



GLEANINGS IN COTTON RESEARCH

SEPTEMBER 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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Title: Effect of foliar application of different hydrogen peroxide concentrations on the biochemical traits of several cotton cultivars

Authors: Baker T. Hassan^{1*}, Waleed A. T. El-Fahdawi²

Imprint: Euphrates Journal of Agricultural Science-18 (2):2057-2068, (june.2026)

Abstract: A field trial implemented during the 2025 growing season at the first research station of the College of Agriculture, University of Anbar. to evaluate the effect of foliar application of hydrogen peroxide at different concentrations on selected biochemical traits of several cotton cultivars. The trial followed a randomized complete block design (RCBD) with split-plot arrangement. Three concentrations of hydrogen peroxide: 0, 50, and 75 mg/L allocated to the main plot. The sub-plots contained five cotton genotypes: W888, Coker 310, Montana, Lashata, and Spiro. The results showed that plants of the Lashata variety showed the highest catalase enzyme activity. They also had the highest leaf MDA content, SOD enzyme activity, proline acid concentration, and relative water content. These values reached 39.56 absorbance units/min/g fresh weight, 19.10 $\mu\text{mol/g}$ fresh weight, 34.59 absorbance units/g fresh weight, 21.93 $\mu\text{g/g}$ fresh weight, and 89.48%, respectively. Hydrogen peroxide concentrations had a significant effect. The dose of 75 mg/L gave a significant superiority in proline acid concentration, catalase enzyme activity, and leaf MDA content. These values reached 27.80 $\mu\text{g/g}$ fresh weight, 39.48-absorbance units/min/g fresh weight, and 24.78 $\mu\text{mol/g}$ fresh weight, respectively. Meanwhile, the control treatment showed superiority in relative water content of leaves, reaching 89.60%. The concentration of 50 mg/L recorded superiority in SOD enzyme activity, reaching 34.63-absorbance units/g fresh weight. Interactions between study factors were observed. Control treatment combined with the Lashata variety gave a significant superiority in relative water content of leaves, reaching 94.60%. However, the concentration of 75 mg/L combined with the Lashata genotype recorded significant superiority in the rest of the studied traits

Title: Effect of different weed management practices on organically grown cotton

Authors: Vengaldas Chaitanya^{1*}, Parikshit Vinayak Shingrup², Vikas Vasant Goud³, Vijay Kumar Choudhary⁴, Janki Sharan Mishra⁴ & Nalla Charitha²

Imprint: PLANT SCIENCE TODAY Vol 13(sp5): 01–07
<https://doi.org/10.14719/pst.11486>

Abstract: Weeds pose a significant challenge in cotton cultivation by competing with the crop for essential resources such as sunlight, water and nutrients, ultimately leading to reduced yield and fibre quality if not effectively controlled. Although chemical herbicides have been widely used for weed management, rising concerns over herbicide resistance, environmental impacts and the need for sustainable agriculture have encouraged the adoption of organic alternatives. Among these, mulching has been recognised as an effective practice for weed suppression while improving soil health and reducing dependence on synthetic chemicals. A field study was conducted during the kharif seasons from 2020–2024 at the Centre for Organic Agriculture Research and Training, Department of Agronomy, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, to evaluate the effects of different weed management practices in organically grown cotton. The results indicated that crop growth parameters including plant height, leaf area per plant, number of sympodial branches per plant and dry matter accumulation per plant along with yield attributes such as number of picked bolls per plant, boll weight per plant and seed cotton yield per plant were significantly higher under the stale seedbed method combined with twice hand weeding, showing performance comparable to that of straw mulch. This treatment also recorded lower weed density and weed dry weight, along with higher weed control efficiency. Economic analysis revealed that stale seedbed with hand weeding produced higher gross returns, whereas straw mulch was more profitable with better net returns and benefit-cost ratio, indicating its suitability as a sustainable weed management option for organic cotton

Title: Effects of planting density and topping time on the source-sink tributes and photosynthetic carbon production in short-fruited branch cotton

Authors: Huang Yin, Wu Jianfei & Tang Feiyu

Imprint: Cotton Res 9, 36 (2026). <https://doi.org/10.1186/s42397-026-00282-0>

Abstract: Background: Short fruiting branch cotton (SFBC) has normal main-stem growth. However, the growth of fruiting branches is compromised by a short sympodial internode of 2–5 cm, which is suitable for a high-density cropping system. Increasing plant population density (PPD) combined with late topping (LT) has been proven to increase yield for SFBC, but the underlying physiological mechanism remains unclear. An SFBC line, P4D, was employed to examine the dynamics of source-sink attributes and leaf carbon metabolism in the fourth main-stem leaf from the apex during peak flowering (PF) to boll opening (BO) stages in 2023 and 2024. The experiment involved a factorial design with two PPD levels (LD: 5.33 plants m⁻², HD: 8 plants m⁻²) and two topping times (ET: early topping for leaving ten sympodial branches; LT: late topping for leaving fifteen sympodial branches).

Results: Compared with the three other combinations, the combination of HD with LT (HDLT) produced higher lint and seed cotton yields by increasing biological yield and boll density. Averaged across the PF to BO stages and over two years, the greatest leaf area index (LAI) and reproductive biomass per unit ground area (RBGA) were recorded in the HDLT, with increases of 46.30% to 78.52% for LAI and 6.77% to 40.18% for RBGA compared with others. Additionally, the HDLT exhibited the lowest reproductive biomass per unit leaf area (RBLA), with a reduction of 15.20% to 42.74%. The above results showed that the HDLT was characterized by the greatest source and sink strengths as well as the strongest anti-senescence ability among the four treatments. Compared with the ET, the LT improved the activities of adenosine diphosphate glucose pyrophosphorylase and sucrose phosphate synthase and, in turn, increased leaf starch and total nonstructural carbohydrate (TNC) concentrations during the PF to BO stages in both years. Relative to the HD, the LD presented greater starch and TNC levels. Thus, the combination of LT and LD (LDLT) achieved the greatest starch and TNC concentrations, followed by the HDLT.

Conclusion: The higher cotton yield in HDLT is attainable through increasing both source and sink ability, delaying leaf senescence, and improving carbon production capacity. Increasing plant density combined with later topping for SFBC is a promising alternative for sustainable cotton production in Jiangxi province, China and other areas with similar ecology.

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Title: Nitrogen, Phosphorus, and Potassium Concentrations in Cotton Organs under Humic-Based Biostimulants across Different Irrigation and Fertilization Regimes

Authors: Shukhrat Abdualimov · Fayzulla Abdullaev · Shokhjakhon Khamidullayev, Khojiakbar Khasanov

Imprint: DOI: <https://doi.org/10.21203/rs.3.rs-10774407/v1>

Abstract: How humic-based biostimulants affect cotton nutrition under different irrigation and reduced fertilization regimes remains poorly documented on the irrigated serozem soils of Uzbekistan. This study evaluated the biostimulants Reflect and Geohumate in field trials conducted on typical serozem soil in Tashkent province. In the first experiment, the UzPITI-103 cultivar received seed and foliar applications of Reflect (200–400 mL/t) under two irrigation regimes (65–70% and 70–75% relative to field water capacity, FWC). In the second experiment, Geohumate, Bactofert, and their combination were evaluated on the Andijon-37 cultivar against a 40%-reduced N120P84K60 fertilizer background relative to a full N200P140K100 control. Nitrogen, phosphorus, and potassium concentrations in plant organs were determined at the budding, flowering, and boll-opening stages. Changes in NPK concentration under Reflect depended on organ, growth stage, application rate, and irrigation regime, with the most consistent positive responses observed in certain reproductive organs. Under the reduced-fertilizer background, the Geohumate and Geohumate+Bactofert packages matched or exceeded the fully fertilized control across numerous tissue indicators. Yield exceeded the control by 3.1–5.3 c/ha for Reflect treatments and by 3.4–6.6 c/ha for Geohumate/Bactofert treatments, with corresponding gains in net profit and profitability. However, the tissue analyses are based on treatment means, and no biostimulant-free control was included at the reduced-fertilizer level; the results therefore reflect the performance of the tested technological packages rather than the isolated contributions of the biostimulant and the fertilizer reduction.

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Title: A seaweed extract-based biostimulant improves cotton nutrition, physiology, and yield under water scarcity

Authors: Antonia Erica Santos de Souza, Luiz Gustavo Moretti, João William Bossolani, José Roberto Portugal, João Henrique dos Santos Ferreira, Nathália Cristina Marchiori Pereira, Sirlene Lopes Oliveira, Carlos Alexandre Costa Crusciol

Imprint: Agronomy Journal, 118, e70523. <https://doi.org/10.1002/agj2.70523>

Abstract: Cotton (*Gossypium hirsutum* L.) production is constrained by water scarcity, and sustainable strategies are needed to improve resilience and productivity. Seaweed extract-based biostimulants (SEBs) are natural materials with the potential to enhance stress tolerance and nutrient use efficiency. This study evaluated the effects of four foliar SEB application treatments on cotton under water restriction: an untreated control (T1), four foliar applications of SEB at early cotton growth stages (T2), foliar application every 15 days (T3), and monthly foliar application (T4) at two sites. SEB application improved macronutrient and micronutrient uptake (K, Ca, Fe, and Cu). It also reduced oxidative damage by decreasing hydrogen peroxide and malondialdehyde contents.

Additionally, SEB enhanced water-use efficiency, carboxylation efficiency, plant height, and productive parameters. Monthly application was the most effective, increasing seed fiber yield by 9.77% (371.14 kg ha⁻¹) and 6.0% (225.0 kg ha⁻¹) compared with the control in the first and second growing seasons, respectively. Monthly SEB application also improved fiber quality by increasing micronaire and reducing the short fiber index. Our findings indicate that SEB application is a sustainable strategy for enhancing cotton nutrition, physiology, productivity, and quality. A monthly application frequency offers a viable approach to maximizing the benefits of biostimulant use in cotton production and contributing to more sustainable agricultural practices.

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Title: Evaluation of a supramolecular complex based on glycyrrhizic acid as a bioregulator for enhancing the salt tolerance of cotton *Gossypium hirsutum* L.

Authors: Babaeva D T1*, Akhunov A A1 , Khashimova N R1 , Saydullaeva K T2 , Navruzov S B1 , Shomakhamadov S S1 , Gafurov M B2 & Yuldashev K A

Imprint: PLANT SCIENCE TODAY Vol 13(3): 1-7 <https://doi.org/10.14719/pst.11011>

Abstract: This study evaluated the biostimulant activity of a supramolecular complex of glycyrrhizic acid and indole butyric acid (GA-IBA) at various concentrations (10⁻⁵ , 10⁻⁶ , 10⁻⁷ and 10⁻⁸ M) on the growth and development of cotton (*Gossypium hirsutum* L.) variety Sulton under experimental salt stress (100 mM NaCl) under laboratory conditions. Key morphometric parameters, including length, fresh and dry weight of hypocotyls and roots, as well as oxidative stress indicators- concentrations of hydrogen peroxide (H₂O₂), malondialdehyde (MDA) and the activity of the antioxidant enzyme peroxidase (POD)- were studied. The most notable stimulatory effect was observed at 10⁻⁶ M of the GA-IBA, which significantly enhanced elongation, increased the fresh weight of roots and activated POD, while reducing oxidative stress by lowering H₂O₂ and MDA levels. Concentrations above and below this optimal level exhibited comparatively weaker effects. These findings indicate that treatment with GA-IBA at 10⁻⁶ M effectively enhances salt tolerance in cotton and may serve as a promising strategy for mitigating the adverse effects of salinity during early stages of plant ontogenesis.

Title: *Leifsonia* sp. and *Enterobacter* sp. improve physiological and biochemical adjustments in cotton under water deficit

Authors: Ellie José Pereira, Vinícius de Souza, Caliane da Silva Braulio, Franciane Tavares Braga & Adailson Feitoza de Jesus Santos

Imprint: BMC Microbiol (2026). <https://doi.org/10.1186/s12866-026-05545-z>

<https://doi.org/10.1186/s12866-026-05545-z>

Abstract: Background: Drought is a major limiting factor in cotton (*Gossypium hirsutum* L.) cultivation, particularly in semi-arid regions, where water scarcity hinders plant growth. This study investigated the effects of rhizobacteria on the morphological and physiological responses of cotton plants under water stress. The experiment was conducted in a greenhouse using a randomized block design with a $3 \times 3 \times 2$ factorial arrangement and five replicates. Plants were subjected to three water-holding capacity levels (100%, 50%, and 25%) and inoculated with *Leifsonia* sp. CR132 and *Enterobacter* sp. CR14, compared to a non-inoculated control, to evaluate morphological and physiological parameters. Data were subjected to analysis of variance (ANOVA), and means were compared using Tukey's test at a 5% significance level.

Results: Under severe water stress (25%), inoculation with *Leifsonia* sp. CR132 and *Enterobacter* sp. CR14 induced superior responses compared to the control, with increases of up to 1.5-fold in superoxide dismutase, peroxidase, and catalase activities, and an increase of approximately 38% in ascorbate peroxidase activity, indicating enhanced antioxidant efficacy. Under full irrigation (100%), *Leifsonia* sp. CR132 also stood out, showing a more than 100% increase in total soluble proteins compared to the control group and consistently promoting greater stem growth, stem diameter, and root biomass. *Enterobacter* sp. CR14 increased proline accumulation by 27% and resulted in a fourfold higher membrane stability index.

Conclusion: The results demonstrate that rhizobacteria enhance drought tolerance in cotton plants through morphological and physiological responses, highlighting the potential of *Leifsonia* sp. CR132 for the development of sustainable agricultural bioinoculants; however, field trials and molecular analyses are required to validate the strains under real-world environmental conditions.

Title: GhSQS1-mediated squalene accumulation coordinates cotton development and stress resilience

Authors: Yameng Xu , Zhitian Zhang , Le Liu , Shuyuan Jia , Jicheng Wei , Lili Lu , Shuya Ma , Yadi Xing , Ye Wang , Jingjing Zhan

Imprint: Journal of Experimental Botany, 2026,,
erag424, <https://doi.org/10.1093/jxb/erag424>

Abstract: Squalene is a high-value triterpenoid. It is increasingly recognized for its regulatory roles in plant signaling. However, the functions of squalene in cotton remain unexplored. Here, we show that exogenous squalene can promote cotton developmental traits (root elongation and ovule development) and identify GhSQS1 as the predominant functional squalene synthase. Overexpression of GhSQS1 promotes root development, along with metabolic and hormonal reprogramming, including the activation of brassinosteroid (BR)-associated signaling. Furthermore, stable overexpression of GhSQS1 markedly elevates endogenous squalene accumulation, predominantly in leaves. This metabolic enhancement is accompanied by coordinated improvements in root architecture, leaf expansion, fiber elongation, and overall plant vigor. Notably, GhSQS1-OE lines exhibited elevated lignin-associated enzyme activities and increased total lignin content. These changes were correlated with improved tolerance to drought and alkaline stress. Importantly, similar development-promoting phenotypes were recapitulated by heterologous expression of a high-activity fungal SQS (sharing only 39.2% amino acid identity with GhSQS1), confirming that enhanced squalene biosynthesis underlies these effects. Collectively, this study establishes squalene biosynthesis as a central metabolic axis coordinating hormonal reprogramming, cotton-specific development and stress adaptation, while concurrently generating squalene-enriched biomass. These findings provide a new paradigm for crop genetic improvement and tolerance enhancement.

Title: A meta-analysis of the factors regulating evapotranspiration in cotton fields under different drip irrigation regimes in Xinjiang

Authors: Sun Rui, Gao Tian, Zhang Shuo, Liu Zongxi, Li Fadong, Gong Ping, Yang Guang

Imprint: Journal of Irrigation and Drainage, 2026, Vol. 45, No. 9, 115-124 ref. 53

Abstract: Objective: Evapotranspiration (*ET*) is a key determinant of irrigation requirement in agricultural production in arid regions. Under mulched drip irrigation, *ET* is influenced by climate, soil properties and agronomic management, but how irrigation regime affects *ET* across different environmental and management conditions remains poorly understood. This study addressed this knowledge gap by systematically analyzing the response of cotton-field *ET* to irrigation regime and identifying factors that regulate these responses. Method: A meta-analysis was conducted using sufficient drip irrigation as the control to quantify the changes in cotton-field *ET* under over-irrigation, mild, moderate, and severe water-stress drip irrigation, and evaluate how climatic conditions, soil properties and agronomic management practices modified these responses. Result: Compared with sufficient irrigation, mild, moderate, and severe water-stress irrigation significantly reduced cotton-field *ET* by 9.89%, 19.41%, and 30.89%, respectively, whereas over-irrigation significantly increased *ET* by 9.01% ($P < 0.05$). Climatic conditions strongly modulated *ET* responses to irrigation regimes, with the greatest responses occurring when growing-season precipitation exceeded 150 mm, mean temperature ranged from 21 to 24°C, sunshine duration ranged from 1 500 to 2 000 h, and mean wind speed exceeded 2 m/s. Soil texture and agronomic management also modified these responses, with *ET* in sandy loam soils showing the greatest sensitivity to irrigation regimes. A combination of nitrogen application rate of 300-400 kg/hm², planting density of 6×10⁴-12×10⁴ plants/hm², and mulch coverage ≥90% reduced *ET* by more than 30% under severe water-stress irrigation. Conclusion: Irrigation regimes substantially regulated *ET* in mulched drip-irrigated cotton fields in Xinjiang through interactions among climate, soil properties and agronomic management. These findings provide a scientific basis for developing precision irrigation strategies for cotton production in arid regions and improving irrigation water-use efficiency.

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Title: Cotton-stalk biochar relieves sodicity and increases seedcotton yield on saline-alkali cotton land by supplying exchangeable cations rather than by adsorbing sodium

Authors: Changkun Ma a,* Mingjiang Deng

Imprint: Industrial Crops & Products 251 (2026) 124361

Abstract: Secondary salinization and disposal of the crop's own stalk are two constraints on cotton fibre production that a single practice could in principle address, yet how a pyrolyzed stalk amendment relieves sodicity, how much of it is worth applying, and whether fibre quality benefits all remain unresolved. Soil, leaf physiology, seedcotton yield, and fibre grade of cotton (*Gossypium hirsutum* L.) were therefore measured against cotton-stalk biochar rate on saline-alkali land. Four rates (0, 10, 20, and 30 Mg ha⁻¹) were applied once before sowing in 2024 and not renewed in

2025, on three drip-irrigated fields of mild, moderate, and severe salinity in southern Xinjiang. One field represented each class, so effects are within-field and among-field differences are described, not attributed to salinity. At the best-performing rate – 20 Mg ha⁻¹ on the mild field, 30 on the other two – topsoil electrical conductivity fell by 22–29% and exchangeable sodium percentage by 20–24%. Bulk density fell, organic carbon and aggregation rose, and pH did not. Two-season mean seedcotton yield rose by 0.70, 1.58, and 1.90 Mg ha⁻¹ (95% confidence intervals 0.59–0.81, 1.40–1.75, and 1.70–2.10). Yield saturated at 18.9 Mg ha⁻¹ on the mild field but was still rising at the highest rate elsewhere. The exchange charge applied covered between 47% and 63% of the sodium displaced: the calcium, magnesium, and potassium supplied, not adsorption, relieved sodicity. Fibre quality improved on the two more saline fields but not detectably on the mild one. On the moderately saline field, however, the micronaire increase carried the fibre out of the top class of the national standard, so not every measured change in that trait is an improvement. The potassium applied, three to eleven times the fertilizer rate, cannot be separated from the amendment.

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Title: *GhSCL5*, a GRAS transcription factor from cotton, positively regulates drought tolerance by modulating phytohormone signaling and carbon metabolism

Authors: Duofu Shan, Xin Zhang, Haijuan Wang, Xingyue Zhong, Yongxue Xie, Kunduziayi Kudelaiti, Aixia Han, Wanwan Fu, Xilin Wang, Yanlong Yang & Jingbo Zhang

Imprint: *Planta* 264, 115 (2026). <https://doi.org/10.1007/s00425-026-05138-0>

Abstract: Drought is a major abiotic stress limiting cotton production. The GRAS protein family participates in plant development and abiotic stress responses, but the roles of many cotton GRAS members remain unclear. Here, we characterized *GhSCL5*, a GRAS family gene in upland cotton (*Gossypium hirsutum*) whose expression was induced by natural drought, polyethylene glycol (PEG), and exogenous γ -polyglutamic acid (γ -PGA). Silencing *GhSCL5* by virus-induced gene silencing (VIGS) reduced cotton drought tolerance, as indicated by decreased catalase (CAT) and peroxidase (POD) activities, lower proline (Pro) accumulation and leaf relative water content (RWC), and increased malondialdehyde (MDA) content under drought stress. Conversely, heterologous overexpression of *GhSCL5* in *Arabidopsis thaliana* enhanced drought tolerance and maintained longer primary roots under mannitol-induced osmotic stress. Transcriptome profiling identified 7061 differentially expressed genes (DEGs) in *GhSCL5*-silenced cotton leaves under drought stress, comprising 3140 upregulated and 3921 downregulated genes. Notably, upregulated DEGs were enriched in pathways, including plant-pathogen interaction, plant hormone signal transduction, the plant MAPK signaling pathway, amino sugar and nucleotide sugar metabolism,

phenylpropanoid biosynthesis, and arginine and proline metabolism, while downregulated DEGs were enriched in photosynthesis, plant hormone signal transduction, starch and sucrose metabolism, carbon fixation in photosynthetic organisms, glyoxylate and dicarboxylate metabolism, and photosynthesis-antenna protein. Importantly, the plant hormone signal transduction pathway was enriched with both upregulated and downregulated DEGs, suggesting that this pathway may represent a significant component of the transcriptional response. Within the plant hormone signal transduction pathway, genes associated with abscisic acid (ABA) and auxin were the most abundant, which indicates that these two hormonal systems might be key factors in the response associated with *GhSCL5*. Collectively, these findings suggest that *GhSCL5* may contribute to drought tolerance through processes related to antioxidant defense, osmotic adjustment, and carbon metabolism, with transcriptomic evidence suggesting a potential involvement of ABA and Auxin signaling.

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Title: Identifying Late Season Weed Patches in Cotton (*Gossypium hirsutum*) Fields from Satellite Imagery Using DeiT-Tiny/16 Machine Learning Algorithms

Authors: Pearce, Ashley Lynne

Imprint: <https://www.proquest.com/LegacyDocView/DISSNUM/32703078>

Abstract: This study aims to develop an automatic algorithm to detect weeds within cotton fields using extremely high resolution RGB satellite imagery to inform precision weed control efforts. A multi-scale approach was developed over six cotton fields in California. First super resolution UAV imagery was collected from three fields on July 12th, 2024, and six fields on September 6th, 2024, and was segmented into 5×5 m tiles. A random subset of the 1.02 cm resolution UAV tiles was manually annotated into three classes: crop, weed, or bare soil. These high-resolution training labels were then used to train a DeiT-Tiny/16 deep learning model to ascertain the location of weeds from Pléiades Neo 4 satellite imagery collected on July 10th, 2024, and September 5th, 2024. The model achieved an overall accuracy of 95.75% on held-out test data. However, field validation results from the first data collection of July 10th, 2024, revealed that the model had likely learned to predict weeds based on the presence of open canopy in the inter-row space, rather than true identification of weeds. This is a form of spurious feature reliance that resulted in near-total weed classification in fields confirmed to have low weed presence. Field validations on data collected September 5th, 2024, show the additional time allowed vigorous sections of the field to reach a state of canopy closure, while less vigorous areas maintained an open canopy. There was a high rate of weed cooccurrence within the less vigorous areas which produced a more accurate weed map, despite resulting from spurious feature prediction. Because of the high cooccurrence, the map holds some potential for extremely late season rescue weed

treatments such as hand rogueing. If the DeiT-Tiny/16 model was provided additional training data to prevent the spurious feature connection, the limited hand rogueing application could be expanded to broader precision weed control and detection applications.

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Title: Integrated Physiological and Transcriptomic Analyses Reveal Mechanisms of Drought Tolerance in Cotton (*Gossypium* spp.): Omics-Driven Approaches for Sustainable Agriculture

Authors: Dalvand Y, Khayam Nekouei M, Jafari A, Hamid R, Ghaffari M R.

Imprint: Journal of Biosafety 2025; 18 (3) :95-117

Abstract: Drought stress limits cotton yield in arid regions by disrupting physiological and molecular processes. This study examined two genotypes: GISV-328 (sensitive) and G. Cot 16 (tolerant) using phenotypic, physiological, and transcriptomic data. Under water deficit, the tolerant genotype better maintained water status, membrane stability, photosynthetic efficiency, and osmotic adjustment, while the sensitive genotype showed greater oxidative damage. RNA-Seq identified 1,465 differentially expressed genes enriched in hormone signaling (especially ABA), MAPK cascades, amino acid/carbohydrate metabolism, secondary metabolite biosynthesis, and antioxidant responses. Key transcription factors (NAC, WRKY, bHLH, DREB) and stress-related genes (HSPs, LEA) were upregulated, indicating complex regulatory networks. The tolerant genotype exhibited stronger activation of osmotic regulation, antioxidant defense, and energy metabolism, whereas the sensitive genotype showed mostly structural and limited responses. Convergence of calcium, ABA, and ROS signals emerged as a core regulatory hub. Overall, drought tolerance in cotton results from coordinated interplay among signaling, transcriptional, and metabolic pathways that preserve cellular homeostasis and enhance adaptation to water scarcity.

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Title: First report of *Fusarium clavus* and *Fusarium ipomoeae* associated with seedling diseases of cotton (*Gossypium hirsutum*) in New South Wales, Australia

Authors: Duy P. Le a b 1, Chi P.T. Nguyen a 2, Sean Roberts

Imprint: Crop Protection, Volume 211

<https://doi.org/10.1016/j.cropro.2026.107850>

Abstract: We inform here for the first time the pathogenicity of *Fusarium clavus* and *F. ipomoeae* that belong to the *F. incarnatum-equiseti* species complex (FIESC) on cotton seedlings in New South Wales (NSW), Australia. FIESC isolates were often recovered from seedlings that displayed collar rot symptoms which were similar to those of *Rhizoctonia* rot and black root rot. Therefore, it was assumed to be a secondary pathogen. However, in the 2023-24 cropping season, we only recovered putative-FIESC isolates from two collar rot diseased samples that were collected from two geographically distant fields in NSW. Based on the DNA sequences retrieved from the translation elongation factor 1 α and the RNA polymerase II second largest subunit, two representative isolates from each field were identified as *Fusarium clavus* and *Fusarium ipomoeae*. Both species were able to cause pre-emerging damping off in Petri dish assays. In pot trials, both species incited light to dark brown lesions on the collar regions that were similar to those observed in the fields. The pathogens were reisolated and reidentified; thus, fulfilling Koch's postulate. This is the first report of *F. clavus* and *F. ipomoeae* in the FIESC causing pre-emerging damping off and collar rot of cotton in NSW, Australia.

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Title: Assessment of genotype by environment interaction for yield stability and sucking pest resistance in cotton (*Gossypium hirsutum* L.) using AMMI, GGE biplot and multi-trait stability index

Authors: Subhashree Das1*, Bhabani Shankar Nayak1 , Jyoti Rekha Mallick1 , Anshuman Nayak2 , Umasankar Nayak3 , Niranjan Mandi4 , Sujata Das5 , Kishore

Chandra Sahoo⁵ , Biman Ranjan Behera⁶ , Ashirbad Swain¹ , Gopal Mistry¹ , Sambit Kumar Parida¹ , Tapas Panigrahi¹ & Chandramani Khanda⁷

Imprint: PLANT SCIENCE TODAY Vol 13(sp5): 1-13
<https://doi.org/10.14719/pst.13796>

Abstract: Cotton (*Gossypium hirsutum* L.) is a major fibre crop underpinning the global textile industry; however, its productivity is increasingly threatened by climatic variability and the resurgence of sap-sucking insect pests. The interaction between genotype and environment ($G \times E$) further complicates the identification of stable and high-yielding genotypes, particularly under rainfed conditions. The present study evaluated 7 cotton genotypes across 9 environments (three locations over 3 consecutive years: 2021–24) in Odisha, India, to assess $G \times E$ interaction for 14 quantitative traits related to yield and sucking pest resistance using advanced statistical approaches. Combined analysis of variance revealed highly significant ($p < 0.01$) effects of genotypes, environments and $G \times E$ interaction for all traits studied. The interaction component was particularly significant for key traits, including seed cotton yield (SCY), lint yield (LY) and populations of major sucking pests, necessitating a comprehensive stability analysis. High broad-sense heritability coupled with moderate to high genetic advance for yield and pest resistance traits indicated the predominance of additive gene action. Stability analyses using the Eberhart and Russell model, additive main effects and multiplicative interaction (AMMI) and genotype plus genotype by environment (GGE) biplot consistently identified genotype BS 3-17 as superior, exhibiting the highest mean SCY (1978 kg ha⁻¹) and LY (675 kg ha⁻¹), along with the lowest mean populations of aphids (APH) (5.28 per 3 leaves) and jassids (JAS) (1.82 per 3 leaves) across environments. The multi-trait stability index (MTSI) further ranked BS 3-17 as the most desirable genotype (MTSI score = 5.51), indicating its closest proximity to the ideotype. Agronomic validation trials demonstrated that high-density planting (90 × 30 cm) combined with 125 % of the recommended dose of fertilisers significantly enhanced the yield potential of BS 3-17, achieving up to 3114 kg ha⁻¹. These findings establish BS 3-17 as a climate-resilient, high-yielding genotype suitable for commercial cultivation and a promising donor parent for breeding programs targeting yield stability and sucking pest resistance

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Title: Evaluation of pathogenic diversity in *Verticillium dahliae* and defense mechanisms of different cotton cultivars against *Verticillium* wilt disease

Authors: N. Khaledi^{1*}, M. Razi Nataj Aghamahli², A. Hamidi¹, S. Sheidaei¹, F. Hassani

Imprint: Plant Protection (Scientific Journal of Agriculture) 49(2), Summer, 2026

Abstract: Verticillium wilt, caused by the soil-borne hemibiotrophic fungus *Verticillium dahliae* Kleb., is one of the most serious diseases affecting cotton production worldwide. The pathogen persists in soil for prolonged periods as microsclerotia, penetrates host plants through the roots, and colonizes the xylem vessels, resulting in vascular blockage, physiological dysfunction, and significant yield losses. Despite the considerable economic importance of cotton, no cultivar with complete and stable resistance to Verticillium wilt has been reported to date. Therefore, understanding cultivar-specific responses at both agronomic and biochemical levels is essential for identifying relatively resistant genotypes and developing effective disease management strategies. Moreover, pathogen-host interactions can vary substantially depending on environmental conditions and cultivar genetic backgrounds, underscoring the need to evaluate multiple genotypes across diverse settings. This study aimed to (i) evaluate the susceptibility of different cotton cultivars to Verticillium wilt, (ii) examine the effects of the disease on agronomic traits and yield components, and (iii) investigate the biochemical defense mechanisms associated with basal resistance.

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Title: Cotton Farming Pesticides Affect Ileal Microbiota Activity and Expression of Virulome but Not Resistome or Metabolic Pathways in a Sedentary Wild Passerine

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Imprint: Environmental Toxicology, 2026; 0:1–8 <https://doi.org/10.1002/tox.70193>

Abstract: The increased use of agrochemicals to enhance crop production has had detrimental environmental effects including implication in the sharp decline of North American farmland-breeding birds. Here, using a combination of deep shotgun metatranscriptomics and pesticide exposure data, we sought to assess whether exposure to cotton (*Gossypium* spp.) production had a differential effect on ileum multi-kingdom microbial activity, metabolism, anti-microbial resistance, and virulence factors of sedentary northern mockingbirds (*Mimus polyglottos*) sampled from two cotton-producing areas (16 birds in total) and one uncultivated area (7 birds) in Texas, USA. Both Shannon Index values (Adj. $r^2=0.174$, $F(1,21)=5.633$, $p=0.027$) and a Mantel test (Spearman $\rho=0.184$, $p=0.013$) supported a relationship between metabolically active microbiota Bray–Curtis dissimilarities and differences in pesticide mixtures among study areas. Virulence factor richness (Adj. $r^2=0.182$, $F(1,21)=5.890$, $p=0.024$), Shannon Index (Adj. $r^2=0.231$, $F(1,21)=7.612$, $p=0.012$), and load (sum of virulence factor abundances; Adj. $r^2=0.160$, $F(1,21)=5.194$, $p=0.033$) were related to total pesticide load

(total quantity of pesticides). We found no pesticide effects on expression of either antimicrobial resistance genes or metabolic pathways.

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Title: Understanding the role of Cry proteins in Bt Cotton against pink bollworm (*Pectinophora gossypiella*): insights into host-insect interactions and dynamics

Authors: Sachdeva Namrata, Rashmi Mayank, Sharma Soumya, Sahu Sarika, Singh Mahender Kumar, Nagrale Dipak T., Fand Babasaheb B., Jha Girish Kumar & Kumar Sunil

Imprint: J Cotton Res 9, 35 (2026). <https://doi.org/10.1186/s42397-026-00280-2>

Abstract: Background: The pink bollworm (*Pectinophora gossypiella*) is one of the most destructive pests of cotton worldwide, causing substantial yield losses and economic damage. The deployment of Bt cotton expressing insecticidal proteins from *Bacillus thuringiensis* (Bt), including Cry1Ac in Bollgard I (BG-I) and Cry1Ac plus Cry2Ab in Bollgard II (BG-II), initially provided effective control of this pest. However, the evolution of resistance to both Cry1Ac and Cry2Ab has significantly reduced the effectiveness of Bt cotton. Previous studies have implicated ATP-binding cassette (ABC) transporters and mutant cadherin proteins as key factors mediating resistance through altered Bt toxin interactions and detoxification mechanisms. Although resistance mechanisms involving cadherin and ABC transporters have been reported, the comparative structural interactions of Cry1Ac, Cry2Ab, and Cry2Ad with these receptor proteins remain poorly understood in the pink bollworm. This study, therefore, aimed to investigate the molecular interactions of Cry1Ac, Cry2Ab, and Cry2Ad with pink bollworm mutant cadherin (PgMutCad) and ATP-binding cassette transporter (PgABC) using computational modeling, molecular docking, and molecular dynamics simulations.

Results: Protein structures were generated using homology modeling and ab initio prediction, depending on sequence variation and structural homology. Molecular docking and simulation analyses revealed distinct interaction patterns among the Cry proteins and resistance-associated targets. Among the toxins evaluated, Cry2Ab and Cry2Ad exhibited stronger binding affinities, structural stability, more favorable binding energetics, and persistent hydrogen-bond interactions with both PgMutCad and PgABC. These toxin-receptor complexes maintained compact conformations throughout the simulations, indicating stable and robust interactions. In contrast, Cry1Ac showed comparatively weaker interactions with the resistance-associated proteins.

Conclusion: The study provides new insights into the molecular basis of pink bollworm resistance to Bt toxins and highlights the critical role of mutant cadherin and ABC

transporter proteins in this process. The strong and stable interactions observed for Cry2Ab and Cry2Ad suggest that these toxin variants represent promising candidates for the development of next-generation Bt cotton and improved pest management strategies. Although these findings are based on computational analyses and require experimental validation, they provide a structural framework for the rational design of novel Bt toxins and resistance-management approaches aimed at sustaining the long-term effectiveness of transgenic cotton against the pink bollworm.

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Title: Management of external boll rot in cotton using optimized UAV-based fungicide application

Authors: Ragiman, S., Gawande, S. P., Nagrale, D. T., Thube, S. H., Fand, B. B., Gandhiji Idapuganti, R., ... Waghmare, V. N

Imprint: Archives of Phytopathology and Plant Protection, 59(16), 1355–1369. <https://doi.org/10.1080/03235408.2026.2720144>

Abstract: Efficient fungicide delivery within dense cotton canopies limits control of canopy-associated diseases such as external boll rot. This study evaluated the effects of UAV spray parameter optimisation on canopy deposition and disease control under semi-arid conditions. A three-factor, three-level orthogonal design assessed spray volume (18, 20 and 22 L ha⁻¹), flight height (2, 3, 4 m) and flight velocity (3.5, 4.0, 4.5 m s⁻¹) based on density, uniformity and penetrability. Spray volume had the greatest influence on deposition ($p < 0.01$), followed by flight velocity, while flight height showed a smaller effect. The optimised combination (20 L ha⁻¹, 2 m, 4.0–4.5 m s⁻¹) enhanced deposition and penetration into inner canopy layers. Field validation over two seasons showed that UAV spraying reduced boll rot severity by 16–19% and increased seed cotton yield by 5% compared to conventional spraying. Results demonstrate that improved deposition enhances disease control and supports UAV-based fungicide application in cotton.

Title: Inheritance Pattern and Combining Ability of Yield and Yield-Related Traits in *Gossypium hirsutum* L.

Authors: Haiqa Mustafa*, Khatir Ali and Abdul Wahab

Imprint: J Genet Appl Biotechnol, 2026: e2026037

DOI: <https://doi.org/10.66432/hdch8293>

Abstract: *Gossypium hirsutum* L. is a significant fibre crop and is a key element in the textile industry. The present study investigated the inheritance and combining ability of yield and yield related traits in upland cotton in a complete 3×3 diallel mating design. The three genetically different parental genotypes Cyto-608, CIM-343 and MNH-1026 were crossed in all possible combinations to generate six F_1 combinations with 9 genotypes; these were then tested for plant height, monopodial branches, sympodial branches, bolls per plant, boll weight, seed cotton yield per plant and lint percentage. Analysis of variance showed significant differences between genotypes for all traits, thus statistically significant variation in the material evaluated was noted. Several traits had significant GCA and SCA effects, indicating a contribution from additive and non-additive genetic effects, per Griffing's Model I analysis. MNH-1026 was superior for a number of traits, but exhibited mixed breeding value for the different traits, with boll number, seed cotton yield, plant height, and lint percentage being superior. Specific crosses also exhibited beneficial SCA effect for certain traits. The differences in the reciprocal crosses were significant for boll number, seed cotton yield, and lint percentage, suggesting direction-specific differences, but the effects cannot be definitely classified as maternal or cytoplasmic inheritance. Interpretation of the relative magnitude of variance components was done in conjunction with statistical significance of GCA and SCA but not as proof of gene action by only the magnitude of the variance components. The overall results suggest that there is a preliminary indication that both additive and non-additive gene effects are involved in the inheritance of yield and yield related traits in the cotton material evaluated. The results are, however, based on only three parents and two replications, and need to be replicated in other genetic material, locations, and growing seasons.

Title: Molecular characterization of SGR genes related to abiotic stress resistance in cotton

Authors: Fei Wei · Linjuan Wang · Lingyu Du · Jiaxin Yao · Weijun Wu · Yuefeng Deng · Qi Zhang · Jinbo Li · Pengyun Chen

Imprint: BMC Plant Biology <https://doi.org/10.1186/s12870-026-09856-1>

Abstract: Background: Stay-green (SGR) genes encode Mg-dechelatase and play critical roles in chlorophyll degradation. Increasing evidence suggests that SGR genes also participate in abiotic stress responses, including drought and salinity tolerance, in various plant species. However, systematic identification and functional analysis of the SGR gene family in cotton (*Gossypium hirsutum*) remain limited. Results: In this study, we performed genome-wide identification, evolutionary characterization, and stress expression analysis of GhSGR genes. A total of six GhSGR genes were identified and were unevenly distributed across six chromosomes of the At and Dt subgenomes. Phylogenetic analysis divided these genes into SGR and SGR-like subgroups, with conserved gene structures, protein domains, and syntenic relationships across cotton species, indicating high evolutionary conservation. Transcriptome profiling revealed that most GhSGR genes were induced by salt and PEG-simulated drought stress. Quantitative real-time PCR (qRT-PCR) further confirmed that GhSGR1 and GhSGR3 exhibited distinct, dynamic expression patterns under stress treatments. Co-expression network analysis suggested that GhSGR genes are co-expressed with stress-related transporters and transcription factors, suggesting potential involvement in stress regulation. Conclusions: These results demonstrate that GhSGR genes are highly conserved during evolution and are involved in the response to salt and drought stress in cotton. This study provides key candidate genes and a theoretical basis for further functional dissection and molecular breeding of stress resistance in cotton

Title: Cytogenetic and flow cytometric analysis of new allotetraploid forms derived from wild cotton species with A1 and G genomes

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Imprint: J Genet Appl Biotechnol, 2026: e2026042 DOI: <https://doi.org/10.66432/kdhxfr21>

Abstract: Wild Australian and Afro-Asian cotton species are characterized by their natural resistance to diseases and pests, serving as valuable genetic resources for the introgression of these beneficial traits into cultivated cotton varieties. This study presents the results of research aimed at determining the ploidy level of novel allopolyploid hybrid forms derived from wild Australian (*Gossypium nelsonii*) and Afro-Asian (*G. herbaceum*) cotton species using interspecific hybridization and experimental polyploidy methods. Cytogenetic analyses demonstrated that the interspecific F1 hybrids possess a diploid chromosome set ($2n=2x=26$), whereas the synthetic F1C hybrids developed via experimental polyploidy exhibited a multiplied chromosome set ($2n=4x=52$). Furthermore, flow cytometry analysis conclusively confirmed this chromosome doubling, showing that the nuclear DNA content doubled from an average value of - 12.8 in the diploid parental forms to 25.492 in the F1C allotetraploids. The study evaluated the interspecific crossability of species belonging to different genomic groups and successfully generated genetically stable synthetic allotetraploids. This demonstrates the feasibility of utilizing wild diploid species in genetic and breeding research.

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Title: Six-parameter genetic analysis of yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L.)

Authors: Ashita Patel^{1*}, K N Chaudhari², C V Kapadia³, Sanyam Patel⁴, K G Modha¹, R K Patel¹ & Alok Shrivastava⁵

Imprint: PLANT SCIENCE TODAY Vol 13(3): 1-12 <https://doi.org/10.14719/pst.13977>

Abstract: Cotton (*Gossypium hirsutum* L.) is a major commercial crop and an important source of natural fibre, making the understanding of its genetic architecture essential for crop improvement. The present study employed generation mean analysis using six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) to investigate the nature of gene action governing yield-contributing and fibre quality traits. Significant scaling tests and chi-square (χ^2) values for several traits indicated the presence of epistatic gene interactions. The analysis revealed that both additive and non-additive gene effects contributed to trait inheritance, with duplicate epistasis predominating for several economically important traits. These findings suggest that the inheritance of yield and fibre quality traits is complex, involving multiple gene interactions. Therefore, breeding strategies that exploit both additive and non-additive genetic variation, including selection in advanced generations and population improvement approaches, are likely to be more effective for developing superior cotton genotypes

Title: Six-parameter genetic analysis of yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L.).

Authors: P. Ashita, K. N. Chaudhari, C. V. Kapadia, P. Sanyam, K. G. Modha, R. K. Patel, S. Alok

Imprint: Plant Science Today, 10 August 2026, Vol. 13, No. 3, 13977 ref. 28
[10.2134/agronmonogr57.2013.0019](https://doi.org/10.2134/agronmonogr57.2013.0019)

Abstract: Cotton (*Gossypium hirsutum* L.) is a major commercial crop and an important source of natural fibre, making the understanding of its genetic architecture essential for crop improvement. The present study employed generation mean analysis using six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) to investigate the nature of gene action governing yield-contributing and fibre quality traits. Significant scaling tests and chi-square (χ^2) values for several traits indicated the presence of epistatic gene interactions. The analysis revealed that both additive and non-additive gene effects contributed to trait inheritance, with duplicate epistasis predominating for several economically important traits. These findings suggest that the inheritance of yield and fibre quality traits is complex, involving multiple gene interactions. Therefore, breeding strategies that exploit both additive and non-additive genetic variation, including selection in advanced generations and population improvement approaches, are likely to be more effective for developing superior cotton genotypes.

Title: Identification and comprehensive evaluation of cold resistance of *Gossypium hirsutum* L. resource materials during germination period.

Authors: Bing-yue Wang, Jun-duo Wang, Ni Yang, Jun-hao Wang, Ju-yun Zheng, Ya-jun Liang, Zhao-long Gong, Shi-wei Geng, Feng-lei Sun, Shuai-shuai Qian, Xue-yuan Li, Yan-ying Qu

Imprint: Xinjiang Agricultural Sciences, 2026, Vol. 63, No. 1, 1-18 ref. 25

Abstract: Objective: To utilize the germplasm resources of *Gossypium hirsutum* L., in the hope of selecting excellent resource materials with strong cold resistance, thus providing parent and resource materials for the genetic improvement of cold tolerance traits and the breeding of new varieties. Methods: 271 *Gossypium hirsutum* L. germplasm resources were taken as test materials, two environmental conditions of control (28°C) and low temperature stress treatment (4°C) were set to test the average root length,

germination rate, germination potential, germination index, average germination speed, average germination days, cold tolerance coefficient of 12 traits, and correlation analysis, principal component analysis and cluster analysis were conducted to carry out comprehensive evaluation of the germination of different upland cotton germplasm resources cold tolerance. Results: Principal component analysis converted the six cold tolerance indexes into three mutually independent comprehensive indicators, reflecting 92.99% of the information content of the six indicators. Using comprehensive cold resistance value (D), 271 germplasm resources of terrestrial cotton were divided into 4 categories; Class I belonged to strong cold resistance with 17 materials; category II belonged to cold resistant type, in which there were 31 materials; the third category was of not cold resistant type with 201 materials; class IV was cold sensitive category with 22 materials; they covered 6.27%, 11.44%, 74.17% and 8.12% of the test materials, respectively. Using multiple regression analysis, the prediction model of cold tolerance of upland cotton was established as $Y=0.14+0.129X_3+0.109X_4+0.098X_2$, and three cold tolerance indexes were selected, which were the cold tolerance coefficient of germination rate, germination potential and germination index. Conclusion: 17 strong cold tolerance materials are selected by 4°C low temperature treatment, and the cold tolerance coefficient of germination rate, germination potential and germination index can be used as the cold resistance index of germination period of *Gossypium hirsutum* L.

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Title: The putative inositol transporter *VdIPT1* negatively regulates *Verticillium dahliae* virulence: A cautionary example for cotton RNAi target selection

Authors: Yongtai Li ¹, Tiange Sun ¹, Ao Feng, RuiXiang Yuan, Qiuwei Liang, Feng Liu, Xinyu Zhang, Jie Sun, Yanjun Li

Imprint: Industrial Crops and Products, Volume 252, 2026, 124274, ISSN 0926-6690,

<https://doi.org/10.1016/j.indcrop.2026.124274>.

Abstract: Upland cotton (*Gossypium hirsutum*), the world's dominant natural fiber crop, suffers severe yield and quality losses from *Verticillium* wilt. This highly destructive vascular disease, caused by the soilborne hemibiotrophic fungus *Verticillium dahliae*, poses a persistent threat to global cotton production. Nutrient transporters are increasingly recognized as candidate targets for innovative disease management, yet their functional roles and involvement in pathogenicity remain largely unexplored for non-canonical functions in *V. dahliae*. Here, we identified and functionally characterized *VdIPT1* encoding a putative inositol transporter in *V. dahliae*. Deletion of *VdIPT1* ($\Delta VdIPT1$) unexpectedly promoted mycelial proliferation, conidiation capacity, and carbon/nitrogen assimilation, leading to enhanced virulence towards cotton seedlings. In agreement with fungal knockout

phenotypes, both transient Host-Induced Gene Silencing (HIGS) and stable expression of VdIPT1-RNAi constructs in cotton effectively silenced fungal VdIPT1 but compromised host defense rather than conferring disease resistance, resulting in exacerbated disease symptoms and elevated fungal biomass accumulation. Transcriptome profiling demonstrated that the impaired resistance in VdIPT1-RNAi cotton was tightly linked to the transcriptional repression of core defense modules, particularly phenylpropanoid biosynthesis and plant-pathogen interaction signaling cascades. Our findings establish this putative inositol transporter VdIPT1 as a negative modulator of fungal virulence. Critically, silencing VdIPT1 is not a feasible HIGS-based resistance strategy. This work provides an important cautionary example, emphasizing that target genes must undergo thorough functional validation prior to their application in RNAi-mediated crop disease resistance breeding.

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Title: Heterosis And Combining Ability For Yield And Fibre Quality In Gms-Based Bt Hybrids Of Upland Cotton Across Three Environments

Authors: S. B. Mitkari, K. S. Baig, H. V. Kalpande, V. N. Chinchane, R. R. Dhutmal, B. V. Bhede, S. G. Shinde, S. S. Deshmukh

Imprint: DOI: <https://doi.org/10.4238/meshyh93>

Abstract: Cotton hybrid breeding requires simultaneous exploitation of heterosis and informed parent choice. This study quantified heterosis, general combining ability (GCA), specific combining ability (SCA), and the associated gene-action pattern for yield, yield components, and fibre quality in a GMS-based Bt upland-cotton population. Forty F1 hybrids generated by crossing four GMS lines with ten Bt testers were evaluated with 14 parents and four standard checks in a randomized block design with two replications across three environments during Kharif 2025–26. Genotypic differences were significant for every studied trait in the pooled analysis. The cross mean for seed-cotton yield was 118.97 g plant⁻¹, compared with 98.71 g for lines, 98.29 g for testers, and 125.86 g for checks. The leading hybrid, GNH-105A × NH22065Bt, yielded 169.57 g plant⁻¹ and expressed 53.59% heterobeltiosis, 34.92% heterosis over NHH 44 BG II, and an SCA effect of 39.52. Other high-value combinations were GNH-101A × NH22160Bt and GNH-111A × NH22037Bt. Non-additive gene action predominated for seed-cotton yield, bolls plant⁻¹, sympodia plant⁻¹, boll weight, seed index, lint index, and uniformity ratio, whereas additive action predominated for flowering time, plant height, ginning outturn, UHML, fibre fineness, and fibre strength. GNH-105A was the strongest female general combiner for yield architecture; NH22037Bt was the strongest tester for yield and boll number; and GNH-101A, GNH-111A, and NH22158Bt contributed complementary fibre-quality effects.

Title: Effects of the GDSL Lipase Gene GhGELP23D from *Gossypium hirsutum* on Plant Cell Elongation Development

Authors: CHEN HaoHua, CHEN Gang, FENG JianTing, XIE Jing, LI QianQian, WANG Fei

Imprint: Scientia Agricultura Sinica

DOI: 10.3864/j.issn.0578-1752.2026.16.003

Abstract: **【Objective】**The GDSL esterase/lipase (GELP) family comprises a group of multifunctional hydrolases with broad substrate specificity and catalytic versatility, playing an essential role in plant growth and developmental processes. The GDSL lipase gene GhGELP23D from *Gossypium hirsutum* is highly expressed during cotton fiber elongation development. This study aims to investigate its function in plant cell elongation and provides references for the mechanism elucidation of GELP-mediated regulation of cell growth. **【Method】**The GhGELP23D was cloned from upland cotton fibers. Bioinformatic analyses were performed to characterize its physicochemical properties, structural features, and phylogenetic relationships. The promoter region was analyzed with PlantCARE to identify putative cis-elements. Expression patterns were detected based on public transcriptomic data and RT-qPCR validation. A GUS reporter construct driven by the GhGELP23D promoter was generated to examine the tissue-specific expression of GhGELP23D in stably transformed *Arabidopsis*. Subcellular localization of GhGELP23D was determined through transient expression in *Nicotiana benthamiana* leaves. Transgenic *Arabidopsis* lines heterologously expressing GhGELP23D (GhGELP23D-OE) were obtained using the floral-dip method, and phenotypic analyses were conducted. Additionally, virus-induced gene silencing (VIGS) was employed to suppress GhGELP23D expression in cotton. Silencing efficiency was verified by RT-qPCR, and the resulting changes in fiber length were assessed in GhGELP23D-VIGS plants. **【Result】**GhGELP23D encodes a 356-amino-acid protein that is stable, weakly basic, and hydrophilic, containing a typical signal peptide but no transmembrane domain. Transcriptomic analysis and RT-qPCR detection showed that GhGELP23D was highly expressed during cotton fiber elongation. Subcellular localization analysis revealed that GhGELP23D is predominantly localized to the extracellular space. Analysis of the GhGELP23D promoter indicated the presence

of multiple cis-elements related to light responsiveness, hormone signaling, and stress response. Histochemical GUS staining showed that the GhGELP23D promoter can drive reporter gene expression in various Arabidopsis tissues, indicating broad tissue expression activity. Heterologous expression of GhGELP23D in Arabidopsis (GhGELP23D-OE) significantly enhanced plant growth and development, resulting in increased plant height and longer primary roots and root hairs. Furthermore, complementation of GhGELP23D in the mutant resulted in a pronounced recovery of primary root and root hair length similar to that of the wild type (WT). In cotton, the fiber length of GhGELP23D-VIGS lines was significantly reduced compared with that of empty-vector control plants, with an average decrease of approximately 13.14%.【Conclusion】GhGELP23D encodes an extracellular GDSL lipase that is highly expressed during the fiber elongation stage of upland cotton and plays an important role in plant cell elongation development.

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Title: Comparative transcriptome analysis identifies ABA/ethylene signaling components and WGCNA hub genes underlying defoliant sensitivity in *Gossypium barbadense*

Authors: Caixia Li ¹ , Meng Wang¹, Zixin Zhou, Zhiqing Liu, Jianping Li, Yaohua Li, Yahui Deng, Yifan Wang, Lingfang Ran, Jiahui Zhu, Alifu Aierxi, Weiran Wang ^{*} , Jie Kong ^{*} , Nan Zhao

Imprint: Plant Gene 48 (2026) 100613

<https://doi.org/10.1016/j.plgene.2026.100613>

Abstract: Elucidating the mechanisms governing plants responsiveness to defoliating agents is essential for developing crop cultivars optimized for mechanized harvesting. Here, we evaluated a pair of Sea Island cotton (*Gossypium barbadense* L.) genotypes possessing contrasting traits: XH35 (defoliant-sensitive) and XKK4102 (defoliants-insensitive). Foliar tissues were collected at 12, 24, and 48 h following the application of a thidiazuron-diuron combination. Transcriptomic profiling and comparative expression analyses revealed a time-dependent amplification in the abundance of differential expression genes (DEGs), reflecting a cumulative physiological response. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses demonstrated that these DEGs predominantly partitioned into pathways associated with plant hormone signal transduction, plant-pathogen interaction, and mitogen-activated protein kinase (MAPK) signaling pathway. Among these, key loci potentially modulating defoliation responsiveness were prioritized, specifically Gbar_A11G002580, Gbar_A05G004030, Gbar_D05G022860, and

Gbar_A08G023130. Furthermore, weighted gene co-expression network analysis (WGCNA) established that the MEbrown module exhibited an exceptionally strong linkage with endogenous abscisic acid (ABA) content ($r = 0.98$). Within this network, two hub determinants (Gbar_D02G007850 and Gbar_D10G005190) were identified as prospective regulators of leaf abscission. Concurrently, the transcription factor Gbar_A09G007510 displayed a strong positive correlation with defoliant sensitivity, whereas the transcription of Gbar_D05G019730 underwent near-total suppression post-treatment. Collectively, these insights advance our comprehension of the macromolecular networks driving cotton defoliation and offer invaluable candidate targets for marker-assisted breeding and genetic modification.

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Title: GhMYB94-activated *GhLTP1* couples cuticle barrier formation with membrane lipid remodeling to confer water-deficit tolerance in cotton

Authors: Chong Yang ¹, Ruiting Zheng ¹, Yanjun Li ¹, Fei Xue ¹, Shuaishuai Cheng ¹, Jie Sun ¹, Xinyu Zhang ¹, Feng Liu

Imprint: Plant Physiology and Biochemistry

<https://doi.org/10.1016/j.plaphy.2026.111714>

Abstract: Water-deficit severely limits cotton (*Gossypium hirsutum*) yield, yet how plants coordinate cuticle barrier formation with membrane lipid remodeling under water-deficit remains unknown. Through WGCNA of water-deficit transcriptomes, we identified GhLTP1, a lipid transfer protein, as the hub gene of the water-deficit-responsive module. GhLTP1 encodes a secreted protein localized to the epidermal cell wall and apoplast. Silencing GhLTP1 impaired water-deficit tolerance and caused intracellular accumulation of cutin precursors (O-acyl- ω -hydroxy fatty acids) coupled with reduced epicuticular waxes, particularly C29 and C31 n-alkanes, indicating that GhLTP1 is required for cuticular lipid accumulation. Notably, GhLTP1 silencing also triggered adaptive remodeling of cellular and thylakoid membrane lipids, by increasing unsaturation, very-long-chain fatty acid incorporation, and adjusting phospholipid-to-galactolipid ratios, consistent with cuticle defects exacerbating water loss while redirecting carbon flux from wax synthesis toward membrane lipids. We further show that GhMYB94 directly binds the GhLTP1 promoter to activate its expression, and GhMYB94-silenced plants phenocopy GhLTP1-RNAi lines. Our findings establish the GhMYB94-GhLTP1 module as a regulatory node that coordinates cuticle formation with membrane lipid remodeling to confer water-deficit tolerance in cotton.

Title: Whole genome identification and analysis of cotton(*Gossypium hirsutum* L.) pyruvate kinase gene family and functional analysis of GhPK5 gene

Authors: CHEN Long¹, CHEN Shan¹, ZHOU Bingbing¹, WANG Xiaoyue¹, LI Shujuan¹, ZHAI Xue^{1,2}, WEI Zihao¹, KE Liping^{1*}, SUN Yuqiang

Abstract: Background: Pyruvate kinase (PK) is a key rate-limiting enzyme in the glycolytic pathway, playing a central role in plant energy metabolism, growth, development, and stress responses. Although the PK gene family has been characterized in several model plants, systematic identification and functional analysis of PK genes in cotton (*Gossypium hirsutum* L.) remain limited. Results: In this study, we identified 41 PK genes in the upland cotton genome and classified them into two subfamilies (PKc and PKp) based on phylogenetic analysis. Chromosomal distribution analysis revealed that these genes are unevenly distributed across 19 chromosomes, with segmental duplication serving as the predominant expansion mechanism. Gene structure and conserved motif analyses demonstrated that members within the same subfamily share similar exon-intron organizations and motif compositions. Cis-acting element analysis indicated that GhPK promoters are enriched with stress-responsive and hormone-responsive elements. Transcriptome profiling showed diverse expression patterns of GhPK genes across different tissues, with GhPK5 exhibiting high and broad expression. Under salt, drought, heat, and cold stresses, GhPK5 displayed a strong and sustained induction, particularly under salt and combined stress conditions. Virus-induced gene silencing (VIGS) of GhPK5 resulted in increased SOD, POD, CAT activities and MDA content under salt stress, along with impaired pyruvate accumulation, suggesting that GhPK5 plays a positive role in cotton salt tolerance. Conclusions: Our genome-wide characterization of the cotton PK gene family provides a foundational understanding of their evolutionary and functional diversity. GhPK5 was identified as a candidate gene positively regulating salt stress response, offering a potential target for molecular breeding aimed at improving stress tolerance in cotton.

Title: Genome-wide characterization and temperature responsive expression profiling of the NF-X1-type zinc finger gene family in upland cotton

Authors: Muhammad Aneeq Ur Rahman · Zhang Rui · Muhammad Asif Saleem · Mirza Muhammad Ahad Baig · Saman Hanif · Zoya Batool Naqvi · Abdulsamad Baig · Yunxiao Wei · Muhammad Tanveer Altaf

Imprint: <https://doi.org/10.1186/s12870-026-09887-8>

Abstract: NF-X1-type Zinc finger (ZF) proteins are important regulatory factors involved in transcriptional control and stress-responsive signaling in plants. However, their evolutionary features and potential functions in upland cotton (*Gossypium hirsutum* L.) remain largely unclear. In this study, we systematically interrogated genomewide identification and comprehensive characterization of NF-X1-type ZF genes in *G. hirsutum* using integrated bioinformatic and transcriptomic analyses. Four NF-X1-type ZF genes were identified and found to be distributed across the A and D sub-genomes. Phylogenetic analysis showed that these proteins are closely related to homologs from dicotyledonous species, especially those in the Malvaceae lineage, suggesting strong evolutionary conservation. The identified proteins were predicted to be large, hydrophilic, and alkaline, with conserved motifs, domains, and exon-intron structures between homologous gene pairs. Promoter study demonstrated multiple cis-acting elements linked with hormonal signaling, light responses, and regulation of abiotic stresses. Structural prediction indicated conserved conformations dominated by random coil regions, and model validation supported their reliability. Transcriptomic analysis showed tissue-specific and stress-responsive expression patterns, with GhChrA09G0713 and GhChrD09G0661 showing relatively higher expression across multiple tissues and stress treatments. Notably, qRT-PCR validation demonstrated that GhChrA09G0713 and GhChrD09G0661 were significantly induced by both heat (42 °C) and cold (4 °C) stress, although with distinct temporal expression profiles. GhChrA09G0713 exhibited sustained upregulation under both temperature treatments, whereas GhChrD09G0661 showed a rapid response to heat stress and stronger induction during prolonged cold exposure. Overall, this study provides a comprehensive overview of NF-X1-type ZF genes in cotton and offers a basis for future functional dissection of their roles in developmental programs and environmental stress tolerance.

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Title: Fingerprint map construction and genetic diversity analysis of 5 Xinjiang upland cotton varieties based on SSR markers

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Imprint: Xinjiang Agricultural Sciences, 2026, Vol. 63, No. 1, 38-47 ref. 24

Abstract: Objective: This study aimed to construct DNA fingerprints of the certified variety Yuanmian 8 and four self-bred *Gossypium hirsutum* varieties using simple sequence repeat (SSR) molecular markers, and to analyze their genetic diversity. Methods: Sixty-four pairs of screened core primers were used for SSR molecular marker detection on Yuanmian 8 and four self-bred upland cotton varieties from Xinjiang. DNA fingerprints were constructed and genetic diversity was analyzed. Results: A total of 88

polymorphic bands were amplified by 64 polymorphic SSR primers across the five cotton varieties (lines). The observed number of alleles (N_a) was 128. The Shannon's information index (I) per locus ranged from 0.5004 to 0.6730, and the average Nei's gene diversity index (H) was 0.4375. Genetic diversity analysis showed that the genetic similarity coefficient between Yuanmian 8 and Yuanmian 1278 was the highest, while that between Yuanmian 8 and Yuanmian 1280 was the lowest. The genetic distance among the five germplasm materials ranged from 0.3730 to 0.8133, indicating a low level of overall genetic diversity. Exclusive QR codes were generated based on the fingerprint information of the five cotton varieties constructed by SSR markers, which could effectively distinguish different cotton varieties. Conclusion: The five Xinjiang upland cotton germplasm resources represented by Yuanmian 8 exhibit low genetic diversity. The SSR fingerprints and QR codes constructed in this study can be used for variety identification of cotton.

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Title: Cloning of GhMYB1 gene and promoter of upland cotton and expression analysis under drought induction.

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Imprint: Shandong Agricultural Sciences, 2026, Vol. 58, No. 7, 1-9

Abstract: The MYB transcription factor family is one of the largest and most widely distributed gene families in plants, playing critical roles in various biological processes including growth and development, disease resistance, and stress tolerance. In the previous study, the GhMYB1 transcription factor from upland cotton (*Gossypium hirsutum* L.) was found to interact with the elite promoter of the drought-responsive gene GhHSP70-26, suggesting its potential involvement in drought response pathways. To investigate the drought-responsive characteristics of GhMYB1, we cloned its full-length coding sequence. The results revealed that its coding sequence was 1 244 bp in length, encoding a protein of 413 amino acids. Subcellular localization prediction indicated that GhMYB1 was targeted to the nucleus and belongs to the R2R3-type MYB transcription factor subfamily. Transcriptome data analysis showed that GhMYB1 exhibited the highest expression level in leaves compared with roots and stems in upland cotton, and its expression was induced by salt, heat and drought stresses, with the maximum transcript abundance at 12 h of drought treatment. To validate the expression pattern of GhMYB1 under drought stress, quantitative real-time PCR (qRT-PCR) was performed to measure its expression levels in leaves of drought-tolerant and drought-sensitive upland cotton accessions subjected to natural drought stress. The results demonstrated that GhMYB1 expression reached its peak at 7 days after drought treatment in both genotypes. To elucidate the regulatory mechanism underlying

drought-induced expression of GhMYB1, a 1 737 bp fragment of its promoter region was cloned. PlantCARE analysis revealed the presence of multiple cis-acting elements associated with stress responsiveness and phytohormone signaling. Furthermore, a pGhMYB1:GUS plant expression vector was constructed and transiently transformed into tobacco leaves. Compared with non-stressed controls, GUS activity gradually increased following 3 h and 12 h of mannitol-simulated drought stress. Collectively, these findings indicated that GhMYB1 was responsive to drought stress in upland cotton and its promoter possessed drought-inducible activity, implying that GhMYB1 might play an important role in drought tolerance. This study could provide a solid theoretical foundation for further functional characterization of GhMYB1 and elucidation of its molecular regulatory mechanisms in drought stress responses.

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Title: Characterization and Expression Analysis of KCS Genes in Cotton: Insights Into Temperature-Regulated Fuzz Development

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Imprint: *Plant Mol Biol Rep* **44**, 128 (2026). <https://doi.org/10.1007/s11105-026-01760-0>

Abstract: The synthesis of very-long-chain fatty acids (VLCFAs), regulation of membrane lipids, and responses to external stimuli all rely on 3-ketoacyl-CoA synthase (KCS). Nevertheless, the regulatory mechanisms of KCS genes in response to temperature during cotton fiber development remain poorly characterized. Herein, a comprehensive analysis of the KCS gene family was conducted across four *Gossypium* species, identifying 167 fatty acid elongase 1 (FAE1)-type and 44 elongation of very-long-chain fatty acids (ELO)-type KCS genes. Synteny analysis revealed that whole-genome and segmental duplications primarily contributed to the expansion of the KCS gene family. intragenomic paralogs underwent strong purifying selection, while intergenomic orthologs experienced pronounced positive selection following polyploidization. The subcellular localization of KCS proteins was highly conserved. Transcriptome analysis and RT-qPCR revealed that, at 4 days post-anthesis (DPA), high temperature significantly increased the expression of five FAE1-type and two ELO-type genes. Analysis of cis-elements in the promoters revealed numerous stress- and hormone-responsive motifs, suggesting a potential association between temperature and hormone signaling. Comparison of *Gossypium hirsutum* and *Gossypium arboreum* with contrasting fuzz phenotypes revealed differences in KCS gene expression. Except for GhKCS12, the expression levels of the other seven genes were positively correlated with the fuzz phenotype in *G. hirsutum*, while these genes were either barely expressed or showed no correlation with the fuzz phenotype in *G. arboreum*. The present study uncovered a KCS-VLCFA-ACO-ethylene-fuzz signaling cascade

responsive to temperature. Importantly, the functional divergence of KCS genes between allopolyploid and diploid cotton provides insights into cotton adaptation to environmental conditions and epidermal cell differentiation and lays a solid foundation for cultivating temperature-adaptive cotton varieties with desirable fuzz traits.

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Title: BSA-Seq-Based QTL Mapping for the Height of the First Fruiting Branch Node of Cotton and the Development of Molecular Markers.

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Imprint: *Genes* **2026**, *17*, 1030. <https://doi.org/10.3390/genes17091030>

Abstract: The height of the first fruiting branch node (HFFBN) is a core indicator for mechanical harvesting of cotton, and the development of molecular markers for this trait is important for accelerating the breeding process. In this study, using bulked segregant analysis coupled with whole-genome sequencing (BSA-seq), one quantitative trait locus (QTL) associated with the HFFBN was mapped; a molecular marker, qFBH7, associated with the HFFBN of cotton was developed; and its application value was systematically evaluated. A total of 20 lines with extreme phenotypes were selected from the recombinant inbred lines constructed using upland cotton Z3-146 and Z3-147 as parental lines. The screened lines with extreme phenotypes were used to construct the extreme high-HFFBN pool and the extreme low-HFFBN pool, which were subsequently used for BSA-seq. Using the upland cotton genome as a reference, relevant QTLs were mapped by BSA-seq. One relevant candidate region was identified, with a total length of 2.25 Mb. The validation experiments revealed that the genotyping results of the KASP_FBH7_03 molecular marker in the parental lines Z3-146 and Z3-147 were completely consistent with the BSA-seq data: Z3-146 had the TT genotype, and Z3-147 had the CC genotype. Among the 66 samples from the natural population, there was a significant difference ($p < 0.05$) in the HFFBN between the CC and TT genotypes, and the mean HFFBN of the TT genotype was greater than that of the CC genotype. In summary, the KASP_FBH7_03 molecular marker can be effectively used for selective breeding for the HFFBN of cotton, and the TT genotype has a positive regulatory effect on the HFFBN. This study not only provides resources for breeding cotton varieties suited to mechanical harvesting but also offers a robust tool for molecular marker-assisted selection.

Title: A Model for Cotton Emergence Based on Thirty Years of Seed Treatment Trials Conducted by the National Cotton Seed Treatment Committee

Authors: Z.A. Noel, T.W. Allen, M. Bragg, M. Bayles, K. Bissonnette, T. Faske, C.A. Floyd, T.S. Isakeit, H. Kelly, R. Kemeraït, T. Kirkpatrick, K. Lawrence, P. Price, E. Rogenkamp, A. Rojas, C. Rothrock, I. Small, T. Spurlock, A. Strayer, Scherer, T. Wheeler, and T. H. Wilkerson

Imprint: <https://doi.org/10.1094/PHYTO-04-26-0137-R>

Abstract: Over 30 years, the National Cotton Council's National Cottonseed Treatment program has conducted coordinated seed treatment trials across the U.S., resulting in a comprehensive dataset of over 500 field trials. After data curation compiled from annual reports published in the Cotton Beltwide Proceedings, we used data from 409 field trials to develop beta regression models for upland cotton (*Gossypium hirsutum* L.) seedling emergence that integrates environmental and pathogen variables and to evaluate the efficacy of seed treatments. The minimum air temperature nine days post-planting and the cumulative precipitation three days post-planting were identified as key environmental predictors of emergence. The successful isolation of *Pythium* spp. from cotton roots was significantly associated with reduced emergence. Seed treatments containing at least three active ingredients targeting both true fungi and oomycetes improved emergence by an average of 10.2% and significantly reduced the risk of falling below the critical threshold of 35,000 emerged plants per hectare, often cited as the population to maintain yield. The resulting model introduces a benchmark tool with an associated error rate of approximately 16 to 20%, enabling future refinement. These findings highlight the long-term value of multi-state field trials and support the development of data-driven tools to guide planting or scouting decisions and optimize seed treatment strategies.

Title: Dynamic Gene Expression Changes During Cotton Seed Germination Under Salt Stress.

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Imprint: Journal of Agricultural Science & Technology (1008-0864), 2026, v. 28, n. 7, p. 39, doi. 10.13304/j.nykjdb.2026.0129

Abstract: Cotton is an important economic crop in China, and salt stress severely inhibits seed germination and seedling establishment. To reveal the dynamic changes in gene expression during cotton seed germination under salt stress, Kezimidian 73 was used as material, and mass volume fraction of 0.6% and 0.8% NaCl stress treatments were set. Samples were collected at 0, 4, 8 and 24 h during germination for RNA-Seq analysis. Differentially expressed genes (DEGs) were identified, and enrichment analysis and transcription factor analysis were conducted. The results showed that a total of 114 139 977 clean reads were obtained, and 26 650 DEGs were identified, which were significantly involved in transcription regulation, signal transduction, carbohydrate metabolism, stress response and protein processing. Under low-salt stress, DEGs were primarily enriched in pathways such as sugar metabolism, secondary metabolite synthesis and glutathione metabolism. In contrast, under high-salt stress, DEGs were mainly enriched in pathways related to plant-pathogen interaction, chaperones and folding catalysts, environmental adaptation and protein processing in the endoplasmic reticulum. A total of 1 053 differentially expressed transcription factors from 74 families were identified, which were predominantly ERF, bHLH, WRKY, NAC and ARF families, with specific distribution patterns across different germination stages. Under low-salt stress, genes encoding key sugar metabolism enzymes such as PFP and PFK showed significant differential expression. Under high-salt stress, antioxidant genes like PER12 exhibited time-specific expression patterns, with SRC2 identified as an early-response gene and LBD41 as a late-response gene. Above results revealed the dynamic transcriptional regulatory network governing cotton seed germination under salt stress, identifying key genes and transcription factors including PFP, PFK, PER12 genes and ERF, WRKY transcription factors etc, which provided crucial genetic resources for the genetic improvement of salt tolerance in cotton.

Title: GADC 4 (Wagad Resham): First Cotton (*Gossypium Herbaceum*) Variety With Superior Fibre Characteristics

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Imprint: Plant Archives Vol. 26, Supplement 2, 2026 pp. 2842-2849

Abstract: The herbaceum cotton variety Gujarat Anand Desi Cotton 4 (GADC 4: Wagad Resham), designated during testing as GVhv 936, was developed through systematic breeding at the Regional Cotton Research Station, Anand Agricultural University, Viramgam. The variety was officially released and notified in 2021 for commercial cultivation in the Northwest Agro-Climatic Zone-V and the Bhal and Coastal Agro-Climatic Zone-VIII of Gujarat. GADC 4 has demonstrated a consistent yield advantage over existing check varieties, coupled with superior fiber quality traits, making it a suitable choice for enhancing productivity and profitability in desi cotton-growing regions of the state. The variety, Gujarat Anand Desi Cotton 4 (GADC 4: Wagad Resham), is a derivative of the inter-specific varietal cross of GVhv 585 × 824. It is an early maturing, long-linted, bold-seeded, open-boll type herbaceum cotton with red-coloured anther filaments. The variety was developed at the Regional Cotton Research Station, Anand Agricultural University, Viramgam, and represents the first-ever long staple desi cotton variety released from this centre in 2021. In multi-location trials, GADC 4 recorded an average seed cotton yield of 1403 kg/ha under rainfed conditions of Gujarat. It exhibited yield superiority of 14.9, 30.8, 11.0, and 11.4% over the check varieties G. Cot. 21, GADC 2, G. Cot. 23, and GN. Cot. 25, respectively. Similarly, lint yield was enhanced by 4.4, 10.8, 14.0, and 16.0% over the same checks, demonstrating its potential as a high-yielding and superior quality desi cotton variety for the target region. It recorded an upper half mean length of 29.4 mm, fibre fineness of 4.5 µg/inch, and bundle strength of 30.6 g/tex under HVI fibre quality testing. The seeds contain 17.1% oil. Field screening for biotic stresses revealed that GADC 4 exhibits moderate tolerance to root rot, bacterial leaf blight, and alternaria leaf blight. Keywords : *Gossypium herbaceum*, GADC 4, Superior fibre quality, Desi cotton

Title: Genome-Wide Identification and Expression Analysis of the TIM Gene Family in Sea-Island Cotton (*Gossypium barbadense*) During Fiber Development

Authors: Zixin Zhou † , Weiran Wang † , Meng Wang, Caixia Li, Yaohua Li, Lingfang Ran, Jianping Li, Zhiqing Liu, Jiahui Zhu, Jing Yang, Yifan Wang, Yahui Deng, Wumaierjiang Kuerban, Alifu Aierxi, Jie Kong * and Nan Zhao

Imprint: Curr. Issues Mol. Biol. 2026, 48, 929

Abstract: The translocase of the inner membrane (TIM) family plays an essential role in mediating the transport of nuclear-encoded precursor proteins across the inner mitochondrial membrane and regulating cellular energy metabolism. Sea-island cotton (*Gossypium barbadense*) is valued for its superior fiber quality, yet the composition, evolution, and expression patterns of its TIM genes remain unclear. To address this, we performed a genome-wide analysis of the TIM family in *G. barbadense*, using the diploid cotton *G. arboreum*, and *G. raimondii* and the allotetraploid *G. hirsutum* as comparative references. A total of 44 GbTIM genes were identified in *G. barbadense* and characterized through phylogenetic, structural, collinearity, promoter, and expression analyses. The TIM family expanded during cotton polyploidization, with tetraploid species containing approximately twice as many genes as diploids. Phylogenetic analysis categorized TIM proteins into seven subfamilies, with Group VI representing the largest clade. Promoter regions were enriched in light- and phytohormonerresponsive elements. Interspecific synteny analysis demonstrated extensive collinearity between *G. barbadense* and its diploid ancestors but limited collinearity with *G. hirsutum*, indicating divergence among tetraploids. Transcriptomic profiling revealed highly spatiotemporal expression patterns. Gbar_A11G001280 was abundantly expressed during fiber initiation and upregulated in low-lint-percentage germplasm, whereas Gbar_D07G010770 was continuously expressed throughout fiber development. This study clarifies the evolutionary lineage of the TIM family across four cotton species, with a primary focus on *G. barbadense*, and provides candidate genes for molecular breeding of high-quality fiber. Functional validation of these candidate genes is recommended in future studies.

Title: Thermal comfort qualities of hybrid woven fabrics with cotton/tencel fibers used in home textiles

Authors: Ali Beyit, Abdulkadir Pars, Fatma Zehra Engin Sagirli, Merve Yarali Kinli, and Erhan Sancak

Abstract: Home textiles that combine comfort and aesthetics are becoming more popular among consumers. Bedding materials contribute to the thermal environment surrounding the body through their heat- and moisture-transfer characteristics. Material parameters such as fiber type, finishing processes, and fabric structure may therefore influence the thermal comfort conditions experienced during sleep. This study aimed to characterize key thermal comfort parameters of home textile products, including thermal resistance (expressed in Tog units), heat retention ability, water vapour resistance (determined using the sweat-guarded plate method), and air permeability. Fabrics manufactured in two different patterns using cotton and cotton/Tencel hybrid yarns were subjected to a raising process, and the different fabric compositions were examined for thermal comfort. Fabric thicknesses, the type of raw material used, the types of patterns, and the finishing processes applied were evaluated by comparison in adherence to ISO standards. Raising and various weaving structures affected heat resistance qualities, while raising lowered air permeability. The thermal resistance (Tog) values of the developed fabrics ranged from 0.11 to 0.43 Tog, with the highest value obtained for the raised twill fabric produced from 50% cotton/50% Tencel yarns. Thermal resistance increased by approximately 290%, demonstrating the combined influence of fabric weight, fiber composition, weave structure, and particularly the raising treatment on thermal insulation performance. In addition, heavier fabrics exhibited lower cooling rates and improved heat-retention ability, while the raising treatment significantly reduced both air and water vapour resistance. These findings demonstrate that structural design and surface modification play a key role in optimizing the thermal comfort performance of woven fabrics intended for home textile applications.

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Title: Cotton fiber quality responses to tillage, irrigation, and plant density

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<https://doi.org/10.1002/ael2.70099>

Abstract: Understanding how management practices interact with environmental conditions is critical for stabilizing cotton yield and fiber quality. A 2-year field study (2024–2025) assessed the effects of tillage (conventional tillage [CT]; no-till [NT]), irrigation regime (all-row irrigation [ARI]; skip-row irrigation [SRI]), and planting

density (7, 10, and 13 plants m⁻²) on cotton (*Gossypium hirsutum* L.) yield and fiber quality. Year had the strongest influence on fiber quality, with 2025 producing fibers that were significantly longer (+2%), stronger (+3%), more uniform (+1%), but with poorer color grade (+12%) compared to 2024. Irrigation affected micronaire and color, as SRI reduced micronaire by 5%. NT increased seed cotton yield by 19%. Plant density influenced fiber quality through interactions; for example, plant density had an irrigation × plant density interaction for color grade. Overall, despite strong seasonal effects, context-dependent interactions among tillage, irrigation, and planting density indicated that management could contribute to fiber quality variation across years.