Master genes in cotton fiber development

Cotton fibers are seed trichomes, which are single celled and arose from the epidermal layers of ovules. Fibre formation in cotton has divided into four distinct stages viz; fibre initiation, elongation, secondary cell wall accumulation and maturation. In fiber initiation stage up to 15-25% of epidermal cells of cotton ovules are differentiated into lint fibers which generally occurs between 0 to 1 DPA, then these fibre initials are begin to elongate until 5-20 DPA by diffusion growth mechanism followed by it secondary cell wall accumulation will take place with cellulose. Whereas, primary cell wall accumulation will done with variety of carbohydrate polymers in the elongation phase. This secondary cell wall biosynthesis will last up to 40-45 DPA, then the bolls will turn to open and maturation of lint fibre will take place by exposing to air (Seagull et al. 2000; Lee et al. 2007).

Despite knowing clear cut physiology of cotton fiber development there was not much improvement in fiber development with respect to yield and quality. Therefore, one should clearly understand the molecular mechanism underlying the process of fiber development and investigate master regulatory genes involved in fiber development will certainly helps to improve the yield and quality of fiber through breeding or genetic engineering technology. In view of this several researchers has worked extensively to find out the specific genes involved in the fiber initiation, elongation process through advanced molecular techniques. Based on the cDNA microarray technology, wu et al. (2006) identified 11 genes which are differentially expressed between fiber and fiberless mutant ovules in the early phases of fiber initiation out of 10, 000 cDNA microarrays. Among these 11 differentially expressed genes, regulatory genes like *GhMyb* 25, *GhHD* 1

and *GhCycD* 3 and structural genes like expansions, sucrose synthase, transporter genes, and fatty acid elongase genes were identified. Yang et al. (2006) also reported regulatory genes like *WRKY* and *MYB* transcription factors along with genes of auxin, brasinosteroid, GA3, ABA, ethylene signaling pathways during fiber cell initiation in wild type ovules compared to N1N1 mutants of the same genotype. Lee et al. (2006) also analyzed gene expression analysis using spotted oligo gene microarray technology between the TM 1 and its naked seed mutant lines (N1N1) and identified ~23 differentially expressed genes which were again regulatory and structural genes involved in early stage of fiber development.

In all these experiments transcription factors like *HD* and *MYBs* are well noticed and functions of these genes were already well determined in leaf trichome development of *Arabidopsis thaliana* and therefore these genes might be has the same role in seed trichome development of cotton. Furthermore, role of different phytohormones were well determined in *in vitro* development of lint fibers from ovules are agreeable with the results of cDNA microarray analysis data of Yang et al. (2006). Moreover, functions of many of these reported genes were not known but some of the important regulatory and structural genes were functionally characterized either by over expressing or silencing in model crops as well as in cotton crop. For example over expression of potato sucrose synthase (*Sus*) under S7 viral promoter resulted in an average 18% increase of seed number, 22% increases of fiber weight and 20-33% increase of fiber length per boll has reported compared to null plants by Xu et al. (2012). In the similar way Haigler et al. (2007); Jiang et al. (2012) also proved in the improvement of

fiber quality and yield in terms of micronaire, maturity ration and fiber length compared to wild types by over expression of spinach sucrose phosphate synthase (*Sps*) gene and *GhSusA1* gene respectively. Further Ruan et al. (2003) was reported repression of fiber initiation, elongation and seed development by suppression of sucrose synthase gene, which clearly indicates the key role of sucrose synthase related genes in the fiber development especially in the initiation and cell wall depositions. Apart from the structural genes regulatory genes like *MYBs* were also functionally characterized. In cotton more than 200 *MYBs* are reported, among them *GhMYB* 25 a homologue of *Am MIXTA* was functionally characterized by developing over expressed and silenced lines of the *GhMYB* 25 (Machado et al. 2009). They reported the crucial role of *GhMYB* 25 in trichome development in various organs including ovules of cotton especially in the time of cell expansion and elongation stages.

An increased 15-35% number of fiber initials were observed relative to wild types in over expressed lines, where as 10-20% lesser fiber initials were reported in silenced lines which ultimately results in short mature fiber. Similarly *R2R3 MYB* gene *GhMYB* 109 function was evaluated in cotton by suppressing native gene through RNAi technology, the silenced lines showed reduced bolls with short fibers having ~2. 3 cm in length compared to ~3. 4 cm length of wild types. Further they also examined the regulatory effect of this transcription factor on other key genes involved in fiber development through RT PCR and found that substantial decrease in expressions of phytohormonal genes like *GhACO* 1, *GhACO* 2 and cytoskeletal genes like *GhACT* 1, *GhTUB* 1. Similarly improved fibre quality was reported through

RNAi approach also by Ibrokhim et al. (2014). Furthermore, over expression of a steroidal gene *GhDET* 2 lead to increase in fiber number by 22. 6% and fiber length by 10. 7% in T_2 generation over the controls. Apart from genes involved in fiber initiation, the genes which are involved in fiber elongation were also functionally characterized in cotton such as *GhTUB* 1 (Li et al. 2002), *GhACT* 1 (Li et al. 2005) and xyloglucan endotransglycosylase/hydrolase (Lee et al. 2010). Recently Zhang et al. (2011) reported an increase of > 15% of lint yield after conducting three years of field experiments in transgenic cotton expressing *iaaM* gene a IAA biosynthetic gene. Apart from the plant origin genes, transgenic cotton was also reported with animal origin genes for fiber development with *acsA* and *acsB* genes of *A. xylinum* (Li et al. 2004) and silk warm fibroin gene (*fbn*) with increased fiber length and strength by ~28% and ~18%, respectively (Li et al. 2009).

To summarize, there is a much scope to find out master genes involved in cotton fiber development and functional characterization of already known differentially expressed genes especially the roles transcription factors how they are regulating other network of genes and whether this regulation is directly or indirectly influence the cotton fiber development. Further, the reported cotton transgenics has to undergone the critical quality and yield evaluations under field conditions, because most of the times the transgenics plants developed for fiber yield might be associated with trichome development in other parts or throughout plant which may not be accepted by farmers some times and also to translate the benefits of transgenics to the farmers. In addition to these, reports are also available for

cotton seed oil improvement by reducing gossypol a hepato toxic terpinoid compound (Sunilkumar et al. 2006). Apart from insect,