



GLEANINGS IN COTTON RESEARCH

AUGUST 2026



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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.

*Chetali Rodge
In charge Library*

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1

Title: Potassium Fertilization Effects on Soil and Tissue Potassium Dynamics in Modern Cotton Cultivars

Authors: Smith, Mitchell

Imprint: Dissertation or Thesis

Abstract: Expansion of cotton production into non-traditional regions of Oklahoma has increased the need to better understand potassium (K) dynamics in the soil and plant system for modern cotton cultivars. Although soil tests often indicate adequate K availability, in-season deficiencies are frequently observed. Improved understanding of how fertilizer management influences soil and tissue K dynamics is critical for effective nutrient management. The objective of this study was to evaluate the effects of K fertilizer rate and application timing on soil K pools and tissue K dynamics and to characterize differences in K uptake and partitioning among modern cotton cultivars across Oklahoma environments. Field experiments were conducted during the 2024 and 2025 growing seasons at four locations representing irrigated and dryland production systems. Three cotton cultivars were evaluated with and without K fertilizer applied either preplant or as split applications. Soil K concentration and relative availability was assessed using water, Mehlich-3, and ammonium acetate extraction methods at two points during the growing season. Whole plant tissue samples were collected at three key growth stages to evaluate K concentration and redistribution among vegetative and reproductive tissues over the growing season. Potassium fertilization influenced soil K pools and tissue K concentration, with responses dependent on environment and fertilizer timing. Split K applications maintained greater amounts of readily available K later in the season under irrigated conditions. Tissue K concentration declined in vegetative tissues and increased in reproductive tissues as the season progressed, indicating substantial internal K remobilization. Cultivars differed in K uptake, storage, and allocation patterns, demonstrating distinct K use characteristics. Understanding cultivar-specific K dynamics and environmental influences on K availability is essential for developing more effective, site- and variety-specific K management strategies for modern cotton production systems.

Title: Quantifying nitrogen release behavior of enhanced efficiency fertilizers in rainfed cotton through field-based and combustion methods

Authors: Akash Shah¹ Kulpreet Singh¹ Anmoldeep Singh¹ Satinderpal Singh¹ Ejaz A. Dar¹ Nkem Nwosu¹ Ednaldo A. Borgato¹ Lakesh K. Sharma² Hardeep Singh

Imprint: Agric Environ Lett. 2026;11:e70089. <https://doi.org/10.1002/ael2.70089>

Abstract: The effectiveness of enhanced efficiency nitrogen fertilizers (EENFs) depends on how well the nitrogen (N) release synchronizes with crop demand. A 2-year (2024-2025) mesh-bag study was conducted to quantify N release from six N fertilizer sources under field conditions. The release trajectories were well described by three-parameter logistic model ($R^2 > 0.94$). By 63 days after fertilization, urea + polymer-coated urea (PCU 43-0-0) in 50:50 ratio released the greatest proportion of total N, reaching 91% in 2024 and 86% in 2025. In contrast, PCU (42-0-0) released 46% in 2024 and 57% in 2025, whereas PCU (41-0-0) released the lowest across both seasons (37% in 2024 and 34% in 2025). The N release from the field-based method was significantly correlated with the combustion method ($r = 0.958$, $p < 0.001$). The findings of this study provide field-based information for selecting EENF source with a release pattern that better aligns with cotton (*Gossypium hirsutum* L.) N demand.

Title: Energy Budgeting, Economic Feasibility and Productivity of Diversified Cotton–Wheat Cropping Systems in Dryland Areas

Authors: Alisher Rajabov, Farmon Mamatov, Obidjon Sindarov, Shavkat Salomov, D Dilshod Mamatov, Sitara Umarova, Bakhodir Zhumadurdiyev, Nilufar Nadiroxanova, Shukur Djumaev, Rokhila Hasanova, Shoxnazar Bobokulov, Odinakhon Khasanova, Anora Abduraximova, Zilola Khurramova, Abubakir Tog'ayev, Gulzira Narkizilova, Yo'ldoshbek Muhammadov, Botir Khaitov ¹

Imprint: <https://www.frontiersin.org/journals/sustainable-food-systems/articles/10.3389/fsufs.2026.1799715/abstract>

Abstract: Resource-efficient agricultural production is critical for improving energy efficiency, strengthening agroecosystem resilience and ensuring food security under current climate variability. To address this, the present study evaluated energy efficiency within the cotton (*Gossypium hirsutum* L.)–wheat (*Triticum aestivum* L.) cropping system in a two-cycle field

experiment. The inclusion of mungbean (*Vigna radiata* L.), potato (*Solanum tuberosum* L.), and maize (*Zea mays* L.) as follow-up crops was assessed using energy indices, productivity and soil quality characteristics. Among the tested systems, the highest energy output was recorded in the cotton-wheat-potato sequence (76.8×10^4 MJ ha⁻¹), followed by cotton-wheat-maize (47.19×10^4 MJ ha⁻¹) and cotton-wheat-mungbean (43.66×10^4 MJ ha⁻¹). Furthermore, energy productivity (0.63 kg MJ⁻¹) and the output-to-input ratio (12.15) were also greatest in the cotton-wheat-potato system. Conversely, the lowest energy consumption was recorded in the cotton-wheat-fallow rotation (32,451 MJ ha⁻¹), followed by cotton-wheat-mungbean (46,785 MJ ha⁻¹) and cotton-wheat-maize (56,724 MJ ha⁻¹). Despite high energy input in the cotton-wheat-potato rotation (63,264 MJ ha⁻¹), this system also generated substantial energy output (768,810 MJ ha⁻¹). Integrating mungbean into the cotton-wheat cropping system played a crucial role in enhancing soil fertility, promoting energy efficiency and contributing to food security. These findings provide critical insights into resource productivity within cotton-wheat systems and identify the most suitable cropping strategy for achieving energy efficiency alongside maximum profitability.

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Title: Nanoceria improves leaf hydraulic conductance and mesophyll conductance to CO₂ in drought-stressed cotton by modifying leaf anatomy

Authors: Yuanli Yang a 1, Nan Cao b 1, Zhao Yang a, Sijia Song a, Wenye Yang a, Jing Wang a, Ting Tao a, Wenqing Zhao a, Shanshan Wang a, Zhiguo Zhou a, Wei Hu

Imprint: Industrial Crops and Products, Volume 250, 2026,
<https://doi.org/10.1016/j.indcrop.2026.123993>.

Abstract: Drought negatively impacts photosynthesis and water transport in plants, so new technologies to enhance drought tolerance are urgently needed. Here, a hydroponic experiment revealed that foliar application of polyacrylic acid-coated nanoceria (PNC, 100 mg L⁻¹) to cotton leaves under drought stress (DS, 5% (w/v) polyethylene glycol 6000, 5 d) significantly improved the growth performance and biomass accumulation. Compared with the DS control, foliar application of PNC under DS conditions (DP) significantly improved leaf hydraulic conductance (K_{leaf}) and mesophyll conductance (g_m) by 73.4% and 34.9%, respectively, thereby leading to 42.2% higher net photosynthetic rate (A). Moreover, compared with the DS control, the DP treatment considerably increased the volume fraction of intercellular airspace and the surface area of mesophyll cells exposed to intercellular airspace by 24.5% and 56.3%, respectively, which contributed to the simultaneous improvements in g_m and outside-xylem hydraulic conductance (K_{ox}). Furthermore, relative to the DS control, the DP treatment considerably decreased hydrogen peroxide and superoxide anion levels by

45.2% and 65.4%, respectively, which largely explained the variations in above mentioned leaf anatomy. Additionally, compared with the DS control, enhancement in K_{ox} under the DP treatment was also ascribed to the increased leaf vein density. Therefore, these findings indicated that foliar application of nanoceria could improve both K_{leaf} and g_m by modifying leaf anatomy, thereby improving the A of drought-stressed cotton seedlings.

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Title: Epigenetic pathways for stress tolerance mechanisms and improved yield in cotton; an adaptation mechanism under extreme conditions

Authors: Youchang Zhang ^a, Changhui Feng ^a, Songbo Xia ^a, Qionshan Wang ^a, Lintao Niu ^b, Xiaogang Wang ^a, Jiaohai Zhang

Imprint: Plant Stress, Volume 23, 2026, 101488, ISSN 2667-064X,

<https://doi.org/10.1016/j.stress.2026.101488>

Abstract: Cotton (*Gossypium spp.*) is a globally important crop providing natural fibre and livelihoods, its productivity is increasingly threatened by climate change-induced stresses such as heat, drought, and soil salinity. Epigenetic regulation has emerged as a promising strategy to enhance stress resilience and yield stability in cotton. Recent advances reveal that epigenetic mechanisms, including DNA methylation, histone modifications, and small non-coding RNAs, modulate the expression of stress-responsive genes without changing the DNA sequence. DNA methylation-mediated gene silencing and chromatin remodelling are linked to key adaptive traits e.g., antioxidant defense, stomatal regulation, and hormonal signalling. Epigenetic memory across generations has been observed in cotton, suggesting heritable stress tolerance mechanisms. These processes directly contribute to fiber quality, boll retention, and biomass allocation under adverse conditions, supporting sustainable yield. Despite these advances, critical gaps remain in understanding the stability, specificity, and inheritance of epigenetic marks, and the integration of epigenomic tools into cotton breeding is still at an early stage. Future research should focus on identifying robust epigenetic biomarkers, generating high-resolution cotton epigenome maps, and developing precision epigenome editing strategies. Such efforts are essential for translating epigenetic insights into climate-resilient cotton cultivars and ensuring sustainable production in the face of escalating environmental challenges.

Title: Impact of climatic factors on cotton production: A forecasting study using time series, machine learning, and regression models

Authors: Mohsin Abbas, Huaping Sun, Moiz Qureshi, Muhammad Awais, Kassim Tawiah, Richard Kwame Ansah

Imprint: *Agronomy Journal*, 118, e70469. <https://doi.org/10.1002/agj2.70469>

Abstract: Cotton (*Gossypium hirsutum*) production is highly sensitive to climatic variability, including rainfall fluctuations, temperature extremes, drought, and flooding, which collectively introduce substantial uncertainty into agricultural output. This study investigates and forecasts cotton production using an integrated framework that combines classical time series models, machine learning techniques, and regression model-based approaches. Specifically, Box–Jenkins ARIMA (autoregressive integrated moving average), autoregressive moving average with exogenous variables (ARIMAX), exponential smoothing, Holt's exponential method, artificial neural networks, and multilayer perceptron (MLP) models are implemented and compared using standard metrics including root mean square error, mean absolute error, mean absolute percentage error, Akaike information criterion (AIC), and Bayesian information criterion (BIC). Empirical results indicate that while classical models outperform in all terms of information criteria (AIC/BIC), machine learning models, particularly MLP, achieve superior predictive accuracy based on error measures. To leverage the strengths of both approaches, an ensemble model combining ARIMA (1,2,2) and an MLP is developed, yielding improved forecasting performance compared with most individual models. Furthermore, the ARIMAX model incorporating exogenous variables (area, rainfall, and flood) highlights the dominant role of cultivated area in driving production, while rainfall exhibits a positive but less consistent effect, and flooding remains statistically insignificant. Complementary multiple regression and distributed lag analyses further confirmed the importance of area and rainfall, while capturing temporal lag effects of climatic influences. Forecast results reveal a divergence between modeling paradigms: classical time series models suggest a declining trend in cotton production, whereas machine learning models indicate potential recovery driven by nonlinear dynamics. The study provides actionable insights for policymakers and stakeholders to anticipate production trends under climate variability better and to design informed agricultural interventions.

Title: Assessment and Analysis of Cotton Development Growth in Pivot Irrigation Areas Using Satellite Imagery

Authors: Bakhtiyar Babashli Huseyn

Imprint: Agricultural Economics * Kənd Təsərrüfatının İqtisadiyyatı * Экономика сельского хозяйства - 2026, № 1 (49)

Abstract: The management of irrigation and the proper utilization of water resources are essential for enhancing agricultural output and maintaining the environment. Cotton fields irrigated with pivot systems are especially vulnerable to water stress and uneven distribution, both of which have a direct impact on yield. In this context, effective and dependable monitoring of water conditions and vegetation health is crucial for enhancing agricultural decision-making. The research shown that the integration of Sentinel-2 multispectral satellite data with water-sensitive spectral indices is exceptionally successful in monitoring water regimes, moisture dynamics and stress processes in pivot fields. The NDMI, NDWI and LSWI indices are essential for evaluating irrigation cycles and the soilplant water balance, whereas the GNDVI and SWIR-based indices facilitate the early detection of vegetation responses and water stress. Stress maps indicated that the majority of the pivot fields exhibit a good condition of vegetation, with low and non-systematic water stress, whereas the primary risk factor identified is controlled nutritional stress. This methodology establishes an effective scientific and practical foundation for the early identification of water stress and the optimization of moisture management

Title: Efficacy and selectivity of vegetation herbicides in cotton (*Gossypium hirsutum* L.).

Authors: Teodora Barakova

Imprint: Bulgarian Journal of Crop Science, (50–58), Agricultural Academy of Bulgaria

Abstract: During the period 2022-2024, a study was conducted in the experimental field of the Field Crops Institute - Chirpan with the cotton cultivar Helius (*Gossypium hirsutum* L.). The efficacy and selectivity of two vegetation herbicides and their herbicide combination were studied: Staple, containing 33.6% pyriithiobac-sodium at a dose of 100 ml/ha and Envoke, containing 75% trifloxysulfuron-sodium at a dose of 20 g/ha. The herbicides and the herbicide combination were applied once and twice during the 4-5 leaf and budding stages of the cotton. From the results obtained, it was found that the herbicide combination Staple - 100 ml/ha Envoke - 20 g/ha, applied once

and twice during the crop's growing season, respectively - 89.0% and 96.2%, had the highest efficacy. It controls very well the broadleaf weeds that form secondary weeding in the cotton, including self-sown sunflower (*Helianthus annuus* L.) plants. When applying the herbicides independently, once and twice during the 4-5 leaf and budding stages of the crop, the herbicide Staple is more efficacy than the herbicide Envoke. This is due to the fact that it more successfully controls the weeds with a waxy coating, such as *Chenopodium album* L., as well as the self-sown sunflower (*Helianthus annuus* L.) plants. The herbicides Staple at a dose of 100 ml/ha, Envoke at a dose of 20 g/ha and their herbicide combination have excellent selectivity towards the cotton, regardless of the stage of the crop development in which they are applied.

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Title: Priming-induced drought memory in rapeseed and cotton: A meta-analytic assessment

Authors: Amenehsadat Hashemi a, Elham Faghani b, Thomas Georg Roitsch

Imprint: Plant Physiology and Biochemistry, Volume 237, 2026, 111558, ISSN 0981-9428, <https://doi.org/10.1016/j.plaphy.2026.111558>

Abstract: Seed priming is increasingly used to enhance crop resilience to drought, yet whether it induces functional stress memory, and how this varies across crops, remains unclear. We conducted a global meta-analysis of 28 studies comprising 761 effect sizes to evaluate priming-induced drought memory in two major crops, rapeseed (*Brassica napus*) and cotton (*Gossypium hirsutum*). Effect sizes were calculated as standardized mean differences (Hedges' g) and synthesized using a random-effects model. Responses were evaluated across physiological, biochemical, and yield-related traits, while drought intensity and priming type were tested as key moderators to explain variation among studies. Priming significantly improved drought tolerance in both crops, but through divergent strategies: rapeseed responses were generally consistent with enhanced cellular protection via robust antioxidant activation (superoxide dismutase, catalase, ascorbate peroxidase) and reduced oxidative damage (malondialdehyde and hydrogen peroxide), particularly under moderate drought stress. In contrast, cotton may reflect a reproductive assurance strategy, sustaining leaf water status (RWC), accumulating proline, and significantly enhancing seed and boll yield, even when antioxidant responses were non-significant. Nutrient/mineral and microbial priming were most effective in cotton, whereas nutrient/mineral and hormonal/biochemical priming excelled in rapeseed. High heterogeneity in cotton ($I^2 = 90.99\%$) indicates that priming responses are strongly influenced by experimental context, including drought severity and priming treatment. Overall, our findings are compatible with a functional,

phenotypic interpretation of stress-memory-related responses rather than direct evidence of epigenetic memory, and highlight the potential value of crop-tailored priming strategies for improving drought resilience and supporting climate-smart agricultural production under increasingly water-limited conditions.

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Title: A silicon-based formulation enhances antioxidant defense and biochemical stability in heat-stressed cotton

Authors: Malika Mamasolieva^{1*}, Ilyos Huhudoynazarov², Gulchekhra Nabyieva¹, Dilafruz Makhkamova¹, Mamlakat Makhmudova³, Muxamad Axmedov⁴, Odiljon Sharipov⁵, Moxidil Yusupova⁶, Ulugbek Mirzayev⁷, Khusnida Abdukhakimova⁷, and Alimardon Abduraxmonov⁷

Imprint: Journal of Agricultural Science and Technology (JAST), 29(3)

Abstract: Global temperature rise increasingly exposes crops to heat stress, leading to oxidative damage and reduced productivity. The present study investigated the effects of seed priming with a silicon-based formulation on antioxidant defense mechanisms and biochemical responses in two cotton (*Gossypium hirsutum* L.) cultivars (Bukhara-8 and Bukhara-102) under short-term heat stress (45 °C for 6 h). Seeds were primed with the commercial silicon-based formulation Aminosid-Silicon (170 mg Si L⁻¹) and evaluated using a 2 × 2 × 3 factorial experimental design. Heat stress increased oxidative damage, whereas treatment with the silicon-based formulation enhanced antioxidant enzyme activities. The greatest response was observed for POD activity, which increased from 22.0 to 29.6 U mg⁻¹ protein in Bukhara-102, while H₂O₂ content decreased from 158.2 to 119.4 nmol g⁻¹ FW under heat stress. The silicon-based formulation also promoted proline accumulation, and Pearson correlation analysis revealed coordinated relationships among antioxidant enzymes, oxidative stress markers, and proline. Overall, the results indicate that seed priming with the silicon-based formulation enhanced biochemical protection against acute heat stress by strengthening antioxidant defense and reducing oxidative damage in cotton seedlings.

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Title: Automated machine learning for soil salinity prediction and explainable driver analysis in drip-irrigated cotton fields of arid regions

Authors: Fukui Gao, Haixue Cui, Yifei Wang, Yadan Wang, Baiyu Li, Daokuan Zhong, Djifa Fidele Kpala, Hao Liu

Abstract: Accurate monitoring of soil salinity is essential for optimizing water-salt regulation strategies and ensuring sustainable agricultural production in drip-irrigated cotton fields in arid regions. Although machine learning has become an effective tool for characterizing complex water-salt transport processes due to its strong nonlinear mapping capabilities, traditional modelling approaches face the dual challenges of low efficiency in manual trial-and-error and difficulties in interpreting "black-box" mechanisms, making it difficult to simultaneously achieve global architectural optimization and effective physical mechanism analysis. To overcome these limitations, this study developed and systematically evaluated the performance of four automated machine learning (AutoML) frameworks, including AutoGluon, H2O AutoML, FLAML, and TPOT, in predicting soil salinity based on in-situ field measurement data. SHAP (Shapley additive explanations) and PDP (Partial dependence plot) analyses were used to reveal the driving mechanisms of soil salt transport and their nonlinear response characteristics to environmental factors. The results indicated that AutoGluon achieved the optimal balance between computational efficiency and generalization accuracy through its multi-layer stacking ensemble strategy. In the 0–20 cm surface soil layer where water-salt transport was intense, the R^2 on the validation set reached 0.91–0.96, with the RMSE as low as 0.80–1.18 g·kg⁻¹, effectively correcting the systematic underestimation bias observed in the other AutoML frameworks within the dataset-defined high-salinity range exceeding 10 g·kg⁻¹. Variable importance and SHAP analysis further demonstrated significant vertical differences in salt-driving mechanisms. Compared with H2O AutoML, which relied excessively on biological indicators such as stem diameter, AutoGluon accurately captured physical driving processes, showing that salt transport in the 0–20 cm soil layer was primarily influenced by irrigation volume and growth stage, with a combined contribution exceeding 50%, while the 60–80 cm deep layer transitioned to being meteorologically dominated, with the contribution of cumulative *ETo* increasing to 29%. PDP analysis quantified the nonlinear physical response boundaries of key environmental factors, objectively identifying cumulative *ETo* in the 420–500 mm range as the critical threshold for inducing deep layer water upward movement and root zone salt accumulation, while also revealing a significant diminishing marginal benefit of leaching as irrigation approached 600 mm. This study confirms that AutoGluon achieves the unification of accurate soil salinity prediction and physical interpretation, and the quantified dynamic environmental response intervals provide a reliable data-driven basis for formulating precision irrigation schedules to suppress salinization and optimize water use in drip-irrigated cotton fields in arid regions.

Title: Influence of a new nanoensemble of graphene oxide and indole-3-acetic acid on the morphophysiological, biochemical, and ultrastructural characteristics of upland cotton (*Gossypium hirsutum* L.)

Authors: Nurlan Amrahov¹, Ulviyya Hasanova, Gunel Aliyeva, Goncha Aghazada, Fuad Rzayev, Eldar Gasimov, Solmaz Aliyeva, Lala Gahramanli, Elvin Ibrahimli, Ruhangiz Mammadova, Zarema Gakhramanova, Cem Bayram, Goncha Eyvazova, Sibel Hasanova, Ziyaddin Mammadov

Imprint: Turkish Journal of Botany 50 (4): 318-340. <https://doi.org/10.55730/1300-008X.2908>

Abstract: The exogenous application of phytohormones plays a crucial role in the activation of adaptive mechanisms in plants under both normal and stress conditions. Therefore, the present study investigates the synthesis, characterization, and application of nanoensembles based on indole-3-acetic acid (IAA) and graphene oxide (GO) nanolayers. The surface of GO synthesized by the modified Hummer method was noncovalently functionalized with IAA molecules. The structure and morphological properties of the prepared materials were analyzed by Fourier transform infrared spectroscopy, X-ray diffraction, UV-Vis spectroscopy, and transmission electron microscopy. The IAA and IAA+GO nanoensemble enhanced the morphological parameters, lateral root formation, catalase and peroxidase activities, and nitric oxide production of upland cotton (*Gossypium hirsutum* L.). It also promoted stem elongation more effectively than pure IAA. Additionally, it significantly boosted polyphenol oxidase activity in leaf tissues. However, IAA+GO reduced the primary root length compared to IAA alone at the same concentration. In summary, the IAA+GO nanoensemble offers a promising approach for enhancing plant growth and development. Its impact on stem elongation, lateral root development, and the activation of enzymatic defense systems points to its potential application in agricultural practices aimed at improving crop productivity and stress resilience. Light and ultrastructural microscopy demonstrated that both IAA and IAA+GO induced cellular gigantism across all examined vegetative organs of cotton plants. Overall, the IAA+GO nanoensemble exhibits a synergistic effect on plant stem elongation and antioxidant defense mechanisms, enhancing nitric oxide-mediated signaling without inducing osmotic stress.

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Title: Field Efficacy of Green Chemistry Molecule for Management of Pink Bollworm in Cotton

Authors: Vijay Kumar, Amandeep Kaur*, Jasjinder Kaur¹, Jasreet Kaur¹, Vikas Jindal, Satnam Singh², Suneet Pandher², Jagdish Arora

Imprint: Pesticide Research Journal Vol. 38 (1) 6367, June 2026
doi: 10.5958/2249524X.2026.00009.1

Abstract: *Pectinophora gossypiella* gained resistance against Bt cotton throughout India. Number of insecticides was screened against this pest. During 2024, study was conducted by Punjab Agricultural University at six locations to evaluate the efficacy of green chemistry and other commonly used insecticides against pink bollworm and the safety to natural enemies. Among the treatments, spinetoram 11.7 SC @ 50 g ai ha⁻¹ was found highly effective followed by emamectin benzoate 5 SG @ 9.5 g ai ha⁻¹, cypermethrin 25 EC @ 50 g ai ha⁻¹, profenophos 50 EC @ 625 g ai ha⁻¹, chlorantraniliprole 18.5 SC @ 30 g ai ha⁻¹ and chlorpyrifos 20 EC @ 250 g ai ha⁻¹ against pink bollworm. Chlorantraniliprole 18.5 SC and spinetoram 11.7 SC recorded higher number of natural enemies as compared to other insecticides. The seed cotton yield was significantly higher in the spinetoram 11.7 SC (20.82 q ha⁻¹) being at par with profenophos 50 EC (20.51 q ha⁻¹) and emamectin benzoate 5 G (20.71 q ha⁻¹).

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Title: Utilizing YOLOv7 Algorithm for Gossypium sp. Detection: An Implementation Study

Authors: Bianda Shafira Kartika Anggraini, Dina Tri Utari & R. B. Fajriya Hakim

Imprint: Advances in Computer Science Applications and Research, vol 13. Springer, Cham. https://doi.org/10.1007/978-3-032-32458-0_10

Abstract: *Gossypium sp.*, commonly known as cotton, is versatile plant used for its fiber and seeds and holds medicinal properties. However, cotton cultivation is susceptible to various plant diseases, primarily affecting the leaves, reducing the production and quality of cottonseed and fiber. Early detection and identification of these diseases are crucial for effective pest control and increased production. Farmers rely on their experience to identify conditions that may not always be optimal. In this research, we propose utilizing the YOLO version 7 algorithm for real-time detection and classification of healthy and infected cotton leaves. The study focuses on two classes: healthy and infected. The model is configured with specific hyperparameters, including a batch size of 16, a network size of 416×416 pixels, 100 epochs, and a dataset split into 80% training data and 20% validation data. The implemented model achieves a mAP@IoU0.5 result of 97.5% and an F1-score of 94% at a confidence level of 54.8%. These results demonstrate the effectiveness of the YOLOv7 algorithm in accurately detecting and classifying healthy and infected cotton leaves in real time. By leveraging this technology, farmers can enhance disease identification and control measures, leading to improved production and quality of cottonseed and fiber.

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Title: Potential of Cerrado endophytic fungi in mitigating biotic stress induced by *Fusarium oxysporum* in cotton plants

Authors: Luciana Cristina Vitorino, Damiana Souza Santos Augusto, Alex Santos Macedo, Nayelly Luzia Silva Santos, Cintia Faria da Silva, Thais Cristina Sousa Oliveira & Layara Alexandre Bessa

Imprint: *Eur J Plant Pathol* (2026). <https://doi.org/10.1007/s10658-026-03284-5>

Abstract: Vascular wilt induced by *Fusarium oxysporum* hinders water and nutrient circulation in plants, severely affecting the yield of globally important crops such as cotton. In this context, the use of endophytic microorganisms emerges as a promising perspective for the biocontrol of *Fusarium* wilt. We hypothesized that endophytic fungal strains isolated from the roots of *Butia purpurascens*, an endemic palm of the Brazilian Cerrado, could control the symptoms caused by *F. oxysporum* f. sp. *vasinfectum* in *Gossypium hirsutum* L. plants. To test this, we induced biotic stress in cotton plants using *F. oxysporum* and evaluated the effect of inoculating seven fungal strains in mitigating the damage caused by this phytopathogen. Biotic stress was assessed through changes in growth, gas exchange (resulting in increased leaf temperature), chlorophyll *a* fluorescence, antioxidant enzyme synthesis, proline, malondialdehyde (MDA) levels, and the incidence of necrosis, leaf wilting, and floral abortion. Overall, the inoculation of cotton plants with endophytic fungi significantly mitigated the effects of the pathogen, promoting vegetative growth, maintenance of

photosynthetic pigments, improved physiological performance, regulation of antioxidant activity, favorable leaf anatomical changes, and reduction of symptoms such as necrosis, wilting, and floral abortion. Specifically, strains BP10EF and BP52EF (*Gibberella moniliformis*), and BP16EF (*Penicillium purporogenum*) stood out as multifunctional agents in mitigating *F. oxysporum* wilt in cotton, resulting in responses similar to those observed in healthy plants. These results highlight the potential of these endophytic strains to be explored not only as plant growth-promoting agents but also as resistance inducers in cotton against the stress caused by *F. oxysporum*.

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Title: Synthesis of a kinetin and graphene oxide nanoensemble and its effects on defense responses of cotton against *Verticillium dahliae*

Authors: N. R. Amrahov*, U. A. Hasanova*, M. Levy**, G. S. Aliyeva*, G. A. Aghazada*, R. B. Mammadova***, S. A. Alizade***, F. H. Rzayev****, E. K. Gasimov****, S. S. Hasanova*, N. A. Malikova*, Z. M. Mammadov*

Imprint: Regulatory Mechanisms in Biosystems, 2026, 17(4), e26077

Abstract: In this study, a kinetin-graphene oxide nanoensemble (KN+GO) was synthesized via non-covalent interactions. Its structure and morphology were characterized by transmission electron microscopy (TEM), Fourier transform infrared (FTIR) spectroscopy, and powder X-ray diffraction (XRD), confirming the successful immobilization of kinetin on graphene oxide. The loading efficiency of kinetin on GO was determined by UV-Vis spectroscopy. The effects of the KN+GO nanoensemble on the physiological and biochemical responses of two cotton genotypes (*Gossypium hirsutum* L. TM-1 and *G. barbadense* L. Pima 3-79) were investigated during infection with *Verticillium dahliae*. Morphometric traits, seedling survival, antioxidant enzyme activities (catalase, peroxidase, and polyphenol oxidase), nitric oxide and proline levels, and photosynthetic pigment composition were analyzed. Pathogen infection induced oxidative stress and significantly altered the growth and biochemical parameters in both genotypes. Free kinetin exhibited genotype-dependent effects, whereas the KN+GO nanoensemble consistently enhanced stress tolerance, particularly under pathogen pressure. In the TM-1 plants, KN+GO markedly improved seedling survival, increased antioxidant enzyme activity, promoted proline accumulation, and stabilized photosynthetic pigment levels. In the Pima 3-79 plants, the nanoensemble mainly supported survival and redox balance, although the responses were less pronounced. These findings demonstrate that graphene oxide-based kinetin nanoensembles modulate cotton defense responses in a genotype- and stress-dependent manner, highlighting their potential as nano-enabled phyto-hormone delivery systems for improving resistance to fungal pathogens.

Title: *GhGH3.1*-Mediated auxin homeostasis coordinates cell wall defense and jasmonate signaling for verticillium wilt resistance in cotton

Authors:

Ying Liu a b 1, Zhaoyuan Ba a b 1, Juyun Zheng c 1, Jingxuan Guo a b, Xueyuan Ma d, Zhaoqi Wang a b, Zhenyu Wang a b, Xiaoyu Pei a b, Xiang Ren a b, Yu Liang a b, Meng Kang a b, Xingxing Wang a b, Xueyuan Li c, Xiongfeng Ma

Imprint: Industrial Crops and Products, Volume 250, 2026, 123970, ISSN 0926-6690, <https://doi.org/10.1016/j.indcrop.2026.123970>

Abstract: Auxin homeostasis is hypothesized to play an important role in the growth-defense trade-off in plants; however, the potential mechanisms by which auxin metabolism correlates with cell wall dynamics and immune signaling during vascular pathogen infection in cotton warrant further investigation. In this study, we characterized GhGH3.1, an IAA-conjugating candidate belonging to the GH3 class II lineage, and explored its potential involvement in defense responses against *Verticillium dahliae* (*V. dahliae*) infection in *Gossypium hirsutum*. GhGH3.1 appears evolutionarily conserved across *Gossypium* species, exhibited a root-predominant expression pattern, and was induced upon *V. dahliae* challenge. Functional investigations via transient virus-induced gene silencing (VIGS) indicated that the knockdown of GhGH3.1 in cotton was associated with an altered host susceptibility; complementarily, its heterologous expression within *Arabidopsis thaliana* was associated with relative tolerance. Pairwise interaction assays tentatively showed that the GhGH3.1 protein physically associates with the epidermis development-related protein GhPDF1. Comparative transcriptomic and physiological profiling further indicated that GhGH3.1 deficiency was accompanied by transcriptional co-alterations in jasmonic acid (JA) signaling marker genes, secondary cell wall structural components, and reactive oxygen species (ROS) accumulation. Collectively, these findings tentatively present a preliminary working model where GhGH3.1, potentially through its interaction with GhPDF1, may contribute to *V. dahliae* defense, likely by modulating auxin-amido conjugation and aligning downstream JA signaling, cell wall reinforcement, and redox balance during the immune response.

Title: Long-term monitoring of insecticide resistance in pink bollworm in Israeli pima cotton fields

Authors: A. Rami Horowitz, Michal Axelrod, Carolina Guzman, Shlomo Sarig, Ariela Niv, Shai Morin

Imprint: Journal of Pest Science (2026) 99:105
<https://doi.org/10.1007/s10340-026-02061-x>

Abstract: Long-term insecticide resistance monitoring is essential for sustainable management of the pink bollworm (PBW), *Pectinophora gossypiella* (Lepidoptera: Gelechiidae), in cotton. We present 13–15 years of field data from Israel, where Pima (*Gossypium barbadense*, Malvales: Malvaceae) -Bt (*Bacillus thuringiensis*) cotton is not available; therefore, chemical control remains the primary management tool. Resistance was assessed in adults collected from cotton fields and compared with a susceptible laboratory strain. Reference-line probit analyses identified chlorpyrifos, bifenthrin, and methomyl as the most potent compounds, with cypermethrin the least effective. Resistance ratios in field populations were ~ 15-fold for cypermethrin, ~ 20-fold for chlorpyrifos, and ~ 45-fold for bifenthrin; no resistance to methomyl was detected. Despite moderate resistance levels, field control was sometimes ineffective, likely due to localized high-resistance populations or suboptimal application methods. Temporal trends showed increasing survival at diagnostic doses for both pyrethroid compounds. Reliance on broad-spectrum insecticides has declined following the phase-out of key organophosphates, accompanied by a growing emphasis on integrated pest management (IPM); approaches such as area-wide control, mating disruption, drone-applied SPLAT-PBW (a compound containing PBW female pheromone) sprays, and post-harvest residue destruction are increasingly implemented. These results underscore the importance of continued surveillance, the integration of non-chemical tactics, and the evaluation of new insecticides with minimal environmental and human health risks to sustain PBW control in Israeli cotton systems. It should be Rami A. Horowitz

Title: *Alternaria* leafspot of cotton in northern Argentina: disease progress, cultivar resistance and fungicide effects under subtropical field conditions

Authors: Lorenzini, Fernando Gabriel^{1,2}, Scarpin, Gonzalo Joel¹, Cereijo, Antonela Estefanía¹, Dileo, Pablo Nahuel¹, Longhi, Tulio Sergio¹, Muchut, Robertino José¹,

Roeschlin, Roxana Andrea^{1,2}, Sartor, Gonzalo Javier¹, Winkler, Horacio Martín¹, Zanel, Walter Javier¹, Tarragó, José Ramón^{3,4}, Paytas, Marcelo Javier

Imprint: J Genet Appl Biotechnol, 2026: e2026044 DOI: <https://doi.org/10.66432/3vvdkh17>

Abstract: Alternaria leaf spot of cotton is a widespread foliar disease worldwide; however, information regarding disease progress and cultivar response under field conditions in northern Argentina is limited. This study aimed to evaluate disease progress, commercial cultivar performance, and the effects of fungicide application on plant growth, yield, and fiber quality. Field experiments were conducted during two growing seasons (2021–22 and 2022–23) in Reconquista, Santa Fe, Argentina, using three commercial upland cotton cultivars grown under fungicide-treated and untreated conditions, under high plant density and narrow row system. A commercial mixture of pyraclostrobin and epoxiconazole was applied at 50, 70, and 100 days after sowing. Disease incidence and severity were assessed over time, and plant growth, yield, and fiber quality traits were evaluated. Disease showed clear temporal progression in both growing seasons, reaching 100% incidence at 110 days after sowing, however, mean severity values remained moderate (<10%). The fungicide neither reduced incidence or severity nor improved yield or fiber quality. However, fungicide-treated plots showed significantly higher aboveground biomass, nearly 20% over control, suggesting a physiological effect unrelated to disease suppression, which warrant further research. Despite low disease pressure, cultivars differed in their response to infection, with NuOpal showing the highest susceptibility and Guazuncho 4 the lowest disease accumulation. Alternaria leaf spot of cotton progresses in northern Argentina even under unfavorable environmental conditions for fungal epidemics. Significant and consistent differences among cultivars were detected across seasons. Under low disease pressure observed in both seasons evaluated, fungicide applications did not significantly affect disease severity, yield or fiber quality.

Title: Genetic Diversity, Population Structure, and Salinity Tolerance of Upland Cotton (*Gossypium hirsutum* L.) Germplasm Revealed by SSR Markers

Authors: Abdulahat Azimov, Jaloliddin Shavkiev

Imprint: <https://doi.org/10.21203/rs.3.rs-10358861/v1>

Abstract: Soil salinity is a major abiotic constraint limiting cotton (*Gossypium hirsutum* L.) productivity and fiber quality, particularly in arid and semi-arid regions. The identification of genetically diverse germplasm with superior salinity adaptation is essential for developing resilient cotton cultivars through marker-assisted breeding. In this study, the genetic diversity, population structure, and salinity adaptation potential of 17 upland cotton genotypes were investigated using 20 genome-wide simple sequence repeat (SSR) markers. A total of 53 alleles were detected, with an average of 2.65 alleles per locus. The SSR markers revealed substantial genetic polymorphism, with polymorphism information content (PIC) values ranging from 0.00 to 0.76 (mean = 0.38). Among them, NAU2277, MUCS223, BNL3545, JESPR65, and NAU6315 were the most informative markers for differentiating the studied germplasm. Cluster analysis, neighbour joining analysis, and principal component analysis consistently classified the genotypes into three major groups, indicating considerable genetic diversity. The first two principal components accounted for 34.7% of the total genetic variation. Analysis of molecular variance (AMOVA) showed that 58% of the genetic variation occurred within populations and 42% among populations. High genetic differentiation ($\Phi_{ST} = 0.42$) and low gene flow ($N_m = 0.35$) indicated restricted genetic exchange among the identified groups. The genotypes T-2000, T-1003, T-1005, and T-1080 were identified as promising parental lines for salinity-tolerance breeding, whereas T-1002, Mehnat, Yulduz-2, and T-1004 represented genetically divergent accessions with high breeding value. These findings demonstrate that Uzbek upland cotton germplasm constitutes a valuable genetic resource for developing salt-tolerant cultivars with improved fiber quality through marker-assisted breeding.

Title: Future Climate Risks to Cotton Production in Brazil: Evidence from Ec-Earth3 Projections and From the Sensitivity of Genetic Parameters

Authors: Edson Magrine de Souza Cavalcante¹, Nicolas Rian Stenico², Iêdo Peroba de Oliveira Teodoro³, Maria Deyse Silva dos Santos⁴, Maria Damiana Rodrigues Araújo⁵, Sérgio Nascimento Duarte⁶

Imprint: <https://doi.org/10.56238/revgeov17n7-164>

Abstract: This study used the DSSAT/CROPGRO-Cotton model and climate projections from EC-Earth3 (SSP2-4.5 and SSP5-8.5 scenarios) up to 2059 to assess the response of cotton yield components to climate change and the sensitivity of the crop genetic parameters in three municipalities representative of Brazilian producing regions: Sapezal (MT), Coromandel (MG) and Luiz Eduardo Magalhães (BA). In order to isolate the climate effect, soil, cultivar and management were kept constant across municipalities; simulations were run under rainfed conditions and without nitrogen limitation. Projections indicate progressive warming and increased interannual variability of maximum temperature and rainfall under SSP5-8.5, with median maximum temperatures approaching 40 °C in Luiz Eduardo Magalhães (BA). The yield response was regionally heterogeneous: Coromandel (MG) showed an increase in productivity up to the 2050s under SSP5-8.5, whereas Luiz Eduardo Magalhães (BA) exhibited a decline after the initial decade and Sapezal (MT) remained relatively stable. The Morris sensitivity analysis identified the maximum leaf photosynthesis rate (LFMAX) as the dominant parameter for total above-ground biomass (CWAD). For lint yield (LIWAM), threshing percentage (THRSH) became the main limiting factor, indicating that the bottleneck under future stress lies in reproductive allocation rather than in maximum carbon assimilation. The duration of the seed-filling phase to physiological maturity (SD-PM) showed increased sensitivity in Coromandel, associated with heat-induced cycle shortening. The σ/μ^* ratio revealed a predominantly linear behaviour for LFMAX and THRSH and a non-linear or interaction-dominated response for SFDUR and PODUR. The results, which are comparative in nature across scenarios, support breeding strategies focused on THRSH and on reproductive thermal tolerance for the resilience of Brazilian cotton production

Title: Transgenic cotton containing synthetic ω -ACTX-HV 1a gene confers broadspectrum protection against major bollworms and leaf army worms

Authors: Muhamamd Arshad, Shaheen Asad, Yusuf zafar , Zahid Mukhtar

Imprint: <https://doi.org/10.21203/rs.3.rs-10132352/v1>

Abstract: Incorporation and stable expression of different Bt and non-Bt genes in cotton have demonstrated an effective control of different insect pests of cotton crop. In present study, a synthetic insecticidal transgene encoding ω -ACTX-HV1a toxin (Hvt) of an Australian funnel web spider (*Hadronyche versuta*), when transformed into cotton (Coker-312) through *Agrobacterium* method, showed insecticidal activity against three major cotton pests i.e. spotted bollworm (*Earias vittella*), American bollworm (*Helicoverpa armigera*) and leaf army worm (*Spodoptera littoralis*). Fertile transgenic cotton (T0 generation) plants were developed from six selected independent transgenic events through tissue culture process and established successfully in the soil. Putatively transgenic T0 cotton plants were analyzed by PCR and Southern hybridization confirming transgene presence and integration in 1-3 copies. Northern blots revealed a high Hvt expression among transgenic lines. Under in-vitro conditions, entomocidal assays showed high level of 1-2nd instar in both major *H. armigera* and *S. littoralis* reaching 80-100 % mortality after 72-96 hrs of their release on detached leaves. Similarly, transgenic hvt cotton plants showed exclusive protection against infestation of spotted bollworm under in-vivo conditions in containment. Insecticidal activity was observed in T0 regenerated cotton plants but also inherited in subsequent generations. Development of Hvt cotton may have significant commercial contribution for sustainable insect pest management and it can be used in combination with other (Bt/non-Bt) genes to circumvent resistance development in cotton insect pests. To our knowledge, this is first transgenic cotton 1 expressing nerve toxin that possess significant mortality against spotted bollworm (*Earias insulana*) and it will be give innovational supplement to already insect resistant bt cotton.

Title: A cis-regulatory variant in GhWRKY21-D08 contributes to pleiotropic salt tolerance revealed by multi-trait GWAS in upland cotton

Authors: Jiahao Duan^{1,2}, Shuting Mu², Ming Chen², Shuqi Zhao^{2,3}, Yijin You², Yu Hu², Ming Tan², Zehua Qiu², Feifei Li², Xuke Lu⁴, Shuxun Yu^{1,2}, Zhen Feng^{2#}, Libei Li

Imprint: Journal of Integrative Agriculture

Abstract: Salt tolerance during germination is a complex trait involving coordinated regulation of multiple developmental processes, yet its shared genetic architecture remains largely unknown. Here, we integrated genome-wide association study (GWAS) and multi-trait GWAS (MTAG) to dissect the pleiotropic basis of salt tolerance in 355 upland cotton accessions by using 2.52 million high-quality SNPs. A total of 517 and 534 significantly associated SNPs were identified by GWAS and MTAG, respectively, revealing 79 salt-tolerance-related QTLs. A major locus, qRST-D08-8, was refined to a 73.8 kb interval containing 12 candidate genes, among which GhWRKY21-D08 (Ghir_D08G020650) was supported by expression profiling and functional assays. Virus-induced gene silencing (VIGS) indicated that GhWRKY21-D08 enhances salt tolerance in cotton by increasing antioxidant enzyme activities to scavenge reactive oxygen species (ROS). Notably, a cis-regulatory SNP (-718 C/A) in the promoter region significantly altered transcriptional activity, linking regulatory variation to phenotypic divergence. Population genetic analyses suggest that the favorable haplotype (Hap1) has undergone recent positive selection during breeding without compromising yield-related traits. These findings highlight the role of cis-regulatory variation in shaping adaptive traits and provide a valuable target for molecular breeding of salt-tolerant cotton.

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Title: Regulatory networks underpinning climate resilience in cotton: From molecular mechanisms to precision breeding

Authors: Rasmieh Hamid ^a, Zahra Ghorbanzadeh ^b, Bahman Panahi

Imprint: Plant Stress, Volume 23, 2026, 101501, ISSN 2667-064X,
<https://doi.org/10.1016/j.stress.2026.101501>.

Abstract: Background: Cotton (*Gossypium hirsutum* L.), the world's leading natural fibre crop, is increasingly challenged by climate change, with drought, salinity, waterlogging, temperature extremes, nutrient limitations, and their frequent co-occurrence substantially reducing yield, fibre quality, and production stability. Although extensive studies have identified numerous stress-responsive genes and pathways, a comprehensive understanding of the integrated regulatory networks governing climate resilience and their translation into breeding strategies remains fragmented.

Aim of review: This review aims to provide a comprehensive systems-level synthesis of the regulatory mechanisms underlying cotton stress resilience by integrating advances in stress signalling, molecular regulation, multi-omics, and precision breeding into a unified framework for developing climate-resilient cultivars, explicitly distinguishing field-validated, breeding-ready targets from mechanistically supported but field-

untested candidates and from speculative, discovery-stage leads across the major bottlenecks constraining translation.

Key scientific concepts of this review: This review systematically integrates the regulatory networks controlling cotton adaptation to major abiotic stresses, encompassing stress perception, signal transduction, transcription factor networks, phytohormone crosstalk, reactive oxygen species homeostasis, ion transport, epigenetic regulation, and downstream physiological responses. Particular emphasis is placed on the emerging biology of combined-stress responses, highlighting regulatory interactions that cannot be explained by single-stress paradigms. Furthermore, the review critically evaluates how functional genomics, multi-omics integration, pan-genomics, genome editing, high-throughput phenotyping, and artificial intelligence-assisted prediction are converging to accelerate precision breeding for climate resilience. By bridging mechanistic understanding with translational breeding strategies, this review provides a forward-looking roadmap for developing climate-resilient cotton cultivars capable of sustaining productivity and fibre quality under increasingly unpredictable environments.

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Title: Assessment of genetic variability and selection potential in F₂ segregating populations of upland cotton (*Gossypium hirsutum* L.)

Authors: Madeeha Memon, Abdul Wahid Baloch, Piar Ali Shar, Zaheer Ahmed Deho, Tanweer Fatah Abro, Amber Memon, Sadam Hussain, Nadia Sipio

Imprint: The Kashmir Journal of Academic Research and Development | 2(6), 63-75, 2026

Abstract: Knowledge of the magnitude of genetic and phenotypic variability present in a crop species is fundamental to designing effective breeding programmes for developing superior cultivars. In this study, eight F₂ segregating populations of upland cotton (*Gossypium hirsutum* L.) was (IUB-2013 × NIA-95, Chandi-95 × M-23, NIA-Ufaq × M-35, NIAB-878 × Chandi-95, NIA-Noori × IUB-2013, Sadori × M-32, Sohni × NIA-Ufaq, ZAD-1 × Sadori) along with their twelve respective parents (IUB-2013, NIA-95, Chandi-95, M-23, NIA-Ufaq, M-35, NIAB-878, NIA-Noori, Sadori, M-32, Sohni, ZAD-1), generated from selected intra-specific crosses, were evaluated together with their twelve parental genotypes at the experimental field of the Nuclear Institute of Agriculture (NIA), Tandojam, during the 2025 Kharif season, using a randomized complete block design with three replications. Analysis of variance detected significant differences among genotypes for plant height, sympodial branches plant⁻¹, bolls plant⁻¹, boll weight, seed cotton yield plant⁻¹, ginning outturn percentage, staple length and micronaire, confirming that exploitable genetic variability was present in the breeding

material. Among the parents, NIA-Ufaq combined the tallest plant stature, the greatest number of bolls plant⁻¹ and the highest seed cotton yield plant⁻¹, while the F₂ crosses NIAB-878 × Chandi-95 and NIA-Noori × IUB-2013 recorded the highest seed cotton yield among the segregating populations. Broad-sense heritability estimates varied widely across traits and crosses, ranging from 3.66% (ginning outturn, Chandi-95 × M-23) to 99.17% (boll weight, Chandi-95 × M-23), while genetic advance ranged from 0.05 to 70.53 depending on the trait and cross combination considered. Seed cotton yield plant⁻¹ combined moderate-to-high heritability with substantial genetic advance in several crosses, most notably Chandi-95 × M-23 and NIA-Ufaq × M-35, indicating predominance of additive gene action and good scope for direct phenotypic selection in early generations. The crosses Chandi-95 × M-23, NIA-Ufaq × M-35, NIAB-878 × Chandi-95 and NIA-Noori × IUB-2013 displayed transgressive segregation for seed cotton yield, exceeding both respective parents, and are recommended as promising material for pedigree breeding aimed at developing high-yielding upland cotton genotypes.

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Title: Comparative genome-wide analysis and characterization of galactinol synthase (*GolS*) gene family in diploid and tetraploid cotton species

Authors: Umm e Abaida Noor, Muhammad Shaban, Muhammad Abubakkar Azmat, Saman Arshad, Abdul Hafeez & Kamran Javed

Imprint: *Biologia* **81**, 202 (2026). <https://doi.org/10.1007/s11756-026-02278-2>

Abstract: Galactinol synthase (*GolS*) is a key enzyme in the synthesis of raffinose and plays a vital role in plant adaptation to abiotic stresses. However, *GolS* gene family has not been comprehensively analysed in cotton. In this work, 36 *GolS* genes were screened across four cotton species (*Gossypium arboreum*, *G. raimondii*, *G. hirsutum* and *G. barbadense*). Their conserved domains/motifs, exon/intron structure, phylogeny, chromosomal distribution, syntenic relationship, and cis-acting elements were systematically studied in detail. Phylogenetic analysis revealed clustering of cotton *GolS* genes into three major groups, with close relationships to *Arabidopsis* *GolS* genes, suggesting functional conservation across species. Chromosomal mapping showed uneven distribution, while synteny and collinearity analyses identified multiple paralogous and orthologous pairs, with segmental duplication emerging as the primary driver of *GolS* gene family expansion. In silico prediction revealed that members of the *GhGolS* gene family are extensively targeted by multiple cotton-specific miRNAs. Expression profiling using transcriptomic data further revealed tissue-specific regulation and responsiveness of *GhGolS* genes to major abiotic stresses. Interestingly, the wide distribution of cis-regulatory elements

associated with light, growth, development, hormones, and stress responses supports the observed expression patterns and highlights their potential roles in stress adaptation. Overall, this work sets a starting point for further investigation into cotton *GolS* genes and provides novel resources for breeding programmes aimed at enhancing abiotic stress tolerance in cotton.

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Title: Genome-wide association study of yield-component traits in US upland cotton (*Gossypium hirsutum* L.)

Authors: Rakesh J. L. Gowda, B. Todd Campbell, S. Anjan Gowda, HuiFang FredM, Bourland MichaelA Gore, Don C. Jones, Vasu Kuraparthi

Imprint: Crop Science. 2026;66: e70334. <https://doi.org/10.1002/csc2.70334>

Abstract: Genetic improvement of cotton (*Gossypium* spp.) yield is challenged by the complex and polygenic nature of yield and its underlying component traits. In this study, an elite diversity panel of 348 upland cotton accessions, genotyped using the CottonSNP63K array, was evaluated across 10 environments in the US Cotton Belt for four yield-component traits: lint percent (LP: %), boll weight (BW: g), seed index (SI: g), and lint index (LI). All traits exhibited high broad-sense heritability (>60%), and all except for SI showed high genomic heritability. Positive correlations were observed among BW, SI, and LI, whereas SI was negatively correlated with LP. Genome-wide association study of the four traits identified 308 significant marker-trait associations (MTAs), including 80 stable MTAs distributed across 19 genomic regions, of which 15 are novel associations. These 19 genomic regions included MTAs detected in at least three environments and explained 7.23%–11.46% phenotypic variation. Notably, this study confirmed the pleiotropic region influencing SI and BW on chromosome D11 and identified a novel co-localized group on D12 associated with LP

Title: Identification of KNOX gene family in *Gossypium barbadense* and analysis of its expression patterns under drought and salt stress.

Authors: Wan-li Han, Yu Yu, Xian-hui Kong, Xu-wen Wang, Gang Wang, Li Liu, Fu-xiang Zhao, Jin-xin Qiao, Ai-jun Si, Qin Tian

Imprint: [Shandong Agricultural Sciences](#), 2026, Vol. 58, No. 6, 12-20, 32

Abstract: KNOX (knotted1-like homeobox) transcription factor play important roles in plant growth, development and stress responses. In this study, members of the KNOX gene family in cotton were identified based on available cotton genome data. The evolutionary relationships of the gene family members were analyzed using bioinformatics approaches. Transcriptome data were used to investigate the expression pattern of KNOX genes under drought and salt stresses, and quantitative real-time polymerase chain reaction (qRT-PCR) was performed to further validate their expression profiles under these stress conditions. A total of 44 KNOX genes were identified in the *Gossypium barbadense* genome, which were distributed across 20 chromosomes. These KNOX genes could be divided into three subgroups and was highly conserved during cotton evolution, and they contained abundant cis-acting elements associated with methyl jasmonate and abscisic acid responses. Based on integrated analyses of RNA-seq data, promoter cis-acting elements and qRT-PCR results, GbKNOX5, GbKNOX13, GbKNOX22, GbKNOX27 and GbKNOX35 were inferred to be potentially involved in the responses of *G. barbadense* to drought and salt stresses. Among them, GbKNOX13 and GbKNOX35 exhibited consistent expression patterns under both drought and salt stresses and might serve as candidate genes for subsequent functional validation. These findings could provide a theoretical basis for further study on the functions of the KNOX gene family and the molecular mechanisms underlying stress resistance in cotton.

Title: Preliminary functional analysis of carbonic anhydrase *GhaCA3-D* regulating drought stress in *Gossypium hirsutum*.

Authors: Run-Run Sun, Jia-Hui Li, Yuan-Yuan Cao, Yuan-Yuan Wang, Ya-Qi Xu, Qing Zhang, Qing-Lian Wang

Imprint 10.16213/j.cnki.scjas.2026.5.012

Abstract: Objective: Carbonic anhydrase (CA) is an important gene family that regulates plant growth and development as well as responses to drought stress. The aim of the study is to investigate the function of the CA family member *GhaCA3-D* in regulating drought stress, which will lay a foundation for cotton drought-resistant molecular breeding. Method: Bioinformatic characterization of *GhaCA3-D* was analyzed, and functional analysis of *GhaCA3-D* was conducted using virus-induced gene silencing (VIGS) technology. Result: *GhaCA3-D* encoded 261 amino acids. *GhaCA3-D* was a hydrophilic protein, which contained one transmembrane domain, multiple phosphorylation sites and a signal peptide. Additionally, the promoter region of *GhaCA3-D* contained cis-acting elements associated with salicylic acid, hormones and abiotic stress, suggesting that the gene may be involved in salicylic acid and stress responses. Natural drought treatment was used in the study. The results showed that TRV :00 plants exhibited leaf wilting, while TRV : *GhaCA3-D* silenced plants maintained better growth status under drought stress. Stomatal width measurements revealed that TRV : *GhaCA3-D* silenced plants exhibited significantly smaller stomatal width compared to TRV :00 control plants, which suggested that silenced plants decreased water loss. The trypan blue staining results showed that the TRV :00 leaves had more dead cells than that of TRV: *GhaCA3-D*. The measurement of proline and malondialdehyde (MDA) content revealed that the TRV *GhaCA3-D* gene silenced plants had significantly higher proline levels and significantly lower MDA levels compared to TRV :00, indicating that the drought tolerance of TRV:*GhaCA3-D* silenced plants was enhanced compared to the control. Conclusion: These results demonstrate that silencing *GhaCA3-D* enhances drought resistance in upland cotton, which provides candidate genes for drought resistant breeding and lays the foundation for cultivating drought tolerant cotton varieties.

Title: Genome-wide identification of GhAOX gene family and its expression and regulation in cotton CMS line Jin A

Authors: Jinlong Zhang, Li Zhang, Yuekai Su, Jinjiang Shi Junfang Yang, Xiuqing Yang, Jinling Huang, Yunfang Qu

Imprint:

<https://www.frontiersin.org/journals/plantscience/articles/10.3389/fpls.2026.1898123/abstract>

Abstract: Alternative oxidase (AOX) is a core functional protein that mitigates excessive mitochondrial reactive oxygen species (ROS) accumulation and modulates plant stress adaptation, and its biological activity is tightly controlled by sophisticated regulatory networks. The cotton cytoplasmic male sterile (CMS) line Jin A represents an optimal model for dissecting the functional characteristics of GhAOX genes, as it exhibits pronounced ROS overaccumulation and aberrant GhAOX transcriptional profiles in anthers during the critical developmental stage of pollen mother cell degeneration, relative to its maintainer Jin B. In this study, we conducted a genome-wide identification of the GhAOX gene family in upland cotton (*Gossypium hirsutum*) and systematically characterized the molecular features of GhAOX members in Jin A at the transcriptional, translational, post-translational modification, and gene structural levels. A total of eight GhAOX genes were identified, among which GhAOX2b1/2 and GhAOX2c1/2 displayed anther-preferential expression patterns and were significantly upregulated in response to multiple abiotic stresses, including osmotic stress (PEG), salinity (NaCl), cold (4°C) and heat (37°C). Functional validation via overexpression and virus-induced gene silencing (VIGS) assays verified the ROS-scavenging capacity of GhAOX. Notably, in Jin A, despite elevated GhAOX protein abundance, its enzymatic activity was substantially compromised, which was attributed to perturbed transcriptional regulation, isoform-specific differential activation by tricarboxylic acid (TCA) cycle intermediates, and reduced abundance of mitochondrial effector molecules. This dysregulation was likely implicated in the aberrant ROS accumulation underlying the pollen abortion phenotype in Jin A. Collectively, this study establishes a comprehensive molecular framework for elucidating the multi-level regulatory mechanisms of AOX in response to intracellular microenvironmental perturbations and uncovers its pivotal role in regulating reproductive fitness in upland cotton.

Title: Biotech Innovation in Cotton: Enhancing Crop Resilience through Precision Pest Control

Authors: Saqlain Ali Saddique, Inzamam ul Haq, Muhammad Ahsan, Muhammad Umar Asghar, Muqaddas Faisal Batool, Amna Saeed, Muhammad Shahzaib Khan and Samra Irem

Imprint: The Life, Book Chapter No: 029, pg 247-254

Abstract: Cotton is one of the most economically and socially significant fiber crops throughout the world, which supports the production of textiles and provides rural livelihood, especially in developing areas. However, cotton yield is reduced by insect pest attack, resistance to the control measures, weather unpredictability, salinity of soils, and the rising cost of production. The history of cotton biotechnology is followed, starting with the use of *Bacillus thuringiensis* and herbicide-tolerant cultivars to molecular technologies like RNA interference, CRISPR/Cas-based genome editing, and genomics-assisted breeding. Furthermore, the molecular processes of pest resistance, environmental and biosafety aspects of biotech cotton, regulatory and socio-economic challenges that determine the adoption of technology, especially by smallholders in developing nations, are addressed. Sensor networks unmanned aerial vehicles, remote sensing, artificial intelligence, and phenotyping technologies currently allow monitoring of crop health, pest pressure, nutrient status, and abiotic stress to allow more accurate and efficient agronomic decisions. Future trends are prefigured, such as climate-smart cotton ideotypes, polygenic and stacked resistance qualities and integrated Aigenomics platforms which combined breeding, field management, and sustainability purposes. The sustainability of cotton productivity depends on the system-wide combination of biological innovation, management practices, and supportive regulatory frameworks to ensure resilient, resource-efficient and environment-friendly cotton production.

Title: Non-Coding RNAs in Cotton: Regulators of Stress Adaptation

Authors: Arooj Fatima¹, Saqlain Ali Saddique^{2*}, Hajra Khan¹, Samreen Gul³, Muhammad Bilal Bashir¹, Muhammad Hussnain Sardar¹, Bilal Mustafa², Amna Saeed⁴, Faiza Anwar¹ and Muhammad Naqeeb Raza²

Imprint: The Life, Book Chapter No: 027

Abstract: Cotton is a vital global fiber and oil crop, but its productivity is facing mounting setbacks of drought, salinity, heat stress and new biotic challenges in changing climatic conditions. Recent studies have proved that non-coding RNAs (ncRNAs) such as microRNAs, long non-coding RNAs, small interfering RNAs, and circular RNAs play crucial functions in perception of stress, signal perception and adaptations in cotton. In this chapter, a holistic summary of ncRNA mediated stress adaptation in cotton has been provided, including the classification of ncRNA, their

biogenesis, regulatory signals, validation of their functions and the new roles of ncRNA in stress memory and transgenerational adaptation. It displays the role of ncRNA in fine-tuning hormone signaling, reactive oxygen species homeostasis, chromatin dynamics and growth-stress trade-offs during drought, salinity, heat and disease pressure. Recent developments in high throughput sequencing, degradome assays and plant specific bioinformatics pipelines have enabled genome wide identification of stress responsive ncRNAs whereas functional studies have used virus induced gene silencing, transgenic and CRISPR based methodologies to associate given ncRNA module with stress tolerance. Through the combination of molecular, physiological, and breeding views, this chapter makes ncRNAs the main regulating centers and promising molecular candidates in the generation of climate-resilient cotton varieties.

SEED SCIENCE AND TECHNOLOGY

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Title: Seed treatment with endophytic *Bacillus* enhances initial development and increases peroxidase and polyphenol oxidase activities in cotton

Authors: Livian Yumi Iwaoka ^a, Natieli Jenifer Mateus Corniani ^b, Luana Thais Varize Marcusso ^c, Carlos Augusto Corniani da Silva ^c, Willian Martire Marcusso ^c, João Arthur dos Santos Oliveira

Imprint: Biocatalysis and Agricultural Biotechnology, August 2026, Article: 104200, Volume: Volume 76

Abstract: *Bacillus* spp. are widely recognized as plant growth-promoting agents; however, their effects as bioinoculants in cotton (*Gossypium hirsutum*) remain poorly characterized. This study investigated the effects of seed treatment with fermented broths produced by the endophytic bacteria *B. subtilis* SB008, *B. velezensis* SB009, and *B. amyloliquefaciens* SB012 on germination, seedling development, and physiological parameters. All three fermented broths exhibited hydrolytic enzyme activities, including amylase, cellulase, and chitinase, and produced indole-3-acetic acid (IAA). Under laboratory conditions, seed treatment elicited significant dose-dependent responses in germination and seedling development, with strain-specific effects. Under greenhouse conditions over a 40-day period, SB009 and SB012 significantly increased plant height (16.34 and 16.58 cm, respectively) compared with controls (13.64 cm), in

addition to elevating foliar carotenoid contents. Furthermore, SB012 significantly increased peroxidase activity (2996 nmol/min/mg protein) and polyphenol oxidase activity (237 nmol/min/mg protein) relative to controls (638 and 58.9 nmol/min/mg protein, respectively). Although the observed responses were statistically significant under laboratory and greenhouse conditions, their agronomic relevance remains to be confirmed under field conditions. Collectively, these findings support the potential application of endophytic *Bacillus* strains as bioinoculants for cotton production.

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Title: Comparative Study of Castor, Cotton and Neem Oil Samples As Sources Glycerin

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Abstract: The study focused on the comparative analysis of castor oil (*Ricinus communis*), cottonseed oil (*Gossypium hirsutum*), and neem oil (*Azadirachta indica*) as sources of glycerin. The oil samples were characterized to ascertain their proximate analysis. Castor oil, cottonseed oil, and neem seed oil had saponification values of 182.71 mg/g, 185.06 mg/g, and 193.45 mg/g, respectively. Other physicochemical properties evaluated included acid value, free fatty acid content, iodine value, density, and peroxide value using standard titrimetric and analytical methods. The oil samples are appropriate for the synthesis of glycerin, according to the recorded average saponification values as well as the properties of the oils. Glycerin was synthesized from the oils through transesterification using methanol in the presence of an alkaline catalyst under controlled temperature and reaction time. After the reaction, phase separation was allowed to occur, and the crude glycerin layer was separated, washed, and dried before further analysis. The produced glycerin samples were characterized by determining their kinematic viscosity, moisture content, and chemical composition using standard laboratory procedures and spectroscopic techniques. The presence of heteroatoms (N and O) in each glycerin product indicates that glycerin is a possible raw material for the synthesis of bio-grease. Trimethylolpropane, 4-ethoxy-4-oxobutanoic acid, dihydro-2-methyl-3-furanone, linoleic acids, neopentyl glycol, methyl ester, and pentaerythritol were identified as the chemical constituents of the glycerin. The glycerin made from castor oil, cottonseed oil, and neem seed oil has kinematic viscosities of 928 cP, 931 cP, and 933 cP, respectively. Additionally, the glycerin made from castor oil, cottonseed oil, and neem seed oil had moisture contents of 1.92%, 2.15%, and 2.04%, respectively. Castor oil outperformed cottonseed and neem seed oil in terms of the glycerin yield. The yield was influenced by the increase in oil/methanol ratio, catalyst concentration, temperature, and time. Overall, the results show that all three oils are

suitable sources of glycerin, with castor oil giving the highest yield under the studied conditions. The study confirms their potential for industrial glycerin production and related applications.

FIBER AND FIBER TECHNOLOGY

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Title: The mitogen-activated protein kinase GhMPK3 participates in ethylene signaling regulating fiber elongation in cotton (*Gossypium hirsutum*)

Authors: Wen-Xiu Zhang, Qiao-Mei Zhao, Hua-Zhi Xie, Ling-Jie Zhang, Ting Jiang & Na-Na Wang

Imprint: Plant Cell Rep **45**, 232 (2026). <https://doi.org/10.1007/s00299-026-03902-w>

Abstract: Cotton is an important economic crop worldwide. Understanding the regulatory mechanisms that govern cotton fiber development is essential for enhancing both fiber yield and quality. Mitogen-activated protein kinases (MAPKs) play critical roles in plant growth, development, and physiological metabolism; however, their specific functions in cotton fiber development remain largely unexplored. Our previous research demonstrated that GhMPK3 is predominantly expressed during the elongation of cotton fiber cells and exhibits a sustained high level of phosphorylation. This study reveals that silencing GhMPK3 in cotton fibers impedes fiber elongation. Additionally, GhMPK3 enhances the transcriptional activity of the key ethylene signaling pathway transcription factor GhEIN3cA by phosphorylation to promote the expression of ethylene biosynthesis enzyme GhACO3, thereby facilitating cotton fiber elongation. This investigation elucidates the mechanism through which GhMPK3 mediates the ethylene signaling pathway to regulate cotton fiber development. The findings will aid in refining the regulatory network of cotton fiber development and provide a scientific foundation for improving cotton fiber quality.

Title: Effects of silicon fertilizer on growth, yield, and fiber quality traits of cotton (*Gossypium hirsutum* L.)

Authors: Muhammad Zeeshan, Luo Yanpei, Li Pengcheng, Zhang Zhenggui, Sun Guilan, Wang Jian, Zhang Yaopeng, Zhao Wenqi, Li Xin, Li Junhong, Zhai Menghua, Wang Lizhi, Pan Zhanlei & Wang Zhanbiao

Imprint: *J Cotton Res* 9, 32 (2026). <https://doi.org/10.1186/s42397-026-00278-w>

Abstract: Background: Cotton is a leading cash crop worldwide, yet its productivity is severely subject to diverse biotic and abiotic stresses. Silicon (Si) effectively enhances crop yields and quality by improving their stress tolerance. However, little is known about how Si additions improve cotton yield and fiber quality by enhancing its physiological stress tolerance. Thus, this field study was launched to explore the effects of different Si foliar spraying concentrations on agronomic traits, leaf physiological indicators, yields, and fiber quality, to identify the optimal concentration.

Results: Si foliar spraying significantly increased plant height, stem diameter, number of fruit branches, and number of main stem leaves, with the greatest increases under Si₂ concentration (7.15%–23.95%). Meanwhile, total and reproductive dry matter were observed to be significantly increased by Si foliar spraying, especially under Si₂ and Si₃ concentrations in 2024 (8.10%–21.65%). Si foliar spraying obviously improved the seasonal mean SPAD value in 2024. Additionally, it was found that Si foliar spraying (i.e., Si₂ and Si₃ concentrations) sharply reduced the marker of oxidative stress injury (i.e., malondialdehyde) while boosting osmotic regulatory substances (i.e., proline) and antioxidant enzyme activities (i.e., superoxide dismutase, peroxidase, catalase, and glutathione reductase). Although Si foliar spraying significantly increased boll weight, especially under Si₂ and Si₃ concentrations (13.79%–17.29% in 2024), there were slight increasing trends for seed cotton and lint yields in both years. Furthermore, Si foliar spraying markedly improved fiber strength, especially at Si₁ and Si₃ concentrations, in 2025.

Conclusions: Our results implied that Si foliar spraying decreased the markers of oxidative stress and injury, elevated the contents of osmotic regulatory substances and antioxidant enzyme activities in cotton leaves, and thereby improved cotton fiber quality, despite no significant effects on yields. In the future, more in-depth studies on Si additions in the cotton field are needed to obtain higher fiber quality.

Title: Genome-wide integrative dissection of genetic basis of fiber color and whiteness regulation in upland cotton (*Gossypium hirsutum*)

Authors: Shiguftah Khalid, Zhenzhen Wang, Tahir Mahmood, Xiaoli Geng, Hongge Li, Xiaomeng Zhang, Shoupu He & Xiongming Du

Imprint: BMC Biol (2026). <https://doi.org/10.1186/s12915-026-02662-z>**Background**

Abstract: Naturally colored cotton has gained renewed interest due to increasing environmental concerns over synthetic dyes. The genetic regulatory characteristics of fiber color are discovered by two perspectives in this study.

Results: Genome-wide association studies (GWAS) identified two major loci D11: 24.3–24.7 Mb and A07: 20.4–22.3 Mb controlling fiber color variation. Integrative QTL mapping and transcriptome profiling revealed three candidate genes *Gh_D11G208100*, *Gh_D11G207100*, and *Gh_D11G207600* with distinct expression profiles in fiber whiteness on D11. In contrast, the A07 locus harbors key transcription regulators *TT2*, *C1*, and *bHLH82* which are implicated in flavonoid-mediated brown pigmentation along with differentially expressed genes, *Gh_A07G015400*, *Gh_A07G019500*, and *Gh_A07G019400*, further supporting their potential role in regulating fiber pigmentation. Segregation analysis of fiber color across three different F₂ populations revealed three gene models. The *W1_W2*_loci were proposed to determine fiber whiteness located on D11 chromosome, while the fiber color gene locus *Lb_* determined by genetic analysis is related to the key locus for transcription regulators *TT2* on the A07 chromosome. The interaction of these three genes controls fiber color. Inheritance patterns were consistent pigment loss and a graded dilution model for pigmented phenotypes, with stable extreme classes white and near white, whereas intermediate pigmentation classes shifted between populations. We also identified overlapping QTLs of fiber quality and color attributes, indicating strongly linked genetic mechanisms.

Conclusions: This integrated analysis supports a model of coordinated regulation, where transcriptional control from A07 influences pigment biosynthesis, while D11 modulates fiber surface or secondary metabolism to fine tune color intensity and whiteness.

Title: Paired high volume instrument (HVI) and advanced fiber information System (AFIS) dataset for global cotton characterization

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Imprint: Data in Brief, Volume 68, 2026, 113110, ISSN 2352-3409, <https://doi.org/10.1016/j.dib.2026.113110>.

Abstract: The article presents a comprehensive dataset of physicochemical descriptions of commercial cotton fibers (*Gossypium hirsutum* L.) that grow in a wide range of agro-climatic- conditions, such as Brazil, West Africa (Mali, Benin, Burkina Faso, Ivory Coast, and Cameroon), Australia, and India. It comprises paired samples from two industry-standard characterization systems, the High Volume Instrument (HVI) to measure the bundle characteristics (e.g., Micronaire, Upper Half Mean Length, and Strength) and the Advanced Fiber Information System (AFIS) to measure the distributions of single fibers (e.g., Neps per gram, Short Fiber Content, Maturity Ratio). To ensure the retention of metadata of various originating file structures, data from industrial-quality reports were digitized with a proven Python-based Optical Character Recognition (OCR) pipeline and subsequently verified manually to achieve high accuracy. The strategic importance of this dataset is that it is the aggregation of ubiquitous HVI trade values and capital-intensive AFIS process values on identical Lot and Bale identifiers. This unique synchronization offers textile-machine learning researchers or data scientists the opportunity to explore various potential linear, non-linear and interdependencies between HVI and AFIS features. Notably, it may pave the way for predicting nep count from the HVI dataset, potentially eliminating the necessity of purchasing an expensive AFIS machine. No predictive analyses or machine learning models were conducted in this current study. Besides, it can be used for various classification-based works through standard commercial classification-level data.

Title: Pan-Genome Analysis of the *Tubulin* Gene Family Reveals Candidates for Fiber Strength in *Gossypium barbadense*

Authors: Yajie Duan, Ruihong Zeng, Yongsheng Cai, Yongsheng Cai, Xiaoju Liu and Fenglei Sun

Imprint: *Genes* **2026**, 17(8), 873; <https://doi.org/10.3390/genes17080873>

Abstract: Background/Objectives: *Tubulins (Tub)* are central components of microtubules, but intraspecific variation and developmental expression of the *Tub* family in *Gossypium barbadense* remain poorly characterized. This study aimed to characterize the *GbTub* family using a pan-genome framework and identify candidates associated with fiber development and strength. **Methods:** A total of 50 *GbTub* genes were identified in the *G. barbadense* 3-79 reference genome, and their orthologous presence-absence patterns were subsequently assessed across 12 additional *G. barbadense* accessions. Phylogenetic, presence-absence variation (PAV), Ka/Ks, structural variation (SV), RNA-seq, RT-qPCR, co-expression, and GO enrichment analyses were integrated. **Results:** Among the 50 reference-defined *GbTub* genes, 43 were classified as core genes, 6 as near-core genes, and 1 as an accessory gene, and the encoded proteins were classified into α -, β -, and γ -*tubulin* clades. All genes showed Ka/Ks < 1. Twenty-three *GbTub* genes differed between the fiber-strength-contrasting accessions 5917 and PimaS-7, and representative expression trends were supported by RT-qPCR. Network analysis prioritized 10 *GbTub* candidates based on degree centrality. *GbTub21* was the sole SV-associated *GbTub* gene displaying significant differential expression between accessions harboring versus lacking the corresponding SV. Non-*Tub* neighbors of the candidate hub genes were enriched for cytoskeletal, intracellular-transport, and plasma-membrane functions. **Conclusions:** The pan-genome analysis reveals strong conservation with limited intraspecific variation in the *GbTub* family. Co-expression profiles nominate candidates associated with fiber secondary-wall development, and their causal contribution to fiber strength awaits functional dissection.

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Title: Pumping Life into Fibers: Roles of Vacuolar H⁺- ATPases in Cotton Development and Stress Adaptation

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Imprint: The Life, Book Chapter No: 053

Abstract: Vacuolar H⁺ ATPases (V-ATPases) and plasma membrane H⁺-ATPases (PM H⁺-ATPases) are vital constituents of ion homeostasis, pH control, and energy conversion in plant cells. These proton pumps produce electrochemical gradients to power nutrient transportation, vesicle trafficking and cell homeostasis processes which are essential to cell growth and adaptation to stress. V-ATPases have been found to be central to fiber elongation and abiotic stress-tolerance in cotton. The catalytic subunit GhVHA-A increases osmotic balance, antioxidants, and dehydration resistance; silencing of this protein, on the contrary, decreases tolerance to stress. Equally, PM H⁺ ATPases maintain ion movements and stomatal activity, and thus, maintain stability of

plants during unfavorable situations. This has been recently clarified by molecular biology and genomics discoveries of the structural organization, regulation and crosstalk between these ATPases and hormonal and redox signaling networks. The dynamic adaptation to environmental changes is achieved by modulation via phosphorylation, redox rule, and protein-protein interactions, including 14-3-3 proteins. New technologies such as CRISPR/Cas based genome editing and synthetic biology have provided the avenue of creating stress-inducible ATPase control and thus increasing resilience and productivity. Extensive knowledge of these processes offers a basis on which development of climate-sensitive, resource-efficient cotton breeds can be designed that combines a basic idea of molecular understanding and practical crop enhancement.