GLEANINGS IN COTTON RESEARCH

FEBRUARY 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.

Swati Dixit	*Chetali Rodge*
In charge Library	*Technical Officer (T5)*

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Subject **Page No.**

AGRONOMY, SOIL SCIENCE AND PLANT PHYSIOLOGY

1

Title: Assessing the Profitability of Cotton Cultivation in Northern Gujarat.

Author: Dharmik G Borisagar, O P Singh and Vaishnavi Singh

Imprint: Journal of Agricultural Development and Policy, 2025 Volume 35, No. 1, 73-79
https://doi.org/10.63066/23220457.35.1.010

Abstract: Cotton has been a leading cash crops in India since the introduction of Bt technology, ever since farmers in Gujarat shown enthusiastic adoption. The state recorded agricultural growth rate more than double the national average between 2001–02 and 2014–15, a trend largely attributed to the widespread adoption of Bt cotton. This study, conducted in the northern districts of Gujarat viz. Patan and Mehsana, assessed the economics of cotton cultivation by analysing input costs and returns. A detailed analysis in both districts revealed that labour constituted the largest portion of the total cultivation cost. Additionally, expenses related to machinery for land preparation and pesticides were also significant. Mehsana farmers achieved higher net returns of Rs. 80,952.16/ ha with operational costs of Rs. 74,438.58/ha, while Patan farmers had lower returns of Rs. 57,127.22/ha on costs of Rs. 75,451.78/ha. The Benefit-Cost Ratio (BCR) over variable costs was observed to be 2.09 for Mehsana and 1.76 for Patan. The study further observed that, in recent years, cotton is increasingly being adopted by large farmers, as the effectiveness of Bt cotton against bollworms has declined. This trend highlights the need for renewed efforts in pest management and technological advancement to strengthen cotton productivity and help transition India from being a net importer to a net exporter of cotton.

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Title: An Efficient Cotton Yield Prediction Framework Using Remote Sensing Images.

Author: Porandla Srinivas & A. Suresh
Imprint: Sensing and Imaging , Volume 26, article number 127, (2025)

Abstract: Cotton is a crucial role in the world textile trade, which is threatened by environmental factors and climate change, Making yield prediction necessary for both sustainability and economic stability. Conventionally, remote sensing-assisted crop yield estimation is usually done using Machine learning methods. However, conventional techniques using machine learning may face problems when using yield regression functions in farming. Hence, a new deep learning-aided cotton yield prediction framework is implemented using remote sensing images. At first, the required remote sensing images are aggregated from available data sources. Then, 3D Yolo-Transformer Unet++ (3D YTUnet++) is introduced and the 3D convolution in this model helps to extract hidden features and segment anomalies. The segmented images are then processed through a Vision Transformer (ViT)-aided Adaptive ShufflenetV2 (ViT-ASNetv2) for accurate yield prediction. Here, the Improved Hermit Crab Optimizer (IHCO) is employed for optimizing the parameters of the ShufflenetV2 technique. The performance evaluation represents with integration of these sophisticated techniques provides a more accurate and reliable model for predicting cotton yields from remote sensing data. The accuracy score achieved by the designed model in cotton yield prediction is 96.4%.

3

Title: Temporal dynamics and optimal dose effects of biochar on soil properties, cotton growth, and bacterial community assembly in saline-alkali soils.

Author: Yuting Wang, Guangli Tian, Qingqing zhao, Dongwei Li & Shuai He

Imprint: BMC Plant Biology , Volume 25, article number 1337, (2025)

Abstract: Biochar is widely recognized as an effective soil amendment, yet its residual effects on saline soils remain underexplored. This study investigates the residual impact of a single biochar application on soil properties, bacterial community assembly, and cotton growth over three years. A controlled pot experiment was conducted using four biochar treatments − 0%, 1%, 3%, and 5% (w/w) - along with two cotton varieties: salt-sensitive and salt-tolerant. Results showed that biochar reduced soil salinity by 0.80–1.39 g·kg^{-1} in the second year, with no effects observed in years 1 and 3. By the third year, biochar at 5% increased soil pH by 0.34–0.44 units. Biochar application enhanced soil organic carbon by 135.15%–763.19%, total nitrogen by 12.88%–241.92%, and available potassium by 22.00%–168.84%, in a dose-dependent manner. However, available phosphorus was unaffected by biochar and showed a gradual decline over time. Biochar altered bacterial community composition but had limited impact on alpha diversity. A shift from homogeneous to heterogeneous selection in bacterial community assembly was observed in the third year, correlating with soil nutrient changes. Cotton growth exhibited an “A-shaped” response, with Limited benefits in the first and third years but improvement in the second year. The 1% biochar promoted cotton growth by at least 12.07%, whereas higher concentrations (3% and 5%) had no effect, emphasizing an optimal dose effect. These findings highlight biochar’s potential as a tool for improving saline soils, while underscoring the importance of optimizing application rates and considering its long-term residual effects.

4

Title: Agronomic efficiency of nano-integrated nutrient management on cotton yield traits under arid farming conditions.

Author: Inomjon Israilov, Obidjon Sindarov, Shavkat Salomov, Shoxnazar Bobokulov, Ilkhom Begmatov, Khasimbek Isabaev, Bekjan Uspankulov

Imprint: Front. Sustain. Food Syst., 12 November 2025, Sec. Climate-Smart Food Systems, Volume 9 - 2025 https://doi.org/10.3389/fsufs.2025.1695604

Abstract: Cotton (Gossypium spp.) is a globally cultivated climate resilience fiber crop known for its potential to produce substantial biomass and yield in stress environments. However, its production requires a huge amount of chemicals, bringing harm to the environment and ecosystem services. Field studies during the 2023–2024 growing seasons were focused on agronomic parameters of cotton in response to nano (Si and Uzbi) and three chemical fertilizer regimes (N150 P105 K75; N200P140 K100; N250P175K125) under arid condition of Uzbekistan. The experiment was arranged in a split-plot design with three replications. The application of nano Si improved nutrients uptake and yield parameters of cotton under open-field arid environment due to a positive synergism between nano and chemical fertilization. The effect of Si nano compound was more pronounced at the lower fertilizer regime (N150P105K75), exhibiting the increase of cotton yield by 31.3% and 1000 seed weight by 5.32% than those in the control. On the other hand, the Uzbi treatment exhibited high efficacy at the intermediate fertilizer level (N200P140K100), enhancing total cotton biomass by 12.9% and total yield by 26.3% relative to the control. The Si nano was found to be relatively efficient in terms of NUE, crop yield and may help reduce the reliance on excessive chemicals in current climate changing scenario. This study explored the cost-effective pathways toward more sustainable cotton production through the synergistic combination of nano and chemical fertilizers in irrigated arid agricultural regions.

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Title: An AI-Enabled System for Automated Plant Detection and Site-Specific Fertilizer Application for Cotton Crops.

Author: Arjun Chouriya, Peeyush Soni, Abhilash K. Chandel and Ajay Kumar Patel

Imprint: Automation 2025, 6(4), 53; https://doi.org/10.3390/automation6040053

Abstract: Typical fertilizer applicators are often restricted in performance due to non-uniformity in distribution, required labor and time intensiveness, high discharge rate, chemical input wastage, and fostering weed proliferation. To address this gap in production agriculture, an automated variable-rate fertilizer applicator was developed for the cotton crop that is based on deep learning-initiated electronic control unit (ECU). The applicator comprises (a) plant recognition unit (PRU) to capture and predict presence (or absence) of cotton plants using the YOLOv7 recognition model deployed on-board Raspberry Pi microprocessor (Wale, UK), and relay decision to a microcontroller; (b) an ECU to control stepper motor of fertilizer metering unit as per received cotton-detection signal from the PRU; and (c) fertilizer metering unit that delivers precisely metered granular fertilizer to the targeted cotton plant when corresponding stepper motor is triggered by the microcontroller. The trials were conducted in the laboratory on a custom testbed using artificial cotton plants, with the camera positioned 0.21 m ahead of the discharge tube and 16 cm above the plants. The system was evaluated at forward speeds ranging from 0.2 to 1.0 km/h under lighting levels of 3000, 5000, and 7000 lux to simulate varying illumination conditions in the field. Precision, recall, F1-score, and mAP of the plant recognition model were determined as 1.00 at 0.669 confidence, 0.97 at 0.000 confidence, 0.87 at 0.151 confidence, and 0.906 at 0.5 confidence, respectively. The mean absolute percent error (MAPE) of 6.15% and 9.1%, and mean absolute deviation (MAD) of 0.81 g/plant and 1.20 g/plant, on application of urea and Diammonium Phosphate (DAP), were observed, respectively. The statistical analysis showed no significant effect of the forward speed of the conveying system on fertilizer application rate ($p > 0.05$), thereby offering a uniform application throughout, independent of the forward speed. The developed fertilizer applicator enhances precision in site-specific applications, minimizes fertilizer wastage, and reduces labor requirements. Eventually, this fertilizer applicator placed the fertilizer near targeted plants as per the recommended dosage.

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Title: Altered cell wall properties in domesticated cotton enhance CO_2 diffusion conductance.

Author: Dongsheng Sun , Zhangying Lei , Jaume Flexas , Cuncang Jiang ,
Ziliang Li , Hao Ding , Fang Liu , Yinglang Wan , Wangfeng Zhang ,
Marc Carriquí

Imprint: Journal of Experimental Botany, eraf441, https://doi.org/10.1093/jxb/eraf441, 08 October 2025

Abstract: The cell wall plays a key role in determining mesophyll conductance (gm) and photosynthetic capacity. While the impact of wall thickness (Tcw) on gm is well understood, the influence of wall composition and structural interactions

on Tcw and gm remains unclear, and it is unknown whether these factors have been affected during crop domestication. In this study, we examined 25 wild and 13 domesticated Gossypium genotypes to investigate whether variations in Tcw, composition, and structure affected gm and photosynthesis. X-ray diffraction was used to analyze internal cell wall structure. Cotton domestication reduced Tcw by modifying the pectin-to-(cellulose+hemicellulose) ratio and increasing cellulose crystallinity. However, cell wall composition and structure regulate gm differently in wild and domesticated genotypes. In wild genotypes, the pectin-to-(cellulose+hemicellulose) ratio influences CO2 diffusion, while in domesticated genotypes, the pectin matrix may be more compact, making 1/(pectin+cellulose+hemicellulose) a better predictor, reflecting the internal property differences of the cell wall. We suggest that the exceptionally low Tcw values reported in cotton domesticated genotypes indicate that they have reached the lower limit, which may impose physical constraints on component proportions and conformation.

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Title: Microbial mechanisms underlying organic phosphorus mineralization and inorganic phosphorus solubilization in arid cotton fields under brackish water drip irrigation and phosphorus fertilization.

Author;Yang Ye, Xiang Li, Tao Xu, Wei Min,

Imprint: Industrial Crops and Products, Volume 236, 2 November 2025, 121983

Abstract: Phosphorus (P) fertilizer utilization is globally constrained by strong soil fixation, which reduces its effectiveness in improving crop yield and quality—a challenge particularly pronounced in arid regions like Xinjiang, China. In arid regions facing freshwater scarcity and soil salinization, integrating brackish water drip irrigation with P fertilization is a potential strategy to enhance cotton productivity. However, the microbial mechanisms particularly functional genes involved in organic phosphorus mineralization (OPM) and inorganic Phosphorus solubilization (IPS), remain poorly understood. This study, conducted in a fixed-site field experiment with consistent long-term treatments, assessed four treatments: fresh water without P (FW), fresh water with P (FWP), brackish water without P (BW), and brackish water with P (BWP), brackish water irrigation significantly reduced cotton growth with biomass, P uptake, and yield decreasing by 27.1 %, 36.1 %, and 17.2 %, respectively. It also altered soil properties, increasing water content, electrical conductivity, organic carbon, and bulk density, while decreasing pH and porosity. P fertilization mitigated these effects, boosting biomass, P uptake, and yield by 51.3 %, 57.9 %, and 10.4 %, respectively. Microbial analysis revealed that brackish water irrigation increased the relative abundance of Pseudomonadota, Bacteroidota, and the gene *phnP,* while decreasing *phoD, gcd,* and *pqqC*. P fertilization increased the abundance of Pseudomonadota, Bacteroidota, Gemmatimonadota, and Planctomycetota, with regulatory effects on functional genes varying under salinity levels. These findings elucidate the regulatory impacts of long-term brackish water drip irrigation and P fertilization on OPM and IPS associated genes in arid cotton soils, offering theoretical guidance for optimizing P management in saline environments.

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Title: Reasoning Behind Soil Fertilisation under Cotton Crops Based on the Relationship between the Sum of Exchangeable Bases (SEB) and Mineralisable Nitrogen (N-NH4 +) .

Author: KOUASSI Koffi Djinkin Samuel , TOURE Bessimory , ABOBI Akré Hébert Damien , ZORO Bi Gohi Fernand and BAKAYOKO Sidiki

Imprint: International Journal of Plant & Soil Science Volume 37, Issue 10, Page 109-123, 2025;

Abstract: Contributing to improving cotton productivity by fertilising the soil in a sustainable manner. The experiment was conducted in a farming environment, with two one-hectare plots of farmland demarcated in each section. The study was conducted in 2019–2020 in the cotton-growing region of Ouangolodougou, Côte d'Ivoire. Two one-hectare plots of farmland were marked out. One plot served as a control and was fertilised solely with 15-15-15 NPK. The second plot, known as the test plot, received inputs corresponding to the predetermined recommendation using the N-NH4 + approach (Tié, 1995). This involved applying 200 kg of NPK (15-15-15), 100 kg of dolomite with 30% CaO, 50 kg of urea with 46% N and 50 kg of KCl with 60% K2O per hectare. Observations focused on plant height, number of fruiting and vegetative branches, internodes, bolls and yield. The study showed widespread potassium deficiency, as well as calcium and magnesium deficiency in some cases. Agronomic results revealed a significant improvement in growth parameters (plant hight, number of fruiting branches, internodes, bolls and yields (increased by a factor of 8 to 12) in plots fertilised according to the recommended approach. Statistical analysis confirmed the effectiveness of this adapted fertilisation, showing that the approach based on N-NH4 + and SBE diagnosis optimises the use of inputs, increases productivity and preserves soil quality. The study validates the hypothesis that rational fertilisation, based on an accurate fertility diagnosis, significantly improves cotton yields, unlike standard doses that are not tailored to specific needs. It illustrates the importance of localised and rational fertiliser management in ensuring the sustainability and competitiveness of the Ivorian cotton industry

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Title: Planting dates and rate of nitrogen fertilization influences whitefly population dynamics and incidence in cotton (*Gossypium hirsutum* L.).

Author: Rishi Kumar, Amarpreet Singh & Debashis Paul

Imprint: Discover Ecology, 07 October 2025, Volume 1, article number 11, (2025)

Abstract: A two-year study examined impact of planting date and nitrogen fertilizer on cotton yield and whitefly population dynamics and incidence. The study compared a local cotton variety and a hybrid variety planted at different sowing time and with varying nitrogen levels, under both protected and unprotected conditions. Very late planting of cotton led to 9.2–14% higher mean whitefly populations, especially during the whitefly's peak activity period (15.82 and 21.67 whiteflies per three leaves during 2018-19 and 2019-20, respectively) at 38 Standard Meteorological Week (SMW). Observation recorded on nymphal counts revealed comparatively a smaller number of mean nymphs per three leaves (8.01 and 8.59 during 2018-19 and 2019-20, respectively) at early stages of crop growth (at 27 SMW) in very late sown crop having poor vegetative growth. As delayed sowing attained optimum growth it attracts comparatively higher nymphal population (13.36 and 10.96 during 2018-19 and 2019-20, respectively) at later stages of crop growth (at 33 SMW). Interestingly, there wasn't much difference between protected and unprotected plots. Using more nitrogen fertilizer than recommended resulted in significantly higher whitefly numbers (14.21 and 15.60, during 2018-19 and 2019-20, respectively) throughout the season. Early (32.00 and 32.75 q/ha seed cotton yield, during 2018-19 and 2019-20, respectively) and timely planted cotton (30.94 and 32.50 q/ha seed cotton yield, during 2018-19 and 2019-20, respectively) produced significantly higher yields compared to very late planted cotton (19.66 and 21.63 q/ha seed cotton yield, during 2018-19 and 2019-20, respectively). Thus, timely sowing of cotton genotypes along with application of recommended doses of nitrogen is recommended for better cotton yields and to effectively manage whiteflies.

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Title: Morphological Variability of the Cotton Boll Weevil in the Principal Cotton-Growing Region of Argentina.

Author: Carolina V. García, Mauricio Tcach, María A. Simonella, Melina S. Almada, Julio González, Silvia B. Lanzavecchia, Ana L. Nussenbaum

Imprint: Entomologia Experimentalis et Applicata, First published: 01 October 2025, https://doi.org/10.1111/eea.70020

Abstract: The cotton boll weevil (*Anthonomus grandis grandis* Boheman) (Coleoptera: Curculionidae) is the main pest of the cotton (*Gossypium hirsutum* Linnaeus) (Malvaceae) crop in South America. First reported in Argentina in 1993, it rapidly dispersed throughout the main cotton-growing region, severely impacting the crop production. However, little is known about the external morphometry and variability of these populations. The main objective of the present study was to assess morphological variability among five boll weevil populations collected in the main cotton-growing region of Argentina during two seasons (winter and growing seasons) using traditional morphometry. Nine morphological variables were measured in 30 individuals per population. Sexual dimorphism was not detected for any of the variables. Significant differences among populations were found based on location and season of collection. Principal component analysis (PCA) and a dendrogram revealed that winter populations clustered together, showing intermediate morphological values and low variability across the three sampled localities. Populations collected during the growing season grouped into two distinct clusters: one comprising populations from the Chaco province and the other from the remaining locations. One-way ANOVA further supported these patterns, indicating significant differences among *Anthonomus grandis grandis* populations for "elytra length" and "total body length" variables. The results were discussed in relation to climatic conditions, cotton management practices, and alternative food sources, providing morphological records that could help optimize control strategies. Larger individuals, likely key reproducers, may require early control, whereas smaller ones may reflect suboptimal development due to limited nutritional resources or high intraspecific competition. These traits may also affect the survival of overwintering populations. Overall, these findings contribute to a better understanding of boll weevil population dynamics and their implications for integrated pest management.

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Title: Spatio-Temporal Distribution of Fusarium Wilt and Floral Virescence, Two Major Diseases of Cotton in Côte D’ivoire: Agronomic Implications.

Author: KOUAKOU Malanno, GNAPI Diane Estelle, KOUADIO Houphouët, KOFFI Kouakou Jean Innocent

Imprint: https://doi.org/10.21203/rs.3.rs-7213160/v1, This work is licensed under a CC BY 4.0 License

Abstract: Background: Vascular fusarium wilt and floral virescence are two major cotton diseases in Côte d’Ivoire, responsible for significant yield losses. Despite their impact, current knowledge about their distribution and dynamics remains limited, as most studies date back several decades. Given this situation, it is necessary to update the data in order to better understand the evolution of diseases in the main cotton-producing areas. The objective of this study is to analyze the spatial-temporal distribution of vascular fusarium wilt and floral virescence based on monitoring carried out on 600 smallholder plots between 2022 and 2024. Results: The results of the seasonal variation show that the incidence of fusarium wilt varies from one crop year to another, with no statistically significant difference between the three seasons ($p = 0.351$). Spatially, the disease is mainly localized in the southern part of the cotton basin (below the 9th parallel), with three foci identified in the northern part. With regard to floral virescence, the seasonal dynamics exhibit a nearly similar pattern across the three cropping seasons, with varying levels of incidence. The 2022 cropping season exhibited the highest incidence rates. Unlike fusarium wilt, inter-season variations in floral virescence are statistically significant. The most affected areas are mainly located in the North of the cotton basin (above the 8th parallel). Conclusion: These results highlight the need to implement targeted phytosanitary strategies, including vector control and the introduction of resistant cotton varieties. They may also guide the choice of plots for seed production.

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Title: Distribution of thrips in cotton canopy under subtropical conditions of Punjab, India.

Author: Amandeep Kaur, Vijay Kumar, Nitika Saini

Imprint: Journal of Entomological Research, Year: 2025, Volume: 49, Issue: 3

Abstract: The experiment was conducted for two consecutive years to study distribution of thrips population within plant. Among the upper, middle and lower canopy, maximum thrips population was recorded on upper canopy (19.77 thrips/3 leaves) as compared to the middle (2.41 thrips/3 leaves) and lower (0.58 thrips/3 leaves) canopy. Thrips prefer to feed more on Bt cotton (4.64 thrips/3 leaves) than non-Bt cotton (4.27 thrips/3 leaves). The peak activity period of thrips was recorded during 26th and 27th standard meteorological week of year 2022 and 2023, respectively. Thrips showed significant positive correlation with rainfall and significant negative correlation with morning relative humidity.

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Title: Classification of cotton leaf disease using YOLOv8 based k-fold cross validation deep learning method for precision agriculture.

Author: Kamaldeep Joshi, Yashasvi Yadav, Sahil Hooda, Rainu Nandal, Baljinder Singh, Kashmir Singh, Narendra Tuteja, Ritu Gill & Sarvajeet Singh Gill

Imprint: *Scientific Reports* volume 15, Article number: 35602 (2025)

Abstract: Cotton production is a crucial agricultural industry, a raw material source for the textiles sector and a major source of livelihood for more than 30 million farmers globally. The yield and quality of cotton (*Gossypium*) are influenced by different types of stress and diseases. Deep Learning as a solution for disease prevention, detection, and management can increase the yield, reduce the cost and improve the quality of crop. This study presents a robust method using 10-fold cross-validation with the YOLOv8 DL model for precise cotton leaf disease recognition. The k-fold cross-validation mitigates overfitting by training the model on diverse data subsets, which leads to enhanced generalizability while ensuring reliable performance. The proposed method achieved 99.60% and 100% as Top_1 and Top_5 accuracy, respectively. The method also achieved a recall of 99.53%, a precision of 99.53%, and an F1 score of 99.60%. During 10 trials, the method consistently performed with an average. Top_1 and Top_5 accuracy of 98.41% and 100% respectively, recall 98.53%, precision 98.39% and F1 score 98.42%.This study is among the first to apply YOLOv8 classification with 10-fold cross-validation for multi-class cotton leaf disease identification using field-captured images.

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Title: Resistance mechanism of cotton (Gossypium *hirsutum) against* verticilum wilt (*Verticillium dahlia*); A review.

Author: Shiguftah Khalid, Junaid Ahmed, Humera Amin, Salman Alrokayan, Hankui Wu, Rashid Iqbal, Aamir Ali Abro, Xiongming Du & Fang Liu

Imprint: Functional & Integrative Genomics, Volume 25, article number 224, (2025)

Abstract: : Verticillium dahliae, a soil-borne pathogen, poses a threat to cotton production, causing wilting and quality issues. While progress has been made in understanding the interaction between cotton and *V. dahliae*, many molecular aspects of the defense mechanisms of cotton remain unclear. Cotton primarily relies on preformed defense structures, including cuticle synthesis and phenolic compound production, along with physiological and biochemical reactions. Current defense strategies involve preventing reactive oxygen species accumulation and inducing systemic acquired resistance. This study underscores the importance of these mechanisms and highlights the potential for genetic and molecular engineering to enhance resistance of cotton against Verticillium wilt, offering insights for future breeding of resilient cotton varieties.

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Title: A New Model of the Mechanisms behind Glucose Oxidase Action in Plant Insect Interactions.

Author: Jared Griffin, Sahil Pawar & Gary W. Felton
Imprint: Journal of Chemical Ecology ,, Volume 51, article number 100, (2025)

Abstract: Plants and insect herbivores are in a constant co-evolutionary arms race. Plants are always under the threat of insect herbivory and need to employ defenses against insect herbivores, which in turn employ counter defense strategies. The salivary enzyme glucose oxidase (GOX), found in many caterpillar species, has been documented to attenuate defenses in plants such as *Nicotiana tabacum* (cultivated tobacco). However, in *Solanum lycopersicum* (cultivated tomato), glucose oxidase elicits defensive responses. Multiple mechanisms have been proposed for how GOX affects plant signaling, but there is still considerable disagreement about which is correct. In this review, we review existing models on the mode of GOX action and propose a new model to fill in research gaps and better explain the mechanism behind GOX action. Our model, coined the "ROS Threshold-Dependent Defense Toggle Model", proposes that whether a plant activates jasmonic acid or salicylic acid-mediated defenses depends on the amount and persistence of hydrogen peroxide whose levels are dependent upon ROS-scavenging capabilities of the plant. We also emphasize the use of cultivated tomato as a model system to test our proposed model.

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Title: Environmental pressures shape regional patterns of genetic diversity and ancestry in cotton.

Author: Avinash Shrestha, Maximus A. Gudino, Rosalyn B. Angeles-Shim

Imprint: Front. Plant Sci., 21 November 2025, Sec. Plant Breeding, Volume 16 - 2025 https://doi.org/10.3389/fpls.2025.1707011

Abstract: Upland cotton has undergone extensive domestication and breeding, leading to substantial genetic improvement but also a pronounced narrowing of its genetic base. To better characterize and leverage the diversity preserved in traditional gene pools, we examined the population structure, phylogenetic relationships, and genomic signatures of selection in a globally sourced panel of cotton landraces and elite cultivars. STRUCTURE and neighbor-joining analyses based on whole-genome SNP genotyping identified four ancestral populations divided into nine major clusters. The landrace accessions formed deep, regionally coherent lineages characterized by high heterozygosity and an abundance of private alleles. Consistent with these patterns, Nei's genetic distance and pairwise FST estimates revealed strong divergence between Mesoamerican and Central American landraces relative to modern breeding lines. Flowering time, a key adaptive trait, was strongly associated with genetic clusters, with photoperiod-sensitive genotypes primarily originating from highland and tropical regions. Genome-wide scans of Tajima's D further differentiated landraces from cultivars, revealing signatures of balancing selection and ancestral polymorphism in the landraces, and selective sweeps in cultivated accessions. Notably, flowering-related genes on chromosomes D05 and A05 were located in regions exhibiting contrasting Tajima's D values between the two gene pools. These findings demonstrate that cotton landraces have retained valuable genomic regions lost from modern cultivars through domestication and decades of intensive improvement. As such, they represent an important reservoir for enhancing resilience, adaptation, and fiber traits in modern cotton. Collectively, our results provide a high-resolution framework for targeted pre-breeding and conservation initiatives, underscoring the untapped potential of landraces in broadening the genetic base of cultivated G. hirsutum.

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Title: Assessment of heterosis and combining ability for yield and oil traits in cotton (Gossypium hirsutum L.) contributing to the revival of India's cotton sector.

Authors: Patel, J. D.; Dubey, N.; Delvadiya, I. R.; Avinashe, H.; Keerthana, Sai

Imprint: Journal of Applied & Natural Science, 2025, Vol 17, Issue 3, p1227

Abstract :Cotton is a major commercial crop with global importance, especially in the textile sector. Enhancing its yield and fibre quality through hybrid breeding is a key goal in crop improvement. This study was conducted during Kharif 2024 at Lovely Professional University, School of Agriculture, Genetics and Plant Breeding Research Farm in Phagwara, Punjab, to evaluate combining ability, gene action, and heterosis in cotton (Gossypium hirsutum L.). A total of 24 F1 hybrids were developed using 10 cotton genotypes (6 lines and 4 testers) along with a standard check (G. Cot. Hy 18) in a line × tester design. Analysis of variance revealed significant variability in seed yield, boll weight, and fibre quality traits, indicating potential for improvement. Nonadditive gene action was observed for seed yield, boll production, and fiber quality, whereas additive gene action was prominent for earliness traits like flowering and boll bursting. The lines 761H20 and GJHV-510, along with the tester Sanjay (CJ-73), were identified as effective general combiners for seed yield, boll weight, and fiber quality. Among the hybrids, 761H20 × V-797, GJHV-503 × Guj. Cot.-15, and 761H20 × Deviraj stood out as the top performers, exhibiting strong performance, high SCA effects, and improved heterosis for yield and fiber traits. Additionally, the hybrid GJC-101 × V-797 showed excellent performance in boll production and weight. These hybrids have strong potential for commercial through heterosis breeding. The variance ratio (σ^2GCA/σ^2SCA) being less than one confirmed the predominance of non-additive gene action. This study provides insights for developing superior cotton hybrids.

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Title: The regulation of *GhAAO9* expression by *GhGATA1* during pollen development is essential for male fertility in cotton.

Author:Zhe Wang, Lina Ma, Jin Wang , Qibo Jia, Ningna Wang , Kaikai Qiao, Juxin Hao , Chenglong Zhao , Yonglin Yang

Imprint: Plant Physiology and Biochemistry, Volume 229, Part D, December 2025, 110638

Abstract: As an important part of the plant reproductive system, pollen tubes play a key role in maintaining normal male fertility. Abnormal pollen tube germination severely impacts male fertility, yet its regulatory mechanisms remain poorly understood. Ascorbic acid oxidase (AAO) plays an important role in pollen tube germination, and the functional role of AAO in male sterility of flowering plants such as *Arabidopsis thaliana* and barley has been reported. However, molecular cloning and functional identification of AAO in cotton remain unclear. In this study, the *GhAAO9* gene, which is closely associated with male sterility in cotton, was successfully cloned and characterized. Following its knockout using CRISPR-Cas9, it was observed that the mutant pollen failed to disperse properly and exhibited a near-complete loss of viability (96 %), which is the primary cause of the male sterility phenotype. A minority of mutant pollen grains (~4 %) that retained partial viability displayed severely impaired pollen tube germination and elongation in vitro… qRT-PCR analysis confirmed a significant reduction in *GhAAO9* transcript levels in *ghaao9* mutant anthers/pollen relative to the WT, which, together with the frameshift mutations, substantiates that the observed male sterility arises from deficient *GhAAO9* function during pollen development. The electrophoretic mobility shift assay (EMSA) further confirmed the in vitro interaction between *GhGATA1* and the regulatory region of *GhAAO9*. The dual-luciferase reporter assay confirmed that *GhGATA1* suppresses the expression of *GhAAO9*, which subsequently results in the manifestation of a sterile phenotype. This study demonstrated that *GhGATA1* regulates *GhAAO9* expression, influencing pollen tube germination in cotton and offering valuable insights into the mechanisms underlying male sterility. While AAO functions have been characterized in Arabidopsis and cereals, cotton (*Gossypium hirsutum)*—an allotetraploid species with complex reproductive biology—remains unexplored. Given cotton's global agricultural importance and the unique challenges in its pollen tube guidance mechanisms, elucidating GhAAO9's role addresses a critical gap in understanding male sterility in fiber crops.

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Title*: GhCYP704B1* is essential for pollen Exine and anther Cutin biosynthesis and plays a critical role in cotton male fertility.

Author: Yuling Li, Jie Gao, Qian Yang, Hongli Zheng, Nnaemeka E. Vitalis, Liping Ke, Jianxin Chen, Yanyan Zhao & Yuqiang Sun

Imprint: Molecular Breeding , Published: 04 October 2025, Volume 45, article number 78, (2025)

Abstract: Cotton hybrids offer significant advantages, the application of male sterile lines in cotton hybrid breeding can reduce the cost of artificial castration and ensure hybrid seed purity. Pollen and anther development are a crucial aspect of plant fertility, sporopollenin synthesis provides the major component of the outer walls in pollen (exines) for preserving pollen grains activity, mutations in the genes involved in sporopollenin synthesis affect pollen development and fertility formation. The differentially expressed genes (DEGs) between the developing anthers of genic male sterile mutant (*ms1*) and its genetic background Coker 312 were identified, the genes related to pollen exine and anther cutin biosynthesis were screened from the DEGs. *GhCYP704B1* (Gh_D12G2768) was the DEGs with a significantly down-regulated expression level in *ms1* anthers, kept very low expression level in *ms1* developing anthers. At the same time, we also screened 20 homologies of *GhCYP704B1* from DEGs data, and the results showed that only *GhCYP704B1* was predominantly expressed in cotton anthers, while other homologies did not show significant expression changes. We used VIGS technology the expression level of *GhCYP704B1* in cotton C312, resulting in disrupted callose formation during the tetrad formation of microspore development, partial defect of the pollen exine, weakened pollen activity, low pollen germination rate, and poor plant fertility. The expression levels of genes related to pollen exine and anther cutin synthesis changed significantly, the composition and content of cutin monomers in cotton anthers were significantly reduced in *GhCYP704B1*-silenced lines. Abnormalities in callose caused blockage of sporopollenin synthesis and failure to synthesize the pollen exine properly. The findings indicate that *GhCYP704B1* affects cotton fertility and is involved in pollen exine biosynthesis, thus providing a candidate gene for creating new male sterile lines in *G. hirsutum*.

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Title: Genetics and evolution of the GoP_1 gene regulating yellow pollen coloration enhancing pollinator attraction in cotton .

Author: Chujun Huang , Wanying Zhang , Yu Cheng , Sunyi Yan , Lu He , Zesheng Rui , Yiwen Cao , Jinwen Chen , Zhanfeng Si , Yan Hu

Imprint: Journal of Experimental Botany, Volume 77, Issue 2, 12 January 2026, Pages 431–444, https://doi.org/10.1093/jxb/eraf448

Abstract: Pollen is produced in the anthers of angiosperm stamens and serves a crucial role in pollination and plant reproduction. The coloration of floral organs is known to attract pollinators, thereby enhancing pollination efficiency and seed production. However, the genetic basis of pollen pigmentation in tetraploid cotton, a major source of renewable fiber worldwide, remains obscure. In this study, we found that yellow pollen pigmentation significantly increased pollinator honeybee visitation to cotton flowers. Here, we fine-mapped and identified a dominant yellow pollen gene, GoP1, which encodes phytoene synthase (PSY), a gateway enzyme in the carotenoid biosynthesis pathway. Silencing GoP1 in the yellow pollen parent J8891 using virus-induced gene silencing and CRISPR/Cas9-mediated targeted mutagenesis disrupted synthesis of carotenoid and other pigments, resulting in significantly reduced carotenoid levels in mature pollen and a white pollen phenotype. Additionally, genomic analysis of a resequencing panel comprising 497 cotton accessions revealed that the yellow pollen trait was gradually lost under negative selection during the domestication and improvement of upland cotton. White pollen plants, which attracted fewer pollinators, helped maintain higher variety purity in production, making them more favored by breeders. Our findings provide new perspectives on the genetic mechanisms of pollen coloration and uncover a promising approach to enhance cotton productivity.

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Title: GhWRKY41 Confers Salt Tolerance by Enhancing Photosynthetic Capacity in Cotton (*Gossypium hirsutum*).

Author: Shenghua Xiao, Mingkun Chen, Lifang Zeng, Kai Chen, Mingjing Liao, Yuqing Ming, Keyi Luo, Shiming Liu, Xiyan Yang, Baoqi Li

Imprint: Plant cell & Environment, 13 October 2025, https://doi.org/10.1111/pce.70224

Abstract: Cotton is a vital textile resource; however, its productivity and fibre quality are severely affected by soil salinity. Identifying salt-tolerant genes is critical for improving cotton resilience, yet the molecular mechanisms linking photosynthesis and chlorophyll metabolism to the salt stress response remain poorly understood. In this study, the WRKY transcription factor *GhWRKY41* was identified as a key regulator of salt tolerance by screening WRKY family members responsive to salinity stress. Functional validation demonstrated that *GhWRKY41* overexpression significantly enhanced salt tolerance in cotton and *Arabidopsis*, whereas gene knockdown increased the sensitivity of cotton to salt stress. GhWRKY41 directly binds to and activates the expression of two salt-responsive genes, *GhMPK3* and *GhLEA3*. Global transcriptomic analyses revealed that GhWRKY41 and its *Arabidopsis* homologues regulate a set of genes involved in photosynthesis and salt stress responses. Notably, GhWRKY41 knockdown downregulated genes encoding photosystem reaction centre proteins, impairing photosynthetic capacity under salt stress. These findings indicate that GhWRKY41 enhances salt tolerance primarily by maintaining elevated photosynthetic activity in cotton under saline conditions. This study provides novel insights into the complex regulatory network underlying the response of cotton to salt stress and presents a valuable genetic resource for breeding salt-tolerant cotton varieties.

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Title: Genome-wide identification and functional characterization of the CP12 gene family in cotton reveals its critical role in heat stress response.

Author: Chao Li, Shuguang Li , Juan Xu , Ziling Han

Imprint: Front. Plant Sci., 30 October 2025, Sec. Plant Abiotic Stress, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1707567

Abstract: Introduction: Calvin Cycle Protein 12 (CP12) is a key regulator of the Calvin-Benson-Bassham (CBB) cycle that mediates CO_2 assimilation through dark/light modulation. Beyond its canonical role, emerging evidence indicates that CP12 may also function as a molecular chaperone and participate in plant stress responses. However, its gene family characteristics and roles under heat stress remain unclear in cotton.

Methods: We performed a genome-wide identification and characterization of the CP12 gene family in four cotton species (Gossypium hirsutum, G. barbadense, G. arboreum, and G. raimondii). Phylogenetic classification, conserved motif analysis, gene structure, synteny, and promoter cis-element analyses were conducted. Transcriptome datasets from flowers, leaves, and buds under heat stress were analyzed to determine expression patterns, and these were further correlated with physiological indicators.

Results: A total of 11, 10, 5, and 4 CP12 genes were identified in G. hirsutum, G. barbadense, G. arboreum, and G. raimondii, respectively. Phylogenetic analysis grouped them into three clades (I–III), supported by conserved motif and structural features. Synteny analysis indicated that whole-genome and segmental duplications were the primary drivers of expansion. Promoter analysis revealed enrichment of stress-responsive elements. Expression profiling showed clade-specific divergence: Clade I genes were strongly induced by heat stress, with Ghir_CP12_10 displaying ~10-fold upregulation in flowers, while Clade II genes were generally downregulated. These expression trends were associated with physiological changes, including reduced net photosynthetic rate and elevated malondialdehyde, catalase, and peroxidase levels.

Discussion: Our findings demonstrate that the cotton CP12 gene family has undergone functional divergence. Clade I members act as positive regulators of thermotolerance, potentially stabilizing photosynthetic complexes and protecting enzymes from oxidative damage under heat stress. This study provides new insights into the evolution and function of CP12 genes and establishes a foundation for future functional validation and breeding of heat-tolerant cotton varieties.

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Title: Genome-wide identification and comparative analysis of CCCH-type zinc finger genes in diploid and tetraploid cotton (Gossypium) species.

Author: Gaofei Sun, Panhong Dai, Xinquan Tian, Renhai Peng, Boshen Li, Lei Ma, Xiaomeng Zhang

Imprint: Front. Plant Sci., 18 November 2025, Sec. Plant Breeding, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1694549

Abstract: Introduction: *CCCH*-type zinc finger proteins are important transcriptional regulators involved in plant growth, development, and responses to abiotic stress.

Despite their significance, a comprehensive characterization of *CCCH* genes in cotton is lacking.

Methods: We systematically identified *CCCH* genes in four cotton species (*Gossypium arboreum*, *G. raimondii*, *G. hirsutum*, and *G. barbadense*) and performed phylogenetic classification, gene structure, conserved motif, and physicochemical property analyses. Collinearity analyses were conducted to assess gene expansion. Promoter regions were examined for hormone- and stress-responsive cis-elements, and expression profiles were analyzed across tissues, developmental stages, and under abiotic stress conditions.

Results: A total of 183 *CCCH* genes were identified and grouped into eight phylogenetic clusters. Comparative analyses revealed both evolutionary conservation and lineage-specific diversification. Gene expansion in tetraploid cotton mainly arose from polyploidization, with most genes retained from diploid progenitors, whereas *GhCCCH21* and *GhCCCH47* were specific to *G. hirsutum*. Promoter analysis uncovered numerous hormone- and stress-responsive elements, including ABRE, CGTCA-motif, and LTR. Tissue-specific expression patterns showed that *GhCCCH24* and *GhCCCH14* are preferentially expressed in ovules and fibers, respectively, while *GhCCCH23*, *GhCCCH51*, and *GhCCCH55* are strongly induced by abiotic stress.

Discussion: These findings reveal the functional diversification of *CCCH* genes in cotton and identify promising candidates for improving stress tolerance and fiber quality, providing a foundation for future functional studies.

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Title: Independent component analysis deciphers the genetic basis of cotton fiber elongation through eQTLs and sQTLs.

Author:Mingjun Zhang, Lan Yang, Rui Liu , Baibai Gao , Renju Liu , Ye Wang , Fuguang Li, Zuoren Yang , Yanli Chen , Zhaoen Yang

Imprint: Journal of Advanced Research, Available online 27 October 2025

Abstract: The formation of agronomic traits is regulated by a complex network consisting of transcriptional and post-transcriptional mechanisms. However, the coordination between these regulatory layers in cotton fiber elongation remains poorly understood. Here, we performed a comprehensive analysis of both transcriptional and post-transcriptional regulation for fiber elongation using a population-level transcriptome approach. A total of 50,501 and 53,211 alternative splicing (AS) events were identified at 5 days post-anthesis (DPA) and 10 DPA, respectively. Among these, skipped exon and retained intron events contribute to the protein diversity by modulating the presence of functional domains. These AS events were controlled by

2,930 and 3,116 independent splicing quantitative trait loci (sQTLs) at 5 DPA and 10 DPA, respectively. Although sQTLs and eQTLs independently regulate gene expression, they synergistically control fiber development through independent components analysis (ICA). Notably, *FL2*, a major fiber length locus, regulates fiber elongation via M103 module. *GhMYB16*, a M103 module gene, regulates fiber length with expression enhanced by GhBEE3. Our study reveals the genetic basis and regulatory network of fiber development through transcriptional and post-transcriptional mechanisms at the population level, and provides valuable resources for molecular breeding.

PLANT BIOTECHNOLOGY

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Title: Understanding the role of G*hRCC1.61* in flowering time in upland cotton through integrated analyses of gene family, RNA-seq, VIGS and allelic variation.

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

Imprint: Plant Cell Reports, 28 October 2025, Volume 44, article number 248, (2025)

Abstract: The regulator of chromosome condensation 1 (RCC1) superfamily is closely related to plant growth and development; however, in-depth studies on the role of *GhRCC1s* in the flowering time of upland cotton are lacking. In this study, 62 members of the *RCC1* superfamily were identified from the upland cotton genome using a bioinformatics approach, and these members were comprehensively and systematically characterized. RNA-seq and qRT-PCR analyses revealed that a gene, *GhRCC1.61*, was significantly differentially expressed between early- and late-maturing varieties. When the expression of *GhRCC1.61* was reduced via virus-induced gene silencing, the plants presented significantly delayed budding and flowering. By integrating existing genome-wide association studies we identified a single-nucleotide polymorphism locus (A/G; D13:1,391,542) within the exonic region of *GhRCC1.61* that was significantly associated with flowering time. By calculating fixation index and nucleotide diversity, we found that the genomic region of *GhRCC1.61* differed between early- and late-maturing varieties. An investigation of the frequency distribution of *GhRCC1.61* allelic variants across the four cotton ecological zones in China was conducted. The frequency of the G allele was relatively high in the Northwest Inland Region and Northern Special Early-Maturity Region. These findings suggest that this gene might be affected by natural or artificial selection during the variety enhancement process. Furthermore, a kompetitive allele-specific PCR marker was developed based on its allelic variation. These findings not only deepen the understanding of *GhRCC1s* but also offer valuable genetic resources for the molecular breeding of early-maturing upland cotton.

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Title: Ethylene enhances cold resistance through GhDREB1/CBF in cotton (Gossypium hirsutum L.).

Author: Yaxin Dong , Huijuan Ma , Yanhui Shen, Pengzhen Li, Changwei Ge , Qian Shen, Jinglin Li, Ruihua Liu, Siping Zhang , Shaodong Liu , Chaoyou Pang
Imprint: Plant J, . 2025 Oct;124(1):e70517. doi: 10.1111/tpj.70517.

Abstract: Although the role of ethylene in plant growth and development has been widely studied, its regulatory effect on cold tolerance varies among crops, and the mechanisms underlying this variability remain unclear. We used weighted gene co-expression network analysis (WGCNA) to analyse cotton transcriptome changes under low-temperature stress. Differentially expressed genes were significantly enriched in those related to ethylene signalling pathways, suggesting their potential role in cold stress responses. The positive effect of ethylene on cold tolerance in cotton was demonstrated by the effects of exogenously applied ethylene precursor 1-aminocyclopropane-1-carboxylic acid and ethylene synthesis inhibitor α-aminoisobutyric acid. Using CRISPR/Cas9, virus-induced gene silencing, as well as overexpression in tobacco, we obtained evidence indicating that the ethylene synthesis gene GhACO1 enhanced plant cold tolerance. Transcriptome analysis showed that the C-repeat/DRE binding factor (GhDREB1/CBF) was highly expressed in cotton and significantly upregulated by low-temperature stress. The CUT&Tag approach suggested that GhDREB1 binds to the GhACO1 promoter. The direct regulation of GhACO1 by GhDREB1 was further confirmed through luciferase reporter gene and yeast one-hybrid detection. These results suggest that GhACO1 enhances cold tolerance of cotton via the CBF-dependent pathway. Transgenic cotton plants overexpressing GhDREB1 exhibited elevated GhACO1 expression and improved cold resistance, further supporting the regulatory role of GhDREB1. Our results revealed that GhACO1-mediated ethylene synthesis is modulated by GhDREB1, which positively regulates cold tolerance in cotton. These findings provide valuable insights into the molecular mechanisms underlying cold tolerance in cotton and lay the foundation for improving crop resilience to low-temperature stress.

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Title: An R2R3 MYB transcription factor GhMYB5: regulator of *CHS* expression and proanthocyanin synthesis in brown cotton (*Gossypium hirsutum* L.).

Author: Long Chen, Shichang Cheng, Xu Sun, Junshan Gao, Dahui Li, Yujiang Zhang & Ning Guo

Imprint: BMC Genomics, Volume 26, article number 884, (2025)

Abstract: Cotton (*Gossypium spp.*) serves as a vital global crop for textile production, with naturally pigmented brown cotton has gained industrial interest due to its eco-friendly coloration. However, the molecular mechanisms underlying variation in color intensity in brown cotton fibers remain poorly characterized. In this study, we investigated the genetic and biochemical basis of fiber color differentiation in hybrid-derived cotton lines spanning white, light-brown, middle-brown, and deep-brown phenotypes. Biochemical quantification revealed significantly elevated proanthocyanidin levels in brown cotton fibers compared to those in white counterparts, with their content positively correlating with color intensity. Transcriptomic profiling identified significant activation of flavonoid biosynthesis pathway genes in pigmented fibers. Among differentially expressed transcription factors, GhMYB5 (Ghir_D07G002110), an R2R3-type MYB regulator, exhibited gradual upregulation corresponding to color deepening. Functional characterization through qRT-PCR demonstrated GhMYB5's potential regulation of key flavonoid pathway genes *GhCHS1* (Ghir_A10G012390), *GhCHI3* (Ghir_A05G041560), and *GhF3H* (Ghir_D11G018670). Protein-DNA interaction assays (DAP-seq), yeast one-hybrid validation and LUC analysis confirmed direct binding of GhMYB5 to the promoter region of *GhCHS1*, establishing a regulatory node in proanthocyanidin biosynthesis.Our findings reveal that GhMYB5-mediated transcriptional activation of *GhCHS1* promotes proanthocyanidin accumulation in brown cotton fibers, providing a molecular explanation for color intensification. The identified MYB-CHS regulatory module offers potential targets for molecular breeding of naturally colored cotton varieties with enhanced pigmentation properties. This study advances our understanding of plant pigment biosynthesis and supports sustainable textile production through engineering of natural fiber coloration.

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Title: GhAOS integrates circadian rhythm and jasmonic acid signaling to regulate high temperature stress responses in cotton and Arabidopsis.

Author: Aamir Hamid Khan, Qingyuan Li, Anyu Luo, Huanhuan Ma, Marcin Kiedrzyński, Abdullah Shalmani, Adnan Akbar, Adnan Iqbal, Jing Cao, Longfu Zhu, Xianlong Zhang & Ling Min

Imprint: BMC Biology , Published: 07 October 2025

Abstract: Cotton (*Gossypium* spp.) cultivation is significantly challenged by high temperatures (HT), especially during reproductive stages, leading to male abortion and yield losses. This study investigated the complex interplay between circadian rhythm (CR), HT, and jasmonic acid (JA) signaling in cotton and Arabidopsis. Disruption of CR led to reduced JA content, triggering bud yellowing and abscission at the tetrad stage (TS) in the HT-sensitive cotton line H05 and longer stigma in Arabidopsis. To elucidate the role of JA under continuous light (CL), targeting the JA biosynthesis gene *GhAOS* in cotton and using Arabidopsis mutants *aos* and *aoc2* revealed accelerated drying, decreased JA content, and male sterility, alongside altered expression patterns of pivotal bioclock-associated genes (*PRR1* and *LHY*). Additionally, mutant anthers manifested elevated ion leakage and H_2O_2 levels, coupled with reduced activities of antioxidant enzymes SOD and POD during CL + HT stress. Current study investigated the complex interplay between CR, HT, and JA signaling pathways in cotton and Arabidopsis, focusing on their impact on male fertility under HT stress. These findings highlight the importance of JA and CR in plant fitness, crucial for future crop improvement and sustainable agriculture.

SEED SCIENCE AND TECHNOLOGY

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Title: Crop Management to Minimize Risk and Optimize Resource Use Efficiencies in Georgia.

Author: Lee, Joshua Mark
Imprint: University of Georgia ProQuest Dissertations & Theses, 2025. 32047254.

Abstract: Cotton (Gossypium hirsutum) and corn (Zea mays) are two widely grown row crops in the state of Georgia, so profitable and sustainable production of these two commodities is essential for producers. The objective of the first project of this dissertation research was to assess stand establishment, crop growth and development, and lint yield in response to varying cultivars and seed sources. Findings from this study illustrate the need to utilize well-adapted cultivars but to also be mindful of seed quality to minimize early season risk of stand loss without sacrificing yield potential. Project two evaluated thrips prevalence, plant injury, crop development, and lint yield in response to cultivar (with or without ThryvOn™, a new gene technology for thrips control) and insecticide treatment under high thrips pressure. ThryvOn™ cotton exhibited lower thrips densities and plant injury due to thrips than non-ThryvOn™ cotton, regardless of insecticide treatment. When interactions between cultivar and insecticide were observed, insecticide treatment reduced pest pressure and positively impacted plant growth to a larger extent in non-ThryvOn™ cotton compared to ThryvOn™ cotton. Lint yields were not affected by cultivar or insecticide treatment in either year, despite significant plant injury in the early season. Project three assessed biomass, nutrient uptake, lint yield, and resource use efficiency in cotton grown under two different irrigation treatments, three N application rates, and three MC treatments. Overall, we can conclude that management practices with the potential to alter canopy growth, nutrient uptake, and lint yield also have the potential to influence resource use efficiency. Project four evaluated the effect of irrigation scheduling approach on grain yield and water, nitrogen, and radiation use efficiencies for field corn in southern Georgia. Across both years of the study, soil moisture-based approaches and the UGA checkbook method maximized grain yields, yet among these treatments, only the 60kPa SWT maximized intrinsic nitrogen use efficiency (iNUE), radiation use efficiency (RUE), and irrigation water use efficiency (IWUE). Using this threshold for irrigation scheduling has the greatest potential to maximize yield and profitability for the producer, while also optimizing the intrinsic resource use efficiencies of the crop.

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Title: Study of Correlation and Path Coefficient Analysis for Seed Cotton Yield, Yield Attributing and Fibre Quality Traits in Upland Cotton (Gossypium hirsutum L.).
Author: Ch. Mohan Mani Kanta , N Chamundeswari , K Reddy , B Sreekanth

Imprint: Journal of Advances in Biology & Biotechnology, 2025, 28 (10), pp.515-526. ⟨hal-05301327⟩

Abstract: The study was conducted with 56 genotypes of cotton in alpha lattice design with two replications at Regional Agricultural Research Station, Lam Farm, Guntur during Kharif season 2024. Upland cotton (Gossypium hirsutum L.) is an important fibre crop contributing significantly to the textile industry and the agricultural economy. Improving its yield and fibre quality traits remains a major breeding objective. In this context correlation and path coefficient analysis were assessed for 19 characters among 56 genotypes of upland cotton. Correlation studies revealed that no. of sympodia per plant, no. of bolls per plant, boll weight, seed index, lint index, seed cotton yield per plant at 140 days after sowing, seed cotton yield per plant at 165 days after sowing and oil content recorded significant positive association with total seed cotton yield per plant indicating more emphasis should be given to these traits during breeding programme to make selection effective. Further partitioning of correlation into direct and indirect effects showed that characters no. of sympodia per plant, no. of bolls per plant, lint index, seed cotton yield per plant at 140 days after sowing, seed cotton yield per plant at 165 days after sowing, tenacity value had direct positive effect on total seed cotton yield per plant. Thus, correlation and path analysis clearly indicated that direct selection based on no. of sympodia per plant, no. of bolls per plant, lint index, seed cotton yield per plant at 140 days after sowing, seed cotton yield per plant at 165 days after sowing may be helpful in developing high yielding varieties in upland cotton.

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Title: Engineering Gossypol-Free Cottonseeds for Future Global Food Security and Agricultural Sustainability.

Author: Teame Gereziher Mehari, Muhammad Yousaf Shani, Junfeng Tang, Hui Fang, Muhammad Jawad Umer, Fang Liu, Kai Wang, Dengbing Yao, Muhammad K. R. Khan, Baohua Wang

Imprint: Food Frontiers, 2026; 7:e70138 https://doi.org/10.1002/fft2.70138

Abstract: Cottonseed, a protein and oil rich byproduct of cotton (Gossypium spp.) fiber production, represents a valuable but underexploited food and feed resource. Its utilization is severely constrained by the presence of gossypol, a toxic sesquiterpenoid aldehyde that accumulates in seeds but plays a critical defensive role in vegetative tissues. Recent advances in biotechnology have enabled precise manipulation of gossypol biosynthesis and gland formation, offering strategies to decouple nutritional quality from plant defense. Targeted approaches such as CRISPR/Cas9 mediated genome editing, RNA interference (RNAi), and virus-induced gene silencing (VIGS) have successfully surpassed key regulators, including GoPGF and CGP1, resulting ultralow gossypol cottonseed (ULGCS) while maintaining protective gossypol levels in leaves and stems. Stable transmission of these traits across generations positions cotton as a dual-purpose crop that simultaneously provides fiber and safe, high-quality protein. Integrating ULGCS into food systems could alleviate protein malnutrition, potentially benefiting over 500 million people annually, while also expanding the $7.4 billion global cottonseed oil market. Future research should integrate multi-omics, precision breeding, genomic selection, and advanced genome engineering to further enhance ULGCS nutritional value, seed composition, and agronomic performance. In addition, assessing metabolic trade-offs and ecological implications will be critical to ensure longterm sustainability. Reprogramming cottonseed gossypol content thus represents a transformative strategy at the interface of plant biotechnology, food security, and sustainable agriculture.

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Title: Multivariate screening of upland cotton genotypes reveals key traits for salt tolerance at the seedling stage.

Author: Zunaira Anwar, Allah Ditta & Muhammad Kashif , Riaz Khan

Imprint: BMC Plant Biology, Volume 25, article number 1448, (2025)

Abstract: Soil salinity poses a serious threat to cotton production worldwide by impairing growth, yield, and fiber quality. Salt stress disrupts key morphological, physiological, and biochemical processes in cotton plants, leading to considerable reductions in productivity. Therefore, identifying salt-tolerant cotton genotypes is essential for improving crop performance in saline environments. Methods- In this study, fifty-one cotton genotypes were evaluated for their response to salinity stress at the seedling stage. Plants were grown in hydroponic culture under controlled glasshouse conditions and subjected to 200 mM NaCl to simulate salt stress. The experiment followed a completely randomized design (CRD) with three replications, and data were analyzed using two-way analysis of variance (ANOVA) and multivariate approaches, including principal component analysis (PCA), heatmap analysis, and the multi-trait genotype-ideotype distance index (MGIDI).

Results- ANOVA showed significant variation among genotypes for all traits. Salt stress caused significant reductions in growth traits, including shoot and root length, fresh and dry biomass, water relation traits, gaseous exchange traits and photosynthetic pigments. In contrast, excised leaf water loss (ELWL), sodium (Na^+)accumulation in roots and shoots, oxidative stress markers like hydrogen peroxide (H_2O_2) and malondialdehyde (MDA), osmolytes including proline, glycine betaine (GB), and saponin, and antioxidant enzyme activities like superoxide dismutase (SOD), peroxidase (POD), catalase (CAT) increased, while potassium contents (K^+) and sodium to potassium ratio (K^+/Na^+) decreased. Under control conditions, PCA showed little variation, whereas under salt stress, it explained 64.8% of the variance and separated growth- from stress-related traits. Heatmap analysis confirmed these patterns and grouped genotypes into three clusters based on ion homeostasis and oxidative stress traits. MGIDI index integrated all traits into a single score and identified superior genotypes like G2 (NIAB-868), G22 (NIA-Noori), G32 (FH-530), G3 (NIAB-878-B), G49 (FH-911), G28 (FH-416), G33 (FH-534), and G39 (FH-546). Conclusion- These findings suggest that multivariate and multi-

trait screening at the seedling stage is a useful method for identifying cotton germplasm with salt tolerance, providing a foundation for breeding programs and further field evaluation that may contribute to stable yields under saline conditions.

FIBER AND FIBER TECHNOLOGY

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Title: Spatiotemporal methylome remodeling during fiber differentiation in *Gossypium hirsutum.*

Author: Zhipeng Yu, Haijuan Cao, Xiaolian Xiong, Shuhan Wen, Xia Huang, Ying Jin, Junkang Rong & Mingquan Ding

Imprint: BMC Genomics, 09 October 2025, Volume 26, article number 901, (2025)

Abstract: Whole-genome methylome analysis reveals DNA methylation dynamics during upland cotton (*Gossypium hirsutum*) fiber development. DNA methylation levels initially increased and then decreased from -3 days post-anthesis (DPA) to 5 DPA, with a significant rise during the rapid elongation stage (5 DPA to 14 DPA), particularly in CHH methylation levels. Integrated transcriptome analysis links elevated DNA methylation to reduced demethylase gene expression (*DME*, *ROS1*, *DML3*). DNA methylation remodeling modulates fiber development through coordinated regulation of lipid metabolism, DNA replication, phosphatidylinositol signaling system and hormonal signaling pathways. Several key transcription factors, such as *TCP14*, *HD1*, *HOX3*, and *MYB25-like*, showed a strong correlation with DMRs, suggesting their regulation by DNA methylation. Furthermore, Multi-omics integration posits that DNA methylation may regulate genes related to fiber development, particularly those related to fatty acid biosynthesis and metabolism, ultimately influencing upland cotton fiber development. Analysis of genes highly correlated with changes in differentially methylated regions (DMRs) indicates DNA methylation can modulate the expression of KCS family genes, including *KCS13*, as well as *KCRL1*, thereby participating in the fatty acid elongation pathway.

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Title: A light-governed cascade of ubiquitin modifications regulates cotton fiber development by coordinating PIN3a proteolysis.

Author: Liuqin Zhang , Yanling zhou , Xingxian Fu , Changzheng Xu ,

Lina Liu , Xinyue Du , Yahong An , Mingxuan Xu , Liman Mu ,

Qingqing Li

Imprint: *The Plant Cell*, Volume 37, Issue 10, October 2025, koaf237, https://doi.org/10.1093/plcell/koaf237

Abstract: PIN-mediated auxin transport is crucial for light-regulated plant organogenesis; however, how light modulates PIN localization remains elusive. Cotton (Gossypium hirsutum), a key textile crop, requires ample sunlight for optimal growth and fiber development. Yet, the mechanism underlying light-regulated fiber development is obscure. Our research shows that light promotes fiber initiation and elongation through inhibiting ubiquitylation degradation of GhPIN3a and subsequently enhancing GhPIN3a plasma-membrane localization. In fiber cells, where GhPIN3a undergoes preferential ubiquitylation, GhCOP1 was identified to control ubiquitylation degradation of GhPIN3a in response to light. Dark-stabilized GhCOP1 targets GhUCH3, which interacts with GhPIN3a to balance its stability through deubiquitylation. This regulatory cascade converts light signals into developmental cues in cotton fibers. Intriguingly, while GhCOP1 promotes GhUCH3 degradation via the ubiquitin–proteasome system (UPS), GhUCH3 modulates GhPIN3a proteolysis through both the UPS and the vacuolar degradation pathway. Our findings reveal a light-regulated GhPIN3a stability mechanism through the GhCOP1–GhUCH3 module, consequently influencing cotton fiber development.