

Cotton fibers: Attributes of specialized cells and factors affecting them

Jehanzeb Farooq¹, Amjad Farooq¹, Muhammad Rizwan¹, I. Valentin Petrescu-Mag^{2,3}, Muhammad Amjad Ali⁴, Khalid Mahmood¹, Asia Batool⁵

¹Cotton Research Institute, AARI, Faisalabad, Pakistan;

²University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Romania;

³University of Oradea, Oradea, Romania;

⁴Department of Plant Pathology & Centre of Agricultural Biochemistry and Biotechnology, University of Agriculture 38040, Faisalabad, Pakistan;

⁵Assistant Plant Pathologist, Pulses Research Institute, Faisalabad, Pakistan.

Corresponding author: J. Farooq, drjehanzeb.pbg@gmail.com

Abstract. Micro and macro environmental factors influence the genetics and physiology of plants during production season which creates the difficulties among the empirical evaluation of plant characters. Fiber quality of cotton is greatly influenced by temperature that seems to be the main barrier in early stages of fiber development whether the crop is sown early or late. Cotton fiber developments comprises four distinct discrete overlapping stages i.e. initiation, elongation, secondary cell wall deposition (SCWD) and maturation/dehydration which are accomplished in -3 to 50 days post anthesis (dpa). The fiber cell, internally occupied a large central vacuole (lumen), is progressively filled with cellulose deposited inside the primary cell wall (PCW) and secondary cell wall. Growth mechanism (diffuse versus tip) for rapid final elongation of cotton fiber is still debatable and no genes are still known to be specific for tip-growing cell types. Plant hormones including GAs (Gibberellic acid), Ethylene, Brassinosteroids (BRs), Auxin are also involve in fiber growth and development. The optimum use of various nutrients like N, P, and K play an important role in physiological maturity of cotton fiber. Most of the fiber traits are quantitatively controlled by the major and minor genes including their additive effects. The negative correlation is commonly observed between fiber quality and yield of seed cotton. Moreover, the amount of heterosis for fiber traits was usually lower (5-10%) than that for yield and its components as fiber traits are more affected by environmental factors. Various studies have supported simple selection methods to maintain the high heritabilities (h_2 and H_2) and genetic gain for fiber characters. Similarly, recurrent breeding followed by selection within the race population is useful for the accumulation of favorable dominant genes for good fiber quality. Marker-assisted selection and Linkage-Disequilibrium (LD) based association mapping is an alternative molecular strategy to dissect and utilized the natural genetic diversity conserved in cotton germplasm. High fiber quality is vital because its affects various modern textile technologies including dye ability properties, speed spinning methods to increase the textile products quality, yield and performance of machines.

Key Words: Environmental factors, fiber quality, heterosis, linkage.

Introduction / History / Importance in Textile Industry. Cotton belongs to the genus *Gossypium*, which comprises of more than 50 species, however, approximately 90% of valuable fiber is produced by four cultivated species including two Asiatic A-genome diploid species *Gossypium arboreum* L. and *Gossypium herbaceum* L. ($2n = 26$) and two allotetraploid AD-genome species, *G. hirsutum* L. and *G. barbadense* L. ($2n = 4x = 52$). *G. hirsutum* L. and *G. barbadense* L. are also known as Upland and Island cotton respectively (Farooq et al 2011; Wilkins & Arpat 2005). According to Bradow & Davidonis (2000), the perfect cotton fibers are those which are as white as snow, strong like steel, fine like silk and as elongated as wool. However, it is difficult to integrate these qualities favored by cotton processors into a breeding strategy or to set them as quantitative objectives for cotton producers. Fiber quality can be described as a set of measurable fiber properties (length, fineness strength, uniformity and elongation) that improves the

spinning performance during textile processing (Dutt et al 2004; Ali et al 2008; Shen et al 2011). Cotton fiber is the single cell elongation of the cotton seed (ovule) epidermis that is anatomically classified as a trichome which is composed of almost 89-100% cellulose (Basara & Malik 1984; Ryser 1985; Delmer & Amor 1995; Haigler et al 2005). Nevertheless, only around 30% of fiber primordial (trichome) have the potential of morphogenesis and successfully differentiate into mature fibers producing approximately 20,000 fibers per ovule (Berlin 1986; Tiwari & Wilkins 1995).

Cotton fiber quality is complex interaction of genetics and physiology of plant under prevailing environment during production season (Rehman et al 2007; Ali et al 2008). Different micro environments have shown significant effects on within boll fiber properties on the same plant, same field and same cropping season (Bradow & Davidonis 2000). A complex association among lint yield, fiber strength and fiber length has also been elucidated (Coyle & Smith 1997; Smith & Coyle 1997; Ali et al 2009a).

Cotton fiber quality is becoming an increasingly important aspect in modern textile industry (Ali et al 2008). The higher demand for fiber quality and lint yield started since 1990s' because of modern textile technologies including speed spinning methods are rotors, friction and air jet which require high fiber strength and uniformity (Rowe 1992; Chen 1999; Saha et al 2008), whereas fiber length influence the yarn regularity during spinning process (Rowe 1992). Therefore in order to fulfill the growing demands of modern textile industry there is a dire need to improve fiber quality in the dominating *G. hirsutum* genotypes. Cotton fiber quality is mainly affected by factors like variety, environment, and cultural practices. Along with other factors, cleaning during the ginning process could have a significant impact on certain fiber quality parameters (Li et al 2007). Under-cleaning would not provide clean cotton fiber and could result in price penalization to cotton growers, while over-cleaning would create excessive short fibers and lower fiber uniformity. There must be a balance between the clean cotton and long fiber. Therefore, the understanding of fiber quality parameters is also critical to enable cotton growers to achieve the maximum profit. This review constitutes process of fiber development, influence of various biotic and abiotic factors on various fiber quality parameters, genomic organization in fiber development, genetics of fiber quality traits and recommendations on the improvement of fiber quality.

Fiber Constituents and Developmental Physiology, Anatomy / Shapes. Cotton fibers are the longest single cells in higher plants with 2.5 to 4.0 cm in length in case of mature ovular fibers (Liu et al 2008). Cotton fiber developments contain four distinct overlapping stages, i.e. initiation, elongation, secondary cell wall deposition (SCWD) and maturation/dehydration (Basara & Malik 1984; Wilkins & Jernstedt 1999). **Initiation** (stage 1) of lint begins around the time of anthesis (-3 to 3 dpa) whereas shorter fuzz fiber starts initiation approximately a week later (Stewart 1975; Turley & Kloth 2008; Tiwari & Wilkins 1995). In **elongation** (stage 2, 0 to ~25 dpa) cell demonstrate high accentuate polarized expansion with peak growth rates of >2mm/day from ~10 to 12 dpa until fiber attains the final length (John & Keller 1996; Smart et al 1998). **Secondary cell wall biogenesis** (stage 3, ~21 to 45 dpa) exhibits massive deposition of pure cellulose for the thickness of secondary cell wall (SCW). Finally, **maturation/dehydration** (stage 4) completes in 45 to 50 dpa with the accumulation of minerals and simultaneous decrease in water potential, resulting into a mature cotton fiber (John & Keller 1996).

Fiber maturity is affected by secondary cell wall thickness followed by cellulose deposition which improves the dyeing ability of cotton fiber and results in immense economic consequences (Goynes et al 1996). Non-dyeing fibers may be immature or abnormally developed on "motes" which are developmentally arrested seed (Rea 1928; Pearson 1949). Motes further divided into short-fiber motes and long fiber motes (Davidonis et al 1996). The length of motes do not affect the dyeability, however, long fiber motes are enough to gin. But they are still thin walled and develop into neps during textile processing and result into poor colouring of the fabrics (Smith 1991). Variation in secondary fiber wall development was observed and found to be associated with the location of the seed in the locule and position of the fiber on the seed (Iyengar 1941;

Davidonis & Hinojosa 1994). The cell wall thickness of fibers on single normal seed, medium seed and mote resulted from chalazal seed fiber may result in imperfection (Weis et al 1999). This advocates that fiber initiation is not dependent on fully normal, pollinated or fertilized ovule, it begins 2-3 days before elongation and secondary wall deposition may be (Berlin 1986). The secondary wall thickness of cotton fiber is the main component of fiber development and maturity which is governed by the deposition of cellulose. Cellulose deposition may be 3-6 μm around the circumference up to approximately 20 μm diameter of fiber (Haigler et al 2005). The fiber internally occupies a large central vacuole (lumen) which is progressively filled by cellulose deposition inside the primary wall (Goynes et al 1995). This is why PCW and SCW are markedly different in term of structure and composition (Carpita & Gibeau 1993). In cotton fibers, a thin (0.2–0.4 μm) PCW deposited during fiber elongation contains <30% cellulose, whereas the thick (8–10 μm) SCW is composed of >94% cellulose, no lignin and few proteins (Meinert & Delmer 1977). The elongation of cotton fiber is completed in almost 3 weeks (15-20 dpa) and massive increase of cellulose contents in secondary wall occurs during this period (Dutt et al 2004; Basara & Malik 1984; Haigler et al 2005).

The growth mechanism for rapid elongation of cotton fiber (diffuse versus tip) is hotly debated for decades (Seagull 1990; Wilkins & Jernstedt 1999); however the structural and physiological data provide the compelling evidence in support of diffuse growth (Tiwari & Wilkins 1995). In diffuse growth mechanism, numerous vesicles are formed which are bearing cellulose into extracellular matrix along the length of fiber preferentially in tip region during the final days of elongation (Wilkins & Arpat 2005). To the date, there is no existence of genetic evidence specifically for tip-growing cell types, supporting this mechanism during rapid polar elongation. Similarly no existing evidences support these contentions that fiber is supposed to be switched from a diffuse to a tip-growth mechanism (Wilkins & Arpat 2005).

Several research results showed that the plant hormones also are involved in fiber growth and development (Beasley & Ting 1973; Seagull & Giavalis 2004; Sun et al 2004, 2005; Shi et al 2006; Luo et al 2007; Yu et al 2011). Fiber cell elongation is collectively affected by GA, Ethylene and Brassinosteroids. However, fiber differentiation and initiation are affected by auxin production in the plant.

Genomics and Transcriptomics of Cotton Fiber and its Development. The high magnitude of genetic complexity is found in cotton fiber. Around 45-50% of the total cotton genes are expressed in cotton fiber in both diploid and tetraploid species (Wilkins & Arpat 2005). Xu et al (2008) investigated genes distribution in upland cotton (*Gossypium hirsutum* L.) genome for fiber discrete developmental stages and found the gene-rich islands/clusters based on expression profiles. Their results revealed 10 fiber gene-rich islands. Out of these, 3 fiber gene-rich islands were found to be associated with fiber initiation on chromosomes 5 while 3 islands were related with the early to middle elongation stage on chromosome 10. Similarly, 3 islands were involved in the middle to late elongation stage on chromosome 14 and 1 island on chromosome 14 and 15 was functional in primary to secondary cell wall deposition. On the other hand Wilkins & Arpat (2005) found about two major groups of gene-rich islands which contribute towards fiber development. Domestication of cotton has resulted in significant changes in the gene expression. Recently, Rapp et al (2010) have demonstrated that the expression profiles of genes involved in fiber development have been massively alter by domestication of upland cotton.

Cotton fiber cytoskeleton is also regulated by the presence of tubulin isotypes that govern the level and type of tubulins which are stage-specific along with gene-rich islands on chromosomes 5, 10 and 14, whereas chromosomes 5 and 10 bear 20 genes which are differentially expressed in early elongation and primary cell wall synthesis (Wilkins & Jernstedt 1999; Dixon et al 1994). Liu et al (2008) observed four genes, *GhAGP2*, *GhAGP3*, *GhAGP4* and *GhFLA1* and their product Arabinogalactan proteins (AGPs) which play an important role in fiber development. *GhAGP2* and *GhFLA1* are highly expressed in *G. hirsutum* fiber from 5 to 20 dpa whereas, *GhAGP3* and *GhAGP4* are abundantly present during the stage elongation to secondary cell wall synthesis.

Furthermore fasciclin-like AGP gene expressed not only in *G. hirsutum* fiber also exists in *Gossypium barbadense* fiber. *Gh14-3-3L* gene, involved in regulating fiber elongation, is expressed during early fiber development and its expression reached to the peak at 10 dpa (Shi et al 2007). MYBs transcriptomes factors *GhMYB 25-like* was found to be expressed from -3 to +3dpa. High expression levels of this gene was demonstrated in the epidermal layers of cotton ovules before anthesis (-3 dpa), increasing in expression at 0-dpa ovules, and in epidermal cells expanding into fibers and then elongation fiber at +3dpa (Walford et al 2011; Machado et al 2009).

Various genes involved in initiation, elongation and biosynthesis of cell wall can be identified by comparing the wild type and fiber mutant of *G. hirsutum* (Wu & Liu 2005; Wu et al 2006). *CAP* gene coding for Adenylyl cyclase associated protein is highly expressed in fiber development during earlier stages. However, *Sus 1* gene codes for sucrose synthase and is involved in fiber initiation, elongation and secondary wall thickening. Similarly, lipid transfer protein *LTP3* is involved in the synthesis of cutin and formation of primary wall (reviewed by Mansoor & Paterson 2012). Moreover, some genes have specified functions for example expansin gene from upland cotton, *GhExp1* loosen the cell walls of cotton fibers by breaking non-covalent bonds between their compartments (Harmer et al 2002).

At 10 and 25 days post anthesis, variation in expression of gene occurs that are very important in determining the impact on quality of fiber (Chen et al 2012). In the fiber elongation cell wall enzymes and hormones play an important character. The improvement in fiber length has been attained by down regulation of ABA and ethylene and induction of auxin hormone during elongation of fiber (Chen et al 2012). Fiber fineness could be improved by maintaining turgor pressure and extension in secondary cell wall synthesis (Mansoor & Paterson 2012). The specific mechanism involved in signalling of auxin and modification of pectin is directly linked with elongated fiber. Additionally, upregulation of antiauxin-resistant 3 (AAR3) and pectin methylesterase (*PME*) occurs when fiber elongation is driven by elevation in turgor pressure (Chen et al 2012).

Several genes like *SUS*, *EXP1*, *EXP2* and *TUB1* are specifically expressed in cotton fiber and are mainly activated by ethylene synthesis (Shi et al 2006; Chen et al 2011; Chen et al 2012). The main functions of these genes are cytoskeleton rearrangement, loosening of wall and cell wall biosynthesis. Qin et al (2007b) reported that ethylene biosynthesis genes, induced by very long chain fatty acids promote cotton fiber elongation. Ethylene and H_2O_2 act synergistically and modulate development of fiber (Qin et al 2008). Hydrogen peroxide homeostasis is mainly regulated by *GhAPX1* gene. Ethylene accumulation activates H_2O_2 production which in turn, as a result of feedback mechanism, stimulates ethylene production during fiber growth (Li et al 2007; Qin et al 2008). Fibre quality and yield enhanced by brassinosteroid (BR) biosynthesis also (Xiao et al 2010). Interaction of ethylene, BR, GA, H_2O_2 and VLCFAs is a novel molecular mechanism involved in fiber initiation and development (Chen et al 2011; Qin et al 2007a,b; Qin et al 2008).

In early stages of fiber development in cotton genome may be due to stress caused by increased level of H_2O_2 . The optimal quantity of H_2O_2 is essential for expansion of cell wall but toxic for the cell in higher concentration. Some of the genes that regulate ROS and H_2O_2 levels result in the production of spinnable fiber (Havov et al 2008). For instance, three gene identified that regulate the level of H_2O_2 . (1) *GAST1* like gene which was previously induced by H_2O_2 and gibberellin belongs to cysteine rich protein family. Elongation is inhibited when *GAST1* is suppressed whereas upregulation of this gene stimulate H_2O_2 removal (Shi & Olszewski 1998). (2) *Cop1/BONZAI* is Ca^{2+} dependent and belongs to membrane binding protein family and stimulates cell growth by inactivating the stress promoting R genes (Hua et al 2001; Jambunathan et al 2001). (3) Biogenesis of peroxisome is encoded by *Pex1* gene which protects the cell from toxic substances as H_2O_2 (Lopez-Huertas et al 2000).

The main purpose of transcriptomics of cotton fiber is to identify the functional genes that help in the improvement of quality and yield of fiber. However, like several other developmental processes in plants, cotton fiber development is also transcriptionally

regulated. Four types of genes were mainly involved in fiber initiation viz; *GaMYB2*, *GaRDL1*, *GaHOX1* and *GhMYB109* (Wang et al 2004; Shangguan et al 2008; Guan et al 2008; Pu et al 2008). It is actually a regulatory network involved in the transcriptional regulation of fiber development. In *G. hirsutum*, 535 genes were involved in fiber development out of which, 173 were simple sequence repeat (SSR) -containing expressed sequence tags (ESTs) and 103 were transcription factors (Xu 2010).

Similarly, microRNAs (miRNA) are also found to be expressed during fiber development which are could have regulatory functions (Zhang & Pan 2009; Zhang et al 2007). Gou et al (2007) reported that fast growth of fiber cell requires cell wall and plasma membrane biosynthesis along with expansion and loosening mechanism. Transcription factors, Myb109 and Myb2 are expressed in the floral parts 1 day after flowering and extended to elongation fiber stage of cotton (Taliercio & Boykin 2007).

Termination of fiber elongation is accompanied by corresponding decrease in growth rate, transcriptional activities (Kosmidou-Dimitripoulou 1986) and protein complexity (Graves & Stewart 1988). Cross-linking of cellulose microfibrils and non-cellulosic matrices presumably "fix" the structure of the PCW (Wilkins & Jernstedt 1999), resulting in the first significant increase in fiber strength (Hsieh 1999). At 15 dpa cotton fiber enter in transition phase, switch from PCW to SCW synthesis, whereas microtubule (MT) cytoskeleton is responsible for polar elongation. Consequently, microtubule cytoskeleton is aborted by MT inhibitors along with actin cytoskeleton which results in growth hinderance of cotton fiber (Wilkins & Arpat 2005).

Factors Affecting Fiber Quality

Biotic Factors

CLCuD. Cotton leaf curl virus disease not only affect yield but also deteriorate fiber quality traits like ginning turnout percentage, staple length, fiber uniformity index, fiber fineness, fiber bundle strength, maturity ratio. Fiber quality is negative affected due to change in composition of major fiber components including cellulose, protein, wax and pectin (reviewed by Farooq et al 2011; Iqbal & Khan 2010).

Insect pest. One of the limiting factors that contribute in the reduction of fiber quantity and quality is the attack of different insect pests (Khan et al 2009; Shahid et al 2012). Various environmental factors like temperature, relative humidity and precipitation contribute in the incidence and development of various insect pests in cotton. According to Nath et al (2000) American cotton (*G. hirsutum*) is more susceptible to the attack of sucking insect pests.

Abiotic Factors

Fiber quality traits are affected by soil properties such as water content, porosity, aeration, aggregation and fertilization (Bilalis 1999; Rabadia et al 1999; Sawan et al 2001; Gormus 2002). Similarly, environmental factors like temperature, relative humidity and precipitation were also strongly associated with fiber strength and fineness which prevent the full realization of fiber quality potential of cotton genotype (Green & Clup 1990). Mean fiber length of the same cultivars sown in consecutive years is influenced by different weather conditions (Avgoulas et al 2005). The early stages of fiber elongation were highly influenced by the temperature than the late fiber elongation stage (Xie et al 1993). Likewise, lint percentage increased due to low temperature and high light intensity (Roussopoulos et al 1998). Fiber length was shortest at high temperature and light whereas, fiber strength, fineness and maturity ratio was high. However, the finest and the most uniform fibers were produced under high light intensity and low temperature (Rehman et al 2007).

Planting Dates. In planting dates experiments, temperature during different growth stages influenced the fiber length. It was observed that there is little increase in 2.5% and 50% span length in late planting dates (Aguillard et al 1980; Greef & Human 1983). Fiber fineness was decreased significantly due to fiber wall thickening, immature fiber fraction and cross-sectional area in four upland cotton cultivars (Porter et al 1996;

Bradow et al 1997). Rehman et al (2007) reported that fiber length, strength, uniformity, fineness of late planting in June (non-stressed) were high as compared to April (heat-stressed) regime. Similarly, plastic mulching along with seedling transplanting system enhanced the plant growth and yield components including lint yield as compared to the use of transplantation only (Dong et al 2007).

Heritable variation controlling fiber traits. Highly significant differences were found under normal agronomic conditions among the tested genotypes for the traits under study including staple length, fiber strength, fiber fineness and fiber uniformity ratio which attribute the presence of dominance effects than the additive ones (Hussain et al 2010). Similarly non-additive gene action was found in upland cotton genotypes for fiber length, strength and fineness (Meredith & Bridge 1972). In contrast, Mingbaao et al (2008) found that fiber length has both additive as well as dominance effect while dominance effect was slightly more than additive effect. Larger additive and absence of dominance effects were observed for uniformity, fineness and fiber strength. However, Ahmad et al (1997) and Iqbal et al (2005) found non-additive type of gene action for fiber quality traits.

A three way interaction (cultivar \times region \times year) for lint yield was studied in North Carolina which demonstrated that fiber quality traits are affected by all these factors with main emphasis on the cultivar (Miller et al 1962). Most of the agronomic and fiber traits are quantitatively controlled by the major and minor effects of the genes (Rong et al 2004; Lacape et al 2005; Ulloa et al 2005; Zhang et al 2005). There were no linkage associations of glandless gene with agronomic traits, fiber and seed characters in upland cotton (Yuan et al 2000). Similarly, dwarf germplasm population had smaller bolls, smaller lint index, lower micronaire and shorter fibers due to the presence of dwarfing genes (Hinze et al 2011).

Genetic analysis of the data also exhibit highly significant effects due to general and specific combining ability (GCA and SCA respectively) for fiber quality characters studied under appropriate field conditions (Hussain et al 2010). Furthermore, Pavasia et al (1999) described GCA and SCA of fiber traits was significantly influenced by environments.

Correlation studies for fiber characters. Positive association between the fiber strength and staple length was found (Avgoulas et al 2005), whereas fiber fineness displayed negative association with staple length and fiber strength (Hussain et al 2010). Malik et al (2009) found the negative correlation between fiber fineness and fiber length and similar to the reports of Lancon et al (1993) and Rehman (2007). The fiber fineness had positive correlation with ginning out-turn (Rehman 2007; Ulloa & Meredith 2002). Moreover, Ying & Jun (2004) and Ulloa (2006) reported that fiber length was positively correlated with fiber strength. Zeng & Meredith (2009) reviewed numerous studies and concluded a negative relationship between yield components and fiber quality specially length and strength. This negative correlation is commonly observed when the breeders aim to accumulate the alleles for maximizing the fiber quality which in turn leads to the reduction in the plant's yield potential.

Heritability of fiber quality traits. The amount of heterosis for fiber traits is usually lower (5-10%) than that for yield and its components (Luckett 1989; Meredith & Brown 1998). Higher environmental interaction with genotypes results in low heritability estimates that can reduce probability of efficient selection (Falconer 1989). The broad sense heritability for fiber traits in high temperature regimes was lower than 10% which indicated the large share of environmental variability in phenotypic expression of traits thus reducing the prospects of favourable selection (Rehman et al 2007). Fiber quality traits (fiber length, fiber fineness and uniformity ratio except fiber strength) exhibited no epistasis with lack of dominance in F_1 and F_2 populations. The inheritance of micronaire due to the prevalence of over dominance increase the value, thus leads towards coarse fiber, so simple selection maintain the fineness, high heritabilities (h_2 and H_2) and genetic gain in F_2 hybrids were also encouraging (Khan et al 2009; Verhalen et al 1971; Khan 2003; Verhalen & Murray 1969; McCarty et al 2004; Wu et al 2006; Aguiar et al 2007; Tang et al 1993; McCarty et al 1996; Tang et al 1996; Hussain et al 1998; Yingxin & Xiangming 1998; Ali et al 2009a,b).

Constraints in Improvement of Fiber Quality

- Despite of economic importance, the available cotton cultivars have narrow genetic base for most of the fiber characters (Bradow & Davidonis 2000; Bowman et al 2003).
- Quality traits being polygenic in inheritance, are highly influenced by the several environmental factors which cause difficulties in breeding for the improvement of these traits (Yuan et al 2005; Ali et al 2009b).
- Lack of high magnitude of additive type of genetic variability, low narrow sense heritability and genotype \times temperature regime interactions created difficulties in improvement of fiber traits through mass and pedigree selection method (Rehman et al 2007).
- Genetic diversity of cultivated cotton is declining due to repeated use of the same elite germplasm as parental material (Van Esbroeck & Bowman 1998).
- The cotton growers only looking for high seed cotton yield, early maturity, disease resistant, etc. while modern spinning mills industry is not interested in these traits rather than fiber properties (Curran 1992).

Prospects for Improvement

- Germplasm of *Gossypium* is diverse with over 50 species including six tetraploid species which can solve the problem of narrow genetic base via interspecific introgression and development of backcrossed chromosome substitution lines (CS-B) between *G. hirsutum* L. and *G. barbadense* (Saha et al 2008).
- The stability of additive effects for fiber length, fineness and fiber uniformity can be improved through simple selection in segregating generations (Khan et al 2009; McCarty et al 2004).
- Recurrent breeding followed by selection could be useful for accumulating the favorable dominant genes for high fiber quality traits (Rehman et al 2007).
- Selection could be made within the race population to raise lint yields and within the fiber population to increase fiber length (Hinze et al 2011).
- Cotton fiber transcriptome reveals the chances of anchored marker-assisted selection for the genetic improvement of fiber traits and therefore has immediate application in cotton biotechnology (Arpat et al 2004).
- Linkage-Disequilibrium (LD) based association mapping is an alternative molecular tool to dissect and utilized the natural genetic diversity conserved in cotton germplasm which could be a handful to improve fiber quality (Abdurakhmonov et al 2008).

Conclusions. The most important fiber traits, dependent on the shape, size, structure and composition of the fiber cell, are determined during the stage of fiber growth and development. Genetic control of fiber size and shape is governed by the rate and duration of fiber expansion and elongation, which in turn, positively correlates to fiber length. Fiber transcriptome during fiber development at molecular level elucidate the regulatory mechanism of fiber morphogenesis, important fiber properties in response to developmental and environmental signals, for which genetic improvement strategies could be designed.

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Authors:

Jehanzeb Farooq, Cotton Research Institute, AARI, Faisalabad, Pakistan, drjehanzeb.pbg@gmail.com, Tel.92333838263.

Amjad Farooq, Cotton Research Institute, AARI, Faisalabad, Pakistan.

Muhammad Rizwan, Cotton Research Institute, AARI, Faisalabad, Pakistan.

Ioan Valentin Petrescu-Mag, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Faculty of Agriculture, Department of Environment and Plant Protection, 3-5 Calea Manastur Street, Cluj-Napoca, Cluj, Romania.

Muhammad Amjad Ali, Department of Plant Pathology & Centre of Agricultural Biochemistry and Biotechnology, University of Agriculture 38040, Faisalabad, Pakistan.

Khalid Mahmood, Cotton Research Institute, AARI, Faisalabad, Pakistan.

Asia Batool, Assistant Plant Pathologist, Pulses Research Institute, Faisalabad, Pakistan.

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