

IDT7-053 | Comparative and evolutionary analysis of drought-responsive transcription factor families in maize

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Drought is one of the major factors limiting maize production worldwide. However, maize possesses a variety of physiological and molecular responses at cellular and morphological levels. Transcriptional regulation of gene expression provides a molecular mechanism by which plants modulate the developmental processes and respond to water stress. The regulation is mediated by various transcription factors through recognizing specific DNA motifs in regulatory elements of genes. A comparative analysis of all the drought-responsive transcription factors gives an insight into drought tolerance mechanism in maize, which could be effectively utilized in breeding drought-tolerant maize cultivars. In the present investigation, thousands of genes falling under 15 drought-responsive TF-families of maize were structurally and functionally characterized. The major drought related functions of the selected genes were ABA signaling,

ROS scavenging, photosynthesis and stomatal development. The evolutionary studies identified several duplication events, including tandem duplications, block duplications and paralogs in the genome. Among several *cis*-regulatory elements identified in TF families, a few were found to be common across all the drought-responsive TFs. These elements are the key determinants in the temporal and spatial expression of TFs in maize. Intron analysis of the genes revealed that the 72% of genes were intron-rich. Expression analysis showed maximum differentially-expressed TFs in roots and leaves. Additionally, TFs interaction analysis identified several intra and inter interactions in imparting drought tolerance in maize. The information generated from the study will be useful for customizing TFs for enhanced drought tolerance through marker assisted selection and genome-editing approaches.

IDT7-054 | Utilizing genomic resources for understanding the stay-green QTLs interactions in Sorghum

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Sorghum [*Sorghum bicolor* (L.) Moench] is a fifth most important cereal crop in the world providing food, fodder/forage and bio-fuel. The post-rainy sorghum crop in India is grown on residual moisture and inadvertently faces terminal drought. "Stay-green" (delayed senescence) is a post-flowering drought tolerance response, which help plants to maintain photosynthetically active leaf area and continue to fill their grains normally under stress.

Sorghum crop is referred to express functional type of stay-green and the trait has been mapped to six major QTLs viz., Stg1, Stg2, Stg3A, Stg3B, StgC and Stg4. However, the gap in understanding the key mechanism has not been deciphered clearly. In this scenario to understand the actual mechanism of the stay-green pathway the information from different crops on candidate genes responsible for stay-green phenotype

were considered viz., STAY-GREEN (SGR) along with one or two homologous (SGR1or NYE1/SGRL); Pheophytin Pheophorbide Hydrolase (PPH); Pheophorbide a Oxygenase (PAO); Red Chlorophyll Catabolite Reductase (RCCR); Non-Yellow Coloring (NYC) and it's homologous NYC1-Like (NOL); 7-Hydroxymethyl Chlorophyll a Reductase (HCAR) from *Zea mays*, *Arabidopsis thaliana* and *Orzya sativa*. Apart from these, senescence associated genes SAG2, SAG102 and SAG39 were also considered from *Arabidopsis thaliana* and *Orzya sativa* respectively. The sequence and functional/annotation information for these genes retrieved for sequence similarity search and it has revealed 45 to 88 % of similarity in sorghum. The mapping of these candidate gene sequences within the defined QTL regions contributing for Stay-green has given an insight to utilize the re-sequencing data for improved drought tolerance in sorghum.