



# GLEANINGS IN COTTON RESEARCH

## JULY 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  
In charge Library*

*Chetali Rodge  
Technical Officer (T5)*

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**Title:** Potassium dynamics in cotton with a white clover living mulch: A Georgia Piedmont case study.

**Author:** Chandler Gruener, Matthew Levi, Nicholas Basinger, Miguel Cabrera, Nicholas Hill

**Imprint:** Agrosyst Geosci Environ. 2025;8:e70103. [wileyonlinelibrary.com/journal/agg2](https://doi.org/10.1002/agg2.70103)  
1 of 12 <https://doi.org/10.1002/agg2.70103>

**Abstract:** Cover crop utilization is an important strategy for improving row crop sustainability and plays a critical role in managing plant–soil nutrient relations needed to maintain cotton (*Gossypium hirsutum* L.) yields in the southeastern United States. Most cover crops are annual species, but perennial cover crops, sometimes called “living mulches” (LMs), can provide year-round benefits. The effects of LM on nitrogen and carbon dynamics have been explored in corn systems. However, information on these dynamics and effects on other nutrients are limited in cotton systems. This project quantified the effect of a white clover LM on nutrient cycling of macro- and micronutrients (excluding N) in a cotton production system in the Georgia Piedmont. This included soil, plant, and pore water samples collected at important cotton reproductive states for 2 site-years with different soil fertility. Additional samples were taken between cotton growing seasons to evaluate soil–clover interactions. Nutrient responses in the system (specifically K) were connected to soil test levels for nutrients at the start of reproduction. Only when the soil had above optimum K levels (2021), the LM luxury consumed excess K from the soil. Cotton leaves had the greatest fluctuations in K concentrations when LM was present from pinhead to cutout when soil K was below optimum. In winter, the soil had the greatest concentration in treatments with the most clover relative to bare ground. Using optimal LM coverage can prevent excess K from potentially being lost from the system while not affecting cotton leaf K nutrition during reproductive growth.

**Title:** History And Present Day Of Cotton Culture In Ukraine.

**Author:** Sonets T. D, Kyienko Z. B.

**Imprint:** Publishing House “Baltija Publishing”, 2025, International scientific conference, DOI <https://doi.org/10.30525/978-9934-26-543-3-7>

**Abstract:** The year 2024 marked the resurgence of cotton cultivation in Ukraine. Analyzing archival data from 200 years of history, we can note repeated attempts to introduce cotton cultivation in Ukraine in order to displace foreign raw materials from Central Asia, Transcaucasia, India, Egypt, etc., for which many millions of rubles were paid in gold. The first attempts to develop cotton cultivation in Ukraine were at the beginning of the 18th century and for 100 years did not bring successful results, primarily due to the lack of early-ripening varieties and methods of its cultivation. In particular, in Ukraine they sowed seeds obtained from Marseilles in the village of Demiiivtsi (80 km from Odesa) [1, c. 96].

**Title:** Water and heat resource utilization influence cotton yield through sowing date optimization under varied climate.

**Author:** Hamad Khan , Nangial Khan , Zeeshan Khan , Han Yingchun , Yang Beifang , Lei Yaping , Zhi Xiaoyu , Xiong Shiwu , Shang Shilong , Ma Yunzhen, Jiao Yahui , Lin Tao

**Imprint:** Agricultural Water Management, Volume 313, 31 May 2025, 109491

**Abstract:** Drought threatens to destroy almost 70 % of the world's cotton supply. Optimizing sowing dates is an agricultural strategy that may help synchronize ecology and productivity. Field data on the coupling impact of various environmental resources on cotton and its response to climate change under sowing date control is still lacking, though. This study examined how resource use efficiencies like water use efficiency (WUE), water consumption, water productivity and heat production efficiency (PEsoil) changed during six sowing dates (S1-S6) over two years (2023 and 2024), characterized by distinct temperature and rainfall. Results revealed that in 2023, optimal climatic conditions and well-timed rainfall events led to a maximum seed cotton yield under S4 (+178 % increase), whereas late sowing (S6) led to a -10 % decrease compared to S1. However, in 2024, delayed sowing had a more adverse impact, with yield declined up to -39 %, likely due to irregular rainfall and suboptimal temperature distribution

during critical reproductive stages. The highest water use amounted to the flowering and boll development stages, exceeding 700 mm in late sowing treatments. However, WUE and WPc in delayed sowing were substantially lower than in early sowing, indicating inefficient resource conversion. Furthermore, statistical analysis of year-to-year specific positive correlations with resource use metrics were found to be significant with seed cotton yield. In 2023, WUE ( $R^2 = 0.8350$ ), WPc ( $R^2 = 0.7189$ ), and PEsoil ( $R^2 = 0.8586$ ) were correlated (strongly) with early sowing dates (S1 and S2) due to optimal timing of growth stages with respect to temperature and rainfall regimes. Though the overall  $R^2$  values were slightly reduced with changed rainfall pattern and cooler peak temperatures, early sowing still had a positive correlation with WUE ( $R^2 = 0.81$ ), WPc ( $R^2 = 0.69$ ), and PEsoil ( $R^2 = 0.78$ ) during 2024, implying stable performance under variable climatic conditions. Similarly, these early sowing treatments also had more stable aboveground biomass, had higher LAI and demonstrated the ability to synchronize phenological state with hydrothermal availability. Principal component analysis (PCA) also confirmed that early sowing increased resource use coupling and yield resilience under the two climatic years. This study introduces a novel integration of temporal sowing optimization, multi-sensor environmental monitoring, and resource coupling analysis. Future studies should focus on integrating climate forecasting models with sowing date recommendations to enable dynamic, site-specific cotton management.

#### 4

**Title:** Ensemble Feature Selection of Cotton Hyperspectral Reflectance to Predict Soil Health Genes.

**Author:** Josh Waldbieser; Rocker D'Antonio; Martin J. Wubben; John P. Brooks

**Imprint:** SoutheastCon 2025, Date of Conference: 22-30 March 2025, DOI: 10.1109/SoutheastCon56624.2025.1

**Abstract:** Monitoring soil microbiome metrics is currently costly and low-throughput. However, by measuring hyperspectral reflectance of cotton (*Gossypium hirsutum*), machine learning models can predict abundance levels for certain genes in the adjacent soil, increasing throughput. In this study, the prediction capabilities of elastic net models were measured for five soil health genes (16S rRNA, 18S rRNA, phoA, cbbLR, and ureC) using cotton hyperspectral reflectance values from 350–2500 nm. phoA, cbbLR, and ureC were partially predictable, but 18S rRNA was not predictable using this methodology. 16S rRNA, though, was consistently predictable using hyperspectral data. Knowing which regions of the spectrum are most influential for predicting gene levels can reduce data size, improve future modeling, and depending on the region, allow more accessible sensors. To find the important regions, this study tested five

feature selection methods: mutual information, agglomerative clustering, embedded linear coefficients, permutation importance, and genetic algorithms (both standalone and on the results of the other methods). No method gave consistently superior or inferior results for all genes, but the methods tended to select wavebands from the visible light regions (particularly yellow-orange light) over infrared regions. Additionally, this study demonstrated that restricting wavebands to visible light improved the model predicting 16S rRNA (RMSE = 0.724, MAE = 0.576, R2 = 0.501 on the standardized variable). The results suggest that infrared wavebands are less important than visible light wavebands in predicting soil microbiome genes, allowing future studies to use more accessible sensors.

## 5

**Title:** A Recent Review On Cotton And Climate Change In Pakistan: Impacts, Mitigation, And Adaptation.

**Author:** Asma, Maimoona Illyas, Neelam Zeb

**Imprint:** Vol. 3 No. 2 (Health & Rehab) (2025): Volume 3 Issue 2 2025

**Abstract:** Cotton (*Gossypium* spp.), a key member of the Malvaceae family, is one of Pakistan's most important cash crops, often referred to as "white gold" due to its significant contribution to the national economy and rural livelihoods. However, the sustainability of cotton production is increasingly threatened by the effects of climate change, including altered temperature patterns, irregular rainfall, pest outbreaks, glacial melting, and extreme weather events such as the catastrophic floods of 2010 and 2022. **Objective:** This narrative review aims to explore the impact of climate change on cotton production in Pakistan and to examine mitigation and adaptation strategies that can enhance the crop's resilience under changing climatic conditions. **Main Discussion Points:** The review discusses the various climate-induced stressors affecting cotton yields, such as heatwaves, drought, unpredictable monsoons, pest invasions, and soil degradation. It highlights the vulnerability of small-scale, rain-fed cotton farmers and underscores the urgent need for adaptive interventions. Climate-smart agriculture (CSA) is presented as a robust approach, encompassing water-smart practices (e.g., micro-irrigation, rainwater harvesting), weather-smart tools (e.g., agro-met advisories, stress-tolerant varieties), nutrient-smart inputs (e.g., precision fertilizers, IPM), and carbon-efficient methods (e.g., zero tillage, crop rotation), alongside institutional and educational supports.

## 6

**Title:** Nitrogen Application Enhances the Radiation Use Efficiency and Quality of Cotton (*Gossypium Hirsutum* L.) Under Divergent AgroEcological Conditions of Pakistan .

**Author:** Amjad Ali, Safdar Hussain, Wajid Nazeer, Muhammad Sarwar

**Imprint:** Journal of Bioresource Management, 12 (1). 2025

**Abstract:** Cotton being a cash crop plays a pivotal role in the economy of Pakistan. Climate change has a pronounced impact on radiation use efficiency and quality of cotton fiber. To find out how nitrogen affected the radiation use efficiency and fiber quality of cotton cultivars in Punjab, a field study using a split-plot design was carried out. The study under representation was conducted in three different locations over the course of two years (2016 and 2017): Adaptive Research Farm in Dera Ghazi Khan, The Regional Agriculture Research Institute, Bahawalpur and The College of Agriculture, University of Sargodha. Three cotton cultivars viz., FH-Lalazar, FH-142, and MNH-786 were treated to six different nitrogen levels (0, 60, 120, 180, 240, and 300 kg ha<sup>-1</sup>) at each of the experimental location. The data collected from the experiments were used as input to run the CROPGRO-model. Input data from 2016 and 2017 were used to calibrate the CROPGRO-cotton model, and its evaluation involved comparing the simulated and observed values. This model accurately predicted radiation use efficiency, cotton fiber quality, and nitrogen impact on three cotton cultivars. For cotton productivity, the arid climate of Bahawalpur is far superior to the semi-arid climates of Sargodha and Dera Ghazi Khan, Pakistan.

## 7

**Title:** Selectivity and stability of herbicides and herbicide combinations applied during the vegetation of cotton (*Gossypium hirsutum* L.).

**Author:** T. Barakova

**Imprint:** AGRICULTURAL SCIENCE AND TECHNOLOGY, VOL. 17, No 1, pp 59-65, 2025

**Abstract:** The experiment was conducted during the period 2019-2021 in the experimental field of the Field Crops Institute - Chirpan. The cotton cultivar grown for the purposes of the study was "Viki". The herbicidal products Bazagran 480 SL /bentazone/ - 1.5 l ha<sup>-1</sup>, Pendistar 40 SK /pendimethalin/ - 4 l ha<sup>-1</sup>, Pulsar 40 /imazamox/ - 1.2 l ha<sup>-1</sup>, Express 50 VG /tribenuron-methyl/ - 50 g ha<sup>-1</sup> and their herbicide combinations - Pulsar 40 - 1.2 l ha<sup>-1</sup> + Bazagran 480 SL - 1.5 l ha<sup>-1</sup>, Pulsar 40

- 1.2 l ha<sup>-1</sup> + Pendistar 40 SK - 4 l ha<sup>-1</sup>, Express 50 VG - 50 g ha<sup>-1</sup> + Bazagran 480 SL -1.5 l ha<sup>-1</sup>, Express 50 VG 50 g ha<sup>-1</sup> + Pendistar 40 SK - 4 l ha<sup>-1</sup> were studied. The herbicides were applied alone and in combinations in the cotton's growth stage BBCH 51 (First floral buds detectable). The aim was to study the selectivity and the stability of the performances of a group of herbicides and their herbicide combinations on cotton under different weather conditions. It was found that the herbicides Bazagran 480 SL and Pendistar 40 SK have excellent selectivity for the cotton cultivar Viki. The herbicides Pulsar 40 and Express 50 VG and their herbicide combinations with Bazagran 480 SL and Pendistar 40 SK showed higher phytotoxicity on cotton, and the highest phytotoxic effect was observed after the treatments with the herbicide mixtures Pulsar 40 + Pendistar 40 SK and Express 50 VG + Pendistar 40 SK. High yields were obtained after the alone application of the herbicides Pendistar 40 SK and Bazagran 480 SL. The remaining herbicides and herbicide combinations showed higher negative impact on the raw cotton yield. The herbicide mixtures Pulsar 40 + Pendistar 40 SK and Express 50 VG + Pendistar 40 SK had the lowest yields. The herbicides Bazagran 480 SL and Pendistar 40 SK and the herbicide combinations Express 50 VG + Pendistar 40 SK were technologically the most valuable as well. These treatments combined high yield values and high stability of this indicator in the different years.

## 8

**Title:** The Fertilizer Recommendation Support Tool: A relational database and decision interface tool.

**Author:** Megan Bourns, Greg Buol, John T. Spargo, Luke Gatiboni, Matt A. Yost, Nathan A. Slaton, Deanna L. Osmond

**Imprint:** Agric Environ Lett. 2025;10:e70016. [wileyonlinelibrary.com/journal/ael2](https://doi.org/10.1002/ael2.70016) 1 of 6  
<https://doi.org/10.1002/ael2.70016>

**Abstract:** The Fertilizer Recommendation Support Tool (FRST) Project is a collaborative effort involving most land grant institutions, USDA branches, nonprofit organizations, and private industry. The FRST objectives are to develop a soil fertility community of practice, preserve soil test correlation and calibration data in a relational database, and develop a decision tool to provide consistent soil test interpretations. Released in April 2024, the interactive tool acts on an evolving database that contained 1455 P trials, 1316 K trials, and 143 S trials from 44 states and Puerto Rico by March 1, 2025. Decision tool outputs include an interactive county-level map of available data and an estimated critical soil test value. The FRST relational database is a repository for soiltest-based P, K, and S data to support data-driven management recommendations. Continued success of the FRST project and decision tool utility rely on collaboration and support from the soil-test-based nutrient management community.

**Title:** Identifying seed cotton yield and abiotic stress response in cotton (*Gossypium hirsutum* L.) grown in the Arizona low desert .

**Author:** Alison L. Thompson, Kelly R. Thorp, Matthew T. Herritt

**Imprint:** Crop Science. 2025;65:e70058. [wileyonlinelibrary.com/journal/csc2](https://doi.org/10.1002/csc2.70058) 1 of 15  
<https://doi.org/10.1002/csc2.70058>

**Abstract:** Cotton (*Gossypium* sp.) is an important natural fiber crop that supports a multibillion-dollar textile industry worldwide. Improved breeding strategies are needed to develop heat- and drought-tolerant cotton. Six upland cotton entries were grown in the Arizona low desert at the Maricopa Agricultural Center, and seed cotton yields were recorded. Cotton responses to abiotic stressors, including high heat and low soil water content, were estimated from leaf chlorophyll and nitrogen content and chlorophyll fluorescence throughout the growing season. Statistical analysis identified important relationships and temporal patterns between the measured traits within each cotton entry. The data showed that leaf chlorophyll and nitrogen content and chlorophyll fluorescence can indicate degrees of abiotic stress tolerance along with improved seed cotton yields. These results agree with previous reports that low and stable leaf chlorophyll content and increased photochemical efficiency during heat stress are indicators of thermotolerance in cotton. The data also indicate that measurements collected just before and during peak flower are most informative for breeding programs when compared to a control.

**Title:** Evaluation of drought tolerance in naturally colored cotton (*Gossypium hirsutum*) under water deficit conditions.

**Author:** S. A. Khamdullaev, S. M. Nabiev, A. A. Azimov

**Imprint:** Vol 16 No 1 (2025): Regulatory Mechanisms in Biosystems

**Abstract:** Drought stress is one of the major environmental factors limiting cotton (*Gossypium hirsutum* L.) productivity, particularly in arid and semi-arid regions. Naturally colored cotton (NCC) has gained attention due to its eco-friendly fiber production; however, its drought tolerance remains insufficiently studied. This study aimed to evaluate the drought tolerance of colored cotton genotypes under water deficit conditions by assessing key agronomic traits and conducting molecular marker screening. Field experiments were conducted under two irrigation regimes: well-watered conditions (4,800–5,000 m<sup>3</sup>/ha) and drought stress conditions (2,800–3,000

m<sup>3</sup>/ha). The results showed that drought stress significantly reduced boll number, boll weight, fiber yield percentage, and total seed cotton yield across all genotypes. However, genotypes A-800, 011250, and 010108 exhibited higher Drought Tolerance Index (DTI) and Stress Tolerance Index (STI) values, indicating their superior drought resilience. Molecular screening using the NAU1190 DNA marker identified the 220 bp allele in genotypes 011460 and 011250, suggesting its potential association with drought tolerance. The ANOVA analysis revealed significant genotype × water regime interactions, indicating that both genetic and environmental factors influence drought tolerance. These findings provide valuable insights for breeding drought-tolerant colored cotton varieties, contributing to sustainable fiber production in water-limited regions.

## 11

**Title:** Physio-biochemical insights into Arsenic stress mitigation regulated by Selenium nanoparticles in *Gossypium hirsutum* L.

**Author:** Muhammad Mahmood Ahmed, Muhammad Mukheed, Tuba Tariq, Murtaza Hasan, Muhammad Shaaban, Ghazala Mustafa & Mehrnaz Hatami

**Imprint:** *BMC Plant Biology* volume 25, Article number: 482 (2025)

**Abstract:** Arsenic is a nonessential toxic metalloid hampering the growth and development of plants. The cotton (*Gossypium hirsutum*) is of great economic importance in the textile industry as well as in the production of edible oil. In developing countries, especially Pakistan, the export of cotton has a distinct position. However, there has been a significant decline in cotton production over the past few years due to climate change, heavy metals induction and biotic stresses. A notable decrease in cotton growth and product is observed in response to arsenic stress. Selenium nanoparticles (Se NPS) were prepared by green chemistry approach and characterized by UV-Vis, FTIR, and XRD to mitigate the heavy metals induced toxicity in cotton seedling. Results shows that arsenic toxicity causes a drastic decrease in photosynthesis, phenolics, proteins, growth of seedlings, relative water content, and overall plant biomass. However, these physio-biochemical attributes were upregulated by applications of Se NPs. Moreover, As stress causes severe oxidative damage by overproduction of MDA, H<sub>2</sub>O<sub>2</sub> and reactive oxygen species (ROS). The supplementation of SeNPs positively regulate the As stress in cotton seedlings by altering important antioxidant enzymes involved in ROS detoxification such as SOD, POD, and CAT. Se NPs ameliorate the toxicity by increasing activities of enzymatic and non-enzymatic antioxidants. The accumulation of As in roots alter the architecture of roots including reduced branching of roots. Current results suggest that the applications of selenium nanoparticles especially 20 mg/L concentration confidently alleviate the As induced toxicity in cotton seedlings.

**Title:** TCotton domestication modified strategies for optimizing photosynthesis by altering cell wall properties that influence CO<sub>2</sub> diffusion conductance.

**Author:** Dongsheng Sun,Zhangying Lei,Jaume Flexas, Cuncang Jiang,Ziliang Li,  
Hao Ding,Fang Liu

**Imprint:** Authorea. April 10, 2025. DOI: [10.22541/au.174427082.29860541/v1](https://doi.org/10.22541/au.174427082.29860541/v1)

**Abstract:** The cell wall plays a key role in determining mesophyll conductance ( $g_m$ ) and photosynthetic capacity. While the impact of wall thickness ( $T_{cw}$ ) on  $g_m$  is well understood, the influence of wall composition and structural interactions on  $T_{cw}$  and  $g_m$  remains unclear, and it is unknown whether these factors have been affected during crop domestication. In this study, we examined 25 wild and 13 domesticated *Gossypium* genotypes to investigate whether variations in  $T_{cw}$ , composition and structure affected  $g_m$  and photosynthesis. X-ray diffraction was used to analyze internal cell wall structure. Cotton domestication reduced  $T_{cw}$  by modifying pectin-to-(cellulose+hemicellulose) ratio and increasing cellulose crystallinity. In contrast, this ratio only correlated with  $g_m$  in wild genotypes, while in domesticated ones,  $1/(\text{pectin}+\text{cellulose}+\text{hemicellulose})$  ratio better explained  $g_m$  variation, reflecting internal property differences of cell wall. Cell wall composition and structure regulate  $g_m$  differently in wild and domesticated genotypes. In wild genotypes, pectin-to-(cellulose+hemicellulose) ratio influences CO<sub>2</sub> diffusion, while in domesticated ones, pectin may behave structurally, making  $1/(\text{pectin}+\text{cellulose}+\text{hemicellulose})$  a better predictor. We suggest that the exceptionally low  $T_{cw}$  values reported in cotton domesticated genotypes indicate they have reached the lower limit, which may impose physical constraints on component proportions and conformation.

### 13

**Title:** Widespread distribution and infestation of pink bollworm, *Pectinophora gossypiella* (Saunders) (Lepidoptera: Gelechiidae), in Bt cotton growing regions of India.

**Author:** Tadagavadi Nagaraju Madhu, Kamanur Muralimohan, Vakudavath Chinna Babu Naik, Dinesh Kumar Yadav

**Imprint:** Crop Protection, Volume 195, September 2025, 107257

**Abstract:** The pink bollworm (PBW), *Pectinophora gossypiella* (Lepidoptera: Gelechiidae), is a major pest of cotton, causing significant economic damage. However, comprehensive data on its prevalence and impact across India's cotton-growing regions (North, Central, and South) is limited. To fill this knowledge gap, extensive surveys were conducted from 2019 to 2021 in 164 locations across 41 cotton-growing districts in 10 states, assessing PBW distribution and its potential damage to Bt cotton. We evaluated PBW incidence and severity at various crop stages, including flowering, boll formation, and maturation stages. The findings indicated that PBW was widely distributed across India's cotton-growing regions, with field infestations ranging from 8 to 29 % during flowering and 40–92.5 % at boll maturation. As the season progressed, locule damage ranged from 36 to 86 %, and boll occupancy was in the range of 0.65–1.83. Central India (Maharashtra and Gujarat) exhibited the highest PBW infestation, followed by North India, while South India generally experienced lower damage severity, except for a few regions in Karnataka and Telangana. The widespread presence of PBW across diverse agro-climatic zones poses a significant threat to cotton production. To effectively manage PBW infestations in Bt cotton, it is essential to implement targeted control strategies at regular intervals throughout the reproductive phases of the crop.

### 14

**Title:** MYB regulation of *GST/GT* mediates red petal spot development in cotton.

**Author:** Sujun Zhang, Jie Chen, Tao Jiang, Haitao Wang, Xiao Cai, Cunjing Liu, Liyuan Tang

**Imprint:** The Crop Journal, Available online 28 April 2025

**Abstract:** Red petal spots are beneficial for attracting cotton pollinators and **producing** hybrid seeds, and the anthocyanin pathway is generally regarded as a metabolic cause

of petal coloration. The current study identified an MYB-encoding gene (*Gar07G09390*, *GaMYB*) as a candidate gene involved in cotton coloration by map-based cloning, and this MYB could positively regulate a candidate glutathione S-transferase gene (*Gar07G08900*, *GaGST*). To unveil potentially involved genes within the *GaMYB*-regulating-*GaGST* route, color metabolites of both *GaMYB*- and *GaGST*-virus-induced gene silencing (VIGS) petals were investigated, revealing that they were largely glycosyl-decorated flavonoids. Accordingly, a transcriptomic survey of both VIGS petals identified a glycosyl-transferase gene (*GaGT*, *Gar02G15390*). Notably, this *GaGT* is adjacent to one of the genome-wide association study loci concerning petal spots in *Gossypium arboreum*, and it is also positively regulated by *GaMYB*. This new regulatory route including both *GST* and *GT* regulated by MYB is conserved among the three cotton species examined in this study (*Gossypium arboreum*, *Gossypium hirsutum*, and *Gossypium barbadense*). Accordingly, comprehensively evaluating the influence of these candidates and their homologs on cotton coloration may provide a more in-depth understanding of cotton coloration, ultimately facilitating the breeding of more colorful cotton.

## 15

**Title:** A panoramic view of cotton resistance to *Verticillium dahliae*: From genetic architectures to precision genomic selection .

**Author:** Xiaojun Zhang, Shiming Liu, Peng Wu, Wanying Xu

**Imprint:** iMeta. 2025;4:e70029. [wileyonlinelibrary.com/journal/imeta](https://doi.org/10.1002/imt2.70029) | 1 of 24  
<https://doi.org/10.1002/imt2.70029>

**Abstract:** Investigating the genetic regulatory mechanisms underlying complex traits forms the foundation for crop improvement. *Verticillium wilt* (VW), caused by *Verticillium dahliae* (*V. dahliae*), is one of the most devastating diseases affecting crop production worldwide. However, the genetic basis underlying crop resistance to *V. dahliae* remains largely obscure, hindering progress in the genomic selection for VW resistance breeding. Here, we unraveled the genetic architectures and regulatory landscape of VW resistance in cotton by combining genome-wide association studies (GWAS) and transcriptome-wide association studies (TWAS) using 1152 transcriptomes derived from 290 cotton accessions. We identified 10 reliable quantitative trait loci (QTLs) associated with VW resistance across multiple environments. These QTLs showed a pyramiding resistance effect and exhibited promising efficacy in the genomic prediction of cotton's VW resistance supported by an F2:3 population. Moreover, trace analysis of these elite alleles revealed a notably increased utilization of *Lsnp1*, *Lsnp4*, *Lsnp5*, *Lsnp8*, and *Lsnp9*, which potentially contribute to the improvement of VW resistance in Chinese cotton breeding since the 1990s. We also identified remarkable gene modules and expression QTL (eQTL) hotspots related to the regulation of reactive

oxygen species (ROS) homeostasis and immune response. Furthermore, 15 candidate causal genes were prioritized by TWAS. Knocking down eight genes with a negative effect significantly enhanced cotton resistance to *V. dahliae*. Among them, GhARM, encoding an armadillo (ARM)-repeat protein, was verified to modulate cotton resistance to *V. dahliae* by regulating ROS homeostasis. Overall, this study updates the understanding of the genetic basis and regulatory mechanisms of cotton's VW resistance, providing valuable strategies for VW management through genomic selection in cotton breeding.

## 16

**Title:** Relationship between phytochrome photoactivity and the degree of auxin binding to the receptor in cotton genotypes differing in wilt tolerance.

**Author:** Akhmedzhanov I.G, Tonkikh A.K., Khotamov M.M., Merzlyak P.G.

**Imprint:** MIKOLOGIÂ I FITOPATOLOGIÂ,  
<https://doi.org/10.31857/S0026364825010076>, Vol 59, No 1 (2025)

**Abstract:** The paper studies some characteristics of three groups of cotton varieties that differ in their resistance to wilt: non-resistant, moderately resistant and resistant. The activity of the phytochrome system in etiolated cotton seedlings was studied using the low-temperature luminescence method, and the ability of red light to increase the specific binding of auxin to its binding sites was studied using the method of studying the binding of radioactively labeled auxin <sup>3</sup>H-IAA to auxin-binding sites in membrane preparations and soluble proteins from cotton hypocotyls. It has been shown that the higher the resistance to wilt in different cotton varieties, the higher their activity of the phytochrome system and the higher the increase under the influence of red light, the specific binding of <sup>3</sup>H-IAA with membrane preparations and soluble proteins obtained from these cotton varieties. Establishing a direct correlation between cotton resistance to wilt, phytochrome photoactivity and the level of auxin affinity for its receptor creates prospects for further progress in the study of phytochrome-phytohormonal interactions in the regulation of cotton plant resistance to *Verticillium dahlia*.

## 17

**Title:** *Verticillium dahliae* Secretory Aspartyl Protease VdSAP Targets Cotton GhARP to Modulate Plant Defence and Defoliation .

**Author:** Haiyuan Li, Xiaotong Gai, Xiangming Xu, Jun Qin, Steve J. Klosterman, Krishna V. Subbarao, Wenjing Shang, Xiaoping Hu

**Abstract:** *Verticillium dahliae* isolates causing devastating vascular wilt in cotton plants can be divided into defoliating and nondefoliating pathotypes. The mechanisms underlying how *V. dahliae* uses secretory proteins to manipulate plant physiological processes and suppress immunity in cotton plants have received renewed research focus over the past several years. Here, we describe the role of a secretory protein named VdSAP (secretory aspartyl protease) from the defoliating *V. dahliae* strain XJ592 in virulence and defoliation. Deletion of VdSAP in strain XJ592 led to significantly reduced virulence and cotton plant defoliation. VdSAP functioned as a protease that targeted cotton plant GhARP (auxin-repressed protein), and VdSAP negatively regulated GhARP content in plants. Transient expression of GhARP in *Nicotiana benthamiana* enhanced the expression of plant defence signals and inhibited plant abscission signals. Furthermore, GhARP negatively regulated the ethylene (ET) signal and positively regulated the salicylic acid (SA) signal. In addition, GhARP interacted with 1-aminocyclopropane carboxylate oxidases (GhACOs), suggesting that it might function through the ET signal during *V. dahliae*-cotton plant interactions. These results suggest that GhARP is a molecular link between plant defence and abscission signals, and that VdSAP decreases accumulation of GhARP and enhances the virulence and defoliation caused by *V. dahliae*.

## 18

**Title:** Bottom-up effects of nitrogen fertilizer on cotton growth and population expansion of *Aphis gossypii* (Hemiptera: Aphididae).

**Author:** Yu Gao , Huatong Li , Yanhui Lu

**Imprint:** *Journal of Economic Entomology*, toaf080, <https://doi.org/10.1093/jee/toaf080>, 13 April 2025

**Abstract:** Bottom-up effects, triggered by fertilization regimes, can be key ecological forces regulating pest populations. In this study, we investigated the effects of 5 different concentrations of  $\text{Ca}(\text{NO}_3)_2$  (0, 2, 4, 6, and 8 mM) on cotton plants and the performance of *Aphis gossypii*. Our results demonstrated that nitrogen application significantly enhanced the growth indices of cotton seedlings (eg plant height, aboveground fresh weight) and plant biochemistry parameters (eg nitrogen, chlorophyll, and tannin). Nitrogen also affected the life history parameters of *A. gossypii* (eg longevity, reproductive days, fecundity, intrinsic rate of increase, finite rate of increase, and net reproductive rate). Notably, the positive effects on cotton seedling growth and *A. gossypii* performance observed at the 6 mM level diminished at the 8 mM level. Additionally, the highest soluble sugar content was observed in the unfertilized plants (the 0 mM treatment). Electrical penetration graph analysis revealed

that *A. gossypii* spent less time on intercellular probing and more time feeding on phloem with increasing nitrogen levels, suggesting improved nutrient acquisition from phloem, which supported the observed increase in fecundity. The above results indicate that the bottom-up effects of nitrogen fertilizer could trigger outbreaks of *A. gossypii*. These findings provide a scientific basis for optimizing nitrogen fertilizer within integrated pest management programs so as to protect yields, reduce the risk of aphid outbreaks, as well as the costs for labor and ecological environment.

## 19

**Title:** *Verticillium dahliae* effector Vd06254 disrupts cotton defence response by interfering with GhMYC3- GhCCD8-mediated hormonal crosstalk between jasmonic acid and strigolactones.

**Author:** Jianhui Ma, Fan Jiang, Yan Yu, Haodan Zhou, Jingjing Zhan, Jianing Li, Yanli Chen

**Imprint:** Plant Biotechnology Journal (2025), pp. 1-14 doi: 10.1111/pbi.70098

**Abstract:** *Verticillium dahliae* is among the most destructive plant pathogens, posing a significant threat to global cotton production. Cotton plants have developed sophisticated immune networks to inhibit *V. dahliae* colonization. Ingeniously, *V. dahliae* employs numerous virulent effectors to surmount plant immune responses. However, the pathogenic mechanisms of *V. dahliae*-derived effectors remain elusive. In this study, we demonstrate that the Vd06254 effector from *V. dahliae* disrupts the synergistic interaction between jasmonic acid (JA) and strigolactones (SL), thereby suppressing cotton immunity. Ectopic expression of Vd06254 enhanced susceptibility to both viral and *V. dahliae* infections in *Nicotiana benthamiana* and cotton, respectively. Vd06254 directly interacts with the JA pathway regulator GhMYC3. The nuclear localization signal (NLS) was found to be essential for the virulence of Vd06254 and its interaction with GhMYC3. Additionally, overexpression and knockout of GhMYC3 in cotton modified the plant's resistance to *V. dahliae*. Our findings further reveal that GhMYC3 inhibits the expression of GhCCD8 by binding to its promoter, potentially regulating SL homeostasis in cotton through a negative feedback loop. This repression was enhanced by Vd06254, highlighting its crucial role in modulating cotton immunity and illustrating how *V. dahliae* effectors reprogram cotton transcription to disrupt this regulatory mechanism.

**Title:** RNAi-mediated down-regulation of the endogenous *GhAIP10.1* and *GhAIP10.2* genes in transgenic cotton (*Gossypium hirsutum*) enhances the earliness and yield of flower buds.

**Author :** Marcos Fernando Basso , Thuanne Pires Ribeiro , Isabela Tristan Lourenço-Tessutti, Nelson Geraldo Oliveira , Reneida Aparecida Godinho Mendes

**Imprint:** Plant Physiology and Biochemistry, Volume 225, August 2025, 109937

**Abstract:** Armadillo BTB Arabidopsis protein 1 (AtABAP1) plays a central role in the cell cycle. ABAP1-interacting protein 10 (AtAIP10, a Snf1 kinase interactor-like protein) is a protein that interacts with AtABAP1. Down-regulation of the *AtAIP10* gene in *A. thaliana* resulted in an altered cell cycle and increased photosynthesis, chlorophyll content, metabolites, plant growth, root system, seed yield, and drought tolerance. Herein, aimed to test whether the down-regulation of *GhAIP10* genes can stimulate the cotton plants in a manner similar to those observed in *A. thaliana*. Cotton transgenic events containing transgenes carrying RNA interfering (RNAi) or artificial miRNA (amiRNA) strategies were successfully generated to down-regulate the endogenous *GhAIP10.1* and *GhAIP10.2* genes. From these 15 transgenic events, five RNAi-based transgenic lines and five amiRNA-based transgenic events were selected for further analyses. The down-regulation of the *GhAIP10.1* and *GhAIP10.2* genes was confirmed by real-time RT-PCR. Phenotypic and physiological analyses revealed that these transgenic lines exhibited earlier production and opening of flower buds, increased vegetative growth over time and root biomass, no reduction in susceptibility to root-knot nematodes, and improved drought tolerance indicated by a higher photosynthetic rate and better intrinsic water-use efficiency. Based on the high identity of amino acid sequences, motifs, domains, subcellular localization, tertiary structure, down-regulation of *GhABAP1* (partner of *GhAIP10*), up-regulation of *GhCdt1* (a marker of the ABAP1 network), up-regulation of *GhCyclinB1* (a marker of the cell cycle), up-regulation of *GhAP3* (involved in vegetative to reproductive transition), and the up-regulation of *CAB3*, *NDA1*, *DJC22*, and *DNAJ11* genes (involved in plant resilience) suggested that *GhAIP10.1* and *GhAIP10.2* proteins may act in cotton similarly to the *AtAIP10* protein in *A. thaliana*. Furthermore, *GhAIP10.1* and *GhAIP10.2* genes are suggested as biotechnological targets for cotton genetic engineering based on genome editing.

## 21

**Title:** Stem trichome polarity development in *Gossypium hirsutum*: insights into GhPRP gene regulation.

**Author:** Huanying Deng, Longen Ma, Li Yu, Yanhao Zhao, Yurong Jiang & Junkang Rong

**Imprint:** Plant Cell Reports , Published: 26 April 2025, Volume 44, article number 102, (2025)

**Abstract:** Stem trichomes in cotton are essential for pest resistance and stress tolerance, yet their molecular regulation remains poorly understood. Significant differences in trichome number and length were observed under 25 °C and 30 °C, with more and longer trichomes at the first stem node under 25 °C. The side above the first true leaf (M side) showed more number of trichomes than the opposite side (L side), indicating polarity distribution. Transcriptome sequencing (RNA-seq) identified differentially expressed genes (DEGs), and 17 key DEGs were selected for further analysis, including 9 upregulated genes encoding proline-rich cell wall proteins (*PRPs*), flavonol synthase (*FLS*), prolyl endopeptidase (*PREP*), and diacylglycerol O-acyltransferase 3 (*DGAT3*). Quantitative real-time PCR (qRT-PCR) confirmed higher *GhPRP* expression on the M side. When *GhPRP1*, *GhPRP2*, or *GhPRP10* was silenced using virus-induced gene silencing (VIGS) technique, trichome density decreased, and polarity was disrupted, highlighting their regulatory roles. Bioinformatics analysis revealed hormone signal transduction-related domains in *PRP* gene promoters, potentially linking them to trichome polarity regulation. This study advances understanding the mechanisms of trichome polarity distribution and offers insights for improving pest resistance and stress adaptation in cotton.

## 22

**Title:** BLUP and AMMI synergy: a comprehensive approach for *Gossypium barbadense* genotype stability and yield assessment.

**Author:** Kari Baghyalakshmi, Ariyapalayam Rajendran Priyanka, Aravindan Shanmugam, Govindaraj Sarathapriya, & Sadhasivam Manickam

**Imprint:** New Zealand Journal of Crop and Horticultural Science , <https://doi.org/10.1080/01140671.2025.2491587>, Published online: 23 Apr 2025

**Abstract:** Increasing temperatures and irregular weather patterns make the selection of stable, high-performing, regional-specific *G. barbadense* cultivars essential. Nineteen *G. barbadense* genotypes were evaluated over five consecutive seasons (2019–2024). The

PCA of the first two interactions revealed 96.2% of the variation, with significant genotype–environment interactions. According to Additive Main Effects and Multiplicative Interactions-1 analysis, genotypes G8 and G18 consistently excelled across all environments with high mean yields. Genotypes G4, G14, and G16 were more stable throughout the tested years. Genotypes G18, G13, G2, G5, and G7 were identified as stable and high yield based on Best Linear Unbiased Prediction (BLUP) – Harmonic Mean of Genotypic Values (HMGV), Relative Performance of Genotypic Value (RPGV), and Harmonic Mean of the Relative Performance of Genotypic Value (HMRPGV) according to their stability parameters. Based on the Weighted Average of Stability (WAASB) and Mean Performance (Y) (WAASBY), genotypes G12, G18, G13, and G7 exhibited high stability and yield performance. BLUP outperformed all other AMMI family members in accuracy when more genotypes were tested. The WAASB is an ideal tool for discerning variations and identifying stable genotypes among all methods, and these genotypes can be used as the best parental lines in breeding programmes for changing climate conditions.

## 23

**Title:** Identification and functional characterization of the SCL gene related to gland formation in upland cotton (*Gossypium hirsutum* L.).

**Author:** Chaofeng Wu, Xuemei Ma, Shuyan Li, Yupeng Cui, Ruifeng Cui & Guoli Song

**Imprint:** Planta, Volume 261, article number 114, (2025)

**Abstract:** In this study, we identified a transcription factor named GoSCL, which was involved in the regulation of pigment gland in the stem. Silencing of *GoSCL* decreased not only the number of pigment glands but also the accumulation of gossypol in the stem of the treated plants. *GoSCL* showed a temporal and spatial pattern of expression in various organs of glanded and glandless cotton plants and demonstrated the inducible expression under exogenous ethylene treatment. The relationship between *GoSCL* and genes involved in gland formation and gossypol synthesis was also discussed. These results advance our understanding of the molecular basis of cotton gland formation and gossypol synthesis and accelerate the molecular breeding of cotton with low-gossypol seeds and high-gossypol plants.

## 24

**Title:** *Gossypium latifolium* genome reveals the genetic basis of domestication of upland cotton from semi-wild races to cultivars.

**Author:** Chao Fu, Nian Wang, Qingying Meng, Zhiyong Xu, Yu Le, Xianlong Zhang, Yangyang Wei, Renhai Peng, Chao Shen, Zhongxu Lin

**Imprint;** The Crop Journal, Available online 12 April 2025

**Abstract:** The genetic basis for *Gossypium hirsutum* race *latifolium*, the putative ancestor of cultivated upland cotton, emerging from the semi-wild races to be domesticated into cultivated upland cotton is unknown. Here, we reported a high-quality genome assembly of *G. latifolium*. Comparative genome analyses revealed substantial variations in both gene group composition and genomic sequences across 13 cotton genomes, including the expansion of photosynthesis-related gene groups in *G. latifolium* compared with other races and the pivotal contribution of structural variations (SVs) to *G. hirsutum* domestication. Based on the resequencing reads and constructed pan-genome of upland cotton, co-selection regions and SVs with significant frequency differences among different populations were identified. Genes located in these regions or affected by these variations may characterize the differences between *G. latifolium* and other races, and could be involved in maintenance of upland cotton domestication phenotypes. These findings may assist in mining genes for upland cotton improvement and improving the understanding of the genetic basis of upland cotton domestication.

## 25

**Title:** Examining photosynthetic induction variation among historical cotton cultivars through time-integrated limitation analyses

**Author:** Yonghui Pan , Margaret M Barbour , Tao Liu , Sen Rao

**Imprint:** *Plant Physiology*, kiaf157, <https://doi.org/10.1093/plphys/kiaf157>

**Abstract:** A thorough understanding of the biochemical, stomatal, and mesophyll components that limit photosynthetic induction is crucial for targeted improvement of crop productivity. However, compared with biochemical activation and stomatal conductance (gs), mesophyll conductance (gm) remains underexplored in induction studies. The fluorescence method (the variable J method) is a valid and widely accessible tool for gm measurement under steady-state conditions. Here, we experimentally validated the applicability of the fluorescence method under non-steady-state conditions, demonstrating comparable induction kinetics of gm with the well-established carbon isotope method. Building on this validation, we combined the fluorescence method with gas exchange measurements to comprehensively examine the induction kinetics of photosynthetic rate (A) and its associated components in a set of historical cotton (*Gossypium hirsutum* L.) cultivars. Our results showed no significant effect of the year of cultivar release on A during induction, suggesting that dynamic photosynthesis has not benefited from past selection efforts in cotton. Nonetheless, significant among-cultivar variations were observed in all measured induction traits, hinting at breeding opportunities for leveraging dynamic photosynthetic variation to

boost crop productivity. Through induction-period-integrated limitation analysis, we further identified gs as the single most important limiter of photosynthetic induction across all cotton cultivars. Moreover, the analysis also demonstrated that accurately accounting for gm kinetics is essential for the unbiased acquisition of mechanistic insights into non-steady-state photosynthetic physiology. We recommend that future induction studies incorporate gm measurements whenever possible to strengthen the knowledge base necessary for genetically enhancing dynamic carbon gain and crop yield in the field.

## PLANT BIOTECHNOLOGY

### 26

**Title:** Genome-wide identification of *LOX* gene in four cotton species and revealed its function in callus induction and drought tolerance.

**Author** :Sani Muhammad Tajo , Zhaoe Pan , K.M. Yusuf , Salisu Bello Sadau , Guowei Lv , Shoupu He , Xiaoli Geng , Xiongming Du

**Imprint:** Plant Gene, Volume 43, September 2025, 100516

**Abstract:** Cotton is one of the important fiber crops. Drought is the primary abiotic factor that restricts cotton growth and development and lowers its output. Plant *LOX* (lipoxygenases) genes catalyze the oxidation of polyunsaturated fatty acids into a variety of functional oxylipins. The *LOX* gene family has been thoroughly investigated under biotic and abiotic stressors; however, knowledge of their functions on callus induction and regeneration in cotton is still scarce. This study identified 34, 38, 23, and 20 *LOX* genes in the *Gossypium hirsutum*, *Gossypium barbadense*, *Gossypium arboreum*, and *Gossypium raimondii*, respectively. The *LOX* genes were found to be divided into three main categories, 9-*LOX*, 13-*LOX* Type I, and 13-*LOX* Type II. Three accessions of *G. hirsutum* were used to generate callus from hypocotyl, cotyledon, and shoot tip and we observed that the highest expression of the *GhLOX* genes were in the hypocotyl callus and most of *LOX* gene expression was up-regulated in one week callus and decreased in two week and four week callus except in the shoot tip induced callus in Jinmian 498. Virus-induced gene silencing of *GhLOX5* (Gh\_A02G037000) revealed that the growth of the silenced plant was significantly decreased compared to WT. Excised leaf water loss and relative electrolyte leakage levels were increased about 23 % and 12 % in the *GhLOX5* silenced plant when compared to the WT. Compared to the WT, the silenced plant had significantly higher antioxidant activity (25 % in MDA content and 45 % in H<sub>2</sub>O<sub>2</sub> content). The importance of *LOX* genes in drought stress and

callus induction is clear, but further research is needed to understand their molecular mechanism.

## 27

**Title:** Unveiling the development of cotton somatic embryos: Integrating spatial transcriptomics and metabolomics.

**Author:** Aizhi Qin , Yaping Zhou , Xiaole Yu , Xiaoyang Ge , Zhixin Liu , Hao Liu , Lam-Son Phan Tran

**Imprint:** Industrial Crops and Products, Volume 230, August 2025, 121077

**Abstract:** Plant development necessitates a diverse array of cell types, metabolites, and intricate gene regulation patterns. Consequently, investigating the spatial localization of cells within tissues, the spatial expression of genes, and the distribution of both primary and secondary metabolites in plants is crucial. The process of somatic embryo development is vital for the genetic enhancement of cotton, yet it remains poorly understood. Moreover, there is currently a scarcity of available data resources on the spatial expression patterns of genes and metabolites in cotton somatic embryo cells. In this study, we employed  $10 \times$  Visium spatial transcriptomics (ST) technology and air flow-assisted desorption electrospray ionization mass spectrometry imaging (AFADESI-MSI) spatial metabolomics (SM) technology to establish sequencing libraries and metabolomes of upland cotton (*Gossypium hirsutum*) somatic embryos, specifically focusing on globular, torpedo, and cotyledonary embryos. Specifically, we have highlighted the spatially regulated gene networks and metabolite gradients critical to embryogenesis. For instance, the integrated analysis of ST and SM revealed that polyamines (putrescine, spermidine, and spermine) and their biosynthesis-related genes (*ADC*, *ODC*, *ARGAH1*, *SPDSYN1*, and *SPMS*) were highly expressed in globular embryos. These findings suggest that polyamines and their biosynthesis-related genes may play a pivotal role in the conversion of embryogenic callus into somatic embryos in cotton. In summary, we propose an integrated spatially resolved multiomics approach, which will aid in deciphering the complex regulatory networks involved in the development of cotton somatic embryos.

## 28

**Title:** Genome-Wide Association Mapping of Seed Shape-Related Traits in Cotton Using SSR Markers.

**Author:** Irfan Ali Siddho, Zixin Zhang, Hang Peng, Shugen Ding, Lin Xu

**Imprint:** <https://doi.org/10.21203/rs.3.rs-5635782/v1>, This work is licensed under a CC BY 4.0 License

**Abstract:** Cotton is a significant crop for fiber production; however, seed shape-related traits have been less investigated in comparison to fiber quality. Comprehending the genetic foundation of traits associated with seed shape is crucial for improving the seed and fiber quality in cotton. Results: A total of 238 cotton accessions were evaluated in four different environments over a period of two years. Traits including thousand grain weight (TGW), aspect ratio (AR), seed length, seed width, diameter, and roundness demonstrated high heritability and significant genetic variation, as indicated by phenotypic analysis. The association analysis involved 145 SSR markers and identified 50 loci significantly associated with six traits related to seed shape. The markers MON\_DPL0504aa and BNL2535ba were identified as influencing multiple traits, including aspect ratio and thousand grain weight. Notably, markers such as HAU2588a and MUSS422aa had considerable influence on seed diameter and roundness. The identified markers represented an average phenotypic variance between 3.92% for seed length and 16.54% for thousand grain weight (TGW). Conclusions: The research finds key loci for seed shape-related traits in cotton, providing significant potential for marker-assisted breeding. These findings establish a framework for breeding initiatives focused on enhancing seed quality, hence advancing the cotton production.

## 29

**Title:** Genome-wide QTL mapping and candidate gene analysis reveal elite yield-, fiber- and seed-associated alleles in *Gossypium hirsutum* race *purpurascens*.

**Author:** Jichun Xia, Zhongni Guo, Disen Zhang, Xuyuan Yang, Yi Yu, Wenhui Song, Jing Lin, Shuxin Wang, Hongyu Tian, Xueying Liu,

**Imprint:** Industrial Crops and Products, Volume 230, August 2025, 121067

**Abstract:** Traditional and effective crossbreeding techniques are widely used to introduce and create desired genetic variation, while integrating main characteristics of elite parents into the progeny. Improvement of cultivars using alleles from wild and semi-wild species has become a current focus in cotton genetic improvement and resources research. In this study, we created a backcrossed inbred lines (BIL) population from parents *Gossypium hirsutum* cultivar and *G. hirsutum* race *purpurascens* and identified Quantitative Trait Loci (QTL) for yield-, fiber- and seed-related traits. Specific locus amplified fragment sequencing (SLAF-seq) technology was used to develop single nucleotide polymorphism (SNP) markers and construct a high-density genetic linkage map. QTL localization was performed by utilizing phenotype data for yield-, fiber- and seed-related traits under seven environments. A total of 633 QTL were identified, among which 318 favorable alleles derived from *G. hirsutum* race *purpurascens*. One hundred and fifty stable QTL were identified in more than two environments, and candidate genes for two QTL were further analyzed. These results highlight the great

potential of utilizing *G. hirsutum* race *purpurascens* germplasm to improve yield-, fiber- and seed-related traits in *G. hirsutum*.

## SEED SCIENCE AND TECHNOLOGY

30

**Title:** Effects of Low Temperature at Seedling Stage on Cotton Floral Bud Differentiation and Cotton Plant Yield.

**Author:** YuXuan ZHAO, JiYuan MIAO, Wei HU, ZhiGuo ZHOU

**Imprint:** Scientia Agricultura Sinica, 2025, 58(7): 1311-1320. <https://doi.org/10.3864/j.issn.0578-1752.2025.07.005>

**Abstract:** This study aimed to investigate the harm of low temperature in the cotton (*Gossypium hirsutum* L.) seedling stage on floral bud differentiation and the effect on seedcotton yield, to analyze the change characteristics of cotton floral bud differentiation phenotypes and terminal buds endogenous hormones under low temperature, so as to provide the theoretical basis for the high-quality and high-efficiency cultivation technology of cotton under low temperature. Method- Using the early-maturing and high-quality cotton variety Zhong 425 as the material, a pot experiment was conducted in the smart greenhouse of the Pailou Experimental Station of Nanjing Agricultural University from 2022 to 2023 to simulate the daily average temperature environment during the cotton seedling stage in Aksu, southern Xinjiang. Two temperature treatments were set up: the control (CK, with a daily average temperature of 27 °C, and daily maximum and minimum temperatures of 32 and 22 °C, respectively) and the low-temperature treatment (LT, with a daily average temperature of 20 °C, and daily maximum and minimum temperatures of 25 and 15 °C, respectively). The number, size, and morphological anatomical structure of cotton flower bud differentiation were investigated, and the changes in endogenous hormones in shoot apices under low temperature during the seedling stage were analyzed. Additionally, the changes in cotton bolls and their component biomass, as well as relevant indicators of seed cotton yield, were examined after the removal of low temperature stress during the seedling stage. Result- During the differentiation of cotton flower buds, the increase in Indole-3-acetic acid (IAA) content and the decrease in trans-Zeatin-riboside/Gibberellin A3 (ZR/GA3) ratio in the terminal buds of cotton under low temperature during the seedling stage inhibited flower bud differentiation. Meanwhile, the content of abscisic acid Abscisic Acid (ABA), GA3, and ZR increased in response to the adverse effects of low temperature. Changes in endogenous hormones in the shoot

tips caused by low temperature during the seedling stage slowed down the process of flower bud differentiation. When the flower buds of the first fruit node on the first fruit branch differentiate from the bract differentiation stage to the sepal differentiation stage, petal-stamen differentiation stage, pistil differentiation stage, and sexual organ formation stage, the leaf age increased by 16.6%-19.4%, 26.5%-31.3%, 17.6%-29.0%, 16.6%-23.3%, and 26.6%-30.0%, respectively; the number of flower buds at the 4-leaf-1-heart, 5-leaf-1-heart, and 6-leaf-1-heart stages of cotton seedlings decreases by 33.3%-55.2%, 24.0%-53.1%, and 26.8%-32.9%, respectively. Due to the slow growth and development of cotton seedlings under low temperature during the seedling stage, the number of flower buds in cotton seedlings exposed to the same number of days of temperature treatment decreased more significantly, with reductions of 66.7%-85.7%, 74.0%-87.8%, and 70.7%-81.7% compared with the control group at the 4-leaf-1-heart, 5-leaf-1-heart, and 6-leaf-1-heart stages, respectively; the sizes of flower buds at these stages also decreased by 33.3%-36.4%, 70.7%-71.6%, and 44.6%-48.3%, respectively. After the removal of low temperature stress during the seedling stage, the development of cotton bolls was still affected, with significant reductions in boll and its component biomass. Specifically, the biomasses of boll shell, fiber, and cottonseed decreased by 64.6%, 65.5%, and 66.7%, respectively. The number of cotton bolls decreased by 65.4%, ultimately leading to a 65.5% reduction in seed cotton yield.

## 31

**Title:** Integrated transcriptomics and metabolomics analyses reveal jasmonic acid metabolic pathways for improving the chilling tolerance in cotton seedlings.

**Author:** Luyao Wang , Yaping Jiang , Yupeng Hao , Li Yu

**Imprint:** Plant Physiology and Biochemistry, Volume 224, July 2025, 109935

**Abstract:** Cotton (*Gossypium* spp.) originated in tropical and subtropical regions, spreading to higher latitudes through domestication while retaining thermophilic characteristics. Xinjiang, a major cotton-producing area in China, frequently experiences 'late spring cold snaps' due to its location, causing chilling injury during critical sowing periods. Current research on cotton chilling stress primarily focuses on physiological studies such as evaluations of chilling stress and biochemical indices but lacks systematic investigation into the difference among varieties. Phenotypic screening across seed germination, cotyledon, and seedling stages identified upland cotton (*Gossypium hirsutum*) cultivar, Junmian1 exhibits superior cold tolerance relative to the sensitive genotype C1470. Under chilling stress, Junmian1 protects chloroplasts and other cellular structures in its first true leaf to survive the chilling stress. Weighted gene co-expression network analysis (WGCNA) analysis pinpointed Module Brown as a chilling-tolerance responsive hub, with subsequent validation via virus-induced gene silencing (VIGS) confirming the regulatory roles of *GhRBL* (Ribulose-bisphosphate carboxylase), *GhGI* (GIGANTEA), and lncRNA *MSTR.1631* in cold tolerance.

Additionally, integrated metabolomic and transcriptomic analyses demonstrated that jasmonic acid plays a crucial role in enhancing cotton's chilling tolerance at seedling stage. The primary difference in chilling tolerance between Junmian1 and C1470 is attributed to the signaling efficiency of the jasmonic acid synthesis and metabolism pathways. These findings establish JA metabolic engineering as a viable approach for enhancing cold resilience in early-stage cotton seedlings.

## 32

**Title:** Genetic insights into cold tolerance in cotton: GWAS identified GhPRL1 gene responsible for cold tolerance in cotton at seedling stage.

**Author:** Aamir Abro, Mubashir Abbas, Qiankun Liu, Zheng Jie, Yanchao Xu

**Imprint:** <https://doi.org/10.21203/rs.3.rs-6283010/v1>, This work is licensed under a CC BY 4.0 License

**Abstract:** Cold stress during the seedling emergence stage severely affects the growth and development of cotton (*Gossypium hirsutum*), leading to reduced yield and plant health. Despite its importance, the molecular mechanisms underlying cold tolerance in cotton remain poorly understood. In this study, we analyzed 302 cotton accessions from the Cotton Research Institute in Anyang, China, to assess phenotypic and genetic responses to cold stress. Statistical analysis revealed significant reductions in primary root length (PRL) under cold stress, with a notable increase in genetic variation in root growth. Genome-wide association studies (GWAS) identified key genetic loci associated with cold tolerance, particularly on chromosome A11, where a cluster of SNPs exhibited strong associations with PRL. Fine mapping revealed high linkage disequilibrium in this region, indicating evolutionary selection for cold tolerance. Among the candidate genes, Gh\_A11G315100 (GhPRL1) was identified as a major gene linked to cold tolerance. Virus-Induced Gene Silencing (VIGS) of GhPRL1 confirmed its essential role in maintaining plant health under cold stress, with GhPRL1-silenced plants showing greater phenotypic damage, increased ion leakage, and reduced antioxidant activity. This study provides valuable insights into the genetic basis of cold tolerance in cotton and identifies GhPRL1 as a critical target for future breeding efforts aimed at enhancing cold resilience.

**Title:** Alleviation of saline stress by the bio-priming of cotton (*Gossypium hirsutum*) seeds with prominent indigenous bacterial isolates under axenic conditions.

**Author:** Jagjot Kaur & Gulab Pandove

**Imprint:** Journal of Plant Nutrition , Received 16 Jun 2024, Accepted 09 Apr 2025, Published online: 24 Apr 2025, <https://doi.org/10.1080/01904167.2025.2493327>

**Abstract:** Salinity is an edaphic stress that significantly limits agricultural productivity. Nonetheless, plant growth promoting rhizobacteria (PGPR) has the potential to escalate the resilience of plant against biotic and abiotic stresses. Therefore, the present investigation was designed to examine the effect of seed bio-priming with liquid inoculants of *Acinetobacter lwoffii* strain PAU\_31LN, *Bacillus thaonhiensis* strain PAU\_43RN, *Klebsiella pneumoniae* strain PAU\_35TP, *Pseudomonas brassicacearum* strain PAU\_34RN and *Pseudomonas fluorescens* strain PAU\_43TN on the biometric growth parameters of cotton seedlings under different salinity levels (50, 100 and 150 mM). Also, the bacterial strains were observed to maintain a constant viability at 150 mM NaCl. The production of plant growth promoting traits by all the bacterial strains was found to be in desirable quantity at different salt concentrations. However, the maximum production of indole-acetic acid, gibberellic acid, ammonia and phosphate solubilization was recorded by the strain PAU\_31LN and PAU\_43RN at all the salt conditions. During *in-vitro* plant growth assay, it was demonstrated that seed bio-priming with *B. thaonhiensis* improve the seedling length (6.50 cm shoot and 3.60 cm root length), dry shoot and root biomass (0.037 and 0.0023 g respectively), vigor index (765.9), and germination percentage (79%) under 150 mM salt content. Hence, the study encourages that bio-priming of cotton seeds with *Bacillus thaonhiensis* strain PAU\_43RN can mitigate the pernicious effect of high osmolarity to enhance cotton plant growth.

**Title:** Evaluating Cotton Seed Treatment Efficacy, Effects On Seedling Diseases and Microbial Diversity in Arkansas.

**Author:** Mariana Araujo Alves Gomes de Souza

**Imprint:** A THESIS Submitted to Michigan State University in partial fulfillment of the requirements for the degree of Plant Pathology – Master of Science 2025

**Abstract:** Cotton is one of the most significant crops primarily grown worldwide for fiber, feed, and oil production. In the United States, it is primarily cultivated in the ‘Cotton Belt’, a region spanning from Virginia to California and covering approximately

10 million acres. In Arkansas, where cotton is typically grown from late April to October, the crop is susceptible to various fungal diseases that can reduce both lint quality and yield. Among the main diseases of economic importance, the seedling disease complex is a significant global issue affecting the establishment and production of cotton stands. It refers to a range of diseases, primarily caused by *Pythium* spp., *Rhizoctonia solani*, *Fusarium* spp., and *Thielaviopsis basicola* (*Berkeleyomyces basicola*), that compromise cottonseed germination and seedlings' emergence, survival, and development. Fungicide seed treatments are a key tool in managing cotton seedling diseases, offering critical protection against soilborne and seedborne pathogens. However, their effectiveness depends on the composition and prevalence of pathogen populations, which vary annually and regionally, as well as environmental conditions. The objectives of this study were to evaluate the effectiveness of four standard fungicide seed treatments in improving seedling emergence and survival across multiple years and locations in cotton fields in Arkansas. Additionally, we aimed to characterize the soil- and root-associated microbial communities in cotton, investigating how microbial composition varies by location, year, and seed treatment. For that, a field trial was conducted in Judd Hill (2019 – 2023) and Marianna (2021 – 2023), Arkansas. Four treatments containing a base insecticide (imidacloprid) were evaluated. Treatments consisted of no fungicide (T1), metalaxyl (T2), penflufen (T3), and a mix of prothioconazole, myclobutanil, penflufen, metalaxyl (T4). Our results suggest that the use of seed treatments is effective in controlling seedling disease complex, but their efficacy depends on environmental conditions and surrounding microbes.

## FIBER AND FIBER TECHNOLOGY

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**Title:** Two duplicated *GhMML3* genes coordinately control development of lint and fuzz fibers in cotton.

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**Imprint:** Plant Commun.. 2025 Feb 12;6(4):101281. doi: 10.1016/j.xplc.2025.101281

**Abstract:** Cotton produces two types of fibers: fuzz and lint. Cotton yield is determined by the number of epidermal cells that develop into lint fibers. Despite numerous studies, the genetic and molecular mechanisms that control lint and fuzz fiber development remain unclear. Here, using the recessive naked-seed or fuzzless-linted mutant ( $n_2$ NSM) in combination with gene editing and complementation, we found that

the recessive fuzzless gene  $n_2$  encodes the MYBMIXTA-like (MML) transcription factor *GhMML3\_D12*. Overexpression of *GhMML3\_D12* in  $n_2$ NSM restored fuzz fiber development, whereas CRISPR-Cas9 knockout of *GhMML3\_D12* in wild-type cotton (J668) resulted in a fuzzless-linted phenotype. Interestingly, simultaneous edits to *GhMML3\_D12* and its duplicate *GhMML3\_A12* resulted in plants with a fiberless (fuzzless-lintless) phenotype. Detailed investigation of the seed fiber phenotypes of segregating progeny derived from a cross between J668 and a fiberless gene-edited mutant of *GhMML3* (#*mml3s*) not only identified progeny that mimicked natural fuzzless and fiberless mutants but also revealed that the duplicated *GhMML3\_A12* and *GhMML3\_D12* regulate the development of fuzz and lint fibers in a dose-dependent manner. Comparative transcriptome analysis and single-cell RNA sequencing identified *GhMML3* as the central hub of the gene network that regulates fiber initiation and early-stage elongation. The gene regulatory network revealed potential candidate genes and key regulators that may contribute to fiber initiation and development, and a model for the control of lint and fuzz fiber development by *GhMML3* was proposed. We also found that the *GhMML3\_D12* protein can bind directly to the promoters of *GhHD-1* and *GhMYB25*, two key genes involved in fiber initiation, thereby activating their expression. This study provides new insights into the fundamental mechanisms that underlie cotton fiber development.