Available online at www.agrifarming.org

DOI: http://dx.doi.org/10.18782/2582-7146.151

ISSN: 2582 – 7146

Curr. Rese. Agri. Far. (2021) *2*(4), 9-25

Current Research in Agriculture and Farming

Review Article

Peer-Reviewed, Refereed, Open Access Journal

Hormones Performs a Crucial Role in the Regulation of Cotton Fiber Synthesis

Ahtasham Hassan[1], Muhammad Nouman Khalid[2*], Zia Ur Rehman[3], Ifrah Amjad[4], Muhammad Mudasir[5], Zaid Rasheed[6], Urooj Fatima Chaudhry[7]

[1]Department of Plant Breeding and Genetics, University of Haripur, Pakistan

[2,3,4,6,7]Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan

[5]Department of Plant Breeding and Genetics, Bahauddin Zakariya University Multan, Pakistan

*Corresponding Author E-mail: noumankhalidpbg@gmail.com

Received: 11.06.2021 | Revised: 26.07.2021 | Accepted: 13.08.2021

ABSTRACT

Cotton is the world's most important source of renewable fiber, and it is largely utilized in the textile industry to make clothes. In contrast to the ovule epidermis, cotton fibers are single cells that have differentiated from it, making them an attractive model system for the study of polyploidization, production of cell wall and elongation of cell. Plant hormones, that are present in very small low quantities in the plant, play essential roles in a variety of developmental processes, and new research has found that hormones play a critical role in controlling cotton fiber formation, as well as other developmental processes. For example, it has been demonstrated that the exogenous administration of hormones can stimulate the start and development of fiber cells. However, there is currently a lack of a thorough knowledge of phytohormones that regulate the formation of fiber. This paper focuses on latest developments in the understanding of the roles of different phytohormones involved in fiber development, including brassinosteroid, gibberellin, cytokinin, auxin, ethylene and abscisic acid. This paper reviews the discovery of genes associated in hormone biosynthesis and signaling pathways, as well as the methods by which these phytohormones control the commencement and elongation of fiber cells in cotton. All of the hormones involved in fiber formation are beneficial; however, cytokinin and abscisic acid are detrimental. Auxin, gibberellin, brassinosteroid, ethylene, jasmonate, and strigolactones are among the hormones involved in fiber development. A complete analysis of the function of phytohormones in cotton fiber development is our goal.

Keywords: *Fiber elongation, Fiber initiation, Signaling pathway, Gene expression, Phytohormone.*

INTRODUCTION

Gossypium hirsutum known as American cotton is one of the major essential crops, and the fibers generated by this crop are the world's basic raw materials for the textile sector. Naturally growing cotton plants are evergreen woody shrubs but now a day cotton is annual growth crop.

Cite this article: Hassan, A., Khalid, M. N., Zia Ur Rehman, Amjad, I., Mudasir, M., Rasheed, Z., & Chaudhry, U. F. (2021). Hormones Performs a Crucial Role in the Regulation of Cotton Fiber Synthesis, *Curr. Rese. Agri. Far. 2*(4), 9-25. doi: http://dx.doi.org/10.18782/2582-7146.151

Every cotton fiber is an epidermal cell of a single extraordinarily lengthened cotton seed coat. A very difficult process is involved in the differentiation and growth of cotton fiber cells. This process started from origination (initiation), primary wall synthesis (elongation), secondary cell wall formation and maturation are four different and overlapping phases of fiber formation. (Patel et al., 2016).

Fiber length plays a crucial role in determining cotton fiber quality in the worldwide textile sector. The hormonal regulation and molecular mechanism of initiating fiber can be highly effective for staple length and quality enhancement. Multiple hormones can influence a single cell type, and the development and differentiation of various tissues can also be controlled by the single hormone. (Chow & McCourt, 2006). These signaling molecules can target particular transcription factors responsible for gene expression control. Salih et al. (2016) Identified various transcription factors such as leucine zipper, zinc finger, MYB, and described their link with hormones controlling fiber initiation such as ABP and ACO. Similarly, Islam et al. (2016) explained variable expression of genes participated in the assembly of crystal cellulose regulated by RLK and ethylene in the formation of fiber in various cotton lines.

Phytohormones, namely cytokinin, auxin, JA (jasmonic acid), GA (gibberellin acid), ethylene, ABA (abscisic acid), BR (brassinosteroid), SL (strigolactone) and salicylic acid are tiny internal signaling molecules that plants have (Davière & Achard, 2016). Most of these hormones were demonstrated to participate directly in cell enlargement, cell expansion and plant growth. An investigation of internal hormone levels in fibers and bolls and the impact of exogenous hormones in ovules reveals the formation of fiber cells in cotton by phytohormones (Ahmed et al., 2018). While in Arabidopsis scientist has found the signal pathways and receptors of these hormones in the last twenty years, it is still uncertain how the different elements of the phytohormone are involved in signaling pathways which play critical role in the formation of fiber cells. Taking benefits of the entire cotton genomic sequence (Wang et al., 2012; Paterson et al., 2012; Li et al., 2014, 2015a; & Zhang et al., 2015), The research of cotton fiber formation has swiftly evolved and led to more findings on the hormones engaged in fiber cell formation. Below are new experimental findings on the involvement of phytohormones in regulating the growth of cotton fibers.

2.1 DIFFERENT STAGES OF COTTON FIBER DEVELOPMENT

2.1.1 Cotton Fiber Initiation

The 1st stage in cotton fiber morphology is the development of chosen epidermal ovule cells into beginnings or spherical protrusions above the egg surface. Beginning of fiber normally starts on the day of anthesis and proceeds at least five DPA (days to post-anthesis) while each ovule contains roughly sixteen thousand fiber beginnings in current cultivars (including immature lengthening of fibers) (Fig. 1; Stewart, 1975; & Seagull & Giavalis, 2004). With the fiber beginning growing, the central vacuole develops and the nucleus relocates from the base to the center of the forming fiber. In 5 Gossypium hirsutum cultivars, fiber beginning at 0 and 1 DPA were strongly linked with lint index and lint %. (Liao et al., 2009). Human beings chosen for increased density and synchronous fiber initiation while cotton domesticated. (Butterworth et al., 2009). (Ruan et al., 2003) reported that Turgor pressure generation in the central vacuole leads to the extension of the first fibers. In the transgenic cotton, both the commencement of fiber and the elongation of fiber were hindered by the suppression of the SS3 isoform of Sus (sucrose synthase). In comparison to wild-type cotton, plants with a reduced Sus protein generated fewer fibers, which were shortened and crushed easily visible through electron microscopy. The transgenic fibers displayed reduced Sus function, which was linked to decreasing starch and hexose concentrations but not sucrose. Perhaps the lowered hexoses caused a

lower osmotic potential and decreased turgor, but at least some of the fiber defects may have been explained by factors like less UDP glucose generated by Sus to supply the substratum for the synthesis of cell wall (see further debate below) and disruption of hexose-dependent signaling.

2.1.2 Cotton Fiber Elongation

The polar expansion and fast fiber elongation continue from two to twenty DPA after start until the fiber is 2-3 cm long. From 2–3 DPA, elongated fibers twist together and form fiber bundles. (Fig. 1B, C; Singh et al., 2009a; See detailed information about middle lamella cotton fiber below). The GhVIN1 (cotton vacuolar invertase) newly identified appears to have a function during early extension by enhancing turgor control through osmotic. Expression of GhVIN1 and VIN activity peaked 0 to 5 DPA in G. hirsutum fiber, whereas VIN production increased to 10 DPA in G. barbadense fiber, which was also prolonged than in G. hirsutum, and remained at a very high level. (Wang et al., 2010b). Further cellular processes promote the fastest extension of cotton fiber. For instance, enhanced cellulose synthesis associated with plasmodesmata closures on the foot of the fiber between 10-16 DPA. The separation of the fibers from the ovule was proposed in resulting for greater turgor pressure, which in turn made the most rapid elongation of the fibers easier. (Ruan, 2007). Aquaporins, protein membrane that facilitates water passage through biological membranes, can also play a role in the extension of cotton fibers. Aquaporins include GhγTIP1 present in tonoplast while GhPIP1-2 in the cellular membranes (Liu et al., 2008). Both genes have been expressed with fiber elongation at 5-15 DPA and more investigation is required to elucidate the potential involvement of aquaporins in the regulation of turgor-driven extension. Starch existed in the elongating of cotton, and at 10 DPA the genes encoding the sub-units ADP-glucose pyrophosphorylase necessary for starch manufacture were at maximal expression. (Taliercio, 2011). Starch, only contributed ~0.3 percent of dry fiber, which coincides with only uncommon little starch granules seen in TEM (transmission microscope electron) levels in cotton fiber.

2.1.3 Secondary Wall Synthesis

Cotton fiber thickening of the 2ndary wall is caused by the deposition of almost pure cellulose. No additional component has been identified among the cellulose fibrils in the unique 2ndary cotton fiber wall. The proportion of crystalline cellulose was 90% in wild type fiber with a maturity ratio of 0.89, as determined by the fiber cross-sections image analysis. Transgenic fiber with a comparable perimeter of fiber rose to around 92 percent with a maturity ratio increase to 0.95-0.99 (Haigler et al., 2007). After chemical dehydration and extraction of sulfuric acid, 85-90% cellulose was identified for two G. hirsutum genotypes (Abidi et al., 2010b). The crystalline cellulose concentration in the isolated secondary wall may be underestimated by all these because: (a) Fiber weight includes the whole fiber including the cuticle primary wall; and 182 Stiff and Haigler (b) Some less organized cellulose may have dissolved by the acids which employed as extractants. The 2ndary cotton fiber wall probably consists of less than 95 percent cellulose, making it the purest plant-synthesized cellulose. 2ndary wall thickening is characterized by a faster rate of synthesis of cellulose, a larger extension of single cellulose chains and more steep orientation of densely packed cellulose fibrils on the fiber axis (Fig. 1F). The microfibrils of cellulose also change their orientation from helical journeys at intervals, causing "reversals" in the structure of the secondary wall (reviewed in Seagull, 1993).

2.1.4 Fiber Maturation

The signal for an end to the production of secondary wall cellulose is not understood but later the final, undefined fiber maturation stage starts. Late-stage fiber nucleic acid and protein extraction difficulties prevent mechanistic research (Kim & Triplett, 2001). In line with Xylem trachea components, programmed cell death processes, which at least partially regulated by ROS, can also act

during this period. (Kim & Triplett, 2001). The planned processes of cell death involve caspase-like activities, nuclear blabbing, cytoplasmic and DNA degradation. (Love et al., 2008); However, DNA degradation experiments were including for cotton fiber (Roche, 2009). Early after opening, the cotton fiber dries and compresses into the cross-sectional form of the kidney bean, which helps to spin into a yarn, provided the fiber has an ideal maturity ratio. Many seed fibers flow into the bulk of the exposed cotton boll.

2.2 Action and interaction of phytohormones in fiber development

Plants employ many hormone types as signaling molecules to regulate a wide variety of processes, which synchronize their development and growth. The significance of phytohormones as major regulators for the growth of these economically significant fiber cells development was studied through experiment. Prior research has shown that bowl, gibberellins and auxin support the growth of cotton fibers in vitro. EST ovula study identified several supposed plant growth regulators that relate to the majority of auxins, abscisic acids, gibberellic acids and bowl of plant hormones. During different phases of fiber formation, these plant hormones are plentiful role in normal growth.

2.2.1 AUXIN

Throughout many developmental stages, including embryogenesis, vascular differentiation, apical dominance, plant root growth, and reactions to internal and external stimuli, auxin plays a critical role (Xi et al., 2016). Auxin has also been shown to have a key function in the formation of cotton fiber. Exogenous IAA (Indole-3-acetic Acid) may be a feasible alternative for compensating for problems involved in elongation of cotton fiber. (Lakdawala et al., 1977). Exogenous IAA, a major natural auxin, also causes a substantial rise in total fiber volume. Auxin starts to build before blooming, reaches a peak of around 2-3 DPA, and then begins to decrease to a level of 10 DPA, in accordance with its function in fiber synthesis (Chen & Guan, 2011). Furthermore, it was discovered that driving the IAA biosynthetic M a gene that is controlled by the Floral Binding Protein 7 (FBP7) fiber box gene increased the initiation of fiber cells in the epidermis from 2-10 DPA in the ovule epidermis and increased the total quantity of lint fibers, resulting in a 15% upsurge in lint fiber yield. (Zhang et al., 2011). According to this study, the primary source of auxin in fiber cells is not in situ production, but rather originates from outside rather than from within the egg. The polar auxin transporters PIN-FORMED are responsible for transporting auxin from the ovules to the fibroblasts (GhPINs). The main regulator of auxin flow in fiber cells and hormone gradients is GhPIN3a, a protein present in epidermal ovule cells. The expression of the GhPIN3a gene is much higher in external cells from 0 DPA ovules. Many GhPIN genes are suppressed in the ovule, resulting in a substantial decrease in commencement and elongation of fiber cells (Zhang et al., 2016). The expression of the ghPIN8 at GhPIN1a Dt and GhPIN6 at genes is enhanced during fiber initiation and elongation, as well as the length and density of the leaf trichomes, which are fiber cell-like bodies (Zhang et al., 2017a, b). The results should be verified using genetic data. In addition to helping with biosynthesis and transport routes, the auxin signaling system also helps in the formation of cotton fiber cells. The expression of five potential auxin response genes (6 to 12 DPA) is substantially elevated during cell lengthening (Gou et al., 2007). At the start of fiber-cell development, the auxin response factors GhARF18 and GhARF2 are strongly expressed, and over-expression of these two genes substantially accelerates the commencement of trichome formation in Arabidopsis leaf trichomes (Xiao et al., 2018). As a consequence of these findings, GhARF18 and GhARF2 seem to be staters of fiber's cell positive regulators. GhIAA16 has a negative impact on fiber initiation and elongation despite the presence of GhARF2 and GhARF18 are two genes that have been identified (indoleacetic acid induced protein 16). GhIAA16 levels are quite low in wild-type ovules. GhIAA16 transcripts are

best produced early in the blooming cycle in the lint less (fuzz less) mutant, whereas they are best produced later in the blooming cycle in the wild type (Han et al., 2012). Auxin is also needed for the growth of fiber cells to their maximal length, which was found via expression profiling. From 0 to 10 DPA, the expression level of GhABP (auxin binding protein) rises by approximately 59-fold. According to further study results, GhABP was only discovered to be articulated in long fibroblasts, not in villous mutations or unexplained epidermal cells. Based on the findings, it was suggested that GhABP may have a function in the development and extension of cells of cotton fibers, according to these results. While ABP is required for Arabidopsis growth and development, it is unclear what role GhABP has in cotton growth and development. In order to further understand the function of the GhABP gene, over-expression and deletion studies in cotton should be carried out in the future. Rac is a tiny protein that is in charge of translating the auxin signal inside the cell. in 2011; (Wu et al., 2011). So far, a number of Rac genes have been discovered in cotton. GhRac1 is strongly expressed during the elongation of cotton fibers, although it progressively declines when secondary wall development in fiber cell membranes begins (Kim & Triplett, 2004). The most abundantly expressed GhRacA and GhRacB are located in the stems, leaves, roots, and fiber cells throughout the initiation and extension phases, with the least amount found in the remainder of the plant. (Li et al., 2005). GhMAPK, a member of the auxin signal pathway family MAPK, is the most frequently expressed protein in elongated fiber cells (Chen et al., 2001). Auxin was a crucial induction for all Agamous subfamily members and was needed for their existence (Moura et al., 2016). The majority of GhSAUR genes increase their expression levels in response to exogenous IAA treatment (Li et al., 2017). The addition of auxin is essential for the thickening of the fiber wall, which is achieved through the addition of auxin during the cell wall strengthening stage. Due to the activities of the superoxide and IAA oxidase enzymes in the cells, the levels of IAA in secondary wall thickening fibers were four times higher than in late elongation fibers. Auxin may be involved in the regulation of main cell wall growth as well as secondary wall synthesis in plant cells, according to Singh et al. (2009). Injection of a synthetic analogue of auxin, 1-naphthaleneacetic acid (NAA), which was discovered to be auxin-like, in addition to exogenous administration of auxin, revealed that auxin is required for the production of secondary cellulose in the cell wall (Zhang et al., 2011). Auxin is needed at the early stages of cell development and expansion in cotton fiber, according to the facts given above (Figure 1). More study, including overexpression and silencing of particular genes which are involved in auxin production and signaling networks, is required to prove that this finding is correct.

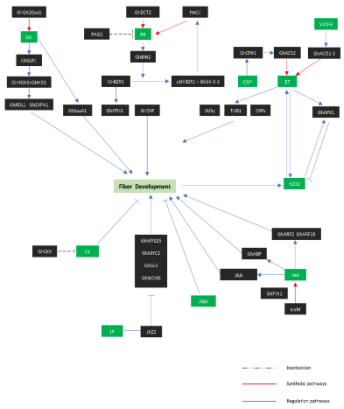

Figure 1: A organized labeled diagram which exhibited phytohormones participation in cotton fiber formation

2.2.2 GIBBERELLIC ACID

GA is a hormone that controls several physiological functions, including seed germination, epidermal hair growth, fruit development, and stem expansion in plants and animals (Huang et al., 2015; & David et al., 2016). In earlier studies, it was discovered that the extracorporeal injection of GA considerably increased the extension of cotton fibers (Kim & Triplett, 2001). In contrast, adding the GA formation inhibitor to the medium of the ovule culture resulted in fewer fibers being formed that were shorter in length compared to the number of fibers produced in the lack of the treatment (Liao et al., 2009). In a study using natural-colored cotton fibers, gibberellic acid was administered throughout the fiber development stage, and the findings revealed an increase in the content of IAA and ABA, as well as improvements in fiber strength, micronaire, and maturity (Zhang et al., 2017a, b). The accumulation of GA in cotton fibers is also linked with the elongation of the fibers. The quantity of GA in the plant increases quickly immediately after flowering, reaching its maximum of 10 DPA fiber cells, and then rapidly declines. (Xiao et al., 2010). While long-staple cotton cultivars have much higher endogenous levels of GA3, a bioactive form of the amino acid Glycine (GA), long-staple cotton cultivars have significantly lower endogenous levels of GA2 (Aleman et al., 2008). A team of researchers discovered that overexpression of the GA 20-oxidase1 gene in transgenic cotton caused the plant to grow longer and produce more fiber. According to the researchers, this greatly increased expression of the GA2 and GA4 bioactive forms and a significant increase in the quantity of both long and fibrous GA fibres were found (Xiao et al., 2010). DELLA proteins play a critical role in promoting GA signaling by blocking transcription factors and regulatory proteins from binding to genes and starting transcription. DELLA proteins are degraded, and essential transcription factors involved in the control of GA-sensitive genes' expression are released as a consequence of GID1 receptor activation (Davière & Achard, 2016). GA has been shown to co-localize with the DELLA proteins GhGID1 and GhSLR1, and this association enables GhGID1 to interact with GhSLR1. GA-responsive genes are greatly activated when GhSLR1 is ectopically expressed in Arabidopsis, and this triggers the growth of dwarf plants and enhances the expression of GA-responsive genes (Aleman et al., 2008; & Dong et al., 2009). Researchers gained a better understanding of the processes via which GA promotes cell elongation as well as the identification of new GA-responsive genes. Combining the GA and EXP genes gives rise to two new genes: the XTH (xyloglucan endotransglucosylase/hydrolase) and cell elongation genes (EXP) (Aleman et al., 2008). GA 20 O-oxidase is expressed in transgenic fibrous cells that are overexpressing GA 20 O-oxidase, and the amount of GA 20 O-oxidase mRNA and the activity of GhSus A1 sucrose synthase are enhanced in those transgenic fibrous cells (Bai et al., 2014). GA (from the environment) has the ability to upregulate GhSusA1 expression in plant fibres and hypocotyls, and this may be of benefit to plant growth (Bai et al., 2014). Cotton cells were discovered to have a higher chance of producing secondary cell wall formation with the help of GA because it controls the expression of sucrose synthesis genes (Figure 1). The technique for increasing cotton fiber elongation has recently been created using GA. In order for the GA signaling pathway to be carried out correctly, the GhHOX3 transcription factor is needed (Shan et al., 2014). When GA levels are low, GhSLR1 (which functions in a more particular manner when GA levels are low) establishes a more precise contact with GhHOX3, indicating that the protein is more active. Given that it has the ability to disrupt the control of the genes it targets, GHHOX3 may upset the proper gene regulation. The GhSLR1 protein is active, which indicates that the protein degrades and releases GhHOX3 in response to high GA concentrations. In this way, GhHOX3 will interact with GhHD1, which is required for cell wall construction.

2.2.3 BRASSINOSTEROIDS

BRs are a family of steroid hormones involved in wide range of processes, such as cell replication and reproductive development, extension, differentiation of tissues of the vascular system biotic stress tolerance and senescence (Ming et al., 2008). For cotton fiber growth, BRs are also significant. In cotton, the administration of the small concentration of brassinolide, a bioactive, plant-insulated, BR, greatly stimulates the elongation of fiber cell, whereas the use of brassinozole (BRZ) (Sun et al., 2005). Applying BRZ exogenously to cotton flower buds results in significant fiber cell differentiation abnormalities. Steroid reduction is recognized as an important speed limitation step in BR biosynthesis by catalyzed by the 5α-reductase (DET) steroid. GhDET2, the 5α-reductible cotton steroid, is abundantly expressed and exceeds the GhDET2 transcription by silencing, which both inhibits the initiation and elongation of cell fiber (Ming et al., 2008). Finasteride, a 5α-reduktase steroid inhibitor, also decreases fiber elongation substantially which may be reversed by BR. The seed coat-specific promoter (pFBP7) over-expression of GhDET2 enhances both the quantity and length of fiber. GhSMT1, another key gene for production of sterols, is widely expressed in ten DPA fiber cells (Shi et al., 2006). GhPAG1, a BR biosynthetic regulates the growth of cotton fiber by controlling the level of BR's endogenous (Yang et al., 2014). BR processes can return the cotton pag1 mutant to a decreased fiber length. In summary these results show that both the start and the elongation of fiber cells need BR (Figure 1). It is also important to better clarify during developmental processes of cotton, GhBZR1 and GhBES1 genes play an important role. In the fiber cell development, the elements in the BR signaling pathway are identified. A BR receptor is a Plasma membrane-localized leucine-rich kinase recipient, which includes the BR Brazilion INSENSITIVE 1 (BRI1) (Peng et al., 2018). GhBRI1 gene is mostly expressed in cells of the fibers during elongation and complements the Arabidopsis 1–5 mutant phenotype fully (Sun et al., 2005). Arabidopsis controls root-epidermal cell specification ENHANCRE OF GLABRA 3 (EGL2) and TRANSPARENT TESTA GLABRA 1 (BIN2), the major negative regulator in the pathways for BR signals. Over-expressing GhBIN2 Arabidopsis plants recover decreased growth due to the lack of gene function (Sun & Allen, 2005). The main transcription factor of the BR signal pathway controls transcripts of its targeted genes by connecting them to a BRRE box in a developer region BZR 1 (BRASSINAZOLE-RESISTANT 1) (Guo et al., 2013). 14-3-3 proteins associated with BZR 1 in response to BR signaling and alter its nucleocytoplasmic shuttle (Gampala et al., 2007). Gh14-3-3 L overexpression also increases elongation processs of fiber, leading to increased fiber length whereas silencing of Gh14-3-3 L dramatically decreases fiber cell start and elongation (Zhou et al., 2015). By exogenous administration of BR, this short fiber phénotype can be partly restored. More analysis has showed that Gh14-3-3 L interacts with GHBZR1 and GhBZR1 can bind the GhXTH1 and GhEXP promoters directly to control the expression of genes in the stage of fiber-cell extension (Zhou et al., 2015). A newly discovered gene, GhbHLH282, has recently been shown to not only control fiber growth, but also to signal BR. Interestingly, GhBZR1 cotton fiber growth regulations because of extreme sterile conditions owing to overexpression of GhBZR1 in cotton are not reported.

2.3.4 ETHYLENE

Ethylene performs a crucial role in growth processes of the plants and controls functions such as hypocotyl growth, production of apical hooks and root hair (Dubois & Van den Broeck Inzé, 2018). Two stages are involved in the ethylene biosynthesis: S-adenosylmethionine is transformed to ACC-carboxylic acid (ACC) catalyzed by synthesis of ACCs (ACS). In addition, ACC is transformed by catalyzing ACC oxidase into ethylene (Yang et al., 2015). Ethylene

stimulates hair development from the root by modulating EIN3 (ethylene insensitive 3) and Arabidopsis root hair defects (RHD6) (Feng et al., 2017). Recently, cellulose synthase D3 was shown to operate reduction of ethylene for root development and cell elongation in Arabidopsis and GhCSLD3 in *G. hirsutum* (Hu et al., 2018). Ethylene in vitro in cotton greatly increases fiber elongation and the L-(2-aminoethoxyvinyl)-glycine (AVG) ethylene synthesis inhibitor reduces elongation of cells (Shi et al., 2006). One of the most important metabolic processes during the fiber extension stage is the ethylene production pathway. During this stage, GhACO1-3 is clearly expressed in line with the high level of synthesis of ethylene in elongated fiber cells. Transcripts of three GhACO genes have been identified in ten DPA fibers specifically. In recent years, Gossypium raimondii was discovered to accumulate high AC O1 and ACO3 transcript levels and ethylene, leading to fiber cell abortions. The protein kinase 1 reliant on ca2+ interacts with cotton ACS2, thereby boosting the activity of cotton and increasing the synthesis of ethylene significantly (Wang et al., 2011). In contrast it has been discovered to be substantially fostering the synthesis of an adequate quantity of ethylene in cotton. BR will not restore the AVG-induced fiber limitation; however, ethylene may be able to reverse the AVG-induced reduction of fiber growth. Cotton fiber is made up of genes such as inositol synthase, tubulin, and expansion (Shi et al., 2006). Another kind of ROS (reactive oxygen species) generated when ethylene promotes fiber elongation is hydrogen peroxide (Qin et al., 2008). The intracellular reactive oxygen species (ROS) enzyme APX (ascorbate peroxidase) regulates the amount of ROS generated inside the cell (Jiang et al., 2017). Fluting ovules express five times more GhAPX1 than five wild-type cotton DPA fiber cells (Li et al., 2007). GhAPX1 transcripts are substantially increased by exogenous H2O2, which enhances APX activity (Qin et al., 2008). During cotton fiber elongation, exogenous ethylene increases the production of H2O2, suggesting that H2O2-mediated fiber elongation is feasible downstream of the Ethylene pathway. GhCaM7 also supports fiber elongation over expression of calmodulin, while GhCaM7 RNAi plants have postponed the beginning of fiber and hindered fiber elongation (Tang et al., 2014). GhCaM7 over-expressing fiber cells, as opposed to wild type, have elevated ROS levels and GhCaM7 RNAi fibers dramatically decreased roosted accumulation, showing that GhCaM7 promotes the elongation of cotton fiber cell by controlling formation of roosts. Interestingly, the Ca2+ inflow in fiber cells may be increased by H2O2. The synthesis of Ethylene is also supported by saturated long-chain fatty acids (VLCFAs) (Qin et al., 2007). The use of C24:0 in vitro fatty acids lead to a large increase in ACO mRNA and considerable synthesis of ethylene. So, ROS controls the buildup of Ca2+ which subsequently increases the elongation of fiber, perhaps via encouraging the synthesis of ethylene. VLCFA can also support ethylene production to improve the elongation of fiber cells (Qin & Zhu, 2011).

2.3.5. CYTOKININS

Cytokinin affects several elements of the growth of plants including cell division, plant tissue and organ senescence, and apical dominance (Liu et al., 2017). Cytokinin has been shown to play a role in the formation of ovules. The incorporation of exogenous cytokinin's in the ovule media enhances ovule development but hampers fiber cell prolongation (Beasley et al., 1974). This is because fast division of the cell happens during the development of embryos, while single cells grow during elongation of the fiber cell (Sawan et al., 2000). But, because to the significant cost and time necessary, substantial commercial uses of cytokinin's in plants are not realistically possible (Li et al., 2004; & Chen et al., 1997). Although unfertilized ovules contain tiny amounts of cytokinin, the hormone's levels rise after the ovules are fertilized (Beasley et al., 1974). For modifying hormones like cytokinin and examining the phenotypes that result, genetic modification is

a useful method. The rate-limiting enzyme in cytokinin synthesis, isopentenyl Transferase (IPT), may be overexpressed, resulting in increased cytokinin levels (Spallek et al., 2017). Although fiber production and quality are unchanged, the accumulation of cytokinin in cotton is significantly increased (Zhu et al., 2012). The cytokinin oxidase/dehydrogenase (CKX) enzyme is a well-known cytokinin metabolism negative regulator. It catalyzes cytokinin N6's unsaturated side chain breaking, leading to a reduction in cytokinin activity in cells (Niemann et al., 2018). When CKX expression is suppressed, endogenous cytokinin levels in plants increase. Using RNA (RNAi) interference to silence transcripts in transgenic cotton plants, seeding development has been enhanced and the fiber output is improved somewhat (Jones & Schreiber, 1997; & Zhao et al., 2015). Cytokinin, which is found in seeds of greater quantities, slows the development of cotton fiber cells. Because GhCKX gene overexpress transgenic cotton plants are being studied, seed and fiber development should be evaluated.

2.3.6 ABSCISIC ACID

Seed dormancy and stress responses are considered to be the most significant functions of ABA (Tuan et al., 2018). In vitro, ABA inhibits the elongation of cell fibers and the formation of cotton fibers, according to previous studies (Beasley et al., 1974). A rise in ABA levels is strongly related to the suppression of this mechanism. As determined by measuring the endogenous ABA content in various fiber-cell types, As ABA concentration increased during the early stages of the fiber-cell and elongation phases of the development cycle, so did the growth rate (0-10 DPA). The initial low-level maturation period (30-50DPA) was reestablished when the elongation-speed (10-20DPA) phase was reached (Davis & Addicott, 1972). About 16 DPNs are required for the process to be completed once ABA begins secondary cell fiber wall production (Yang et al., 2001). The potential production of secondary wall proteins from ABA is brought to the forefront. various fibres have variable quantities of ABA in their composition, however fibres with a short and long staple have a larger percentage of ABA in their fibres (Nayyar et al., 1989). This has been demonstrated to be related to the little quantity of fibres plants produce because of the presence of ABA in their ovules (Ma et al., 2011). the ABA level of Ligon-lintless1 in the 0 DPA ovule was found to be greater in the kind of cotton with mutant ABA levels, compared to the type of cotton with normal ABA levels (Gilbert et al., 2013). the usage of ABA and GA may be controlled when using GbEXPA2 cotton fibres (Li et al., 2015a, b). Complementing this, it has been shown that ABA may limit synthesis of fibres in transgenic cotton overexpressing ABA synthetic genes at ABA concentrations or via the application of JA at high concentrations of ABA. In this manner, it is believed that there is a negative regulation (Figure 1). The above results (Yoshida et al., 2009) Increased JA production is correlated with increased trichome development, a major component of which is GL3 expression. even though proteins having the ZIM (JAZ) domain and therefore playing a role in removing the negative JA signal have been found in the scientific literature (Song et al., 2011). a JAZ is associated with the production of trichomonas by means of the transcriptional WD-repeat/bHLH/MyB complex, which consists of the GL1, EGL3, and BHLH genes (Qi et al., 2011). When J, GL1, and GL3 are missing, the 26S proteasome frees up JAZ and translocates transcription factors to initiate trichiasis. This is an example of a blockage of the 26S proteasome. Cotton fiber synthesis is directly reliant on the specific metabolic requirement for JA (Wang et al., 2015a, b). In fiber initiation, higher amounts of GJAZ2 were found, and its overexpression led to a delay in the onset of fiber, which in turn led to a decrease in the fiber cell length (Hu et al., 2016). With GhJAZ2 proteins, the W-D/bHLH/Myb transcription-component transcriptional, and GhMYB25, the GhGL1, the MYC2, and the GhWD40 proteins, increased fiber synthesis is possible. Fibers are formed when manufacturing processes are

performed (Figure 1). The discovery of genes involved in phytohormone synthesis and cell identification has been made in the cotton plant (Table 1). It is essential to study the roles and activities of genes in the cotton production process in the future.

Table 1: Genes intricated in phytohormone formation

Gene	Method	Up/downregulated	Transgenic/ non-transgenic
GhGA20ox1	1. PCR	Upregulated	Transgenic
GhSLR1	PCR	Upregulated	Transgenic
GhHOX3	PCR	Upregulated	Transgenic
GhHD1	PCR	Upregulated	Transgenic
GhRDL1	PCR	Upregulated	Non-transgenic
GhEXPA1	PCR	Upregulated	Non-transgenic
GhDET2	PCR	Upregulated	Transgenic
GhDWF4	PCR	Upregulated	Transgenic
GhARF2	PCR	Upregulated	Non-transgenic
GhARF18	PCR	Upregulated	Non-transgenic
Gh14–3-3	PCR	Upregulated	Transgenic
GhAPX1	PCR	Upregulated	Non-transgenic
GhBIN2	PCR	Upregulated	Non-transgenic
GhXTH1	PCR	Upregulated	Non-transgenic
GhEXP	PCR	Upregulated	Non-transgenic
GhPIN1	PCR	Upregulated	Non-transgenic
GhMYB25	PCR	Upregulated	Non-transgenic
GhMYC2	PCR	Upregulated	Non-transgenic
GhGL1	PCR	Upregulated	Non-transgenic
GhWD40	PCR	Upregulated	Non-transgenic
GhSusA1	PCR	Upregulated	Transgenic
GhBZR1	PCR	Upregulated	Non-transgenic
GhACO1–3	PCR	Upregulated	Non-transgenic
GhSuSy	PCR	Upregulated	Transgenic
GhTUB1	PCR	Upregulated	Non-transgenic
GhABP	PCR	Upregulated	Non-transgenic
GhJAZ2	PCR	Downregulated	Transgenic
GhPAG1	PCR	Downregulated	Transgenic
GhCPK1	PCR	Upregulated	Transgenic
GhACS2	PCR	Upregulated	Transgenic
GhCKX	PCR	Downregulated	Transgenic

3. FUTURE PROSPECTS

Despite the fact that auxin, GA, BR, ethylene, and JA have all been proven to indorse the development of cotton fiber cells, and numerous genes have been identified as being engaged in the production of cotton fiber, further study is required in order to understand how cotton fiber is formed (Ahmed et al., 2018). According to recent research (Zhang et al., 2017a & b), auxin polar transport vehicles (PINs) and core auxin controls (RFS) play a critical role in the development of cotton fibers. However, the exact mechanisms of transportation of auxin between ovules and fibers, as well as the targets of ARF proteins, are still unknown at this time. It may one day be feasible to produce genetically modified cotton that has PIN overexpression or deletion, and it may also be possible to study the allocation of auxin to ovules and transgenic cotton fibers using transgenic technology. A very beneficial approach to studying the auxin signaling mechanism and molecular pathways involved in the formation of cotton fibers is the identification and exploitation of GhARF2 and GhARF18 target genes. In cotton, exogenous administration of BR stimulates the growth of cotton fiber, and overexpression of the BR biological gene GhDET2 leads to a substantial increase in the length of the cotton fiber cell (Sun et al., 2005). The roles of BZR 1 and BRI1-EMS-SUPPRESSOR 1 (BES1), two key components of the BR Signal Pathway that have yet to be determined,

remain a mystery despite the identification of the BR Signal Pathway. Our knowledge of how JA controls the development of fibers is still in its infancy, and further research is needed. Understanding the mechanism by which the JA signaling system controls molecular fiber production will be improved as a result of the identification of the downstream JA signaling pathway target genes GhMYB25-like, GhGL1, GhMYC2, and GhWD40. The linkages between major regulators of different hormone signaling pathways will be utilized to show the cross-talking between distinct phytohormones involved in fiber initiation and elongation throughout the fiber initiation and elongation process. The interconnections between major regulators of several hormone signaling pathways are discussed in detail. A new family of plant hormones, the SL family, has recently caught the attention of scientists, and the path to understanding SL is becoming increasingly obvious (Khosla & Nelson, 2016). Cook et al. (1966) reported the first time that SL was isolated from the roots of cotton, and more recent research has shown that SL is mainly used as a shoot branch inhibitor in cotton (Yao et al., 2016). It has been discovered that SL controls the elongation of root hairs in Arabidopsis, which is very intriguing (Kapulnik et al., 2011a, b). Elongating root hair may be dependent on cross-speaks between the hormones sodium chloride (SL), ethylene, and auxin, which are comparable to cotton fiber cells in their capacity to lengthen root hair (Kapulnik et al., 2011a, b). However, while the biological role of SLs and the pattern of SL signaling in Arabidopsis have been thoroughly investigated, the role of SLs in cotton growth, especially fiber-cell expansion, is still not completely understood. The issue of whether or not SL is involved in the manufacture of cotton fiber is an important one that needs more investigation and investigation. In order to better understand the relationship between selenium and fiber growth, as well as the length of the fiber cotton cells in the research, it is possible to overexpress or remove genes involved in selenium production and signaling pathway. Arabidopsis is well-known for its hormone biosynthesis genes and signaling pathways, as well as for its capacity to generate the hormones that are produced by these genes.

REFERENCES

Abidi, N., Hequet, E., & Cabrales, L. (2010). Changes in sugar composition and cellulose content during the secondary cell wall biogenesis in cotton fibers. *Cellulose*, *17*(1), 153-160.

Ahmed, M., Shahid, A. A., Din, S. U., Akhtar, S., Ahad, A., Rao, A. Q., & Husnain, T. (2018). An overview of genetic and hormonal control of cotton fiber development. *Pak J Bot*, *50*(1), 433-43.

Aleman, L., Kitamura, J., Abdel-Mageed, H., Lee, J., Sun, Y., Nakajima, M., & Allen, R. D. (2008). Functional analysis of cotton orthologs of GA signal transduction factors GID1 and SLR1. *Plant molecular biology*, *68*(1-2), 1.

Bai, W. Q., Xiao, Y. H., Zhao, J., Song, S. Q., Hu, L., Zeng, J. Y., & Pei, Y. (2014). Gibberellin overproduction promotes sucrose synthase expression and secondary cell wall deposition in cotton fibers. *PLoS One*, *9*(5), e96537.

Beasley, C. A., & Ting, I. P. (1974). Effects of plant growth substances on in vitro fiber development from unfertilized cotton ovules. *American Journal of Botany*, *61*(2), 188-194.

Butterworth, K. M., Adams, D. C., Horner, H. T., & Wendel, J. F. (2009). Initiation and early development of fiber in wild and cultivated cotton. *International Journal of Plant Sciences*, *170*(5), 561-574.

Chen, J. G., Du, X. M., Zhou, X., & Zhao, H. Y. (1997). Levels of cytokinins in the ovules of cotton mutants with altered fiber development. *Journal of Plant Growth Regulation*, *16*(3), 181-185.

Chen, J. G., Ullah, H., Young, J. C., Sussman, M. R., & Jones, A. M. (2001). ABP1

is required for organized cell elongation and division in Arabidopsis embryogenesis. *Genes & development*, *15*(7), 902-911.

Chen, Z. J., & Guan, X. (2011). Auxin boost for cotton. *Nat. Biotechnol. 29*, 407–409. doi: 10.1038/nbt.1858.

Chow, B., & McCourt, P. (2006). Plant hormone receptors: perception is everything. *Genes & development*, *20*(15), 1998-2008.

Cook, C. E., Whichard, L. P., Turner, B., Wall, M. E., & Egley, G. H. (1966). Germination of witchweed (Striga lutea Lour.): isolation and properties of a potent stimulant. *Science*, *154*(3753), 1189-1190.

Davière, J. M., & Achard, P. (2013). Gibberellin signaling in plants. *Development*, *140*(6), 1147-1151.

Davière, J. M., & Achard, P. (2016). A pivotal role of DELLAs in regulating multiple hormone signals. *Molecular plant*, *9*(1), 10-20.

Davis, L. A., & Addicott, F. T. (1972). Abscisic acid: correlations with abscission and with development in the cotton fruit. *Plant physiology*, *49*(4), 644-648.

Dubois, M., Van den Broeck, L., & Inzé, D. (2018). The pivotal role of ethylene in plant growth. *Trends in plant science*, *23*(4), 311-323.

Feng, Y., Xu, P., Li, B., Li, P., Wen, X., An, F., & Guo, H. (2017). Ethylene promotes root hair growth through coordinated EIN3/EIL1 and RHD6/RSL1 activity in Arabidopsis. *Proceedings of the National Academy of Sciences*, *114*(52), 13834-13839.

Gampala, S. S., Kim, T. W., He, J. X., Tang, W., Deng, Z., Bai, M. Y., & Wang, Z. Y. (2007). An essential role for 14-3-3 proteins in brassinosteroid signal transduction in Arabidopsis. *Developmental cell*, *13*(2), 177-189.

Gou, J. Y., Wang, L. J., Chen, S. P., Hu, W. L., & Chen, X. Y. (2007). Gene expression and metabolite profiles of cotton fiber during cell elongation and secondary cell wall synthesis. *Cell research*, *17*(5), 422-434.

Haigler, C. H. (2007). Substrate supply for cellulose synthesis and its stress sensitivity in the cotton fiber. In *Cellulose: Molecular and Structural Biology* (pp. 147-168). Springer, Dordrecht.

Han, X., Xu, X., Fang, D. D., Zhang, T., & Guo, W. (2012). Cloning and expression analysis of novel Aux/IAA family genes in Gossypium hirsutum. *Gene*, *503*(1), 83-91.

Hu, H., He, X., Tu, L., Zhu, L., Zhu, S., Ge, Z., & Zhang, X. (2016). Gh JAZ 2 negatively regulates cotton fiber initiation by interacting with the R2R3-MYB transcription factor Gh MYB 25-like. *The Plant Journal*, *88*(6), 921-935.

Hu, M. Y., Ming, L. U. O., Xiao, Y. H., Li, X. B., Tan, K. L., Lei, H. O. U., & Yan, P. E. I. (2011). Brassinosteroids and auxin down-regulate DELLA genes in fiber initiation and elongation of cotton. *Agricultural Sciences in China*, *10*(8), 1168-1176.

Huang, D., Wang, S., Zhang, B., Shang-Guan, K., Shi, Y., Zhang, D., & Zhou, Y. (2015). A gibberellin-mediated DELLA-NAC signaling cascade regulates cellulose synthesis in rice. *The Plant Cell*, *27*(6), 1681-1696.

Islam, M. S., Fang, D. D., Thyssen, G. N., Delhom, C. D., Liu, Y., & Kim, H. J. (2016). Comparative fiber property and transcriptome analyses reveal key genes potentially related to high fiber strength in cotton (Gossypium hirsutum L.) line MD52ne. *BMC plant biology*, *16*(1), 1-19.

Lakdawala, R. T., Sing, Y. D., & Chinoy, J. J. (1977). Auxin metabolism in

developing cotton hairs. *Journal of Experimental Botany*, *28*(5), 1111-1116.

Jiang, L., Wang, W., Chen, Z., Gao, Q., Xu, Q., & Cao, H. (2017). A role for APX1 gene in lead tolerance in Arabidopsis thaliana. *Plant Science*, *256*, 94-102.

Jing, D. O. N. G., Meng-Hui, Y. I. N., Fan, Y. A. N. G., Juan, Z. H. A. O., Shan, Q. I. N., Lei, H. O. U., & Yue-Hua, X. I. A. O. (2009). Cloning and expression profile of gibberellin insensitive dwarf GID1 homologous genes from cotton. *Acta Agronomica Sinica*, *35*(10), 1822-1830.

Jones, R. J., & Schreiber, B. M. (1997). Role and function of cytokinin oxidase in plants. *Plant Growth Regulation*, *23*(1), 123-134.

Kapulnik, Y., Delaux, P. M., Resnick, N., Mayzlish-Gati, E., Wininger, S., Bhattacharya, C., & Koltai, H. (2011). Strigolactones affect lateral root formation and root-hair elongation in Arabidopsis. *Planta*, *233*(1), 209-216.

Kapulnik, Y., Resnick, N., Mayzlish-Gati, E., Kaplan, Y., Wininger, S., Hershenhorn, J., & Koltai, H. (2011). Strigolactones interact with ethylene and auxin in regulating root-hair elongation in Arabidopsis. *Journal of experimental botany*, *62*(8), 2915-2924.

Khosla, A., & Nelson, D. C. (2016). Strigolactones, super hormones in the fight against Striga. *Current opinion in plant biology*, *33*, 57-63.

Kim, H. J., & Triplett, B. A. (2001). Cotton fiber growth in planta and in vitro. Models for plant cell elongation and cell wall biogenesis. *Plant physiology*, *127*(4), 1361-1366.

Li, F., Fan, G., Lu, C., Xiao, G., Zou, C., Kohel, R. J., & Yu, S. (2015). Genome sequence of cultivated Upland cotton (Gossypium hirsutum TM-1) provides insights into genome evolution. *Nature biotechnology*, *33*(5), 524-530.

Li, F., Fan, G., Wang, K., Sun, F., Yuan, Y., Song, G., & Yu, S. (2014). Genome sequence of the cultivated cotton Gossypium arboreum. *Nature genetics*, *46*(6), 567-572.

Li, H. B., Qin, Y. M., Pang, Y., Song, W. Q., Mei, W. Q., & Zhu, Y. X. (2007). A cotton ascorbate peroxidase is involved in hydrogen peroxide homeostasis during fiber cell development. *New Phytologist*, *175*(3), 462-471.

Li, X. B., Fan, X. P., Wang, X. L., Cai, L., & Yang, W. C. (2005). The cotton ACTIN1 gene is functionally expressed in fibers and participates in fiber elongation. *The Plant Cell*, *17*(3), 859-875.

Li, X., Liu, G., Geng, Y., Wu, M., Pei, W., Zhai, H., & Yu, J. (2017). A genome-wide analysis of the small auxin-up RNA (SAUR) gene family in cotton. *BMC genomics*, *18*(1), 1-22.

Li, Y., Duan, H., Wu, Y. H., McAvoy, R. J., Pei, Y., Zhao, D., & Luo, K. (2004). Transgenics of plant hormones and their potential application in horticultural crops. *Genetically modified crops, their development, uses, and risks. The Haworth Press, New York*, 101-117.

Li, Y., Tu, L., Ye, Z., Wang, M., Gao, W., & Zhang, X. (2015). A cotton fiber-preferential promoter, PGbEXPA2, is regulated by GA and ABA in Arabidopsis. *Plant cell reports*, *34*(9), 1539-1549.

Liao, W. B., Ruan, M. B., Cui, B. M., Xu, N. F., Lu, J. J., & Peng, M. (2009). Isolation and characterization of a GAI/RGA-like gene from Gossypium hirsutum. *Plant growth regulation*, *58*(1), 35-45.

LiI, X. B., Xiao, Y. H., Luo, M., Hou, L., Li, D. M., Luo, X. Y., & Pei, Y. (2005). Cloning and expression analysis of two Rac genes from cotton (Gossypium hirsutum L.). *Yi chuan*

xue bao= Acta genetica Sinica, *32*(1), 72-78.

Liu, D., Tu, L., Wang, L., Li, Y., Zhu, L., & Zhang, X. (2008). Characterization and expression of plasma and tonoplast membrane aquaporins in elongating cotton fibers. *Plant cell reports*, *27*(8), 1385-1394.

Liu, J., Moore, S., Chen, C., & Lindsey, K. (2017). Crosstalk complexities between auxin, cytokinin, and ethylene in Arabidopsis root development: from experiments to systems modeling, and back again. *Molecular plant*, *10*(12), 1480-1496.

Love, A. J., Milner, J. J., & Sadanandom, A. (2008). Timing is everything: regulatory overlap in plant cell death. *Trends in plant science*, *13*(11), 589-595.

Ma, J., Liu, F., Wang, Q., Wang, K., Jones, D. C., & Zhang, B. (2016). Comprehensive analysis of TCP transcription factors and their expression during cotton (Gossypium arboreum) fiber early development. *Scientific reports*, *6*(1), 1-10.

Nayyar, H., Kaur, K., Basra, A. S., & Malik, C. P. (1989). Hormonal regulation of cotton fiber elongation in Gossypium arboreum L. in vitro and in vivo. *Biochemie und Physiologie der Pflanzen*, *185*(5-6), 415-421.

Niemann, M. C., Weber, H., Hluska, T., Leonte, G., Anderson, S. M., Novák, O., & Werner, T. (2018). The cytokinin oxidase/dehydrogenase CKX1 is a membrane-bound protein requiring homooligomerization in the endoplasmic reticulum for its cellular activity. *Plant physiology*, *176*(3), 2024-2039.

Paterson, A. H. (2012). Genomes for jeans: cotton genomics for engineering superior fiber. *Trends in biotechnology*, *30*(10), 521-527.

Peng, Y., Chen, L., Li, S., Zhang, Y., Xu, R., Liu, Z., & Li, Y. (2018). BRI1 and BAK1 interact with G proteins and regulate sugar-responsive growth and development in Arabidopsis. *Nature communications*, *9*(1), 1-13.

Qin, Y. M., & Zhu, Y. X. (2011). How cotton fibers elongate: a tale of linear cell-growth mode. *Current opinion in plant biology*, *14*(1), 106-111.

Qin, Y. M., Hu, C. Y., & Zhu, Y. X. (2008). The ascorbate peroxidase regulated by H2O2 and ethylene is involved in cotton fiber cell elongation by modulating ROS homeostasis. *Plant signaling & behavior*, *3*(3), 194-196.

Roche, M. C. (2007). *A study of programmed cell death in cotton (gosypium hirsutum) fiber* (Doctoral dissertation, Texas A & M University).

Ruan, Y. L. (2007). Rapid cell expansion and cellulose synthesis regulated by plasmodesmata and sugar: insights from the single-celled cotton fiber. *Functional Plant Biology*, *34*(1), 1-10.

Ruan, Y. L., Llewellyn, D. J., & Furbank, R. T. (2003). Suppression of sucrose synthase gene expression represses cotton fiber cell initiation, elongation, and seed development. *The Plant Cell*, *15*(4), 952-964.

Salih, H., Leng, X., He, S. P., Jia, Y. H., Gong, W. F., & Du, X. M. (2016). Characterization of the early fiber development gene, Ligon-lintless 1 (Li1), using microarray. *Plant Gene*, *6*, 59-66.

Sawan, Z. M., Mohamed, A. A., Sakr, R. A., & Tarrad, A. M. (2000). Effect of kinetin concentration and methods of application on seed germination, yield components, yield and fiber properties of the Egyptian cotton (Gossypium barbadense). *Environmental and experimental botany*, *44*(1), 59-68.

Seagull, R. W. (1993). Cytoskeletal involvement in cotton fiber growth

and development. *Micron*, *24*(6), 643-660.

Seagull, R. W., Giavalis, S., Seagull, R. W., & Giavalis, S. (2004). Molecular biology and physiology pre-and post-anthesis application of exogenous hormones alters fiber production in Gossypium hirsutum L. cultivar maxxa GTO.

Shan, C. M., Shangguan, X. X., Zhao, B., Zhang, X. F., Chao, L. M., Yang, C. Q., & Chen, X. Y. (2014). Control of cotton fiber elongation by a homeodomain transcription factor GhHOX3. *Nature communications*, *5*(1), 1-9.

Shi, Y. H., Zhu, S. W., Mao, X. Z., Feng, J. X., Qin, Y. M., Zhang, L., & Zhu, Y. X. (2006). Transcriptome profiling, molecular biological, and physiological studies reveal a major role for ethylene in cotton fiber cell elongation. *The plant cell*, *18*(3), 651-664.

Singh, B., Avci, U., Eichler Inwood, S. E., Grimson, M. J., Landgraf, J., Mohnen, D., & Haigler, C. H. (2009). A specialized outer layer of the primary cell wall joins elongating cotton fibers into tissue-like bundles. *Plant physiology*, *150*(2), 684-699.

Singh, B., Cheek, H. D., & Haigler, C. H. (2009). A synthetic auxin (NAA) suppresses secondary wall cellulose synthesis and enhances elongation in cultured cotton fiber. *Plant cell reports*, *28*(7), 1023-1032.

Song, S., Qi, T., Huang, H., Ren, Q., Wu, D., Chang, C., & Xie, D. (2011). The Jasmonate-ZIM domain proteins interact with the R2R3-MYB transcription factors MYB21 and MYB24 to affect Jasmonate-regulated stamen development in Arabidopsis. *The Plant Cell*, *23*(3), 1000-1013.

Spallek, T., Melnyk, C. W., Wakatake, T., Zhang, J., Sakamoto, Y., Kiba, T., & Shirasu, K. (2017). Interspecies hormonal control of host root morphology by parasitic plants. *Proceedings of the National Academy of Sciences*, *114*(20), 5283-5288.

Stewart, J. M. (1975). Fiber initiation on the cotton ovule (Gossypium hirsutum). *American Journal of Botany*, *62*(7), 723-730.

Sun, Y., & Allen, R. D. (2005). Functional analysis of the BIN2 genes of cotton. *Molecular Genetics and Genomics*, *274*(1), 51-59.

Sun, Y., Veerabomma, S., Abdel-Mageed, H. A., Fokar, M., Asami, T., Yoshida, S., & Allen, R. D. (2005). Brassinosteroid regulates fiber development on cultured cotton ovules. *Plant and Cell Physiology*, *46*(8), 1384-1391.

Taliercio, E. (2011). Characterization of an ADP-glucose pyrophosphorylase small subunit gene expressed in developing cotton (Gossypium hirsutum) fibers. *Molecular biology reports*, *38*(5), 2967-2973.

Tang, W., Tu, L., Yang, X., Tan, J., Deng, F., Hao, J., & Zhang, X. (2014). The calcium sensor G h C a M 7 promotes cotton fiber elongation by modulating reactive oxygen species (ROS) production. *New phytologist*, *202*(2), 509-520.

Tuan, P. A., Kumar, R., Rehal, P. K., Toora, P. K., & Ayele, B. T. (2018). Molecular mechanisms underlying abscisic acid/gibberellin balance in the control of seed dormancy and germination in cereals. *Frontiers in Plant Science*, *9*, 668.

Wang, H., Guo, Y., Lv, F., Zhu, H., Wu, S., Jiang, Y., & Zhang, T. (2010a). The essential role of GhPEL gene, encoding a pectate lyase, in cell wall loosening by depolymerization of the de-esterified pectin during fiber elongation in cotton. *Plant molecular biology*, *72*(4-5), 397-406.

Wang, H., Mei, W., Qin, Y., & Zhu, Y. (2011). 1-Aminocyclopropane-1-carboxylic acid synthase 2 is

phosphorylated by calcium-dependent protein kinase 1 during cotton fiber elongation. *Acta Biochim Biophys Sin*, *43*(8), 654-661.

Wu, H. M., Hazak, O., Cheung, A. Y., & Yalovsky, S. (2011). RAC/ROP GTPases and auxin signaling. *The Plant Cell*, *23*(4), 1208-1218.

Xi, W., Gong, X., Yang, Q., Yu, H., & Liou, Y. C. (2016). Pin1At regulates PIN1 polar localization and root gravitropism. *Nature communications*, *7*(1), 1-10.

Xiao, G., He, P., Zhao, P., Liu, H., Zhang, L., Pang, C., & Yu, J. (2018). Genome-wide identification of the GhARF gene family reveals that GhARF2 and GhARF18 are involved in cotton fiber cell initiation. *Journal of experimental botany*, *69*(18), 4323-4337.

Xiao, Y. H., Li, D. M., Yin, M. H., Li, X. B., Zhang, M., Wang, Y. J., & Pei, Y. (2010). Gibberellin 20-oxidase promotes initiation and elongation of cotton fibers by regulating gibberellin synthesis. *Journal of plant physiology*, *167*(10), 829-837.

Yang, C., Lu, X., Ma, B., Chen, S. Y., & Zhang, J. S. (2015). Ethylene signaling in rice and Arabidopsis: conserved and diverged aspects. *Molecular plant*, *8*(4), 495-505.

Yang, Y., Chu-Nian, X., Bao-Min, W., & Jun-Zhen, J. (2001). Effects of plant growth regulators on secondary wall thickening of cotton fibres. *Plant Growth Regulation*, *35*(3), 233-237.

Yang, Z., Zhang, C., Yang, X., Liu, K., Wu, Z., Zhang, X., & Li, F. (2014). PAG1, a cotton brassinosteroid catabolism gene, modulates fiber elongation. *New phytologist*, *203*(2), 437-448.

Yao, R., Ming, Z., Yan, L., Li, S., Wang, F., Ma, S., & Xie, D. (2016). DWARF14 is a non-canonical hormone receptor for strigolactone. *Nature*, *536*(7617), 469-473.

Yoshida, Y., Sano, R., Wada, T., Takabayashi, J., & Okada, K. (2009). Jasmonic acid control of GLABRA3 links inducible defense and trichome patterning in Arabidopsis.

Zhang, F., Liu, X., Zuo, K., Zhang, J., Sun, X., & Tang, K. (2011). Molecular cloning and characterization of a novel Gossypium barbadense L. RAD-like gene. *Plant Molecular Biology Reporter*, *29*(2), 324-333.

Zhang, M., Zeng, J. Y., Long, H., Xiao, Y. H., Yan, X. Y., & Pei, Y. (2017). Auxin regulates cotton fiber initiation via GhPIN-mediated auxin transport. *Plant and Cell Physiology*, *58*(2), 385-397.

Zhang, M., Zheng, X., Song, S., Zeng, Q., Hou, L., Li, D., & Pei, Y. (2011). Spatiotemporal manipulation of auxin biosynthesis in cotton ovule epidermal cells enhances fiber yield and quality. *Nature biotechnology*, *29*(5), 453-458.

Zhang, X., HU, D. P., Yuan, L., Yuan, C., Abidallha, E. H., DONG, Z. D., & Zhang, L. (2017). Developmental and hormonal regulation of fiber quality in two natural-colored cotton cultivars. *Journal of integrative agriculture*, *16*(8), 1720-1729.

Zhang, Y., He, P., Yang, Z., Huang, G., Wang, L., Pang, C., & Xiao, G. (2017 a). A genome-scale analysis of the PIN gene family reveals its functions in cotton fiber development. *Frontiers in plant science*, *8*, 461.

Zhao, J., Bai, W., Zeng, Q., Song, S., Zhang, M., Li, X., & Pei, Y. (2015). Moderately enhancing cytokinin level by down-regulation of GhCKX expression in cotton concurrently increases fiber and seed yield. *Molecular Breeding*, *35*(2), 1-11.

Zheng, M., Wang, Y., Liu, K., Shu, H., & Zhou, Z. (2012). Protein expression changes during cotton fiber elongation in response to low temperature stress. *Journal of plant physiology*, *169*(4), 399-409.

Zhou, Y., Zhang, Z. T., Li, M., Wei, X. Z., Li, X. J., Li, B. Y., & Li, X. B. (2015). Cotton (Gossypium hirsutum) 14-3-3 proteins participate in regulation of fiber initiation and elongation by modulating brassinosteroid signaling. *Plant biotechnology journal*, *13*(2), 269-280.

Zhu, H., Lv, J., Zhao, L., Tong, X., Zhou, B., Zhang, T., & Guo, W. (2012). Molecular evolution and phylogenetic analysis of genes related to cotton fibers development from wild and domesticated cotton species in Gossypium. *Molecular phylogenetics and evolution*, *63*(3), 589-597.