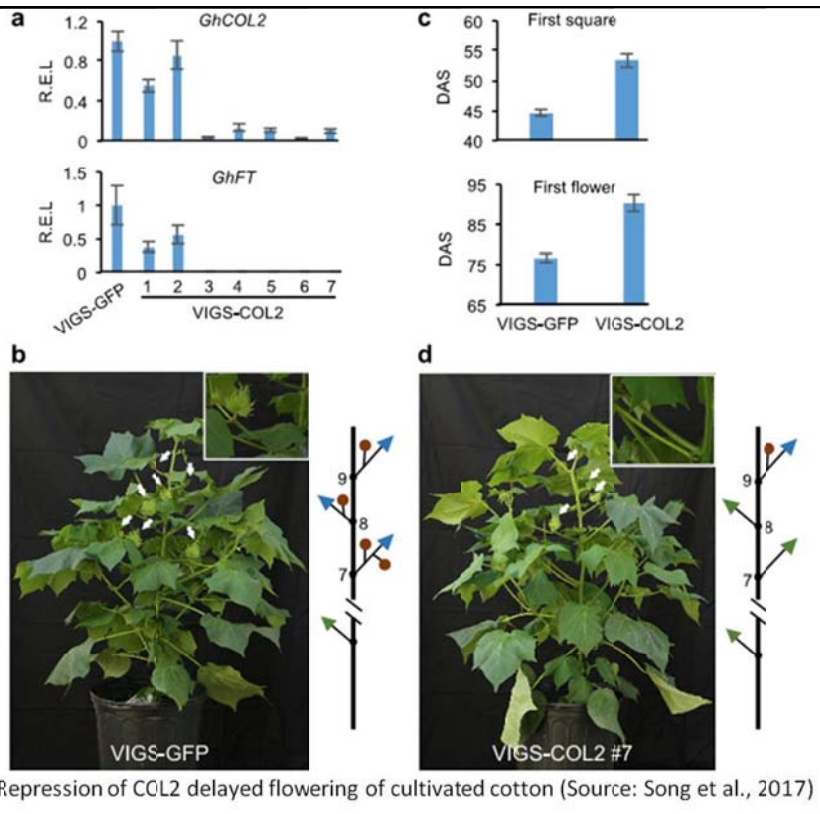
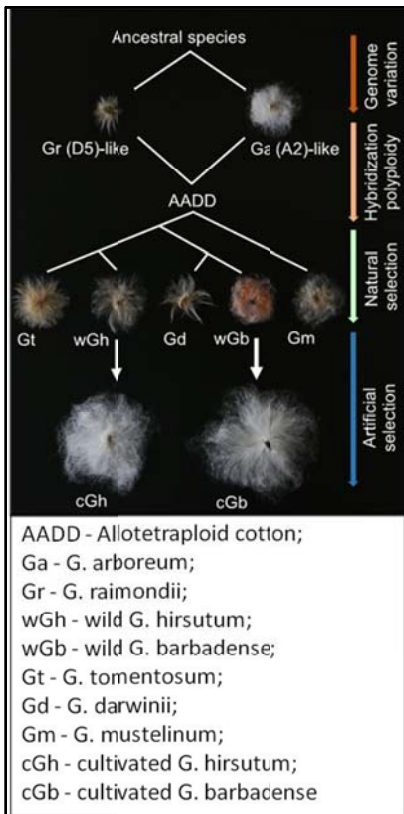




Epi-Genetically Modified (EGM) Cotton

- H. B. Santosh and J. Annie Sheeba

Most of the characters in living organisms are governed by genes, a stretch of DNA code with four alphabets viz., A (adenine), T (thymine), G (guanine) and C (cytosine). Of late, scientists have discovered that there are processes outside the DNA that determine or influence the expression of character on spatial and temporal basis which are collectively called as 'Epigenetics'. Epigenetics unravels the possibility of entirely new methods of breeding plants and animals. Plant breeders thus can develop new varieties without altering the genes or nucleotide sequence. Methylation of DNA is one of the important epigenetic processes in living organisms. DNA methylation is a process by which methyl groups are added to the DNA molecule. Methylation can change the activity of a DNA segment without changing the sequence.



A team of researchers led by Z. Jeffrey Chen at The University of Texas, USA and Nanjing Agricultural University, China have taken the first step toward a novel way of breeding cotton through epigenetic modification. In their latest study published in the journal *Genome Biology*, these researchers have identified genes that are epigenetically modified between wild and domesticated cotton. Many of these are known to be related

to traits of agronomic importance like yield, quality and stress tolerance. One important finding of this study is that the change that provided capacity to cotton plant to adapt to different conditions across the world from earlier adapted tropics has epigenetic basis. They studied domesticated allotetraploid cottons and their tetraploid and diploid relatives to comprehensively analyse the epigenomic variation. They found evolution is faster for methylated genes compared to unmethylated genes. DNA methylation changes can produce meiotically stable epialleles, which are transmissible through selection and breeding. The genes like CONSTANS (CO) and CO-LIKE (COL) are known to regulate response

of flowering to daylight in Arabidopsis. They have studied COL2 gene which is an epiallele in allotetraploid cottons. They observed that COL2A is hypermethylated and silenced, while COL2D is repressed in wild cottons but highly expressed due to methylation loss in all domesticated cottons they tested. Inhibition of DNA methylation activates COL2 expression and repression of COL2 expression in cultivated cotton delays flowering. The present study discovers epigenomic signatures of domestication traits during cotton evolution. The suitability of cotton for worldwide cultivation could have been contributed by the demethylation of COL2 which increases its expression, inducing photoperiodic flowering.

The present study provides insights into 'methylome' - a list of genes and genetic elements that have been switched on or off through a natural process called DNA methylation in cotton. This understanding can supplement the process of genetic breeding and cotton improvement. Authors opine that modern breeders can modify gene methylation with chemicals or through modified gene-editing technologies such as CRISPR/Cas9 and enabling them make targeted changes to a plant's epigenome and create new cotton cultivars with improved traits.

Suggested readings:

- Song Q, Zhang T, Stelly DM and Chen ZJ (2017). Epigenomic and functional analyses reveal roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons. *Genome Biology*, 18(1). DOI: 10.1186/s13059-017-1229-8.
- Paterson AH, Wendel JF, Gundlach H, Guo H, Jenkins J, Jin D, Llewellyn D, Showmaker KC, Shu S, Udall J, et al. (2012) Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibres. *Nature*, 492: 423–427.
- Quadrana L and Colot V (2016) Plant Transgenerational Epigenetics. *Annual Review of Genetics*, 50: 467–491.

Meetings attended

Dr D. Monga Head, CICR, Regional Station, Sirsa and Dr Rishi Kumar, Principal Scientist (Entomology) attended the meeting on whitefly management held at KVK, Sirsa under the chairmanship of Dr S. S. Sethi, Director of Research, CCSHAU Hisar and Dr S. S. Siwach, Principal Scientist (Cotton) on 13.09.2017. Dr K.K. Dahiya, Principal Scientist Entomology, Dr. Omender Sangwan, Cotton Breeder and Deputy Director of Agriculture of Cotton Growing Districts of Haryana attended the meeting. The meeting was attended by DDAs from all the cotton growing districts. Dr. Rishi Kumar presented the survey and surveillance report of entire zone with respect to whitefly. Dr. Monga presented a scenario of CLCuD of the zone in the meeting. The queries regarding whitefly and CLCuD were addressed by them.



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