



# GLEANINGS IN COTTON RESEARCH

## APRIL 2025



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## **Preface**

*Information plays a vital role in just about everything we do in modern society. Today, the Internet is one of the most effective and efficient ways to collect information. The internet gives us the opportunity to connect with all kinds of different people and read news and information from all over the world.*

*Information literacy is the ability to find, evaluate, organize, use, and communicate information in all its various formats, most notably in the acquisition of knowledge. The diversity of news sources thus makes the internet a source of information and knowledge.*

***Gleanings in Cotton Research** is an attempt made by the Library to scan, collect, edit and present, ongoing research in Cotton using the information available on the Internet in a concise manner.*

*Articles related to Cotton subject area are represented by Agronomy, Soil Science, Plant Physiology, Genetics, Biotechnology, Crop Protection, Seed Technology, and Fiber Technology.*

*The information collected is arranged under these broad subject headings. The Title of the research paper is followed by the Imprint, wherein Names of the authors and Journal are given. Names of the journals are followed by year of publication, volume number, issue number in brackets and inclusive pages. The DOI (Digital Object Identifier) wherever applicable is also mentioned. The abstract follows the citation.*

*Information has been mainly retrieved from Google Scholar, Science Direct and GAIN website.*

*We duly thank The Director, Dr V. N. Waghmare for providing inspiration and support for this publication.*

*Suggestions are welcome for further improvement on [cicrlib@yahoo.co.in](mailto:cicrlib@yahoo.co.in).*

*Swati Dixit  
Incharge Library*

*Chetali Rodge  
Technical Officer (T5)*

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1

**Title:** Soil pH influence on cotton lint yield and quality.

**Author:** R. L. Sharry, M. Smith, H. Moulay, J. Souza, S. Sharma, D. B. Arnall

**Imprint:** Agrosyst Geosci Environ. 2025;8: e70065.

wileyonlinelibrary.com/journal/agg2 1 of 9 <https://doi.org/10.1002/agg2.70065>

**Abstract:** Increases in cotton (*Gossypium hirsutum* L.) production across Oklahoma due to various circumstances have led to cotton planted on soils that have been traditionally managed for differing crops, specifically winter wheat. Many of these soils are possibly acidic in nature due to natural and anthropogenic activities such as excessive ammonia-based fertilizer applications. Common wheat production practices such as banding phosphorus fertilizers with seed and planting aluminum (Al) tolerant varieties may have masked potential problems associated with crop performance in acidic soils. In response, this study was initiated to evaluate the impact of soil acidity on cotton production. This experiment was conducted in central Oklahoma in the 2019 and 2020 growing seasons. Cotton lint yield and lint quality were evaluated across a range of soil pH levels and associated potassium chloride extractable Al across a soil pH gradient of 4.0–8.0. Two cotton cultivars were planted to identify possible differences in response between genotypes. Soil acidity negatively impacted in-season growth parameters such as plant height, node count, and boll count, as well as the primary variable of lint yield. A critical threshold at a soil pH level of 5.2 was identified as detrimental to cotton lint yield, corresponding with a lint yield loss of approximately 4.5% per pH unit decrease below the critical soil pH level of 5.2. This equates to a lint yield loss of 44.5 kg ha<sup>-1</sup> per 0.1 change in soil pH, assuming 100% yield potential is approximately 989 kg ha<sup>-1</sup> of lint for this specific growing environment.

2

**Title:** PGPR and nutrient consortia promoted cotton growth, antioxidant enzymes, and mineral uptake by suppressing sooty mold in arid climate.

**Author:** Muhammad Luqman, Maqshoof Ahmad, Abubakar Dar, Azhar Hussain

**Imprint:** Front. Microbiol., 20 March 2025, Sec. Terrestrial Microbiology, Volume 16 - 2025 | <https://doi.org/10.3389/fmicb.2025.1551465>

**Abstract:** Introduction: Cotton (*Gossypium hirsutum* L.) plays a vital role in Pakistan's economy, providing significant employment opportunities and supporting the country's textile industry. However, cotton productivity is severely impacted by pests and diseases, such as black spots caused by sooty mold, posing critical challenges to sustainable agriculture. This study investigates a novel integration of plant growth-promoting rhizobacteria (PGPR) with recommended NPK fertilizers and micronutrients to enhance cotton growth, yield, disease resistance, and post-harvest soil properties. Methodology: A consortium of *Bacillus megaterium* (ZR19), *Paenibacillus polymyxa* (IA7), and *Bacillus* sp. (IA16) were evaluated under six treatments: control (T1), PGPR (T2), recommended NPK (T3), recommended NPK + PGPR (T4), recommended NPK + micronutrients (T5), and recommended NPK + micronutrients + PGPR (T6). Results: The results depicted a significant increase in antioxidant activities of 19% in superoxide dismutase (SOD), 29% peroxidase (POX), 28% peroxidase dismutase (POD), and 14% catalase (CAT) activity under T6 as compared to control. Similarly, growth parameters substantially improved root length (39%), shoot length (19%), and root and shoot biomass by up to 31 and 20%, respectively, under T6. Moreover, the yield attributes like single boll weight and lint percentage were also enhanced by 32 and 13%, respectively, under the integration. In contrast, the PGPR consortium demonstrated considerable biocontrol potential against sooty mold, as disease incidence was reduced by 68% in cotton, the disease index was 75%, and control efficacy reached 75%. The PGPR consortium also substantially improved post-harvest soil biological and chemical properties, including bacterial populations, microbial biomass nitrogen, organic matter, and essential nutrient availability. Discussion: So, these findings witnessed the dual behavior of the *Bacillus* and *Paenibacillus* strains with balanced nutrition and can lead us to the development of an effective biopesticide cum biofertilizer for the sustainable production of cotton in arid conditions by combating sooty mold effectively.

### 3

**Title:** Application of Fermented Manure Improves the Growth and Antioxidant Potential of Cotton (*Gossypium hirsutum* L.) and Soil Health under Semi-Arid Conditions.

**Author:** Muhammad Ali<sup>1</sup>, Raheela Jabeen, Fahad Al-Asmari, Özhan Şimşek, Özlem Şimşek, Tolga İzgü, Fayez Althobaiti, Eman Fayad

**Imprint:** Pol. J. Environ. Stud. Vol. XX, No. X (XXXX), 1-10

**Abstract:** Using organic manures appears to be a promising strategy to promote plant performance and improve soil health in arid and semi-arid regions under the threat of changing climate. The objective of the current field-based study was to investigate the

beneficial effects of cow dung manure (CDM) fermented at different days, including 7, 14, and 21 days, on cotton crop growth and soil health compared with synthetic fertilization. It was noticed that chemical fertilizer application showed the lowest values for cotton seedling growth, physio-biochemical attributes, and soil organic matter content. Results regarding CDM also showed that under all applied treatments, treatment in which 21 days of fermented manure was applied performed better in terms of cotton plant growth and soil properties, as evidenced by the cotton plant's higher biomass, chlorophyll, and water contents, activities of antioxidant enzymes, lower soil pH, increased organic matter contents, and higher amounts of moisture and essential plant nutrient retention in soil. In summary, our study suggests that using CDM could be an efficient practice to improve the growth and development of crop plants and soil health.

#### 4

**Title:** Lower Demand for Boll Dry Matter Accumulation and Higher Harvestable Bolls Ensure the Yield and Quality Advantages of Small Boll Cotton Under Water-Deficit Conditions.

**Author:** Yongchao Han, Honghai Luo, Qian-Hao Zhu, Chong Yang, Ruiting Zheng, Fei Xue, Jie Sun, Xinyu Zhang, Feng Liu

**Imprint:** First published: 25 February 2025, Journal of Agronomy and Crop Science, <https://doi.org/10.1111/jac.70035>

**Abstract:** Water deficiency has a serious effect on cotton productivity. Development of cotton bolls determines cotton fibre yield and quality and is affected by many environmental variables, including water availability. However, we know little about the effect of water stress on boll development and the final fibre yield and quality of the varieties with different boll sizes. In this study, cotton varieties with different boll sizes were used to compare the effect of water availability on boll development, characteristics of fibre yield and quality, seed components and seed vigour. The results showed that under the well-watered (WW) and water-deficit (WD) irrigation conditions, large boll (LB) and small boll (SB) varieties had a similar overall trend of boll volume change and accumulation of boll dry matter during boll development but differed in the rate of dry matter accumulation and boll volume growth. Under WW treatment, the dry matter accumulation per boll of LB was significantly higher than that of SB at 42 days postanthesis (DPA), with a difference of 29.17%. WD led to a reduction in dry matter accumulation of bolls, and the dry matter accumulation in seed cotton and boll shell for LB varieties decreased by 20.45% and 3.24%, respectively, at 42 DPA. The corresponding decrease in SB varieties was, respectively, 16.76% and 2.81%, but the harvestable boll numbers per plant of SB varieties were 36.28% higher than that of LB

varieties under WD irrigation. The lint yield of the SB varieties was 1042.45 kg ha<sup>-1</sup> and the seed cotton yield was 2459.67 kg ha<sup>-1</sup>, which were also comparable to those of the LB varieties. WD treatment also reduced fibre length and strength, with a more significant impact on LB varieties. In addition, WD significantly increased the relative protein content of cottonseed but decreased the relative oil content, leading to a decrease in seed vitality. Under WD irrigation, compared to seeds of LB varieties, the seeds of SB varieties have higher germination potential. Compared with LB varieties, SB varieties required less dry matter accumulation for boll maturation and produced more harvestable boll numbers, resulting in a smaller impact on yield and quality under WD irrigation. In general, SB varieties are more tolerant to WD stress and are expected to have a better performance in severe arid areas.

## 5

**Title:** Genetic mapping and transcriptome profiling revealed leaf lobe formation and leaf size are regulated by GhRL4 in *Gossypium hirsutum*.

**Author:** Hui Jiang, Xue Li, Chao Zhang, Mingwei Gao, Yongcui Wang,

**Imprint:** Theoretical and Applied Genetics, Published: 24 February 2025, Volume 138, article number 53, (2025)

**Abstract:** Leaf shape determines canopy structure and cotton productivity. Except for the *L-D<sub>1</sub>* locus, which determines the okra-leaf shape, the genetic control of other leaf shapes remains unknown in cotton. In the current study, using BSA-seq, RNA-seq, and molecular methods, *GhRL<sub>4</sub>* was mapped to chromosome A01, and it was identified as a key regulator of round-leaf shape in the cotton accession (M113116). Transcriptional suppression of *GhRL<sub>4</sub>* by virus-induced gene silencing (VIGS) led to the formation of leaf lobes and enlarged leaf size. Compared to the wild-type, the coding sequence of round-leaf alleles of *GhRL<sub>4</sub>* had a 21 bp deletion at the potential target site of miR319c. *GhRL<sub>4</sub>* belongs to the TCP (*Teosinte Branched1*, *Cyclodea*, and *Proliferating Cell Factor*) 4 subfamily, previously implicated in the regulation of leaf shape in model plants. Further, transcriptome analysis indicated that PILS (Pin-Likes), GIF (Grf-Interacting Factor), WIP (Wip Domain Protein), CUC (Cup-Shaped Cotyledon), and TCP family genes might be involved in the development of the round-leaf. Identifying the genetic and biochemical basis of phenotypic variation for leaf shape diversity would enable the use of genetic diversity and genomic tools for development of climate resilient high yielding cotton cultivars.

## 6

**Title:** *Cytokinin Dehydrogenase* suppression increases intrinsic water-use efficiency and photosynthesis in cotton under drought.

**Author:** Wei Hu, Dimitra A Loka, Yuanyu Luo, Huilian Yu, Shanshan Wang, Zhiguo Zhou

**Imprint** : *Plant Physiology*, Volume 197, Issue 3, March 2025, kiaf081, <https://doi.org/10.1093/plphys/kiaf081>

**Abstract:** Drought reduces endogenous cytokinin (CK) content and disturbs plant water balance and photosynthesis. However, the effect of higher endogenous CK levels (achieved by suppressing cytokinin dehydrogenase [CKX] genes) on plant water status and photosynthesis under drought stress is unknown. Here, pot experiments were conducted with wild-type (WT) cotton (*Gossypium hirsutum*) and 2 GhCKX suppression lines (CR-3 and CR-13) to explore the effect of higher endogenous CK levels on leaf water utilization and photosynthesis under drought stress. The GhCKX suppression lines had a higher leaf net photosynthetic rate (AN) and intrinsic water-use efficiency (iWUE) than WT under drought. This increase was attributed to the decoupling of stomatal conductance (gs) and mesophyll conductance (gm) in the suppression lines in response to drought. GhCKX suppression increased gm but maintained gs relative to WT under drought, and the increased gm was associated with altered anatomical traits, including decreased cell wall thickness (Tcw) and increased surface area of chloroplast-facing intercellular airspaces per unit leaf area (Sc/S), as well as altered cell wall composition, especially decreased cellulose levels. This study provides evidence that increased endogenous CK levels can simultaneously enhance AN and iWUE in cotton under drought conditions and establishes a potential mechanism for this effect. These findings provide a potential strategy for breeding drought-tolerant crops or exploring alternative methods to promote crop drought tolerance.

## 7

**Title:** Unveiling Drought Tolerant Cotton Genotypes: Insights from Morpho-Physiological and Biochemical Markers at Flowering.

**Author:** Muhammad Yousaf Shani, Muhammad Yasin Ashraf, Muhammad Ramzan

**Imprint:** *Plants* 2025, 14(4), 616; <https://doi.org/10.3390/plants14040616>

**Abstract:** Drought stress substantially restricts cotton growth, decreasing cotton production potential worldwide. This study evaluated cotton genotypes at the

flowering stage to identify drought-resilient genotypes under moderate and severe drought conditions using physio-morphic and biochemical markers. Five genotypes were examined in a completely randomized design with three replicates across three treatments. Growth and biochemical traits were measured after 14 days of drought stress. The Multi-trait Genotype-Ideotype Distance Index (MGIDI) identified the most drought-tolerant genotypes. Severe drought had a pronounced negative effect on growth and biochemical traits, followed by moderate drought. Among the genotypes, FH-912 exhibited the strongest resilience, with significant increases in proline, peroxidase, catalase, and total chlorophyll. In contrast, chlorophyll a and transpiration rates were largely unaffected. Genotypes VH-351, VH-281, and GH-99 showed moderate drought tolerance, while FH-556 was highly sensitive to water stress. Statistical analyses, including ANOVA, PCA, and heatmaps, confirmed FH-912's superior performance under drought stress. The drought-resilient genotype, FH-912, holds promise for breeding drought-tolerant cotton varieties to sustain cotton productivity in water-limited environments, especially in drought-prone regions.

## 8

**Title:** Better root length distribution in the deep soil profile enhances upland cotton performance.

**Author:** Om Prakash Ghimire, Vasu Kuraparthy, Michael Jones, B. Todd Campbell, William C. Bridges Jr., Femi P. Alege Christopher Delhom, Sruthi Narayanan

**Imprint:** Field Crops Research, Volume 325, 15 April 2025, 109805

**Abstract:** Intense selection for lint yield and fiber quality traits can impose an unintended limitation on the attainable yield of modern cotton cultivars, as the root systems fail to support boll growth. Despite the importance, little progress has been made in enhancing cotton root systems. We evaluated a subset of the U.S. cotton diversity panel under field conditions in 2022 and 2023 to identify the root architectural traits that enhance effective water use and aboveground performance. We found that increased water use efficiency (WUE, shoot biomass/soil water depletion) of the cotton genotypes was associated with enhanced shoot biomass (correlation coefficient,  $r$ , 0.80 in 2022 and 0.96 in 2023). Potential root phenotypes that enhanced resource capture and shoot biomass production were better root length distribution in deep soil profile (~40–60 cm) and fine root (0.25–0.5 mm diameter) production. Shoot biomass was correlated with root length in the deep profile ( $r$ , 0.69 in 2022 and 0.45 in 2023) but not in the shallower profile (<40 cm). Root length in the deep profile was also correlated with WUE in the dryer year 2022 ( $r$ , 0.45). The cotton root system was dominated by fine roots (46–66 % in 2022 and 53–62 % in 2023). Genotypes Station Miller, Paymaster HS26,

and PD 2164 possessed beneficial root architecture which was linked to their high shoot biomass, leaf area index, WUE, and seed cotton yield. These genotypes can be used as germplasm sources for improved root traits and to study their genetic regulation.

## 9

**Title:** Photosynthetic Efficiency and Water Status as Determinants for the Performance of Semiarid-Adapted Cotton Cultivars Under Drought in Greenhouse

**Author:** Renato Oliveira de Sousa

**Imprint:** *Agronomy* 2025, 15(2), 500; <https://doi.org/10.3390/agronomy15020500>

**Abstract:** Searching for crop cultivars that are resilient to environmental stresses is crucial for maintaining global agricultural production. Our study aimed to screen semiarid-adapted cotton cultivars performing well under water-restricted conditions. Trials were conducted in a greenhouse involving six cotton cultivars (FM 911, FM 912, FM 970, FM 974, FM 978, and FM 985) subjected to four water levels (100, 80, 60, and 40% field capacity –FC). At 20 days post-drought imposition, the growth, leaf succulence, osmotic potential, gas exchanges, photosynthetic pigments, and lipid peroxidation were measured. Cotton plants showed reduced growth and gas exchanges at 60% and 40%, displaying elevated sensibility at 40% FC. Under 60% FC, FM 970 and FM 985 exhibited a superior dry biomass, leaf area, and growth, indicating high drought tolerance. FM 911, FM 912, and FM 978 displayed higher rates of net photosynthesis, transpiration, stomatal conductance, and chlorophyll content under 60% and 40% FC, but also demonstrated an increased lipid peroxidation. Additionally, FM 911, FM 970, and FM 974 had the lowest osmotic potential values. Field capacity at 60% and 40% represent moderate and severe drought conditions for cotton. The superior performance of FM 970, FM 978, and FM 985 under drought is attributed to pigment accumulation and photosynthetic efficiency. Our findings suggest that a water-saving strategy with an 80% FC can enhance sustainable production and identify promising cotton cultivars for cultivation in water-scarce regions.

**Title:** Mannose-binding lectin 1.1A interacts with hypersensitive-induced response 4 to promote hypersensitive cell death and defense responses in cotton upon *Verticillium dahliae* infection.

**Author:** Leitian Yuan, Min Wu, Deming Tan, Shuling Zhang, Huanyang Zhang, Jing Li, Guixian Xia, Fuxin Wang

**Imprint:** Plant J., 2025 Feb;121(4):e70018. doi: 10.1111/tpj.70018

**Abstract:** Increasing evidence indicates that mannose-binding lectins (MBLs) act as a lectin-receptor-like protein in plant immune responses, yet the functional basis remains elusive. In this study, we dissected the functional mechanism of GbMBL1.1A in defense against *Verticillium dahliae* infection in sea island cotton (*Gossypium barbadense*). GbMBL1.1A expressed preferentially in cotton roots and significantly upregulated upon *V. dahliae* infection. Transgenic expression of GbMBL1.1A in upland cotton (*Gossypium hirsutum*) and *Arabidopsis* remarkably improved the disease resistance of the plants, while silencing of GbMBL1.1A resulted in an increased susceptibility of cotton plants in response to *V. dahliae* attack. Protein interaction assays revealed that GbMBL1.1A interacted with the cotton hypersensitive-induced response protein 4 (GbHIR4, a scaffold protein for immune signaling in the plasma membrane microdomain) through PAN domain. GbHIR4 expression was upregulated in response to *V. dahliae* invasion, and silencing of GbHIR4 seriously attenuated the disease tolerance of cotton plants. GbMBL1.1A enhanced the cell death phenotype induced by the transient expression of GbHIR4, and meanwhile promoted HR-PCD and GbHIR4-dependent resistance upon *V. dahliae* infection. The results suggested that GbMBL1.1A employed GbHIR4 as a downstream component to trigger the hypersensitive responses and therefore contributed to cotton resistance against *V. dahliae*. In addition, we observed that GbMBL1.1A overexpression could alter the phytohormone-mediated defense and growth signaling under both normal and *V. dahliae* infection conditions. Collectively, these results demonstrated that the lectin receptor-like protein GbMBL1.1A interacts with GbHIR4 in cotton immunity to induce the hypersensitive response, which is associated with phytohormone-mediated defense and growth signaling.

## 11

**Title:** Evaluation of genetic diversity of cotton genotypes using morphological and molecular markers and evaluation for leaf hopper resistance.

**Author:** Alagarsamy Manivannan, Thomas Cheeran Amal, Aravindan Shanmugam

**Imprint:** South African Journal of Botany, Volume 179, April 2025, Pages 206-215

**Abstract:** Diverse populations are an important resource for any breeding programme for broadening the genetic base and molecular markers would be the most effective way to dissect the genetic divergence among the populations. Majority of the cotton cultivars under commercial cultivation is highly susceptible to leaf hopper incidence and also possess narrow genetic base with less genetic variation. Thus, this study evaluated a panel of 26 cotton genotypes for genetic variation, leaf hopper resistance, and 14 agronomic traits. Using 63 simple sequence repeat (SSR) markers, polymorphic information content ranged from 0.336 to 0.485 (average 0.384), with alleles per locus varying from 2 to 9. Population structure analysis grouped the genotypes into two clusters, while Ward's D<sup>2</sup> analysis classified them into three, with cluster III comprising 88.5 % of the genotypes. AKH 1355, a *G. hirsutum* genotype, uniquely clustered with *G. barbadense* in structure analysis but formed a solitary cluster in D<sup>2</sup> analysis. Plant types ranged from compact to spreading, with leaf lobing varying from 3 to 5 lobes and boll locules ranging from 1 (Suvin) to 11 (H1454). Genotypes displayed wide variation in plant height (24.0–116.0 cm), internode length (2.0–7.0 cm), monopodia (0–2), and sympodia (6–18), reflecting significant phenotypic diversity within the panel. Unique traits were observed in DCH32 and Suvin, which exhibited frego bracts, glabrous stems, and conical pitted bolls, contrasting with the round smooth bolls of GISV 267 and GISV 216. Leaf hopper resistance was significantly correlated with leaf lobing ( $r = 0.48^*$ ), indicating a potential link between leaf morphology and resistance traits. Notably, genotypes GSHV 171, AKH 2006-2, NH 630, GSHV 173, RS 2765, AKH 2012-8, and AKH 1351 were comparable to the resistant check (NDLH 1938) and identified as promising sources of leaf hopper resistance. These findings provide valuable insights into genetic divergence, phenotypic diversity, and potential resistance sources, contributing to the development of resilient cotton cultivars with improved productivity and pest tolerance.

## 12

**Title:** Reduced survivorship, host preference, and feeding damage by *Helicoverpa zea* (Lepidoptera: Noctuidae) on cotton plants colonized by the endophyte *Beauveria bassiana* (Ascomycota: Hypocreales).

**Author:** Hadi Farrokhzadeh, Stefan T Jaronski, Arash Rashed

**Imprint:** *Journal of Economic Entomology*, toae302, <https://doi.org/10.1093/jee/toae302>

**Abstract:** The GHA strain of *Beauveria bassiana* (Balsamo) Vuillemin (Ascomycota: Hypocreales) is known to establish symbiotic relationships with some plant species. The present study was developed to determine whether the foliar application of *B. bassiana*-GHA and *B. bassiana* ANT-03, another commercial *B. bassiana*, results in the successful colonization of cotton, *Gossypium hirsutum* L., and examine whether the endophyte can influence the survivorship and feeding damage by the corn earworm, *Helicoverpa zea* Boddie (Lepidoptera: Noctuidae). Using polymerase chain reaction, colonization success by *B. bassiana*-GHA, 3, 7, 14, and 21 days after inoculation was estimated at 83.3%, 100%, 91.7%, and 83.3%, respectively. The colonization success based on the mycelial outgrowth method was 41.7%, 66.7%, 58.3%, and 50%, 3, 7, 14, and 21 days after inoculation, respectively. *Beauveria bassiana* ANT-03 did not colonize cotton. Corn earworms preferred untreated plants over the neonicotinoid and *B. bassiana*-GHA treatments. The *B. bassiana* ANT-03-treated plants and controls were not distinguished from one another by the corn earworms. The corn earworm survivorship was higher on the control plants, compared to plants treated with *B. bassiana* ANT-03, *B. bassiana*-GHA, and the neonicotinoid insecticide. The neonicotinoid insecticide, *B. bassiana*-GHA, and *B. bassiana* ANT-03 reduced corn earworm damage compared to the untreated controls. Our results demonstrated the potential for *B. bassiana*-GHA to be used as a biological control agent against *H. zea* in cotton.

## 13

**Title:** Efficacy and Utility of MPP51AA2-Traited Cotton as a Management Tool for Cotton Fleahoppers [*Pseudaatomoscelis seraitus* (Reuter)]

**Author:** Arthur, Brady Paul

**Imprint:** <https://hdl.handle.net/1969.1/1582837>

**Abstract:** In Texas the cotton fleahopper (*Pseudaatomoscelis seriatus* (Reuter)) is considered a highly economically damaging pest of cotton (*Gossypium hirsutum* L.). Current control methods rely heavily on the use of foliar applied chemical insecticides during the growing season. The Mpp51Aa2.834\_16 gene in cotton (ThryvOn) has proven effective against thrips and *Lygus* spp. with piercing and sucking feeding behaviors, suggesting the trait may also provide similar efficacy on cotton fleahoppers. Field trials were conducted in 2019, 2020, and 2021 comparing a ThryvOn cultivar to a non-traited isolate under insecticide-treated and untreated conditions. While cotton fleahopper population differences between the traited and non-traited plants were not consistently noted during the pre-bloom squaring period, there was a consistent increase in square retention in cotton expressing Mpp51Aa2 relative to non-traited

cotton. Additionally, cotton expressing Mpp51Aa2 offered similar square protection relative to non-treated cotton treated with insecticides for cotton fleahopper. These findings indicate that the Mpp51Aa2 protein should provide benefits of delayed nymphal growth, population suppression, and increased square retention. In the choice assay, feeding by cotton fleahoppers significantly reduced square retention in the non-treated cotton to 46%, while ThryvOn cotton retained 60% of squares. In the no-choice assay, cotton fleahopper nymph feeding significantly reduced square retention in the non-treated cotton to 61%, whereas ThryvOn cotton was unaffected. Our findings indicate that the Mpp51Aa2 protein influences cotton fleahopper feeding preference and the susceptibility of cotton plants to damage caused by cotton fleahoppers. To evaluate the feeding behavior of the cotton fleahoppers on ThryvOn cotton an electropenetrography (EPG) coupled with a Giga-8 DC EPG amplifier was used to monitor the probing activity cotton fleahopper nymphs on ThryvOn and non-treated cotton squares. Nymphs were placed on a square for 8 hours and waveforms were characterized as non-probing, cell rupturing, and ingestion. There were significantly more cell rupturing events on ThryvOn (14.8) than on non-treated squares (10.3) but there were no differences in ingestion events. However, the duration of ingestion events was significantly shorter at 509s on ThryvOn compared to 914s on non-treated squares. The results of this study provide evidence that ThryvOn affects the feeding behavior of cotton fleahoppers.

## PLANT BREEDING AND GENETICS

### 14

**Title:** Genome-wide identification and characterization of FORMIN gene family in cotton (*Gossypium hirsutum* L.) and their expression profiles in response to multiple abiotic stress treatments.

**Author:** Suronjeet Kumar Paul, Md Shohel Ul Islam, Nasrin Akter, Fatema Tuz Zohra, Shuraya Beente Rashid, Md. Shakil Ahmed, Shaikh Mizanur Rahman, Md. Abdur Rauf Sarkar

**Imprint:** PLOS One, Published: March 3, 2025,  
<https://doi.org/10.1371/journal.pone.0319176>

**Abstract:** FORMIN proteins distinguished by FH2 domain, are conserved throughout evolution and widely distributed in eukaryotic organisms. These proteins interact with various signaling molecules and cytoskeletal proteins, playing crucial roles in both biotic and abiotic stress responses. However, the functions of FORMINs in cotton

(*Gossypium hirsutum* L.) remain uncovered. In this study, 46 FORMIN genes in *G. hirsutum* (referred to as *GhFH*) were systematically identified. The gene structures, conserved domains, and motifs of these *GhFH* genes were thoroughly explored. Phylogenetic and structural analysis classified these 46 *GhFH* genes into five distinct groups. *In silico* subcellular localization, prediction suggested that *GhFH* genes are distributed across various cellular compartments, including the nucleus, extracellular space, cytoplasm, mitochondria, cytoskeleton, plasma membrane, endoplasmic reticulum, and chloroplasts. Evolutionary and functional diversification analyses, based on on-synonymous ( $Ka$ ) and synonymous ( $Ks$ ) ratios and gene duplication events, indicated that *GhFH* genes have evolved under purifying selection. The analysis of *cis*-acting elements suggested that *GhFH* genes may be involved in plant growth, hormone regulation, light response, and stress response. Results from transcriptional factors TFs and gene ontology analysis indicate that FORMIN proteins regulate cell wall structure and cytoskeleton dynamics by reacting to hormone signals associated with environmental stress. Additionally, 45 putative ghr-miRNAs were identified from 32 families targeting 33 *GhFH* genes. Expression analysis revealed that *GhFH1*, *GhFH10*, *GhFH20*, *GhFH24*, and *GhFH30* exhibited the highest levels of expression under red, blue, and white light conditions. Further, *GhFH9*, *GhFH20*, and *GhFH30* displayed higher expression levels under heat stress, while *GhFH20* and *GhFH30* showed increased expression under salt stress compared to controls. The result suggests that *GhFH20* and *GhFH30* genes could play significant roles in the development of *G. hirsutum* under heat and salt stresses. Overall these findings enhance our understanding of the biological functions of the cotton FORMIN family, offering prospects for developing stress-resistant cotton varieties through manipulation of *GhFH* gene expression.

## 15

**Title:** Post-polyploidization centromere evolution in cotton.

**Author:** Hu Yan, Jinlei Han, Shangkun Jin, Zegang Han, Zhanfeng Si, Sunyi Yan,

**Imprint:** Nature Genetics (2025)

**Abstract:** Upland cotton (*Gossypium hirsutum*) accounts for more than 90% of the world's cotton production and, as an allotetraploid, is a model plant for polyploid crop domestication. In the present study, we reported a complete telomere-to-telomere (T2T) genome assembly of Upland cotton accession Texas Marker-1 (T2T-TM-1), which has a total size of 2,299.6 Mb, and annotated 79,642 genes. Based on T2T-TM-1, interspecific centromere divergence was detected between the A- and D-subgenomes and their corresponding diploid progenitors. Centromere-associated repetitive sequences (CRCs) were found to be enriched for Gypsy-like retroelements. Centromere size expansion,

repositioning and structure variations occurred post-polyploidization. It is interesting that CRC homologs were transferred from the diploid D-genome progenitor to the D-subgenome, invaded the A-subgenome and then underwent post-tetraploidization proliferation. This suggests an evolutionary advantage for the CRCs of the D-genome progenitor, presents a D-genome-adopted inheritance of centromere repeats after polyploidization and shapes the dynamic centromeric landscape during polyploidization in polyploid species.

## 16

**Title:** Tissue-Specific RNA-Seq Analysis of Cotton Roots' Response to Compound Saline-Alkali Stress and the Functional Validation of the Key Gene GhERF2.

**Author:** Aiming Zhang, Qiankun Liu, Xue Du, Baoguang Xing, Shaoliang Zhang

**Imprint:** Plants 2025, 14(5), 756; <https://doi.org/10.3390/plants14050756>

**Abstract:** Saline-alkali stress is one of the major abiotic stresses threatening crop growth. Cotton, as a “pioneer crop” that can grow in saline and alkali lands, is of great significance for understanding the regulatory mechanisms of plant response to stresses. Upland cotton has thus become a model plant for researchers to explore plant responses to saline-alkali stresses. In this study, RNA sequencing was employed to analyze tissue-specific expression of root tissues of TM-1 seedlings 20 min after exposure to compound saline-alkali stress. The RNA-Seq results revealed significant molecular differences in the responses of different root regions to the stress treatment. A total of 3939 differentially expressed genes (DEGs) were identified from pairwise comparisons between the non-root tip and root tip samples, which were primarily enriched in pathways including plant hormone signal transduction, MAPK signaling, and cysteine and methionine metabolism. Combined with the expression pattern investigation by quantitative real-time PCR (qRT-PCR) experiments, a key gene, GhERF2 (GH\_A08G1918, ethylene-responsive transcription factor 2-like), was identified to be associated with saline-alkali tolerance. Through virus-induced gene silencing (VIGS), the GhERF2-silenced plants exhibited a more severe wilting phenotype under combined salt-alkali stress, along with a significant reduction in leaf chlorophyll content and fresh weights of plants and roots. Additionally, these plants showed greater cellular damage and a lower ability to scavenge reactive oxygen species (ROS) when exposed to the stress. These findings suggest that the GhERF2 gene may play a positive regulatory role in cotton responses to salt-alkali stress. These findings not only enhance our understanding of the molecular mechanisms underlying cotton response to compound saline-alkali stress, but also provide a foundation for future molecular breeding efforts aimed at improving cotton saline-alkali tolerance.

**Title:** Registration of three cotton germplasm lines with extremely high fiber strength derived from crosses between Upland cotton and diploid *Gossypium* species.

**Author:** Linghe Zeng, Erik J. Sacks, David D. Fang, Jinfa Zhang

**Imprint:** First published: 28 February 2025, Journal of Plant Registrations, <https://doi.org/10.1002/plr2.20422>

**Abstract:** USDA-ARS-GMD 2427 (Reg. no. GP-1158, PI 706599), USDA-ARS-GMD 2442 (Reg. no. GP-1159, PI 706600), and USDA-ARS-GMD 24141 (Reg. no. GP-1157, PI 706598) are noncommercial breeding lines of cotton (*Gossypium hirsutum* L.) released by the USDA-ARS at Stoneville, MS, in 2024. Tetraploid hybrids of tri-species, *G. arboreum* L./*G. hirsutum*/*G. aridum* Skovst (AADD) was derived from crosses between *G. arboreum* (AA) and a hexaploid bridge line, *G. hirsutum*/*G. aridum* (AADD) followed by three backcrosses to Upland cotton. Lines were selected in F<sub>5</sub> progenies and were evaluated at Stoneville in 2017, 2018, and 2019 and at seven locations across the US Cotton Belt in 2020 in the Regional High Quality test. In all tests, the three lines had significantly higher fiber strength than checks, 5% to 25% higher than the high fiber quality check, MD 15, and 10% to 18% higher than commercial checks. Other fiber properties including fiber length, uniformity, elongation, and micronaire were in acceptable ranges. Yield of the three lines was low to moderate compared with the high-yielding checks. The three lines had significantly different fiber strength and lint yield among themselves. USDA-ARS-GMD 24141 had high fiber strength with yield equivalent to SureGrow 747 and higher than MD 15. This line had intermediate resistance to *Fusarium* wilt race 4 compared to the susceptible checks and resistant checks. USDA-ARS-GMD 24141 is registered with another two sister lines, USDA-ARS-GMD 2427 and USDA-ARS-GMD 2442. The released germplasm lines can be used by breeders for genetic improvement of fiber strength and by molecular scientists for identification of high fiber strength genes and their genomic locations.

**Title:** The History of the Development Of Old-World Cotton Species.

**Author:** KH. Muminov , B. Amanov , A. Buronov , N. Tursunova , L. Valiyev , O. Omonov , S. Kodirova , E. Pirnazarov , and A. Iskandarov

**Imprint:** SABRAO Journal of Breeding and Genetics 57 (1) 126-136, 2025 <http://doi.org/10.54910/sabrao2025.57.1.13>

**Abstract:** Several laws have reached creation for studying the world cotton diversity, with an enormous theoretical and practical importance. For practical selection, the characteristics of special value are the bush shape, its durability and non-recumbency, types of branching, and the branches" structure: the size, shape, and opening rates of the ripe bolls, quick entry into the crop, and quick ripening. Therefore, it is necessary to study its relationship with the day length and light period, to irrigation, soil fertility, characteristics of the saline soil, and the existence of other similar signs. From such diversity, it showed cotton is an extremely flexible crop with great opportunities for selection, including the selection of base material. Specifically, the diploid species, such as, *Gossypium herbaceum* and *Gossypium arboreum*, have great significance to selection. These old-world cotton species are the results of centuries of evolution. Concepts about the origin, botanical composition, relations, evolution, and geographical distribution of cultivated and wild cotton species have been inaccurate until now. Therefore, it is obligatory to revise and update, correct, and supplement the existing information.

## 19

**Title:** The Analysis of the Glycosyltransferase Activity Gene Family in *Gossypium hirsutum* and Functional Verification of GTs Conferring Resistance to *Verticillium* Wilt.

**Author:** Mingli Zhang, Fang Zhu, Guo Sun, Yingjie Mi, Xuekun Zhang, Sifeng Zhao, Yu Yu \*, Hui Xi \*

**Imprint:** Posted Date: 25 February 2025, doi: 10.20944/preprints202502.2038.v1

**Abstract:** Glycosyltransferases (GTs) play an important role in plant growth and development, and responses to biotic and abiotic stresses. However, the function of GTs gene family in cotton resistance to *Verticillium* wilt is limited. In the present study, transcriptome analysis revealed eight GTs upregulated in susceptible cotton varieties and downregulated in resistant cotton varieties during early *Verticillium dahliae* inoculation, indicating which were involved in regulating the infection of *V. dahliae* in cotton. Promoter analysis revealed a high prevalence of MeJA (methyl jasmonate) and ABA (abscisic acid) -related cis-acting elements among these GTs. Genome-wide and location analysis of the homologous genes showed that these GTs were relatively conserved in evolution. Furthermore, a virus-Induced Gene Silencing (VIGS) experiment results demonstrated a reduction in disease resistance after *GhGT61* silencing. These insights not only deepen our understanding of the GT family's role in cotton but also provide a foundation for future research on the disease resistance mechanisms of these genes.

**Title:** Late embryogenesis abundant gene *GhLEA-5* of semi-wild cotton positively regulates salinity tolerance in upland cotton

**Author:** Chunyan Tian, Abdul Rehman, Xiaoyang Wang, Zhenzhen Wang, Hongge Li, Jun Ma, Xiongming Du, Zhen Peng, Shoupu He

**Imprint:** Gene, Volume 949, 15 May 2025, 149372

**Abstract:** The productivity and quality of cotton are significantly compromised by salt stress. In this study, the full length of encoding region and genomic DNA sequences of *GhLEA\_5A/D* (*Gh\_A10G166600* and *Gh\_D10G188300*), which belong to the late embryogenesis abundant gene family in allotetraploid upland cotton (*Gossypium hirsutum* L.) and semi-wild cotton (*Gossypium purpurascens*), were isolated and their salt tolerance was experimentally confirmed. Analysis of sequence alignments and phylogenetic trees indicated a significant level of homology between *GhLEA-5A* and *GhLEA-5D*. Additionally, a conserved protein motif was consistently identified across these sequences. The transcriptome data analysis showed that the expression level of *GhLEA-5A/D* was substantially enhanced in the leaves of salt-tolerant *G. purpurascens* accessions compared to salt-sensitive materials. In the real-time quantitative reverse transcription PCR (qRT-PCR) assays, notable expression levels of the *GhLEA-5D* gene were detected in salt-tolerant upland cotton materials following exposure to salt stress at 3 and 12-hour time points. The suppression of *GhLEA-5A/D* transcription via Virus-induced Gene Silencing (VIGS) technology significantly exacerbates salt sensitivity in cotton. This is evidenced by nearly 50 % increase in malondialdehyde (MDA) content alongside a 60 % reduction in peroxidase (POD) levels in salt-treated plants when compared to the control group. The overexpression of the *GhLEA-5A/D* gene conferred enhanced salt tolerance in *Arabidopsis*, resulting in a 25 % increase in root length, a 30 % improvement in survival rate, a 15 % increase in water retention, and a 15 % boost in photosynthetic efficiency. The chlorophyll fluorescence parameters, enzyme activities, diaminobenzidine, and nitroblue tetrazolium staining suggested that *GhLEA-5A/D* likely exhibited a positive regulatory role for cotton responding to salt stress. Furthermore, we identified 76 candidate proteins that potentially interact with *GhLEA-5* in the yeast two-hybrid screening library. These results provide a theoretical basis for studying the mechanism of cotton salt tolerance and offer new resources for improving cotton salt tolerance genes.

**Title:** Time-course RNA-seq analysis of upland cotton (*Gossypium hirsutum* L.) responses to Southern root-knot nematode (*Meloidogyne incognita*) during compatible and incompatible interactions.

**Author:** Sameer Khanal, Pawan Kumar, Mychele B. da Silva, Rippy Singh, Nelson Suassuna,

**Imprint:** BMC Genomics, Published: 24 February 2025, Volume 26, article number 183, (2025)

**Abstract:** The Southern root-knot nematode (*Meloidogyne incognita*) poses a substantial threat to cotton (*Gossypium hirsutum* L.) by causing significant agricultural losses. Host plant resistance is the most plausible approach for minimizing these losses. QTL mapping and early transcriptomic studies have identified candidate genes within the QTL regions on chromosome 11 (*qMi-C11*) and chromosome 14 (*qMi-C14*). Although these QTL regions have been fine-mapped and candidate genes identified, expression profiling of *Meloidogyne-Gossypium* interactions across different stages of infection could further refine the list of candidate genes. This study advances our understanding of the molecular mechanisms underlying the resistance conferred by *qMi-C11* and *qMi-C14* against Southern root-knot nematode. Results -Using time-course RNA-seq analyses across nematode developmental phases, we uncovered transcriptomic events—both genome-wide and within QTL intervals—underlying defense responses during compatible interactions (with Cocker 201, a susceptible line) and incompatible interactions (with M-120 RNR, a resistant line). Basal defense responses were observed in both compatible and incompatible interactions, with stronger expression in the incompatible interaction. Nematode-responsive genes associated with defense pathways showed distinct dynamics, characterized by repression during compatible interactions and early induction, greater diversity, and heightened upregulation during incompatible interactions. This study uncovers a broad repertoire of disease resistance and putative resistance genes, as well as pathogenesis-related genes, ligands, and receptors, that are differentially expressed in response to nematode parasitism. Mapping of these genes across the cotton genome identified promising candidates, including Gh\_A11G3090 (*PUB21*) and Gh\_A11G2836 (*RPPL1*) within the chromosome 11 QTL region, and Gh\_D02G0257 (*RLP12*) and Gh\_D02G0259 (*RLP12*) within the chromosome 14 QTL region. Conclusions- The findings of this study deepen our understanding of host-nematode interactions, identify candidate genes for downstream

applications, and contribute to advancements in resistance breeding and sustainable nematode management strategies.

22

**Title:** Genome-Wide Characterization of Gibberellin Oxidase Genes (*GbGAoxs*) and Illustration of Their Molecular Responses to Exogenous GA<sub>3</sub> in *Gossypium barbadense*

**Author:** Zixin Zhou, Weiran Wang, Nan Zhao, Meng Wang

**Imprint:** *Int. J. Mol. Sci.* 2025, 26(5), 1985; <https://doi.org/10.3390/ijms26051985>

**Abstract:** As key enzymes in the gibberellin (GA) biosynthesis pathway, GAoxs function as regulators of bioactive GA levels and plant architecture, yet little is understood about GAoxs in *Gossypium*. In this study, 78 GAox genes identified in four cotton species were divided into three subgroups: GA2ox, GA3ox, and GA20ox. Syntenic relationships of GAoxs in *Gossypium* suggested that divergencies in gene function may be attributed to whole-genome duplication during evolution. *Cis*-acting element analysis suggested that the *GbGAox* genes might participate in plant growth, development, and hormone responses. Moreover, transcriptome analysis was performed to characterize the molecular response of the exogenous GA<sub>3</sub> application. It was found that DEGs (differentially expressed genes) are widely involved in cell division and cell wall modification, in which the most *XTH* (xyloglucan endotransglucosylase/hydrolase) and *GAox* genes responded actively to the exogenous GA<sub>3</sub> treatment. Some transcription factors and protein kinases cooperated with those *GbGAoxs* in response to GA<sub>3</sub>. These findings underline the biological function of *GAox* genes and their responses to GA<sub>3</sub> in regulating plant growth in *Gossypium barbadense*.

### 23

**Title:** Evaluation of seed treatment fungicides for cotton seedling disease management near Belle Mina, AL, 2024

**Author:** Bisho Ram Lawaju, Claire Schloemer, and Kathy Lawrence

**Imprint:** Published Online:26 Feb 2025<https://doi.org/10.1094/PHP-01-25-0033-PDMR>

**Abstract:** Cotton seedling diseases caused by fungal pathogens (*Rhizoctonia solani*, *Thielaviopsis basicola*, *Pythium* spp., *Fusarium* spp.) can reduce plant survival and yield, posing a significant challenge to production. Common symptoms include damping-off, root rot, and stunted growth. This study evaluated the effectiveness of seed treatment fungicides for improving cotton (*Gossypium hirsutum* 'DP 2038 B3XF') establishment and yield. The trial was conducted in 2024 at the Tennessee Valley Research and Extension Center, Belle Mina, AL. Findings will help growers select effective treatments to enhance seedling health and optimize yield, contributing to improved cotton production under varying environmental conditions.

### 24

**Title:** Evaluation of Salt-Tolerant Germplasms and Identification of Salt Tolerance-Related Proteins in Upland Cotton at the Seedling Stage.

**Author:**Xiawen Li, Abdul Rehman, Zhenzhen Wang, Hongge Li

**Imprint:** *Int. J. Mol. Sci.* 2025, 26(5), 1982; <https://doi.org/10.3390/ijms26051982>

**Abstract:** Currently, developing cotton cultivation in saline-alkali soils is a vital focus for restructuring the cotton industry in China. The seedling stage, specifically the three-leaf stage, is a crucial period for assessing the salt tolerance of cotton. This research examined 430 natural populations of upland cotton, including 45 semi-wild germplasm lines of *Gossypium purpurascens*. We measured the phenotypic responses of salt stress injury on seedlings as well as potassium (K), calcium (Ca), sodium (Na), and magnesium (Mg) concentrations in the roots, stems, and leaves following a 72-h exposure. The comprehensive salt tolerance index (CSTI) was determined using a membership function, principal component analysis, and cluster analysis based on 48 phenotypic

traits related to salt tolerance. The results revealed significant variations in the phenotypic traits of the ion group under salt stress. Salt stress greatly affected the relative contents of Mg, K, and Ca ions in the above ground parts of cotton, and correlations were observed among the 48 indices. The CSTI was calculated using seven principal component indexes, identifying 30 salt-tolerant, 114 weakly salt-tolerant, 39 salt-sensitive, and 4 highly sensitive materials based on cluster analysis. Among the 45 *G. purpurascens* cotton resources, 28 were weakly salt-tolerant, while 17 were salt-sensitive. Through TMT (Tandem Mass Tag)-based quantitative analysis, we identified 3107 unique peptides among 28,642 detected peptides, resulting in 203,869 secondary mass spectra, with 50,039 spectra successfully matched to peptides. Additionally, we identified several salt tolerance-related pathways (carbon metabolism; glutathione metabolism; the biosynthesis of amino acids, etc.) and proteins classified within the CAZy (Carbohydrate-Active Enzyme) family and expansin proteins. The results of this study concerning salt-tolerant materials provide a crucial theoretical foundation for the identification and evaluation of salt-tolerant breeding parents in cultivated cotton.

## 25

**Title:** Melatonin-mediated methylglyoxal homeostasis and regulation of autophagy during seed germination under PEG-induced drought stress in upland cotton.

**Author:** Deepika Dake, Laha Supriya, Amarjeet Kumar and Padmaja Gudipalli

**Imprint:** bioRxiv preprint doi: <https://doi.org/10.1101/2025.02.18.638685>; this version posted February 23, 2025.

**Abstract:** Methylglyoxal (MGO), toxic byproduct of glycolysis, acts as a signaling molecule at low levels, but its over-accumulation during drought stress disrupts redox balance and accelerates cell death. Contrarily, melatonin maintains redox balance, particularly during stress. The redox status and MGO level might differ in drought-sensitive and drought-tolerant varieties, so shall the melatonin's effect. The study evaluated the effect of melatonin-priming on MGO detoxification and autophagy during polyethylene glycol (PEG)-induced drought stress during seed germination in drought-sensitive (L-799) and drought tolerant (Suraj) varieties of upland cotton. Melatonin-priming increased endogenous melatonin content, reduced MGO accumulation and advanced glycation end-products (AGEs), and downregulated the expression of MGO biosynthesis genes in L-799 under stress. The expression and activities of glyoxalases and non-glyoxalases were upregulated, showing melatonin's effectiveness in MGO detoxification. Additionally, priming upregulated expressions of TPI1, PGK5, and PK1 and downregulated HK3 expression, allowing better conversion of glucose to pyruvate, leading to reduced MGO in L-799. The downregulation of necrosis-related genes with reduced cell death in L-799 shows the potential of priming

in maintaining cell viability under stress. Furthermore, upregulated expression of SnRK1.1, SnRK2.6 genes and KIN10 protein levels, with enhanced autophagy markers (ATGs, MDC-stained bodies, lipidated-ATG8), confirmed improved autophagy in melatonin-primed L-799 under stress. Despite lowering ABA, melatonin-mediated MGO homeostasis likely activated MAPK6, preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission. bioRxiv preprint doi: <https://doi.org/10.1101/2025.02.18.638685>; this version posted February 23, 2025. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission. This article is intended to highlight the biological processes independent of ABA in stressed plants. Conversely, Suraj, with higher endogenous melatonin and inherent stress tolerance, showed limited response to priming. Thus, the study illustrates melatonin's role in regulating MGO homeostasis and autophagy under drought stress in cotton.

## 26

**Title:** Longevity of neonicotinoid seed treatments in cotton seedlings under various deficit irrigation levels.

**Author:** Aqeela Sehrish, Suhas Vyavhare, Megha Parajulee, Cade Coldren, Haydee Laza & Catherine Simpson

**Imprint:** *Scientific Reports* volume 15, Article number: 6576 (2025)

**Abstract:** Neonicotinoids are one of the most widely used classes of insecticides in agriculture. They are systemic insecticides mainly used as seed treatments to manage sucking insect pests in a wide range of field crops. Environment and growing conditions can impact the efficacy of neonicotinoid seed treatments. To evaluate this, an experiment was conducted to study the interactive effect of soil, water levels on the neonicotinoid concentration and plant growth in cotton. The experiment was laid out in a split-plot design, with three water levels, 30%, 60%, and 100% (control) of recommended irrigation and four seed treatments, including clothianidin, thiamethoxam, imidacloprid and an untreated control. Cotton seedlings were collected and analyzed for physiological changes and neonicotinoid concentrations at 15, 30 and 45 days after germination (DAG). Data were collected on plant height, fresh biomass and leaf area. The neonicotinoid concentrations were analyzed in leaf tissues using LC-MS/MS. The 30% and 60% of recommended irrigation treatments resulted in significantly taller seedlings with greater biomass and leaf area compared to the 100% water saturation (control) treatment. Thiamethoxam-treated seedlings had greater plant height and shoot fresh mass compared to clothianidin and the untreated control, whereas imidacloprid-treated seedlings had greater leaf area than thiamethoxam, clothianidin, and control at all water levels. 30% recommended irrigation increased neonicotinoid concentrations in leaf tissues, with clothianidin showing higher levels

compared to other neonicotinoids at 45 DAG. Neonicotinoid seed treatment efficacy may vary with environmental factors, impacting sustainable pest control.

## 27

**Title:** Suppression of Seeds Mycoflora Involved on Cotton Seedling Damping-Off Disease by Chitinolytic Actinomycetes.

**Author:** Ashour, A. Z. A. and Aida H. Afify

**Imprint:** J. of Agricultural Chemistry and Biotechnology, Mansoura Univ., Vol. 16 (2):15 - 19, 2025

**Abstract:** Actinobacteria as biological pesticides are considered an economical and safe method, especially for improving plant growth. In this study, five actinobacterial isolates were obtained from farming soil samples and evaluated for their biocontrol capacity against five or more fungal isolates that cause seedling damping-off disease in cotton. From non-sterilized cotton seeds, the frequency (%) of isolated fungi was as follows: *Rhizoctonia solani* (25.12%), *Fusarium* spp. (24.82%), and *Macrophomina phaseolina* (22.12%) were the most dominant fungi. Other fungi were found at lower frequencies, including *Penicillium* sp. (5.44%) and *Aspergillus* sp. (5.12%). When Koch's postulates were applied, the fungal isolates caused the same symptoms of pre- and post-emergence damping-off, as well as reduced seedling survival. *R. solani*, *Fusarium* spp., and *M. phaseolina* exhibited high virulence in cotton seedlings, while *Penicillium* sp. and *Aspergillus* sp. were considered moderately virulent. Several morphologically distinct actinomycete isolates were screened for chitinase production. The actinomycete isolate that produced the highest chitinase activity, indicated by the formation of a clear zone, was identified. This isolation was found to match *Streptomyces gelaticus* with 99.73% similarity. Antagonistic tests showed that this *Streptomyces gelaticus* strain inhibited all fungal pathogens. The highest inhibition zones were observed against *Rhizoctonia solani*, *Fusarium* spp., *Penicillium* sp., and *Aspergillus* sp., while *Macrophomina phaseolina* exhibited the lowest inhibition. In conclusion, actinomycetes, particularly *Streptomyces* spp., hold great potential as biocontrol agents for sustainable agriculture and the management of plant diseases.

### 28

**Title:** Formation of the structure of naturally colored cotton fiber.

**Author:** R. B. Rahmonova; M. X. Ravshanova; N. P. Shomurodov; M. A. Raxmatullayeva

**Imprint:** *AIP Conf. Proc.* 3268, 040038 (2025), <https://doi.org/10.1063/5.0257992>

**Abstract:** The structure of the cotton fiber is formed during its maturation. During the formation of the structure of cotton fiber, cellulose biosynthesis and the ordered arrangement of macromolecules of this substance occur. The composition of the plant cell of cotton fiber contains substances of the tannin group, substances of phenolic compounds that contribute to the development of colored cotton fiber, also perform the function of tanning and antiseptic components. Tannins are able to form strong bonds with proteins, polysaccharides and other organic compounds. The article provides information on the stages of the formation of the structure of colored cotton fiber, the effect of pigments on the natural coloring of fibers in yellow, green and brown colors. At the moment, one of the promising directions is the development of the use of natural colored cotton fiber and its production, since the chemical processing of cotton fiber in the textile industry requires a large amount of water, energy, chemicals and other resources. The process of dyeing fabrics pollutes the environment due to the use of carcinogenic chemical dyes and by-products. Naturally, colored cotton is considered an environmentally friendly raw material for textiles, it can be considered as a product completely free of chemicals, so the demand for colored cotton is growing every day.

### 29

**Title:** GhMYB102 affects cotton fibre elongation and secondary wall thickening by regulating GhIRX10 in cotton.

**Author:** Aimin Wu, Tong Shen, Jianhua Lu, Xiaokang Fu, Miaoqian Yang, Mengxi Sun, Liang Ma, Boying Lian, Hongmei Wu, Yiran Li, Shuxun Yu, Hengling Wei, Hantao Wang

**Imprint:** *Plant Biotechnol J.* . 2025 Apr;23(4):1329-1344.  
doi: 10.1111/pbi.14588. Epub 2025 Feb 18.

**Abstract:** Upland cotton (*Gossypium hirsutum*) is a principal economic crop and a fundamental raw material for the textile industry. The quality of cotton fibres is significantly influenced by the synthesis of cell wall polysaccharides. This study focuses on GhIRX10, a beta-1,4-xylosyltransferase crucial for xylan backbone synthesis. Overexpression of GhIRX10 enhances xylan synthesis, which impacts fibre elongation and secondary cell wall thickening. GhMYB102, identified as a direct regulator of GhIRX10 expression, was confirmed through comprehensive validation. Overexpression of GhMYB102 resulted in a similar phenotype as OE-GhIRX10: increased cell wall thickness and reduced fibre length. Overexpression of GhMYB102 upregulated the expression of key cell wall synthesis-related genes, including GhCESA4/7/8, GhIRXs, GhCESAs, GhGUXs, GhTBLs, GhXTHs, and GhXXTs. Consequently, the cellulose and hemicellulose contents in OE-GhMYB102 lines were significantly increased. GhMYB102 was also validated as a target gene regulated by GhFSN1 and GhMYB7, with the ability to reciprocally regulate GhFSN1 expression. In summary, we propose a regulatory model where GhMYB102 promotes the expression of GhIRX10 and other cell wall-related genes, thereby affecting fibre quality. This study elucidates the regulatory network of secondary cell wall synthesis in cotton and provides potential targets for improving fibre quality through molecular breeding.

## 30

**Title:** Specific expression of a fusion gene Lc-GhPAP1D results in colored cotton fibers with increased flavonoid and lignin synthesis, but impaired elongation and secondary cell wall deposition.

**Author:** Lingfang Ran, Yaohua Li, Long Chen , Tong Mo , Nian Liu , Shijia Xu , Yucheng Su , Chuannan Wang , Aimin Liang , Jianyan Zeng , Wanting Yu , Jie Kong , Yuehua Xiao

**Imprint:** Journal of Integrative Agriculture Received 14 November 2024 Accepted 22 January, 2025

**Abstract:** Naturally colored cotton (NCC) represents a kind of eco-friendly and sustainable textile material. Limited colors and inferior yield and quality are the major obstacles to the wide application of NCCs. The present work aimed to generate new colored cotton by synthesizing and accumulating anthocyanins in fibers. Two anthocyanin regulatory genes Lc and GhPAP1D were fused and specifically expressed in fibers of the secondary cell wall (SCW) stage. The transgenic fibers exhibited pronounced purplish-red color at 20 to 30DPA (days post anthesis), and reddish-brown color at maturation. Meanwhile, expressing Lc and GhPAP1D led to reduced elongation rate and impaired SCW deposition in fibers, finally decreased fiber strength and length, and low lint percentage at maturation. Metabolomic and transcriptomic analyses

indicated that the whole flavonoid pathway was significantly up regulated, and multiple flavonoids, including anthocyanins, proanthocyanidins and flavonols, were accumulated in developing and mature fibers. It was also found that lignin biosynthesis and accumulation were significantly increased in fibers of the SCW synthesis stage. Our results provided a feasible strategy to promote anthocyanin synthesis and accumulation in cotton fibers, and also its side effects on fiber coloration and development, which laid the foundation for future NCC color innovation.

## 31

**Title:** Histone H3 lysine 27 trimethylation (H3K27me3) modulates the fiber cell initiation in upland cotton.

**Author:** Zhiqiang Zhang, Yingqiang Long, Yangai Liu, Wenqi Huo, Jintao Li, Zhongying Ren, Kunlun He, Fei Zhang, Jinfeng Guo

**Imprint:** Industrial Crops and Products, Volume 226, April 2025, 120751

**Abstract:** Histone methylation is pivotal in regulating the expression of numerous essential functional genes in plants. However, its specific function and mechanism in cotton fiber cell initiation remain poorly understood. The upland cotton (*Gossypium hirsutum* L.) variety Xuzhou142 (Xu142) and its *fuzzless-lintless* mutant Xu142 *fl* are ideal model materials for studying cotton fiber cell development. *In vitro* ovule culture analysis showed that the histone H3 lysine 27 trimethylation (H3K27me3) inhibitor RDS 3434 could inhibit fiber cell initiation and development. Cleavage under targets and tagmentation (CUT&Tag) and RNA sequencing (RNA-seq) data of -1-, 0-, and 1-day post-anthesis (DPA) ovules showed that H3K27me3 regulates fiber cell initiation by accumulating in Xu142 than in Xu142 *fl*. It was also found that H3K27me3 was negatively correlated with gene transcription, as 227 expressed genes showed an opposite trend to the H3K27me3 modification level and were identified to participate in multiple signaling pathways. Furthermore, the expression levels of ten potential genes related to fiber development were confirmed to correlate with H3K27me3 levels. The results demonstrate the critical role of H3K27me3 in fiber development process and present evidence supporting its involvement in cotton fiber cell initiation. The study lays the foundation and provides genetic resources for further investigations into genes related to fiber development.