GLEANINGS IN COTTON RESEARCH

October 2025

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Preface

Information plays a vital role in just about everything we do in modern society. Today, the Internet is one of the most effective and efficient ways to collect information. The internet gives us the opportunity to connect with all kinds of different people and read news and information from all over the world.

Information literacy is the ability to find, evaluate, organize, use, and communicate information in all its various formats, most notably in the acquisition of knowledge. The diversity of news sources thus makes the internet a source of information and knowledge.

Gleanings in Cotton Research *is an attempt made by the Library to scan, collect, edit and present, ongoing research in Cotton using the information available on the Internet in a concise manner.*

Articles related to Cotton subject area are represented by Agronomy, Soil Science, Plant Physiology, Genetics, Biotechnology, Crop Protection, Seed Technology, and Fiber Technology.

The information collected is arranged under these broad subject headings. The Title of the research paper is followed by the Imprint, wherein Names of the authors and Journal are given. Names of the journals are followed by year of publication, volume number, issue number in brackets and inclusive pages. The DOI (Digital Object Identifier) wherever applicable is also mentioned. The abstract follows the citation.

Information has been mainly retrieved from Google Scholar, Science Direct and GAIN website.

We duly thank The Director, Dr V. N. Waghmare, for providing inspiration and support for this publication.

Suggestions are welcome for further improvement on cicrlib@yahoo.co.in.

Swati Dixit
In charge Library

Chetali Rodge
Technical Officer (T5)

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1

Title: Reducing Nitrogen Input Increases the Efficacy of Soil Nitrogen Utilization by Regulating Cotton–Arbuscular Mycorrhizal Fungi–Soil Nitrogen Interactions.

Author: Hushan Wang, Yunzhu He, Zihui Shen, Mengjuan Liu, Wangfeng Zhang and Xiaozhen Pu

Imprint: *Nitrogen* 2025, *6*(3), 55; https://doi.org/10.3390/nitrogen6030055

Abstract: Crops and arbuscular mycorrhizal (AM) fungi can enhance nitrogen (N) transformation and utilization efficiency in the soil, and this effect is regulated by soil N application rates. However, it remains unclear whether the N utilization efficiency of cotton can be improved through the symbiosis of cotton with AM fungi under reduced N application rates. Therefore, we conducted ^{15}N labeling experiments using a compartmentalized culture system with *Gossypium hirsutum* L. as the experimental plant. We established three N treatments (0.15 g·kg^{-1}, 0.10 g·kg^{-1} and 0 g·kg^{-1}) to investigate the effects of different fertilization rates on N utilization, soil N priming effects, and differences in N accumulation in various parts of cotton plants within the soil–AM fungi–cotton system. The results indicate that under reduced N application, symbiosis between cotton and AM fungi increased the N fertilizer utilization efficiency and the soil N priming effect. Specifically, reducing the fertilization dosage from 0.15 g·kg^{-1} to 0.10 g·kg^{-1} increased the N fertilizer utilization efficiency and soil N priming effect by 8.87% and 11.67%, respectively, and decreased the N loss rate by 7.02%. The symbiosis between cotton and AM fungi after N reduction significantly increased N accumulation in the roots and leaves. Moreover, the N fertilizer content accounted for 5.89% of the total N content in roots. Overall, when N application was reduced, symbiosis with AM fungi effectively promoted the rhizosphere N priming effect, which reconciled the conflict in N nutrient allocation within cotton and thus enabled the efficient utilization of soil N.

2

Title: Modeling leaf and crop water use efficiency of rainfed Cotton: Interplay of environmental and biophysical drivers.

Author: Shreedevi Moharana, Syam Chintala, BVN P. Kambhammettu

Imprint: Agricultural Water Management, Volume 317, 1 August 2025, 109626

Abstract: Being the key eco-hydrologic trait linking carbon fixation (photosynthesis) and water consumption (transpiration), water use efficiency (WUE) plays a vital role in the plant-atmosphere continuum. However, ecological drivers and scaling relations on WUE represented at different scales is poorly understood. This study is aimed at simulating WUE of rainfed Cotton at leaf 'WUE_L' and crop 'WUE_C' scales, and further investigates the role of environmental and biophysical factors on WUE dynamics. The simulated leaf and crop WUE fluxes were used to establish the scaling relations. Stomatal conductance 'g_s' and WUE_L of Cotton leaves exposed to ambient CO_2 are simulated using modified Ball-Berry model with instantaneous gas exchanges measured around noon used to validate the model. We observed a large diurnal (4.3 ± 1.9 mmolCO_2 mol$^{-1}H_2O$) and seasonal (5.16 ± 1.51 mmolCO_2 mol$^{-1}H_2O$) variations in WUE_L. Model simulated g_s and WUE_L are in agreement with measurements ($\rho>0.5$, RMSE<0.3). Meteorological, phenologic, and management conditions during the crop cycle were used to simulate WUE_C using FAO-AquaCrop. Model calibration was performed with gravimetric measurements of soil water content ($\rho = 0.95$, RMSE = 21.8) and eddy covariance (EC) measurements of evapotranspiration ($\rho = 0.57$, RMSE = 0.88). Seasonal variations in WUE_C ranged from 1.7 to 7.3 kg/m^3 during crop cycle. We observed strong linear relations between WUE_L and WUE_C during maturity stage ($\rho = 0.84$) followed by growth stage ($\rho = 0.75$). Eight climate and biophysical factors were considered to see their dependence on WUE at both scales. Our results conclude that WUE_L is governed by soil moisture content ($\rho = -0.75$) and leaf area index ($\rho = 0.57$), whereas WUE_C is controlled by canopy cover ($\rho = 0.86$) and vapor pressure deficit ($\rho = -0.63$). Our findings can help in developing effective water management strategies to improve WUE in rainfed Cotton.

3

Title: Effect of nutrient management practices on growth, yield attributes and yield of coloured cotton (Gossypium hirsutum L.).

Author: Selvakumar, S , Ragavan, T , Gurusamy, A , Gunasekaran, M , Sivakumar, T , Prabhaharan, J , Thiruppathi, M , Subramanian, E , Arthirani, V, Rani, S

Imprint: Plant Science Today; Vol. 12 No. 2 (2025), 2348-1900, 10.14719/pst.2025.12.2

Author: The field experiment was carried out at the Central Farm, AC &RI (Agricultural College and Research Institute), TNAU, Madurai, Tamil Nadu during Kharif season 2024. The study aimed to evaluate the effects of different nutrient management strategies on the growth, yield components and productivity of coloured cotton. The experiment followed a randomized block design (RBD) with nine treatments based on nitrogen equivalence, incorporating different organic manures in comparison to inorganic fertilizers, with each treatment replicated three times. The

results revealed that growth parameters such as plant height, dry matter production, leaf area index, chlorophyll content, number of monopodial branches plant-1 , days to 50% flowering and days to 50% boll bursting were significantly enhanced by the application of 100% NPK based on site-specific recommendation (T2), which statistically at par with 100% NPK through blanket recommendation (T1). Yield attributes including number of fruiting branches plant-1 , number of fruiting points plant-1 , number of bolls plant-1 , number of bolls m-2 , boll setting percentage and boll weight, along with seed cotton yield, lint cotton yield, stalk yield and biological yield, which also showed a significant increase with the application of 100% NPK through site-specific recommendation (T2). Organic treatments, including the complete organic package (T9), cover cropping with 75% N through vermicompost (T4) and cover cropping with 75% N through poultry manure (T5), exhibited comparable results to inorganic treatments. Future research should focus on optimizing organic nutrient management strategies and integrating cover crops to enhance soil health and ensure sustainable cotton production.

4

Title*: Gossypium 3rboretum* (L.): A review on its agronomic and industrial potential for sustainable cotton production.

Author : Samar Gogari, Radha

Imprint: Physiological and Molecular Plant Pathology, Volume 139, September 2025, 102797

Abstract: *Gossypium arboretum* (L.), an ancient diploid cotton species native to the Indian subcontinent, holds substantial agronomic and industrial value due to its resilience to biotic and abiotic stresses and its potential for sustainable cotton production in the face of climate change. This review synthesizes current research on the agronomic, industrial, biochemical, and pharmacological attributes of *G. 3rboretum*, emphasizing its relevance as a resilient and multifunctional crop. Unlike the widely cultivated *G. hirsutum*, the species is naturally adapted to rainfed and low-input agricultural systems, displaying strong resistance to drought, pests, and major cotton diseases, making it suitable for organic and environmentally sustainable farming. Despite limitations in fiber length and fineness compared to tetraploid species like *G. hirsutum*, it has industrial applications in absorbent cotton, handlooms, and coarse yarn, and is now gaining recognition in niche markets for its naturally pigmented varieties. Recent breeding programs have aimed to improve its fiber quality while maintaining stress tolerance. *G. 3 rboretum* also maintains fiber quality under water-deficit conditions, reinforcing its value in stress-prone regions. Unique biochemical features, particularly its GaCYP722C-mediated strigolactone biosynthesis, distinguish it from other *Gossypium* species, offering novel genetic insights for plant growth regulation and soil symbiosis. Phytochemically, it is rich in flavonoids, tannins, and terpenoids, which

contribute to antidiabetic, antioxidant, and wound-healing properties. This pharmacological potential, along with its compatibility with sustainable textile applications, expands its industrial scope. By integrating genetic, agronomic, and phytochemical perspectives, this review identifies *G. 4rboretum* as a vital genetic resource for cotton improvement and climate-resilient agriculture.

5

Title: Yield and economics following 5 years of integrated weed management in cotton .

Author: Amar S. Godar, Jason K. Norsworthy, L. Tom Barber, Roger Farr, Ty Smith

Imprint: Agronomy Journal. 2025;117:e70101. Wileyonlinelibrary.com/journal/agj2 1 of 10 https://doi.org/10.1002/agj2.70101

Abstract: The implementation of integrated weed management (IWM) practices in conventional management systems involves additional costs and can influence both short-term and long-term cotton (Gossypium hirsutum L.) yields, ultimately affecting economic viability. This study, conducted from fall 2018 to fall 2023 near Marianna, AR, evaluated four IWM practices in a large-plot, fixed-plot factorial design: zero tolerance for weed seed rain, soil inversion deep tillage every third year in the fall, a preplant terminated cereal rye cover crop, and dicamba-resistant cotton technology. Long-term economic impacts were assessed using the 5-year average cost-adjusted yield, with the base program (excluding all IWM practices) serving as the control. Zero tolerance did not influence cotton yield and, due to a significant decline in hand hoeing time over time, had no adverse effect on economic outcomes. Most IWM combinations produced cotton yield comparable to the base program. However, the deep tillage–dicamba combination resulted in a 9% reduction. When costs were incorporated, cost-adjusted yields for the all-present, dicamba alone, and deep tillage–dicamba combinations were 5%–8% lower than the base program. Integration of a cover crop, except when combined with both deep tillage and dicamba, consistently resulted in cost-adjusted yield similar to the base program. While the progressive reduction in labor costs over time enhances zero tolerance practice's practicality as a foundational element within long-term IWM systems, the evaluated IWM practices, whether implemented individually or in combination, generally did not affect cotton yields, and many combinations, including those up to triplet levels, imposed no long-term economic burden.

6

Title: Physiological responses of cotton roots and soil microbial adaptation to drought hardening.

Author: Xin Li, Yuhao Zhao, Kunkun Wu, Xiaoya Li, Gaoqiang Lv, Yi Chen

Imprint: This is a preprint; it has not been peer reviewed by a journal. https://doi.org/10.21203/rs.3.rs-6703288/v1, This work is licensed under a CC BY 4.0 License

Abstract: Background: As global climate changing significantly exacerbated the frequency and intensity of drought stress, posing severe challenges to the sustainable development of agriculture in arid regions.

Aims: This investigation employed integrated physiological and metagenomic analyses to unravel the physiological responses of cotton roots and the changes of soil microbial communities induced by drought hardening. Then, by integrating the physiological responses of the aboveground parts and yield performance, a comprehensive analysis was conducted to provide optimized irrigation strategies for cotton fields in moisture-limited regions.

Methods: The experiment was conducted in 2024 at Huaxing Farm in Changji, Xinjiang, using the Zhongmian 113 variety, with three drought hardening treatments during the seedling stage. These treatments were saving 20% (D1), 30% (D2), and 40% (D3) of irrigation amount respectively, comparing to the control (CK, conventional full irrigation).

Results: The results showed that the D1 treatment was identified as moderate drought hardening, which based on cotton growth and yield; The D1 treatment significantly enhanced the antioxidant capacity and membrane integrity maintenance in cotton roots; Additionally, the D1 treatment altered soil microbial diversity, partially optimizing the microbial community structure and forming a dominant bacterial group—Gemmatimonadales.

Conclusions: This integrated microbial-plant analysis hypothesized that Gemmatimonadales might interact synergistically with cotton roots during the budding stage to enhance the drought resistance of cotton. The research provided a foundation for revealing the enhancing drought- resistance- mechanisms of root-microbe interactions in cotton via drought hardening in arid regions.

7

Title: Organic water-soluble fertilizers promote cotton growth and phosphorus uptake by stimulating indigenous microbiota-mediated soil phosphorus activation.

Author: DENG Wanglan, CHEN Wangzun, FENG Gu

Imprint: Chinese Journal of Eco-Agriculture, Jul. 2025, 33(12): 1−14

Abstract: To elucidate the common mechanisms and concentration effects of six typical organic water-soluble fertilizers (OWSFs) on soil phosphorus (P) activation mediated by indigenous microorganisms, crop P uptake, and growth enhancement, a pot experiment with cotton in slightly saline soil was conducted. The study investigated two factors: 1) OWSF types (including six representatives: alginic acid powder, alginic acid aqueous solution, polyglutamic acid-based, chitin-based, fish protein-based, and molasses-based fertilizers) and 2) organic carbon (C) application rates (0, manufacturer-recommended dose, 40, 80, 160, and 240 mg·pot−1). The effects of C rates within each OWSF type and across different OWSF types under the same C rate were evaluated for cotton seedling growth (plant height, leaf area dynamics, biomass, and P uptake), soil microbial activity (microbial biomass P and phosphatase activity), and soil available P content. The C priming effect (i.e., changes in microbial biomass P, phosphatase activity, bioavailable P, and plant P uptake per unit C input) of the six OWSFs was quantified. The key findings showed that 1) all six OWSFs enhanced soil P activation, cotton P uptake, and seedling growth in a C dose-dependent manner, with dose-response relationships well fitted by linear-plateau models. Threshold C rates (30~60 mg·pot−1) for growth stimulation varied among OWSF types. 2) At equivalent C rates, OWSF types showed no significant differences in promoting cotton growth but exhibited distinct priming effects on microbial biomass P, phosphatase activity, and P availability ($P < 0.05$). This indicates that OWSFs enhance plant growth indirectly by stimulating microbially mediated soil P activation rather than through direct effects. 3) The efficiency of the priming effect of six OWSF-C sources varied significantly, with molasses-based OWSF demonstrating the highest priming effect on microbial biomass P among the six types. We further discuss the current definition of OWSFs, proposing that their "fertilizer" function is primarily achieved through water-soluble organic C priming microbial activity to activate soil P turnover.

8

Title: Cotton production in the Yellow River Basin of China: reforming cropping systems for ecological,economic stability and sustainable production.

Author: Yuexia Su, Xuewen Wei, Zhanbiao Wang, Lei Gao and Zhenggui Zhang

Imprint: Front. Sustain. Food Syst. 9:1615566. Doi: 10.3389/fsufs.2025.1615566

Abstract: Cotton cropping systems are critical for ensuring the stability and sustainability of cotton production, which is of vital importance to both the agricultural and economic sectors of China. This review examines the historical evolution, challenges, and potential reforms of cotton cropping systems in Shandong Province, a key cotton-producing region in China. The study highlights the effects of economic, technological, and ecological factors on cotton production in the region, emphasizing the importance of optimizing cotton cropping systems to stabilize production, enhance efficiency, and promote rural revitalization. Based on empirical evidence, the review suggests several innovative approaches, including advanced cotton cultivation systems and large-scale mechanization, designed to enhance the sustainability of cotton farming. Furthermore, the research highlights the critical need to balance cotton cultivation with national food security goals by addressing the challenges of saline and alkaline soils and promoting sustainable cotton industry development in the Yellow River Basin; it further offers forward-looking policy recommendations for Shandong, advocating for the integration of advanced agricultural technologies, the establishment of robust agricultural insurance systems, and the implementation of region-specific strategies to ensure both ecological resilience and economic viability—ultimately positioning cotton farming as a key driver of rural revitalization and green development. The findings of this study provide valuable insights for policy-making, guiding the sustainable development of cotton farming in Shandong and other regions with similar requirements.

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Title: High Planting Density Combined with Delayed Topping Improves Short Fruiting Branch Cotton Yield by Enhancing Biomass Accumulation, Canopy Light Interception and Delaying Leaf Senescence.

Author: Yin Huang, Tao Wang, Xiaoxia Luo, Jianfei Wu, Yanfeng Deng, Qingquan Kong

Imprint: Agronomy 2025, 15(6), 1495; https://doi.org/10.3390/agronomy15061495

Abstract: Short fruiting branch cotton (SFBC) has a compact plant architecture suitable for dense planting. Plant population density (PPD) and topping are important agronomic practices to achieve high yielding by optimizing cotton plant structure. However, their individual and interactive effects on SFBC growth and yield are poorly understood. This study aimed to explore cotton growth and yield responses to various combinations of PPD and topping time (TT) and the underlying physio-ecological mechanism. Four combinations were included in a two-year field experiment (2023–2024) involving two PPD levels (5.3 plants m^{-2}, low density LD; 8 plants m^{-2}, high density HD) and two TT levels (early topping for leaving ten sympodials per plant ET; late topping for leaving fifteen sympodials per plant LT), and compared in terms of biomass accumulation, photosynthetically active radiation capture, and leaf senescence

during entire reproductive growth period. Compared to the other three combinations, the combination of HD and LT (HDLT) achieved a higher lint yield due to a greater biological yield, which was predominantly attributed to the higher average rate during the rapid biomass increasing period. Owing to delayed leaf senescence caused by the HD and the LT, the HDLT performed better in leaf senescence-related attributes at the late growth stage. Moreover, these improved attributes also contributed to a higher radiation interception rate and photosynthetic efficiency at the late growth stage. Taken together, combining high density with later topping tends to increase the lint yield of SFBC through increasing dry matter accumulation, delaying leaf senescence, and enhancing canopy radiation interception rate at the late growth.

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Title: Sustainable nutrient management in Cotton: Impact of nitrogen application through vermicompost on yield, growth attributes, and economic returns .

Author: Chinthala Mounika, PR Kadu, Peram Nagaseshi Reddy and NM Konde

Imprint: International Journal of Research in Agronomy 2025; 8(6): 566-571

Abstract: A field investigation titled " Sustainable Nutrient Management in Cotton: Impact of Nitrogen Application through Vermicompost on Yield, Growth Attributes, and Economic Returns " was conducted during the Kharif season of 2021-22 at COART (Centre for Organic Agriculture Research and Training), Dr. PDKV, Akola to evaluate the effect of different nitrogen levels applied through vermicompost on the productivity, growth, and economics of rainfed organic cotton (Gossypium spp.). The experiment was laid out in a factorial randomized block design (FRBD) with eight treatments, each replicated three times, using vermicompost as the nutrient source. Treatments included the application of 40 or 60 kg N ha^{-1} via vermicompost to cultivars of G. hirsutum and G. 8rboretum. Results revealed significant variation in seed cotton yield, stalk yield, and key growth parameters across treatments. The highest seed cotton yield (1508 kg ha^{-1}) and stalk biomass (3685 kg ha^{-1}) were recorded under 60 kg N ha^{-1} applied to G. hirsutum (T4), reflecting a 52.3% yield improvement over the lowest-yielding treatment T1. Enhanced growth attributes, such as plant height, number of sympodia, and boll production, were also observed in T4. Although differences in harvest index were statistically non-significant, the mean value (28.88%) suggested efficient biomass partitioning under organic nutrient regimes. Economic analysis indicated that T4 yielded the highest gross returns (₹1,13,400 ha^{-1}), net returns (₹59,400 ha^{-1}), and benefit-cost ratio (2.1). The study affirms that vermicompost, when applied at 60 kg N ha^{-1}, can substantially improve cotton yield, profitability, and sustainability under organic farming systems. These findings support the integration of vermicompost into organic nutrient management strategies for improved productivity and soil health. Further studies should assess the long-term soil fertility impacts and adaptability across agro-climatic zones to refine organic cotton cultivation practices.

11

Title: Current status of herbicide resistance in global cotton production: trends and perspectives.

Author : Christos A. Damalas, Spyridon D. Koutroubas

Imprint: Crop Protection, Volume 197, November 2025, 107320

Abstract: The evolution of herbicide innovations continues to deliver benefits to cotton growers, but the threat of resistant weeds with repeated application of the same active ingredients has been steadily increasing over the last 20 years. In this study, a critical overview of herbicide resistance cases in cotton production globally is reported following data retrieved from the International Herbicide-Resistant Weed Database and the scholarly literature. The first case of herbicide resistance in cotton dates back to 1973, referring to trifluralin-resistant *Eleusine indica* in the United States. Since then, one hundred and nineteen (119) cases refer to resistant weeds in cotton during the period from 1973 to 2020. More than three-fourths of the resistant-weed cases (76.5 %) in cotton come from the United States. The cases increased dramatically after 2000. The most frequently reported broadleaf weeds with herbicide resistance are *Amaranthus palmeri*, *Amaranthus tuberculatus*, and *Xanthium strumarium*. The most frequently reported grasses with herbicide resistance are *Eleusine indica* and *Sorghum halepense*. Most cases of herbicide resistance refer to glyphosate (HRAC Group-9) and ALS inhibitors (HRAC Group-2), followed by microtubule assembly inhibitors (HRAC Group-3) and ACCase inhibitors (HRAC Group-1). To ensure the value of herbicides, growers must change weed control towards a more sustainable way, re-implementing an integrated approach to weed control with rotation of herbicide groups as a key principle for reducing herbicide resistance. Moreover, residual herbicides should be backed up with additional practices, such as tillage, cultivation plus chipping, and knockdown herbicides, other than glyphosate.

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Title: The Impact of Applying Phosphorus and Mycorrhiza on the Morphological Parameters of Cotton Roots and Shoots, as well as Their Phosphorus Uptake and Dry Matter Yield.

Author: Mehmet IŞIK* and İbrahim ORTAŞ

Imprint: International Journal of Agricultural and Applied Sciences, June 2025, 6(1): 99-105

Abstract: This study aimed to investigate the effects of Phosphorus and mycorrhiza application on cotton root and shoot morphological parameters, phosphorus uptake,

and dry matter yield. The hypothesis to be tested is that mycorrhiza and P applications increase cotton growth yield and P uptake. The experiment was established under greenhouse conditions in May 2022 and harvested in July 2022, as a pot experiment. In the experiment, two P levels (0 mg P2O5 kg-1, and 50 mg P2O5 kg-1), three mycorrhizae species (control (without mycorrhiza), indigenous mycorrhiza (IM) and *Rhizophagus clarus* inoculated by May 505-cotton (*Gossypium hirsutum* L.) variety were used with three replications. Before harvesting, plant height and stem diameter were measured. At harvest, shoot and root dry matter weight (DW), P concentration and root morphological characteristics were determined. Mycorrhizal Dependency (MD) was calculated. The results showed that there was no statistically significant difference in terms of plant height, but P and mycorrhiza treatments made a significant difference in terms of stem diameters. In addition, mycorrhiza application made a significant difference in DW. IM application had 45.1 g pot-1 and *Rh. Clarus* had 47.38 g pot-1 total DW. The results showed that mycorrhiza and P dose applications increased root growth parameters. Mycorrhizae dependency of cotton plant was found to be 8.0 to 12.3%, and MD was lower in P-treated pots (8.1%) compared to non-P-treated pots (11.3%). Results show that mycorrhiza inoculation and 50 mg P2O5 kg-1 applications seem to be suitable for cotton growth.

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Title: Dynamic approaches to precision irrigation of cotton.

Author: A. Ben-Gal, A. Barski, O. Bukris, H. Yasuor, S. A. O'Shaughnessy, N. C. Hansen, A. Peeters & Y. Cohen

Imprint: Precision Agriculture , Published: 03 July 2025, Volume 26, article number 64, (2025)

Abstract: Zones for spatial irrigation management are often assumed to be static, dictated by non- or slowly-changing parameters, including elevation and slope, soil depth, texture and hydraulic properties, and other landscape properties. Sensing allows for the integration of static management zones (MZ) with a dynamic characterization of water status. Temporal remote sensing data, indicating crop status and, particularly, thermal imaging, indicating water status, suggests that, rather than static, dynamic re-zoning within crop seasons could be beneficial to precision water management. Methods: MZ delineation and precision irrigation for cotton were evaluated using a variable rate center pivot sprinkler system. The objectives were to evaluate precision management over time with both static and intra-seasonal dynamic zoning. Spatial distribution and irrigation decision-making were re-evaluated on a weekly basis. Irrigation followed commercial best management, based on target values of plant size (growth rate) in the early vegetative growth period and of plant water status (leaf water potential, LWP) in the reproductive and cotton boll production periods. Site-specific decision-making used drone-acquired normalized difference vegetation index as a

proxy for crop height and growth rate and a thermal image-based crop water stress index as a proxy for LWP. Results and conclusionDynamic precision irrigation of cotton based on weekly decisions using the remote sensing products slightly decreased spatial variability while improving water productivity by 12% using static MZs and by 19% using dynamic MZs, compared to commercial uniform irrigation. The costs and benefits of implementing intra-seasonal dynamic zoning are discussed.

CROP PROTECTION

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Title: Developing eco-friendly, pest-resistant cotton by a heterologous multi-gene transformation system for caffeine synthesis.

Author:Yibo Fan , Yingchao Tang , Yuanmei Miao , Yanchang Zhao , Lu Yu , Peng Han, Xiangqian Zhu, Tingwan Li , Guanying Wang , Zhongping Xu , Lu Long , Wei Gao , Lis ong Hu , Shuangxia Jin

Imprint: The Crop Journal, Available online 3 July 2025

Abstract: Cotton production faces significant challenges from insect pests, with chemical pesticide use becoming increasingly limited by resistance and environmental concerns. This study explores the potential use of caffeine, a natural plant alkaloid, as an environmentally friendly insect resistance strategy in cotton. Exogenous caffeine application demonstrated potent insecticidal effects against cotton bollworm (*Helicoverpa armigera*) larvae, with concentrations ≥ 2 mg mL^{-1} causing near-complete feeding cessation and up to 70% larval mortality. Building on this, we engineered transgenic cotton (Gossypium hirsutum cv. Jin668) for heterologous caffeine biosynthesis by introducing three key N-methyltransferase genes (*CaXMT1*, *CaMXMT1*, *CaDXMT1*) by multiple gene transformation. Transgenic lines expressing all three genes showed remarkable caffeine accumulation (up to 3.59 mg g^{-1} dry weight), whereas two-gene combinations exhibited wild-type-level production. Feeding preference assays revealed that caffeine-enriched cotton strongly deterred feeding by *H. armigera*. Non-choice feeding trials demonstrated reduced leaf consumption and reduced larval growth in *H. armigera* fed on caffeine-producing cotton. The study highlights the effectiveness of synthetic biology approaches using the TGSII-UNiE multigene stacking system, despite challenges in transgene stability. This work advances plant-derived insect resistance research and provides a sustainable framework for reducing chemical pesticide reliance in cotton production, while underscoring unique potential of cotton as a synthetic biology platform for secondary metabolite engineering.

15

Title: Development of biocontrol agents for cotton verticillium wilt using microbiome analysis.

Author: Wanyi Zhang, Jingjing Wang, Peng Wu, Yan Pang, Shijia Dai, Xiaoxia Zhang,

Imprint: This is a preprint; it has not been peer reviewed by a journal.https://doi.org/10.21203/rs.3.rs-6884856/v1

Abstract: Verticillium wilt is one of the most devastating diseases of cotton. However, effective biocontrol strains are still lacking. The aim of this study is to inform the selection of effective biocontrol strains by comparing the microbiomes of healthy and diseased cotton plants. Our results revealed that Verticillium dahliae V991 (V991) is the causal agent of cotton Verticillium wilt, significantly altering the bacterial and fungal communities in the roots, rhizosphere and bulk soil. Compared to the diseased cotton in the V991 inoculation group (D), the healthy cotton in the V991 inoculation group (H) and the control cotton in the V991 non-inoculation group (C) both suppressed Verticillium and Fusarium and enriched taxa of Bacilli, Clostridia, Archacosporales, Glomerales, unclassified Basidiomycota and unclassified Glomeromycota in the roots, both enriched Burkholderiales in the rhizosphere soil, both enriched Archaeosporales and Verrucomicrobiota in the bulk soil. A total of 20 strains were screened for antagonism to V991, most of them were isolated from the roots of the C group. Bacillus amyloliquefaciens M9 (BM), which was screened from the rhizosphere soil, exhibited the strongest antifungal activity, whereas Bacillus cereus R19 (BR), which was screened from the root, exhibited weaker antifungal activity. Pot experiments showed that the application of BR and BM (109 CFU/mL) reduced the disease incidence by 44.44% and 33.33%, respectively, compared to the control. Field experiments showed that BR reduced the disease incidence by 88.46%, while BM reduced it by 50.01%. These results demonstrate the effectiveness of comparative microbiome analysis in guiding the selection of highly effective biocontrol strains.

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Title: Herbivore-induced plant volatile (Z)-3-hexenyl acetate impairs larval performance and adult fecundity of cotton bollworm.

Author: Baojuan Zeng, Mina Jiang, Shan He, Jiong Liu, Yongkang Huang, Lu Li, Guanqing Zhai, Xi Zhang

Imprint: Journal of Pest Science , Published: 17 June 2025

Abstract: Herbivore-induced plant volatiles (HIPVs) are crucial chemical cues guiding insect herbivores and their natural enemies to the potential hosts. However, the effects

and underlying mechanisms of HIPVs on insect development and reproduction remain underexplored. This study investigated the cotton bollworm *Helicoverpa armigera*-induced cotton volatiles as well as their impacts on larval performance, adult fecundity and transcriptome of *H. armigera*. Upon cotton bollworm feeding, the volatile compositions of cotton leaves, calyxes, and bolls were altered, with (*Z*)-3-hexenyl acetate (HAC) being the most significantly induced volatile. HAC exposure had negative effects on *H. armigera*, including reduced food intake, slower larval growth, prolonged larval lifespan, and a significant decrease in adult fecundity. RNA-Seq and qRT-PCR analysis revealed that HAC exposure altered the expression of genes related to cuticles, muscles, and juvenile hormone metabolism in larvae. In adults, the transcriptome changes were less pronounced and mainly associated with carbohydrate metabolism. Our results suggest that cotton bollworm feeding induces HAC production, which negatively impacts bollworm development and reproduction by modulating gene expression. These findings provide new insights into the role of HIPVs in insect herbivore physiology and their potential for biological control.

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Title: Molecular Detection and Quantification of Fusarium oxysporum f. sp. vasinfectum Race 4 in Cotton Plants and Soils.

Author: Chagoya, Jennifer C.

Imprint: https://hdl.handle.net/2346/102428, Collections- TTU Electronic Theses and Dissertations

Abstract:The highly virulent soilborne fungal pathogen Fusarium oxysporum f. sp. vasinfectum race 4 (FOV4) causes the inoculum density-dependent disease Fusarium wilt in cotton (Gossypium spp.), leading to vascular necrosis, plant death, and yield loss. Managing FOV4 relies on planting resistant cultivars, but no commercially available Upland (G. hirsutum L.) cultivars are resistant. Furthermore, detecting FOV4 in Upland cotton is more challenging due to fewer observable foliar symptoms than Pima (G. barbadense L.) cultivars. In two independent studies conducted over two years, Upland and Pima cultivars with varying responses to FOV4 were evaluated in naturally infested fields. In-season assessment of soil inoculum densities was performed by quantitative PCR (qPCR) at planting, first flower (midseason), and crop maturity (late season). Field measurements included plant mortality, visual root necrosis ratings, and yield. Highly susceptible Pima cultivars had the highest mortality rates, most severe necrosis, and the lowest yields. In contrast, publicly available resistant cultivars showed the lowest mortalities and necrosis, along with intermediate yields. Commercial Upland cultivars, assumed to have some degree of susceptibility, demonstrated intermediate levels of mortality and necrosis, but with greater yield potential, had the highest yields. Midseason soil inoculum densities significantly differed among cultivars, with highly susceptible Pima cultivars having the greatest

densities, although most cultivars were not significantly different from each other. However, positive relationships were observed between at-plant and late season inoculum densities with mortality and necrosis in both Upland and Pima cultivars regardless of resistance. Despite being resistant, yield loss was observed in Pima PHY 881 RF with increasing inoculum density, but yield losses were not observed in Upland cultivars at the inoculum densities in this study. A separate effort aimed to develop a multiplex qPCR assay for the rapid race-specific identification of FOV in planta, simultaneously detecting races 1, 2, and 3 separately from FOV4. This assay was utilized in a limited survey of Fusarium in Texas cotton and demonstrated high specificity and reliable identification, enabling the identification of FOV4 directly from root tissue in one day. This molecular tool can also be used in future studies to quantify inoculum density within the plant, enhancing the understanding of FOV4 and other races of FOV in Upland cotton. Overall, this research highlights the importance of cultivar selection and effective diagnostic tools in managing FOV4.

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Title: Multispectral Imaging and CNN Architectures for Cotton Leaf Disease Classification: A Comprehensive Review .

Author: Gajanan Ankatwar , Chitra Dhawale

Imprint: International Journal for Multidisciplinary Research IJFMR250347769 Volume 7, Issue 3, May-June 2025

Abstract: This review paper presents a comprehensive cotton leaf disease dataset designed to enhance detection and classification models using deep learning. The dataset comprises over 50,000 high-resolution images across seven classes: Bacterial Blight, Curl Virus, Herbicide Growth Damage, Leaf Hopper Jassids, Leaf Reddening, Leaf Variegation, and Healthy Leaves. Images were captured in diverse environments and growth stages to facilitate the development of robust, scalable convolutional neural network (CNN) models. We review prior datasets, highlighting limitations in class diversity, environmental inconsistency, and image quality, and demonstrate how our dataset addresses these challenges. The dataset construction methodology is detailed, from multi-modal data acquisition and expert labeling to augmentation and preprocessing techniques. We explore the biological basis and visual patterns of each disease class, enabling both human and algorithmic recognition. State-of-the-art CNN architectures like ResNet, DenseNet, and MobileNet are benchmarked, with a focus on explainable AI techniques like Grad-CAM for decision transparency. The integration of multispectral and hyperspectral imaging is shown to enhance classification performance. Deployment strategies for mobile and edge AI systems are discussed, along with challenges in rural connectivity and user adoption. Future research directions include addressing dataset biases, cross-regional validation, and extending to

pest and weed detection. This work establishes a new standard for data-driven plant pathology, empowering farmers with timely, accurate, and scalable disease diagnostics.

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Title: Gh_FBL43 regulates the resistance of Gossypium hirsutum to Verticillium wilt through jasmonic acid and flavonoid-related pathways.

Author: Jieyin Zhao, , uening Su, Wenju Gao, Tingwei Wang, Yuxiang Wang

Imprint: Front. Plant Sci., 17 July 2025, Sec. Functional and Applied Plant Genomics, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1620947

Abstract: F-box-LRR (FBL) genes play crucial roles in the response of plants to pathogen stress. This study involved a systematic analysis of the evolution of the FBL gene family in Gossypium hirsutum from a whole-genome perspective, and through expression pattern analysis combined with virus-induced gene silencing (VIGS), Gh_FBL43 was identified as a gene associated with resistance to Verticillium wilt in G. hirsutum. Further RNA-seq analysis revealed key pathways and genes regulated by Gh_FBL43. The G. hirsutum genome contains 57 FBL genes, which can be divided into five subgroups that were relatively conserved during the evolution of cotton. Expression analysis revealed that the expression level of Gh_FBL43 significantly increased under Verticillium wilt stress, with notable differences observed among extreme varieties. VIGS-meditated silencing of Gh_FBL43 was performed, and the leaves of the silenced plants presented chlorosis and necrosis, with the disease severity index (DSI) and disease severity rate (DSR) being significantly greater than those of the empty vector control plants. RNA-seq data from Gh_FBL43-silenced and control plants at 0 h and 24 h post-infection revealed 10,928 differentially expressed genes (DEGs), including 2,051 shared DEGs. Enrichment analysis combined with expression pattern analysis indicated that the silencing of Gh_FBL43 reduced the expression of genes in jasmonic acid (JA) and flavonoid-related pathways. In conclusion, our findings demonstrate the important role of the Gh_FBL43 gene family in conferring resistance to Verticillium wilt in G. hirsutum, potentially regulating this resistance through JA and flavonoid-related pathways, thereby laying a foundation for further elucidation of the molecular mechanisms by which Gh_FBL43 confers resistance to Verticillium wilt.

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Title: Gene genealogies reveal recent population expansion of cotton root rot incitant, *Macrophomina phaseolina* (Tassi) Goid in North-Western India.

Author:Shubham Saini , Rakesh Kumar , Minakshi Jattan, Karmal Singh, Oshin Saini , G utha Venkata Ramesh, Jagdeep Singh, Adesh Kumar , Rupesh Kumar Arora , Prashant B. Sandipan, Pradeep Kumar

Imprint: Physiological and Molecular Plant Pathology, Volume 139, September 2025, 102803

Abstract: Cotton root rot, incited by Macrophomina phaseolina is one of the most devastating fungal disease of the crop. The present study marks the inception of comprehensive population genetic analysis of *M. phaseolina* across the North Western cotton belt of India, encompassing 55 geographically distinct isolates of the pathogen collected from four states of India: Haryana, Punjab, Rajasthan, and Gujarat. The isolates were subjected to ITS and *EF-1a* region sequencing. All four *M. phaseolina* populations display haplotype and nucleotide diversity patterns indicative of historical bottlenecks followed by rapid population expansion, as evidenced by high haplotype diversity (0.714) coupled with low nucleotide diversity (0.0025). The star-like structure observed in the median-joining network also support the assumption of a departure from neutrality in the context of a constant population size, hence providing an evidence of population expansion. *M. phaseolina* populations in different geographical locations appear to form a largely panmictic or weakly structured metapopulation rather than being strongly subdivided as evident from low levels of genetic differentiation. Neutrality tests on *M. phaseolina* showed significant deviations from neutrality, with strongly negative Tajima's D, Fu and Li's D∗, and F∗ values, indicating recent positive selection or population expansion. Mismatch distribution analysis further supported a recent demographic expansion in the population. The results of hierarchical AMOVA analysis implied a lack of clear genetic boundaries between different populations of *M. phaseolina*, as supported by the low percentage of variation between populations compared to within-population differences.

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Title: Exploring the Impact of Weather Parameters on Cotton Leaf Curl Disease Progression and Whitefly Population Dynamics: A Decadal Analysis (2011–2020).

Author: N. K. Yadav, Yogesh Kumar, Navish Kumar Kamboj, Preeti Vashisht

Imprint: Journal of Phytopathology, First published: 26 June 2025,

https://doi.org/10.1111/jph.70115

Abstract: Cotton leaf curl disease (CLCuD) has become a potential menace to the production of cotton (*Gossypium hirsutum*) in Africa and South Asia. Whitefly (*Bemisia tabaci*) is the potential vector of this virus. Due to the dearth of resistant cultivars and effective management strategies of whitefly, yield loss in cotton is witnessd regularly. To ensure the timely application of management practices, there is a dire need for a reliable regression model that can forecast the CLCuD with high speed and accuracy. Keeping this in view, long-term studies were conducted during 2011–2020 at Cotton Research Station, Sirsa. The influence of weather parameters on the modulation of the disease progression and whitefly dynamics was recorded and analysed through

correlation and regression. A prediction equation for disease incidence and vector population was developed through regression. Minimum temperature, maximum temperature and evening relative humidity (RH) significantly influenced the disease development, with the former two having negative significant effects. The coefficient of determination (R^2) ranged from 0.19 to 0.90 for disease development with the weather parameters. The best fitted regression equation based on the decadal study for prediction of CLCuD incidence was $Y = -12.913_{Tmax} + 2.489_{Tmin} + 0.242_{RHm} - 0.197_{RHe} - 0.890_{Rf} + 459.368$ and for percent disease intensity (PDI) of CLCuD was $Y = -8.962_{Tmax} + 2.608_{Tmin} + 0.232_{RHm} - 0.567_{RHe} - 0.570_{Rf} + 306.433$. Additionally, a significant positive correlation between the CLCuD incidence, PDI and population of whiteflies was observed, as reflected by high values of the correlation coefficient (r) for most of the years during the period of study. The vector, whitefly (*B. tabaci*) population was also significantly influenced by the ambient weather conditions. High relative humidity favoured the whitefly population. Regression analysis revealed 25%–62% variability in whitefly population due to weather parameters, and the best fitted regression model for whitefly incidence is $Y = -0.194_{Tmax} - 1.610_{Tmin} - 0.439_{RHm} + 0.911_{RHe} + 0.020_{Rf} + 44.733$. On the basis of these equations, the main meteorological factors, such as temperature, relative humidity and rainfall, have a substantial impact on the emergence of CLCuD over the years.

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Title: Identification of potential target sites in cotton leaf Curl Multan Virus (CLCuMuV) after hybridization through candidate miRNAs in cotton to induce virus resistance.

Author: Momna Dar, Tauheed Suddal, Mudassar Fareed Awan, Muhammad Farhan Sarwar, Sana Shakoor & Safia Obaidur Rab

Imprint: 3 Biotech, Published: 02 July 2025, Volume 15, article number 234, (2025)

Abstract: The present study focuses on the computational identification and experimental validation of *Gossypium hirsutum*-derived miRNAs capable of targeting the *CLCuMuV* genome. The retrieved *CLCuMuV* genome sequence and 80 mature miRNAs were subjected to the identification of six key open reading frames (ORFs) encoding viral proteins: AC4 (100 amino acids), AC3 (134 amino acids), AC2 (150 amino acids), Rep (363 amino acids), AV2 (121 amino acids), and coat protein (256 amino acids). Using a combination of computational tools, including psRNATarget, RNA22, RNAhybrid, and miRanda, potential miRNA–mRNA interactions were predicted based on sequence complementarity and free energy calculations. The computational analysis revealed multiple cotton miRNAs manifesting increased binding potential to viral mRNAs. The potential miRNAs included ghr-miR390a, ghr-miR7486a, and ghr-miR7503 which emerged as highly promising candidates for RNA interference. Among

these, ghr-miR390a witnessed the highest level of binding efficiency equipped with duplex free energy (ΔG Duplex) of − 18.70 kcal/mol with binding energy (ΔG Binding) of − 16.78 kcal/mol, indicating the maximum potential of inhibiting viral gene expression. These cotton-derived potential miRNAs target essential viral genes involved in replication, coat protein synthesis, and movement immensely critical for the survival and proliferation of *CLCuMuV*. Phylogenetic analysis revealed that *CLCuMuV* isolates share common evolutionary ancestors, suggesting potential cross-resistance mechanisms that could be exploited. To experimentally validate these computational predictions, the identified miRNAs were cloned and highly expressed in transgenic cotton lines. Real-time PCR (RT-PCR) was employed to confirm the expression level of the target miRNAs in the transgenic plants while enzyme-linked immunosorbent assay (ELISA) validated the presence of key *GhDCL3* proteins in transgenic in contrast to the control. The transgenic lines expressing the ghr-miR390a encoding gene *GhDCL3* witnessed a significant reduction in symptoms of *CLCuMuV*, and incommensurable presence of *CLCuMuV* infection, while control plants exhibited typical disease symptoms, including leaf curling and vein thickening. This study identifies three highly promising miRNAs ghr-miR7486a, ghr-miR390a, and ghr-miR7503 that can effectively target critical genes in the *CLCuMuV* genome, providing a molecular mechanism to inhibit viral replication and mitigate the impact of the disease. The successful integration of these miRNAs into cotton via genetic engineering offers a novel and sustainable approach to control *CLCuMuV*.

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Title: Non-Conventional Treatments of Imidacloprid, Ascorbic acid, and Salicylic Acid against the Cotton Aphid Aphis gossypii (Glover).

Author: Noura M. Abd-El Hamid1; A. A. EL-hady; A. E. Abd-El Mageed and Salwa E. Negm

Imprint: J. of Plant Protection and Pathology, Mansoura Univ., Vol. 16 (6): 339- 348, 2025

Abstract: The present study was conducted to investigate the effects of selected inducers, including salicylic acid (SA), ascorbic acid (ASA), and the insecticide imidacloprid (IMI), on the cotton aphid, Aphis gossypii. All treatments demonstrated strong to moderate effects against aphids. Notably, (ASA) applied at concentrations of 2 and 4 mM significantly increased shoot and root lengths compared to both (IMI) and (SA) treatments. In the first season, based on the overall mean reduction in aphid populations, (IMI) showed the highest significant reduction 64.12% and 67.58% at application rates of 3.5 and 7 g/kg of seed, respectively. This was followed by IMI at 1.75 g/kg and SA at 2 mM, which resulted in reductions of 61.04% and 60.51%, respectively. The lowest reduction was observed with (ASA) at 1 mM, which achieved only 39.01%. Among all treatments, T18 (S&F with IMI at 7 g/kg + 0.75g/L) was the

most effective, reducing cotton aphid populations by 64.12%, followed by T17 (S&F with IMI at 3.5 g/kg +0.375g/L) with 58.91%, and T11 (S&F with SA at 2 mM) achieving a 54.60% reduction. In contrast, seed treatment with ASA at 1 mM was the least effective, showing only a 27.32% reduction in aphid populations. Treatments with IMI, SA, and ASA significantly increased polyphenol oxidase activity and total protein levels compared to the control. Moreover, seed treatment with ASA at 4 mM resulted in a highly significant increase in chlorophyll content specifically, chlorophyll A, chlorophyll B, and total chlorophyll content increased by 20.51%, 41.42%, and 29.79%, respectively.

PLANT BREEDING AND GENETICS

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Title: A comprehensive study on the stability of Desi cotton (Gossypium arboreum) genotypes under rainfed conditions using AMMI and GGE biplot analysis.

Author: Sheeba, A, Yogameenakshi, P, Ramakrishnan, S H, Aanandhi, N Baskar, K

Imprint: Plant Science Today; Vol. 12 No. 1 (2025), 2348-1900, 10.14719/pst.2025.12.1

Abstract: The present study aims to assess the stable and adaptable cotton genotypes under rainfed vertisol conditions using Additive Main effects Multiplicative Interaction and Genotype and Genotype × Environment (GGE) biplot analyses. Seventeen cotton genotypes were evaluated for seed cotton yield at the Agricultural Research Station, Kovilpatti, over three years (2020, 2021 and 2022), treated as distinct environments. Seed cotton yield was subjected to pooled ANOVA, AMMI and GGE biplot analysis, revealing significant variation between genotypes, environment and GEI, with the climate and G × E interaction accounting for 33.8 % and 27.8 % of the total variation, respectively, in seed cotton yield. Based on AMMI I analysis, the genotypes G5 (TKA 0856) and G13 (TKA 1336) were found to have overall adaptability in all the environments (years) studied and considered stable genotypes. GGE biplot was plotted for seed cotton yield using PC1 and PC2, accounting for 70.2% and 26.2 %, respectively, explaining 96.4 % of the total GEI variance. The winning genotypes identified for three mega-environments are G2 (TKA 0612), G16 (TKA 1104) for the first, G6 (TKA 1035), G13 (TKA 1336) for the second and G11 (TKA 1326), G4 (TKA 0848) for the third respectively. The genotype G6 (TKA 1035) was chosen as the most ideal genotype based on mean vs. stability analysis. Among the test environments, E1 was considered the most discriminating environment suitable for selecting widely adapted genotypes.

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Title: A single-nucleotide mutation of G301A in GaIAA14 confers leaf curling in Gossypium arboretum.

Author: Pengfei Miao, Huan Zhang, Yifan Xu, Ruowen Zhang, Yunfei Hao, Ji Liu

Imprint: Front. Plant Sci., 22 July 2025, Sec. Plant Breeding, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1645239

Abstract: Cotton is a crucial fiber and oil crop, playing a significant role in the textile and food industries. Its yield heavily relies on photosynthesis, a process that primarily occurs in the leaves. Consequently, leaf morphology stands as a vital agronomic trait in cotton breeding. However, research on the molecular mechanisms underlying cotton leaf morphogenesis remains relatively limited. Here we identified a curly leaf mutant (CU) in Gossypium arboreum by ethyl methyl sulfonate (EMS) mutagenesis. The genetic analysis revealed that the curly leaf trait in this mutant is a semi-dominant characteristic controlled by a single gene. The map-based cloning of the CU locus showed a single-nucleotide mutation from G to A at the 301st positions in AUX/IAA14 protein (GaIAA14), which resulted in an amino acid substitution from valine (V) to isoleucine (I). After silencing GaIAA14 through virus-induced gene silencing (VIGS) technology in CU mutant, the leaves exhibited a flattened phenotype, indicating that GaIAA14 is a key gene regulating leaf curling in cotton. Comparative transcriptomic RNA-Seq analysis revealed significant changes in the expression levels of most auxin-related genes, suggesting that the mutation disrupts auxin signaling transduction. These findings establish a foundation for further functional studies of this gene and provide research strategies for leaf morphology improvement.

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Title: GWAS analysis reveals a novel *ERF* family gene *GH_A03G1754* in upland cotton under cold stress.

Author: Jianbin Li, Xiaokang Feng, Bangxin Chen, Qian-Hao Zhu, Xinyu Zhang, Yonglin Yang, Fei Xue

Imprint: Plant Stress, Volume 17, September 2025, 100932

Abstract: Low temperature is a critical abiotic stress during the early growth stages of cotton, affecting crop establishment and causing yield reduction. A thorough insight into the genetic factors governing cold tolerance is critical for formulating breeding strategies aiming for enhanced cold tolerance. This study measured the primary root length (RL), fresh weight (FW), and dry weight (DW) of 343 upland cotton (*Gossypium hirsutum* L.) germplasm under sustained low-temperature stress during the seedling stage. The single nucleotide polymorphisms (SNPs) identified based on resequencing of

the 343 accessions were used in a genome-wide association analysis of the three traits, which identified two, six and eight SNPs significantly associated with RL, FW, and DW, respectively. Two major loci on chromosomes A03 and D04 contributing to FW- and DW-based cold tolerance were evident due to their occurrence in at least two datasets. Within these two loci, multiple genes were found to be cold responsive, with *GH_A03G1754* being a potentially positive contributor of cold tolerance, because silencing the gene in cold-tolerant variety reduced its cold tolerance. This study provides molecular markers and candidate gene for molecular breeding of cold tolerance in cotton.

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Title: Assessment of genetic architecture of cotton germplasm for drought tolerance: A focus on morpho-physiological and biochemical attributes.

Author: Zoha Chaudhary, Athar Mahmood, Abdel-Halim Ghazy, Sajid FIAZ, Ayesha Arshad, Muhammad T. Chaudhary, Muhammad M. Javaid, Kotb A. Attia, Inzamam UL Haq

Imprint: Notulae Botanicae Horti Agrobotanici Cluj-Napoca, Volume 53, Issue 2, Article number 14205, DOI:10.15835/nbha53214205

Abstract: Cotton (Gossypium hirsutum) is a vital fiber and cash crop, but water scarcity significantly impacts its development and production. The drought tolerance of 15 genotypes was evaluated at the seedling stage under three water regimes: control, 40%, and 20% field capacity. Significant variations in sodium ions (Na+) were observed across all morphological and physiological traits. Key traits like fresh root weight, shoot length, total chlorophyll, hydrogen peroxide (H2O2), K+/Na+, and potassium ions (K+) showed strong interactions between drought stress and genotype (D × G). Excised leaf water loss (ELWL) was positively correlated with shoot length (SL) under both control and drought conditions, while negatively associated with fresh root weight. Shoot length had a positive correlation with all attributes except Na+. Fresh root weight was negatively correlated with H2O2 but positively with other traits. Potassium ions were positively associated with SL, fresh root weight, and chlorophyll content. Genotypic correlations showed positive relationships for all biochemical traits except H2O2. Traits like root length, shoot length, ELWL, relative water content, proline, peroxidase

(POD), H2O2, and K+/Na+ can differentiate drought-tolerant genotypes. Genotypes RH-622, FH-144, CIM-608, and MNH-886 showed potential for developing drought-resistant cotton cultivars.

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Title: Genome-wide identification and functional analysis of *TCX* gene family and the critical role of *GhTCX17* in response to drought and salt stress in cotton.

Author: Yangyang Wei, Jingjing Zhai, Shuaikang Geng, Shaoliang Zhang, Yongqing Zhao, Bingkai Cui, Huiyun Shan, Yanhua Li, Cong Wang, Pengtao Li, Yuling Liu, Quanwei Lu, Baohong Zhang

Imprint: Functional & Integrative Genomics, Published: 16 June 2025, Volume 25, article number 129, (2025)

Abstract: Cotton is an important natural fiber crop. The Tesmin/TSO1-like CXC (*TCX*) gene family plays an important role in plant resistance to environmental stress, and its mechanism is still not clear in cotton. In this study, we systematically identified the potential functions of *TCX* family genes in cotton were investigated based on genome identification, phylogenetic and genomic analyses, chromosome mapping and cis-regulatory element prediction. A total of 79 *TCX* genes were identified in the genome-wide analysis of four cotton species. Chromosomal localization and synteny analysis revealed that the *TCX* gene family was relatively conservative and fragment replication was the main amplification mode of *TCX* gene family during cotton evolution. Cis-element analysis showed that there were a plenty of elements related to light response, hormone response and abiotic stress response in the *TCX* gene promoter. Gene expression analysis based on RNA-seq and qRT-PCR showed that *TCX* genes were responsive to abiotic stress. The key gene *GhTCX17* was cloned for functional verification. *GhTCX17* protein was localized in the nucleus. Under drought and salt stress, silencing *GhTCX17* gene plants showed leaf wilting aggravation, decreased total antioxidant capacity, increased malondialdehyde content compared with control plants, implied the reducing drought and salt tolerance of silencing *GhTCX17* gene in cotton. This study revealed the evolution and function diversity of the *TCX* gene family and laid an important foundation for further study to dissect *TCX* gene family functioning mechanisms on cotton stress resistance arch.

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Title: Genetic dissection of lint percentage in an introgression population between *Gossypium hirsutum* and *G. mustelinum.*

Author: Yang Yang, Bo Li, Yuanxue Li, Zhiyong Xu, Xiaorong Li, Zumuremu Tuerxun, Xunji Chenginal Article

Imprint: Theoretical and Applied Genetics , 13 June 2025, Volume 138, article number 152, (2025)

Abstract: Cotton (*Gossypium* spp.) is an important natural fiber crop for the textile industry worldwide. Lint percentage (LP) is one of the most essential yield components of cotton. However, the genetic and molecular mechanisms underlying LP in cotton remain unclear. Here, 264 introgression lines of the *G. mustelinum* acc. P0811704 in the background of *G. hirsutum* cv. Emian22 were used to dissect the LP phenotype in ten

individual environments. A total of 14 stable quantitative trait loci (QTL) were identified in at least two environments, with phenotypic variation explained by them ranged from 1.12 to 13.14%. Among them, *qLP-D12-3*, a main-effect QTL, was validated in IL-derived F_2 segregating population ($n = 2836$), and was fine-mapped to a 110-kb physical region by selected $F_{2:3}$ recombinants. Among the seven annotation genes in this region, only one gene, encoding allene-oxide cyclase (*AOC4*), exhibited a significant expression difference between near-isogenic lines and recurrent parent when lint fibers are initiating. *AOC4* contains *G. mustelinum*-specific variation in the promoter region, and highly expressed in fiber cells of the outer layer of ovule. This research would lay a solid foundation for further elucidating the molecular mechanism of cotton fiber initiation.

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Title: Unravelling the Genetic Basis of Fusarium Wilt Resistance and Abiotic Stress Tolerance in Cotton.

Author: Gulzira Narkizilova, O. S. Turaev, Sayfulla Boboyev, Mirvakhob Mirakhmedov, Muhammad Zafar, Salman Majeed, Mohamed Fawzy Ramadan, Trobjon Makhkamov, Muhammad Rizwan Khan, Aleena Gul, Ankeela Pńisyer

Imprint: Journal of Phytopathology First published: 24 June 2025, https://doi.org/10.1111/jph.70107

Abstract: Cotton (Gossypium hirsutum L.), often referred to as 'white gold', is a vital global crop, yet its productivity and fibre quality are significantly affected by abiotic stressors like drought and salinity, as well as biotic threats such as Fusarium wilt (Fusarium oxysporum f. sp. vasinfectum). To enhance stress tolerance, disease resistance and fibre quality, this study employs marker-assisted selection (MAS) as a more efficient alternative to conventional breeding. Genomic DNA from eight cotton genotypes, including hybrids and varieties, was analysed using polymerase chain reaction (PCR) with molecular markers (BNL1604, Gh247, BNL3255, JESPR220, SOC1 and CAT) linked to economically significant traits. Results indicated that the BNL1604 marker (102 bp allele) was associated with fibre quality in most samples, while the Gh247 marker (125 bp allele) suggested additional genetic influences on fibre characteristics. The BNL3255 marker (225 bp allele) was consistently linked to Fusarium wilt resistance, whereas the JESPR220 marker showed allele variation. The SOC1 gene, related to early maturation, exhibited polymorphism but failed to amplify in the Kamolot-79 variety. Stress tolerance variability was reflected in fragment size differences of the CAT gene, associated with abiotic stress resilience. These findings highlight the significance of molecular markers in accelerating cotton improvement through MAS, enabling the development of high-yield, disease-resistant and stress-tolerant cultivars. Future research should focus on validating these markers across broader genetic populations to optimise their use in cotton breeding programmes.

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Title: Thermotolerance in Cotton: Comparative Analysis of Antioxidant Gene Expression Under Heat Stress.

Author: Shomakhamadov Shoakbar Shoazim o'g'li , Navruzov Sanjar Botirovich , Babayeva Dildora Tuygunovna , Khashimova Nigora Rustamovna , Akhunov Ali Akhunovich

Imprint: International Scientific and Practical Conference "The Role of Plant Genetics and Experimental Biology in Global Climate Change and Food Security", May 15-16, 2025

Abstract. This study investigated the expression of key antioxidant genes—CAT1 (catalase), POD (peroxidase), SOD (superoxide dismutase), and APX (ascorbate peroxidase)— in three cotton (Gossypium hirsutum L.) cultivars: Ravnaq-2, Porloq-1, and Buxoro-102, under heat stress (45°C for 6 hours) and a subsequent recovery period. Gene expression was assessed by quantitative PCR (qPCR) and analyzed using the 2^(-ΔΔCt) method [8]. Under heat stress, CAT1, POD, and SOD expression significantly increased in all cultivars, whereas APX expression declined. During the 6-hour recovery at 30°C, most gene expression levels returned toward baseline, indicating stress alleviation. Notably, Buxoro-102 exhibited the strongest induction of CAT1 and SOD, suggesting superior thermotolerance. These findings provide a molecular basis for selecting heat-tolerant cotton cultivars based on antioxidant gene expression profiles.

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Title: Genome assembly of two allotetraploid cotton germplasms reveals mechanisms of somatic embryogenesis and enables precise genome editing.

Author: Zhongping Xu, Guanying Wang, Xiangqian Zhu, Ruipeng Wang, Longfu Zhu, Lili Tu, Yuling Liu, Renhai Peng, Keith Lindsey, Maojun Wang, Xianlong Zhang & Shuangxia Jin

Imprint: *Nature Genetics* volume 57, pages2028–2039 (2025)

Abstract: Somatic embryogenesis is crucial for plant genetic engineering, yet the underlying mechanisms in cotton remain poorly understood. Here we present a telomere-to-telomere assembly of Jin668 and a high-quality assembly of YZ1, two highly regenerative allotetraploid cotton germplasms. The completion of the Jin668 genome enables characterization of ~30.1 Mb of centromeric regions invaded by centromeric retrotransposon of maize and *Tekay* retrotransposons, an ~8.1 Mb 5S rDNA array containing 25,190 copies and a ~75.1 Mb major 45S rDNA array with 8,131 copies. Comparative analyses of regenerative and recalcitrant genotypes reveal dynamic transcriptional patterns and chromatin accessibility during the initial regeneration process. A hierarchical gene regulatory network identifies *AGL15* as a contributor to regeneration. Additionally, we demonstrate that genetic variation affects sgRNA target sites, while the Jin668 genome assembly reduces the risk of off-target effects in CRISPR-based genome editing. Together, the complete Jin668 genome reveals the complexity of genomic regions and cotton regeneration, and improves the precision of genome editing.

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Title: Melatonin bridges timekeeping and survival: coordinating diurnal rhythms, autophagy, and energy balance in upland cotton.

Author:Laha Supriya , Deepika Dake, Nyanthanglo Woch, Kritika Chauhan, Richa Lobi yal, Mehanathan Muthamilarasan, Gudipalli Padmaja

Imprint: Plant Stress, Volume 17, September 2025, 100969

Abstract: Melatonin is widely recognized for its regulatory role in animal circadian rhythms, but its functional significance in plant chronobiology, especially its integration

with energy metabolism and autophagy, remains poorly understood. To address this gap, we examined the interplay between melatonin oscillation, clock gene expression, carbohydrate metabolism, and autophagic activity in *Gossypium hirsutum*. Plants were subjected to four treatments: control, melatonin inhibition (melatonin inhibitor (Tip60 Histone Acetyltransferase inhibitor (MG-149), melatonin rescue (MG-149 + exogenous melatonin), and excess melatonin. Across a 24-hr cycle, we quantified melatonin levels, circadian gene expression-*LATE ELONGATED HYPOCOTYL1 (LHY1), CIRCADIAN CLOCK ASSOCIATED1 (CCA1), PSEUDO-RESPONSE REGULATOR7 (PRR7), and TIMING OF CAB EXPRESSION 1 (TOC1), Sucrose non-fermenting-1-related protein kinase 1 (SnRK1)* pathway activity, autophagy markers, and carbohydrate dynamics. Control and melatonin-rescue treatments displayed robust diel oscillations in melatonin content, clock gene expression, energy signaling (SnRK1), and autophagy-related markers *(*ATG8-PE*, ATG5/7/9),* with starch and ATP levels following rhythmic trends. In contrast, melatonin-deficient and melatonin-excess treatments disrupted these rhythmic patterns, leading to deregulated sugar metabolism, suppressed *SnRK1* expression, and loss of autophagic cycling. Notably, the rhythmicity, rather than mere presence of melatonin, emerged as critical for synchronizing internal timekeeping with cellular metabolic processes. This study identifies melatonin as a central coordinator of plant diurnal regulation, linking diel gene expression with energy and stress-adaptive homeostasis, and opens promising avenues for chronobiology-based crop improvement.

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Title: Green synthesized silver nanoparticles enhance drought tolerance in cotton plants cultured in vitro.

Author: Gizem Şafak Baransel, Oğuz Yücel, Eren Yıldırım, Göksenin Kalyon, Serkan Emik, Ayşe Erol & Neslihan Turgut Kara

Imprint: Physiology and Molecular Biology of Plants , Published: 28 June 2025, Volume 31, pages 959–978, (2025)

Abstract: The study investigated the effects and potential applications of green-synthesized silver nanoparticles (AgNPs) on cotton plants under in vitro drought stress. AgNPs were synthesized using cotton seed oil cake extract (CSOCE) as a stabilizing and reducing agent. The secondary metabolite content of CSOCE was analyzed using High Performance Liquid Chromatography (HPLC). Characterization of synthesized AgNPs was performed using Dynamic Light Scattering (DLS), polydispersity index (PDI), Zeta Potential (ZP), Scanning Electron Microscopy and Energy Dispersive X-Ray Spectroscopy (SEM-EDS), X-Ray Diffraction Analysis (XRD), Ultraviolet-Visible Light Spectroscopy (UV-Vis spectroscopy), and Fourier Transform Infrared Spectrometry (FTIR) analyses. According to SEM, the nanoparticle sizes varied between 50 and

100 nm. ZP was − 28.7 mV and PDI value was 0.65 according to DLS results. The experimental groups were: (1) MS medium (control group), (2) PEG, (3) AgNP, and (4) PEG + AgNP. Plants were transferred to the respective media, cultured for three days, and subsequently analyzed. Morphological parameters including root number, root and shoot lengths, and leaf surface area were measured, while physiological traits such as relative water content, biomass accumulation, osmolyte accumulation, and photosynthetic pigment contents were assessed. Molecular analyses were conducted to examine the relative gene expression of drought stress-associated genes, including *CAT*, *POD*, *Cu/Zn SOD*, *MnSOD*, *MPK17*, *CAX2*, and *IDI-1*. The results demonstrated that the application of AgNPs alleviated the adverse effects of in vitro drought stress on *Gossypium hirsutum* plants. These findings suggest that green synthesized AgNPs hold significant potential as agents to mitigate drought stress in plants.

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Title: Turbo ID-Based Proximity Labelling Identifies MED25 as an Activator of GoPGF-Mediated Gland Formation and Gossypol Biosynthesis in Cotton.

Author: Lu Long, Fu-Chun Xu, Fen Li, Zhen-Nan Zhang, Shen-Zhai Shang, Jing-Ruo Zhao, Gai-Yuan Hu, Jia-Yi Ma, Man Yuan, Jose Ramon Botella, Yingfang Zhu

Imprint: Plant Cell and Environment, First published: 22 June 2025, https://doi.org/10.1111/pce.70026

Abstract: The pigment glands of cotton synthesize the toxic gossypol that contributes to cotton's defence, but also limits the usage of cottonseed as a food source. Previous studies have shown that the gland-localized GoPGF is the master transcription factor controlling the gland morphogenesis and gossypol biosynthesis in cotton. However, the precise mechanism underlying the GoPGF-mediated transcription of downstream genes remains unclear. In this study, TurboID-based proximity labelling was established in cotton using a transient expression system to identify the components of GoPGF-complex. A total of 48 high-confidence GoPGF-proximal proteins were identified, and a mediator subunit, MED25, was shown to control gland formation through phenotypic studies. Several lines of evidence indicate that GhMED25 physically interacts with GoPGF in the nucleus, and GhMED25-GoPGF complex regulates the expression of *GhJUB1* related to gland morphogenesis, and several well-characterized gossypol biosynthetic genes. ChIP-qPCR further revealed that GhMED25 acts as an enhancer of the GoPGF-mediated transcriptional output. Our study shows the value and reliability of the proximity labelling system in studying the low-abundance and cell-type-specific proteins in crops, adding a new role to the multifunctionality of MED25 in plants, and provides new insights into the intricate signalling network governing gland formation and terpene production in cotton.

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Title: Genome-Wide Characterization of the ABI3 Gene Family in Cotton.

Author: Guoyong Fu, Yanlong Yang, Tahir Mahmood, Xinxin Liu, Zongming Xie, Zengqiang Zhao, Yongmei Dong, Yousheng Tian, Jehanzeb Farooq, Iram Sharif, and Youzhong Li

Imprint: Genes 2025, 16(8), 854; https://doi.org/10.3390/genes16080854

Abstract: Background: The B3-domain transcription factor ABI3 (ABSCISIC ACID INSENSITIVE 3) is a critical regulator of seed maturation, stress adaptation, and hormonal signaling in plants. However, its evolutionary dynamics and functional roles in cotton (Gossypium spp.) remain poorly characterized. Methods: We conducted a comprehensive genome-wide investigation of the ABI3 gene family across 26 plant species, with a focus on 8 Gossypium species. Analyses included phylogenetics, chromosomal localization, synteny assessment, gene duplication patterns, protein domain characterization, promoter cis-regulatory element identification, and tissue-specific/spatiotemporal expression profiling under different organizations of Gossypium hirsutum. Results: Phylogenetic and chromosomal analyses revealed conserved ABI3 evolutionary patterns between monocots and dicots, alongside lineage-specific expansion events within Gossypium spp. Syntenic relationships and duplication analysis in G. hirsutum (upland cotton) indicated retention of ancestral synteny blocks and functional diversification driven predominantly by segmental duplication. Structural characterization confirmed the presence of conserved B3 domains in all G. hirsutum ABI3 homologs. Promoter analysis identified key stress-responsive cis-elements, including ABA-responsive (ABRE), drought-responsive (MYB), and low-temperature-responsive (LTRE) motifs, suggesting a role in abiotic stress regulation. Expression profiling demonstrated significant tissue-specific transcriptional activity across roots, stems, leaves, and fiber developmental stages. Conclusions: This study addresses a significant knowledge gap by elucidating the evolution, structure, and stress-responsive expression profiles of the ABI3 gene family in cotton. It establishes a foundational framework for future functional validation and targeted genetic engineering strategies aimed at developing stress-resilient cotton cultivars with enhanced fiber quality.

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Title: Assessment of genetically modified cotton T304-40 for renewal authorisation under Regulation (EC) No 1829/2003 (dossier GMFF-2024-23010).

Author: EFSA Panel on Genetically Modified Organisms (GMO)✉, Josep Casacuberta, Francisco Barro, Albert Braeuning, Ruud de Maagd, Michelle M Epstein, Thomas Frenzel, Jean-Luc Gallois, Frits Koning, Antoine Messéan, F Javier

Moreno, Fabien Nogué, Giovanni Savoini, Alan H Schulman, Christoph Tebbe, Eve Veromann, Tilemachos Goumperis, Paolo Lenzi, Ana M Camargo, Pietro Piffanelli, Tommaso Raffaello

Imprint: EFSA J, . 2025 Jul 22;23(7):e9580. doi: 10.2903/j.efsa.2025.9580

Abstract: Following the submission of dossier GMFF-2024-23010 Regulation (EC) No 1829/2003 from BASF Agricultural Solutions Seed US LLC, the Panel on Genetically Modified Organisms of the European Food Safety Authority was asked to deliver a scientific risk assessment on the data submitted in the context of the renewal of authorisation application for the insect resistant and herbicide tolerant genetically modified cotton T304-40, for food and feed uses, excluding cultivation within the European Union. The data received in the context of this renewal application contained post-market environmental monitoring reports, an evaluation of the literature retrieved by a scoping review, a search for additional studies performed by or on behalf of the applicant and updated bioinformatics analyses. The GMO Panel assessed these data for possible new hazards, modified exposure or new scientific uncertainties identified during the authorisation period and not previously assessed in the context of the original application. Under the assumption that the DNA sequence of the event in cotton T304-40 considered for renewal is identical to the sequence of the originally assessed event, the GMO Panel concludes that there is no evidence in renewal dossier GMFF-2024-23010 for new hazards, modified exposure or scientific uncertainties that would change the conclusions of the original risk assessment on cotton T304-40.

SEED SCIENCE AND TECHNOLOGY

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Title: Identification of novel sources of variation for the improvement of cold germination ability and early seedling vigor in upland cotton (Gossypium hirsutum L.).

Author: Ritchel Bueno Gannaban, B.S.

Imprint: A Thesis In Plant and Soil Science, Submitted to the Graduate Faculty of Texas Tech University in Partial Fulfillment of the Requirements for the Degree of Master of Sciences

Abstract: Cotton production is limited by the adverse effects of low temperature stress especially at the germination and early seedling stages. Due to its tropical and sub-tropical origins, cotton is extremely sensitive to low temperatures from seed germination up to maturity. The germination process is hindered when cotton seeds are

exposed below the minimum cardinal temperature of 15°C. Subsequently at the early seedling stage, cotton genotypes that are susceptible to cold exhibit poor vigor. Although several

mitigating strategies that involves both agricultural practices and the application of plant exogenous regulators are available, the most economical long-term solution would be to develop cultivars and varieties with tolerance to low temperatures at the germination and early seedling stage. The main goal of this study is to identify genetic variation in the available germplasm collections which can be utilized in future breeding programs aiming to improve cold germination ability and early seedling vigor in cotton at the early seedling stage. Through genotypic and phenotypic analysis, a wide variation in response

to cold stress during germination is established within the Gossypium Diversity

Reference Set (GDRS) and fatty acid (FA) mutants. The screening for seedling vigor was carried out using a set of morphological, physiological, and biochemical assays. A total of 18 genotypes from both test germplasm were identified exhibiting varying responses to cold stress during the early seedling stage. In addition, morphological markers such as plant height and biomass were found to be good markers in identifying seedling vigor under cold stress in cotton. Comparative transcriptome profile analysis was conducted to confirm the differences in response to cold stress at the early seedling stage at the genic

level. Through further analysis and gene validation studies, the initial results of this study can be used to identify set of genes or gene networks responsible for vigor under cold stress at the early seedling stage in cotton.

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Title: Parental Diversity and Earliness-Seed-Lint Index of Twelve Cotton (Gossypium hirsutum L.) Genotypes.

Author: Srabone Akter Dhulon; M. S. Raihan; M. S. Alam; Sima Kundu; A. K. M. Aminul Islam

Imprint: Arab Universities Journal of Agricultural Sciences, Volume 33, Issue 1, June 2025, Page 81-92.

Document Type: Original Article, DOI: 10.21608/ajs.2025.349870.1590

Abstract: The study aimed to assess the genetic diversity and relationships among 12 genotypes using RAPD markers. Molecular variance within and between the populations of parental genotypes accounted for 93% and 7%, respectively. The

unweighted neighbor-joining tree, principal coordinate analysis, and heatmap clustered the 12 parental genotypes into three major groups. The population structure model divided the population into two groups, with parents BC-119 and RA-2 being pure. Parents BC-119 and P1(1) required the fewest days for 80% boll opening (166.97 and 168.78, respectively). Parents RA-2 and P1(1) also achieved the highest seed cotton yield per plant (68.47 g and 68.09 g, respectively). Parent BC-119 exhibited strong performance in traits including the number of secondary fruiting branches (10.64 per plant), lint index (5.46), and ginning out-turn (41.26%). The highest value of Bartlett's earliness index was 1.11. CB-15 and CB-17 genotypes produced the highest seed index, while genotype P1(1) recorded the lowest seed index. Parents BC-119 and CB-17 yielded the highest lint index (>5.30 g), whereas P3(8) produced the lowest lint index (2.93 g). Results suggested that molecular marker data are useful in determining the diversity and relatedness of parents, which could be used to identify exceptional lines for future breeding programs.

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Title: Cluster and Principal Component Analysis for Seed Coat Resistibility and Its Related Traits of Cotton (Gossypium spp.) Genotypes.

Author: Fatih KILLI, Tahsin BEYCİOGLU

Imprint: International Journal of Environmental & Agriculture Research (IJOEAR) ISSN:[2454-1850] [Vol-11, Issue-6, June- 2025

Abstract— During the ginning of seed cotton, the seeds can be broken and mixed into the fibers. The number of seed coat particles passing into the fibers and the amount of neps caused by the seed coat is an important factor that negatively affects the yarn quality and creates problems in dyeing. In this study, 200 different cotton genotypes were evaluated in terms of 100-seed weight, seed coat ratio, seed coat thickness and seed coat resistibility. As a result of the study, it was determined that 100-seed weights of genotypes varied between 7.23 - 15.43 g, seed coat ratios between 15.53 - 38.27%, seed coat thickness between 0.41 - 1.00 mm and seed coat resistibility between 41.07 - 107.21 newton. TxNo:142 genotype had the highest seed coat resistibility. In addition, it was determined that there was a positive and significant relationship between seed coat resistibility and 100-seed weight. In principal components analysis, two out of 4 principal components were selected with Eigen value >1. The two principal components contributed 59.3% towards variability. In cluster analysis, 200 genotypes were allocated in five clusters. Cluster II was the largest by having 90 genotypes while cluster V, cluster III, cluster I and cluster IV having 54, 28, 20 and 8 genotypes, respectively.

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Title: Genetic and Molecular Insights into the Inheritance of Fiber Colors in Upland Cotton (Gossypium hirsutum).

Author: Shiguftah Khalid, Tahir Mahmood, Javaria Tabusam, Zhenzhen Wang, Hongge Li, Baojun Chen, Jun Peng, Xiaoli Geng, Shoupu He & Xiongming Du

Imprint: Journal of Plant Growth Regulation , Published: 22 July 2025, Volume 44, pages 4995–5011, (2025)

Abstract: Cotton is a commercially valuable fiber crop, renowned for its unique fiber properties. The distinctive features of cotton fiber result from complex interactions among various genetic and molecular pathways. One intriguing aspect of cotton fiber is its natural color, which offers the potential to develop a diverse spectrum of naturally colored cotton fibers. This review aims to elucidate these complexities by examining the inheritance patterns of different fiber colors. Initially, it was proposed that distinct genes were responsible for the color traits of cotton fiber, such as green, brown, and white, based on Mendelian inheritance patterns. Traditionally, a dominant brown fiber gene was believed to be the primary determinant of brown fiber color. However, recent advancements in cotton genetics have identified numerous genes involved in pigment production, regulatory components influencing fiber color, and genetic variants contributing to the diverse range of fiber colors. Key metabolic pathways have been mapped, revealing genes encoding the corresponding enzymes, such as chalcone synthase (*GhCHS*), which is linked to the flavonoid production pathway and associated with brown and green fiber coloration. Proanthocyanidins and their derivatives, produced via the flavonoid pathway, are the primary pigments in brown fiber. The expression of flavonoid pathway genes is regulated by a major locus *Lc1* linked to the MYB transcription factor gene TRANSPARENT TESTA 2 (*GhTT2*). Brown and green fiber colors are partially dominant traits controlled by single genes, suggesting that gene expression dosage impacts the phenotype of colored cotton. The review highlights the crucial role of genetic and epigenetic processes in determining fiber color. Additionally, it nuanced interaction between dominant brown and white fiber genes and the involvement of multiple loci or modifier genes influencing color intensity.

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Title*: GhHDZ50* regulates cotton fiber elongation in *Gossypium hirsutum* L. through control of fatty acid biosynthesis.

Author:Wenbin Ren, Cuicui Wu, Tao Wang, Yanfeng Deng,Qingquan Kong, Xiu Yang, Shuiping Xiao

Imprint: Plant Science, Volume 359, October 2025, 112641

Abstract: Cotton fibers are highly elongated single-celled trichomes that develop on the ovule of the seed. However, there are still many unknowns about the molecular mechanism of cotton fiber development. In this study, a homologous domain leucine-zipper (HD-Zip) IV gene *GhHDZ50* was reported to play an important role in cotton fiber elongation. *GhHDZ50* was predominantly expressed in fibers at 5 days post-anthesis (DPA), and its gene product was localized to the nucleus. Overexpression of *GhHDZ50* in Arabidopsis resulted in longer leaf trichomes and root hairs, while knocking out of *GhHDZ50* in cotton, resulted in shorter cotton fibers. Knockout of *GhHDZ50* in cotton led to reduce transcript levels of genes associated with fatty acid biosynthesis, ethylene biosynthesis and signal transduction, sucrose synthase and tubulin. Biochemical analysis showed that GhHDZ50 interacted directly with GhTCP3, which further inhibited the transcriptional activity of GhHDZ50 on downstream fatty acid synthesis-related genes *GhLAC6* and *GhLOX5*. In conclusion, *GhHDZ50* positively regulates cotton fiber elongation through fatty acid biosynthesis. The results provide new evidence for involvement of HD-Zip transcription factors in regulation of cotton fiber development and suggest new targets for cotton breeding.

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Title: Study on the analysis of yield and fiber quality characteristics of upland cotton (Gossypium hirsutum L.).

Author: Rajab Ali Kaleri, Naila Gandahi, Mohsin Zulqarnain Hussain Abbasi, Shahla Karim Rukhsar Samoon, Tariq Hussain Majeedano Nabeela Rashid, Aweesha Bughio, Soohanro Khan Kaleri, Farman Ali Kaleri Naeem Ahmed Kaleri, Sarmad Ali Kaleri

Imprint: Pure and Applied Biology (PAB), [S.l.], v. 14, n. 2, p. 440-445, june 2025. ISSN 2304-2478. Available at: https://thepab.org/index.php/journal/article/view/2942>. Date accessed: 25 aug. 2025.

Abstract: The present study was conducted at the Cotton Research Institute (CRI) in Tandojam during the kharif season of 2022. The study aimed to investigate the yield and fiber characteristics of upland cotton (*Gossypium hirsutum* L.) genotypes. The plant material was grown in the field in a randomized complete block design (RCBD) with three replications and eight genotypes, including one check variety. The plant height (cm), sympodial branches per plant, bolls per plant, boll weight, and staple length showed highly significant differences at a probability level of <0.01. Monopodial branches per plant, seed cotton yield, and GOT% indicated differences at a probability level of >0.05. Among the eight genotypes, the TH-26/23 genotype had the maximum

plant height, monopodial branches per plant, boll weight, seed cotton yield, while TH-23/23 had the maximum sympodial branches per plant, bolls per plant, seed cotton yield, and GOT%. According to the correlation analysis, plant height showed a significant favorable relationship with monopodial branches per plant, and a highly significant and favorable relationship with boll weight, seed cotton yield, and GOT%. Monopodial branches per plant showed a highly significant relationship with GOT%. Sympodial branches per plant showed a significant relationship with staple length. Boll weight showed a highly significant correlation with seed cotton yield.

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Title: Digital Classification of Naturally Colored Cotton Fiber by RGB Imagery.

Author: Gabriel Fernandes , Luiza Medeiros , Filipe Matias , Larissa Sousa , Daniel Cardoso , and Elv´ecio Silva J´unior

Imprint: Authorea Preprints, 2025

Abstract: Image-based phenotyping represents an innovative approach in breeding research, allowing rapid and reliable measurements that aid in decision-making. This study used image analysis to quantify the intensity of fiber coloration in Gossypium hirsutum L. genotypes and investigate the impact of bolls from the upper, middle and lower thirds of the plants. Seventeen cotton genotypes (5 cultivars and 12 F2:3 generation genotypes) were evaluated in relation to the intensity of fiber coloration. Three representative bolls were manually harvested per plot, per third development, and were photographed, including a colorcard, and these were processed with ImageJ software for correction of brightness and coloration. Data analysis was performed in R software, and the FIELDimageR package was used to calculate the BI, SI and NGRDI indices. Calibration of the images with colorcards resulted in higher averages but did not change the grouping of the observed averages. Compared with the other thirds, the upper third presented lower fiber staining intensity, with a variation of 6.25%, but there was no interaction between the genotypes and thirds. The SI allowed the distinction of genotypes by the saturation of the fiber color. The BI was correlated with the fiber characteristics UI, STR and UHML, with coefficients of determination of 0.77, 0.80 and 0.88, respectively. This digital cotton fiber quality evaluation method streamlines breeding decisions, enhances data accuracy and reduces costs.

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Title: The Cotton Cinnamyl Alcohol Dehydrogenase 6 Functions in Developing Cotton Fibers.

Author: Wenran Hu, Xuan Ding

Imprint: Agricultural Sciences > Vol.16 No.7, July 2025, DOI: 10.4236/as.2025.167036

Abstract: Cotton fiber is the most important source used natural raw in the textile industry and its productions play a pivotal role in the global economy. Cinnamyl alcohol dehydrogenase (*CAD*) plays crucial roles in the development of cotton fibers, but its functional mechanisms remain largely unknown. Research on improving fiber quality of cotton crop is important. Owing to a fiber-specific *CAD* gene, designated *GhCAD*6 from upland cotton (*Gossypium hirsutum* L.) is expressed predominantly in fiber cells, especially at the secondary wall thickening stage of fiber development, we characterized the function of *GhCAD*6 in cotton fiber development. Through cloning *GhCAD*6 and analyze expression of *GhCAD*6 in cotton fiber development by real-time RT-PCR. *GhCAD*6 overexpression construct was introduced in upland cotton variety Xinluzao 36 using *Agrobacterium tumefaciens*-mediated transformation. A number of *GhCAD*6 transgenic plants were obtained and a single copy of *GhCAD*6 was integrated into the recipient genome of cotton fiber. The expression of *GhCAD*6 in transgenic plants was higher with compared to that in the wild type and the *GhCAD*6 transgenic cottons resulted in changing the content of the fiber cell structural composition phenylpropanoid. Although these transgenic lines in cell wall composition was not obvious difference, except only the phenylpropanoid content in the mature fiber of transgenic plants being slightly lower, the mature cotton fiber cells of transgenic lines had a quite smooth, fine, and dense surface, which led to be changed in the fiber length, strength, uniformity and micronaire value and improved the fiber quality in transgenic lines. These results demonstrate that *GhCAD*6 is involved in regulating cotton fiber development and is a promising candidate gene to improve fiber quality in cotton through genetic manipulation.