GLEANINGS IN COTTON RESEARCH

NOVEMBER 2026

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Preface

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

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

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

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

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

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

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

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

Chetali Rodge
In charge Library

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1

Title: Impact Of Drought Stress On Key Agronomic Traits and Yield Components in Diverse Cotton Genotypes

Authors: Gulshan Abdulaliyeva*, Firuza Yunusova, Naila Mammadova, Shader Alizade

Imprint: Agricultural & Veterinary Sciences, Vol.10, No.2, 2026, pp.88-95
https://doi.org/10.62476/ravs10288

Abstract: Drought stress significantly limits global cotton (Gossypium hirsutum L.) productivity by disrupting physiological processes and reducing yield components. This study evaluated 15 cotton genotypes (14 G. hirsutum L. and one G. barbadense L.) at the Absheron Experimental Station during 2024-2025 to identify drought-tolerant varieties with high economic performance. A split-plot design was employed, comparing normal irrigation (control) with drought stress conditions. Analysis of variance (ANOVA) revealed that drought stress significantly impacted boll weight and yield per plant ($p < 0.05$), while vegetation period and fiber yield remained relatively stable. Genotypes 'Cristina' and 'Ak-Altun' demonstrated notable resilience, exhibiting increased yield per plant under stress. 'Prime- 9811' showed a compensatory increase in boll weight. These findings provide valuable insights for selecting drought-tolerant cotton genotypes to enhance sustainable agricultural productivity in water limited environments.

2

Title: The m6A epitranscriptome and the emerging role of m6Am: Molecular hubs for regulating abiotic stress tolerance in cotton

Authors: Muhammad Nadeem, Muhammad Waqas, Kang Zhao, Jihua Yang, Xue-Rong Zhou, Wuwei Ye

Imprint: Plant Stress, Volume 23, September 2026, 101504

Abstract: RNA modifications, especially N6-methyladenosine (m6A) and N6,2′-O-dimethyladenosine (m6Am), are emerging as important regulators of gene expression during plant responses to abiotic stress. In cotton (Gossypium hirsutum), m6A

improves transcript stability and regulates critical stress signals, including abscisic acid and calcium, which increase drought tolerance. Although m6Am is less studied, it is highly intertwined with m6A and may therefore play a significant role, despite not having been fully explored. The current review is devoted to the chemical characteristics, enzyme regulation and functional activity of m6A and m6Am in the reaction of cotton to abiotic stress. It also presents the recent developments in high-resolution mapping and functional validation methods. It explains how RNA methylation can be utilized in molecular breeding strategies to enhance the stress resilience of cotton. In general, RNA methylation is a dynamic process of epitranscriptomics that is essential in cotton adaptation to the conditions of stress.

3

Title: Foliar Laser Boost increases leaf potassium uptake in field-grown cotton: a randomized proof-of-concept trial

Authors: Alejandro Ponce Flores1, Teresa Flores Reyes1, Luis Ponce Cabrera

Abstract: Foliar potassium (K) correction is common in cotton during flowering and boll fill, but uptake of surface-applied K is limited by the hydrophobic epicuticular wax barrier. Foliar Laser Boost (FLB) uses a pulsed laser to selectively ablate epicuticular wax before a localized nutrient dose. We tested whether FLB improves foliar K uptake in field cotton at late bloom. In a randomized complete block design (5 treatments × 3 blocks, 15 plots) at Agricenter International (Memphis, TN, USA), we compared an untreated check, a conventional backpack KNO_3 spray, a syringe-only localized dose (1.5 mL/plant, no laser), and two FLB treatments (lateral-pattern and midrib-crossing laser followed by the same 1.5 mL syringe dose). Leaf K (% dry matter) was quantified by ICP-OES (Waypoint Analytical). Both laser treatments raised leaf K significantly: midrib-crossing 2.11% and lateral 2.02%, versus the untreated check 1.76%, conventional spray 1.68%, and syringe-only 1.78% (two-way ANOVA $F_{4,8} = 13.2$, $p = 0.0013$; residual CV 4.7%). Critically, the syringe-only dose was statistically indistinguishable from the check, so the gain was driven by the laser step and not by the KNO_3 or the mechanical delivery. The two laser patterns did not differ from each other. These results are a positive proof of concept that laser micro-ablation enhances foliar K uptake in cotton, from a single site, single season, and single sampling timepoint.

4

Title: Brackish water irrigation differentially modulates rhizosphere microbial communities and metabolites under two biochar feedstocks in cotton

Authors: Yonghui Dai, Liping Liu, Xiao Zhao, Jingxiang Hou, Ling Tong, Jian Kang, Jinliang Chen, Taisheng Du, Risheng Ding

Imprint: Industrial Crops and Products, Volume 251, 2026, 124084,

ISSN 0926-6690, https://doi.org/10.1016/j.indcrop.2026.124084

Abstract: Rhizosphere microbe–metabolite associations under biochar amendment may influence crop responses to salt stress, but how biochar feedstock type shapes these associations under brackish water irrigation remains unclear. We investigated the responses of cotton rhizosphere bacterial communities, soil metabolites, soil nutrient availability, plant physiological traits, and seed cotton yield to wheat straw biochar (B1) and apple wood biochar (B2) under freshwater irrigation (S0) and brackish water irrigation (S1) in the field. Brackish water irrigation differentially altered rhizosphere bacterial communities and metabolite profiles under the two biochar treatments. Under B1, S1 was associated with Nitrobacter enrichment and higher predicted nitrification-related functions, with soil NO_3^--N decreasing by 14.7%, compared with 30.2% in the non-biochar treatment. These bacterial responses were accompanied by higher levels of soluble sugars and organic acids, with enrichment of starch and sucrose metabolism, citrate cycle, and carbon metabolism. In contrast, B2 maintained higher alkaline phosphatase activity and was more closely associated with lipid-, phenolic-, and flavonoid-related metabolic responses. Although S1 reduced cotton root growth, photosynthesis, and yield, B1 maintained higher specific root length, aboveground dry biomass, seed cotton yield, and net photosynthetic rate than B2 under brackish water irrigation. Compared with S1B0, B1 increased net photosynthetic rate by 30.3%, whereas B2 increased it by 17.0%. These results suggest that different biochar feedstocks were associated with distinct short-term rhizosphere responses under brackish water irrigation: B1 was mainly linked to soluble sugar and organic acid metabolism, predicted N-cycling functions, and yield maintenance, whereas B2 was more closely associated with lipid- and phenolic-related stress responses.

5

Title: Integrative multivariate analysis of morphological, physiological, and biochemical responses of upland cotton to water deficit at the reproductive stage

Authors: Muhammad Yousaf Shani, Allah Ditta & Muhammad Kashif Riaz Khan

Imprint: https://doi.org/10.1038/s41598-026-60650-3

Abstract: Drought is a major abiotic stress that severely limits cotton productivity by reducing growth, yield, and fiber quality. Understanding genotype-specific responses to reproductive-stage drought is essential for identifying reliable selection traits and improving drought resilience in cotton breeding programs. This study evaluated 54 cotton genotypes at the flowering stage under three irrigation regimes: well-watered conditions (80% FC), mild drought stress (60% FC), and severe drought stress (40% FC). Morphological traits (root and shoot biomass), physiological traits (photosynthetic rate, leaf water loss, and relative water content), and biochemical traits (proline, soluble sugars, amino acids, antioxidant enzyme activities, and reactive oxygen species) were assessed. Drought treatments were imposed for three consecutive weeks during flowering to investigate genotype responses to varying levels of water deficit. The experiment was conducted in a rain-out shelter using a factorial completely randomized design (CRD) with three replications for each genotype–treatment combination. Cotton accessions were grown in plastic containers. Significant genotype-dependent variation was observed across all drought treatments, with responses becoming more pronounced under severe stress. Two-way analysis of variance revealed that ARTICLE IN PRESSACCEPTED MANUSCRIPT ARTICLE IN PRESS drought significantly affected all measured traits. Descriptive statistics and boxplot analyses further illustrated variations in trait performance among genotypes under different stress levels. Principal component analysis (PCA) revealed clear phenotypic divergence among genotypes and highlighted trait associations under contrasting water regimes. Heatmap analysis further confirmed genotype grouping patterns and their relationships with the evaluated traits. Moreover, MGIDI-based selection at 15% selection intensity identified G33 (FH-901), G50 (N-1048), G53 (N-135), G36 (FH-Super-Cotton), G29 (FH-556), G47 (MNH-1035), G54 (N-135-BB-121/38), and G41 (IUB-13) as drought-tolerant genotypes based on their lower MGIDI values and favorable performance. These genotypes exhibited superior performance, greater water retention, lower oxidative damage, and stronger antioxidant defense systems under water-deficit conditions. The findings provide valuable insights for cotton breeding programs aimed at developing drought-resilient cultivars and support sustainable cotton production in water-limited environments.

6

Title: Phenotypic and Agronomic Evaluation of Isogenic and Introgressive Cotton Lines for Yield, Fiber Quality, and Growth Traits under Field Conditions in Uzbekistan

Authors: Abdukayum Bekmukhamedov, Sayfulla Boboev, Mirvakhob Mirakhmedov, Navruzbek Khusanov, Azamat Yuldoshkhonov, Ulug'bek Abdukarimov, Abdusalyamova Shaxida, Dusmuratov Ganiybay, Gulchekhra Khalmuminova, Mukhlisa Turopova, Mukhlisa Kudratova

Imprint: ROMANIAN AGRICULTURAL RESEARCH, NO. 43, 2026 First Online: August, 2026. DII 2067-5720 RAR 2026-199
www.incda-fundulea.ro; doi.org/10.59665/rar4389

Abstract: The present study evaluated the phenotypic and agronomic variability of isogenic and introgressive cotton (Gossypium hirsutum L.) lines under field conditions in Uzbekistan. A total of ten cotton lines and two commercial cultivars were assessed for earliness, yield performance, fiber quality, and morphobiological traits using a randomized complete block design. Significant genotypic differences were observed for all evaluated parameters. Early-maturing lines L-608 and L-454 showed shorter periods from sowing to flowering, indicating their suitability for environments with limited growing seasons. Line L-452 exhibited the highest boll weight and cotton weight per plant, demonstrating superior yield potential. Regarding fiber quality, lines L-454, L-453, and L-452 showed higher fiber yield and fiber index, while L-4112 recorded the longest fiber length. Morphobiological assessment revealed vigorous vegetative growth in L-4112 and L-620, whereas L-608 showed a more compact growth habit associated with earliness. Overall, no single genotype was superior across all traits; instead, different lines expressed specific advantages in yield, earliness, and fiber quality. The results highlight the presence of valuable genetic diversity among the studied materials and their potential use in cotton breeding programs aimed at developing high-yielding, early-maturing, and high-quality fiber cultivars adapted to Uzbekistan agroecological conditions.

7

Title: Effect of Growth Retardant on Growth and Yield of Cotton

Authors: Fensi N. Chaudhari1*, Palav R. Marakana2, H. R. Ramani3 and Harsh N. Patel

Imprint: Plant Archives Vol. 26, Supplement 2, 2026 pp. 1355-1361 e-ISSN:2581-6063 (online), ISSN:0972-5210
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.162

Abstract: To investigate the effect of growth retardants on cotton growth and yield under a high-density planting system (HDPS), a field experiment was carried out during the Kharif season of 2024 at the Main Cotton Research Station, Navsari Agricultural University, Athwa-farm, Surat (Gujarat). Two cotton genotypes, G. Cot-34 and G. Cot-44 and six growth retardant treatments, including control, detopping, mepiquat chloride (45 ppm), cycocel (100 ppm) and their combinations with detopping at the 20th node, were used in the experiment, which was laid out in a Factorial Randomized Block Design (FRBD) with three replications. Findings showed significant differences in growth and yield parameters related to genotypes and growth retardant treatments. Genotype G. Cot-44 produced compact growth with significantly reduced

plant height, lower biomass, more nodes, shorter internodal length and improved sympodial length and boll weight, resulting in a higher seed cotton yield (2075.87 kg ha-1) under high-density planting conditions. Whereas G. Cot-34 produced more bolls per plant and higher biomass, but with excessive vegetative growth and comparatively lower yield (1944.61 kg ha-1). Among the growth retardant treatments, mepiquat chloride @ 45 ppm at 45 DAS combined with detopping at the 20th node was most effective in regulating vegetative growth by reducing plant height, biomass and internodal length, while significantly enhancing yield attributes such as boll weight, number of sympodia and seed cotton yield (2408.86 kg ha-1) which was remained statistically at par with cycocel @ 100 ppm at 45 DAS. The interaction effect showed that G. Cot-44 produced optimum growth and maximum yield under HDPS when combined with mepiquat chloride @ 45 ppm and detopping. The study concludes that, in high-density planting conditions, applying growth retardants along with detopping is an efficient agronomic practice to reduce excessive vegetative growth and increase cotton yields.

8

Title: Impact of Reduced Rates of Trifludimoxazin + Saflufenacil on Early-Season Cotton (Gossypium hirsutum L.) Growth and Yield

Authors: Donnie K. Miller*, Koffi Badou-Jeremie Kouame, Shelly P. Kerns, Matthew R. Foster, L. Tom Barber, and Lawrence E. Steckel

Imprint: The Journal of Cotton Science 30:1–7 (2026) http://journal.cotton.org, © The Cotton Foundation 2026

Abstract: Trifludimoxazin + saflufenacil is a premix protoporphyrinogen oxidase-inhibiting herbicide with both PRE and POST activity pending U.S. Environmental Protection Agency registration for burndown application ahead of planting corn, soybean, grain sorghum, and wheat. Early-season cotton emergence and growth often coincide in the Mid-South with preplant herbicide application in later planted soybean, thereby increasing opportunity for off-target herbicide movement from adjacent fields. Field studies were conducted in 2024 to identify any deleterious impacts of reduced rates of trifludimoxazin + saflufenacil (1/8-1/256x of the lowest proposed labeled application rate of 38.3 g ai ha-1) applied to one- to two-leaf cotton. Visual injury one week after treatment (WAT) with 1/8, 1/16, 1/32, and 1/64x rate of trifludimoxazin + saflufenacil was 93, 84, 66, and 40%, respectively; whereas at four WAT these respective rates resulted in visual injury of 55, 30, 11, and 4%. Trifludimoxazin + saflufenacil at these rates reduced cotton height 30 to 72% and 21 to 60%, two and four WAT, respectively, and reduced seed cotton yield 64, 26, 6, and 1%. Application of trifludimoxazin + saflufenacil directly adjacent to cotton in early vegetative growth should be avoided as severe visual injury will occur. In cases where off-target

movement does occur, impacted cotton should not be expected to fully recover and negative impact on growth and yield will be observed at the three highest reduced rates evaluated.

9

Title: Conservation tillage and cover crop effects on greenhouse gas emissions from furrow-irrigated cotton in southeast Arkansas

Authors: Cassie Seuferling, Kristofor R. Brye, Diego Della Lunga, Michael Daniels, Ashlyn Brown, Lucia Escalante Ortiz, Kelsey Greub, Lisa Wood

Imprint: ***Soil Science Society of America Journal*****, 90, e70306. https://doi.org/10.1002/saj2.70306**

Abstract: Conservation agriculture practices, such as reduced tillage (RT) and cover crop (CC) use, have been identified as methods to potentially reduce soil-surface greenhouse gas (GHG) emissions from the soil surface in row-crop agriculture. Yet, few studies have investigated carbon dioxide (CO2), methane (CH4), and nitrous oxide (N2O) release from furrow-irrigated cotton (Gossypium hirsutum) production. The field study objective was to evaluate the effects of first-year conventional tillage with no CC and RT with CC on GHG fluxes and emissions from furrow-irrigated cotton on a silt-loam soil in southeast Arkansas. A field-portable, GHG analyzer system was used to measure GHG concentrations every 2 weeks for the 2025 growing season to calculate fluxes, season-long emissions, and global warming potential (GWP). Carbon dioxide fluxes differed between treatments over time ($p < 0.01$), where the CO2 flux was 8.9 times greater from the conservation (166.6 mg m−2 h−1) than from the conventional (18.7 mg m−2 h−1) treatment on one (June 10, 2025) of nine total measurement dates, which correlated with the driest recorded soil water content. Methane fluxes were similar between field treatments, but differed over time ($p < 0.01$), with a maximum recorded flux of 0.09 μg m−2 h−1 on August 19, 2025. Field treatments did not affect ($p > 0.05$) N2O fluxes nor season-long CO2, CH4, or N2O emissions or GWP estimates. Results describe early conservation effects in Arkansas cotton production on GHGs are minimal, providing a guide for future GHG studies in upland agriculture.

10

Title: The mechanisms underlying cotton cell damage and leaf sticking induced by the defoliant thidiazuron

Authors: Zexin Wei a, Le Zhang a, Haohao Zhao a, Yuyue Ma a, Haoqi Feng a, Xinyao Liu a, Shuqi Wang a, Xinghua Yu a, Zhaohui Liu b, Mingwei Du a, Fangjun Li a, Xiaoli Tian a, Zhaohu Li

Imprint: Plant Physiology and Biochemistry, Volume 238, 2026, 111658, ISSN 0981-9428,

https://doi.org/10.1016/j.plaphy.2026.111658.

Abstract: Chemical defoliation is essential for mechanized cotton harvesting, but excessive thidiazuron (TDZ), frequently induces a "leaf sticking" phenotype characterized by wilting without abscission, which severely compromises harvest efficiency. We integrated field and greenhouse experiments with anatomical, physiological, and transcriptomic analyses to investigate this abnormal response. TDZ (0.45 and 2.27 mM) was rapidly absorbed by leaf blades within 3–6 h, and accumulation increased with concentration. Early cellular damage (3–24 h) featured membrane integrity loss, and cell death, occurring prior to substantial ROS accumulation or senescence/PCD-related gene activation, suggesting direct membrane perturbation rather than ROS- or transcription-mediated injury. At later stages (48–96 h), excessive ROS and upregulated senescence/PCD transcripts further aggravated cellular damage. The optimal concentration (0.45 mM) promoted abscission zone (AZ) cell separation and complete abscission by 96 h, an excessive concentration (2.27 mM) initiated AZ separation as early as 24 h but halted its progression, causing persistent adhesion and leaf sticking. Localized application revealed that TDZ application to the blade alone was sufficient to induce petiole wilting, confirming that leaves retain the ability to generate signals even under severe injury. Direct AZ application neither induced abscission nor visibly damaged AZ cells. These findings indicate that abscission failure under excessive TDZ is not due to impaired blade-to-AZ signaling or direct killing of AZ cells, but rather to disrupted coordination of blade-derived abscission cues. Collectively, excessive TDZ uncouples leaf damage from AZ differentiation by impairing signal coordination, providing a mechanistic framework for understanding defoliation failure and optimizing TDZ application strategies in cotton production.

11

Title: Chemical Oxidation Synergistically Regulates Surface Chemistry and Pore Structure of Cotton Stalk-Based Hard Carbon for Enhanced Sodium Storage Performance

Authors: Wang, Yuanzhe, Hong Cui, Liang Liu, Jianyuming Zhang, Yue Tang, and Jiantie Xu.

Imprint: *Batteries*, *12*(8), 310. https://doi.org/10.3390/batteries12080310

Abstract: Biomass-derived hard carbon (HC) represents a promising anode candidate for sodium-ion batteries, owing to its disordered structure and abundant micropores. This study systematically investigates three chemical oxidation strategies (NaClO, H2SO4 and H2O2+NaOH) applied to cotton stalk-derived HC carbonized at 1300 °C. The NaClO-treated sample delivers the optimal overall electrochemical performance, achieving a high discharge capacity of 330.2 mAh g−1 at 0.1 C, a high initial Coulombic efficiency (ICE) of 81.7%, and a capacity retention of 81.9% after 1000 cycles at 2 C (from 226.0 to 185.1 mAh g−1). This superiority is attributed to the formation of a three-dimensional hierarchical pore network and optimal oxygen functional groups. The H2SO4 treatment yields a discharge capacity of 323.2 mAh g−1, an ICE of 75.3%, and a capacity retention of 77.1% after 1000 cycles (from 183.5 to 141.5 mAh g−1), benefiting from structural densification. The H2O2+NaOH treatment delivers a capacity of 269.8 mAh g−1 and an ICE of 74.2%, exhibiting a distinct activation behavior likely due to its thin pore walls and abundant open mesopores. Overall, all treated samples significantly outperform the pristine HC, which exhibits a discharge capacity of 320.3 mAh g−1, an ICE of 68.0%, and a retained capacity of 90.4 mAh g−1 after 1000 cycles at 2 C.

12

Title: Improving Cotton Productivity and Fiber Quality Through Implementation of Reduced Tillage and Balanced Nutrition Under Arid Climate

Authors: R. Hussai, K. Usman, A. A. Khan1 and Q. U. Khan

Imprint: J. Anim. Plant Sci., 36 (6) 2026
https://doi.org/10.36899/JAPS.2026.6.0143

Abstract: Cotton (Gossypium hirsutum L.) is a cash crop that plays a crucial role in the textile industry at global scale and Pakistan. However, its sustainable production is restricted by challenges like conventional tillage, imbalanced fertilization, water shortage and soil health degradation. Therefore, a two-year field study was conducted in Agricultural Research Institute, Ratta Kulachi, Dera Ismail Khan to compare the tillage operations coupled with nutritional regimes of balanced nitrogen (N), phosphorus (P), and potassium (K) to maintain the growth, yield and fiber quality traits of the cotton. The research treatments involved the tillage system (TS) reduced vs. conventional as main plots and NPK levels (NPK1 = 0:0:0, NPK2 = 200:0:0, NPK3 = 0:120:0, NPK4 = 0:0:150, NPK5 = 200:120:0, NPK6 = 200:0:150, NPK7 = 0:120:150, NPK8 = 200:120:150, and NPK9 = 250:170:200 kg ha-1) as subplots. The fiber quality and yield attributes of cotton were assessed after the harvest of cotton. The results of interactive effect of TS, NPK and Years were significant which influenced sympodial branches (plant-1), ginning outturn (%) and fiber strength (g tex-1) during both the years 2023 and 2024. However, balance NPK (200:120:150 kg ha-1) in combination with reduced tillage consistently outperformed and yielded maximum sympodial branches (59.2 in

2024 and 57.7 in 2023), plant height (151.5 cm in 2024), bolls plant-1 (60.7 in 2024 and 59.7 in 2023), seed cotton (2696 kg ha-1 in 2024 and 2646 kg ha-1 in 2023) and ginning outturn (71.9% in 2024 and 70.7% in 2023). This optimal fertilizer dose also improved fiber strength (30.0-31.0 g tex-1) which gave the highest net returns (1003.18 US $ ha-1) with benefit cost ratio (BCR) of 2.3. This study concluded that combination of reduced tillage and NPK (200:120:150 kg ha-1) adequately for sustainable cotton production under arid environment.

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Title: Rainfed cotton response to polymer-coated and conventional urea under different placement methods

Authors: Shah, A., Singh, K., Singh, S., Nwosu, N., Dar, E. A., Borgato, E. A., … Singh, H.

Imprint: Journal of Plant Nutrition, 1–28.
https://doi.org/10.1080/01904167.2026.2729340

Abstract: Surface broadcasting of conventional urea is a common method of supplying nitrogen (N) to cotton, but this practice can increase the risk of N losses through volatilization and leaching, especially under a rainfed production system. A 2-year (2023–2024) field study was conducted at the West Florida Research and Education Center in Jay, FL, to evaluate the effects of N source and placement method on cotton growth, plant N status, lint yield, fiber quality, and partial factor productivity of applied N (PFP). Treatments consisted of conventional urea (46-0-0) and polymer-coated urea (PCU; 41-0-0), applied through surface broadcasting and subsurface banding at 100 kg N ha−1. Growing season conditions differed substantially between years, with hotter and drier conditions in 2023 and greater, more evenly distributed rainfall in 2024. Surface-applied conventional urea resulted in 29–31% higher chlorophyll index (CHL) and 51–57% higher nitrogen balance index (NBI) than other treatment combinations at early square stage in 2023 compared to 2024. N source significantly affected leaf area index (LAI), with conventional urea producing ~11.2% higher LAI in 2023 and ~19.4% higher LAI in 2024, on average, compared to PCU-treated plots. Subsurface banded urea generally resulted in the highest petiole nitrate-N (PNN) concentrations across both seasons. Under specific rainfed conditions and N rates evaluated in this study, conventional urea provided greater early or in-season N availability for some physiological indicators than PCU, particularly during the drier season. However, these differences did not result in greater lint yield or PFP.

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Title: Predictive modelling for whitefly control in cotton (Gossypium spp.): Evaluating sprayer efficiency using PLS regression and ANN techniques

Authors: Santosh Kumar, Apoorv Prakash, Anand Gautam, Vijay Kumar and Mandeep Pathania

Imprint: Indian Journal of Agricultural Sciences 96 (6): 000–000, June 2026/Article https://doi.org/10.56093/ijas.v96i6.166850

Abstract: Cotton (Gossypium spp.), a vital fibre cash crop in India, faces challenges from various insects-pestsamong which whiteflies, pose a significant threat. A study was conducted in 2022 at Abhor district of Punjab to evaluate seven sprayers, including high clearance boom sprayer, air-assisted drop-up boom sprayer, auto-rotate gun, air-assisted electrostatic sprayer, engine-powered knapsack, manually operated knapsack, and UAV sprayers, based on droplet density, size, coverage, spray volume deposition, and bio-efficacy. From the experimental results, it was found that the electrostatic sprayer was most effective against whiteflies. An economic analysis considered costs, ANN and PLSR models predicted whitefly populations, with ANN showing superior accuracy (MSE=8.31, R^2=0.74), recommending engine-powered gun sprayers for optimal control. Field assessments favoured high clearance boom and drone sprayers, offering cost efficiencies. Eventually, the optimal choice of a sprayer should align with the specific needs and circumstances of the farm.

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Title: Cotton insect resistance and integrated pest management: current research and future directions

Authors: Xu Xinyue, Zhou Lili, Wang Peilin, Fu Jiayue, Liu Xinyan, Guo Wenfang, Su Xiaofeng, Cheng Hongmei & Guo Huiming

Imprint: J Cotton Res 9, 33 (2026). https://doi.org/10.1186/s42397-026-00274-0

Abstract: Cotton production has long been challenged by combined damage from chewing and piercing-sucking pests. Bt cotton has provided effective control of the

cotton bollworm in many production regions. However, several factors have rendered single-tactic management unsustainable. These include the increasing prominence of piercing-sucking pests, accelerating resistance evolution, and growing concerns over non-target effects. Critically, the lack of standardized, cross-environment protocols for reproducible resistance phenotyping has become the primary bottleneck preventing the translation of laboratory-discovered resistance genes into field-effective cultivars. Over the past three decades, major advances have been made in elucidating resistance mechanisms and developing gene identification technologies. Breeding-to-field transformation efficiency has not improved in parallel. Standardized, cross-environment protocols for reproducible insect-resistance phenotyping are still lacking. Specifically, there is a lack of unified specifications for defining pest pressure levels, selecting sampling time points, determining tissue positions for investigation, and establishing criteria for resistance evaluation. Moreover, agronomic cost assessments that balance resistance with yield have rarely been incorporated into breeding decision pipelines. Consequently, many candidate genes remain at the stage of functional validation rather than deployment. At present, insect-resistance breeding is shifting from simply identifying new resistance genes toward evaluating their effects in combination with yield and performance in field trials. In essence, this transition expands breeding objectives from single resistance indices to a broader assessment of yield stability, multi-pest management, and field ecological function. The overarching objective is to improve yield stability under multi-pest pressure while slowing pest adaptation and preserving field ecological functions. Achieving this objective will require explicitly linking genetic resistance traits with physical, chemical, and biological control measures within a dynamic, threshold-based Integrated pest management (IPM) framework.

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Title: Development of an RPA-CRISPR/Cas12a-based rapid visual detection method for two insecticide resistance-associated mutations in *Aphis gossypii*: A302S in the *ace1* gene and M918L in the *para* gene

Authors: Rujing Kang, Yucheng Qian, Yuanchi Zuo, Ren Li, Lei Zhang,

Imprint: Pesticide Biochemistry and Physiology, Volume 223, 2026, 107303, ISSN 0048-3575, https://doi.org/10.1016/j.pestbp.2026.107303.

Abstract: The resistance of Aphis gossypii to pyrethroids and organophosphate/carbamate insecticides has become increasingly severe. The para M918L and ace1 A302S target-site mutations are the key mechanisms conferring resistance to these two types of insecticides, respectively. However, rapid and field-deployable methods for detecting these mutations are still lacking. In this study, the genotype and allele frequencies of eight field populations collected in 2023 were

investigated, and a rapid visual detection method based on RPA-CRISPR/Cas12a was developed. By optimizing the concentration of the reaction components, specific recognition of both mutations was achieved. The optimized assay could be completed within 1 h under a single-temperature condition of 37 °C, with fluorescence signals directly visualized using a portable 440–460 nm blue-light illuminator without PCR thermocyclers, fluorescence readers or sequencing platforms. Validation using the tested field samples showed complete concordance with Sanger sequencing. In addition, Sanger sequencing further showed that no homozygous susceptible genotype was detected at the para M918 locus across all populations, whereas the 302S allele frequency at the ace1 A302S locus exhibited significant geographic variation, ranging from 0% to 100%. The RPA-CRISPR-based visual detection method developed in this study is rapid, accurate, and does not require expensive instrumentation. Together with previously developed neonicotinoid resistance detection techniques, it forms a comprehensive monitoring system for multiple resistance in A. gossypii, providing a practical tool for rapid field diagnosis and more informed insecticide selection.

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Title: GaRD21A, a cysteine protease gene in Gossypium arboreum is associated with defense response against cotton leaf curl disease

Authors: Muhammad Qasim Aslam, Athar Hussain, Rida Zahid, Afzal Akram, Khalid Pervaiz Akhtar, Rubab Zahra Naqvi, Imran Amin, Shahid Mansoor & Muhammad Saeed

Imprint: Sci Rep (2026). https://doi. org/10.1038/s41598-026-64111-9
https://doi.org/10.1038/s41598-026-64111-9

Abstract: Cysteine proteases (CPs) of the C1-papain family play important roles in plant immunity, particularly in antiviral and antifungal defenses. However, this gene family has not yet been characterized in cotton under Cotton Leaf Curl Disease (CLCuD) stress. Genome-wide diversity analysis and functional annotation revealed the abundance, evolutionary conservation, and conserved peptidase signatures of CP family members across ten Gossypium species and an ancestrally related species Theobroma cacao. Furthermore, a virus-induced gene silencing (VIGS) assay was performed to investigate the role of a papain-like CP gene GaRD21A in resistance response of Gossypium arboreum against CLCuD. Silencing of GaRD21A resulted in increased virus accumulation in both viruliferous whitefly-exposed and graft-mediated CLCuD inoculated ARTICLE IN PRESSACCEPTED MANUSCRIPT ARTICLE IN PRESS plants; however, pronounced vein thickening symptoms were only observed in graft-inoculated plants. To the best of our knowledge, this is the first report demonstrating the involvement of a CP family gene in the immune response of G.

arboreum against CLCuD, providing a potential target for cotton resistance breeding programs.

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Title: First report of *Bacillus pumilus* causing soft rot of cotton (*Gossypium hirsutum* L.) in Turkey

Authors: Deniz Çaplık, Soner Soylu, Mustafa Küsek & Abdurrahman Seyrek

Imprint: *J Plant Pathol* 108, 2405–2406 (2026). https://doi.org/10.1007/s42161-026-02303-y

Abstract: Cotton (Gossypium hirsutum L.) is one of the most significant industrial crops in Turkey, and boll rot disease has a substantial impact on both yield and fibre quality. In August 2023, cotton bolls showing water-soaked lesions and soft rot symptoms were observed in four cotton fields in the Çınar district of Diyarbakır province, Turkey (Fig S1). A total of 37 cotton plants bearing 114 bolls were examined. Fourteen of the 37 plants had at least one symptomatic boll, corresponding to a plant-level symptom incidence of 37.84%. Symptomatic bolls (n = 23) were collected, surface sterilised, and plated on nutrient agar. The bacterial strains (n = 25) were whitish to cream-coloured, Gram-positive, rod-shaped with endospores, motile, catalase-positive and oxidase-negative. All bacterial isolates were capable of inducing hypersensitive reactions on tobacco leaves and soft rot on potato slices two days after inoculation (dai) (Fig S3 A-B). MALDI-TOF mass spectrometry identified all isolates as Bacillus pumilus, with identification scores ranging from 2.005 to 2.117, corresponding to secure genus identification and probable species identification (Fig S2). Because all isolates exhibited consistent phenotypic characteristics and comparable MALDI-TOF MS profiles, CBp08 was selected as a representative isolate for molecular characterization. The 16 S rDNA and gyrB genes were amplified using primer pairs 27 F (5′-AGAGTTTGATCMTGGCTCAG-3′)/1492R (5′-TACGGYTACCTTGTTACGACTT-3′) and gyrB-F (5′-TTGRCGGHRGYGGHTATAAAGT-3′)/gyrB-R (5′-TCCDCCSTCAGARTCWCCCTC-3′), respectively, and sequenced. The resulting sequences were deposited in GenBank under accession numbers PX726042 (16 S rDNA) and PX704420 (gyrB). The 16 S rDNA sequence showed high similarity to several closely related members of the B. pumilus species complex; however, due to the limited discriminatory power of this highly conserved marker, it was not considered sufficient alone for species-level identification. In contrast, the gyrB sequence of CBp08 showed

99.7% identity with B. pumilus ATCC 27142 (AY167870). Thus, species-level identification of CBp08 as B. pumilus was primarily supported by the higher-resolution gyrB sequence analysis together with the MALDI-TOF MS and phenotypic results. The phylogenetic placement of CBp08 based on gyrB gene sequences is shown in Fig S4.

Pathogenicity tests were conducted on immature cotton bolls using three replicates, with four bolls per replicate. A bacterial suspension of representative isolate CBp08 (10^8 CFU/mL) was inoculated into the central region of each boll using a sterile syringe, while control bolls were similarly inoculated with sterile distilled water. Both inoculated and control bolls were incubated at 26 °C. Typical water-soaked and macerated soft-rot lesions resembling those observed on naturally infected cotton bolls in the field developed within 5 days after inoculation (dai), whereas the control bolls remained asymptomatic (Fig S3 C). The bacterium was re-isolated from the induced lesions, and the resulting colonies exhibited phenotypic characteristics consistent with those of the original isolate. The identity of the re-isolated bacterium was confirmed as B. pumilus by MALDI-TOF MS, thereby fulfilling Koch's postulates.

Previous studies have identified B. pumilus as the causal agent of soft rot in muskmelon (Song et al. 2018), potato (Yahyaoui et al. 2023) and cotton (Acharya et al. 2024). To our knowledge, this is the first scientific evidence that B. pumilus can cause soft rot in cotton in Turkey. The association of disease occurrence with fields irrigated using untreated river water highlights the need for further research into the role of irrigation systems in spreading pathogens.

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Title: Deciphering the Genetic Architecture of Whitefly (Bemisia tabaci) Resistance in Cotton: From Resistance Mechanisms to Molecular Breeding and Genome

Authors: Zarar Ahmed, Shahid Majeed and Ayesha Hussain

Imprint: Plant Crop Letters, 8: 144-163. https://doi.org/10.65822/j.pcl/2026.40

Abstract: One of the most significant natural fiber crops in the world is cotton (Gossypium hirsutum L.), but its productivity is severely limited by the whitefly Bemisia tabaci, a deadly phloem-feeding insect that triggers direct feeding damage and spreads Cotton Leaf Curl Disease (CLCuD), which results in significant yield and financial losses globally. Chemical pesticides are still the major management approach, but their widespread usage has accelerated insecticide resistance, upset ecological balance, and raised production costs, underscoring the critical need for long-lasting hostplant resistance. By incorporating recent developments in plant defense

mechanisms, quantitative trait loci (QTLs), resistance genes, transcriptomics, molecular markers, and contemporary breeding technologies, this review thoroughly summarizes the current understanding of the genetic and molecular basis of whitefly resistance in cotton. The morphological, biochemical, and molecular defense mechanisms, candidate resistance genes, marker-assisted selection, genomic selection, CRISPR/Cas-based editing, and multiomics techniques that are transforming resistance breeding are given special attention. Along with discussing the significance of integrated pest management in maintaining resistance, the paper critically looks at some of the main obstacles, such as the polygenic nature of resistance, interactions with the environment, genetic variety of whiteflies, and the scarcity of resistant germplasm. In conclusion, high-throughput genomics, genome editing, artificial intelligence-assisted phenotyping, and climateresilient breeding techniques are identified as future research goals. This analysis offers a thorough framework for creating resilient whitefly-resistant cotton cultivars that can enable sustainable cotton production under shifting climatic conditions by fusing traditional breeding with cutting-edge molecular technology

PLANT BREEDING AND GENETICS

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Title: Sample size for morphological traits of cotton cultivars

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

Imprint: Pesqui. Agropecu. Trop. 56 • 2026 • https://doi.org/10.1590/1983-40632026v5685261

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

of productive branches. Assuming a mean estimation error of 5 % and a confidence level of 95 %, the number of plants needed to measure the traits is 14 for main stem height, and number of leaves and nodes; 38 for main stem diameter and number of primary branches; and 126 for first productive branch height and number of productive branches.

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Title: Epigenetic control of heat stress responses in cotton: Mechanisms and breeding prospects

Authors: Guangming Han, Quanqiu Chen, Shengxi Zhang, Guorong Li, Jiayang Lan

Imprint: Plant Stress, Volume 23, 2026, 101513,
ISSN 2667-064X, https://doi.org/10.1016/j.stress.2026.101513

Abstract: Global climate change intensifies heat stress, severely threatening cotton production by impairing growth, reproduction, and fiber quality. Recent advances highlight that dynamic epigenetic mechanisms—including DNA methylation, histone modifications, chromatin remodeling, and non-coding RNAs (ncRNAs)—orchestrate stress-responsive gene networks and establish heat stress memory in cotton. These reversible modifications provide a crucial regulatory layer for sensing, responding to, and potentially recalling thermal stress. Multi-omics integration has been pivotal in linking these epigenetic changes to physiological and agronomic outcomes. Translational tools such as epigenome editing and marker-assisted selection demonstrate the potential of harnessing epialleles (allelic variants defined by epigenetic modifications rather than DNA sequence changes) for breeding resilient varieties. However, challenges persist, including understanding epigenetic crosstalk and tissue-specificity. This review synthesizes current knowledge on epigenetic regulation in heat-stressed cotton, explores integrative omics approaches, and discusses their application in crop improvement. We conclude by outlining key research priorities to accelerate the development of epigenetics-informed breeding strategies for climate-resilient cotton.

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Title: Heterosis, Combining Ability and Stability Analysis For Yield And Fibre Quality Traits in Upland Cotton (Gossypium Hirsutum L.): A Comprehensive Review

Authors: Rohit Kumar Tiwari, Krishan Pal, Ram Avtar

Imprint: Genetics and Molecular Research 25 (14s): 2026

Abstract: Upland cotton (Gossypium hirsutum L.) is a globally important fibre crop, and improving seed cotton yield and fibre quality remains a primary objective of cotton breeding programs. Over the past decades, extensive research has focused on heterosis, combining ability, and stability analysis to identify superior parental lines and high-performing hybrids. This review critically synthesizes published studies employing classical biometrical approaches such as Line × Tester and diallel mating designs, multi-environment evaluations, and emerging molecular methodologies including transcriptomics, QTL mapping, and multi-omics integration. Previous investigations consistently demonstrate the involvement of both additive and non-additive gene action in controlling yield and fibre traits, while genotype × environment interaction significantly influences hybrid performance and adaptability. Although substantial progress has been achieved through conventional breeding, limitations persist in terms of restricted environmental testing, narrow genetic bases, and limited integration of molecular tools. Recent advances highlight the potential of combining phenotypic selection with genomic-assisted breeding to enhance selection efficiency and hybrid stability. This review further identifies key research gaps and outlines future directions emphasizing integrated breeding strategies, expanded multi-location trials, and utilization of diverse germplasm resources. Collectively, the synthesis provides a comprehensive framework for developing high-yielding, fibre-quality superior, and environmentally stable cotton hybrids to support sustainable cotton production.

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Title: Quantifying naturally colored cotton fiber color intensity using RGB image-based phenotyping

Authors: Gabriel Aragão Fernandes1) Inácio Matias, Luiza Amaral Medeiros, Daniel Bonifácio Oliveira Cardoso, Filipe , Elvécio Gomes Oliveira Junior1 and Larissa Barbosa de Sousa

Imprint: Crop Breeding and Applied Biotechnology 26(3): e55682637, 2026
http://dx.doi.org/10.1590/198470332026v26n3a37

Abstract: Image-based phenotyping has become an innovative approach in plant breeding. This study quantified fiber color intensity in Gossypium hirsutum L. genotypes and evaluated the effect of boll position in the upper, middle, and lower plant canopy thirds. Five cultivars and twelve F2:3 lines were assessed by sampling five plants per plot, collecting three bolls per third, and photographing them with a standard color card. Images were processed using ImageJ and analyzed in R with the FIELDimageR package to calculate the Brightness Index (BI), Saturation Index (SI), and Normalized Green-Red Difference Index (NGRDI). Color card calibration increased mean values without changing genotype groupings. The upper third showed 6.25% lower color intensity, with no significant genotype × third interaction. SI efficiently

discriminated genotypes, while BI strongly correlated with fiber Uniformity Index, Strength, and Upper Half Mean Length (R^2 = 0.77, 0.80, and 0.88, respectively), supporting its use in breeding programs.

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Title: Speed breeding in upland cotton (*Gossypium hirsutum* L): scientific foundations and integrated implementation of a next-generation cotton breeding platform

Authors: Kurbonov AY, Mamedova FF, Isayeva RM, Khamirayev UA, Liu S, Lizhi W, Makhmadjanov SP, Kostakov AK, Aliyev AI, Kostak OA and Makhmadjanov DS

Imprint: Front. Plant Sci., 07 September 2026
Sec. Plant Breeding, Volume 17 - 2026 | https://doi.org/10.3389/fpls.2026.1915693

Abstract: Conventional cotton (Gossypium spp.) variety development requires 8–12 years - a timeline structurally incompatible with the accelerating urgency of climate-change adaptation, soil salinisation, and textile-industry demands for novel varieties within 3–5 years. Speed breeding (SB) compresses the generation interval by 30–80% through synergistic optimisation of LED spectra, temperature, nutrition, and immature embryo rescue (IER). However, SB alone is a temporal accelerator, not a breeding system: its transformative potential is realised only when it functions as the central engine of a genomics-assisted speed breeding (GASB) platform that integrates molecular marker-assisted selection (MAS), genomic selection (GS), CRISPR and New Genomic Technique (NGT) editing, high-throughput phenotyping (HTP), and AI-assisted decision-support tools. Building on previous reviews of cotton speed breeding and genomics-assisted breeding, the present review provides a mechanistic and implementation-oriented synthesis of these complementary technologies within a unified GASB framework. We evaluate: (i) the molecular architecture of photoperiodic flowering in predominantly Gossypium hirsutum, together with currently available evidence from other Gossypium species where appropriate and its manipulation through LED protocol design and CRISPR targeting of flowering suppressors; (ii) the mechanistic basis of multi-channel LED recipe design from SB 1.0 to SB 3.0; (iii) stage-specific thermal management including the operationally critical 33°C pollen safety ceiling; (iv) nutritional physiology, phytohormones, and biochemical monitoring; (v) in vitro biotechnologies—including callus culture, microspore-derived doubled haploids, and immature embryo rescue (IER)—together with the operational coordination of immature embryo rescue and pollen-stage temperature management within speed-breeding facilities; (vi) high-throughput phenotyping technologies experimentally validated in cotton, encompassing five cotton-specific applications reviewed in a dedicated section; and (vii) AI-assisted phenotyping and digital twin architectures for

real-time decision support within the GASB pipeline. Critical analysis identifies allotetraploid genome redundancy, genotype × light environment (G×L) interaction with landrace germplasm, IER scalability, bioinformatics infrastructure gaps, SB-to-field correlation uncertainties, and SVT regulatory requirements as the primary barriers to widespread GASB deployment. A structured 2025–2035 roadmap with three time-horizon priorities and measurable KPIs is presented.

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Title: Egyptian cotton: harnessing genetic diversity, molecular tools, fiber anatomy, and innovation for a climate-smart future

Authors: Mohamed Ibrahim A. A., Abdel Razek Usama Abdel Hameid, Wang Junjuan, Ye Wuwei, Wu Honghong, Liu Qing & Yin Zujun

Imprint: *J Cotton Res* 9, 34 (2026). https://doi.org/10.1186/s42397-026-00279-9

Abstract: Egyptian cotton, derived primarily from Gossypium barbadense L., has shaped the country's agricultural economy and international reputation for nearly two centuries. Among these, the Giza varieties—renowned for their exceptional fiber length, fineness, and strength—have garnered global recognition and made substantial contributions to export revenues and rural livelihoods. This review systematically analyzes more than 120 scientific publications from the past 30 years. It synthesizes research advances in Egypt, focusing on germplasm resources, fiber anatomical characteristics, variety improvement, and the integration of molecular and biotechnological tools. Progress in molecular markers, quantitative trait locus (QTL) mapping, and genome-wide association studies (GWAS) is highlighted for its role in dissecting traits related to fiber quality and stress tolerance. Experimental transformation studies and functional genomics have provided proof-of-concept for genes involved in insect resistance and fiber development. At the same time, genome editing—particularly clustered regularly interspaced short palindromic repeats/CRISPR-associated protein (CRISPR/Cas) systems—represents an emerging frontier for precise trait improvement in G. barbadense. Molecular markers have been used to assess genetic diversity within Egyptian cotton germplasm, enabling the development of unique varietal fingerprints and guiding breeding programs to improve yield, quality, and stress resilience. Techniques such as QTL mapping and GWAS facilitate the identification of genomic regions underlying key traits, thereby establishing a foundation for marker-assisted selection. Specific Egyptian varieties—including Giza 94 (a heat-tolerant variety), Giza 95 (a drought-tolerant variety), and Giza 90/Giza 97 (salinity-tolerant varieties)—have demonstrated measurable stress resilience in controlled and field trials. However, formal release designations for these

traits remain lacking. Concurrently, functional genomics approaches have enabled the characterization of genes involved in fiber development in Egyptian cotton. Furthermore, biotechnological innovations—including experimental Bt-transformation and the emerging precision of CRISPR/Cas genome editing—offer promising pathways to introduce adaptive traits more efficiently.

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Title: Genome-wide identification and expression analysis of Pto-interacting1 (PTI1) gene family in *G. hirsutum* L. under drought and salt stresses

Authors: Ali Ahmad, Umar Akram & Muhammad Baber

Imprint: ***Genet Resour Crop Evol*** **73, 288 (2026). https://doi.org/10.1007/s10722-026-02920-7**

Abstract: Pto-interacting 1 (PTI1) proteins are receptor-like cytoplasmic kinases that play important roles in plant stress signaling. In this study, genome-wide analysis was performed to identify and characterize the PTI1 gene family in Gossypium hirsutum and investigate its potential involvement in abiotic stress responses. Seven GhPTI1 genes were identified and analyzed using integrated bioinformatics approaches, including physicochemical properties prediction, subcellular localization, conserved domain and motif analysis, phylogenetic and synteny analyses, cis-element identification, sequence logo analysis, miRNA target prediction, RNA-seq expression profiling, and qRT-PCR validation. GhPTI1 proteins showed variation in their physicochemical properties, while subcellular localization predicted four proteins in the cytoplasm, two in the chloroplast, and GhPTI1-4 in the mitochondria, suggesting possible functional divergence and a role in ROS signaling. Conserved domain and phylogenetic analyses indicated that PTI1 proteins are highly conserved, with PTI1 members classified into three different clades. All GhPTI1 genes were located in clades II and III, suggesting possible lineage-specific gene diversification. Promoter analysis identified numerous hormone- and stress-responsive cis-elements, while twenty-one putative miRNA target sites were predicted across five GhPTI1 genes. This study in upland cotton demonstrated that the family is evolutionarily conserved and predominantly maintained under purifying selection. Expression profiling revealed that GhPTI1-1, GhPTI1-2, GhPTI1-6, and GhPTI1-7 are significantly induced under both drought and salt stress conditions at 1h, 3h, 12h, 24h, highlighting these genes as promising candidates for future functional studies and the development of stress-resilient cotton cultivars.

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Title: From feasibility to predictability: prime editing redefines precision breeding in plants

Authors: Muhammad Jawad Akbar Awan1 · Sameer H. Qari2 · Zujun Yin3 · Niaz Ahmad4 · Shahid Mansoor

Imprint: Trends in Plant Science, 2026

Abstract: Originally developed in mammalian systems as a genome editing strategy without double-strand breaks, prime editing (PE) has been adapted for precise genome modifications. However, its deployment revealed key limitations, including reduced efficiency, strong locus dependency, low germline transmission, and somatic chimerism. Consequently, diverse PE variants have emerged, resulting in fragmented landscape of architectures with context-dependent and inconsistent performance. This review consolidates these advances and outlines emerging design principles behind plant PE systems. It evaluates optimization strategies at multiple levels, discusses their applications in monocots and eudicots, and highlights persistent bottlenecks and future directions, including AI-guided protein engineering and improved delivery strategies. These advances position PE as a rapidly evolving platform toward enabling precision breeding in plants

PLANT BIOTECHNOLOGY

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Title: Assessment of Genetic Diversity in Cotton (Gossypium spp.) Varieties Using RAPD Markers

Authors: G. N. Wade, S. D. Surbhaiyya, A. M. Daude, R. D. Rawat, S. D. Nikam, R. C. Pardeshi

Imprint: ***Journal of Advances in Biology & Biotechnology*, 2026, 29 (8), pp.1092-1099. ⟨hal-05710840⟩**

Abstract: Background: Genetic diversity assessment is essential for the effective characterisation and utilisation of cotton germplasm in breeding programmes. Random

amplified polymorphic DNA (RAPD) markers provide a simple and rapid approach for detecting variation without prior sequence information. Aim: This study assessed genetic diversity and relationships among five cotton (Gossypium spp.) varieties using RAPD markers. Method: Genomic DNA was isolated from Phule Rukumai, Phule Yamuna, Phule Anmol, Phule Dhanwantary, and Phule-688 using a modified rapid extraction protocol. Ten RAPD primers were initially screened, of which five produced reproducible amplification. The amplified fragments were resolved by agarose gel electrophoresis and scored as present or absent. Polymorphic information content (PIC) was calculated to evaluate primer informativeness. Genetic similarity was estimated using Jaccard's coefficient, and cluster analysis was performed using the unweighted pair-group method with arithmetic mean. Results: The five primers generated 23 scorable bands, with an average of 4.6 bands per primer. Thirteen bands were polymorphic and ten were monomorphic, representing 56.52% and 43.48%, respectively. PIC values ranged from 0.016 to 0.384, with a mean of 0.150. Jaccard's similarity coefficients ranged from 0.133 to 0.466. Phule Yamuna and Phule Anmol showed the highest similarity, whereas Phule Rukumai was comparatively distinct. Conclusion: RAPD markers effectively differentiated the evaluated cotton varieties and provided preliminary evidence of their molecular relationships. The findings may support initial germplasm characterisation and parent selection, although wider validation using more genotypes and marker systems is required.

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Title: The need for manual curation of the cotton proteome leads to a solution primed for undergraduate involvement

Authors: Jonathan Zirke | Amanda R. Storm | Grant T. Billings | Amanda M. Hulse-Kemp

Imprint: ***Plants, People, Planet*****, 1–15. https://doi.org/10.1002/ppp3.70233**

Abstract: Societal Impact Statement Cotton is a global crop cultivated worldwide, yet a significant portion of the cotton genome remains functionally unannotated. Attempts have been made to automate this annotation but have been unable to completely bridge the gap. Human curation is still needed for accurate interpretations and predictions to be made. We present a solution leveraging a course-based approach to annotating protein function in a format tailored for undergraduate students. This format produces significant insight into individual proteins while introducing students to research in a low- to no-cost footprint. In this way, this work provides a case study to bridge the gap between the next generation of scientists to deliver cutting-edge science. Summary • Cotton suffers from a modest fraction of functionally unannotated proteome. This problem is unsolvable by our current automated annotation tools. We set out to develop a solution that brings undergraduates into the research pipeline. • We systematically

identified all unannotated proteins and their corresponding genes and compiled a set of thousands of proteins suitable for manual downstream analysis. We devised a mutually beneficial solution, which provides manual annotation of unknown function genes through an analysis pipeline that can be used by undergraduate students as an authentic research experience. This approach ultimately provides valuable annotations disseminated in the form of a microPublication that would otherwise remain inaccessible. • This analysis pipeline solution is modular and adaptable as technology improves and has successfully produced multiple microPublications, each of which provided novel predictions of form and function for an uncharacterized protein in the cotton genome. • These microPublication reports are then shared directly with the cotton community by linking them to the gene in the community database, which ensures the results are broadly findable to provide valuable functional information for downstream research purposes.

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Title: JA-*GhMYC2*-*GhWIND1-A* transcriptional cascade promotes cotton callus enlargement

Authors: Yaqian Zhu, Peng Wang, Lulu Liu, Lu Qiu, Mengna Ding, Yiming Liang, Ying Wang, Wenjing Wang, Yan Zhao, Yadi Xing, Fuguang Li, Maozhi Ren,

Imprint: Industrial Crops and Products, Volume 251, 2026, 124097,
ISSN 0926-6690, https://doi.org/10.1016/j.indcrop.2026.124097.

Abstract: Wound-induced cellular reprogramming is a fundamental process for plant regeneration, yet the molecular mechanisms of this process in cotton remain poorly understood. In this study, we identified and systematically characterized the GhWINDs gene family in upland cotton (Gossypium hirsutum), revealing its plant-specific conserved features. Among these genes, GhWIND1-A, which encodes a nucleus-localized AP2/ERF transcription factor, significantly promoted callus enlargement when overexpressed in both Arabidopsis thaliana and upland cotton. Further analyses demonstrated that GhMYC2, a central regulator of jasmonic acid (JA) signaling, directly binds to and activates the GhWIND1-A promoter and also promotes callus enlargement in cotton hairy roots. Transcriptomic and molecular biology analyses showed that GhWIND1-A acts as a key regulatory hub coordinating the reprogramming of multiple phytohormone pathways and directly activates GhSWEET4, which encodes a sugar transporter, thereby providing the metabolic energy required for rapid callus enlargement. Consistently, treatment with JA inhibitors reduced endogenous JA levels, suppressed GhSWEET4 expression, and significantly inhibited callus enlargement, whereas exogenous MeJA application elevated JA content, induced GhSWEET4 expression, and promoted callus enlargement. Collectively, these findings reveal a JA-

GhMYC2-GhWIND1-A-GhSWEET4 regulatory cascade that links wound-induced hormonal signaling with metabolic energy regulation to promote callus enlargement. Given that cotton is a major industrial fiber crop and that callus enlargement is a critical trait for tissue culture and genetic transformation, this study provides new insights into the molecular basis of callus enlargement in cotton and identifies potential regulatory targets for improving cotton tissue culture systems.

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Title: Genome-wide association mapping identifies *GhGLR4.8* as a major regulator of basal immunity against *Rhizoctonia solani* in cotton

Authors: Peng Wu, Chenglin Liu, Dingyi Yang, Xinyi Li, Junyuan Lv, Yuqing Ming, Wanyin Xu, Xiaojun Zhang, Weiran Wang, Ping Du, Mingde Wu, Wei Gao, Jie Kong, Xinhui Nie, Chunyuan You, Xiaoping Guo, Haiquan Zhao, Ling Min, Xianlong Zhang, Hui Xi, Shiming Liu, Longfu Zhu

Imprint: Industrial Crops and Products, Volume 251, 2026, 124100,
ISSN 0926-6690, https://doi.org/10.1016/j.indcrop.2026.124100.

Abstract: Resistance to the necrotrophic pathogen Rhizoctonia solani is a major bottleneck in cotton breeding, hindered by the lack of resistance germplasm, accurate phenotyping methods, and defined resistance genes. Here, we established a precise phenotyping system and performed a genome-wide association study (GWAS) on a natural population of Upland cotton (Gossypium hirsutum). A major resistance locus on chromosome D03, which explains 19.65% of the phenotypic variation, was identified. GhGLR4.8, encoding a glutamate receptor-like protein, was pinpointed as the causal gene. Clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9 (CRISPR/Cas9)-mediated knockout significantly compromised resistance, whereas overexpression of the elite haplotype GhGLR4.8Hap3 conferred robust protection. Functional characterization indicated that GhGLR4.8 promotes lignin deposition and strengthens cell wall structure while maintaining reactive oxygen species (ROS) balance. Loss-of-function mutants displayed excessive ROS accumulation accompanied by pronounced tissue maceration, suggesting that GhGLR4.8 restricts fungal invasion through coordinated regulation of ROS homeostasis. This study reports the first major resistance gene against R. solani in cotton, providing key insights into the balance between ROS signaling and structural defense, as well as a valuable genetic resource for molecular breeding to stabilize cotton yield.

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Title: Cadmium tolerance mediated by GhBCAT12 through branched-chain amino acid degradation via vacuolar sequestration in cotton.

Authors: Xiao, L., Chen, X., He, Y. et al.

Imprint: Stress Biology 6, 59 (2026). https://doi.org/10.1007/s44154-026-00335-z

Abstract: Soil Cd2+ pollution threatens agricultural safety. Branched-chain amino acid (BCAA) metabolism is involved in stress responses, but its role in cotton Cd2+ tolerance remains unclear. Here, 16 GhBCAT genes were identified in Gossypium hirsutum, among which GhBCAT12 was significantly induced by Cd2+ stress. Silencing GhBCAT12 increased Cd2+ sensitivity, causing growth inhibition, oxidative damage, and cell death. Metabolomic analysis revealed the accumulation of leucine, isoleucine, and valine, with decreased acetyl-CoA, indicating that GhBCAT12 mediates BCAA degradation. This study reveals a novel pathway in which GhBCAT12-mediated BCAA degradation provides acetyl-CoA precursors for the tricarboxylic acid (TCA) cycle, sustaining ATP production, which in turn powers vacuolar Cd2+ sequestration. These findings provide a new target for improving heavy metal tolerance in crops.

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Title: Deciphering thermotolerance in cotton genotypes using integrated morpho-physiological and biochemical markers at early stage

Authors: Iman Fatimaa, Muhammad Yousaf Shania, Muhammad Yasin Ashrafb, Adeel Hussainc, M. Kashif Riaz Khana,b, M Saleemb, Ghulam Faridb, Cataldo Pulvento

Imprint: Research Article, 2026, :38; 17832025
doi: 10.25259/JKSUS_1783_2025

Abstract: Heat stress critically affects plant growth, development, and physiological balance, resulting in substantial yield losses. Understanding early responses to high temperature is crucial to identifying resilient genotypes for breeding activities. In this study, heat tolerance in 25 cotton genotypes was evaluated at the seedling stage using morphological and physio-biochemical indicators. The experiment was carried out under controlled conditions using a completely randomized experimental design with three replications; the plants were exposed to three temperature regimes: normal (T1: 32/28°C), moderate heat stress (T2: 45/30°C, 2 h exposure), and severe heat stress (T3: 48/32°C, 4 h exposure). Increasing temperature stress caused significant reductions in shoot and root length as well as fresh and dry biomass. In contrast, biochemical attributes, including total soluble sugars, proline, superoxide dismutase, catalase, peroxidase, ascorbate peroxidase (APX), sodium, potassium, and electrolyte leakage increased significantly ($P \leq 0.05$), whereas total soluble protein content declined. The multi-trait genotype–ideotype distance index (MGIDI) identified genotypes G9

(National Institute for Biotechnology and Genetic Engineering (NIBGE)-IR-824), G11 (Nuclear Institute for Agriculture and Biology (NIAB)-846), G18 (NIAB-512), and G21 (NIAB-896) as the most heat-tolerant under both moderate and severe stress. These findings provide valuable insights for identifying and utilizing heat-resilient cotton genotypes, supporting future breeding programs aimed at improving thermal tolerance in cotton.

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Title: Poly(acrylic acid) coated Mn3O4 nanozymes enhanced high light stress tolerance in cotton by scavenging ROS and down-regulating the expression level of GhADF7

Authors: Guilan Sun, Lingling Chen, Zihao Dong, Guangjing Li, Huixin Ma, Hezhen Yuan, Dan Wang, Ibrahim A.A. Mohamed, Elsheery Nabil, Jiangjiang Gu, Zhouli Xie, Zhanbiao Wang, Zhaohu Li, Honghong Wu,

Imprint: Plant Stress, Volume 23, 2026, 101522,
ISSN 2667-064X, https://doi.org/10.1016/j.stress.2026.101522.

Abstract: High light stress is common during plant production. However, we still lack powerful tools to deal with high light stress. In this study, poly(acrylic acid) coated Mn3O4 nanoparticles (PMO) were used to increase high light tolerance of cotton. Our results showed that the fluorescence intensity of hydrogen peroxide (H2O2), hydroxyl radical, and superoxide anion (O2•-) was significantly lower in PMO treated cotton plants than control plants under high light, accompanied with increased activities of peroxidase and catalase in PMO treated cotton plants. Further, under high-light stress, PMO treatment significantly downregulated actin depolymerization factor GhADF7 expression by 64.0% (first true leaf) and 41.0% (second true leaf) compared with the control, accompanied by a marked increase in actin filament (AF) fluorescence intensity and integrated density. Under normal growth conditions, foliar application of actin polymerization inhibitor and excessive H2O2 demonstrated that AF depolymerization led to increased ROS accumulation, whereas PMO effectively alleviated high-light-induced ROS accumulation. This result indicated that the ROS content and the stability of AF skeleton were mutually affected. Moreover, cotton plants with silencing of GhADF7 showed increased actin filament fluorescence intensity and integrated density while reducing H2O2 and O2•- levels in seedlings under high-light stress. Collectively, these results demonstrate that PMO enhances high-light tolerance in cotton by suppressing AF depolymerization through downregulation of GhADF7 expression and modulation of ROS homeostasis, thereby maintaining cytoskeletal stability. It highlights the potential of nanotechnology approach as a powerful tool to resist plant high light stress.

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Title: Systematic analysis of cotton beta galactosidases and their expression profiles under abiotic stresses and gibberellin treatment

Authors: Cun Guo, Weifeng Guo, Shuaiguo Ma, Guolong Zhao, Ling Li, Qiang Hu, Xueqi Liang, Jinhao Sun & Guodong Chen

Imprint: ***BMC Genomics*** **(2026). https://doi.org/10.1186/s12864-026-13327-0**

Abstract: Background: In plants, the beta galactosidases (BGALs) function in various biological processes, including growth, development and responses to abiotic stresses. However, the evolutionary patterns and stress-regulatory roles of the BGAL gene family across multiple Gossypium species remain largely unclear.

Results: In this study, a total of 58, 38, 25, and 26 BGAL genes were identified in Gossypium barbadense, Gossypium hirsutum, Gossypium herbaceum and Gossypium raimondii, respectively. Together with Arabidopsis BGALs, the newly identified cotton BGAL members were classified into eight groups, and their chromosome distribution was mapped. Genome-wide gene duplication analysis indicated that segmental duplication played a crucial role in the expansion and evolution of the BGAL gene family. Expression profiling revealed that GhBGAL genes were expressed in multiple tissues and exhibited distinct responses to cold, heat, salt, and drought stresses, suggesting their important roles in abiotic stress adaptation. Promoter analysis and qRT-PCR further showed that most GhBGAL genes contained gibberellin (GA)-responsive cis-elements and their expression responded rapidly responded to GA treatment, suggesting that BGALs may coordinate with GA signaling to regulate cotton development.

Conclusions: Our results systematically reveal the evolutionary and functional characteristics of cotton BGALs, and provide key candidate genes for dissecting stress tolerance mechanisms and facilitating the genetic improvement of cotton.

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Title: Nano Zinc Oxide Seed Treatment and Priming Improve Germination, Seedling Vigour and Root Development in Bt Cotton

Authors: N. Pruthviraj, V. Lakshmi

Imprint: Archives of Current Research International, 2026, 26 (8), pp.525-534. ⟨hal-05709170⟩

Abstract: Poor germination and weak early establishment can reduce plant population and productivity in Bt cotton, while zinc deficiency can constrain enzyme activity, reserve mobilization, and root development during establishment. Against this background, the present study evaluated nano zinc oxide (ZnO) seed treatment and seed priming for improving seed germination, seedling vigour, and root development in Bt cotton (Gossypium hirsutum L.) under controlled laboratory conditions. Eight treatments comprising three nano ZnO seed-treatment doses (0.5, 1.0, and 2.0 g kg^{-1} seed), four seed-priming concentrations (500, 750, 1000, and 1250 ppm), and an untreated control were evaluated in a single laboratory experiment with two independent replications using the between-paper germination method following ISTA guidelines. Germination percentage, seedling vigour indices (SVI-I and SVI-II), and root morphological traits were recorded and subjected to analysis of variance. Nano ZnO significantly improved germination and early seedling growth over the control. Seed treatment with nano ZnO at 1.0 g kg^{-1} seed recorded the highest germination (92%), SVI-I (3119), SVI-II (43001), root length (326.7 cm), root volume (1.92 cm^3), and root surface area (82.8 cm^2). Among seed-priming treatments, 1000 ppm nano ZnO produced superior seedling performance. Thus, nano ZnO at an appropriate concentration enhanced early establishment and root development in Bt cotton; however, these findings are limited to laboratory conditions and require nursery and field validation before agronomic recommendation.

FIBER AND FIBER TECHNOLOGY

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Title: Strigolactones: Shaping the future of cotton fiber production

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Imprint: Crop Design, Volume 5, Issue 3, 2026, 100154, ISSN 2772-8994, https://doi.org/10.1016/j.cropd.2026.100154.

Abstract: Cotton fiber, a single-cell trichome differentiated from the seed coat, represents one of the most important natural textile raw materials worldwide. The development of cotton fiber cells is a highly coordinated process that requires the participation of multiple signaling molecules and transcription factors. Plant hormones such as auxin and gibberellins (GA), as well as reactive oxygen species (ROS), have been demonstrated to play essential roles. In addition, transcription factors (TFs), including the MYB TFs family GhMML3 and GhMML4, and the HD-ZIP IV TFs family GhHOX3, have been identified as critical regulators of fiber initiation and elongation. Strigolactones (SLs), one of the most important plant hormones identified as signaling molecules over the past two decades, participate in multiple aspects of plant development. The discovery of SL receptors in Arabidopsis thaliana and rice represents a remarkable breakthrough in elucidating SLs functions. To date, SLs are increasingly recognized as versatile regulators, controlling tillering in cereals, driving secondary metabolism in horticultural crops, and enhancing disease resistance in major economic species [[1], [2], [3]]. Yet, their roles in the unique single-cell model of cotton fiber development have remained largely unexplored - until recently [[4], [5], [6]]. Independent studies now reveal that SLs critically influence fiber initiation, elongation, and maturation, underscoring their potential as a powerful lever for cotton improvement and future innovations in agricultural productivity.

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Title: Integrative Approaches for Fiber Quality Improvement in Tetraploid Cotton: Progress from QTL Discovery to Genome Editing Tools

Authors: MuhammadAbubakar", HumaSaleem'", MuhammadAzam Kha', Umara Sahar Rana', AliMurtaza' andMuhammadZarar Hasan

Imprint:

Abstract: The global textile industry is made up of cotton (Gossypium spp.), which is the most important natural fiber crop currently. Tetraploid cottons (G. hirsutum and G. barbadense) are mostly prevalent because they have higher yield and spinnability of fiber. Fiber traits are polygenic, highly environmentally and genetically dependent, in nature as they relate to the quality of the fiber in terms of length, strength, fineness and elongation. The unending worldwide need to have high quality cotton fiber requires high-technological methods that exceed traditional breeding requirements. Over the last 20 years, there has been prodigal advancement in the genetic and molecular pathways of fiber development. The discovery ofmany quantitative trait loci (QTLs) and operative genes that relate to fiber elongation, synthesis ofthe cell wall, and secondary thickening has alowed the breeding oftraits specifically through the action of these genes. Genome-wide association studies (GWAS), high-throughput sequencing, and transcriptome genomics have largely complemented cotton genomics, whereas CRISPR /Cas based genome editing currently provide accuracy during the engineering of fiber genes. The current review is a compilation of recent progress in enhancement of fiber quality in tetraploid cotton between traditional QTL mapping and marker-assisted selection (MAS), and contemporary genomic prediction and genome editing. The special attention is paid to essential genes and transcriptional regulators involved in the fiber morphogenesis, the use ofmolecular tools in breeding, and the success stories underpinning the CRISPR/Cas technology. Additionally, the review introduces the concept of combining data on multi-omics, 20pangenome resources, and genomic selection models to enhance faster improvements of fiber and allow the maintenance of yields. Phenotyping bottlenecks, lack of genetic diversity and high-quality fiber production that is sustainable also are mentioned. In the end, these developments provide a pathway to the next generation cotton improvement systems that are based on molecular accuracy, bioinformatics and breeding creativity to satisfy the increasing quality demands of the textile industry.

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Title: From developmental overlap to molecular coordination: regulation of cotton fiber elongation and secondary wall thickening

Authors: Yan Mengyuan, Cao Junfeng & Guo Anhui

Imprint: J Cotton Res 9, 31 (2026). https://doi.org/10.1186/s42397-026-00277-x

Abstract: Elongation and secondary wall thickening determine the length, strength, and fineness of cotton fibers, with inherent trade-offs between these traits. Cotton fiber development involves a partially overlapping transition from rapid elongation to secondary wall cellulose deposition, and the duration and coordination of this transition directly affect fiber length, strength, and fineness. Although this overlap has

long been recognized, the molecular mechanisms that coordinate elongation and wall-thickening programs during this transition remain poorly understood. Recent work by Zhu et al. on the GhCEWT1–GhCEWT2 module provides novel insight into how fiber elongation rate and secondary wall deposition may be jointly regulated during the elongation-to-thickening transition. This emerging framework advances our understanding of fiber developmental coordination and offers new opportunities to overcome long-standing trade-offs and improve fiber quality.

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Title: Fiber quality stability across canopy positions in upland cotton genotypes

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Imprint: https://doi.org/10.21203/rs.3.rs-10501475/v1

Abstract: Fiber quality is a major target of upland cotton (Gossypium hirsutum L.) breeding because it directly affects textile processing and commercial value. However, most studies evaluate fiber quality using composite samples from entire plants, overlooking variation among canopy positions. This study evaluated the effects of genotype and canopy position on fiber technological traits and identified genotypes combining superior fiber quality with greater intraplant stability. The experiment was conducted in a randomized complete block design with four replications using a nested arrangement involving 12 cotton genotypes and three canopy positions. Twenty bolls were collected from each canopy position per plot and analyzed by High Volume Instrument (HVI) for micronaire (MIC), fiber maturity (MAT), upper half mean length (UHML), uniformity index (UI), short fiber index (SF), fiber strength (STR), and elongation (ELG). Genotype significantly affected all evaluated traits, whereas canopy position influenced MIC, MAT, and UHML. DP 1552 B2RF exhibited the most favorable fiber quality profile, combining high UI and ELG, low SF, and stable performance across canopy positions. BRS 372 showed superior UHML and STR, whereas IMA 5675 B2RF displayed the greatest reduction in MIC. These findings demonstrate that evaluating fiber quality together with canopy stability provides an additional criterion for selecting cotton genotypes with more uniform and predictable fiber quality.

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Title: Drought stress reshapes the genetic architecture of fiber quality and developmental traits in Egyptian cotton (*Gossypium barbadense* L.): a line × tester analysis under contrasting irrigation regimes

Authors: A. A. E. Mohamed, W. M. B. Yehia, Asmaa Hamoda, Reem M. E. Jabr, Fouad H. Saleh & Sobhi F. Lamlom

Imprint: *Sci Rep* **16**, 24940 (2026). https://doi.org/10.1038/s41598-026-63583-z

Abstract: Water scarcity is an increasing threat to Egyptian cotton production, yet the mechanisms by which drought stress modifies the genetic control of fiber development and plant architecture remain poorly characterized. This study investigated how water deficit alters the genetic architecture of eight fiber quality and agronomic traits in Egyptian cotton, using a line × tester mating design comprising seven lines crossed with three testers to produce 21 F^1 hybrids, which were evaluated under normal irrigation and drought stress at the Sakha Agricultural Experimental Research Station during the 2025 growing season. Analysis of variance partitioned genetic variation into general combining ability (GCA) and specific combining ability (SCA) components, and estimated gene action, heterosis, and heritability under both environments. Under normal irrigation, fiber quality traits micronaire, fiber length (UHML), uniformity index, and fiber strength were predominantly governed by additive genetic effects, with GCA/SCA variance ratios ranging from 13.0 to 81.6. Under drought stress, all four fiber traits showed lower GCA/SCA ratios (0.13–0.32), consistent with a relatively greater contribution of non-additive (dominance and epistatic) variance in this dataset. Narrow-sense heritability for fiber length declined from 0.980 under normal conditions to 0.206 under drought, while broad-sense heritability remained high (0.979), a pattern consistent with a relative reduction in the additive genetic component under stress. Agronomic traits were predominantly non-additive under both environments, with the notable exception of the first fruiting node under drought, which exhibited an additive-dominant ratio of 1.11, suggesting that the developmental timing of reproductive branching becomes more additively heritable under stress. Among parental genotypes, Giza 85 and Giza 92 emerged as superior donors for fiber quality under drought, while Giza 70 and Giza 87 were the most effective combiners under normal conditions. The cross Giza 85 × Giza 86 showed the highest positive mid-parent heterosis for fiber length (8.48%), uniformity index (2.01%), and fiber strength (6.57%) under drought simultaneously, suggesting complementary genetic interactions that may buffer fiber development against water deficit. These findings suggest that drought is associated with a shift in the relative contribution of additive and non-additive genetic control over fiber quality and developmental traits in this population and environment, with potential implications for climate-resilient cotton breeding strategy. Hybridization-based approaches exploiting non-additive variance may be worth considering for

drought-targeted programs, whereas pedigree selection appears more appropriate under favorable conditions; confirmation across additional environments and germplasm would strengthen these recommendations.

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Title: Automated Segmentation and Quantitative Analysis of Cotton Fiber Cross Sections Using a Deep Learning-Based Workflow

Authors: Shalini P. Etukuri , Chaney L. Courtney, Conner Rhoden , Matthew Laufer , Riley Main , Ryan A. Smith, Damon Kenny , Khushi Patel , Jacob Johnson, Helan Baby Thomas , Neha Kothari , Brooke Shumate , Vikki B. Martin , Trevor W. Rife , Christopher A. Saski

Imprint: DOI: https://doi.org/10.21203/rs.3.rs-10594498/v1

Abstract: Cross-sectional analysis is considered the reference method for measuring cotton fiber fineness and maturity; however, its widespread use has been limited by labor-intensive sample preparation and manual image analysis. The objective of this study was to develop and validate a reproducible deep-learning-based workflow for automated segmentation and quantitative analysis of cotton fiber cross-sections. A total of 249 composite light microscopy images of cotton fiber cross-sections were collected and manually annotated to generate training and validation datasets. A YOLO11m instance segmentation model was developed to identify cotton fiber and lumen regions and automatically extract quantitative traits, including fiber area, lumen area, fiber perimeter, and lumen perimeter. The workflow integrates automated image segmentation, post-processing, quantitative trait extraction, and data export to facilitate reproducible cotton fiber phenotyping. Model performance was evaluated using mean Average Precision (mAP), and workflow outputs were validated against Adobe Photoshop using descriptive comparisons of six cross-sectional traits. The model achieved Box mAP50 scores of 0.984 for cotton fiber regions and 0.789 for lumen regions, demonstrating high segmentation accuracy. The automated workflow substantially reduced manual analysis time while producing measurements with central tendencies comparable to those obtained using Adobe Photoshop. To facilitate reproducibility and adoption, the workflow, trained model weights, and supporting documentation are publicly available through GitHub and a Hugging Face web application. The workflow substantially increases analytical throughput while providing a reproducible and publicly accessible method for automated cotton fiber cross-sectional phenotyping, facilitating quantitative analysis for cotton genetics and breeding research.

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Title: Differential Non-Fiber Agronomic Properties and Biochemically Related Fourier Transform Infrared Spectral Features of Cotton Genotypes with Contrasting Fiber Lengths

Authors: Zhongqi He,* Haile Tewolde, Yongliang Liu, HeeJin Kim, Marina Naoumkina, Sunghyun Nam, Xinhua Yin, and Jack McCarty Jr.

Imprint: ACS Agric. Sci. Technol. 2026, 6, 1761−1774

Abstract: While Fourier transform infrared (FT-IR) spectroscopy is widely used in agricultural research, linking the FT-IR biochemical features to agronomic properties is quite limited. In this work, three cotton mutants with shorter fiber lengths (Li1, Li2, and liy) and two wild types (DP5690 and MD15) were grown under field conditions to characterize their plant biomass parts at three growth stages for nine non-fiber agronomic properties and six biochemically related FT-IR spectral features. Compared to the wild-type, lower values of protein-related FT-IR bands were observed in leaf blade samples of liy and Li1 but not in Li2. FT-IR spectroscopy coupled with correlation analysis pinpointed that the major growth-retardant factor for Li1 and liy was the alteration of the biomass synthesis/accumulation in leaf blades. Leaf blades should be the samples selected for future protein profiling for plant growth and fiber cell initiation due to the gene modifications in the three mutants.

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Title: Understanding Cotton (Gossypium hirsutum L.) Fiber Quality for American Upland Cotton: From Field Factors to Market Consequences1

Authors: Sudeep S. Sidhu, Gabrielle A. Comitre, and Hardeep Singh2

Imprint: doi.org/10.32473/EDIS-AG503-2026

Abstract:Cotton plants produce fruit over a long period while they are still growing (indeterminate growth habit). The amount of cotton a farmer can harvest depends on several factors: good sunlight, the right amount of water, soil fertility, suitable temperatures, and protection from weeds, insects, and diseases (DeLanghe, 1986). Cotton profitability hinges on not only lint yield but also fiber quality. Various cotton quality factors are considered for cotton fiber quality premium. These factors are meticulously measured using precise instruments in a process called HVI (High Volume Instrument) classification, which ultimately determines the final market price and end-use applications of the cotton fiber. Therefore, a bale of cotton will receive a premium or a discounted price depending on quality parameters such as 1) fiber length,

2) fiber uniformity, 3) fiber strength, 4) micronaire, 5) color grade, 6) trash content, 7) leaf grade, and 8) extraneous matter, which includes plastic contamination in cotton fiber. This article discusses the cotton fiber quality characteristics in relation to industry premiums and overall profitability, as well as conditions that impact these qualities, such as 1) variety selection, 2) environmental conditions, and 3) crop management. This article is intended for cotton producers, Extension agents, crop advisors, and consultants.