IDT9-087 | Haplotype for drought responsive genes in pigeonpea

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Pigeonpea is a resilient crop which is relatively drought tolerant compared to many other legumes. To understand the molecular mechanisms of this unique feature in pigeonpea, 51 genes were selected using the Hidden Markov Models (HMM). These genes were validated for their expression on parents of mapping populations (ICPL 151, ICPL 8755, and ICPL 227) segregating for drought tolerance. A total of 10 differentially expressed genes that showed ≥2-fold up-regulation in the higher drought tolerant genotypes was identified. Further analysis of the 10 genes revealed that they encode four different classes of proteins. These include plant U-box protein (four genes), universal stress protein A-like protein (four genes), cation/H(+) antiporter protein (one gene) and an uncharacterized protein (one gene). Subsequently, these 10 candidate genes were used for haplotype analysis in whole genome re-sequencing data of 292 lines. As a result, 10 to 56 haplotypes were identified for the selected 10 genes. In order to validate the haplotype results, a defined set of lines is being phenotyped for induced water stress using polyethylene glycol (PEG) at seedling stage along with the non-stressed control seedlings. Phenotyping data together with the haplotype information of the targeted candidate genes will be useful for the identification of superior haplotypes of genes. The lines possessing superior haplotypes of the candidate genes could be used in genomics-assisted breeding programs for development of more drought tolerant lines.

IDT9-088 | Development of transgenic tomato (*Solanum lycoperscicum* L.) by heterologous expression of osmotin-like protein (*OLP*) and chitinase (*Chi11*) genes for salt and drought stress tolerance

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Tomato (*Solanum lycopersicum* L.) is the second most produced and consumed vegetable, next to potato. Pusa early dwarf (PED) variety of tomato is sensitive to salinity and drought which reduces the yield and fruit quality in tomato. In the present study, tomato transgenics were developed with osmotin-like protein (*OLP*) and chitinase (*Chi11*) genes *via in vitro* and *in planta* transformation methods. Transgene integration and transcript levels were confirmed by multiplex PCR, DNA blot, and multiplex reverse transcriptase PCR. Homozygous T_2 transgenics, when evaluated for salt and drought stress, showed enhanced tolerance compared to wild-type plants. Transgenics showed enhanced root biomass under normal conditions. Transformants also displayed higher proline content, K^+, relative water content, chlorophyll fluorescence, total biomass, vascular conductivity, and fruit yield compared to the wild-type plants under stress conditions. Co-immunoprecipitation revealed that Chi11 co-expresses with phosphofructokinase2 (PFK2), which may play a role in enhanced root biomass. qPCR analysis resulted in higher transcript levels of *OLP*, *Chi11,* and *PFK2* in transgenics as compared to the wild-type plants.