



GLEANINGS IN COTTON RESEARCH

JULY 2026



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NAGPUR - 440010

E Mail: cicrlib@yahoo.co.in

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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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Title: Weed Control and Cotton Yield Response under Sorghum-Cotton Rotation

Authors: Gaganjot Singh Sodhi, Sukhbir Singh, S. V. Krishna Jagadish, Donna McCallister and Rupinder Saini

Imprint: <https://doi.org/10.20944/preprints202607.0586.v1>

Abstract: The Texas High Plains (THP) is a major cotton-producing region facing challenges from continuous cotton monoculture, which has increased weed pressure and reduced system sustainability. Over 90% of cotton acreage relies on herbicides, accelerating herbicide-resistant weed development. Declining Ogallala Aquifer water levels and erratic rainfall further stress the system, highlighting the need for diversified, drought-resilient cropping systems. Sorghum, known for its drought tolerance and allelopathic properties, offers an effective rotational crop to suppress weeds and improve water use efficiency. This study evaluated the effects of sorghum-cotton rotation on weed dynamics, crop growth, and yield. A two-year field experiment (2024-2025) was conducted at the Quaker Research Farm, Texas Tech University, Lubbock, TX, using a split-plot design with crop rotations [sorghum-cotton (S-C), sorghum-sorghum (S-S), and cotton-cotton (C-C)] as main plots and weed management treatments (weeded and unweeded) as subplots, with four replications. Results showed that the C-C system had 41% higher weed density and 57% greater early-season biomass than S-C; cotton growth improved in S-C with 17-22% taller plants and 36-90% more biomass compared to cotton monoculture. Under weeded conditions, lint yield increased by 53% and seed yield by 30% compared with cotton monoculture. Under unweeded conditions, yields were 21% to 41% greater in the S-C system due to improved weed suppression and reduced competition. Overall, integrating sorghum into cotton-based systems reduced weed pressure, enhanced crop performance, and minimized yield losses under limited weed control, supporting more sustainable production in the THP.

Title: An Explainable Vision Transformer Based Framework for Weed Identification in Cotton Production Systems

Authors: Maaham; Zahira Parveen Jamro; Asif Khan; Zakria; Abdul Rehman Qureshi; Hafsa Shaikh

Imprint: 2026 5th International Conference on Computing, Mathematics and Engineering Technologies (iCoMET), Sukkur, Pakistan, 2026, pp. 1-6, doi: 10.1109/iCoMET69771.2026.11591582.

Abstract: The process of sustainable cotton production which requires efficient weed management, suffers from traditional methods that need many workers and cause environmental damage through their chemical application. Deep learning enables automated weed identification, yet conventional Convolutional Neural Networks (CNNs) encounter difficulties when attempting to differentiate between weeds and crops that exist in obstructed field settings. The research solves these issues by using the Vision Transformer (ViT-Base/16) architecture to analyze the CottonWeedID15 dataset which consists of 6,750 images from 15 different species. The ViT model uses a multi-head self-attention mechanism to track global shape relationships which allows scientists to discover yet unidentified plant characteristics that exist between different species. The application of explainable AI (XAI) through Gradient-weighted Class Activation Mapping (Grad-CAM), which we developed to use with transformer tokens helps us to replace "black-box" classification methods. The testing accuracy of our model reached 98% while the XAI heat maps indicated that the model used both leaf venation and margin serration as essential biological indicators to differentiate between species. The results demonstrate that Vision Transformers provide a strong yet understandable system which farmers can use in precision farming to develop trustworthy autonomous weeding solutions.

Title: Comparative Effect of Different NPK Fertilizers on Growth of Cotton (*Gossypium hirsutum* L.) in Alkaline Calcareous Soil

Authors: 1Ahmad Waqas*, 2Saba Tabasum, 3Beenish Butt, 4Muhammad Jamil, 5Fariha Amin, 4Muhammad Umar Hayat Khan, 4Naseem Akhtar, 6Sehrish Jamil, 4Nafeesa Muslim, 7Sajid Ali Shah, 8Muhammad Zubair Ayyoub

Imprint: J. Plant Environ. 05 (01) 2023. 51-55 <https://doi.org/10.33687/jpe.005.01.4584>

Abstract: Cotton is an important commercial crop that supports the world economy by serving as a source of raw materials for the textile sector. It is grown in various regions of the world and is subjected to diverse environmental or nutritional constraints that affect its growth and productivity. Among these constraints, NPK deficiency is a major nutritional constraint in alkaline-calcareous soils. The problem of NPK deficiency in cotton has been addressed by the application of different NPK fertilizers; however, their efficacy in alkaline soils is not well understood. This experiment was carried out to look into the comparative effect of NPK fertilizers, such as DAP, Urea, SOP, CAN, and NP on the growth of cotton. The aim of the findings was to assess the impact of different NPK fertilizers on the growth and productivity of cotton in alkaline-calcareous soils. Five different treatments were used in the experiment, which was carried out using a randomized complete block design, a control treatment and three replications. The results showed that the treatment with NP+CAN+SOP (T5) had the highest number of bolls (46.75), followed by T3 (42.25) with DAP+CAN+SOP, and T4 (36.55) with NP+Urea + SOP. The highest plant height (163.48 cm) and fresh stalk weight (290 g) were observed in T5. Similarly, the maximum yield (2350 kg/ha) was observed in T5 followed by T3 (2081 kg/ha). T5 also showed highest relative water content (94.7%) and staple length (27.4 mm)). In conclusion, the application of NP+CAN+SOP (T5) had a significant optimistic impact on the growth and productivity of cotton in alkaline-calcareous soils. The findings of this investigation offer insightful information on the efficacy of NPK fertilizers for cotton production in these soils and can be used to make informed decisions for future fertilizer management practices.

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Title: GhCHX6A and GhKEA1D Enhance Salt Tolerance by Regulating Na⁺/K⁺ Homeostasis in Cotton

Authors: Quanrun Zhu 1, Yangfan Miao 1, Yu Wang 2, Zhiqiang Zhang 2, Zhongying Ren 2, Xintong Zhai 2 3, Ling Li 1, Suhan Wei 2, Wei Li 1 2, Tong Li 1, Wei Liu 3

Imprint: DOI: [10.1111/pp1.71001](https://doi.org/10.1111/pp1.71001)

Abstract: The cation/proton antiporter (CPA2) family plays key roles in regulating plant ion balance and pH homeostasis, particularly in response to salt stress. In this study, a total of 76 CPA2 members were identified in *Gossypium hirsutum*, phylogenetically classified into 62 GhCHXs and 14 GhKEAs. Through RNA-Seq data analysis, we found that the expression levels of GhCHX6A and GhKEA1D were significantly upregulated under salt stress. The subcellular localization test showed that GhCHX6A is localized to the vacuolar membrane, while GhKEA1D is localized to the thylakoid membrane. Yeast functional complementation assays revealed that GhCHX6A and GhKEA1D exhibit Na⁺ and K⁺ transport activities, respectively.

Silencing of these genes via virus-induced gene silencing (VIGS) dampened cotton salt tolerance, manifested as aggravated wilting, increased accumulation of reactive oxygen species (ROS) and malondialdehyde (MDA), decreased chlorophyll content, and disrupted Na⁺/K⁺ balance in cotton tissues. These results indicate that GhCHX6A and GhKEA1D enhance salt tolerance in upland cotton by regulating Na⁺/K⁺ transport to maintain ion homeostasis and alleviate oxidative damage.

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Title: Modeling the Field-Scale Effects of Regenerative Agricultural Practices in a Semi-Arid Cotton Production System

Authors: Navdeep Kaur Saasan, Ali Mirchi, Zaichen Xiang, Muhammad Umar Akbar, Kevin Wagner, Srinivasulu Ale, Luca Doro, Sara Alian, Tim Propst, Lucas Gregory, Briana Wyatt, Bismark Osei

Imprint: Journal of the ASABE. 69(4): 571-587. (doi: [10.13031/ja.16657](https://doi.org/10.13031/ja.16657)) @2026

Abstract: Integrating regenerative agricultural practices (RAPs) into semi-arid agroecosystems offers a potential pathway to mitigate climate-driven water scarcity and soil degradation. The Environmental Policy Integrated Climate (EPIC) model was used to evaluate eight management combinations of tillage, winter-wheat cover, and water regime over a long-term simulation period (2000–2023). Field operation logs and edge-of-field runoff observations collected during 2022–2023 from a cotton experiment near Altus, OK, aided model calibration. Simulation results indicated that no-till with winter wheat cover crop increased mean crop-available water by 94.5 mm (692.4 vs. 597.9 mm) relative to the conventional irrigated baseline. RAP scenarios reduced mean annual runoff relative to conventional dryland management. Runoff decreased from 149.4 mm under CT-NCC-DRY to 99.8 mm under NT-WWCC-IRR and 94.7 mm under NT-WWCC-DRY, representing reductions of 33.2% and 36.6%, respectively. Cotton yield also increased by ~6% (1.21 vs. 1.14 Mg ha⁻¹) with greater stability in dry years under this set of RAPs. Local one-at-a-time (OAT) sensitivity screening highlighted soil bulk density (1.50–1.75 Mg m⁻³) and saturated hydraulic conductivity (~0.11–1.0 mm h⁻¹) as major factors affecting water dynamics. Overall, the combination of no-till, winter wheat cover crop, and strategic water management improved root-zone storage, reduced runoff, and stabilized cotton yield in this water-limited system. By linking empirical observations with process-based modeling, the study offers actionable guidance for implementing RAPs in semi-arid regions.

Title: Sample size for morphological traits of cotton cultivars

Authors: Mikael Brum dos Reis, Alberto Cargnelutti Filho, Leonardo Cesar Pradebon, Lais Cherobini, Manoela Conterato Della Pace, Debora Luiza Pozzebon

Imprint: Pesqui. Agropecu. Trop., Goiânia, v. 56, e85261, 2026

Abstract: The adequate sample size helps in the experimental precision and in the efficient use of resources in research with cotton. This study aimed to determine the sample size and understand the dissimilarities between traits and between cultivars of cotton at the stages of first visible flower bud and full maturity. Nine uniformity trials were carried out with the cultivars IMA2106GL, IMA5801B2RF, IMA5802B2RF, TMG31B3RF, TMG44B2RF, IMA5045WS3, TMG51WS3, TMG91WS3, and 21064WS3. At the stage of first visible flower bud, the main stem height, first productive branch height, main stem diameter, and number of leaves, nodes, and primary branches were evaluated; and, at the full maturity stage, in addition to the first five traits, the number of productive branches. Assuming a mean estimation error of 5 % and a confidence level of 95 %, the number of plants needed to measure the traits is 14 for main stem height, and number of leaves and nodes; 38 for main stem diameter and number of primary branches; and 126 for first productive branch height and number of productive branches.

Title: Tillage does not impact soil greenhouse gas emissions in a Central Texas rainfed maize-cotton system

Authors: Dorothy Menefee Hal Collins Doug Smith

Imprint: Argosies Geosci Environ. 2026;9: e70386. [wileyonlinelibrary.com/journal/agg2](https://doi.org/10.1002/agg2.70386)
1 of 20 <https://doi.org/10.1002/agg2.70386>

Abstract: Agricultural soils are a significant source of greenhouse gas (GHG) emissions, primarily as N₂O. Monitoring how management practices impact soil gas fluxes (CO₂, CH₄, and N₂O) is useful for making sure conservation practices (e.g., no-till) are sustainable with regards to all potential environmental impacts. Static chambers were used to collect soil gases from a rainfed maize-maize-cotton rotation (*Zea mays* and *Gossypium hirsutum*) with three tillage treatments (conventional till, strip-till, and no-till) in Temple, TX, at a USDA Long-Term Agroecosystem Research network site. Soil available nitrogen (ammonia and nitrate), soil moisture, and soil temperature were also collected alongside gas measurements. Measurements were conducted over three growing seasons to capture the full rotation cycle in each plot. CH₄ fluxes were small

and largely net uptake with some influence of soil temperature and crop selection. Soil CO₂ fluxes were primarily influenced by soil moisture ($p < 0.0001$) and temperature ($p < 0.0001$). Soil N₂O emissions were primarily correlated with soil moisture ($p < 0.0001$), temperature ($p < 0.0001$), and nitrate availability ($p < 0.001$). Tillage practices had no significant effect on soil GHG fluxes, including N₂O, in this agricultural system.

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Title: Best Fertilizer Management Practices for Cotton: A Guide to Optimising Yield, Profit, and Sustainability in Maharashtra

Authors: A Manikandan, D Blaise, Rachana Deshmukh, Chandrashekhar Mundafale, Vikram Fandi and AS Tayade

Imprint: Medicon Agriculture & Environmental Sciences Volume 10 Issue 6 June 2026

Abstract: Cotton, the world's most important natural fibre crop, is a significant contributor to the global textile industry and a crucial economic pillar for many agricultural regions. However, its cultivation is resource intensive, particularly in terms of nutrient requirements (Blaise and Kranti, 2019). Effective fertiliser management is not merely an agronomic task; it is a critical determinant of profitability, fibre quality, and environmental stewardship for cotton cropping systems. Inappropriate fertilizer use can lead to excessive costs, nutrient runoff polluting water systems, soil degradation, and suboptimal yields. Therefore, adopting scientifically sound, site-specific Best Management Practices (BMPs) for fertilizer application is paramount for the future of sustainable cotton production. The foundation of any successful fertilizer programme is a comprehensive understanding of the crop's nutrient demand curve and critical stages. Cotton has a distinct growth pattern i.e., bell shape with a long vegetative period followed by a critical reproductive phase which translates into a specific nutrient uptake schedule. Notably, cotton is a "nutrient hoarder" early in the season, accumulating nitrogen (N), phosphorus (P), and potassium (K) in leaves and stalks before peak demand during boll development. Approximately 60-70% of total N uptake occurs during the flowering and boll-set stages. Failure to meet demand at this juncture severely impacts yield, while excessive or poorly timed N application promotes excessive vegetative growth ("rank growth"), increases susceptibility to pests and diseases, delays maturity, and can detrimentally affect fibre quality. Therefore, the critical stages of cotton (Seedling, squaring, flowering, Boll formation and Boll maturity) and subtending leaves nutrient management is important.

Title: The decline in leaf mesophyll conductance is derived from anatomical traits under multiple stresses of water, salt and high temperature in cotton

Authors: Tong Zhang, Zhangying Lei, Yihan Liu, Xilin Li, Weixi Zhao, Ting Wang, Fubing Liang, Huanyong Han, Youzhong Li, Daohua He

Imprint: Plant Physiology and Biochemistry, Volume 237, August 2026, 111530

Abstract: Climate change-driven extreme abiotic environmental stresses, for instance water stress, salt stress, and high temperature, prominently threaten agricultural crop development and yield. Although we have extensive knowledge regarding how plants react to each of these single stresses, we have limited understanding of how the combination of multiple factors (i.e., multiple stresses) have impact on leaf CO_2 diffusion and photosynthesis. This study examined the response of leaf mesophyll conductance (g_m) and its consequences for photosynthesis and biomass in flower and boll stages of cotton under the multiple stresses of water, salt, and high temperature. The results revealed that the multiple stresses of water, salt, and high temperature stress markedly reduced stomatal conductance (g_s), g_m and net photosynthesis rate (A_N), and A_N was positively associated with g_s and g_m . The decline in g_m was closely associated with reductions in the surface areas of mesophyll cells and chloroplasts exposed to intercellular airspace. Under triple stress, g_m showed a great decline than under individual stresses, whereas the reduction in A_N was comparatively less pronounced. This discrepancy is likely because biochemical limitations became the dominant factor under severe stress. These findings demonstrate that the multiple stresses of water, salt, and high temperature obviously restricts g_m and impairs photosynthetic capacity by changes in leaf anatomical traits, it suggests that optimizing CO_2 diffusion may represent a potential strategy to mitigate the effect of multiple stresses.

Title: Basal application of silicon fertilizer enhances antioxidant defense and mitigates oxidative damage in cotton under neutral salt stress

Authors: Jiaxin Guo, Huijuan Guo, Fenghua Zhang, Wei Min

Imprint: Industrial Crops & Products 249 (2026) 123811

Abstract: Soil salinity-alkalinity is a major constraint limiting crop productivity, highlighting the need to enhance crop tolerance for the sustainable use of saline-alkali

lands. Although silicon (Si) has been widely reported to alleviate salt-induced damage in plants, its mechanisms in improving salt-alkali tolerance in cotton remain poorly understood. In this study, integrated physiological, biochemical, proteomic, and metabolomic analyses were used to investigate the response of cotton to silicon supplementation under control (CK), neutral salt stress (CS), and alkali stress (AS), along with their corresponding silicon-treated groups (CKSi, CSSi, ASSi). Results showed that both CS and AS treatments significantly increased ROS, MDA, and Na⁺ accumulation in cotton leaves. Compared with CS, CSSi markedly reduced Na⁺, ROS, and MDA by 56.00%, 19.63%, and 17.84%, respectively. Si application concurrently increased Si content and enhanced antioxidant enzyme activities (SOD, POD, CAT), proline content, leaf water status, and net photosynthetic rate by 87.32%, 17.93%, 7.07%, 9.81%, 14.38%, 2.49%, and 21.79%, respectively. In contrast, ASSi induced only marginal physiological responses compared with AS. Proteomic and metabolomic analyses identified 1260 differentially expressed proteins and 595 differential metabolites in CSSi. Flavonoids (57 upregulated, 6 down-regulated), coumarins and derivatives (28 up-, 1 down-regulated), and phenolic acids and derivatives (21 upregulated, 8 down-regulated) were strongly induced by Si. These molecules were enriched across 12 metabolic pathways. In ASSi, 1776 proteins and 42 metabolites were differentially expressed, enriched in only 4 pathways. These findings suggest that silicon alleviates neutral salt stress by regulating ion homeostasis, enhancing antioxidant defense, and promoting flavonoid biosynthesis, thereby reinforcing both enzymatic-non-enzymatic system. In contrast, its alleviating effect under alkali stress was limited, likely due to restricted silicon uptake at high pH.

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Title: Formal Verification and Deep Learning for Smart Farming: A Robust Framework for Cotton Crop Monitoring

Authors: Abdul Rehman, Nadeem Akhtar, Muhammad Talal, Naveed Imran, Sana Hameed

Imprint: VFAST Transactions on Software Engineering 343
<https://vfast.org/journals/index.php/VTSE@> 2026, ISSN(e): 2309-3978, ISSN(p): 2411-6246 Volume 14, Number 2, April-June 2026

Abstract: Cotton, a critical global cash crop, faces challenges in disease detection due to wetland and climate-change inconsistency. This work evaluates the Cotton Crop Disease Detection Model that uses an EfficientNet-Convolutional Neural Network (CNN) architecture and the Temporal Logic of Actions (TLA+). The proposed model ensures accurate disease classification and formal verification for correctness, reliability, and availability. EfficientNet-CNN demonstrates robust performance in identifying multiple disease conditions, including aphids, armyworms, and bacterial blight,

achieving an overall weighted accuracy of 94%, with macro-average scores of 0.94 for precision, recall, and F1-score. Class specific performance shows an F1-score of 97% for armyworms and 96% for powdery mildew. TLA+ verifies the model's compliance with disease-monitoring requirements, ensuring correctness, reliability, and availability in industry applications. This integrated framework enhances cotton crop disease detection, supporting sustainable and technology-driven agricultural practices.

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Title: Machine learning models to forecast cotton yield for Punjab

Authors: Opinder Kaur^{1*}, Mohammed Javed¹, Chetan Singla² And Gurjeet Singh Walia³

Imprint: MAUSAM, 77, 3 (July 2026), 1059-1068 DOI:
<https://doi.org/10.54302/mausam.v77i3.6782>

Abstract: Accurate and early predictions in agriculture are essential for sustainable farming and optimizing field management. Crop yield prediction significantly impacts the farmer's decisions on crop insurance, storage demand and other important factors during the growing season. Due to non-linearity in crop yield, the use of non-linear models for forecasting purposes has become popular these days. In this paper, ANN and LSTM models were trained using weather parameters to forecast the cotton yield for Punjab, India. Predicting the yield with minimum error is a main challenge. ANN (10 10 10 1) model with ReLU activation function in hidden layers performed better than other forecasting models with a minimum MSE (0.0182). The analysis using the NN model concluded that the weather parameters played an important role in affecting the plant growth. These variables may enhance or reduce the yield significantly. Sensitivity analysis showed that relative humidity was the most important weather parameter followed by rainfall.

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Title: Enhancing cotton yield (*Gossypium hirsutum* L.) through effective pre-emergence weed control using s-metolachlor and prometryn

Authors: Fatima M. Elnour, Abosofian S. Osman, M. Elkhawad, Dafalla A. Dawoud

Imprint: Gezira Journal of Agricultural Science, [S.l.], v. 20, n. 1, june 2026. ISSN 1728-9556. Available at: <<http://37.60.236.48/index.php/gjas/article/view/2576>

Abstract: The use of pre-emergence (pre-em) herbicides in cotton crop is a key strategy for effective weed control. Therefore, this study aimed to evaluate the efficacy and

selectivity S-metolachlor in tank mixture with prometryn for pre-emergence weed control in cotton. The experiment was carried out at Rahad Research Station Farm (RRSF), Sudan, during seasons 2018/19 - 2019/20. S-metolachlor was applied in mixtures with prometryn. Herbicides were applied immediately after sowing. S-metolachlor at 1.142, 1.370 and 1.599 a.i./ha and prometryn at rates 0.357 and 0.476 a.i./ha, were used with and without supplementary hand weeding at 4 weeks after sowing (WAS). Weeded and un-weeded treatments were included for comparison. Treatments were arranged in a Randomized Complete Block Design (RCBD) with 4 replicates. Results showed that mixtures of S-metolachlor + prometryn, irrespective of the rates, provided effective good to excellent control (70-100%) of grasses (G) in both seasons. The same treatments at all rates without supplementary hand weeding gave moderate to excellent control of broadleaved (BL) weeds in both seasons. The highest tank mixtures rates at (1.599+0.357 and 1.599+0.476 a.i./ha) caused phytotoxicity and reduced plant population and yield. All mixtures reduced weed ground cover throughout the seasons, and significantly reduced man-hour required for supplementary weeding in comparison with the weeded control (WC) and reduced weed biomass in comparison to the un-weeded control(UWC). Unrestricted weed growth significantly reduced cotton seed yield by 60-64% when compared with the weeded control. Consequently, it can be concluded that the pre-emergence herbicides of S-metolachlor + prometryn resulted in good control of both G and BL during the critical period of crop growth, and high cotton yield. The recommended dose at 1.142+ 0.476 a.i./ha of S-metolachlor and prometryn with supplementary hand weeding for effective control of both types of weeds grassy and for seed cotton yield comparable to the weeded control.

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Title: Integrated agronomic strategies for alleviating salinity stress and enhancing cotton yield

Authors: Waqar Ahmad Khan

Imprint: EQA-InternationalJournalofEnvironmentalQualityISSN2281-4485 -Vol.74 (2026):16 -42

Abstract: Salinity is one of the most threatening stress for cotton. Cotton is considered a moderately salt-tolerant crop with a salt tolerance limit of 7.7 dS m⁻¹. Stress is always deleterious for cotton growth, yield, and quality of cotton. The degree of sensitivity to salt stress varies in a dependent position with growth stage and type of salt. Cotton reacts to salinity, and its ability to cope with it and the management methods might prove useful in helping to find ways to enhance the production of cotton under saline environments. Several of the studies have demonstrated that the germination, seedling phases and emergence are much more sensitive to salinity stress in a comparative

perspective from other later phases. Flowering occurs later, and fewer fruiting sites, fruit drop, and smaller boll size ultimately influence seed cotton yield; its partitioning is the major aspect of cotton modulation under salt stress. This study shows that high level of salts in the soil affect the metabolic activities of the cotton plants mostly through osmotic stress, nutritional imbalance and toxicity from the salts' ions; sodium and chloride. The metabolic disorders may suddenly bring down cotton growth and lint yield, most especially in moderate to highly saline soil. In this review, we study different of agronomic practices such as mulching and furrow seeding, plant density management, increasing soil moisture and temp, water management, utilization of root associated microorganism, drip irrigation, crop rotation, biochar, seed priming, flat-sowing technique, ridge planting technique mitigating soil salinity, reducing salinity effects on cotton and improving plant growth of the cotton plant. Cotton genetic studies on salt tolerance indicated that most biochemical, physiological, agronomic, and fiber traits are genetically regulated and have significant QTL effects. But with biochemical and molecular biology tools available now, it has become possible to look at the intricacies of salt tolerance at the transcript level. This review highlighted integrated agronomic strategies for alleviating salinity stress and enhancing cotton yield.

CROP PROTECTION

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Title: Formulation-dependent efficacy of *Bacillus velezensis* BEIB-46 for the biological control of *Meloidogyne incognita* in cotton

Authors: Bergonsi, W., Gobatto, R., da Silva, L.C.O. *et al.*

Imprint: Eur J Plant Pathol (2026). <https://doi.org/10.1007/s10658-026-03272-9>

Abstract: *Meloidogyne incognita* is one of the main phytonematodes affecting cotton productivity, requiring sustainable control alternatives to chemical nematicides. This study evaluated the efficacy of different bioinputs based on *Bacillus velezensis* BEIB-46 for the biological control of *M. incognita* and their effects on cotton development. The strain was identified through high-resolution genomic analyses, followed by production via submerged fermentation and formulation into four distinct forms: fermented broth (6×10^8 CFU/mL), fermented broth supplemented with 10%

composting extract (4×10^8 CFU/mL), concentrated wet biomass of *B. velezensis* BEIB-46 (1×10^{10} CFU/g), and concentrated dry biomass of *B. velezensis* BEIB-46 (1×10^{10} CFU/g), applied at different doses at planting. After 98 days, the final nematode population, reproduction factor, control efficiency, and agronomic parameters were evaluated. All *B. velezensis* treatments significantly reduced the *M. incognita* population compared with the untreated control. The highest control efficiencies were observed for the concentrated formulations, particularly the dry solid form, which achieved up to 83.4% efficiency and reproduction factors of 0.4 and 0.3. In addition to nematode suppression, the treatments significantly increased fresh root mass and shoot dry mass, indicating a biostimulant effect. The concentrated dry formulations (2 and 5 g/ha) demonstrated superior performance by combining high nematicidal efficiency with root or shoot growth promotion, as well as improved commercial attributes and operational feasibility, highlighting the potential of *B. velezensis* BEIB-46 as a sustainable alternative for the management of *M. incognita* in cotton cultivation.

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Title: Diversity of Insect Pest of Cotton Species (*Gossypium hirsutum*) near Mungoli, Tahsil-Wani, District- Yavatmal, Maharashtra, India

Authors: Deulkar Samiksha Arun*, Gaidhane Dnyaneshwar Mahadeo and Telkhade Pravin Madhukarrao

Imprint: Life Science Review <https://doi.org/10.51470/LSR.2026.10.01.11>

Abstract: Cotton accounts for 40% of total global fibre production. India is a major contributor to the cotton market globally in terms of area and production. Nearly 500 species of natural enemies related to cotton pest have been reported by many researchers. The present study carried out for a period of June 2024 to May 2025. The survey conducted in cotton field near Matholi, Jugad and Shivni area, Tahsil Wani, District Yavatmal, Maharashtra. The state the area is located between the latitude 19.887° and the longitude 79.12779° . In the present investigation, total 19 harmful cotton pest species were recorded which damages the leaves, flowers, boll and the stem of cotton plant which affects the production and the quality of cotton fibres. The aim of the study is to collect baseline data of insect pest on cotton plant species.

Title: Status of cotton stem weevil, *Pempherulus affinis* (Faust) (Coleoptera: Curculionidae)

Authors: K Shankarganesh, V Gowtham & A.H Prakash

Imprint: *Int J Trop Insect Sci* (2026). <https://doi.org/10.1007/s42690-026-01926-z>

Abstract: The cotton stem weevil, *Pempherulus affinis* (Faust) (Coleoptera: Curculionidae), has become an important early-season pest of cotton in India, particularly in the southern states of Tamil Nadu, Andhra Pradesh, and Karnataka. Its increased incidence is associated with shifts in pest dynamics following the adoption of Bt cotton, changes in agronomic practices, and climatic variability. The pest causes damage by boring into the stem, disrupting vascular tissues, and weakening plant growth, resulting in high seedling mortality and yield losses of up to 78.9% under severe infestation. This review synthesises available information on the biology, distribution, host range, damage symptoms, outbreak history, anatomical effects, and economic importance of *P. affinis*. Current management approaches include cultural practices, chemical and biological control measures, host plant resistance, and integrated pest management (IPM) strategies. However, effective control remains constrained by the lack of resistant cultivars, limited availability of registered insecticides, and the pest's concealed feeding habit. Recent research efforts have focused on field surveillance, varietal screening, assessment of Bt Cry toxins, and the development of eco-friendly IPM components. Strengthening systematic monitoring, resistance breeding, and farmer awareness is essential for sustainable management of *P. affinis* in cotton production systems.

Title: Isolation and identification of *Bacillus subtilis* and *Pseudomonas fluorescens* bacteria from cotton plant (*Gossypium hirsutum*) rhizospheric soil and potential use as food waste decomposer

Authors: Om Prakash Jat ^a, Prasanta Das

Imprint: Next Sustainability, Volume 8,2026,100394,ISSN 2949-8236,
<https://doi.org/10.1016/j.nxsust.2026.100394>.
<https://www.sciencedirect.com/science/article/pii/S2949823626001492>)

Abstract: The increasing accumulation of food waste and the environmental concerns associated with its disposal have intensified the search for sustainable and eco-friendly

biodegradation methods. In the present study, a total of thirty samples were collected and analyzed for *Bacillus* and *Pseudomonas* species; the isolated bacteria were identified as *Bacillus subtilis* and *Pseudomonas fluorescens* by a number of biochemical analyses. Soil samples were collected from healthy cotton cultivation fields and subjected to serial dilution and culture techniques using selective nutrient media. Morphological, biochemical, and microscopic analyses were performed for the identification of the bacterial isolates. The isolated strains exhibited characteristic features of *Bacillus subtilis* and *Pseudomonas fluorescens*, including Gram-positive rod-shaped endospore-forming bacteria and Gram-negative fluorescent pigment-producing bacteria, respectively. These bacteria are then applied individually to food waste (container 1 for *Bacillus subtilis*, container 2 for *Pseudomonas fluorescens*, container 3 for both bacteria, container 4 without bacteria). The potential application of these isolates as food waste decomposers was evaluated under laboratory conditions using common organic food waste materials. Both bacterial strains demonstrated significant degradative activity through rapid decomposition of organic substrates, reduction in waste volume, and production of nutrient-rich compost-like material. This study examined the temperature, pH, conductivity, phosphorus, nitrogen, potassium, and Carbon/Nitrogen (i.e. C/N) ratio in containers with and without bacteria. The measurements were taken under three distinct circumstances: on the first day, two weeks later, and four weeks later. Enzymatic activities such as protease, cellulase, and amylase production were also observed. The most efficient and nutrient-rich biofertilizer was found in container 3 out of four container containing a bacterial consortium of *Bacillus subtilis* and *Pseudomonas fluorescens* (1:1) after four weeks of adding bacteria to food waste container material. The findings of this study suggest that rhizospheric bacteria associated with cotton plants possess promising potential for sustainable food waste management and organic waste bioconversion. The utilization of these bacterial strains could provide an environmentally friendly alternative to conventional waste disposal methods while contributing to soil fertility and agricultural sustainability.

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Title: Cotton Plant Disease Prediction using CNN based Deep Learning Framework

Authors: Suganya Devi K; Sekar K; Devendar Rao B; Yuvashree A; Subashini B; Dheepa T

Imprint: 2026 4th International Conference on Integrated Circuits and Communication Systems (ICICACS), Raichur, India, 2026, pp. 1-6, doi: 10.1109/ICICACS68679.2026.11578770.

Abstract: Cotton is a most economically important crop in the globe, which is very vulnerable to fungal, bacterial and viral diseases. These diseases greatly lower productivity and have an impact on income of farmers. Conventional diagnosis techniques rely on manual inspection, which is both labor-intensive and prone to errors,

and cannot be applied on large scales. The paper is a deep learning-based automated cotton plant disease detection system that uses the convolutional Neural Network(CNN) architecture. The model is trained on a selected set of twelve disease classes, both biotic stress and healthy leaves. Normalization, augmentation, and class balancing were preprocessing methods used to increase the generalization. The proposed framework has a 95 percent validation accuracy. The model has an advantage of about 3-5 percent over the baseline CNN networks like VGG16 and ResNet50. The data set comprises of more than 8,000 photographs under twelve classes, which guarantee effective training and testing. Experimental findings corroborate that the system provides dependable and fast inference that can be used in the real world in agriculture. This study shows that deep learning and web technologies could be integrated to enable accuracy agriculture and resource-efficient crop management, especially in environments with limited resources like agriculture.

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Title: Field validation of integrated pest management strategy in Bt cotton (*Gossypium hirsutum*) under farmers' participatory mode in central India

Authors: Ajanta Birah, Licon Kumar Acharya, Mukesh Khokhar, Satish Parsai

Imprint: The Indian Journal of Agricultural Sciences96(01):18-24
DOI: [10.56093/ijas.v96i1.168748](https://doi.org/10.56093/ijas.v96i1.168748)

Abstract: A field study was carried out during rainy (kharif) season of 2022 to 2024 in Khandwa district, Madhya Pradesh to evaluate the performance of Integrated Pest Management (IPM) in Bt cotton (*Gossypium hirsutum* L.) under farmers' participatory mode. The experiment was conducted using a randomised complete block design (RCBD) having three treatments, viz. T1, Integrated Pest Management (IPM); T2, Farmers' Practice (FP); and T3, Untreated Control (UC). IPM packages included timely sowing with refugia, border cropping, cowpea intercropping for natural enemy conservation, neem oil sprays (Azadirachtin 1500 ppm), need-based application of Flonicamid for sucking pests, SPLAT pheromone formulations for pink bollworm management, selective insecticides (spinetoram or emamectin benzoate), and crop termination with residue destruction. IPM fields were compared with Farmers' Practice (FP) and Untreated Control (UC). Data were analysed using ANOVA under a mixed-effect model. IPM adoption significantly reduced pest infestations up to 81% over FP across major pests, accompanied by higher populations of beneficial insects. Pesticide sprays were reduced by 46.55% without yield penalty. Instead, seed cotton yield increased by 25.38%, and net returns improved by more than 56% over FP. IPM strategy proved highly effective in reducing major cotton pests, ecologically safer by enhancing natural enemy population, and significantly lowering pesticide use across three seasons along with high benefit-cost ratio. Scaling this validated strategy through farmer field

schools and improved access to pheromone-based tools can support wider adoption in future throughout the country

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Title: Leveraging Soil Microbiome Diversity for the Management of Highly Virulent Fusarium Wilt (FOV4) in Cotton

Authors: Ilham Laadsi, Mostafa Abdelwahed Abdelrahman, Mauricio Ulloa, Mohamed Fokar, Timothy O Jobe

Imprint: Frontiers in Microbiology

Abstract: Cotton (*Gossypium* spp.) is a globally important crop increasingly threatened by *Fusarium oxysporum* f. sp. *vasinfectum* race 4 (FOV4), a soil-borne pathogen responsible for Fusarium wilt. FOV4 has negatively affected cotton production in California and was confirmed in the far west Texas region of El Paso, TX in 2017, where it has caused similar disruptions. Thus, there is a need for improved disease management and the development of resistant cotton cultivars to maintain agricultural productivity. To understand the relationships among soil properties, fungal communities, and disease incidence, we examined the elemental composition and fungal microbiome of five cotton fields in the lower valley of El Paso, Texas, having varying levels of Fusarium wilt incidence. Comparisons between high Fusarium wilt incidence fields (F1, F2, and F5) and low Fusarium wilt incidence fields (F3 and F4) were performed. Metabarcoding analyses identified marked differences in fungal community composition and diversity between the fields. Alpha diversity metrics indicated higher fungal diversity and evenness in the low Fusarium wilt incidence field F4, suggesting that high fungal diversity contributes to decreased disease incidence. In contrast, high Fusarium wilt incidence fields (F1, F2, and F5) exhibited lower diversity, indicative of a less resilient fungal ecosystem. Beta diversity analyses further confirmed the distinct fungal community composition between soils with contrasting Fusarium wilt incidence. Taxonomic profiling showed that the low Fusarium wilt incidence field F4 harbored beneficial fungal taxa, including *Actinomucor*, *Fusarium* (potentially non-pathogenic species), *Penicillium*, *Preussia*, and *Pseudeurotium*, generally recognized for their contributions to soil health and potential to suppress pathogenic organisms. In contrast, the high Fusarium wilt incidence fields were dominated by genera associated with plant pathogenicity, such as *Alternaria*, *Cladosporium*, and *Stachybotrys*, contributing to the higher disease prevalence observed. These findings underscore the crucial role of fungal diversity and soil chemical composition in influencing the incidence of Fusarium wilt in cotton. Soils with low Fusarium wilt incidence, characterized by diverse and complex fungal communities, may suppress the establishment and proliferation of pathogens. Our results provide insights for

developing targeted soil management practices and enhancing cotton resilience, essential for sustainable disease management strategies and breeding resistant cultivars.

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Title: Genome assembly of *Ramulariopsis gossypii*: a pathogen associated with areolate mildew in cotton (*Gossypium* spp.)

Authors: Beffart Schardong I, Hill R, Patel S, Sharma A, Jimenez-Madrid AM, Avant J, Koebernick J, Bissonnette K, Jones DC, Chee PW. 0.

Imprint: Microbiol Resour Announc 0:e00401-26.

<https://doi.org/10.1128/mra.00401-26>

Abstract: Areolate mildew is a foliar disease of cotton, with two fungal species reported as causal pathogens. We announce the first genome of *Ramulariopsis gossypii*. The genome size is 33.34 Mbp, with an N50 of 2.116 Mb and Benchmarking Universal Single-Copy Orthologs completeness of 98.8%, providing a resource for comparative genomics and disease management.

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Title: Regression And Correlation Analysis Of Morphological Traits In Cotton (*Gossypium Hirsutum* L.) Under Different Salinity Levels

Authors: A. Mamajanov, M. Darmanov, I. Normamatov*, N. Khusenov, R. Mukhammadaliev, V. Kamburova and Z. Buriev

Imprint: SABRAO Journal of Breeding and Genetics 58 (3) 1139-1150, 2026

Abstract: Salinity is one of the major abiotic stresses that considerably and adversely affects cotton growth, development, and seed cotton yield. The relevant study aimed to analyze regression and correlation among the morphological traits of 12 cotton (*Gossypium hirsutum* L.) cultivars exposed to different concentrations of sodium chloride (NaCl). Four levels of NaCl stress (0, 100, 150, and 200 mM) were successful in their application under controlled conditions. The results revealed different levels of salt stress conditions negatively influence cotton traits, particularly the fresh plant weight and shoot length, which showed a decrease of about 50% and 29%, respectively. The dry root weight and root length demonstrated a high degree of stability under salt stress conditions. According to the correlation analysis, plant length and root length appeared as positively correlated with other traits under different mM of NaCl stress conditions. These findings provide useful insights for identifying salt-tolerant cotton genotypes through marker-assisted selection and physiological screening.

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Title: A New Case of Uniparental Chromosome Elimination in an Interspecific Hybrid of Cotton F1 (*Gossypium Hirsutum* L. × *G. Barbadense* L.)

Authors: M.F. Sanamyan, Sh.U. Bobokhujayev, Sh.S. Abdukarimov, And A.B. Rustamov

Imprint: SABRAO Journal of Breeding and Genetics 58 (3) 969-979, 2026
<http://doi.org/10.54910/sabrao2026.58.3.2>

Abstract: Cytogenetic and molecular genetic studies of the cotton haploid describe its morpho-biological features in comparison with the parental genotypes. This research

aimed to study the cotton haploid (2772) spontaneously developed through interspecific crossing of monosomic line Mo15 (*Gossypium hirsutum*) with Pima 3-79 (*G. barbadense*) to create the chromosome-substituted cotton lines. With species incompatibility, selective elimination of chromosomes took place in one of the parental genomes observed in interspecific hybrids. The haploid plant displayed characteristics of a thin and tall stem, dense foliage, shortened internodes, small three-lobed leaves, and complete sterility. In the metaphase I of meiosis, 26 univalents manifested random distribution in the pollen mother cells. The haploid stood out by the complete absence of bivalent formation and presence of unpaired chromosomes in the pollen mother cells. Molecular genetic analysis of the haploid using SSR markers revealed the alleles only from the species *G. hirsutum* in all 26 chromosomes of the haploid genome, which confirmed the selective elimination of chromosomes of the entire paternal genome. The promising results indicated the possibility of using haploid inbreeding by developing doubled haploids (DH).

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Title: Registration of three upland cotton germplasm lines with high levels of seed oil oleic acid and elevated resistance to root-knot and reniform nematodes

Authors: Jay Shockey¹ Jack C. McCarty Jr.² Martin J. Wubben² Michael K. Dowd¹ Jacobs H. Jordan¹ Johnnie N. Jenkins

Imprint: J. Plant Regist. 2026;20:e70058. [wileyonlinelibrary.com/journal/plr2](https://doi.org/10.1002/plr2.70058) 1 of 10
<https://doi.org/10.1002/plr2.70058>

Abstract: Three upland cotton (*Gossypium hirsutum* L.) germplasm lines, USDA-ARSGNLO1 (Reg. no. GP-1171, PI 708333), USDA-ARS-GNLO2 (Reg. no. GP-1172, PI 708334), and USDA-ARS-GNLO3 (Reg. no. GP-1173 PI 708335), containing high seed oil oleic acid and increased resistance to root-knot and reniform plant-parasitic nematodes were developed and released by the USDA-ARS. The stability of the high-oleic acid oil trait was evaluated by examining its effects on plant agronomic performance and seed traits across multiple generations and geographic locations. This trait was originally identified in *G. barbadense* L. accession GB713 (PI 608139) and bred into the upland cotton cultivar Sure-Grow 747 (SG747, PVP 9800118) as part of a nematode resistance breeding program. Starting with the previously analyzed F5 seed, plants producing high oleic acid were selected based on seed oil fatty acid distribution analyses. Plants producing >50% seed oleic acid were analyzed for seed oil content, protein and gossypol levels, fiber properties, and warm germination competency. The three lines consistently produced seed oleate levels >50%, which is triple the 15%–19% observed in standard cottonseed oil and higher than the 33%–35% levels found in previously released ‘HOa’ lines (HOa1–HOa4). Oleate levels in the USDA-ARS-GNLO lines surpassed those of the original *G. barbadense* GB713 parent, suggesting synergistic

effects between gene alleles from the *G. hirsutum* and *G. barbadense* parental genotypes in the new germplasm lines. Oil with this composition should demonstrate competitive deep-fat-frying properties and help extend the shelf life of other food products, such as spreads and salad dressings.

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Title: Bivalent chromatin states and epigenetic priming in cotton: the role of H3K4me3 and H3K27me3 in cold stress memory and resilience

Authors: Mayamiko Masangano, Ahmed Nasre, Ferehewoit Deressegn Lakew, Yohannes Gelaye, Yu Gao, Yuzhi Zhang, Gongye Cheng, Usama Arshad, Lin Ziwei, Li Yang, Meng Kang, Yu Liang, Xiaoyu Cao, Xuehong Song, Chengjun Miao, Bei Liubei, Yan Shihong, Xiaoyu Pei, Xiang Ren, Kunlun He, Abdou Mahaman Mahamadou, Nooney Chidwala, Songjuan Tan, Xingxing Wang, Zhenyu Wang & Xiongfen Ma

Imprint: Epigenetics & Chromatin (2026). <https://doi.org/10.1186/s13072-026-00680-3>

Abstract: Cold stress is a significant challenge to cotton (*Gossypium hirsutum* L.) production during seed emergence and early seedling establishment, as cotton is native to tropical and subtropical environments. Low temperatures during these sensitive stages impair photosynthetic efficiency, damage cellular structures, and reduce yield. Although cotton responses to cold stress have been extensively investigated at physiological, molecular, and transcriptional levels, increasing evidence suggests that transient gene expression changes alone are insufficient to explain sustained stress performance. This review synthesizes current knowledge on cotton cold-stress responses, emphasizing the regulatory roles of key histone modifications histone H3 lysine 4 trimethylation (H3K4me3) and histone H3 lysine 27 trimethylation (H3K27me3) in transcriptional control and within-generation (somatic) epigenetic priming. Although cotton cold epigenome profiling is beginning to emerge, cotton-specific, time-resolved chromatin datasets that span chilling, recovery, and recurrent chilling (stress-recovery- re-stress) remain limited; therefore, several mechanistic inferences necessarily rely on indirect evidence from cotton studies under other conditions and on well-characterized model plant systems. H3K27me3 is implicated in Polycomb-mediated gene silencing and may regulate gene reactivation during cold stress and recovery, whereas H3K4me3 is proposed to support rapid induction of cold-responsive genes. Bivalent chromatin domains containing H3K4me3 and H3K27me3 may maintain stress-related genes in a poised transcriptional state, enabling swift activation while preserving developmental regulation. We highlight key knowledge gaps and experimental priorities for establishing cotton-specific chromatin mechanisms of cold memory and for translating these insights into epigenome-assisted breeding and biotechnological strategies to develop cotton varieties with improved and stable cold resilience.

Title: Integrative transcriptomic and epigenomic analyses reveal *GhERF114* as a negative regulator of drought and salt stress tolerance in cotton

Authors: Qiankun Liu, Yanfang Li, Muhammad Jawad Umer, Yuqing Hou a, Aiming Zhang , Xue Du, Yongqing Zhao, Yiman Liu, Yulin Liu, Yangyang Wei, Quanwei Lu, Jie Zheng, Xiaoyan Cai , Zhongli Zhou , Pengtao Li, Fang Liu , Renhai Peng

Imprint: Industrial Crops and Products

Date: 1 April 2026

Article: 123063

Volume: Volume 243

Abstract: Abiotic stresses such as salt and drought severely impair cotton (*Gossypium hirsutum*) productivity by disrupting photosynthesis, growth, and fiber development. Although transcription factors (TFs) are key regulators in the process of abiotic stress adaptation, their specific roles in cotton remain not fully elucidated. Here, we integrated transcriptomic and CUT&Tag analyses to identify *GhERF114*, an AP2/ERF family transcription factor, as a key negative regulator of drought and salt tolerance. *GhERF114* is highly expressed in roots and rapidly induced by salt stress. The functional validation results in cotton using virus-induced gene silencing (VIGS) technology demonstrated that *GhERF114*-silenced plants exhibited enhanced stress resistance, maintaining higher chlorophyll content, relative leaf water content (RLWC), and antioxidant enzyme activity, while accumulating less malondialdehyde and reactive oxygen species (ROS). In contrast, overexpressing *GhERF114* in *Arabidopsis* leads to its hypersensitivity to salt and drought, accompanied by severe wilting, elevated ROS, and weakened antioxidant defenses. Comprehensive metabolomic profiling further revealed that *GhERF114* overexpression disrupted lipid and carbohydrate metabolism under salt stress, reducing metabolites involved in galactose, fructose, and mannose pathways. This metabolic imbalance likely compromises osmotic adjustment and energy homeostasis, aligning with the reduced stress tolerance phenotype. Collectively, these findings demonstrate that *GhERF114* impairs abiotic stress resilience by suppressing ROS scavenging capacity and perturbing key metabolic and hormonal signaling pathways. This study identifies *GhERF114* as a negative regulator of tolerance to salt stress and drought stress, and provides a potential molecular target for enhancing cotton stress resilience through breeding.

Title: Detection of quantitative trait nucleotides (QTNs) and QTN-by-QTN interactions (QQIs) for seed-cotton yield in upland cotton (*Gossypium hirsutum* L.)

Authors: Haihong Zhao, Jianan Li, Jinjing Liu, Mengyuan Li, Nunu Sun, Hui Sun, Chengguang Dong, Yuanyuan Wang & Chengqi Li

Imprint: *Euphytica* 222, 48 (2026). <https://doi.org/10.1007/s10681-026-03699-5>

Abstract: Seed-cotton yield (SCY) is one of the key yield traits and primary breeding targets in cotton. Numerous quantitative trait loci (QTLs) have been identified; however, there are few reports on interactions between QTLs. In this study, a genome-wide association study (GWAS) was performed on 312 upland cotton (*Gossypium hirsutum* L.) accessions by using the CottonSNP80K array. Four GWAS methods, GEMMA-LM, GEMMA-LMM, EMMAX, and FaST-LMM, were employed to identify quantitative trait nucleotides (QTNs) associated with SCY using the best linear unbiased predictors, while the 3VmrMLM method was used to detect QTN-by-QTN interactions (QQIs). The results of the phenotypic analysis showed that SCY exhibited a wide and continuous variation across five environments. The genotypic variance, environmental variance, and genotype-environment interaction variance all reached highly significant levels. Genotyping resulted in 47,894 polymorphic single nucleotide polymorphism markers, dividing the upland cotton accessions into two subpopulations. The four GWAS methods detected 15 significant QTNs, including nine stable QTNs identified by at least three methods. Single-marker/haplotype analysis confirmed that these nine QTNs collectively constituted three novel QTLs: *qSY-D03* (TM53448/TM53452/TM53454/TM53460), *qSY-D10* (TM74930), and *qSY-D12* (TM78919/TM78920/TM78921/TM78922). Gene Ontology enrichment analysis revealed 25 non-redundant candidate genes related to SCY. Further in-silico analysis of RNA-seq data from upland cotton TM-1 indicated that six genes exhibited high expression levels in ovules during specific developmental stages. Additionally, 21 QQIs were detected, including two significant and 19 suggestive interactions, leading to prediction of five pairs of protein-protein interactions involving four QQIs and five gene pairs. This study provides novel insights into the genetic architecture of SCY in upland cotton. The identified QTNs/QTLs and QQIs offer valuable genetic resources for future studies.

Title: Characterization of phytosulfokine peptide family in cotton and its role in cold stress response

Authors: [Shuaiqi Lu](#), [Julan Yang](#), [Yuguo Li](#) & [Fei Xiao](#)

Abstract: Phytosulfokines (PSKs) are plant-secreted peptides that undergo post-translational modifications and play essential roles in regulating plant development, immune responses, and regeneration. However, their presence and functional roles in cotton remain largely unexplored, particularly regarding their involvement in stress responses. In this study, we identified 28, 31, 15, and 15 *PSK* genes in tetraploid *Gossypium hirsutum* (*G. hirsutum*) and *Gossypium barbadense* (*G. barbadense*), as well as diploid *Gossypium arboreum* (*G. arboreum*) and *Gossypium raimondii* (*G. raimondii*), respectively. Phylogenetic analysis classified these cotton *PSK* genes into three distinct subgroups. A comprehensive investigation was conducted on protein characteristics, gene structure, conserved motifs, chromosomal localization, cis-regulatory elements, and expression patterns of the cotton *PSK* gene family. Collinearity analysis suggested that whole-genome duplication (WGD) events have played a pivotal role in the expansion and diversification of *PSK* genes in cotton. Furthermore, virus-induced gene silencing (VIGS) of *GhPSK22* and *GhPSK25* under cold stress revealed that these genes function as positive regulators in the cold stress response. Exogenous application of the mature *PSK*- α peptide, derived from *GhPSK* precursors, significantly enhanced cold tolerance in cotton. Transcriptome and qRT-PCR analyses further demonstrated that *PSK*- α modulates genes involved in DNA-binding transcription factor activity, Plant hormone signal transduction and the MAPK cascade, thereby enhancing cold tolerance in *G. hirsutum*. Collectively, our findings provide the first comprehensive genome-wide analysis of the *PSK* gene family in cotton, revealing that whole-genome duplication contributed to its expansion. Functional characterization demonstrates that *GhPSK22* and *GhPSK25*, along with exogenous *PSK*- α application, enhance cold tolerance by activating transcription factors, hormone signaling, and the MAPK cascade. These results suggest the promising potential of *PSK*- α as an environmentally friendly biostimulant to enhance cold resistance in cotton and possibly other crops under field conditions.

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Title: Economically important Malvaceae species in India: diversity, distribution and utilization

Authors: Bhagwati Prashad Sharma¹ , Arti Sharma² , Arti Khanduri³ , Ishan Acharya⁴ , Sanjeet Kumar⁵ and Sugimani Marndi

Imprint: Mallow Family: Medicinal, Ecological and Economical Aspects; ISBN: 978-81-999177-3-6; 2026

Abstract: Malvaceae includes numerous economically important species that support agriculture, industry, traditional medicine, horticulture and rural livelihoods in India. Present study documented 13 economically valuable species belonging to eight genera based on published scientific literature. These species are utilized for fibre, food, medicine, timber, fodder, ornamental purposes and natural dyes. Fibre crops, particularly *Gossypium* spp., *Corchorus* spp., and *Hibiscus cannabinus*, dominate the textile sector, while *Abelmoschus esculentus* and *Hibiscus sabdariffa* contribute to food security. The review highlighted the importance of Malvaceae in sustainable agriculture, biodiversity conservation, industrial development, and India's growing bioeconomy

PLANT BIOTECHNOLOGY

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Title: Biochemical and molecular response of heavy metals phytoremediation in cotton genotypes

Authors: Abdulsamad H. Noaman , Mohammed Hamdan Al-Issawi , Anas Ibrahim Hasan ,Yas Ameen Mohammed & Zbynek Polesny

Imprint: *International Journal of Phytoremediation*, 1-11.
<https://doi.org/10.1080/15226514.2026.2695200>

Abstract: Heavy metal pollution is major environmental and public health concern because of the widespread toxicity of metals such as Cd and Pb. Using cotton crops for phytoremediation offers sustainable and environmental solution to heavy metal pollution. A pot experiment was conducted to evaluate the phytoremediation capability of six cotton genotypes for their phytoremediation capability, including Cocker310, Lachata, Pak-Cot, Montana, Spearo888, and W888, exposed to Cd (450 mg kg⁻¹) and Pb (1350 mg kg⁻¹) stresses. To achieve this, morphological, biochemical, and molecular evaluation has been made. The results highlighted genotype-dependent variation in response to heavy metal stress. Cocker310, Lachata, and Montana genotypes have relative tolerance to Cd and Pb stress. While W888, Spearo 888, and Pak-Cot showed considerable growth reduction, suggesting higher metabolic reduction associated with detoxification. The antioxidant system was enhanced to contribute to oxidative stress amelioration. The analysis of phytoremediation analysis indicated that Cd mobility and removal were higher in comparison with Pb. Cocker310, W888, and Spearo888 showed

superior Cd accumulation, while Cocker310 showed enhanced Pb removal and translocation. The upregulated expression of *GhHMA1* is related to heavy metal translocation, while *PCS1* expression is involved in intracellular sequestration. In conclusion, selecting suitable genotypes can enhance phytoremediation in contaminated environments.

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Title: Systematic characterization of purple acid phosphatases provides targets for improving phosphorus use efficiency in cotton

Authors: Asif Iqbal, Zhou Junyan, Inam Ullah, Tariq Mahmood, Syed Tanveer Shah, Mazhar Iqbal, Atif Raja, Song Meizhen & Dong Qiang

Imprint *Funct Integr Genomics* 26, 179 (2026). <https://doi.org/10.1007/s10142-026-01964-3>
Funct Integr Genomics 26, 179 (2026). <https://doi.org/10.1007/s10142-026-01964-3>

Abstract: Purple acid phosphatase (PAP) genes are central to plant phosphorus metabolism and stress adaptation. However, their genome-wide characterization and functional roles in cotton remain unclear. Cotton often faces phosphorus limitation, affecting growth and fiber yield. In this study, we performed a comprehensive genome-wide analysis of *PAP* genes in four cotton species to elucidate their evolutionary patterns and potential roles in phosphorus use efficiency, stress response, and fiber development. A total of 202 PAP encoded proteins were identified, with 63 in *G. hirsutum*, 69 in *G. barbadense*, 35 each in *G. arboreum*, and *G. raimondii*, which were classified into eight conserved subgroups. Gene structure, motif composition, and phylogenetic analysis revealed strong evolutionary conservation with evidence of subfunctionalization. Chromosomal mapping, collinearity, and Ka/Ks analysis indicated that segmental and whole-genome duplications primarily drove *PAP* expansion, with most genes retained under purifying selection. Promoter analysis uncovered abundant cis-elements associated with stress and hormone responses, suggesting tight transcriptional regulation under developmental and experimental cues. Expression profiling revealed tissue-specific and Pi-responsive regulation, highlighting the involvement of PAPs in root Pi acquisition, reproductive growth, and fiber development. Co-expression analysis further identified key hub genes, regulating vegetative growth (*Gh_A13G1171*), reproduction (*Gh_D05G1806*), fiber development (*Gh_D05G0522*), and P metabolism (*Gh_A03G0451*). Collectively, this study provides the first systematic characterization of the cotton PAP gene family, offering new insights into their evolutionary dynamics and functional roles, and identifies promising genetic targets for improving P use efficiency and stress resilience in cotton.

Title: Combined genome and transcriptome analysis of boll weight and lint percentage traits in *Gossypium barbadense*

Authors: Xiaohui Song, Yonglin Tan, Guozhong Zhu, Xiujuan Su, Xiaoguang Shang & Wangzhen Guo

Imprint: *Theor Appl Genet* 139, 193 (2026). <https://doi.org/10.1007/s00122-026-05307-5>

Abstract: Compared to *Gossypium hirsutum*, *G. barbadense* exhibits superior fiber quality but relatively lower fiber yield. Exploring the genetic basis of yield-related traits could facilitate yield improvement in *G. barbadense*. Here, we conducted a genome-wide association study (GWAS) on two yield components, boll weight and lint percentage, using 246 *G. barbadense* accessions. We identified a total of 272 main-effect quantitative trait loci (qtls) and 34 QTL-by-environment interaction loci (qtLEs) for these traits, among which 57 qtls and 3 qtLEs overlapped with previously reported loci. To explore the potential mechanism between yield and fiber quality, we extracted the genes located within these loci and compared their expression patterns between *G. barbadense* accessions with extreme differences in fiber quality or yield traits. Gene ontology analysis of differentially expressed genes revealed that sugar- and hormone-related genes were antagonistically expressed during the later stages of fiber development, correlating with high yield and superior fiber quality, respectively. Local association analysis further identified 67 candidate genes associated with the two yield components, 20 of which were located within two introgression segments (ISs) from *G. hirsutum* into *G. barbadense*. Among them, A10-1-Y IS reduced the yield of *G. barbadense*, while D08-1-Y IS increased the yield of *G. barbadense*. Finally, we demonstrated that two haplotypes of the gene *GB_A06G0815* (encoding beta-galactosidase 1), *GB_A06G0815^c* and *GB_A06G0815⁻*, with a 1-bp insertion/deletion of C/- in the 10th exon, were significantly associated with fiber yield. Overexpression of *GB_A06G0815^c* in *Arabidopsis* resulted in longer roots, larger leaves, higher yield, and more vigorous growth and development compared to the control. Our findings provide novel insight into the negative correlation between fiber quality and yield traits and offer potential genetic loci for high-yield breeding in *G. barbadense*.

Title: Assessment of Cotton Wilt Incidence and in Vitro Evaluation of Botanical Extracts and Biocontrol Agents against, Fusarium, Hanumangarh District, Rajasthan, India

Authors: Mohd Aftab Alam , Ramesh Singh

Imprint: *Asian Journal of Microbiology and Biotechnology*, 2026, 11 (2), pp.66-72.

Abstract: Cotton (*Gossypium* spp.) is an important fibre crop, but its production is constrained by Fusarium wilt. The present study assessed the influence of sowing date on wilt incidence and evaluated selected botanical extracts and biocontrol agents against the pathogen under in vitro conditions. Field experiments were conducted at the Agricultural Field Research Centre, Hanumangarh, Rajasthan, during Kharif 2023–24 and 2024–25 in a randomised block design with three replications. Cotton was sown on five dates from 1 June to 29 June, and disease incidence was recorded at 15 days after first symptom appearance, 30 days after symptom appearance, and maturity. Early sowing reduced wilt incidence in both years. The 1 June sowing recorded the lowest mean disease incidence of 8.75%, 14.90%, and 23.30% at the respective stages, whereas the 29 June sowing recorded the highest mean incidence of 34.55%, 53.15%, and 74.00%. The inhibitory effect of six botanical extracts was tested at 2.5%, 5.0%, and 7.5% concentrations using the poisoned food technique. Neem showed the highest inhibition of mycelial growth, with 68.51%, 73.70%, and 79.63% inhibition at the respective concentrations, followed by tulsi with 64.44%, 70.37%, and 76.30% inhibition. Among the biocontrol agents, *Trichoderma harzianum* produced the highest inhibition of 85.19% at 5% culture filtrate concentration, followed by *Trichoderma viride* with 82.96% inhibition. The results indicate that early sowing, neem extract, and effective *Trichoderma* spp. may contribute to integrated management of Fusarium wilt in cotton.

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Title: Biotechnological Enhancement of Cotton Resistance Against Whitefly and Cotton Leaf Curl Virus in Sindh Agroecosystems

Authors: Sheraz Amjad, Nadia Jabeen, Aliya Farman, Kainat Fatima, Aliya, Ayesha Javed

Imprint: Research Consortium Archive, Vol.4 No.2 2026

Abstract: Cotton cultivation in Sindh agroecosystems faces severe threats from a destructive, multi-trophic pest-pathogen complex driven by the phloem-feeding whitefly (*Bemisia tabaci*) and the whitefly-transmitted Cotton Leaf Curl Virus (CLCuV). Intensive reliance on chemical insecticides has escalated production costs, eliminated beneficial natural predators, and catalyzed rapid insecticide resistance in local vector populations. This comprehensive review article evaluates the critical limitations of conventional plant breeding, characterizes the complex tripartite interactions governing pathogen-vector-host dynamics, and assesses the deployment of advanced genetic engineering and biotechnological tools to safeguard cotton crops. It highlights how upland cotton (*Gossypium hirsutum*) inherently lacks durable resistance genes, whereas diploid "Old World" cotton (*Gossypium arboreum*) possesses physical and

biochemical defenses such as dense trichomes and waxy cuticles that are structurally restricted from traditional cross-breeding due to strong hybridization barriers. To overcome these constraints, modern biotechnology offers highly precise alternatives. We examine the mechanism of post-transcriptional gene silencing via RNA interference (RNAi) constructs targeting the viral AC1 and β C1 genes to arrest systemic replication. Furthermore, we analyze the integration of multiplexed CRISPR/Cas9 and Cas12a genome-editing platforms designed to target several viral and satellite loci concurrently, which successfully suppresses the evolution of viable escape mutants. Finally, we review the transgenic expression of insecticidal plant lectins including *Allium sativum* leaf agglutinin (ASAL) driven by phloem-specific promoters to disrupt vector survival. Collectively, integrating these modern biotechnological innovations within Pakistan's evolving biosafety framework provides a sustainable pathway toward durable, engineered resistance against this devastating disease complex.

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Title: Polarimetric Scattering Angle Simulation (SAS) for Cotton and Maize Extent Mapping Using Dual Pol SAR Data

Authors: Harine Karthikeyan; Shoba Periasamy; Narmatha Balachandar Gani; Sabreen Sadhak

Imprint: Conference Proceedings: 2026 IEEE Mediterranean and Middle-East Geoscience and Remote Sensing Symposium (M2GARSS)

Abstract: This study presents a Scattering Angle Simulation (SAS) approach for mapping the extent of cotton and maize crops using multi-temporal Sentinel-1 data. The temporal backscatter profiles were examined to identify the characteristic 'peak-dippeak' signatures typically associated with the phenological development of cotton and maize. Cotton exhibited a narrow VV dip and smaller angular spread, while maize showed a broader dip and larger scattering angles due to higher volumetric scattering.

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Title: Identification and Expression Analysis of the *MLO* Gene Family Under Salt Stress in Cotton (*Gossypium hirsutum* L.)

Authors: Cong-Hua Feng, Junbo Zhen, Linlin Liu, Mengzhe Li, Mengmeng Jiang, Di Liu and Jina Chi

Imprint: *Life* 2026, 16(3), 476; <https://doi.org/10.3390/life16030476>

Abstract: MLO (Mildew Resistance Locus O) genes encode seven-transmembrane proteins that function as critical regulators of powdery mildew resistance and abiotic stress responses. Despite their established importance, the *MLO* gene family in *Gossypium hirsutum* L. has not been systematically investigated under salt stress conditions. Here, we performed genome-wide identification of 46 *GhMLO* members using Hidden Markov Model and BLAST searches based on the latest cotton genome assembly. Phylogenetic analysis classified these genes into four distinct subfamilies. Transmembrane topology and conserved domain analyses revealed that all *GhMLO* proteins contain typical MLO domains and transmembrane structures, maintaining high structural similarity with dicotyledonous model plants. Synteny analysis demonstrated that the expansion of the *GhMLO* family was primarily driven by segmental and tandem duplications. Integration of transcriptomic data from the COTTONOMICS database revealed tissue-specific expression patterns, with higher transcript abundance in receptacles, stems, and roots, but lower levels in stamens and petals. Salt, drought, and cold stress treatments induced upregulation of *GhMLO* family members, with most genes showing increased expression over time. RT-qPCR analysis validated that five candidate *GhMLO* genes were significantly upregulated under salt stress. In summary, this study provides a comprehensive genome-wide characterization of the *GhMLO* gene family, elucidating their phylogenetic relationships and expression dynamics, which establishes a theoretical basis for identifying key regulatory genes involved in abiotic stress responses and offers novel genetic resources for improving stress tolerance in cotton molecular breeding.

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Title: H3K27me3-mediated chromatin remodelling governs salt tolerance in cotton via Na^+/K^+ homeostasis modulation

Authors: Wei Liu, Zhiqiang Zhang, Qiying Du, Jianing Li, Liuqi Yang, Zhongying Ren, Jiameng Guo, Wei Zhu, Zongbin Ma, Yang Zhou, [Wei Li](#)

Imprint: [Journal of Advanced Research](#), <https://doi.org/10.1016/j.jare.2026.03.027>

Abstract: Introduction: Histone modifications are among the key epigenetic regulators of gene expression in plants under abiotic stress, particularly in modulating stress responses by activating or repressing specific genes. Nevertheless, the epigenetic basis of the salt stress response in cotton remains largely unknown, despite its comparative salt tolerance.

Objectives: This study aimed to decode the genome-wide histone H3 lysine 27 trimethylation (H3K27me3) regulatory landscape in cotton under salt stress, establish the relationship between H3K27me3 dynamics and stress resilience, and identify epigenetically controlled target genes with breeding potential.

Methods: Cleavage under targets and tagmentation (CUT&Tag) and RNA sequencing (RNA-Seq) were employed to profile the genome-wide distribution of H3K27me3 and its associated gene expression changes in cotton roots under salt stress. Exogenous application of the H3K27me3 inhibitor RDS 3434 was used to assess its impact on H3K27me3 levels and salt tolerance. Virus-induced gene silencing (VIGS) was employed to validate candidate genes regulated by H3K27me3 under salt stress.

Results: Salt stress significantly reduced H3K27me3 levels in cotton roots, and RDS 3434 treatment further decreased H3K27me3 deposition while enhancing salt tolerance. Genome-wide analysis revealed the expression of 36 genes was negatively correlated with H3K27me3 levels under salt stress. VIGS experiments verified two key genes, GhNCED3 and GhTIFY9, whose H3K27me3 levels were down-regulated and expression levels up-regulated under salt stress, positively contributing to salt tolerance by modulating reactive oxygen species (ROS) accumulation and Na⁺/K⁺ balance in cotton seedlings.

Conclusion: This study provides evidence for the critical role of H3K27me3 in modulating gene expression for salt tolerance in cotton. The findings highlight the epigenetic regulation of salt tolerance and identify GhNCED3 and GhTIFY9 as promising candidates for developing salt-tolerant cotton cultivars. These insights advance our understanding of H3K27me3-mediated epigenetic regulation of abiotic stress adaptation in plants and provide a foundation for future crop improvement strategies.

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Title: A Natural LTR Retrotransposon Insertion in the Promoter of GhNAC140-Dt Boosts Cotton Lint Yield

Authors: Yujia Yu^{1,2,3} | Xiaoguang Shang^{1,2,3} | Haitang Wang^{1,2,3} | Lijie Zhu^{1,2} | Xu Han^{1,2} | Qingfei He^{1,2} | Weixi Li^{1,2} | Yonglin Tan^{1,2} | Guozhong Zhu^{1,2,3} | Wangzhen Guo

Imprint: Plant Biotechnology Journal, 2026; 24:4240–4262
<https://doi.org/10.1111/pbi.70639>

Abstract: Transposable elements (TEs) are fundamental drivers of crop evolution and domestication. Whereas the underlying mechanisms of TE-mediated gene activation remain poorly understood. Lint percentage is an important yield component in cotton. Here, we report a retrotransposon insertion in the promoter of GhNAC140-Dt, a secondary wall NAC encoding gene, to promote the lint production by elevating its expression. We confirm that a 60bp core cis-regulatory module within the TE's LTR (long terminal repeat) specifically recruits the transcription factor GhMYB46 and

increases downstream genes' expression. GhNAC140-Dt overexpression activates the expressions of secondary cell wall development related genes, including GhCESA4-Dt, GhCESA4-At, and GhCOBL9-At, promotes cellulose deposition, and enhances lint percentage. This retrotransposon insertion massively emerges on the domestication transition from *Gossypium hirsutum* races to cultivated cotton accessions, with >80% fixation in modern cultivars. This work deepens our understanding of TE-mediated gene activation; it also provides direct molecular evidence for “transposon-driven yield evolution” in crop domestication.

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Title: Somatic embryogenesis in Egyptian extra-long staple cotton cultivar Giza 96

Authors: Hagar M. Abbad & Ahmed El-Bakry

Imprint: *Discov. Plants* 3, 273 (2026). <https://doi.org/10.1007/s44372-026-00725-7>

Abstract: Egyptian Giza cotton cultivars are known worldwide for their high quality long and extra-long staple. The application of biotechnology to Giza cottons has not been explored to-date. Giza 96, an extra-long staple cultivar (ELS), has been selected to establish somatic embryogenesis and to determine factors necessary for successful regeneration. Naphthalene acetic acid (NAA) and 2,4-dichlorophenoxyacetic acid (2,4-D) at concentrations of 0.1–1.0 mg L⁻¹, in addition to benzyl adenine (BA) at 0.5 mg L⁻¹ were used to screen the frequency of somatic embryo induction. The highest induction frequency was 100% and 87.5% on media containing 0.25 mg L⁻¹ NAA + 0.5 mg L⁻¹ BA and on 1.0 mg L⁻¹ NAA + 0.1 mg L⁻¹ 2,4-D + 0.5 mg L⁻¹ BA respectively. Explants with healthy embryos were transferred onto media containing different cytokinins BA, kinetin (K) and meta-Topolin (mTp) at concentrations of 0.25–0.1 mg L⁻¹ for further embryo growth and maturation. The highest number of embryos was 224.92 ± 23.83 and 189.17 ± 35.93 on media containing a combination of NAA, BA, kinetin, and mTp, at a concentration of 0.25 mg L⁻¹ for NAA and at 2 different concentrations of cytokinins 0.5 and 0.25 mg L⁻¹ respectively. Explant tissue with normally developing embryos were inoculated into liquid media of the same composition adding 2 sugar concentration treatments of 3% and 4.5%. Suspension cultures of different treatments produced profuse embryos at different developmental stages up to the tulip shape. This research presents the first study towards achieving efficient regeneration of the ELS Egyptian cotton cultivars germplasm. Key embryo induction and growth factors reaching the tulip-shaped embryos were identified. Future research is needed to achieve embryo maturation and germination leading to full regeneration of plants, thus laying the foundation for applying biotechnology towards the improvement of Egyptian Giza cotton germplasm.

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Title: Assessment of Some Antioxidant, Phytochemical, Antinutritional, And Nutritional Properties of Cottonseed

Authors: Lawal Nura; A. S. Idoko; M. M. Ibn-Shuaib; & Zainab Mohammed Bonomi

Imprint: Journal of Health, Metabolism & Nutrition Studies (Jhmns) Vol. 12 No. 3

Abstract: Cottonseed, a by-product of cotton fibre production, remains largely underutilized despite its rich nutritional and bioactive composition. This study investigated the phytochemical profile, antioxidant potential, nutritional composition, and antinutritional factors of cottonseed using standard analytical procedures. Qualitative and quantitative phytochemical analyses revealed appreciable levels of alkaloids, flavonoids, tannins, and saponins. Antioxidant activity assessed using 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging and total phenolic content (TPC) assays showed strong, concentration-dependent antioxidant activity with a low IC₅₀ value of 7.6 mg/mL. Proximate analysis indicated that cottonseed is rich in protein (23.80 ± 0.30%), fat (21.20 ± 0.40%), and dietary fibre (14.80 ± 0.40%). Although antinutritional factors such as phytates (15.15 ± 0.28 mg/100g) and oxalates (3.58 ± 0.12 mg/100g) were present, their concentrations were within acceptable limits. These findings suggest that cottonseed possesses significant functional, nutritional, and antioxidant potential and may serve as a valuable ingredient in functional foods and nutraceutical formulations

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Title: Integrated Transcriptome and Metabolome Analysis Elucidates the Regulatory Networks of Salt Stress Response During Cotton Seed Germination

Authors: Yutao Guo, Li Tian, Shaoyu Cheng, Xiang Ren and Xianliang Zhang

Imprint: *Genes* 2026, 17(7), 761; <https://doi.org/10.3390/genes17070761>

Abstract: Background/Objectives: Soil salinization constitutes a critical threat to global agriculture, with cotton (*Gossypium* spp.) being highly susceptible. This abiotic stress most severely impacts cotton during the early sowing and seedling stages,

compromising stand establishment and early growth. Manifestations of this stress include reduced germination rates, uneven emergence, stunted seedlings, and, ultimately, diminished boll set and fiber yield. Methods: To investigate the molecular basis of salt tolerance in cotton seed germination, we performed integrated transcriptomic and metabolomic profiling of *Gossypium hirsutum* cv. ST022-1056m5 under 150 mM NaCl stress at 24 h, 48 h, and 72 h, finding that salt stress significantly inhibited germination. Differentially expressed genes (DEGs) and differentially accumulated metabolites (DAMs) were identified, followed by functional enrichment and Weighted Gene Co-expression Network Analysis (WGCNA) to construct regulatory networks. Results: Transcriptomics revealed stage-specific differentially expressed genes, with predominant downregulation and enrichment in catalytic/transporter activities. Metabolomics showed distinct reprogramming, with 210 shared differentially accumulated metabolites enriched in lipids, organic acids, terpenoids, and phenolic acids. KEGG analysis highlighted time-dependent pathway shifts: sucrose metabolism and MAPK signaling at 24 h, photosynthesis at 48 h, and cuticular lipid biosynthesis at 72 h. Weighted Gene Co-expression Network Analysis (WGCNA) identified stage-associated modules and hub genes (*GH_A02G0892*, *GH_A08G2853*), and multi-omics integration indicated the strongest transcript-metabolite coordination at 24 h. Conclusion: Our study reveals dynamic molecular reprogramming underpinning stage-specific salt adaptation in germinating cotton seeds. These identified DEGs, DAMs, and hub genes represent promising candidate targets for molecular breeding and offer a crucial genetic basis for improving salt tolerance in cotton.

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Title: Factors Affecting the Quality of Cottonseed Oil

Authors: Matrasulova Nazokat Ismailovna

Imprint: Международный научный журнал № 32 (100), часть 1

«Научный Фокус» Январь, 2026

Abstract: This article provides information on the composition of cottonseed oil and its storage conditions. The primary uses of cottonseed oil are food related; it is used as salad oil, for frying, in margarine manufacture, and for manufacturing shortenings used in cakes and biscuits

Title: Systems-level proteomic models of cotton fiber development: a high-resolution data resource to analyze cell dynamics and trait engineering

Authors: Youngwoo Lee , Pengcheng Yang , Heena Rani , Gideon Miller , Sivakumar Swaminathan , Corrinne E Grover , Jonathan F Wendel , Olga A Zabolina , Jun Xie , Daniel B Szymanski

Imprint: Plant Physiology, Volume 201, Issue 3, July 2026, kiag318, <https://doi.org/10.1093/plphys/kiag318>

Abstract: The shapes and material properties of cotton (*Gossypium* spp.) seed coat trichoblasts form the basis of a multibillion-dollar natural fiber industry. As such, these highly specialized cells are low-hanging fruit for intentional trait engineering. However, broad success will require more mechanistic knowledge of their systems-level cellular controls. This time-series study integrates daily measurements of purified fiber transcriptomes and proteomes with multiscale fiber phenotyping datasets that span the same developmental interval. Abundance profiles of the subcellular proteomes are the foundation of the analyses. This resource article provides direct information about which homoeologs operate and offers informative depictions of how compartmentalized cellular systems change during developmental transitions. Prediction accuracy was partially validated by analyzing protein expression group 11, which contained multiple known secondary cell wall (CW) cellulose synthases together with dozens of unknown proteins, and displayed an averaged expression profile that strongly correlated with a sharp state transition in cellulose microfibril alignment and increased cellulose content. The dataset as a whole can serve as a hypothesis-generating tool to guide future experiments related to CW glycome remodeling, morphogenesis, reversible tissue formation, and growth rate control. Integration of mRNA and protein abundance revealed widespread evidence of post-transcriptional control. In addition, there were hundreds of transcriptionally controlled genes with different time points of transition. This latter gene set can be used to more reliably analyze transcriptional control networks and to generate collections of gene expression drivers for cotton fiber research. The protein and transcript abundance profiles are organized into user-friendly tables and a web interface that can be searched using any plant ortholog of interest based on developmental time, abundance, annotations, or phenotypic association.

Title: *GhFIR_A08*: An uncharacterized regulator promotes cotton fiber initiation by integrating into a GhWRKY16-GhRL6 transcriptional hierarchy

Authors: Yuanxue Li, Chao Fu, Yuhuan Xiao, Nian Wang, Ying Liu, Yu Le, Meilin Chen, Xianlong Zhang, Zhongxu Lin

Imprint: Journal of Advanced Research (2026), doi: <https://doi.org/10.1016/j.jare.2026.07.030>

Abstract: Introduction - Cotton is an important global economic crop, and enhancing yield remains a primary breeding objective. Fiber development is controlled by a complex regulatory network, with the initiation stage being pivotal because it determines fiber number and ultimately yield. However, most studies have focused on upstream transcription factors, leaving downstream functional genes largely uncharacterized.

Objectives - To explore the gene function and regulatory network of the unannotated gene *GhFIR_A08* (Fiber Initiation Regulator on chromosome A08), which was identified based on previous structural-variant analyses and highly expressed during fiber initiation.

Methods - Currently high-quality *Gossypium* genome assemblies were compared to investigate the origin of the *FIRs* gene family and the mechanism of transposon-mediated copy number variation. Gene function was evaluated by generating stable homozygous transgenic lines (both knockout and overexpression) in the recipient backgrounds. Interacting proteins were screened and verified by MBP pull-down combined with mass spectrometry, yeast two-hybrid, bimolecular fluorescence complementation, and pull-down assays. The regulatory network was explored by yeast one-hybrid, dual-luciferase reporter, electrophoretic mobility shift assays, RNA-seq, and measurements of related metabolites.

Results - Alongside the evolutionary origin and polyploidization-driven expansion of this gene family in *Gossypium*, a transposon-mediated, haplotype-specific loss of *GhFIR_A08* was uncovered. Overexpressing *GhFIR_A08* increased the number of ovule protrusions and enhanced lint percentage (LP), whereas knockout produced the opposite phenotype. An upstream regulatory hierarchy was further uncovered in which *GhWRKY16* induces another activator, *GhRL6*; both *GhWRKY16* and *GhRL6* bind the respective sites of *GhFIR_A08* promoter, forming a coherent GhWRKY16-GhRL6-*GhFIR_A08* module to activate *GhFIR_A08*. Functionally, *GhFIR_A08* cooperates with Gh14-3-3, GhHSP70, GhSPL13, and GhPPR to regulate cotton fiber initiation by modulating hormone signaling, protein homeostasis, and redox processes.

Conclusion - The uncharacterized gene, *GhFIR_A08* is revealed to positively regulate fiber initiation to increase LP, and provides valuable genetic resources for molecular breeding aimed at improving cotton yield.