



GLEANINGS IN COTTON RESEARCH

September 2025



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RESEARCH***

SEPTEMBER 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
(T5)*

*Chetali Rodge
Technical Officer*

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1

Title: Comparative economic analysis of Bt cotton and SAU cotton varieties in Tamil Nadu.

Author: V Vikanasan, M Manimegalai, KR Sundaravaradarajan, M Vaidheki and Sharath S Yeligar

Imprint: International Journal of Agriculture and Food Science 2025; 7(5): 373-378

Abstract: The cotton sector in Tamil Nadu plays a vital role in rural livelihoods and agricultural income. This study conducts a comparative socioeconomic analysis between cotton varieties released by State Agricultural Universities (SAUs) and Bt cotton cultivated in the Perambalur district. Primary data were collected through structured interviews from 120 cotton farmers using a multistage random sampling technique. Analytical tools such as the Probit Model, Independent Sample t-Test, and Friedman Test were employed to assess varietal preference, income differences, and cultivation challenges. The findings reveal that while Bt cotton offers higher yields and profitability, SAU varieties are preferred for their seed affordability and resilience to climatic stress. However, marketing and pest management challenges persist across both systems. The study underscores the importance of promoting context-specific cotton varieties, enhancing extension services, and ensuring better market linkages for improving farmers' welfare and sustainable cotton cultivation.

2

Title: Soil Applied Potassium Combined with Foliar Application of Macro and Micronutrients Improved Yield and Economic Returns of Cotton (*Gossypium hirsutum* L.).

Author: Hakan Ünal Ağaç & Hasan Haliloğlu

Imprint: Journal of Soil Science and Plant Nutrition , Open access, Published: 11 June 2025

Abstract: Improper or inadequate mineral nutrition is a major issue in cotton (*Gossypium hirsutum* L.) production globally. Therefore, the development of balanced fertilization strategies is essential for sustainable cotton production. This study assessed the impacts of soil-applied potassium (K) doses ($K_0 = 0$, $K_{70} = 70$, $K_{140} = 140$, and $K_{210} = 210$ kg ha⁻¹) combined with water ($F_0 = \text{control}$) foliar-applied humic acid

(F1 = 150 g humic acid in 100 L water), micronutrients (F2 = (250 g of micronutrient mixture containing 7% iron (Fe), 7% zinc (Zn), 1% boron (B), 5% manganese (Mn), 0.05% molybdenum (Mo) and 1% copper (Cu) in 100 L water), and macro + micronutrients (F3 = 500 g urea + 500 g potassium sulfate + 100 g zinc sulfate + 100 g F2 in 100 L water) on yield-related and fiber quality traits, and ginning outturn of cotton during 2020 and 2021. Frequently cultivated genotype 'Fiona' was used in the study. The K was applied at the time of sowing, whereas foliar treatments were applied at square initiation, flowering initiation, and peak flowering. The individual and interactive effects of soil-applied K and foliar applied nutrients significantly altered yield and related traits, whereas fiber quality traits remained unaffected during both years. Overall K210 × F3 interaction resulted in the highest values of yield-related traits and seed cotton yield. The highest seed cotton yield (6428 and 6185 kg ha⁻¹ during 2020 and 2021, respectively) was recorded for K210 × F3 interaction. Similarly, K210 × F3 interaction resulted in the highest net returns (709 and 496 US\$ ha⁻¹ during 2020 and 2021, respectively) and benefit: cost ratio (1.90 and 1.50 during 2020 and 2021, respectively). Overall, the highest seed cotton yield and economic returns were recorded for K210 × F3 interaction. Therefore, it is recommended to apply 210 kg ha⁻¹ K followed by foliar application of macro + micronutrients for higher yield and economic returns.

3

Title: Integrating cover crops and targeted herbicide applications in cotton production.

Author: Tristen H. Avent, Jason K. Norsworthy, Thomas R. Butts, Gerson Drescher

Imprint: Agrosyst Geosci Environ. 2025;8:e70132.
wileyonlinelibrary.com/journal/agg2 <https://doi.org/10.1002/agg2.70132>

Abstract: Cover crops are part of integrated weed control management to help mitigate herbicide resistance evolution. Targeted sprays from the John Deere See & Spray are currently not recommended in cover crops. Experiments were conducted yearly from 2022 to 2024 in Keiser, AR, to evaluate targeted applications (TAs) with cover crops in cotton (*Gossypium hirsutum* L.). Treatments assessed the main effect of winter cover crop (fallow, cereal rye [*Secale cereale* L.], or hairy vetch [*Vicia villosa* Roth]), herbicide application methods (nontreated, broadcast [BC], TA + BC residuals [TA + BCRs], or TA only), and the interaction on cotton tolerance, weed control, and herbicide savings. Cereal rye generally aided weed control efforts across the weeds evaluated, and there were instances of herbicide savings at the preemergence and mid-postemergence (MPOST) timings when using TA or TA + BCR relative to BC. In some instances, TA POST + RES reduced weed control. At layby, TA-only applications reduced Palmer amaranth control by 5–10 percentage points in winter fallow systems compared to the BC in 2022 and 2023. In 2024 at MPOST, low herbicide savings occurred in the winter fallow cover systems (2.9%), whereas TA + BCR saved 29.4% and 26.5% for cereal rye and hairy vetch, respectively. In conclusion, See & Spray improved environmental

stewardship and could detect and treat weeds in standing cover crop biomass, providing comparable control to the BC application at the end of the season ($\geq 92\%$ for all species).

4

Title: Nitrogen uptake kinetics in relation to cotton root morphology subjected to different nitrogen sources.

Author: Wajid Mahboob, Nadeem Sarwar, Muhammad Irfan, Muhammad Abbas, Muhammad Akhtar, Guozheng Yang

Imprint: J. of Plant Nutrition, <https://doi.org/10.1080/01904167.2025.2509133>

Abstract: Nitrogen (N) deficiency is considered one of the key factors limiting cotton growth and productivity. Kinetic and root morphological parameters influencing nutrient absorption efficiency are often overlooked in crop breeding programs. This hydroponic study examined the growth, morphology, and uptake kinetics parameters including maximum absorption velocity (V_{\max}), Michaelis–Menten constant (K_m), minimum concentration (C_{\min}) for NO_3^- and NH_4^+ in cotton varieties, N-efficient Ghotki-Uhad (GH-Uhad) and N-inefficient Faisalabad-Hybrid (FH-444) subjected to 0.5 and 5 mM N supply. The studied parameters considerably responded to N application either in the form of NO_3^- or NH_4^+ . High-N treatment significantly increased shoot dry weight (SDW) (46.7%), root dry weight (RDW) (28.3%), and total biomass (42.7%) compared to low-N and results were more obvious (16% higher biomass) under NO_3^- -N than NH_4^+ -N. Compared to NH_4^+ -N, root length (RL) and root surface area (RSA) increased under low NO_3^- -N while high NO_3^- -N improved mean root diameter and root volume. Furthermore, GH-Uhad had low K_m and C_{\min} for both N forms, suggesting that it functioned in a high-affinity transport system (HATS) under low N-supply. Contrarily, FH-444 exhibited higher V_{\max} for NH_4^+ but had low affinity irrespective of N forms. However, GH-Uhad preferred NO_3^- over NH_4^+ , while FH-444 switched between the two at low and high N levels. Root morphological traits, V_{\max} , C_{\min} , and N content were positively associated with growth attributes while kinetic parameters had a negative correlation with root morphological traits. In crux, GH-Uhad performed better for growth, root morphology, and exhibited high affinity for N uptake, showing its adaptation to N-limited conditions.

5

Title: High-Performing Upland Cotton Shifts Root-Associated Microbiomes Under Water Limitation.

Author: Jimaree A. Legins

Imprint: A Thesis Submitted to the Faculty of the School of Plant Sciences In Partial Fulfillment of the Requirements For the Degree of Master of Science In the Graduate College The University of Arizona 2025

Abstract: Water scarcity significantly threatens cotton productivity, a challenge amplified by climate change and increasing competition for limited water resources. As a major source of natural fiber, cotton's resilience to drought stress is essential for maintaining productivity and supporting global textile production. However, the mechanisms underlying this resilience, particularly the responses of root-associated microbial communities that may influence plant drought stress responses, remain unclear. Here, we quantified the plasticity of microbial communities associated with roots of six cotton cultivars grown under water-limiting and well-watered conditions in a hot, arid environment. The highest-yielding cotton cultivars markedly shifted their root microbial communities between irrigation treatments, whereas low-yielding cultivars were less responsive. Microbiome shifts in high-performing varieties suggest that these plants may leverage symbiotic relationships to cope with water limitation. This study links microbial communities and the performance of cotton and highlights the potential for leveraging these relationships to improve crop resilience in water-limited environments.

6

Title: Transcriptomic exploration yields novel perspectives on the regulatory network underlying trichome initiation in *Gossypium arboreum* hypocotyls.

Author: Yuxing Xie, Luying Yang, Zewei Zhao, Mingquan Ding, Yuefen Cao

Imprint: Front. Plant Sci., 02 July 2025, Sec. Plant Bioinformatics, Volume 16 - 2025 | <https://doi.org/10.3389/fpls.2025.1604186>

Abstract: Trichomes play a crucial role in plant stress tolerance and serve as an excellent model for studying epidermal cell differentiation. To elucidate the molecular mechanisms underlying trichome development in cotton stems, we investigated two *Gossypium arboreum* mutants that exhibit abnormal trichome patterns during hypocotyl growth. Based on morphological characteristics, we classified four developmental stages: preinitiation, initiation, elongation, and maturation. Comparative transcriptome profiling of epidermal cells across these stages identified differentially expressed genes (DEGs) through maSigPro analysis, which revealed that these DEGs were primarily associated with pathways involved in cell wall metabolism. Additionally, integrated weighted gene co-expression network analysis (WGCNA) and Cytoscape analyses identified 20 core regulatory genes from a total of 59 candidates linked to epidermal development. Utilizing three machine learning algorithms (SVM-RFE, Boruta, and LASSO), we consistently prioritized five key regulators: Ga02G1392 (TBR), Ga03G0474 (OMR1), Ga12G2860 (ACO1), Ga11G2117 (BBX19), and Ga12G2864 (CUE). RT-qPCR validation confirmed their stage-specific expression patterns, which were consistent with the RNA-Seq data. Our study establishes a comprehensive framework for research on cotton trichomes and identifies critical genetic components

governing epidermal hair development, thereby providing new insights for the molecular breeding of stress-resistant cotton varieties.

7

Title: Critical Nitrogen Dilution Curve for Diagnosing Nitrogen Status of Cotton and Its Implications for Nitrogen Management in Cotton–Rape Rotation System.

Author: Yukun Qin, Weina Feng, Junying Chen, Cangsong Zheng, Lijuan Zhang, Taili Nie

Imprint: *Agronomy* 2025, 15(6), 1325; <https://doi.org/10.3390/agronomy15061325>

Abstract: Based on a 2-year in situ nitrogen fertilization experiment, this study aims to establish a critical nitrogen concentration (CNC) dilution curve model for cotton under straw incorporation, analyze the effects of the nitrogen application rate on the cotton yield and nitrogen use efficiency (NUE), and determine the optimal nitrogen application rate by integrating the nitrogen nutrition index (NNI). The experiment setup was a randomized block design with five nitrogen application levels under a straw incorporation: 0, 60, 120, 180, and 240 kg N ha⁻¹ (denoted as N0, N60, N120, N180, and N240, respectively). The cotton dry matter accumulation and nitrogen concentration were measured at the flowering and boll stage, peak boll stage, and boll opening stage. The CNC dilution curve was developed using the data from 2021 and validated with those of 2022. Results showed that the cotton biomass and seed cotton yield at the boll opening stage increased with nitrogen application rates up to 180 kg N ha⁻¹. However, no further increase was found in the yield with an N rate higher than 180 kg N ha⁻¹. The CNC dilution curve was formulated as $y = 3.4921x^{-0.416}$ ($R^2 = 0.8741$). The validation using 2022 data yielded a root mean square error (RMSE) of 0.21% and a normalized RMSE (nRMSE) of 13.40%, confirming the model's robustness. The NNI, calculated based on the CNC, indicated that an application rate of 120 kg N ha⁻¹ maintained NNI values close to one across all growth stages, reflecting an optimal nitrogen status. Significant positive correlations were observed between the NNI and both the seed cotton yield and harvest index ($p < 0.05$). Nitrogen use efficiency parameters, including the agronomic NUE (NUEa), nitrogen partial factor productivity (NPFp), and internal NUE (NUEi), exhibited quadratic declines with the increasing nitrogen input. Within the range of 120–240 kg N ha⁻¹, the highest NPFp was achieved at 120 kg N ha⁻¹. In conclusion, the critical nitrogen dilution curve model combined with the NNI effectively diagnoses the nitrogen status in cotton under straw incorporations. Considering the NNI, yield, and nitrogen utilization efficiency, the recommended nitrogen application rate for cotton in a cotton–rape rotation system with a straw incorporation is 120 kg N ha⁻¹.

8

Title: Drip Irrigation of Phosphorus Fertilizer Enhances Cotton Yield and Phosphorus Use Efficiency.

Author: Yuwen Wu, Xiaoqian Wu, Jun Zhang, Leru Zhou, and Bolang Chen

Imprint: *Agronomy* 2025, 15(6), 1328; <https://doi.org/10.3390/agronomy15061328>

Abstract: Root systems are pivotal for nutrient absorption, exhibiting high plasticity in phosphorus (P) acquisition, and significantly influencing soil phosphorus availability. However, the impacts of different P application methods on root parameters and P utilization efficiency in cotton (*Gossypium hirsutum* L.) under Xinjiang conditions are still not well understood. To identify optimal P fertilization strategies, a consecutive two-year field experiment (2023–2024) under mulched drip irrigation was conducted. Three P application methods were tested: no P (CK), basal P application (PB), and drip P application (PD). Results revealed that P application methods significantly affected cotton dry matter, P use efficiency, root morphology, and yield ($p < 0.05$). Over the two years, the optimized treatment (25% P applied at bud stage and 25% at flowering-boll stage, PD) increased yield by 13.62% and 9.50% compared to full basal application (PB), with P use efficiency improved by 22.04–31.51% and agronomic efficiency improved by 6.56–9.75 kg kg⁻¹. PB significantly increased soil-available P in 0–20 cm (34.17–70.09%) and 20–40 cm layers (30.37–70.32%) compared to CK. During the bud stage, PD treatment exhibited higher soil-available P in the 20–40 cm layer than PB. PD enhanced P uptake and dry matter accumulation, with increases of 22.43–36.33% and 7.90–15.55% in reproductive organ P accumulation compared to other treatments. Root parameters followed PD > PB > CK across all treatments. At the seedling stage, PB increased total root length by 19.79% compared to CK, while PD increased root volume by 46.15% compared to PB. During the bud stage, PB increased root volume by 53.33% compared to CK, and PD enhanced root surface area and volume by 39.25% and 47.82% compared to PB. Root volume showed a significant positive correlation with phosphorus absorption across growth stages. The PD treatment significantly enhanced soil P availability and P use efficiency and optimized root spatial distribution. This treatment consistently increased cotton yield by 30.41–39.09% ($p < 0.05$) compared to CK, demonstrating stable positive effects. This study highlights that adjusting P application methods can establish sustainable, high-yield agricultural fertilization systems.

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Title: Morpho-physiology and production of naturally colored cotton under salt stress and foliar application of salicylic acid .

Author: Reynaldo Teodoro de Fatima, Lauriane Almeida dos Anjos Soares, Geovani Soares de Lima, Jackson Silva Nóbrega, Jean Telvio Andrade Ferreira

Imprint: *Ciência Rural*, Santa Maria, v.55:8, e20240164, 2025

ABSTRACT: Cultivation of naturally colored cotton is an alternative to add value to the crop in the northeast region of Brazil, but it is necessary to adopt strategies capable of attenuating the effects of salt stress, increasingly common in this region. In this context, the present study evaluated the morphophysiology and production components of naturally colored cotton cv. ‘BRS Jade’ irrigated with saline water and under foliar

application of salicylic acid. The experimental design was randomized blocks, in a 5×5 factorial scheme, referring to five levels of electrical conductivity of irrigation water - EC_w (0.3, 1.8, 3.3, 4.8, and 6.3 dS m⁻¹) and five concentrations of salicylic acid - SA (0, 1.5, 3.0, 4.5, and 6.0 mM), with three replicates. Irrigation water up to 6.3 dS m⁻¹ did not cause losses greater than 10% in the morphophysiology of colored cotton. Application of salicylic acid at a concentration of 6.0 mM increased CO₂ assimilation rate, but affected negatively the biomass accumulation, lint cotton weight, bract dry mass, and total number of bolls of colored cotton cv. 'BRS Jade'. Salicylic acid did not mitigate the effects of salt stress on the morphology and lint production of naturally colored cotton cv. 'BRS Jade' at 100 days after sowing. Key words: *Gossypium hirsutum* L., cotton crop, salinity, phytohormone, semi-arid region.

10

Title: Synergistic Optimisation of Root Hydraulic Architecture Enhances Drought Tolerance in Cotton.

Author: Shuo Wang, Lingxiao Zhu, Peng Zhang, Xinyue Wang, Hongchun Sun, Ke Zhang, Yongjiang Zhang, Guiyan Wang, Ningxin Zhu, Zhiying Bai, Hezhong Dong, Cundong Li, Liantao Liu

Imprint: Plant Cell Environ, 2025 May 27. doi: 10.1111/pce.15640. Online ahead of print.

Abstract: Optimising the root hydraulic architecture, which is defined by the integration of morphological and hydraulic traits, plays a crucial role in enhancing the drought tolerance of crops. However, the mechanisms by which root hydraulic architecture coordinates structural and functional adaptations under drought remain unclear. In this study, we used paper-based cultured 13 cotton cultivars under no-stressed and drought-stressed conditions, and identified a drought-tolerant (Guoxin 02) and a drought-sensitive (Ji 228) cultivar. The drought-tolerant cultivar exhibited enhanced root hydraulic conductance (L_{pr}) through increased lateral root length and number, reduced lateral root tip angle, and lower root width/depth ratio. Anatomically, drought tolerance was associated with narrower xylem vessels to limit axial conductance (K_x) and reduced cortex cell layers to increase radial hydraulic conductance (K_{ox}), thereby balancing hydraulic efficiency and embolism resistance. Despite lower K_x, the high root hydraulic conductance (K_{root}) in the drought-tolerant cultivar was maintained by lateral root proliferation, demonstrating a synergistic interplay between morphology and hydraulics. These findings highlight the plasticity of root hydraulic architecture as a key target for breeding drought-resilient cotton.

11

Title: Integrated transcriptomic and metabolomic analyses provide new insights into alkaline stress tolerance in *Gossypium hirsutum*.

Author: Shiwei Geng, Wenju Gao, Fenglei Sun, Ni Yang, Teng Ma

Imprint: Front. Plant Sci., 03 June 2025, Sec. Crop and Product Physiology

Volume 16 - 2025 | <https://doi.org/10.3389/fpls.2025.1604606>

Abstract: Introduction: Cotton, one of the most important economic crops worldwide, has long been bred mainly for improvements in yield and quality, with relatively little focus on salt–alkali resistance.

Methods: In this study, transcriptomic and metabolomic sequencing were performed on *Gossypium hirsutum* exposed to alkaline stress for different durations.

Results: The results of sample clustering, principal component analysis (PCA), and the number of differentially expressed genes (DEGs) revealed that 12 hours and 24 hours were the periods during which upland cotton presented the strongest response to salt stress, with flavonoid biosynthesis and alpha-linolenic acid metabolism playing significant roles during this time. A total of 6,610 DEGs were identified via comparison to the 0 h time point, including 579 transcription factors (TFs) that were significantly enriched in pathways such as flavonoid biosynthesis, the cell cycle, the cytochrome P450 pathway, phenylalanine metabolism, phototransduction, and alpha-linolenic acid metabolism. Through ultrahigh-performance liquid chromatography–MS (UPLC-MS), 4,225 metabolites were identified, and 1,684 differentially accumulated metabolites (DAMs) were identified by comparison to the levels at 0 h. A joint analysis of RNA-seq and metabolomic data revealed that the flavonoid biosynthesis and alpha-linolenic acid metabolism pathways play key roles in the response of *G. hirsutum* to alkaline stress, and the key genes in these pathways were identified. The weighted gene correlation network analysis (WGCNA) revealed 15 candidate genes associated with alkali tolerance in cotton, including 4 TFs and 4 genes related to flavonoid and anthocyanin biosynthesis.

Conclusion: In conclusion, our study provides a theoretical foundation for understanding the molecular mechanisms underlying alkali tolerance in cotton and offers new gene resources for future research.

12

Title: Wild and cultivated cotton species: comparative studies on plant biochemistry, soil biology, and soil nutrient status.

Author: Ritika Rajendra Waghmare, Kulandaivelu Velmourougane, Desouza Blaise, Manikandan Angamuthu , Lalita Rameshwar Harinkhede , Pranali Tarachand Bansod , Sanika Bhagawatrao Nasare , Jimmy Bhardwaj Vaidya , Vinita Prashant Gotmare and Yenumula Gerard Prasad

Imprint: *Crop & Pasture Science* 76, CP24265 <https://doi.org/10.1071/CP24265>

Abstract: Among the *Gossypium* species, wild cotton species (WCS) serve as a genetic reservoir of diverse unique traits that are useful for genetic improvement of cultivated

cotton species (CCS). Although cotton-breeding strategies largely use phenotypic and genotypic data for parent selection, plant biochemistry and soil biology have not been considered because of the absence of such data.

Aims: To study the differences in WCS and CCS on plant biochemistry, soil biology, and soil nutrient status.

Methods: A comparative analysis was conducted on 10 WCS (*Gossypium anomalum*, *G. aridum*, *G. australe*, *G. barbosanum*, *G. capitiviridis*, *G. davidsonii*, *G. raimondii*, *G. somalense*, *G. stocksii*, *G. thurberi*) and four CCS (*G. arboreum*, *G. herbaceum*, *G. hirsutum*, and *G. barbadense*).

Key results: CCS had a higher soil basal respiration rate and microbial biomass carbon, whereas WCS had higher glomalin, phosphatase, β -glucosidase, and soil dehydrogenase activities. WCS had higher shoot and root carbohydrates, whereas CCS recorded higher proteins in the shoots and roots. WCS exhibited significantly higher peroxidase, polyphenol oxidase, catalase, and L-phenylalanine ammonia lyase activities in the shoots and roots compared with CCS, whereas CCS had higher phenolic content. In terms of soil nutrients, WCS had higher organic carbon, macro, secondary, and micronutrients concentrations than CCS.

Conclusions: WCS exhibited higher plant defense enzyme activity and soil nutrient status than did CCS.

Implications: Our study has provided a greater understanding on the biochemical and soil biological differences between CCS and WCS, eventually supplementing the cotton database and support cotton breeders in selecting unique traits for crop improvement programmes.

CROP PROTECTION

13

Title: Whitefly-Resistant Population Development Source Selection Among Cotton Germplasms of Pakistan Through Multivariate Tools.

Author: Obad Ul Rahman, Syed Bilal Hussain & Muhammad Javed

Imprint: Plant Molecular Biology Reporter, Published: 28 May 2025

Abstract: Cotton has globally significant economic importance, and cotton contributes 0.8% to GDP and 60% of textile exports in Pakistan. Cotton leaf curl disease (CLCuD) is a whitefly (*Bemisia tabaci*) transmitted disease, which causes a reduction in yield and fiber quality, and cotton faces serious challenges due to biotic stresses like whitefly. Morphological characterization, SSR markers, principal component analysis (PCA), biplot analysis, correlation studies, and cluster analysis were used to estimate whitefly resistance, yield-related traits, and genetic diversity among the morphological characterization of 150 Pakistani genotypes. Field evaluation along with molecular analysis was employed as a comprehensive approach. Strong genetic control was demonstrated by high heritability estimates in most traits. Genotypes demonstrated significant variability including pest resistance and growth parameters. Multivariate analysis demonstrated clear grouping of genotypes based on performance characteristics, with many components explaining the majority of observed diversity. The results described the potential of morpho-molecular screening for selecting superior genotypes in breeding programs. CA-12 and AGC-155 are recommended as parental lines for developing whitefly-resistant, high-yielding cotton varieties while Gomal-105 and SLS-87/175 are recommended as whitefly-susceptible parental lines, supporting improved cotton productivity and sustainable pest management in Pakistan.

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Title: De novo long-read assembly and annotation for genomes of two cotton-associated *Fusarium oxysporum* isolates.

Author: Donald M. Gardiner, Elizabeth A. B. Aitken, Peter van Dam, Duy P. Le, Linda J. Smith & Andrew Chen

Imprint: Australasian Plant Pathology , Published: 04 June 2025, Volume 54, pages 377–386, (2025)

Abstract: *Fusarium* wilt of cotton is a major production constraint worldwide caused by *Fusarium oxysporum* f. sp. *vasinfectum*. Strain variations contribute to differences in disease expression across different geographic locations. Genomes for two Australian isolates of *F. oxysporum* isolated from cotton are presented. The strains differ in their symptomatology on cotton plants and group in distinct lineages, different to those cotton infecting strains found overseas.

15

Title: First report of canker and dieback caused by *Diaporthe ueckeri* in cotton (*Gossypium hirsutum* L.) in Florida.

Author: Fanny B. Iriarte, Hector Urbina, Claudia A. Paez, G. Kelly O'Brien, John McVay, and Ian Small

Imprint: Published Online:7 Jun 2025<https://doi.org/10.1094/PHP-02-25-0072-BR>

Abstract: In July 2024, several plants of cotton (cultivar: Deltapine 2127 B3XF) (Malvaceae, Rosids) were presenting symptoms of canker and dieback in experimental plots at UF/IFAS-NFREC in Quincy, Florida. Pycnidia found on canker lesions presented large number of alpha (α) conidia and small number of beta(β) conidia. Molecular identification was conducted by conventional PCR and sequencing of the internal transcribe spacer (ITS) (White T.J., et al., 1990) (1114 Kb, GenBank acc. numb. PQ422729), β -tubulin (Glass and Donaldson, 1995) (TUB2, 1569 Kb, GenBank acc. numb. PQ435399) and translation elongation factor (Carbone I., and Kohn L. 1999) (TEF1, 362 Kb, GenBank acc. numb. PQ435400) regions. Blast analysis of ITS, TEF1 and TUB2 sequences resulted in > 99% identity with GenBank acc. numbs. NR147543, KJ610881 and KJ590747, respectively), sequences obtained from the ex-type strain of ascomycetous fungus *Diaporthe ueckeri* (as 'euckerae') CBS 139283 (Diaporthaceae, Sordariomycetes) (Udayanga et al., 2015). Pathogenicity studies based on 20 pathogen inoculations sites and 10 plain agar inoculation sites, resulted in similar canker symptoms where the same pathogen was recovered. Molecular identification of the pathogen confirmed *D. ueckeri*. To our knowledge, this is the first report of canker/dieback caused by *D. ueckeri* in cotton in FL and in the United States.

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Title: Estimation of Different Carbon and Nitrogen Sources against *Fusarium oxysporum* f. sp. *vasinfectum* (FOV) Causing Wilt Disease of Cotton.

Author: Twinkle D. Manavadria, Prashant. B. Sandipan, R.K Patel, P.S Patel, Paras N Sangani, et al..

Imprint: Journal of Scientific Research and Reports, 2025, 31 (6), pp.403-411. [10.9734/jsrr/2025/v31i63138](https://doi.org/10.9734/jsrr/2025/v31i63138). [hal-05098526](https://hal.archives-ouvertes.fr/hal-05098526)

Abstract: Cotton (*Gossypium hirsutum* L.) is a major fiber crop that contributes significantly to global economic and social development. It is often referred to as "The White Gold" or "The King of Fibers". Cotton is a major cash crop in our country and belongs to the family Malvaceae. Cotton is a historically important commercial commodity, next to food grains, and serves as the primary raw material for the thriving textile industry. Cotton production, processing, textiles, and allied industries employ approximately 42 million people and sustain their livelihoods. In this present study, seven different carbon and nitrogen sources were tested for their suitability for the growth and sporulation of *F.oxysporum* f. sp. *vasinfectum* of cotton. *Fusarium* wilt caused by *F. oxysporum* f. sp. *vasinfectum* (FOV) is one of the most important and serious diseases. This disease is capable to cause tremendous loss to this crop in no time. Among the different carbon source, the maximum growth was observed in glucose (345.20mg), which was followed by galactose (306.15mg), mannitol (281.10mg), fructose (270.34mg), sucrose (268.16mg), starch (257.91mg) and lactose (172.10mg).While, the poor growth was observed in control (85.38mg). For sporulation category, it was found that the fungus showed abundant (++++) sporulation in glucose, galactose and mannitol. Among the different nitrogen source, the maximum growth was observed in potassium nitrate (310.13mg)which was followed by calcium nitrate (302.30mg), urea (298.37mg), sodium nitrate (288.58mg), ammonium nitrate

(272.57mg), ammonium chloride (183.45mg), ammonium oxalate (162.30mg). While, the poor growth was observed in control (59.11mg). For sporulation category, it was found that the fungus showed abundant (++++) sporulation in potassium nitrate and sodium nitrate.

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Title: A novel cotton miR7814 targeting *GhCNL2* regulates plant defense against *Verticillium dahliae* infection.

Author: Lin Xu, Ye Tang, Ge Zhao, Zhennan Zhang, Xiaoqiong Zhang, Wenwen Liu, Qingzhong Peng, Jiahe Wu

Imprint: Plant Science, Volume 359, October 2025, 112604

Abstract: Many miRNAs can post-transcriptionally regulate expression levels of a type of resistant (R) genes encoding NBS-LRR proteins. However, the underlying resistant mechanisms of various miRNAs-targeted R gene pairs remain explored. Here, we addressed a novel ghr-miR7814 targeting *GhCNL2* function in plant resistance against *Verticillium dahliae* infection. Based on GUS reporter and 5'-RLM RACE analyses, ghr-miR7814 was revealed to directly target *GhCNL2* mRNA for cleavage through post-transcriptional process. Through virus-induced gene silencing (VIGS) or overexpressing assays, we found that ghr-miR7814 knockdown significantly increased plant resistance to pathogen infection, whereas ghr-miR7814 overexpression and *GhCNL2* knockdown significantly reduced plant resistance, which was accompanied by expression changes of defense-related genes including *GhPR1*, *GhPR3*, *GhPR5* and *GhPDF1.2*. Results of DAB staining revealed that H₂O₂ contents in *GhCNL2* knockdown plants were significantly higher than those in the control. The expression levels of SA biosynthesis-related genes including *GhICS1*, *GhEDS1* and *GhPAD4* showed significant differences between *GhCNL2* knockdown and the control plants under *V. dahliae* infection as well as SA accumulation. Taken together, these results demonstrated that the novel ghr-miR7814 targeting *GhCNL2* is able to regulate plant resistance to *V. dahliae* infection possibly via induction of ROS and SA biosynthesis.

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Title: Development and Analysis of Infectious and Fluorescent Clones of Cotton leafroll dwarf virus-AL

Author: Wilson C. Clark, Rachel M. Livingston, Annu Kumari, Kaylee Hirsch, J. Koebernick, S.-H. Kang, A. Price, K.N. Conner, A. Jacobson, and K.M. Martin

Imprint: Running title: - *PhytoFrontiers*, 2025 CLRDV Infectious Clones from Alabama.

Abstract: Cotton leafroll dwarf virus (CLRDV) is a plant viral pathogen first reported in the United States (U.S.) in 2017 that causes yield loss in certain cotton (*Gossypium hirsutum* L) cultivars, but is asymptomatic in others. In Argentina, an infectious clone of the typical and atypical strains of CLRDV were developed to facilitate biological studies and aid in development of resistant cotton cultivars. Two infectious clones derived from the original Alabama isolate (Macon 1) were created using *Agrobacterium tumefaciens* for plant infection. The first one, CLRDV_{Macon1} (CLRDV-Ma1) was constructed by inserting the full length sequence of CLRDV into the pJL89 plasmid, followed by transformation of *Agrobacterium tumefaciens* strain LBA4404. This clone systemically infects cotton and *Nicotiana benthamiana* and was detectable in transfected plants by PCR amplification. A second clone, CLRDV-M-GFP, was constructed by replacing a fragment of the ORF3-5 region of CLRDV-Ma1 with EGFP. This clone expresses EGFP making visualization possible by fluorescence microscopy in infiltrated cotton cotyledons and is detectable using commercial antibodies. However, during the infection cycle, EGFP was found to be truncated resulting from unintended mutations. This study reports the first infectious clones of a U.S. isolate of CLRDV and contributes new knowledge about the biology of Poleroviruses.

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Title: Ghr-miR166b-GhHB14 Pair With GhDLO1 Partner Mediates Cotton Plant Defence Against *Verticillium dahliae* .

Author: Yuan Meng, Ge Zhao, Ye Tang, Lin Xu, Dongliang Li, Xiaoyang Ge, Jiahe Wu

Imprint: Molecular Plant Pathology, 2025; 26:e70104 1 of 13
<https://doi.org/10.1111/mpp.70104>

Abstract: In plants, the class III homeodomain-leucine zipper (HD-ZIP III) transcription factors regulate a broad range of developmental processes. However, less research on HD-ZIP IIIs has been done on *Verticillium* wilt, which is a devastating disease of cotton production worldwide. Here, we report that a cotton HD-ZIP III (GhHB14) targeted by ghr-miR166b participates in plant resistance to *Verticillium* wilt. According to degradome data, RACE sequencing and in vivo fluorescent light assay, ghr-miR166b can target GhHB14 mRNA to directly cleave it at nucleotide position 586, suggesting that GhHB14 expression is mediated by a posttranscriptional process. Yeast two-hybrid and bimolecular fluorescence complementation analyses showed that GhHB14 can interact with GhDLO1 in cells. Plants silenced for ghr-miR166b showed significantly higher susceptibility to *Verticillium dahliae* infection compared to the control, while GhHB14- and GhDLO1-silenced plants exhibited significantly higher resistance. These results suggested that ghr-miR166b is a positive regulator in plant resistance against *Verticillium* wilt, whereas GhHB14 and GhDLO1 are both negative regulators. Therefore, ghr-miR166b-GhHB14 coupled with GhDLO1 regulates cotton plant defence against *V. dahliae*.

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Title: Genetic inheritance and resistance patterns of cotton leaf curl disease in upland cotton (*Gossypium hirsutum* L.).

Author: Ghulam Sarwar, Zai b - U n - N i s a , M u h a m m a d Ihsan Ullah, Muhammad Jamil, Sadia Hakeem, Jodi A. Scheffler, Brian E. Scheffler, Jehanzeb Farooq

Imprint: Gene Reports, Volume 40, September 2025, 102273

Abstract: Cotton Leaf Curl Disease (CLCuD) has been causing substantial yield losses to the cotton crop in South Asia since its first epidemic in the early 1990s. Researchers face several problems while screening and breeding for CLCuD-resistant varieties due to absence of a reliable screening system, controversial inheritance data, limited genetic information about resistance sources, rapid evolution of viral strains, recombination between two virus groups, narrow plant genetic base, poor management practices, and reliance on small segregating populations. These factors have led to the failure of several cotton varieties that were initially released as resistant to Cotton Leaf Curl Virus (CLCuV). Hence, in the present study, a highly CLCuV-susceptible breeding line, Stoneville-47, tagged with a herbicide resistance marker gene (Round-Up-ready cotton), was crossed with newly discovered resistant accessions, Mac-07 and USG13_1087, to gain insights into the genetic inheritance patterns of resistance against CLCuD. Screening of breeding material against CLCuD resulted in thirty-resistant (S-0), and susceptible plants (S1-S4) upon grafting with susceptible scions. The qPCR further validated the results, as no viral or betasatellite DNA was detected in resistant plants, unlike the susceptible ones. The Chi-square test of F₁ and F₂ generations revealed the presence of a single dominant gene or closely linked QTLs with involvement of certain modifying factors or suppressors, controlling CLCuD resistance. These findings suggest that backcross breeding is a suitable method to introduce disease resistance. The circumvention of the suppressors of resistance from the selected progenies can be achieved by raising larger plant populations. However, there is still a need to fine-map the resistance loci, identify key haplotypes, and validate them across diverse genetic backgrounds. Moreover, pyramiding these clusters may be a straightforward approach to advancing the development of CLCuD-resistant cotton varieties.

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Title: Identification of Potential RNAi Targets for Cotton Mealybug (*Phenacoccus solenopsis* Tinsley) Management.

Author: Sanchita Singh, Somnath Rahangdale, Shivali Pandita, Manisha Singh, Gauri Saxena, Gourav Jain & Praveen C. Verma

Imprint: The Protein Journal, Volume 44, pages 464–481, (2025)

Abstract: *Phenacoccus solenopsis* Tinsley (Hemiptera: Pseudococcidae), commonly known as the cotton mealybug, is a highly invasive pest worldwide, particularly in tropical and subtropical regions. Despite posing a significant economic threat to various agricultural crops, a promising, environmentally friendly control strategy against this pest is lacking. Furthermore, the molecular aspects of this insect pest remain understudied. This pioneering study provides the first proteome data for four different developmental stages of the cotton mealybug. A comparative analysis of differential protein expression (DEPs) among six groups revealed the highest number of DEPs (550 up-regulated and 1118 down-regulated) when comparing the egg and first nymphal stages to the second nymphal instar (fold change ≥ 2 , $P < 0.05$). From the generated proteomics data, potential target genes were identified for cotton mealybug management. These genes were further evaluated for RNAi-based pest control and optimization of the dsRNA delivery system in cotton mealybug. Notably, RNAi-based pest management analysis revealed that dsRNA of the Ferritin-like precursor (Psfer) gene (TRINITY_DN17055_c1_g1_i1) induced significant mortality (~ 69%), followed by dsRNA of the probable cytochrome P450 6a14-like (Psp450 6a14) gene (TRINITY_DN47081_co_g1) and odorant-binding protein 2 precursor (Psobp) gene (TRINITY_DN11547_co_g1). This investigation proposes a potential alternative, eco-friendly strategy for managing cotton mealybug populations and related pests. Furthermore, this study provides valuable insights into the proteome of the cotton mealybug and Hemiptera, offering avenues for proteome-based identification of RNAi targets for pest management and crop improvement.

PLANT BREEDING AND GENETICS

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Title: Development of a “Golden fiber” cotton germplasm via carotenoid biofortification.

Author: Yujie Wang, Lu Long, Yanqi Zhang, Kaixuan Wang, Luying Shao, Yingchao Tang, Kun Li, Wei Gao, Jinggong Guo, Salim Al-Babili, Yuchen Miao, Kun-Peng Jia

Imprint: The Crop Journal, Available online 6 June 2025

Abstract: Natural colored cotton (NCC) offers a sustainable, dye-free, and eco-friendly alternative for producing colored textiles. Carotenoids, a group of important natural liposoluble pigments, are known for their diverse color spectrum. In this study, we successfully engineered the carotenoid biosynthesis pathway specifically in cotton fibers by utilizing a fiber-specific *GbEXPA2* promoter and a CaMV 35S promoter to drive the expression of two key carotenoid biosynthesis genes, *CrtB* and *CrtI*, respectively. This approach resulted in the development of a golden fiber cotton germplasm enriched with β -carotene. Notably, the pigmentation was predominantly observed during the early

developmental stages of the fiber (5–20 d post-anthesis). While the presence of carotenoids had no significant effect on plant architecture and growth, it positively influenced the fiber elongation rate, albeit with a slight reduction in fiber length and strength. This study represents a pioneering strategy for the future development of NCCs through carotenoid biofortification.

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Title: Heatmap clustering and performance analysis of cotton genotypes in response to environmental conditions.

Author: Fahmida Sultana, Washu Dev, Xiaowu Zhi, Hasan Sakibul, Yingchun Han, Lu Feng, Beifang Yang, Yaping Lei, Yahui Jiao, Yunzhen Ma & Yabing Li

Imprint: *Scientific Reports* volume 15, Article number: 19297 (2025)

Abstract: Cotton (*Gossypium hirsutum*) is a crucial cash crop in China, with yield performance influenced by genotype, environmental conditions, and management practices. The aim of this study was to assess the yield performance, biomass accumulation, and growth of nine cotton genotypes in Henan Province during three growing seasons (2017–2019) with different climates. Field experiments were conducted using a randomized complete block design (RCBD) at the Institute of Cotton Research, Chinese Academy of Agricultural Sciences (CAAS), Anyang, China. Plant height, true leaf number, and boll number per plant were among the morphological characteristics that showed the most variance across years and genotypes. Reproductive biomass, leaf area index (LAI), and biomass accumulation followed distinct seasonal trends, with LAI rising during boll formation and flowering. Yield parameters such as seed cotton yield, lint percentage, and boll weight vary by genotype and year, with the highest yields recorded in 2019. According to correlation study, temperature and precipitation had a negative impact on seed cotton production and final biomass, whereas climatic parameters had a favorable correlation with the harvest index. The genotypes were divided into distinct categories according to growth and yield characteristics using heatmap clustering. These findings provide insight into the best cotton genotypes for increased productivity and resilience in a variety of climates, allowing breeders and farmers to make more informed cultivar selections.

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Title: Inter and Intra Selection Efficiency of Cotton Families (*Gossypium hirsutum* L.) .

Author: Dawood Salman Madab

Imprint: International Journal of Environmental Sciences ISSN: 2229-7359 Vol. 11 No. 2s, 2025 <https://www.theaspd.com/ijes.php>

Abstract: Offspring families (F3 and F4) derived from superior crosses were grown at an agricultural farm in Baghdad Governorate\ Iraq (33.05N latitude, 44.32E longitude) for two successive years (2021-2022) by using a Randomized Completely Block Design with three replications to investigate responses for selection for seed cotton yield and its components traits. Results showed: Some lines outperformed their parents in yield and its components in both the third and fourth generations. The combinations 2-2, 3-1, and 3-4 demonstrated the best performance and stability in the yield of cotton bolls (135.06 and 145.72), (130.46 and 141.33), and (143.97 and 137.77) for the third and fourth generations, respectively. They also excelled in yield traits compared to other genetic combinations. The coefficients of inbreeding were negative for the number of fruit branches, the number of bolls per plant, and the yield of cotton bolls per plant (-9.33, -21.01, and -14.62, respectively). Genetic divergence indicated that the most distinct genetic combination was line 4-1, which formed a unique group, followed by line 9-2, which included other subgroups. However, group seven, comprising combinations 1-2 and 3-4, stood out with the best performance and highest yield of cotton bolls (139.46 grams per plant), followed by group six, which included combination 3-3 (143.97 grams per plant), and group four, which included combination 2-1 (135.06 grams per plant). These groups can be considered sources for improving the yield traits and their components of cotton bolls. Therefore, it can be concluded that the best performing and productive line was combination 3-4, which was distinguished by a unique group with combination 1-2, making it a promising candidate for selected cotton families.

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Title: Genome-wide association study reveals significant loci and candidate genes for fruit branch length in upland cotton.

Author: Hui Chang, Honghu Ji, Ruijie Liu, Juling Feng, Jiayi Wang, Shuqi Zhao, Wei Li, Zehua Qiu, Nabil Ibrahim Elsheery, Shuxun Yu, Libei Li, Zhen Feng

Imprint: Plant Genome. 2025;18:e70041. wileyonlinelibrary.com/journal/tpg2 1 of 13
<https://doi.org/10.1002/tpg2.70041>

Abstract: The length of fruit branches significantly influences plant architecture in upland cotton (*Gossypium hirsutum* L.), which is crucial for optimizing fiber yield and quality. In this study, a comprehensive genome-wide association study was conducted based on whole-genome resequencing data that identified 249 significant SNPs associated with fruit branch length (FBL), forming 79 distinct quantitative trait loci (QTL) regions. Notably, stable QTL regions qFBL-A10-4 and qFBL-DO3-17 were identified, harboring key candidate genes such as Ghir_A10Go14390 and Ghir_Do3Go11390. Superior haplotypes of these genes significantly enhance FBL, fiber yield, and quality, offering valuable targets for cotton breeding programs focused on optimizing plant architecture and productivity.

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Title: Pangenome analysis reveals yield and fiber-related diversity and interspecific gene flow in *Gossypium barbadense* L.

Author: Qingying Meng, Peihao Xie, Zhongping Xu, Jiwei Tang, Liuyang Hui, Jiaqi Gu

Imprint: *Nature Communications* volume 16, Article number: 4995 (2025)

Abstract: *Gossypium barbadense* is renowned for its superior fiber quality, particularly its extra-long fibers, although its fiber yield is lower compared to *G. hirsutum*. Here, to further reveal fiber-related genomic variants of *G. barbadense*, we de novo assemble 12 genomes of *G. barbadense* that span the wild-to-domesticated continuum, and construct a graph-based pangenome by integrating these assemblies and 17 publicly available tetraploid cotton genome assemblies. We uncover the divergent evolutionary trajectories and subsequent exchanges between *G. barbadense* and *G. hirsutum* through investigation of structural variants (SVs). We perform the SV-based GWAS analysis in *G. barbadense* and identify four, three, and seven candidate SVs for fiber length, fiber strength, and lint percentage, respectively. Furthermore, we detect the underlying candidate genes and uncover the origin and distribution of favorable alleles, and reveal the tradeoff between lint percentage and fiber quality. These pangenome and trait-associated SVs provide insights into and resources for improving cotton fiber.

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Title: Multifactorial ANOVA analysis of genotype and environment effects on morphological and agronomic traits in *G. barbadense* L. cotton.

Author: Shavkiev, J., Azimov, A., Khamdullayev, S., Ahmedjanov, A., Karimov, E., Mamarasulov, U., & Nurmetov, X.

Imprint: *Journal of Wildlife and Biodiversity*, 9(2), 388–408.
<https://doi.org/10.5281/zenodo.15521377>

Abstract: This study investigates the influence of genotype and environmental stress (optimal, drought, and salinity conditions) on morphological and agronomic traits in ten fine-fiber cotton genotypes using multifactorial ANOVA. Traits such as plant height, number of fruiting branches, number of opened bolls, total boll number, boll weight, vegetative period, and overall yield were analyzed. Results showed that genotype had no statistically significant effect on most traits ($P > 0.05$), whereas environmental factors significantly impacted all studied parameters ($P < 0.0001$ in most cases). Genotypes such as *T-2024*, *Duru-gavhar-4 (T-5560)*, *Angor (T-1981)*, and *T-2090* demonstrated relative stability and adaptability to stress conditions and may be considered valuable in breeding programs for stress-tolerant cotton cultivars.

Title: Genome-Wide Identification and Expression Analysis of EBP Genes in Cotton.

Author: Lingyu Hao, Dongyun Zuo, Qiaolian Wang, Limin Lv, Youping Zhang, Yi Yang, Xue Zhang, Shuo Zhang, Guoli Song & Hailiang Cheng

Imprint: Biochemical Genetics , Published: 05 June 2025

Abstract: Most cotton varieties of plants have pigment glands that produce and store terpenes. These terpenes play a vital role in the growth and development of cotton. According to the literature, the marker gene of a pigment gland cell cluster, *TMEM97* (*GH_A12G1754*), belongs to the *EBP* gene family. Promoter element analysis revealed that the promoter of this gene contains multiple G-box elements, so the *EBP* gene family was analyzed. Emopamil-Binding Proteins (EBP) are integral membrane proteins of the endoplasmic reticulum and catalyze the conversion of Delta(8)-sterols to their corresponding Delta(7)-isomers in cholesterol biosynthesis and Cholesterol metabolism. In this study, the EBP proteins of ten plant species, including 4 cotton species (*G. arboreum*, *G. raimondii*, *G. hirsutum*, and *G. barbadense*), were identified and their evolutionary relationships and characteristics were analyzed. All EBP proteins localized in the intracellular membrane, possess transmembrane domains, show low hydrophilic and high lipophilic characteristics, and activate under alkaline conditions. Further, 5, 5, 10, and 10 EBP genes were identified in *G. arboreum*, *G. raimondii*, *G. hirsutum*, and *G. barbadense*, respectively. The EBP gene was found to be expanded in *Gossypium* by tandem repeats. The evolution of the EBP gene family in *Gossypium* has mainly underwent purification selection. This suggests that the EBP gene family arose before the differentiation of the genus *Gossypium* and is conserved during the differentiation of the genus *Gossypium*. Expression pattern analysis of *G. hirsutum* EBP genes in different tissues revealed that they function in roots, stems, leaves, ovules and fiber development. Cotton pigment glands contain terpenes and other secondary metabolites. Transcriptome data and fluorescence quantitative PCR analysis revealed that EBP gene family members *GH_A12G1755*, *GH_D12G1751*, *GH_A12G1754*, and *GH_D12G1750* were differentially expressed in glanded and glandless cotton, and all of them were low-expressed in glandless lines. According to the literature, GhMYC2-like is a transcription factor known to regulate the formation of pigmented glands. Meanwhile, silencing the expression of *GhMYC2-like* resulted in a significant decrease in the expression of EBP gene family members *GH_A12G1755*, *GH_D12G1751*, *GH_A12G1754*, and *GH_D12G1750*. So it is hypothesized that the EBP gene family members may be downstream of GhMYC2-like and involved in the regulation of lipid metabolism in pigment glands. These results provide information for the future study of EBP family genes in cotton.

Title: GhTOPP4aD and GhRAF36 inversely regulate cotton (*Gossypium hirsutum*) response to ABA and salt stress through reversible phosphorylation of GhABI1.

Author: Pengfei Cao, Lin Zhou, Mingwei Du, Xiaoli Tian , Fangjun Li and Zhaohu Li

Imprint: Plant Biotechnology Journal (2025), pp. 1–20 doi: 10.1111/pbi.70166

Abstract: The post-translational phosphorylation modification of stress-related proteins regulated by kinases and phosphatases is one of the crucial regulatory mechanisms for plants in response to salt stress. However, the paired kinases and phosphatases of the same substrate that participate in response to salt tolerance in crops, especially in cotton, remain to be elucidated. Here, we identified GhTOPP4aD as a negative regulator of salt-stress response in cotton. GhTOPP4aD interacted with Raf-like kinase 36 (GhRAF36) and ABA Insensitive 1 (GhABI1) respectively, thereby inhibiting the phosphorylation activity of GhRAF36 and directly dephosphorylating GhABI1 to counteract GhRAF36 regulation. The phosphatase activity of GhABI1 was inhibited by GhRAF36-mediated phosphorylation at two unique residues Thr124 and Ser357 in cotton, whereas it was compromised by GhTOPP4aD. GhTOPP4aD thereby limited ABA signal transduction and orchestrated ABA-responsive gene expression. Together, modulation of the phosphorylation dynamics of GhABI1 by GhRAF36 kinase and GhTOPP4aD phosphatase constitutes an essential mechanism for ABA response and salt tolerance in cotton.

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Title: Callogenesis and Cell Suspensions in Cotton (*Gossypium hirsutum* L.) Cultivars Recalcitrant to Somatic Embryogenesis, Influence of Phytochemical Profile on the Acquisition of Ability to Induce Embryogenic Structures.

Author: Tanoh Hilaire Kouakou, Mongomaké Koné, Alain Decendit & Pierre Waffo-Teguo

Imprint: Natural Products, Living reference work entry, First Online: 01 May 2025, pp 1–27

Abstract: This study aimed to investigate the influence of phytochemical profile, particularly phenolic compounds, on cotton somatic embryogenesis induction. The research focused on identifying significant differences between recalcitrant and embryogenic cultivars. The analysis demonstrated that embryogenic cultivar Coker 312 exhibited a higher concentration of specific phenolic compounds than non-embryogenic cultivar R405–2000. The superior embryogenic capacity of cultivar Coker 312 is linked to catechin accumulation, which is essential for callus induction. Additionally, other compounds, including catechin, kaempferol, quercetin, *E*-resveratrol, and *p*-coumaric

acid, are indispensable for embryogenic structure induction in cell suspensions. These phenolic compounds may be utilized as markers for somatic embryogenesis induction of cotton. Conversely, elevated levels of gentisic, salicylic, caffeic, and ferulic acids, accompanied by diminished concentrations of gallic, *o*-coumaric, and *E*-cinnamic acids induced by cultivar R405–2000, impede the process of somatic embryogenesis. Additionally, it synthesizes genistein, rutin, *E*-2, and *Z*-2 methoxycinnamic acids, which have been demonstrated to have no promoting effect on somatic embryogenesis process. Moreover, incorporation of phenolic compounds identified as markers into the culture medium was unsuccessful in triggering embryogenic structure induction with cultivar R405–2000, indicating that the endogenous synthesis of these phytochemical compounds is the paramount factor. In a nutshell, the impact of the phenolic profile on the embryogenic capacity of cells demonstrates the genotype dependence of somatic embryogenesis in cotton. To overcome this recalcitrance, cells should be capable of synthesizing phenolic markers, potentially through the incorporation of phenolic biosynthesis precursors in the culture medium of callus and cell suspensions.

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Title: Molecular characterization of cotton genotypes using PCR based molecular markers.

Author: C. S. Shinde, L. S. Shitole, T. J. Bhor, D. P. Jadhav, R. D. Nimbalkar, R. S. Wagh

Imprint: Vegetos <https://doi.org/10.1007/s42535-025-01300-3>

Abstract: Total 25 cotton accessions and 25 SSR markers were selected to depict diversity and correlation between the genotypes for fiber quality traits. The existing study was conducted at Biotechnology Laboratory College of Agriculture, Pune and Central laboratory of ICAR-Directorate of Floricultural Research, Keshavnagar, Pune. Out of 25 SSR markers, 17 were amplified and all the markers were polymorphic. Total 71 loci amplified by 17 markers. Out of these, 59 were polymorphic and 12 were monomorphic. The polymorphic information content (PIC) value ranged from 0.18 to 0.82, maximum PIC recorded for JESPR-289 and minimum for CIR-089. The similarity matrix and dendrogram was constructed using Jaccard's similarity coefficient with NTSYS 2.02i software. The value of coefficient of similarity varied from 0.46 to 0.97. The dendrogram revealed that two major clusters were formed among 25 cotton genotypes. Cluster I contain twenty one genotypes while Cluster II contain four genotypes. The correlation was calculated. Total of 7 markers were found to be correlated with fiber quality. Out of that seven markers, BNL-3090 and BNL-3867 were found to positively correlated with all three fiber quality parameters. The remaining five BNL-1059, BNL-3147, BNL-3435, BNL-3510 and CIR-413 were positively correlated with length and strength. BNL-3090 and BNL-3867 are only markers found to be correlated with fineness. These molecular markers can be effectively used in future cotton improvement program as well as integrated with DUS descriptor data supporting with DNA fingerprinting analysis.

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Title: Deciphering the Role of Lipid Transfer Protein (LTP) in Transgenic Cotton Under PEG-Induced Drought Stress.

Author: Aiman Zahra, Sameera Hassan & Bushra Rashid

Imprint: Plant Molecular Biology Reporter , Published: 31 May 2025

Abstract: Drought stress is one of the major threats to cotton production, especially during the reproductive stage, when water deficit severely reduces yield and fibre quality. In this work, the contribution of the lipid transfer protein (LTP) gene in conferring drought resilience to transgenic cotton plants has been studied. In silico analysis revealed conserved regions of LTP and a role in membrane stability, with a binding energy of -5.4 kcal/mol to palmitic acid, stabilized through hydrogen and hydrophobic interactions-suggesting its role in stress resilience. Transgenic plants containing the LTP gene were produced through *Agrobacterium*-mediated transformation with 4.71% transformation efficiency. Transgenic plants performed better under polyethylene glycol (PEG) induced drought at 5%, 7.5%, and 10%. The height of transgenic plants was 78%, 60%, and 45%, while it was 52.4%, 40%, and 30% in control plants at 5%, 7.5%, and 10% PEG application, respectively. Root length of transgenic plants was 6.10 cm, 6.50 cm, and 5.20 cm, while it was 2.92 cm, 3.20 cm, and 2.90 cm in control plants at 5%, 7.5%, and 10% PEG application, respectively. Shoot length of transgenic plants was 4.68 cm, 4.45 cm, and 4 cm, while it was 2.83 cm, 2.10 cm, and 1.80 cm in control plants at 5%, 7.5%, and 10% PEG application, respectively. Similarly, the root-to-shoot ratio of transgenic and control plants was observed under the same applications of PEG stress as mentioned above. Real-time PCR analysis confirmed the 2–fourfold increase in LTP expression in transgenic plants as compared to controls. Hence, this work underlines the importance of LTP concerning the enhancement of drought adaptation in cotton.

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Title: RNA Interference-Mediated Suppression of GhSP (SELF-PRUNING) Modulates the Plant Architecture of Transgenic Cotton in a Dose-Dependent Manner.

Author: Yi Wang, Qinzhaio Liu, Wanting Yu, Junmin Chen, Qingwei Suo, Zhong Chen

Imprint: Biology 2025, 14(6), 601; <https://doi.org/10.3390/biology14060601>

Abstract: Cotton exhibits indeterminate growth potential at its apical meristem. In field cultivation, it is often necessary to restrict plant height by the foliar application of plant growth regulators or artificial topping. The genetic engineering of cotton architecture offers an efficient, environmentally friendly, and low-cost alternative to current field management. Our study aimed to improve the plant architecture of transgenic cotton by the suppression of GhSP, a key flowering repressor, via the RNA

interference method. Sixteen independent transgenic lines were generated and classified as mildly, moderately, and severely suppressed, according to GhSP expression levels. Field evaluation revealed the dose-dependent effects of GhSP silencing on plant height. The mildly suppressed line GhSPi-#5 exhibited a semi-dwarf phenotype of approximately 70~100 cm in height. Negative phenotypes, including excessive dwarf plant architecture and inferior fiber quality and yield traits, were observed in severely GhSP-suppressed transgenic lines. Notably, the mild silencing of GhSP in GhSPi-#5 did not negatively affect leaf and flower organ growth, pollen fertility, major agronomic traits, or fiber quality compared with the wild type. These observations demonstrate the feasibility of manipulating the architecture of transgenic cotton via GhSP silencing.

SEED SCIENCE AND TECHNOLOGY

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Title: Cotton Seed Quality and Storage Physiology in Relation to Harvest and Post-harvest Storage Techniques.

Author: Muhammad Nadeem , Abdul Ghaffar , Muhammad Amir Bakhtavar, Shahid Iqbal , Wazir Ahmed , Muhammad Iqbal and Muhammad Najeeb Rasool

Imprint: Intl J Agric Biol 33:330408. <https://doi.org/10.17957/IJAB/15.2298>

Abstract: Cotton seed mainly loses its viability and vigour during harvesting and storage. This study was designed to evaluate the effect of picking time and post-harvest

storage techniques on germination and vigour of cotton seed. In the first phase of experiment, initial seed quality (seed moisture content, germination and vigour) was determined at four different picking times i.e. 15 August, 15 September, 15 October and 15 November. In the second phase, seed from different picking (Factor A) was dried to 8% moisture contents and stored for six months by different storage techniques i.e., Ginned cotton seed and Un-Ginned seed cotton (Factor B) in different packaging materials i.e. hermetic and jute bags (Factor C). Maximum moisture (17.36%) was recorded from seed cotton picked on 15th September. September picking gave the best quality seed having maximum thousand seed weight (106.13 g) and germination percentage (67.25%). In storage experiment, highest seed vigour index- I (3256.9) and II (29.43), total soluble sugar contents (2.86 mmol g⁻¹ FW), catalase (2.78 U g⁻¹ FW) and peroxidase (1.72 U g⁻¹ FW) was measured from September picked cotton seed stored in hermetic bags after ginning. Highest malondialdehyde contents (3.01 nmol g⁻¹ FW) were measured in August picked un-ginned seed under conventional storage. Maximum seed germination (65%) and lowest seed deterioration was observed in September picked seed stored in hermetic bags after ginning. In conclusion, cotton seed picked during the month of September after drying (maximum 8%) should be ginned and stored in hermetic bags to retain maximum viability for seasonal storage under ambient conditions.

FIBER AND FIBER TECHNOLOGY

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Title: Genome-wide identification of novel alternative splicing events and related isoforms linked to cotton domestication and fiber domestication.

Author: Ying Bao, Xiaoyu Yin, Xiaolin Song, Lindi Liu, Yujie Liu, Shuai Meng

Imprint: Gene, Volume 963, 5 September 2025, 149601

Abstract: Alternative splicing (AS) plays a crucial role in plant co-/post-transcriptional regulation and proteome diversification, thereby affecting plant growth and development, and environmental adaptation. Despite the significant contribution of AS to plant regulation, the extent of AS diversity and complexity remains largely underestimated owing to their evolutionary intricacies. In this study, we used single-molecule real-time isoform sequencing to comprehensively analyze full-length

transcripts from the composite organs and tissues of the leaves, flowers, and fibers of *Gossypium hirsutum*, with a specific focus on novel AS events and their corresponding isoforms. Our investigation revealed 3,022 previously unidentified AS events, involving 2,800 complete AS isoforms which ranged from 269 to 8,300 bp in length, and comprised between one and 51 exons. Subsequent expression analysis using second-generation transcriptomic data revealed significant differences in the expression of 180 isoforms during fibers development. Thus, our study not only extends the list of known AS isoforms but additionally, it deepens our understanding of the intricate transcriptional regulatory diversity behind cotton domestication. The functional roles of these newly identified AS isoforms in cotton warrant further analysis.

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Title: Genetic dissection of lint percentage and seed cotton yield in exotic x elite upland cotton crosses using population-specific and joint population analysis.

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Abstract: Limited genetic diversity for fiber quality and yield traits in the improved gene pool for Upland cotton motivates the exploration of exotic materials. In the present study, we carried out QTL mapping for 2 fiber yield components in five BC₁F₂ and one F₃ resembling intermated population(s) involving 5 ‘converted’ exotic lines of Upland cotton and an elite cultivar “DES56,” as a common parent in all populations. The results indicated a higher frequency of dominant QTLs than additive QTLs. However, the prevalence of negative heterotic effects shows few opportunities to utilize these exotic lines for hybrid production. Most of the dominant QTLs were overdominant. In addition, all additive QTLs for lint percentage indicated the DES56 allele to be superior. These results suggest that selection practices need to be carried out in the later generations along with the implementation of precise marker-assisted selection to avoid the undesirable heterotic effects of these regions and reduce the linkage drag from undesirable alleles in the exotic segments. Moreover, the population-specific analysis and joint analysis showed the inflation of QTL parameters with a decrease in sample size, indicating the importance of larger sample sizes in mapping populations. Overall, the potential for using these exotic race stocks for hybrid production targeting yield components is limited.

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Title: Advancements in AI-driven Cotton Fiber Quality Assessment Through Image Processing: A Comprehensive Review.

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Abstract: The integration of artificial intelligence (AI) and image processing techniques has emerged as a transformative solution to address the limitations of traditional cotton fiber quality assessment methods, particularly the High-Volume Instrument (HVI) and Advanced Fiber Information System (AFIS), which require time-consuming manual labor. This comprehensive review examines the convergence of three key technological domains: image processing, AI/machine learning, and IoT/edge computing, in revolutionizing cotton fiber quality assessment. The review focuses on three primary image processing techniques—feature extraction, segmentation, and classification—that enable precise analysis of critical fiber properties including length, fineness, strength, and maturity. Advanced AI algorithms, particularly convolutional neural networks (CNNs), have demonstrated remarkable success in automating the assessment process, achieving accuracy rates of 82-98% in fiber classification tasks. The integration of Internet of Things (IoT) devices and edge computing has further enhanced the system's capabilities, enabled real-time quality assessments and reduced processing time by up to 60% compared to traditional methods. However, several significant challenges persist, including limited availability of high-quality annotated datasets, variability in image quality due to environmental factors, model generalization across different cotton varieties, and real-time processing constraints in industrial settings. The combination of image data with additional sensor inputs, such as spectral analysis and environmental monitoring, offers potential to further enhance assessment accuracy and robustness. This review emphasizes the transformative potential of AI-driven image processing systems in revolutionizing cotton fiber quality assessment, while also identifying critical areas requiring further research for successful industrial implementation. The findings suggest that continued advancements in AI algorithms, coupled with improved IoT integration and edge computing capabilities, will be crucial for developing more robust and efficient quality assessment systems in the cotton industry.

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Title: Development and Effectiveness Evaluation of InDel Molecular Markers Closely Linked to Fiber Strength QTL in *Gossypium barbadense*. S

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Abstract: The objective of this study is to develop InDel molecular markers for Island cotton, which is characterized by its superior fiber quality, particularly the fiber tensile strength—a key indicator of cotton fiber quality. The study aims to validate these markers using RIL (Recombinant Inbred Line) populations and resource materials, thereby providing a theoretical foundation for breeding new varieties of Island cotton with enhanced fiber quality. **【Method】** - Utilizing a previously established population of

213 Pima S-7 and 5917 F_{5:6} RILs, we conducted QTL (Quantitative Trait Locus) mapping to identify the locus regulating fiber strength in Island cotton, designated qFS-chr17-1. InDel markers were designed based on whole genome sequencing (WGS) data of the parental lines, followed by the identification of polymorphic markers. Preliminary validation of these markers was performed using 40 extreme family materials selected based on phenotypic data. Genotyping was carried out on both the 213 RIL population and the 213 Island cotton resource population, alongside multi-year fiber quality data to assess the markers' effectiveness. **Result-** The genotyping of the RIL and Island cotton resource populations with the two developed InDel markers indicated a close linkage to fiber strength phenotypic data, with significant differences observed in fiber strength traits among the differentiated materials. The analysis of genotypic combinations revealed an upward trend in fiber strength across four combination types, with materials exhibiting the Hap3 (B/A) and Hap4 (B/B) genotypes demonstrating significantly greater fiber strength than those with Hap1 (A/A) and Hap2 (A/B). Furthermore, the InDel-3L2 marker showed significant correlations with fiber length, fiber uniformity, and spinning consistency index, consistent with the observed phenotypic trends. Analysis of multi-year fiber quality data from two experimental sites revealed environmental variability in fiber quality, while temperature data indicated that the developed molecular markers are minimally influenced by environmental factors. Clustering analysis of fiber quality data from 213 Island cotton resource materials, combined with molecular marker genotyping, identified eight materials exhibiting superior fiber quality. **Conclusion-** This study successfully developed two InDel molecular markers closely linked to the fiber strength QTL (qFS-chr17-1), which maintain their effectiveness upon combination. The InDel-3L2 marker demonstrates significant correlations with fiber length, fiber uniformity, and spinning consistency index. These markers can efficiently and accurately identify high-strength fiber resources in Island cotton, contributing to the breeding of improved fiber quality. Additionally, eight materials with excellent fiber quality have been identified.

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Title: Harnessing the acid growth theory to optimize apoplastic acidification for enhancing cotton fiber elongation.

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Abstract: Cotton (*Gossypium* spp.), a major global fiber crop, serves as an ideal model for research on plant cell development. According to the acid growth theory, plasma membrane (PM) H⁺-ATPase (HA) regulates cell wall acidification, thereby promoting cell elongation and providing a mechanistic framework for understanding this process. However, its application to cotton fiber cells has remained limited. In this study, the acid growth theory was utilized to investigate the elongation of cotton fibers. Comparative genomics revealed an expansion in the number of gene family members associated with acid growth, including PM HA and transmembrane kinase (TMK) genes,

in tetraploid cotton. Transcriptomic analysis highlighted the co-expression of these genes during fiber elongation. Functional validation using chemical modulators and CRISPR-Cas9-mediated knockout mutants demonstrated that PM HA activity is essential for apoplastic acidification and fiber elongation. Specifically, GhHA4A and GhTMK3A were identified as potential regulators of proton extrusion; their loss-of-function mutants exhibited elevated apoplastic pH and reduced fiber length. Furthermore, the results indicated that an optimal apoplastic pH is required for fiber elongation, whereas insufficient or excessive acidification inhibits growth. Spatiotemporal modulation of PM HA activity in transgenic cotton plants enhanced fiber length without affecting other fiber- and seed-related traits, demonstrating the potential of the acid growth theory for fiber improvement. These findings not only extend the acid growth theory beyond conventional model systems but also provide an innovative strategy for increasing fiber length in cotton breeding.