

IDT9-097 | Identification of genes and genomic segments for cleistogamy in Pigeonpea (*Cajanus cajan* L.)

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Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the major grain legume crops of the world predominantly grown in semi-arid tropics and sub-tropical regions. Pigeonpea has open or semi-cleistogamous flowers that promote natural out crossing. However, its open pollination behavior causes genetic deterioration in purity of seeds in varieties. In this direction introgression of cleistogamy or self-pollination behavior in pure line varieties can be a genetic tool to maintain purity of elite lines. In pigeonpea a mutant line ICPL 99050 has been identified as a cleistogamous line. However the cleistogamy has been found to link with shriveled seeds which further hampered the breeding efforts. Therefore, efforts have been initiated to identify the molecular

markers/genes/genomic segments associated with cleistogamy and possibly to break its linkage with shriveled seeds. As the first step a recombinant inbred line (RIL) population has been developed from the crossing parents ICPL 99010 (cleisto flowers) and ICP 5529 (open flowers). RILs are being subjected to high density genotyping using 50k SNP array. In parallel RILs are being phenotyped for the cleistogamy and shriveled seeds. Trait phenotyping data together with SNP genotyping data will be used for the identification of genes and genomic segment associated with the target traits. Identified genes/genomic segments for cleistogamy/ shriveled seeds will help in selection of lines with self-pollinating behavior and acceptable seed size.

IDT9-098 | Expression studies of transcription factors under moisture stress in Cotton (*Gossypium hirsutum* L.)

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Cotton (*Gossypium hirsutum* L.) is an important commercial crop playing a significant role in Indian farming and industrial economy. The adverse environmental conditions are the major factors that reduce crop productivity worldwide. The whole process of plant adaptation to the environmental stresses is controlled by orchestration of complex molecular networks. Transcription factors are master-control proteins in all living cells. They often exhibit sequence specific DNA binding and are capable of activating or repressing transcription of multiple target genes. In the present study, six transcription factor genes **viz.**, WRKY 19, LIM, NAC, GeBP, WRKY 70 and C₂H₂,

showing significant difference of expression on exposure to artificial moisture stress in cotton, were selected. The moisture stress was induced by withholding water from 45 DAS. Expression analyses of transcription factor (TF) genes in 27 cotton genotypes were carried out using qRT-PCR. The relative expression profiles of all the six TF genes revealed that, all the TF genes were significantly up-regulated in genotype 5433 A2 A03 N83 (G₁₆) which is known to be drought tolerant from the survey report of the All India Coordinated Cotton Improvement Project (AICCIP). Present study reports the relevance of selected TF genes in drought tolerance.