IDT9-061 | Next generation sequencing based transcriptomic studies for crop improvement in pigeonpea

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Transcriptomic studies are rapidly evolving as a powerful tool with next-generation sequencing technology to understand gene functions and molecular mechanisms. RNA sequencing (RNA-seq) provides a dynamic range for transcript detection and a better quantification of expression levels.With the availability of genome sequence in pigeonpea, RNA-seq was used to link the sequence information to phenotypic traits resulting from specific developmental processes. In pigeonpea, three-line hybrid breeding system is well-established; however, it is technically demanding and cumbersome. In order to explore the possibility of a two-line hybrid breeding system, a coherent transcriptomic approach supported by physiological and cytological data has led to the identification of a temperature-sensitive male sterile (TSMS) line. This line has been characterized for critical (tetrad) stage and temperature (23°C), and the identification of candidate genes involved in abscisic acid signaling for fertility reversion. Furthermore, a gene expression atlas (CcGEA) has been developed and transcriptomic profiles generated for studying pod and seed development with a dataset of 590.84 and 342 million paired-end reads, respectively in pigeonpea. These data have been analyzed for genes with differential, specific, spatio-temporal and constitutive expression. In addition, CcGEA identified a gene network of 28 co-expressed genes, including two regulatory genes, a pollen specific SF3 and a sucrose-proton symporter to be involved in pollen fertility, which has potential implication in seed yield improvement. In summary, this study, especially identification of TSMS and development of CcGEA, will accelerate on-going efforts to enhance genetic gains in pigeonpea.

IDT9-062 | *In silico* analysis of candidate gene from identified QTL regions for drought stress tolerance in wheat

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Drought stress is a complex phenomenon, and many approaches are used to overcome drought stress in wheat. Availability of DNA markers closely linked to drought tolerance QTLs will make the job easier. The QTLs generally span the genomic region containing tens to hundreds of genes, and identification of the most promising regulatory genes within QTL interval will be more effective than using QTL-linked markers. In the present study, efforts were made to identify putative genes within QTL regions. The previously identified three QTLs for drought tolerance were selected between marker intervals *viz.,* xbarc 48 – xbarc 101(QTL1), xbarc 271 – Xgwm337 (QTL2) and Gdm 132 – cfd 42 (QTL3). *In silico* analysis of candidate genes from QTL regions was done, using gene finding algorithms such as FGENESH, GENESCAN and AUGUSTUS. Large numbers of genes were predicted for all three QTLs, which were quarried against *Arabidopsis thaliana* and maize genome in order to find high similarity between the sequences. Finally, three common predicated genes for QTL1 and QTL 2, and five predicted genes for QTL 3 were selected after comparison with FGENESH, GENESCAN, AUGUSTUS, *Arabidopsis,* maize and Genebank data. The selected genes' function was found out using the BLASTx annotation and the gene or protein was queried based upon Query coverage and E value. The identified candidate genes in all three QTLs were mostly governing their function in one or more stress conditions. Primer were designed using primer 3 plus an online primer designing software to validate the identified candidate genes' using qRT-PCR.