea

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Recently released pigeonpea hybrids for cultivation in farmers' fields have shown their potential to elevate the yield levels. For instance, the world's first grain legume hybrid of pigeonpea ICPH 2671 showed 47% yield advantage over the check varieties. Generally, the development of such hybrids is based on selection efficiency of breeding program; breeders make thousands of random crosses between cytoplasmic male sterile (CMS) lines and tester lines. In order to enhance the selection efficiency, genomic diversity along with the phenotyping data have been used for predicting the best possible parental combinations. This approach has been successfully used in defining heterotic pools in many crop species such as maize, rice, sunflower, and rapeseeds.. With an aim to define heterotic pools in pigeonpea, a set of 104 parental lines (09 CMS, 13 maintainers and 82 restorers) have been re-sequenced following whole genome re-sequencing (WGRS) approach. WGRS yielded a total of 511 GB data with the coverage ranging from 5X to 10X. A total of 3.4 million SNPs have been identified across parental lines. Structural variations such as copy number and presence/absence variations have been also identified. In parallel, these parental lines have been used to develop test crosses in factorial mating design. F_1 hybrids along with parental lines were phenotyped for yield and yield related traits at two locations in India, namely ICRISAT, Telangana State and ARS-Gulbarga, Karnataka. The availability of genome-wide SNP variations combined with the phenotypic data will be used for deploying genomic selection to define hetereotic pools in pigeonpea for accelerating hybrid breeding program.

IDT9-078 | Targeted genome mining, comparative modelling and protein structural motifs studies of Δ1-pyrroline-5-carboxylate synthetase (P5CS) in *Zea maize*

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One of the chief concerns of climate change is an escalation in the frequency and severity of abiotic stresses. Proline plays an important in drought tolerance in plants. There are two pathways for proline and one of them is from glutamate, which is converted to proline by two successive reductions catalysed by pyrroline-5-carboxylate synthase (P5CS) and pyrroline-5-carboxylate reductase (P5CR), respectively. During stress, the expression of P5CS, but not of P5CR gene, is correlated with proline content. We hypothesize that it will be possible to associate candidate genes discovered in model species such as *Arabidopsis thaliana*, with corresponding loci in maize. In this study we took up an analysis of the complete maize genome for the similarity/ presence of P5CR protein product. We conducted targeted genome mining, comparative modelling and protein structural motifs studies of P5CS. The best homolog of P5CS protein in maize was identified based on significant sequence similarity. The target sequence was used to identify the close homolog in PDB with better resolution. A homology model was built according to the positive match protein sequence. A comprehensive search for templates was done in all publicly available structure databases of pdb structures solved by X ray crystallography or NMR. InterPro scan was done with other known protein families, domains, regions, repeats, and sites for identifiable features found in known proteins to be applied to the target protein sequence. The resultant putative P5CS protein was subjected to detailed bioinformatics analysis to ascertain it's structural and functional similarly to known P5CS.