GLEANINGS IN COTTON RESEARCH

DECEMBER 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.

Swati Dixit
In charge Library

Chetali Rodge
Technical Officer (T5)

INDEX

Subject	**Page No.**
Agronomy, Soil Science & Plant Physiology	1
Crop Protection	12
Plant Breeding and Genetics	21
Plant Biotechnology	26
Seed Science and Technology	31
Fiber and Fiber Technology	33

AGRONOMY, SOIL SCIENCE AND PLANT PHYSIOLOGY

1

Title: Cotton Canopy Management: A Review of Topping and Pruning Techniques to Enhance Yield and Quality.

Author: Muhammad Abu Bakar Hayat, Fahd Rasul, Xinlu Bai, Runze Wang, Muhammad Zia Ul Haq, Jinhu Zhi

Imprint: * Posted Date: 19 August 2025 doi: 10.20944/preprints202508. 1399.v1

Abstract: Cotton is a significant cash crop globally, so optimizing the yield and quality of fibre is crucial for its sustainability. Managing canopy architecture and planting density in cotton is important because it affects light interception, humidity and temperature that are crucial for boll development and yield. Improper management adversely affects boll numbers, weight and boll setting rates. The present review highlights canopy management and planting density as the critical factors in enhancing productivity and optimizing the microenvironment in the cotton canopy. High density planting maximizes light interception and lint yield by increasing bolls per unit area. However, excessive density can lead to reduced yield due to increased competition within plants. Furthermore, by managing canopy structure with pruning, chemical topping and manual topping, plant canopy can maintain a beneficial microclimate that is essential for higher yield. It also explains the importance of canopy microclimate, including air temperature, relative humidity and light interception in the development of bolls and fibre quality. By optimizing canopy architecture and planting density farmers can achieve higher yields and maintain fibre quality hence contributing to the global significance of cotton as a cash crop.

2

Title: Transcriptomic and metabolomic analyses reveal the molecular mechanisms by which long-day photoperiods promote flowering in Gossypium hirsutum L.

Author: Ning Zhang, Yujie Liu, Yuli Lu, Zhonghua Zhou, Qiming Wang, Aiyu Liu, Xiaoju Tu

Imprint: Front. Plant Sci., 11 September 2025, Sec. Crop and Product Physiology, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1657595

Abstract: Photoperiod is a crucial environmental cue that regulates flowering time in plants, playing a vital role in crop adaptability and early maturity. However, the molecular mechanisms underlying photoperiod-regulated flowering in cotton (Gossypium hirsutum L.) remain unclear. In this study, cotton plants were exposed to different photoperiod treatments during the seedling stage. Phenotypic evaluation, transcriptomic sequencing, and metabolomic profiling were integrated to systematically investigate the effects of photoperiod on flowering time and the associated molecular and metabolic regulatory pathways. The results showed that long-day treatments significantly accelerated budding and flowering in cotton, advancing by 20 and 17 days, respectively, compared to short-day conditions. Transcriptome analysis identified numerous differentially expressed genes (DEGs) involved in photoperiod response, hormone signaling, and metabolic regulation. Weighted Gene Co-expression Network Analysis (WGCNA) further revealed that key photoperiod-related genes, including GhFKF1, were upregulated under long-day conditions and formed co-expression networks with flowering regulators. Integrated transcriptomic and metabolomic analyses revealed significant enrichment in glycerophospholipid metabolism, α-linolenic acid metabolism, and flavonoid biosynthesis pathways. Long-day treatment suppressed the expression of key genes and precursors involved in jasmonic acid biosynthesis, while simultaneously upregulating genes involved in flavonoid biosynthesis, leading to increased accumulation of metabolites such as myricetin. Therefore, we propose a theoretical model in which long-day treatment during the seedling stage integrates hormonal and photoperiodic signals by upregulating the expression of the GhFKF1 gene. This regulation may contribute to the initiation of flowering by simultaneously suppressing jasmonic acid biosynthesis and activating the flavonoid biosynthetic pathway. Our findings offer a theoretical foundation and a novel perspective for understanding the photoperiodic response and molecular mechanisms underlying early maturation in cotton.

3

Title: Insights into the Significance of Nitrogen Fertilizer and Hydraulic Lift with Moisture Depletions in Cotton Quality and Nitrogen Distribution Under Topsoil Drought.

Author: Jia Lu, Longjia Tian, Dan Xu and Guangcheng Shao
Imprint: *Agronomy* 2025, *15*(9), 2094; https://doi.org/10.3390/agronomy15092094

Abstract: Dry topsoil restricts root growth and nutrient uptake in arid regions, thereby significantly reducing crop yield. Hydraulic lifts occur due to the dry topsoil and wet deep soil. This study investigates the effects of topsoil drought intensity (three field capacities in topsoil: 60–70% (W1), 50–60% (W2), and 40–50% (W3)) and nitrogen application rate (N1: 120, N2: 240, and N3: 360 kg ha^{-1}) on cotton quality and the distribution of nitrogen in soil and plant under hydraulic lift using a root-splitting

device. The upper pot of the root-splitting device was 22 cm high, with a 26 cm top diameter and a 23 cm bottom diameter; the lower pot of the root-splitting device was 45 cm high, with a 48 cm top diameter and a 36 cm bottom diameter. Topsoil moisture was maintained at W1 without nitrogen application under the control treatment (CK). The W2 and W3 treatments (representing different topsoil drought intensities) were designed to compare the interactive effects of water and nitrogen fertiliser on nitrogen distribution and cotton quality with the CK treatment. Results indicate that the concentrations of nitrate nitrogen (NO_3^--N) in the 10–20 cm soil were generally higher than those in the 0–10 cm soil. The topsoil drought intensity and nitrogen application rate had significant impacts on nitrogen concentrations in cotton organs. The W2 treatment produced the maximum nitrogen concentration, except for the root nitrogen concentration in 2021. The nitrogen concentration in the roots and stems peaked at 240 kg ha^{-1} of nitrogen application rate. The topsoil drought intensity and nitrogen application rate had considerable influences on the cotton dry matter. The nitrogen application rate had a significant impact on the following indexes: internal nitrogen-fertiliser use efficiency (*INUE*), physiological nitrogen-fertiliser use efficiency (*PNUE*), and nitrogen-fertiliser recovery efficiency (*NRE*), except for *PNUE* in 2020. The *INUE* of other treatments decreased by 13.82–43.44% compared with CK treatment. In 2021, fibre length and elongation were significantly impacted by the topsoil drought intensity, nitrogen application rates, and their interactions. The nitrogen application rate's effects on the uniformity index were significant in 2020 and 2021. The hydraulic lift magnitude, NRE, and NO_3^--N in the 0–10 cm soil were significantly correlated with each other. There were correlations among cotton quality indexes: fibre length and strength, uniformity index and micronaire, and micronaire and elongation. These findings provide a reference for future research on the mechanism by which hydraulic lift participates in nitrogen distribution in soil and crops and also offer a new direction to utilize deep water to improve the utilization rate of water resources.

4

Title: Water footprint, runoff and soil loss assessment of cotton production in central India.

Author: B. Bhargavi, D. Blaise, P. Nalayini

Imprint: Cleaner Water, Volume 4, December 2025, 100119

Abstract: Cotton the major crop grown on the Vertisols of central India is dependent on the monsoonal rains. Most often the high intensity rains are received in short spells and most of it is lost through runoff. Information on runoff, soil loss and water footprint (WF) of cotton grown under rainfed conditions is meagre. We determined the water runoff, soil loss, and the water footprint in a field study conducted during 2019–2022. During the study period, of the total mean annual rainfall, 47 % was effective rainfall (541 mm), and 51 % was lost through runoff. The soil loss was highest (11.5 Mg ha^{-1}) in the year 2022. The average annual soil loss was 8.81 Mg ha^{-1}. It was observed that the

mean crop water use was 541 mm and 624 mm under rainfed and drip irrigated conditions, respectively. The WF of rainfed cotton was 11,339 m^3 to produce 1Mg of lint. The green (WF_{green}) and grey (WF_{grey}) WF values were 9424 and 1915 m^3 Mg^{-1}, respectively, corresponding to 83 % and 17 % of the total WF (WF_{total}).The values obtained for WF_{green}, WF_{blue}, WF_{grey} and WF_{total} under drip irrigated cotton production were 7227, 842, 1891 and 9959 m^3 Mg^{-1}, respectively. These values correspond to 73 %, 8 % and 19 % of the WF_{total}, respectively. The blue water use in drip irrigated cotton was 50–120 mm during non-monsoon months (October to November), which resulted in 0.18 Mg ha^{-1} (28 %) lint yield enhancement and 13 % WF reduction compared to rainfed cotton. Our study indicates scope for enhancing rainfed cotton production by adopting appropriate water and crop management practices making it not only profitable but also addressing the sustainable development goals.

5

Title: Influence of Defoliants on Cotton Production Technology.

Author: Ramunaidu, P. V. S., & Pradhan, J. (2025).

Imprint: *NG Agriculture Insights*, *1*(3), 12-17. https://doi.org/10.5281/zenodo.17038337

Abstract: Uneven boll opening in cotton crops affects yield. Dense leaves obstruct boll opening, delay crop maturity, and create trash during harvesting. Natural leaf drop facilitates mechanical harvesting, but if this process doesn't occur on time, mechanical harvesting becomes challenging. To address this issue, farmers use chemical defoliants, which promote leaf drop and simplify the mechanical harvesting process. Chemical defoliants play an important role in promoting leaf drop and boll opening. The use of these chemicals improves boll maturity, enhances fiber quality, and increases harvesting efficiency. In different countries, defoliation in cotton crops is carried out through various techniques and methods. In developed countries, highly advanced techniques are used for defoliant spraying and monitoring, whereas in developing countries like India, these techniques are comparatively less advanced. Defoliation makes the cotton crop harvesting process more effective and smoother and it also simplifies post- harvest processing activities.

6

Title: Elevated temperature effects on functional yield drivers in cotton.

Author: John L. Snider Comfort O. Adegbenro

Imprint: Crop Science. 2025;65:e70149. wileyonlinelibrary.com/journal/csc2 1 of 15 https://doi.org/10.1002/csc2.70149

Abstract: Gossypium hirsutum L. (cotton) yields are limited by heat stress. Breeding for heat tolerance is an important goal, yet the most important functional contributors to heat-induced yield loss must first be defined. Although Monteith defined crop yield decades ago as the product of intercepted photosynthetically active radiation, radiation use efficiency (RUE), and harvest index (HI), a review of heat stress effects on these functional yield drivers or their underlying processes is still needed for cotton. Heat stress is known to affect canopy development, which could impact radiation interception. Specifically, leaf area declines when plants are exposed to maximum air temperatures greater than 35°C. However, direct evidence for a yield-limiting decline in intercepted radiation under high temperature is lacking. Though information is limited in peer reviewed literature, RUE (photosynthetic efficiency of the canopy) may be an important contributor to heat-induced yield loss, and this review explores the heat sensitivity of RUE and underlying photosynthetic processes. HI is the ratio of economic yield to biological yield, and current evidence indicates that reproductive processes are more heat sensitive than vegetative growth processes. Therefore, lower HI is discussed as a potentially significant contributor to heat-induced yield loss, and the relative heat sensitivity of reproductive processes and specific yield components is explored in detail. In the future, there is a need for (1) field studies addressing the temperature responses of canopy-scale yield drivers, (2) further exploration of nighttime temperature effects, and (3) targeted selection for increased heat tolerance of physiological yield drivers.

7

Title: Long-term economic and yield comparison of organic and conventional cotton-based production systems with wheat and soybean rotations in central India.

Author:Amritbir Riar, Bhupendra Sisodia, Chigusa Keller, Ishwar Patidar, Sabine Stuerz, Eva Goldmann, Akanksha Singh, Gurbir S. Bhullar

Imprint: European Journal of Agronomy, Volume 171, October 2025, 127814

Abstract: The rising demand for organic products has intensified comparisons between organic and conventional farming systems, especially for smallholders. Balancing productivity and profitability is key to supporting sustainable farming. This study assesses the economic and yield performance of organic versus conventional cotton-based systems with wheat and soybean rotations in central India. Conducted over eight cropping cycles, each comprising 2-year rotations, the long-term experiment (LTE) compared biodynamic, organic, conventional, and conventional Bt cotton systems. Organic crops yielded between 77 % (wheat) and 102 % (soybean) of their conventional counterparts. Organic cotton yielded 93 % relative to non-Bt and 82 % relative to Bt conventional cotton, with year-to-year variations. Cotton had the highest total production costs, with Bt conventional costs 5 % higher due to higher seed and fertilizer expenses. Input costs for soybean were approximately 28 % lower in organic systems, while wheat showed 6 % higher costs in conventional treatments. The Bt cotton conventional system showed the highest mean annual gross margins, 11 % higher than other systems, though no significant differences were observed among the other three. Cotton gross margins, influenced by its high production costs, contributed substantially to income variability across all systems. These findings suggest that adaptations in crop management and rotation diversity can play a more crucial role in determining farm income than the choice between organic and conventional practices. This offers insights for similar agro-ecological contexts, emphasizing the importance of tailoring rotations and inputs to local conditions for the economic resilience of smallholders.

8

Title: APSIM-cotton model calibration for phenology-driven sowing and yield optimization in drip irrigated arid climate.

Author:Adnan Arshad, Yue Zhang , Pengzhong Zhang, Xuejiao Wang, Yongfan Chen, Mukhtar Ahmed , Lizhen Zhang

Imprint: Smart Agricultural Technology, Volume 12, December 2025, 101325

Abstract: Climate-driven weather shift poses a serious challenge to cotton production and particularly crop phenology stages in arid, drip-irrigated systems like Xinjiang, China, where temperature extremes events disrupt different growth-development stages and limit yield potential. Our existing research study influences APSIM-cotton model calibration to optimize suitable sowing windows, phenological compatibility with climate-smart favorable planting windows under drip irrigation conditions for yield enhancement in water-limited agricultural systems. To evaluate the impact of warming temperatures on cotton phenology and yield, the APSIM-cotton model was calibrated and validated for sowing-times, phenology, growth, and yield employing 40-years of historical climate data, cotton yield data from six agrometeorological locations, and two years of field trials with five different sowing dates. The model calculates the yield gap and production-limiting variables when surface temperatures rise. Results of APSIM-model validation showed that the difference in sowing-emergence was ±2.7 days, for sowing-squaring ±5.3 days, for squaring-flowering ±6.6 days, and for flowering-boll open ±3.8, and boll open-maturity ±4.8 days. The observed warming trend from 1961 to 2020 represented a predicted yield decrease of 1.4 % decade^{-1} in Xinjiang due to a significant temperature increase of 0.37°C decade^{-1}. Interannual temperature variability influenced cotton growth and yield more than any other climatic factor. APSIM-cotton model simulations optimized the value of different sowing dates in extending the growth period and enhancing natural resource optimization. Quantifications of sowing-emergence, emergence-flowering, flowering-boll open, and full crop maturity phases were negatively interrelated with the rise in temperature -3.14, -2.15, -2.09, and -1.17 days °C^{-1}. The present study concludes that climate-smart adapting sowing windows (15-25 April) of cotton runs a practical approach for increasing yield and mitigating climate change risks.

9

Title: Impact of Abiotic Stress on Cotton Productivity and Strategies to Ameliorate the Effects.

Author: Naeem N*, Ali Q, Akram J

Imprint: Journal of Life and Social Sciences, J. Life Soc. Sci, 2025; Volume, 4: 41

Abstract: Cotton has grown as an important fiber cash crop, which has most significant impact on economies and livelihoods throughout the world. However, its development and productivity are significantly impacted by abiotic
factors like drought, high temperatures, waterlogging, and salinity of the soil. Reduced yields result from these environmental issues that interfere with physiological activities as photosynthesis, metabolism, and fiber growth.
While water and salt stress affect cellular processes and nutrient intake, high temperatures speed up evaporation and change reproductive growth. These stresses can be mitigated with the use of efficient management techniques, such as improved irrigation techniques, genetic innovations, and cultivars resistant to drought. Functional genomics and marker-assisted selection offer encouraging paths toward enhancing cotton's resistance to abiotic stress. Addressing these challenges is crucial for sustaining cotton production under climate change and resource limitations.

10

Title: A 5-year field study to assess interannual variability and determinants of cotton fiber quality in intercropping systems.

Author:Haoyue Qin, Yurui Tang, Xin Li, Yurong Qiu, Jian Wang, Yingchun Han, Guoping Wang, Shiwu Xiong, Minghua Xin, Wenli Du, Lu Feng, Yongjiang Zhang

Imprint: European Journal of Agronomy, Volume 171, October 2025, 127817

Abstract: Climate change and market demands emphasize the importance of both the average quality and long-term stability of end-use fiber quality in cotton production. Intercropping, a sustainable agriculture practice, has demonstrated potential to enhance cotton fiber quality compared to monoculture. However, the impacts of intercropping on cotton fiber quality stability and key factors influencing quality variability remain poorly understood. This study analyzed five years of data to investigate the variability and controlling factors of cotton fiber quality in both monoculture and intercropping. The results indicated that intercropping maintained cotton fiber length within the long fiber range. While intercropping did not influence fiber quality temporal stability or the risk of quality decline, higher stability was associated with a reduced probability of quality deterioration. Trade-offs among fiber quality traits were observed, indicating that improving one trait often negatively impacted another. Intercropping had minimal impact on these trade-offs. Weather factors accounted for 17–33 % of fiber quality variability, with the effects varying by specific quality trait. Precipitation and photosynthetically active radiation positively influenced fiber length, strength, and uniformity index but negatively affected micronaire and elongation. In contrast, temperature positively influenced all measured fiber quality traits. Overall, our results demonstrate intercropping maintained relatively stable fiber quality over time. This study also reveals strong trade-offs among multiple cotton fiber quality traits, underscoring the need to close trade-offs and achieve synergistic improvements in future research.

11

Title: Evaluating the effect of potassium fertilization on mineral nutrients and root parameters in cotton and pigeon pea under water stress.

Author: Meenakshi, Narender Singh, Saroj Kumar Pradhan, Jyoti Rani, Divya Batra, Mohammad Hedayat & Gholamreza Abdi

Imprint: Discover Sustainability , Published: 16 August 2025, Volume 6, article number 835, (2025)

Abstract: This study explored the influence of potassium chloride (KCl) on mineral nutrient levels and root parameters in an intercropping system involving cotton (*Gossypium hirsutum* var RCH-773) and pigeon pea (*Cajanus cajan* var Manak). The experiment followed a randomized complete block design, considering varied irrigation schedules: full irrigation (control), early water stress (no irrigation during vegetative stage), late water stress (no irrigation during flowering stage), and severe stress (no irrigation). Three potassium concentrations (K_0, K_1, K_2) were applied (0, 20, and 60 kg acre^{-1}, respectively) with replication of each analysis. Sampling occurred at the vegetative growth stage (45 days after sowing), 50% flowering (120 days after sowing), and 50% fruiting stage (150 days after sowing). The results revealed that escalating water stress notably reduced mineral nutrient content (nitrogen, phosphorus, potassium, calcium, magnesium) in the plants. Under water stress conditions, fresh and dry root weights notably reduced, with reductions of 11.60%, 27.20%, and 20.50% for cotton and 30.90%, 11.40%, and 20.22% for pigeon pea at the respective stages. Potassium supplementation significantly enhanced root growth, with fresh weight increases of up to 23% in cotton and 14.3% in pigeon pea under severe water stress. Control treatments exhibited the lowest root length for cotton (5.20 cm) and pigeon pea (4.57 cm). Nutrient analysis indicated that severe stress reduced nitrogen content by 11.50% in cotton and 49% in pigeon pea, with the lowest phosphorus levels at 10.03 mg g^{-1} DW in cotton and 0.09 mg g^{-1} DW in pigeon pea under extreme stress. Potassium supplementation of 60 kg acre^{-1} increased nitrogen content by 9.40% in both crops during stress, while phosphorus content rose to 11.89 mg g^{-1} DW in cotton under severe conditions. The study reveals that potassium application can mitigate reductions in root parameters, highlighting its role as a potent osmo-regulator and enzyme co-factor in plants. ANOVA explained significant interactions between crop, potassium treatment and water stress at F value 31.24 and *p* value 0.0092. Principal Component Analysis showed that PC1 and PC2 explained 88.2% of the total variance, distinguishing mineral-rich, well-irrigated treatments from stressed conditions.

12

Title: Economic risk analysis of precision cotton irrigation scheduling method under conservation tillage.

Author: Anukul Bhattarai, Yangxuan Liu, Amanda Smith, Vasileios Liakos, George Vellidis

Imprint: Agronomy Journal. 2025;117:e70127. wileyonlinelibrary.com/journal/agj2 1 of 15 https://doi.org/10.1002/agj2.70127

Abstract: There is a gap in economic understanding regarding post-adoption changes in profitability and income risks, resulting in the limited adoption of precision irrigation scheduling methods. This study investigated the profitability and the associated risks with the adoption of precision irrigation scheduling methods for cotton (Gossypium hirsutum) production under conservation tillage. Two irrigation scheduling methods were compared with a dryland control (Control): a calendar-based checkbook method (Checkbook) and a precision irrigation method using the Smart Irrigation Cotton App (Cotton App) in Camilia, GA. The net return distributions were subsequently ranked using stochastic efficiency with respect to a function to examine the risk preferences of the irrigation methods among cotton growers. The findings revealed significant water saving, ranging from 24% to 77%, when the Cotton App was used instead of the Checkbook. Risk analysis indicated that the Cotton App was preferred over the Checkbook across all levels of producer risk aversion. The utility-weighted risk premiums for the Cotton App ranged from −\$18 to \$42 ha−1 when compared to the Control and from \$284 to \$305 ha−1 when compared to the Checkbook. The positive risk premium value of the Cotton App over the Checkbook suggests that adopting precision irrigation scheduling strategies, such as the Cotton App, could enhance profitability for cotton growers. The findings from the risk analysis provide valuable guidance to risk-averse cotton growers, enabling them to make well-informed decisions regarding the adoption of innovative methods and effectively mitigate income uncertainties while conserving water and thus promoting sustainable agricultural practices.

13

Title: Patterns of domestication in upland cotton (*Gossypium hirsutum*): a perspective from multielement stoichiometry.

Author: Ziliang Li, Zhangying Lei, Mengmeng Jia, Ülo Niinemets, Wangfeng Zhang

Imprint: BMC Plant Biology , Published: 18 August 2025, 5, article number 1093, (2025)

Abstract: Upland cotton (*Gossypium hirsutum*) is one of the most important cash crops in the world, but few studies have investigated its chemical and physiological changes during domestication, especially changes in chemical element stoichiometry. We investigated the concentrations of 15 chemical elements (carbon, nitrogen, calcium, potassium, sulfur, phosphorus, magnesium, iron, silicon, manganese, boron, zinc, nickel, copper, and molybdenum) in the leaves of 41 genotypes of semiwild and domesticated upland cotton. Principal component analysis, network analysis and domestication effect analysis were used to explore the changes in multielement stoichiometry during the domestication of upland cotton. Analysis of the multielement network indicated that calcium became a more important element after domestication. Across the studied genotypes, the concentrations of carbon and phosphorus decreased after domestication, whereas the concentrations of calcium, magnesium and zinc increased. These alterations resulted in significant domestication effects on some elemental ratios. Combined with changes in plant aboveground biomass, a genetic dilution effect of phosphorus was found. We proposed and tested the "elemental domestication effect" (EDE) in upland cotton (the higher the concentration of elements, the easier it is to be changed during domestication), which may provide new directions for potential crop breeding. We suggest further increasing the calcium, magnesium, and zinc concentrations to enhance the potential for cotton yield and quality, and to reverse the continuous decrease in phosphorus concentration through biological fortification.

14

Title: Integrated physiological and agronomic assessment reveals contrasting drought tolerance strategies in cotton genotypes.

Author: Rennan Fernandes Pereira, Jean Pierre Cordeiro Ramos, Pedro Dantas Fernandes, José Jaime Vasconcelos Cavalcanti, Roseane Cavalcanti dos Santos

Imprint*: Pesqui. Agropecu. Trop.*, Goiânia, v. 55, e82375, 2025

Abstract: Drought limits cotton yield by impairing photosynthesis and growth, yet genotypes differ in their adaptive responses. This study aimed to evaluate upland (*Gossypium hirsutum* var. *latifolium*) and perennial (*G. hirsutum* var. Marie- Galante) cotton cultivars in order to identify physiological mechanisms of drought tolerance and promising germplasm for breeding. A greenhouse experiment was conducted with nine cultivars and two water regimes (irrigated control and drought stress). Growth, gas exchanges, cellular water status, boll production and fiber technological traits were assessed. The BRS Rubi, BRS 286, BRS Seridó, CNPA 5M and CNPA 7MH cultivars exhibited distinct drought-tolerance strategies. BRS Rubi and BRS 286 maintained gas exchange rates similar to the control, preserving the photosynthetic capacity throughout the stress period. CNPA 5M and CNPA 7MH adopted a water-conservation strategy, reducing gas exchanges but sustaining a high relative water content, low electrolyte leakage, satisfactory growth and increased root/ shoot ratio. Overall, BRS 286, BRS Seridó, CNPA 5M and CNPA 7MH combined superior physiological performance with higher boll production and improved fiber quality. These genotypes are recommended as parents in diallel crosses, including with high-yielding but drought-sensitive cultivars, to expand breeding opportunities for cotton in water-limited environments.

15

Title: Exploring the Impact of Chemical Defoliants on Morphological, Physiological Traits and Yield Synchronization in Cotton (*Gossypium* spp.)

Author: R. Rajasekar, V. Ravichandran, A. Senthil, A. Subramanian, K. Thirukumaran, R. Jagadeeswaran & S. Anandakumar

Imprint: Russian Journal of Plant Physiology , Published: 16 August 2025, Volume 72, article number 146, (2025)

Abstract: Cotton is one of the most important fiber and cash crops, which plays a dominant role in the industrial and agricultural economics of the world. Most cotton cultivars produce excessive foliage even at crop maturity due to their indeterminate growth habit, which delays boll opening and results in unsynchronized maturation. Due to this, the multiple pickings in cotton require more labour and is also time-consuming process. These problems can be overcome by the practice of mechanical picking in cotton cultivation. For mechanical picking, it is necessary to defoliate the leaves artificially through application of chemicals which will also synchronize the boll opening, finally yield. To address this, we evaluate the various chemicals on morpho-physiological traits, the nutrio- hormonal changes for efficiency in defoliation, boll opening percentage, and synchronization of the entire yield in cotton. The results show that chemical defoliation makes a significant contribution in the improvement in leaf abscission, decreases green leaf retention, and hastens boll opening, allowing for a more even harvest. Among the chemicals, the application of thidiazuron + diuron exhibited the greatest defoliation percentage (96%) and boll opening rate (84%), resulting in enhanced the synchronized boll opening of harvesting efficiency and fiber quality. Overall, this research offers important information for cotton producers seeking to maximize the defoliant application for efficient mechanized harvesting.

CROP PROTECTION

16

Title: RNAi-Based Approach as a Promising Tool for Management of Leafhopper (*Amrasca biguttula biguttula*) in Cotton

Author: K Shankarganesh , V Gowtham , K P Raghavendra , Joy Das

Imprint: Methods Mol Biol, . 2026:2966:283-291., doi: 10.1007/978-1-0716-4746-2_20.
Abstract: Leafhoppers pose a severe threat to cotton crops, causing substantial yield losses. The use of synthetic insecticides for pest control has drawbacks such as resistance development, environmental harm, and health risks. In this context, RNA interference (RNAi)-based strategies have emerged as an alternative for leafhopper management. RNAi involves introducing double-stranded RNA molecules (dsRNAs) that target vital genes, disrupting their function and causing reduced fitness or death. Specific target genes are identified, and corresponding dsRNA molecules are produced and delivered to leafhoppers through various methods. This chapter presents a case study of Amrasca biguttula, showcasing the potential of RNAi in cotton leafhopper control. Despite delivery and cost challenges, RNAi offers precise, safe, and eco-friendly benefits, making it a valuable tool for managing this significant cotton pest. The chapter outlines techniques for mass rearing leafhoppers, gene selection, RNA isolation, cDNA synthesis, primer design, PCR amplification, and in vitro transcription for dsRNA synthesis. It also includes a protocol for RNAi diet bioassay for bio-efficacy testing and molecular characterization of dsRNA-treated insects. Proper handling and use of RNase-free reagents are emphasized throughout these processes. Overall, we present an RNAi protocol as a valuable tool for controlling leafhopper infestations in cotton research experiments.

17

Title: Management of Whitefly the Vector of Cotton Leaf Curl Disease through Synthetic Insecticide.

Author: Ghulam Mustafa Dasti, Abdul Waheed Solangi, Jamal-U-Ddin Hajano

Imprint: Annual Methodological Archive Research, Volume 3,Issue 9 (2025)Reviewhttp://amresearchreview.com/index.php/Journal/about

Abstract: Cotton crop is cultivated throughout the world and contribute the vital role in economy of many countries. As several types of insect pests have been attacked on cotton crop among them cotton whitefly Bemisia tabaci cause huge losses by suck the cell sap of leaves and reduce the yield every year, in addition to transmit the cotton leaf curl diseases (CLCuD). Selective insecticides are the dire need to control the cotton whitefly, because of their target oriented and immediate knockdowneffect. Farmers still depend on old chemistry-based insecticides for controlling this pest which is not work properly. Therefore, field experiment was performed withrandomized complete block design RCBD with triplicate was carried out at theVillage Khair Muhammad Dasti District Naushehro Feroze during 2024todetermine the effectiveness of novel insecticides against cotton whiteflies. The cotton SS-32 variety was sprayed with different synthetic insecticides for whitefly control. Results showed the after first spray overall average of various time intervals that maximum mortality % was recorded from the plots which treated with Polo insecticide such as (77.51±08.09%) followed by Ulala (69.42±10.53%) and Oberon(64.78±09.10) and Lano (57.21±08.16%) respectively. However, after the application of second spray highest mortality % was recorded from the plots which treated with Polo such as (73.70±09.45%) followed by followed by Ulala insecticide(66.39±07.34%) and Oberon insecticide (62.99±10.05) and Lano (59.41±08.25%) respectively. Further, cotton leaf curl diseases (CLCuD) % of incidence were recorded at different days after sowing (DAS) and data revealed that overall seasonal the lowest CLCuD % incidence was observed (12.68 %) from the plots where Polo insecticide was treated followed by Ulala (16.73%), Oberon (17.47%), Lano (18.79%) and control untreated plot (25.53%), respectively. Further, yield of cotton after the applications of different insecticides was recorded and maximum yield was obtained from the plots which traded with Polo insecticide such as (853.0 kg/acre) followed by Ulala insecticide (824.0 kg/acre), Lano (809.00 kg/acre) and Oberon insecticide (724.0 kg/acre) and Control untreated plot (675.0), respectively. Based on the results, it is suggested that Polo synthetic insecticide product should be sprayed on cotton crop under field condition to manage cotton whiteflies for less crop infestation and better yield production.

18

Title: Development of Transgenic Cotton Plants for Insect Resistance.

Author: Janani Sree Sivakumar , Dhandapani Gurusamy, Selvi Chellamuthu , Sakthi Ambothi Rathnasamy , Vasanth Krishnan

Imprint: Methods Mol Biol, . 2025:2973:137-148., doi: 10.1007/978-1-0716-4803-2_12.
Abstract: Genetically engineered plants are emerging as an increasingly popular tactics for combating insect pests, offering the possibility of increased crop yields with reduced reliance on toxic pesticides. A notable instance is the emergence of Bt-transgenic cotton that incorporates a gene obtained from the bacterium Bacillus thuringiensis which

releases a toxin lethal for certain insect pests especially bollworms. This strategy has become extensively utilized because Bt-cotton has enabled for significant rises in cotton production. Concerns are being expressed regarding the possibility for insect resistance to Bt toxins along with the chance of adverse impacts to organisms that are not targets. This work seeks to provide an optimized manual approach for producing Bt-transgenic cotton cultivars that can successfully manage insect pests while reducing potential negative consequences. The main procedures for introducing genes, transforming plants, and choosing transgenic lines exhibiting desired characteristics will all be covered in the protocol. The resultant transgenic cotton will undergo extensive investigation and assessment in order to determine their overall agronomic performance, potential effects on nontarget organisms, and effectiveness against target pests. This research aims to actively contribute toward the ethical creation and implementation of insect-resistant genetically modified cotton by offering a strong and well-characterized manual process, balancing the need for improved agricultural output and preserving the environment. This manual provides a step by step protocol for successful transformation of transgenic cotton.

19

Title: Spider Diversity and Abundance in Bt nd Non-Bt Cotton Crops a in Punjab, India

Author: Mithun Chaudhary, Neena Singla*, Randeep Kaur Aulakh and Amrit Kaur Mahal

Imprint: Indian Journal of Ecology (2025) 52(3): 598-603 DOI: https://doi.org/10.55362/IJE/2025/4543

Abstract: Bt cotton, expressing a gene for Bt-toxin specifically affects lepidopteran larvae, but little is known about its impact on spiders. This study recorded the diversity and abundance of spiders in both Bt (transgenic cotton PAU Bt 1) and non-Bt cotton crops along with the (F 2228) effect of other factors like crop stages and climate for two seasons. Spiders of nine genera and 11 species representing six families: Araneidae (37.68%), Oxyopidae (28.85%), Lycosidae (18.68%), Thomisidae (10.57%), Salticidae (3.80%), and Pisauridae (0.41%) were recorded with maximum species richness of family Araneidae followed by family Lycosidae, and families Oxyopidae, Thomisidae, Salticidae and Pisauridae. The Shannon-Weiner index and species evenness index were 1.42 and 0.59, respectively. Spider abundance was significantly higher in Bt cotton compared to non-Bt cotton indicating no adverse effect of Bt toxin on spiders. In both crops, the spider abundance was higher at the bollbearing and boll-opening stages. Additionally, there was a significant effect on spiders of mean temperature. T he study suggests that rich spider fauna of cotton crops be protected to utilize their full potential in the Integrated Insect Pest Management Program.

20

Title: Performance of different botanical pesticides against pink boll worm on cotton crop review

Author: Sajjad Hussain Rind+, Saiqa Sanam Solangi+, Nazish Mazhar Ali+

Shakira Mushatque+, Mehral Aslam+, Mazia Amber+, Ayaz Ali Hajano+

Imprint: *Planta Animalia* 4 (4): 387-96. https://doi.org/10.71454/PA.004.04.0205.

Abstract: Cotton (*Gossypium hirsutum* L.) is a globally important cash crop, often termed "White Gold," contributing significantly to food, fiber, feed, and fuel production as well as the livelihoods of millions worldwide. However, its productivity is severely threatened by insect pests, of which the pink bollworm (*Pectinophora gossypiella*) is the most destructive, causing substantial yield and quality losses. Dependence on synthetic insecticides for its control has led to resistance development, environmental contamination, and harmful effects on human health and biodiversity. In recent years, botanical pesticides have emerged as eco-friendly, sustainable, and effective alternatives for integrated pest management (IPM). Neem-based products, including neem seed kernel extract, neem oil, and azadirachtin formulations, have shown strong efficacy against pink bollworm larvae without disrupting natural enemies. Other botanicals, such as extracts of tobacco, datura, chili, and *Artemisia annua*, have demonstrated varying levels of effectiveness, particularly when combined with biological control agents or cultural practices. Integration of botanicals with pheromone trapping, biocontrol agents (e.g., *Trichogramma* spp., *Chrysoperlla carnea, Coccinillidae* spp.*, Beauveria bassiana,*), and selective biopesticides enhances management outcomes. This review highlights the role of botanical pesticides in mitigating pink bollworm infestations, reducing reliance on chemicals, and promoting sustainable cotton production systems.

21

Title: Morphological and physiological characterization of Colletotrichum gossypii and C. dematium infecting Cotton (*Gossypium* spp.) .

Author: SA Raut, AD Lokhande, Vinita Yadav, SB Latake, SJ Deshmukh, DP Shinde and DB Wadekar

Imprint: International Journal of Research in Agronomy 2025; 8(7): 95-99

Abstract: A detailed investigation was conducted to characterize the principal fungal agents responsible for cotton anthracnose, Colletotrichum gossypii and Colletotrichum dematium. Comprehensive morphological analyses revealed that C. gossypii is distinguished by cylindrical conidia (14.25-19.00 × 2.7-5.03 µm) and flexible setae, while C. dematium produces falcate conidia (18-24 × 2.5-3.5 µm) and rigid, melanized setae. Both species exhibited optimal growth on potato dextrose agar (PDA) at 25-30°C and pH 5.5-6.5. Physiological studies demonstrated that temperature and pH strongly influence fungal proliferation, with significant growth inhibition observed outside these optimal ranges. Pathogenicity assays highlighted that C. gossypii induces boll rot and ramulosis (witch's broom), whereas C. dematium causes necrotic leaf spots and dry boll rot. The study establishes a robust framework for the identification and characterization of these pathogens, emphasizing the importance of environmental conditions and morphological traits in understanding anthracnose epidemiology in cotton.

22

Title: Integrating ground-based spectral reflectance and machine learning for C*otton Leaf Curl Virus Disease* (*CLCuD*) detection in cotton crop.

Author: Rahul Nigam, Karunesh K. Shukla, Ajanta Birah, Mukesh K. Khokhar, Bimal K. Bhattacharya

Imprint: Advances in Space Research, Volume 76, Issue 9, 1 November 2025, Pages 5126-5145

Abstract: Early detection of *cotton leaf curl virus disease (CLCuD)* is essential for reducing yield losses and minimizing pesticide use in cotton cultivation. This study integrates ground-based hyperspectral reflectance data with machine learning (ML) techniques to establish a robust framework for detecting *CLCuD* severity under field conditions. A total of 1700 hyperspectral samples were collected from healthy and diseased cotton leaves across multiple seasons in Punjab, India. The disease severity grading was refined based on spectral response overlap, allowing for improved class separability. Four supervised classifiers - Random Forest (RF), Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and Decision Tree (DT) - were evaluated using raw, normalized, PCA-transformed, and Multi-Scale Aggregation (MSA)-processed datasets. RF combined with MSA preprocessing achieved the highest overall accuracy (0.87), followed by KNN (0.82). Spectral derivative analysis and recursive feature elimination identified red-edge (680–750 nm) bands as key indicators of disease severity. Comparative analysis of spectral sub-regions revealed that the 400–1200 nm and full 400–2500 nm ranges offered the most reliable discrimination of disease grades. The study demonstrates the potential of combining domain-informed grading, multiscale spectral aggregation, and feature-optimized ML models for early-stage *CLCuD* detection. This approach offers a scalable and non-destructive tool for precision agriculture, enabling timely management of viral diseases and supporting sustainable cotton production.

23

Title: Varietal Response of Cotton (Gossypium hirsutum L.) against Different Sucking Insect Pests.

Author: Muhammad Ihsan Ullah, Muhammad Hasnain, Zaib Un Nisa, Saeed Ahmad, Javeed Shabbir Dar, Naeem Arshad Mann, Asifa Hameed, Muhammad Tauseef, Imran Ali, Shamim Akhtar, Abdul Ghaffar and Muhammad Akram

Imprint: Sarhad Journal of Agriculture, 41(2): 826-834.

DOI | https://dx.doi.org/10.17582/journal.sja/2025/41.2.826.834

Abstract: Nine cotton (Gossypium hirsutum L.) varieties were tested for resistance against whiteflies (Bemisia tabaci), jassid (Amrasca biguttula biguttila), and thrips (Thrips tabaci) at the Cotton Research Institute, Multan. This study investigates the population dynamics of sucking insect pests cross different cotton varieties during the months of July, August, and September. Significant variations in pest populations were observed, with the peak infestations exceeding the Economic Threshold Level (ETL). In September, the highest whitefly population was recorded on FH-1184 (5.20/leaf), while the lowest was noted on MNH-Sultan and CKC-6, at 3.67 and 3.69/leaf, respectively. August also revealed elevated jassid infestations, notably on FH-1184 and MNH-1082 (4.24/leaf). In contrast, thrips populations peaked on CKC-6 (1.17/leaf) while the lowest was recorded on MNH-Shan (0.51/leaf). Results indicate that both July and August were conducive to the growth of whitefly and jassid populations, contrasting with findings by Swidrak et al. (2013), which identified a July peak for jassids. The study enhances understanding of pest resistance among cotton varieties, with MNH-789 exhibiting the highest tolerance to jassids, whereas CKC-6 showed notable resistance to thrips and whitefly. These findings contribute valuable insights into host plant resistance against sucking pests, highlighting the importance of genotype selection in pest management strategies.

24

Title: Field Survey and Assessment of Fusarium Wilt Incidence in Cotton (Gossypium spp.) in Hanumangarh District of Rajasthan, India.

Author: Deepak Mourya, Anjani Khulbe.

Imprint: Journal of Advances in Biology & Biotechnology, 2025, 28 (8), pp.1595-1603. ⟨hal-05215691⟩

Abstract: Cotton (Gossypium spp.) is a vital commercial crop cultivated worldwide for its natural fibre and seed. Among the various biotic stresses affecting cotton production, Fusarium wilt, incited by the soil-borne fungus Fusarium oxysporum f. sp. vasinfectum

(FOV), is one of the most devastating diseases, often leading to considerable economic losses. The pathogen is known for its long-term survival in the soil through chlamydospores and its ability to persist in association with the roots of susceptible, resistant, and non-host plants, as well as within infected seed. In the present study, a systematic survey was conducted in major cotton-growing regions of Hanumangarh district of Rajasthan to assess the incidence of Fusarium wilt. The maximum disease incidence (28.38%) was recorded in Pilibanga (loamy soil), followed by 27.71% in Goluwala (loam), while the lowest incidence (7.82%) was observed in Motsar, which is characterized by loam soil. Morphological observations revealed that microconidia were produced in greater numbers compared to macroconidia. Chlamydospores were found to be abundant, occurring both terminally and intercalarily. The virulent isolate FTH34 (Fatehgarh), the dimensions of macroconidia, microconidia, and chlamydospores were 38.95x6.26µm, 14.67x5.26µm, and 11.88x10.06µm, respectively.

25

Title: *GhCAT1* improved the tolerance of cotton to Verticillium wilt revealed by genome-wide characterization of *CAT* genes family.

Author:Lei Zhang, Huimin Zhang, Han Zhang, Chang Wang, Kaikuo Rong, Youzhong Li , Yongang Yu

Imprint: Industrial Crops and Products, Volume 235, 1 November 2025, 121795

Abstract: Although catalase (CAT) proteins are well established players in plant immunity, their specific regulatory mechanisms in cotton's defense against Verticillium wilt remain unclear. To elucidate the functional roles of CAT proteins in plant defense systems, we conducted a systematic bioinformatics analysis encompassing physicochemical properties, phylogenetic relationships, protein structures, conserved domains, motif composition, duplication patterns, chromosomal localization, *cis*-regulatory elements, and expression profiles of *CAT* gene family members. RNA-seq data were employed to investigate correlations between *GhCAT*s and *Verticillium dahliae* (*V. dahliae*) infection. Furthermore, an RT-qPCR analysis showed that *GhCAT1* exhibits tissue-specific and *V. dahliae*-responsive expression. Functional studies using VIGS in cotton and overexpression in *A. thaliana* confirmed its role in enhancing Verticillium wilt resistance by regulating pathogen-induced reactive oxygen species and jasmonic acid-dependent defense pathways. Yeast two-hybrid (Y2H) screening identified GhHSP70 as a direct interaction partner of GhCAT1 and a positive regulator of cotton Verticillium wilt. This research reveals new findings on CAT protein functions and supplies key genetic materials for breeding cotton varieties resistant to Verticillium wilt.

26

Title: Screening of Predatory Natural Enemies of Lygus pratensis in Cotton Fields and Evaluation of Their Predatory Effects.

Author: Pengfei Li, Kunyan Wang, Tailong Li, Liqiang Ma, Changqing Gou, and Hongzu Feng

Imprint: Insects 2025, 16(9), 903; https://doi.org/10.3390/insects16090903

Abstract: Lygus pratensis is a major pest of cotton, causing serious damage to cotton production. This study designed species-specific PCR detection primers for L. pratensis, established a detection system to identify L. pratensis DNA in the intestinal contents of predatory natural enemies, and investigated the control potential of four species' predatory natural enemies against L. pratensis. The results indicated that 826 predatory natural enemies were collected from cotton fields belonging to two classes, five orders, and twelve families. Among these, 9 species of insecta natural enemies accounted for 54.12% of the total number of predatory natural enemies collected, while 14 species of arachnida predatory natural enemies comprised 45.88%. Of the 806 natural enemies tested, 5.58% were found to be positive for L. pratensis, all of which were arachnid predators, specifically Ebrechtella tricuspidata, Xysticus ephippiatus, Hylyphantes graminicola, and Oxyopes sertatus. The predation response of these four spider species to the fourth to fifth instar nymphs and adults of L. pratensis adhered to the Holling II model. The theoretical predation (a′/Th), daily maximum predation rate (T/Th), and searching effect for the fourth to fifth instar nymphs and adults of L. pratensis of the four spider species were assessed. According to the results, the species can be ranked in terms of their predatory and searching efficiency as follows: O. sertatus > E. tricuspidata > X. ephippiatus > H. graminicola. Four species of spiders had the highest theoretical predation against L. pratensis nymphs, ranging from 23.71 to 60.86, and adults, ranging from 22.14 to 50.25. Therefore, these four spider species could be utilized for L. pratensis management. This study identified the main predatory natural enemies of L. pratensis and their pest control capabilities, providing a scientific basis for selecting and utilizing natural enemies in integrated pest management (IPM) strategies. This will help promote ecological and green pest control of L. pratensis in cotton-growing areas.

27

Title: Antixenosis: mechanism of resistance to whitefly in upland cotton introgression lines.

Author: Harsimran Kaur, Vijay Kumar, Dharminder Pathak & Manjeet Kaur Sangha

Imprint: Arthropod-Plant Interactions , Published: 06 September 2025, Volume 19, article number 76, (2025)

Abstract: Screen house experiments were conducted under free-choice conditions to determine the antixenosis mechanism of host plant resistance in nineteen cotton test entries against whitefly, *Bemisia tabaci* (Gennadius). They were assessed for settling behavior and oviposition preference. The study revealed that introgression line D-12-7-4-P-2 was most preferred for whitefly settling and oviposition and categorized as highly susceptible, whereas synthetic polyploid, C1-P-1, C1-P-31, C1-P-20, and C1-P-36 were least preferred for oviposition by whitefly, falling under the resistant category and exhibiting an antixenosis mechanism of resistance. Various biophysical and biochemical parameters were estimated for each treatment and correlated with both settling and oviposition preference. Among biophysical parameters, trichome density, leaf area, and vascular bundle length showed significantly positive correlations, whereas leaf lamina thickness was negatively correlated with settling behavior and ovipositional preference. Sugars were predominantly higher in whitefly susceptible lines, whereas phenols, tannins, and proteins were comparatively higher in resistant genotypes. Among biochemical parameters, total soluble sugars and reducing sugars registered a positive association, while total soluble proteins, crude proteins, total phenols, and total tannins showed negative correlations with whitefly settling and ovipositional preference. It may thus be concluded that the antixenosis mechanism of resistance is operating in cotton lines and that biophysical and biochemical parameters play a predominant role in imparting resistance against *B. tabaci*. These identified resistant cotton introgression lines can be used to obtain whitefly-resistant cultivars.

28

Title: Evaluation of Beauveria bassiana Strain NI8 and Conventional Insecticides to Control Lygus lineolaris in Cotton.

Author: Maribel Portilla, Nathan S. Little, Blake H. Elkins, Yuzhe Du, Yu-Cheng Zhu, James P. Glover, Quentin D. Read

Imprint: Southwestern Entomologist, 50(2):611-631
(2025). https://doi.org/10.3958/059.050.0225

Abstract: Cotton, Gossypium hirsutum (L), is an economically important crop in the United States, and the tarnished plant bug, (TPB) Lygus lineolaris Palison de Beauvois (Hemiptera: Miridae) is currently its most significant pest. The efficacy of Beauveria bassiana (Bb) and synthetic insecticides (imidacloprid, sulfoxaflor, novaluron, and acephate) commonly used to control TPB in the Mid-southern U.S. was evaluated significant different when compared with the mortality (32% and35%) of the TPB exposed to leaves under field and laboratory conditions. Its effectiveness was determined by the application of each treatment on cotton leaves sprayed with acephate and reached 78% and 68% 10-days post exposure (DPE) for 2015 and 2016. This was highly was highly sprayed with Bb, 10-DPE for 2015 and 2016. The laboratory bioassay showed no significant differences in the mortality of TPB between Bb, imidacloprid, sulfoxaflor, and sulfoxaflor + novaluron 10-DAE for 2015. However, there were significant differences in yield in the plots sprayed with Bb (1,401 ± 90 kg of lint/ha) from those sprayed with any of the four synthetic set of insecticides (1,530 ± 91 kg of lint/ha) for 2015. Unexpectedly, little to no variation was observed in the cotton yield between the Bb-treated plot (940 ± 30 kg of lint/ha) in 2016. Overall, these results indicated that the use of Bb in controlling the TPB population is as effective as those of synthetic insecticides. However, its performance could vary between the applications in comparison to consistent or better performance of acephate for the control of TPB because Bb is probably degraded negatively affected by environmental factors.

PLANT BREEDING AND GENETICS

29

Title: Genetic Insights into Heterosis and Inbreeding Effects on Yield and Quality Attributes in Cotton (Gossypium hirsutum L.)
Author: Hemali Pandya , K. V Vadodariya , Krunal Baria , Vishwa Gohil , Naresh Chaudhary , Priyanka A Antala , Riya Pate

Imprint*:* Journal of Advances in Biology & Biotechnology, 2025, 28 (8), pp.1669-1678. ⟨hal-05215701⟩

Abstract: Background Information: Cotton (Gossypium hirsutum L.) is an economically important fiber crop, also valued for its seed, which serves as a source of oil and protein. Genetic enhancement of complex traits such as seed cotton yield, fiber quality and oil content remain primary objective in cotton breeding programs. The exploitation of heterosis offers a potential avenue for improving these traits through the development of superior F_1 hybrids. Conversely, inbreeding depression resulting from successive selfing leads to a decline in trait performance due to increased homozygosity and expression of deleterious alleles. Assessing the magnitude and direction of heterosis and inbreeding depression provides critical insights into the genetic architecture of target traits and aids in formulating effective selection strategies for the development of high-performing genotypes. Methodology: The present investigation carried out at Regional Cotton Research Station, Navsari Agricultural University, Bharuch during kharif 2023-24 with a view to estimate heterosis and inbreeding depression by adopting generation mean analysis. The experimental materials were consisting of four different crosses of cotton viz., GBHV 276 × GBHV 278, GBHV 276 × GN Cot32, G. Cot 16 BG II × GBHV 281 and BC-68-2 BG II × GBHV 217to estimate genetic parameters on various five characters viz., seed cotton yield per plant (g), fibre length (mm), fibre fineness (mv), fibre strength (g/tex) and oil content (%). Results: Highly significant and positive relative heterosis as well as heterobeltiosis were recorded in majority of the crosses for most of the characters. For the seed cotton yield per plant, the best heterotic cross was the cross III [G. Cot 16 BG II × GBHV 281] which also showed significant heterosis and heterobeltiosis in the desired direction for fibre length, fibre fineness, fibre strength and oil content. Hence, heterosis breeding in this cross i.e., cross III [G. Cot 16 BG II × GBHV 281] would be a more practical approach for getting higher seed cotton yield. With respect to the inbreeding depression, significant inbreeding depression was observed for majority of crosses for most of the characters included in present investigation.

30

Title: The National Plant Germplasm System cotton collection—a review of germplasm resources, phenotypic characterization, and genomic variation.

Author: Lori L. Hinze, Joshua A. Udall, John Z. Yu & James E. Frelichowski Jr.

Imprint: Theoretical and Applied Genetics, Volume 138, article number 220, (2025)

Abstract: This review is an investigation of the status of phenotypic and molecular characterization efforts in the National Plant Germplasm System (NPGS) cotton collection, highlighting progress to date to maximize the efficiency and effectiveness of future characterization efforts. We considered recent publications of large-scale characterization activities involving the cotton collection. Reports of qualitative descriptors and quantitative phenotypes were considered as well as reports of molecular genotypes. Approximately 80% of cotton accessions are characterized with standardized descriptors and digital images; in addition, large numbers of accessions have recently been screened for resistance to Fusarium wilt, bacterial blight, and cotton leaf curl virus. Many studies have measured genotypes of accessions using a range of technologies—31% of accessions have been genotyped using simple sequence repeat markers, 5% have been genotyped with single nucleotide polymorphism (SNP) arrays, 7% have been genotyped with SNPs from resequencing, and 0.2% of accessions have been sequenced genomically de novo. These efforts ensure that valuable genetic resources are well-characterized, although only a small fraction of the genetic variability in the cotton collection has been surveyed to date. The integration of NPGS cotton collection resources with phenotypic and genotypic information has illuminated the value of cotton genetic variation and genes associated with important traits such as disease resistance and stress tolerance. The cotton collection is a premier information source and critical foundation of variation essential for cotton research and breeding programs aimed at developing resilient cultivars with superior yield and fiber quality in support of U.S. cotton production.

31

Title: Genome-wide identification and analysis of paclobutrazol-resistance gene family in cotton and the positive role of *GhPRE3* in salt stress and drought stress resistance.

Author: Shuaikang Geng, Jingjing Zhai, Bingkai Cui, Huiyun Shan, Zili Liu, Jiahui Li, Cong Wang, Yuling Liu, Pengtao Li,

Imprint: Functional & Integrative Genomics , Published: 29 September 2025, Volume 25, article number 201, (2025)

Abstract: Compared with other transcription factors, much less studies have been performed on paclobutrazol-resistance (PRE), a subgroup of the extensive bHLH transcription factor gene family, and the research in cotton was also limited. By utilizing the PRE genes and their conserved domains identified in Arabidopsis, a total of 23, 22, 11, and 12 PRE genes were identified from two major cultivated cotton species and their two ancestors, respectively. The cotton PRE gene family was categorized into three subgroups based on evolutionary tree analysis. Motif and intron analyses indicated that the PRE gene has remained highly conserved throughout evolution. Collinearity analysis indicated that gene duplication, particularly through fragment replication, has significantly contributed to the expansion of the cotton PRE family. An exploration of the conserved elements within the PRE gene family uncovered numerous elements associated with plant stress resistance. Additionally, cotton transcriptome and qRT-PCR analysis showed that PRE genes were associated with a variety of abiotic stresses, including salt, drought, and cold treatments. Subcellular localization experiments indicated that the *GhPRE3* gene is associated with membrane proteins. Finally, we selected the *GhPRE3* gene for a VIGS experiment, which revealed that under salt stress and drought stress conditions, the wilting of leaves in the *GhPRE3*-silenced plants was significantly more severe than that observed in the control group, with T-AOC levels notably lower and MDA levels significantly higher. Overexpression of *GhPRE3* enhanced seed germination and root development in transgenic *Arabidopsis thaliana* under salt stress and drought stresses. This suggests that *GhPRE3* plays a positive regulatory role in cotton tolerance to salt and drought stressed, providing a reference for molecular genetic breeding of cotton with salt and drought tolerance.

32

Title: Prioritising *D*-Value in Multivariate Evaluation Identifies High-Yield and Drought-Resistant Cotton Genotypes.

Author: Jinglin Li, Ruihua Liu, Shaodong Liu, Guo Zhigang, Huijuan Ma, Qian Shen, Siping Zhang, Changwei Ge, Chaoyou Pan

Imprint: Journal of Agronomy & Crop Sc. : 13 August 2025, https://doi.org/10.1111/jac.70113

Abstract: In order to screen out agronomic traits closely related to drought resistance of cotton, seven agronomic traits were measured, including morphological traits: plant height (PH), first vegetative shoot length of single plant (FVSL) and all vegetative shoot length of single plant (AVSL), and yield traits: boll number (BN), single boll weight (SBW), lint percentage (LP) and seed cotton yield (SCY). All agronomic traits were significantly affected by drought stress, and the morphological traits were significantly correlated, while the yield traits were opposite. Among them, the plant height and seed cotton yield were closely related to drought resistance of cotton. Comprehensive drought resistance coefficient (CDC), comprehensive drought resistance comprehensive evaluation value (D) and weighted drought resistance coefficient (WDC) value are the three comprehensive evaluation indexes of drought resistance. This study is the first to systematically validate that the D value is more scientific to reflect the differences between various agronomic traits and drought resistance of cotton than the CDC value and WDC value. Among the 199 cotton genotypes, there were large differences in drought resistance, and by using cluster analysis, they were divided into five groups: high drought resistance, drought resistance, medium drought resistance, drought-sensitive and high drought sensitivity groups. Four cotton genotypes with high drought resistance were selected; UC072 and UC002 can be widely used as drought resistant genotypes with high yield.

33

Title: Utilizing of RUBY as a Visual Marker and Developmental Regulatory Genes for Genotype-Independent Genetic Transformation in Cotton.

Author: Lekkala, Sai Krishna

Imprint: Files Citable Link, https://hdl.handle.net/2346/103353Collections, TTU Electronic Theses and Dissertations

Abstract: Genetic transformation of cotton (Gossypium hirsutum) continuously faces significant challenges due to strong genotype dependence, limited regeneration capacity in commercial cultivars, and the need for efficient, non-destructive selection systems. To address these barriers, this study explored a combined strategy involving visual marker development, genotype evaluation, and application of developmental regulatory (DR) genes to enhance transformation outcomes. The RUBY reporter gene, encoding a synthetic betalain biosynthesis pathway, was first validated as a visual selection marker in the regeneration-amenable cultivar Coker 312. When introduced through Agrobacterium-mediated transformation using somatic embryogenesis, RUBY-expressing explants developed distinct red pigmentation visible to the naked eye. Approximately 40% of these explants produced pigmented embryogenic calli, and eight fully regenerated RUBY-positive plants were recovered, confirming RUBY's utility as a reliable, equipment-free marker that does not interfere with any regeneration in cotton. To assess genotype responsiveness, transformation protocols were extended to four additional commercial cultivars BSD 598, BSD 4X, BSD 9X, and Ton Buster using both somatic embryogenesis and embryo-axes methods. All genotypes supported transformation, but regeneration remained highly genotype-dependent; only Coker 312 consistently produced somatic embryos, while Ton Buster demonstrated promising transformation frequencies but poor shoot regeneration. To overcome this limitation, three DR genes WUSCHEL (WUS), SHOOT MERISTEMLESS (STM), and ISOPENTENYL TRANSFERASE (IPT) were introduced via the embryo-axis transformation method. While WUS and STM showed limited improvements, IPT significantly enhanced regeneration in both Coker 312 and Ton Buster, inducing multiple shoot formation per explant and effectively mitigating genotype-based constraints. Collectively, these results establish RUBY as a robust visual selection tool and underscore the potential of IPT-driven hormonal modulation to improve regeneration efficiency, offering a practical path toward genotype-independent cotton transformation workflows.

34

Title: Genome-wide evolution and function analysis of ALOG gene family in cotton.

Author: Zhen Liu, Siyu Shen, Zhijuan Cui, Tao Wang, Pengtao Li, Yangyang Wei, Renhai Peng

Imprint: Front. Genet., 10 September 2025, Sec. Computational Genomics, Volume 16 - 2025 | https://doi.org/10.3389/fgene.2025.1625634

Abstract: Background: The ALOG (*Arabidopsis thaliana LSH1* and *Oryza sativa G1*) gene family is a class of transcription factors present in various plants. To elucidate the roles of ALOG genes in cotton, we systematically investigated the ALOG gene family across four cotton species (*Gossypium hirsutum*, *Gossypium barbadense*, *Gossypium arboreum* and *Gossypium raimondii*). Results: In this study, a total of 43, 42, 23 and 27 ALOG genes were identified from *G. hirsutum*, *G. barbadense*, *G. arboretum* and *G. raimondii*, respectively. The results indicated that cotton ALOG gene duplications originated before the speciation of *Gossypium* species, whole genome duplication, segmental duplication and transposable elements all play important roles in its expansion. In addition, cotton ALOG genes had undergone purifying selection during the evolution. Cis-element analysis revealed that TATA-box and CAAT-box are the most abundant in the promoters of cotton ALOG genes. Transcriptome analysis showed that the expression of ALOG genes in specific tissue is significantly higher than that in other tissues. Conclusion: This study enhances our comprehension of cotton ALOG genes, and these findings lay the foundation for functional characterizations of ALOG gene family.

PLANT BIOTECHNOLOGY

35

Title: Identification of the full-length *GbERD7* gene family in *Gossypium barbadense* and functional analysis of the role of the *GbERD7g* gene in drought and salt tolerance.

Author:Zheng Zong, Xue Sun, Junchen Chen, Yuehua Yu, Zhiyong Ni,Yi Wang

Imprint: Plant Science, Volume 360, November 2025, 112715

Abstract: *ERD* (early response to dehydration) genes are promptly upregulated under dehydration stress and are pivotal in plant development. Nonetheless, the precise impact of the *ERD7* gene on the response of cotton to abiotic stress remains unclear. The physical and chemical characteristics, gene architecture, gene collinearity, and transcriptomic profiles were examined. Using bioinformatics techniques, we investigated the evolutionary relationships among the genes within the *GbERD7* gene family of sea island cotton. The *GbERD7* genes are unevenly distributed across the seven chromosomes of sea island cotton, with multiple gene duplications. The *GbERD7* gene family was subjected to phylogenetic analysis, leading to the classification of its members into the SENA and SENB subfamilies. The expression of the *GbERD7* genes was investigated in relation to heat, low-temperature, salt (NaCl), and polyethylene glycol (PEG) treatments. Some genes presented greater expression in specific organs and different periods of fiber development. The functional role of *GbERD7g* was subsequently investigated using molecular biological techniques. *GbERD7g* exhibited pronounced expression in sea island cotton leaves and was upregulated following exposure to PEG, NaCl, and ABA. Subcellular localization studies revealed that the GbERD7g protein is located within the nucleus as well as the plasma membrane of the cell. When the *GbERD7g* gene was silenced under drought and salt stress, the sea island cotton plants were significantly less resistant to drought and salinity and exhibited lower survival than the control plants. The proline levels, catalase activity, and superoxide dismutase activity were reduced, and the malondialdehyde and hydrogen peroxide levels were elevated. In addition, compared with those in the control plants, the expression of all three stress-responsive genes, namely, *GbRD22*, *GbRD26*, and *GbCDPK1*, was significantly lower in the mutant plants.

36

Title: Agrobacterium Infection in Cotton for the Development of Transgenic Cotton Plants.

Author: Masoud Tohidfar

Imprint: Methods Mol Biol, . 2025:2973:207-214., doi: 10.1007/978-1-0716-4803-2_19.
Abstract: Cotton (Gossypium hirsutum L.) is an important fiber crop in the world. Abiotic and abiotic stresses are the main challenges of yield reduction in cotton. Traditionally, four to six times of spraying per growing season of environmentally harmful chemical insecticides is used for pest control. There are various methods for producing transgenic cotton, among which the Agrobacterium tumefaciens method is widely used. In order to produce transgenic cotton tolerance to stresses, explants are transformed with Agrobacterium tumefaciens. Also, selectable marker gene is used as a marker. Inoculated tissue sections are placed onto co-cultivation medium. Transformed tissues are selected on culture medium containing suitable antibiotic. Plantlets are subsequently regenerated from putative transgenic explants. In this chapter, the steps of genetic transformation of cotton by Agrobacterium method using embryogenic calli have been completely explained.

37

Title: Genome-wide identification of *GhEDS1* gene family members in cotton and expression analysis in response to biotic and abiotic stresses.

Author: Rasmieh Hamid, Bahman Panahi, Amin Nezarat, Zahra Ghorbanzadeh, Feba Jacob, Komal G. Lakhani & Mohammad Reza Ghaffari

Imprint: BMC Plant Biology Published: 29 September 2025, Volume 25, article number 1229, (2025

Abstract: Enhanced Disease Susceptibility 1 (EDS1) genes are central regulators of plant immunity and abiotic stress responses. Although well studied in model species, their genome-wide characterisation in cotton (*Gossypium* spp.) remains lacking. Results- We identified 268 putative *EDS1* genes across four Gossypium species (*G. hirsutum*, *G. barbadense*, *G. arboreum*, and *G. raimondii*) using HMMER-based domain searches. Phylogenetic analysis grouped the genes into five subfamilies, reflecting both conserved ancestry and subgenome-specific diversification. Chromosomal mapping, collinearity, and Ka/Ks analyses revealed that segmental and whole-genome duplications were the primary drivers of expansion, with most duplicates under purifying selection. Promoter analysis using PlantCARE uncovered cis-regulatory elements responsive to abscisic acid, jasmonic acid, drought (MBS), and light signals (G-box). miRNA target prediction via psRNATarget revealed *ghr-miR414* as a key regulator targeting multiple GhEDS1 transcripts. Functional enrichment indicated roles in lipid metabolism and ubiquitin-mediated proteolysis. Finally, RNA-seq data and qRT-PCR confirmed that *GhEDS1A-13*, *GhEDS1D-57*, and *GhEDS1D-48* were significantly upregulated under PEG-induced drought stress, implicating them in ABA-linked stress adaptation. Conclusions- This study provides the first comprehensive characterisation of the EDS1 gene family in cotton, highlighting its evolutionary dynamics, regulatory complexity, and potential in improving drought tolerance through molecular breeding.

38

Title: Qualitative Screening of Cry1Ac and Cry2Ab Genes in Nigerian Cotton Genotypes Prior to Commercial Release.
Author: Zango, I. A., Yahaya, A. I., & Mohammed, M. S.

Imprint: Researchers Journal of Science and Technology, 5(6), 56–63. Retrieved from https://www.rejost.com.ng/index.php/home/article/view/214

Abstract: A study was conducted during the 2016 dry season at the Institute for Agricultural Research (IAR), Samaru, in the Northern Guinea Savannah of Nigeria to screen fifty-one (51) cotton (*Gossypium hirsutum* L.) genotypes for the presence of Cry1Ac and Cry2Ab genes. These Bt-derived genes encode insecticidal proteins that provide resistance against bollworms, major pests of cotton. Two qualitative detection methods were employed: Bt lateral flow strips for Cry1Ac and ELISA for Cry2Ab. The genetic materials tested included multi-adversity lines, northern zone lines, eastern zone lines, commercial varieties, and Sabuwa lines. Of the 51 genotypes screened, only two Sabuwa lines tested positive for both Cry1Ac and Cry2Ab, while all others were negative. Limited to qualitative detection, the study nonetheless provides the first baseline evidence of Bt gene presence in Nigerian cotton germplasm prior to the 2018 official approval of Bt cotton. These findings underscore important biosafety and regulatory concerns, highlighting the need for systematic monitoring, enhanced seed certification, and regional harmonization to safeguard varietal integrity and compliance with international biosafety standards.

39

Title: Mapping the Phosphorylation Regulatory Network of Single-Celled Fibre Elongation Mediated by GhBIN2 in Cotton.

Author: Le Liu, Mengli Yu, Longfei Wang, Ghulam Qanmber, Liqiang Fan, Yujun Li, Zhao Liu, Xuwen Wang, Li Liu, Fuguang Li1, Shuangxia Jin, Zuoren Yang

Imprint: Plant Biotechnology Journal, 2025; 0:1–18 https://doi.org/10.1111/pbi.70311

Abstract: Protein phosphorylation plays a pivotal role in cellular signal transduction and plant development. The plant steroid hormone Brassinosteroids (BRs) signal transduction relies primarily on protein kinase-mediated phosphorylation cascades. However, the specific mechanisms of phosphorylation regulation in BR signalling remain to be fully elucidated. This study focuses on BIN2, an indispensable protein kinase in the BR signalling pathway, utilising single-celled cotton fibre to investigate the mechanisms by which phosphorylation regulates cell elongation. Firstly, we confirmed the inhibitory role of GhBIN2 in fibre elongation through its overexpression. Subsequently, we employed 4D-fastDIA quantitative phosphoproteomics and proteomics analysis to map the GhBIN2-mediated phosphorylation regulatory network. Through a comprehensive analysis of this network, we identified six credible substrates of GhBIN2. Further investigation revealed that GhBIN2 interacts with substrate GhIQD14 and increases its abundance through phosphorylation to negatively regulate fibre elongation. This study deepens the understanding of BR signalling in cotton fibre elongation and provides experimental evidence and new insights for comprehending the regulatory role of protein phosphorylation in plant cell elongation processes.

40

Title: Genome-wide association study reveals novel SNP loci and candidate genes linked to flowering time in upland cotton.

Author: Xuefeng Guo, Junning Yang, Dandan Li, Xueli Zhang, Wenmin Yuan, Ying Li, Fuxiang Wang, Qi Ma, Caixiang Wang & Junji Su

Imprint: Theoretical and Applied Genetics Volume 138, article number 214, (2025)

Abstract: Flowering time (FT) is one of the main traits associated with early maturity in upland cotton; however, genetic basis and candidate genes underlying FT remain inadequately understood. In this study, 1,574,032 high-quality single nucleotide polymorphisms (SNPs) were identified on the basis of resequencing data from 619 upland cotton lines, and among them, 418 core germplasms were selected and genome-wide association studies (GWASs) were conducted to identify 456 SNPs that were significantly associated with FT. Variant annotation of significant SNPs revealed that 25 of these SNPs resulted in nonsynonymous mutations in eight genes. Three early-flowering-favouring haplotypes (A02_Hap3, D10_Hap3 and D11_Hap3) and two early-flowering-favouring alleles (D09_6523710_GG and D09_50028094_AA) were identified by haplotype/allele analysis. By RNA–seq and qRT–PCR, three candidate genes (*GhFRO7*, *GhCML1* and *GhPCMP-E88*) were also shown to be differentially expressed between early-flowering and late-flowering varieties. Virus-induced gene silencing (VIGS) experiments further verified the critical roles of the three genes, which were important regulators underlying the late-flowering phenotype in upland cotton, in the regulation of FT. Moreover, selection pressure analysis revealed that these three candidate genes might have experienced artificial or natural selection. In addition, we developed two cleaved amplified polymorphic sequence (CAPS) markers, which have potential application value. These findings will provide a new theoretical basis for the genetic improvement of early maturity-related traits in upland cotton and lay the foundation for the breeding of excellent early maturing varieties.

41

Title: Genome-wide identification of *VOZ* gene family in ten cotton species and the function analysis of *GhVOZ2* involved in heat stress response.

Author: Xiangxiang Hu, Kailu Chen, Shuangquan Xie, Quanliang Xie, Xifeng Chen, Zhuang Meng, Asigul Ismayil, Xiang Jin, Shandang Shi, Fei Wang & Hongbin Li

Imprint: BMC Genomics, Published: 18 August 2025, Volume 26, article number 753, (2025)

Abstract: Vascular plant one zinc-finger protein (VOZ) is a type of special transcription factor and plays important roles in regulating various biological processes in plants. However, a genome-wide analysis of *VOZ* gene family in cotton is still not clear, which greatly limits the further understanding of *VOZ* gene function and regulatory mechanism. Results- We identified 44 *VOZ* family genes in ten cotton species including 3 in *Gossypium herbaceum*, *G. arboretum*, *G. thurberi*, and *G. Raimondii*, 6 in *G. hirsutum*, *G. barbadense*, *G. tomentosum*, and *G. mustelinum*, and 5 in *G. darwinii*. The phylogenetic tree analysis indicated that *VOZ* gene family was subdivided into four subgroups. Chromosome location and collinearity analysis revealed that this gene family had experienced segment duplication events. The exon-intron structure and conserved motif analysis showed high conservations in each branch of the cotton *VOZ* genes. *Cis*-acting element component analysis displayed that *VOZ* gene family may be involved in various stresses. Expression profile analysis of *GhVOZ* genes through both publicly available RNA-seq data from *G. hirsutum* and quantitative reverse transcription PCR (RT-qPCR) indicated that *GhVOZ* members are involved in tissue development and biotic and abiotic responses, especially *GhVOZ2* showed continuous high expressions in different tissues and stress treatments, with the most significantly induced accumulation under heat stress. Suppressing *GhVOZ2* expression in virus-induced silencing (VIGS) cotton lines significantly decreased the tolerance to heat stress. Further RNA-seq analysis of *TRV::GhVOZ2* showed that the down-regulated differentially expressed genes (DEGs) were mainly enriched in hormone signal pathways (auxin and BRs), phenylpropanoid and flavonoid biosynthesis, fatty acid elongation, starch and sucrose metabolism pathways, suggesting their potential important roles in heat response mediated by GhVOZ2. Conclusions- A total of 44 *VOZ* genes were obtained in ten cotton species, and *GhVOZ2* might perform significant positive function in cotton in response to heat stress via regulating the pathways of hormone signal and metabolisms. Our results provide insights into the function and regulatory mechanism of *VOZ* gene family and the further utilization of excellent cotton material breeding.

SEED SCIENCE AND TECHNOLOGY

42

Title: Identification of stress tolerance in cotton during the germination stage and analysis of its correlation with seed composition.

Author: Yaping Guo, Quanjia Chen, Zehui Du, Pengfei Liu, Yujie Chang and Xiaojuan Deng

Imprint: Plant Genetic Resources, Published online by Cambridge University Press: 26 August 2025

Abstract: Drought, salt and low-temperature stress significantly reduce the germination rate of cotton seeds. Additionally, the seed composition of seeds, including protein, oil and gossypol, are also closely linked to germination performance. This study assessed the seed composition of 120 cotton genotypes and their ability to germinate under drought, salt, and low-temperature stress, and compared with under standard conditions (control). Stress resistance during the germination stage was comprehensively evaluated using principal component analysis (PCA), which categorized the genotypes into three groups: 35 high-stress tolerance, 74 medium-stress tolerance and 11 medium sensitivity. Subordinate function analysis revealed that the comprehensive resistance D values of the 120 genotypes ranged from 0.20 to 1.12. Correlation analysis showed a significant negative correlation between seed oil content and germination under drought and salt stress ($R = -0.27^{**}$ and $R = -0.24^{**}$). Additionally, germination under drought and salt stress were positively correlated ($R = 0.58^{***}$). SNP_A07_90682411-based Kompetitive Allele-Specific PCR (KASP) markers identified that AA-type genotypes had significantly higher D values for comprehensive stress tolerance, drought resistance and salt resistance at the germination stage compared to GG-type genotypes ($P = 0.0003$, $P = 0.010$, and $P = 0.0004$, respectively). This study identified highly resistant and sensitive genotypes to various abiotic stresses, during germination and demonstrated that the ability of the newly developed KASP molecular markers effectively differentiate comprehensive germination performance under stress. These findings provide valuable references for understanding stress tolerance mechanisms during germination and breeding stress-tolerant cotton varieties.

43

Title: Decreased active cytokinin levels inhibited the cytokinin signaling pathways to increase the lateral root number in mepiquat chloride-treated cotton (*Gossypium hirsutum* L.) seedlings.

Author: Zhang Man, Zhang Jiaqi, Chen Yujie, Wu Yixuan, Shi Yang, Xing Haiyan, Chen Xiaojiao & Wang Baomin

Imprint: Journal of Cotton Research, Published: 29 August 2025, Volume 8, article number 30, (2025)

Abstract: Mepiquat chloride (MC) is a widely used plant growth regulator in cotton *(Gossypium hirsutum* L.*)*. It regulates endogenous hormone content and crosstalk to control plant height and promote lateral root (LR) development. However, the roles of cytokinins (CTKs) in the MC-induced increase in LR number in cotton seedlings remain unclear. Therefore, in this study, whole-genome transcriptome analysis was performed to elucidate the molecular mechanisms, CTK transformation, and CTK signaling pathway response to MC in cotton roots. **Results**- In the present study, MC reduced the contents of the active CTK *trans*-zeatin (tZ) and N^6-isopentenyladenine (iP) but increased the levels of the nucleoside CTK *trans*-zeatin riboside (tZR) and N^6-isopentenyladenine riboside (iPR). RNA-seq data showed that the CTK biosynthesis genes *GhIPTs* and active CTK catabolism genes *GhCKXs* were obviously upregulated after MC treatment. The CTK-activating enzyme gene *GhLOGs* was repressed compared with the control. Furthermore, MC inhibited the expression of *GhAHK4* and *GhARR2/12*, which are involved in the CTK signaling pathway, and activated the IAA-IAA14-ARF7/19 signaling module. Meanwhile, MC increased the expression levels of genes involved in sucrose synthesis, the cell cycle, cell division, and cell wall biosynthesis pathways. Silencing the *GhCKX* family separately decreased the LR number and active indole-3-acetic acid (IAA) level. The expression levels of *GhPIN1*, *GhARF7*, *GhARF19*, *GhLBD16*, *GhLBD18*, *GhLBD29*, and *GhLBD33* were downregulated, but *GhARR2/12* and *GhIAA14* were upregulated. The total content of active CTKs was noticeably increased. The results of silencing the *GhLOGs* family were opposite to those of silencing *GhCKXs*. Silencing *GhARR12* could upregulate *GhPIN1* expression and increase LR number. In addition, the silenced *GhCKXs*, *GhLOGs*, and *GhARR12* were less responsive to MC-induced LR growth than the control. **Conclusion**- These results suggested that MC treatment could upregulate CTK-nucleoside biosynthesis and CTK metabolism genes to decrease active CTK levels, promoting crosstalk between CTKs and auxin signaling pathways to enhance LR initiation.

44

Title: Genome-wide identification and characterization of DUF789 genes in cotton: implications for fibre development.

Author: Rasmieh Hamid, Bahman Panahi, Zahra Ghorbanzadeh, Feba Jacob, Mehrshad Zeinalabedini & Mohammad Reza Ghaffari

Imprint: BMC Plant Biology , Published: 02 September 2025, Volume 25, article number 1192, (2025)

Abstract: Proteins containing domains of unknown function (DUFs) play a crucial role in plant growth, development and stress adaptation, but many of them are still uncharacterized. The DUF789 family is one of the least studied of these, especially in economically significant crops like cotton (*Gossypium* spp.), whose possible function in fibre production and abiotic stress response is yet unknown. **Results**- In a comprehensive genome-wide analysis, a total of 91 *DUF789* genes were identified in four *Gossypium* species: *G. arboreum*, *G. barbadense*, *G. raimondii* and *G. hirsutum*. Evolutionary and phylogenetic analyses placed the *GhDUF789* proteins into different clades, with purifying selection identified as the major evolutionary force. Analyses of gene structure and conserved motifs revealed considerable structural diversity, with closely related genes showing similar exon–intron patterns and motif compositions. Synteny and duplication analyses showed that segmental and tandem duplications contributed to the DUF789 family expansion in cotton. Analysis of cis-regulatory elements revealed that the GhDUF789 promoters are enriched in motifs responsive to hormonal, developmental, light-induced and abiotic stresses. GO enrichment analyses, prediction of protein–protein interaction and secondary and tertiary structure modelling, indicated that GhDUF789 proteins are involved in clathrin-mediated vesicle trafficking and membrane trafficking. The miRNA target prediction revealed regulatory interactions with conserved miRNAs from cotton, in particular ghr-miR414 and ghr-miR396. Expression profiling based on transcriptome analysis, supported by validation using qRT-PCR, revealed that several *GhDUF789* genes are differentially expressed during fibre development and respond strongly to drought, heat, salinity and cold stress, especially in drought-tolerant genotypes. **Conclusions**- This study provides the first comprehensive characterization of the DUF789 gene family in cotton and offers new insights into its evolutionary dynamics, structural features and potential role in fibre development and adaptation to abiotic stress. The results provide a solid foundation for future functional studies and identify candidate *GhDUF789* genes for targeted genetic improvement of stress resistance and fibre quality in cotton.

45

Title: Molecular dissection of quantitative variation in fiber elongation between *Gossypium hirsutum* and *Gossypium barbadense* in reciprocal near-isogenic lines.

Author: Jeevan Adhikari, Deepak Vitrakoti, Wiriyanat Ployaram, Sameer Khanal

Imprint: Front. Plant Sci., 16 September 2025, Sec. Plant Breeding, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1657140

Abstract: In reciprocal interspecific near-isogenic lines developed by crossing elite cultivars Acala Maxxa (Gossypium hirsutum) and Pima S6 (G. barbadense) representing the two major domesticated species of cotton, we identified genomic locations underpinning an important fiber quality trait - fiber elongation (ELO). Phenotypic evaluation of these lines in three environments revealed a total of 36 QTLs, including 14 (38.89%) on the D subgenome, from a progenitor that does not produce spinnable fiber. Nearly half (16, 44.4%) of the 36 QTLs identified in the study explained less than 6% of phenotypic variation, and two (EL07.1 and EL25.1) were new, justifying the use of near-isogenic lines for analysis. Significantly larger additive effects of these QTLs in comparison to those reported using early generation backcrosses, F2 and F2 derived populations as well as recombinant inbred lines (RILs) show that NILs offer an advantage in estimating more precise QTL effects by removing background noise due to segregating genomic regions. Seven genomic regions on chromosomes 2, 6, 9, 12, 15 and 18 were consistently associated with ELO in two of the three environments tested. A total of 11 (30.56% of) QTLs had transgressive allele effects, i.e. which were opposite of what would be predicted from the parental phenotypes, indicating opportunities to breed superior interspecific lines; and three QTLs (8.33%) had heterotic alleles that may contribute to the striking fiber quality of F1 hybrids between these species. Limited reciprocity of QTLs in the two backgrounds is attributed to the combined consequences of epistasis, small phenotypic effects and imperfect coverage of donor chromatin in the recipient background. The availability of DNA markers linked to both G. barbadense and G. hirsutum QTLs identified in this and other studies promise to assist breeders in transferring and maintaining valuable traits from exotic sources during cultivar development.