



## Breeding Approaches for Drought Resistance in Cotton

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Cotton (*Gossypium* spp.), ( $2n=2x=26$ ,  $4x=52$ ) belongs to the family *Malvaceae* and tribe *Gossypieae*. It includes about fifty species, out of which four species are cultivated and forty-six species are in wild forms. It is native to the tropical and subtropical regions from both the Old and New world. Cotton is the most preferred natural fibre in the world and plays a major role in the economy of agriculture and industry. Among the four cultivated species *G. hirsutum* and *G. barbadense* are grown for world cotton fiber production in modern days and diploid cotton species *G. herbaceum* and *G. arboreum* are known for its inherent ability to sustain biotic and abiotic stresses.

### Drought

Drought is one of the major significant environment stress in agriculture worldwide threatening the sustainability of agriculture, limiting plant growth and crop productivity around the world. Improving yield under drought stress is major goal of plant breeding. The main effect of drought in plants is the reduction of vegetative growth. Even though cotton originates from arid and semi-arid regions of the tropics and sub-tropics, it is not identified as a drought tolerant crop. It is known that improving yield and maintaining yield stability of cotton crop under normal as well as drought condition is essential for the global population.

### Mechanism of Drought Resistance

- Drought Escape: Drought susceptible variety performs well under drought environment simply by avoiding the drought period.
- Drought Avoidance: Ability of plants to maintain favourable internal water balance under moisture stress. (1) Reduced Transpiration (2) Increased Water Uptake
- Drought Tolerance: Ability of crop plants to withstand at low tissue water content.
- Drought Resistance: It refers to survival of plant under water deficit or scarcity condition without injury.

### Important traits related to drought

- **Morphological traits:** Earliness, Stomatal characters, Leaf characters, Root characters and Growth habit.
- **Physiological traits:** Higher rate of photosynthesis, Lower rate of transpiration, Higher leaf turgidity, Higher osmotic concentration
- **Biochemical traits:** Proline content, Glycine betaine content

### Methods for drought resistant

1. **Conventional methods:** Introduction, Mass selection, Pureline selection, Pedigree method, Backcross method and Mutation breeding.
2. **Non conventional methods:** Genetic engineering, Tissue culture

## Case Study

**Case study 1:** Anonymous (2013) Seventeen genotypes of *G. hirsutum* were evaluated under water stress (rainfed) and normal condition. The plant height, stomatal conductance, relative water content, transpiration rate, number of bolls, biomass, boll weight and yield were declined under water stress. Genotypes ARBH-2004, LRA-5166, H-1454/12, CA-105 and HAG-805 showed tolerance as they attained higher yield stability with least drought susceptibility index. A correlation was worked out between yield under rainfed and various screening indices. PHSI DMSI, YSI and S were significantly correlated with each other.

Seventeen genotypes (*G.hirsutum*) were grown under rainfed as well as irrigated conditions and the leaf samples were analysed for various biochemical parameters. Free amino acid and proline content were higher in the leaf under rainfed condition as compared to irrigated condition except few genotypes while reducing sugar and protein declined under rainfed condition. Genotypes ARBH-2004, LRA-5166, H-1454/12, CA-105 and HAG-805 showed tolerance as they attained higher yield stability with least drought susceptibility index.

**Case study 2:** Chen *et al.* (2013) investigated molecular mechanism of cotton drought resistance by employing RNA-Sequencing technology to identify differentially expressed genes (DEG) in the leaves of two different cultivars (drought resistant cultivar “J-13” and drought sensitive cultivar “Lu-6”) of cotton. The results indicated that all the unigenes differentially expressed in drought resistant sample and drought sensitive control wherein the number of DEG was increased along with prolonged drought treatment. DEG analysis showed that the normal biophysical profiles of cultivar J-13 were affected by drought stress and some cellular metabolic processes including photosynthesis were inhibited in cotton under drought conditions. Furthermore, the experimental data revealed that there were significant differences in expression levels of the genes related to abscisic acid signaling, ethylene signaling and jasmonic acid signaling pathways between cultivar J-13 and Lu-6, implying that these signaling pathways may participate in cotton response and tolerance to drought stress.

**Case study 3:** Saleem *et al.* (2015) crossed a drought tolerant (B-557) and a drought susceptible (FH-1000) to develop F<sub>2</sub> population. The parents and the F<sub>2</sub> population were studied under osmotic stress in hydroponic culture. A survey of 524 SSR and EST-SSR primers revealed a lot of DNA polymorphism between the drought resistant and drought susceptible cultivar. Two QTLs for relative water content were identified. One QTL was mapped on chromosome 23 with nearest marker NAU2954 and another QTL was mapped on chromosome 12 with nearest marker NAU2715. One QTL for excised leaf water loss was found on chromosome 23 with nearest marker NAU2954.

**Case study 4:** Guo *et al.* (2017) studied that plant specific NAC proteins comprise one of the largest transcription factor families in plants and play important roles in plant development and the stress response. In this study, the NAC domain gene GhNAC79 was functionally characterized in detail. GhNAC79 was located on scaffold 42.1, containing three exons and two introns. GhNAC79 was a transcription activator, and its activation domain was located at its C-terminus. The results of qRT-PCR proved that GhNAC79 was preferentially expressed at later stages of cotyledon and fiber development, and it showed high sensitivity to ethylene and meJA treatments. Overexpression of GhNAC79 resulted in the improving drought tolerance in cotton. Furthermore, VIGS-induced silencing of GhNAC79 in cotton led to a drought sensitive phenotype.

## Conclusions

- Biochemical, physiological changes and structural modifications occur in resistant plants which are responsible for drought resistance.
- Wild species and land races especially of Asiatic cottons are good sources of drought resistance.
- Effectiveness of resistant breeding program depends on the availability of efficient screening procedures, identification of adequate sources of resistance and knowledge of inheritance of resistance.
- Overexpression of gene like GhNAC79 responsible for drought tolerance.

## Future Thrust

- Drought is a complex trait. However rapid advances in the omics technologies will make it possible to use a system biology approach to understand cotton plant response.
- Molecular techniques were mostly studied under greenhouse or tested in the field under artificial water-deficit conditions at a smaller scale. Thus, for improvement of drought tolerance it could be studied in more realistic environment.
- Application of CRISPR/Cas9 in cotton genome editing will be useful for inducing drought tolerance.
- Molecular markers have significant value in future cotton genetic-breeding. Specific chromosome regions with important QTLs can be identified and utilized for efficient selection of drought tolerant traits.

## References

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