# GLEANINGS IN COTTON RESEARCH

## NOVEMBER 2025

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# Preface

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

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

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

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

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

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

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

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

*Swati Dixit*
*In charge Library*

*Chetali Rodge*
*Technical Officer (T5)*

# INDEX

# AGRONOMY, SOIL SCIENCE AND PLANT PHYSIOLOGY

## 1

**Title**: The erosion of agrobiodiversity of cotton in India: interplay of politics, science, and technology.

**Author**: Avik Ray

**Imprint**: Science, Technologie, Développement 2025, vol. 5, n° 1, 84-98 pages, DOI: 10.21494/ISTE.OP.2025.1339

**ABSTRACT**. The dissection of the contemporary cotton crisis in India has cast light on knowledge and deskilling, capitalism and commodification, biotechnology and public policy, Bt cotton and yield, diseases and management, etc. Whereas how agricultural-technology, plant breeding and biotechnology, have influenced cotton agriculture reciprocating to global demand is rarely invoked in the political-ecological analyses. Here, employing various data, I reconstructed the trajectory of cotton agrobiodiversity and underlying drivers nestled in the broad techno politics of the last century. It revealed that a major change in the twentieth century was steered by cotton improvement through breeding when a few varieties of American cotton with industry-set staple-length have gained precedence, causing the continued abandonment of native species. The process was exacerbated by the large-scale adoption of the hybrids in the seventies and eighties. Increasing genetic homogeneity unleashed bollworm infestation that raised the pesticide application and cost of cultivation. Later, genetically modified Bt cotton was widely adopted in the twenty-first century to circumvent this problem. Genetic erosion driven by global technopolitical change has raised the vulnerability to major diseases, especially bollworm, wreaking havoc across geographies and culminating in agrarian distress. The study seems to lay a foundation for future research on the entanglement between technopolitical, bio-cultural, and agrarian change.

## 2

**Title**: Effects of a combination of biochar and cow manure on soil nutrients and cotton yield in salinized fields.

**Author**: Cheng Huang, Shengtong Hou, Bao Wang, Yuchuan Song, Aikeremu Abulatijiang, Jiuzhou Min, Jiandong Sheng, Ping'an Jiang, Ze Wang & Junhui Cheng

**Imprint**: Journal of Arid Land , Published: 29 July 2025, Volume 17, pages 1014–1026, (2025)

**Abstract**: Biochar and animal manure application can improve crop yields in salt-affected soil. Previous studies have primarily applied biochar and animal manure either alone or at fixed ratios, while their combined effects with varying combination proportions are still unclear. To address this knowledge gap, we performed a 2-a experiment (2023–2024) in a salinized cotton field in Wensu County of Xinjiang Uygur Autonomous Region of China with the following 6 treatments: control; application of biochar (10 t/hm²) alone (BC100%); application of cow manure (10 t/hm²) alone (CM100%); application of 70% biochar (7 t/hm²) combined with 30% cow manure (3 t/hm²) (BC70%+CM30%); application of 50% biochar (5 t/hm²) combined with 50% cow manure (5 t/hm²) (BC50%+CM50%); and application of 30% biochar (3 t/hm²) combined with 70% cow manure (7 t/hm²) (BC30%+CM70%). By measuring soil pH, electrical conductivity, soil organic matter, available phosphorus, available potassium, and available nitrogen at 0–20 and 20–40 cm depths, as well as yield components and cotton yield in 2023 and 2024, this study revealed that soil nutrients in the 0–20 cm depth were more sensitive to the treatment. Among all the treatments, BC50%+CM50% treatment had the highest value of soil pH (9.63±0.07) but the lowest values of electrical conductivity (161.9±31.8 μS/cm), soil organic matter (1.88±0.27 g/kg), and available potassium (42.72±8.25 mg/kg) in 2024. Moreover, the highest cotton yield (5336.63±467.72 kg/hm²) was also observed under BC50%+CM50% treatment in 2024, which was 1.9 times greater than that under the control treatment. In addition, cotton yield in 2023 was jointly determined by yield components (density and number of cotton bolls) and soil nutrients (available phosphorus and available potassium), but in 2024, cotton yield was only positively related to yield components (density, number of cotton bolls, and single boll weight). Overall, this study highlighted that in salt-affected soil, the combination of biochar and cow manure at a 1:1 ratio is recommended for increasing cotton yield and reducing soil salinity stress.

## 3

**Title**: Quantifying the impact of environmental conditions on the effectiveness of mepiquat chloride in modulating canopy architecture, yield, and quality of drought-stressed cotton (Gossypium hirsutum L.)

**Author**: Mashenene Malima, Orhan Kurt and Muhammet Safa Hacikamiloglu

**Imprint**: Journal of Current Opinion in Crop Science, 6(1), 6-17. https://doi.org/10.62773/jcocs.v6i1.296

**Abstract**: This study, conducted in the semi-arid region of Turkey, during the 2022/23 cropping season, employed a split-split-plot design with three replications to evaluate the impact of Mepiquat chloride (MC) on the growth, yield, and quality of newly developed cotton varieties. The main plot comprised two cotton varieties, while the sub-plots represented two MC application timings and the sub-sub plots included four MC dosages. Although statistical analysis revealed that treatment differences were generally not significant for most parameters, notable trends were identified. In 2022, MC treatments delayed cotton development, whereas in 2023, they improved fiber quality. The highest fiber percentage was recorded under the control treatment in 2023, while in 2022, it peaked at a dosage of 400 mL•ha⁻¹. Among the varieties, Selin showed the highest fiber percentage when MC was applied during the Bolling stage. Additionally, the shoot-root ratio reached its maximum at 400 mL•ha⁻¹ during harvest in 2022 and at 0 mL•ha⁻¹ during the reproductive stage in 2023. These results indicate that the effectiveness of MC in promoting physiological traits and alleviating drought stress appeared to be closely associated with weather variability, underscoring the necessity for site-specific management strategies to achieve optimal outcomes.

## 4

**Title**: Growth-stage-dependent relationship between photosynthetic capacity and leaf biochemical traits in cotton.

**Author**: Xiaojin Qian, Yongjiang Zhang, Liangyun Liu

**Imprint**: Industrial Crops and Products, Volume 235, 1 November 2025, 121650

**Abstract**: Quantifying the seasonal dynamics of leaf photosynthetic capacity and its coupling with biochemical traits is critical for refining terrestrial carbon cycle models. This study investigated the seasonal variations in leaf photosynthetic parameters, especially the maximum carboxylation rate at 25 °C ($V_{cmax,25}$) and the maximum electron transport rate at 25 °C ($J_{max,25}$), and their linkages with leaf nitrogen (N) and chlorophyll (Chl) content in cotton (*Gossypium hirsutum L.*) over two growing seasons. Gas exchange measurements and biochemical analysis revealed that $V_{cmax,25}$ and $J_{max,25}$ peaked during vegetative stages (seedling to squaring) and declined during reproductive growth, mirroring shifts in nitrogen allocation. Strong correlations were observed between photosynthetic parameters and both N ($r = 0.84–0.90$) and Chl ($r = 0.55–0.67$), though these relationships exhibited growth-stage dependency. A saturation threshold of leaf nitrogen content per unit area ($N_{area}$) at $3.7\ g\ m^{-2}$ was identified for the $N_{area}$−$V_{cmax,25}$ relationship, indicating a nitrogen storage strategy in cotton leaves. The relationship between leaf chlorophyll content per unit area ($Chl_{area}$) and $V_{cmax,25}$ varied significantly between vegetative and reproductive growth stages. Mixed-effects modeling confirmed that the growth stage significantly modulated these linkages. The results highlight the importance of stage-specific and threshold-based parameterization in photosynthesis models to better support precision agriculture and global carbon flux simulations.

## 5

**Title**: PSY4-mediated carotenoid biosynthesis confers yellow anther and enhances heat tolerance in cotton.

**Author**:Yujie Wang, Daowu Hu, Kaixuan Wang, Xiaoli Geng, Hangyuan Guo, Kun Li, Baojun Chen, Jinggong Guo

**Imprint**: The Crop Journal, Available online 28 July 2025

**Abstract**: Carotenoids are lipophilic isoprenoid pigments with essential roles in plants. While the cultivated allotetraploid cotton exhibit distinct mature anther coloration — yellow in *Gossypium barbadense* versus predominantly white in *G. hirsutum* — the genetic basis of this divergence remains unclear. The purpose of this study was to identify the genetic basis of anther-color variation in cotton (*Gossypium*) species. We firstly identified carotenoids as the primary pigments underlying yellow-anthers coloration. Comparative transcriptomics of anthers revealed that the carotenoid biosynthesis gene *GbPSY4* was expressed as a key regulator in *G. barbadense*. Functional validation via tissue-specific expression, subcellular localization, *in vivo* enzymatic assays, and virus-induced gene silencing confirmed its role in carotenoid biosynthesis and yellow pigmentation. Genome-wide association studies in a *G. hirsutum* population revealed *GhPSY4_At*, an ortholog of *GbPSY4*, as the causal gene of anther-color variation. We conclude that *PSY4*-regulated carotenoid biosynthesis governs yellow pigmentation. Furthermore, a finding that *G. hirsutum* accessions with yellow anthers showed greater pollen viability under high-temperature stress than those with white anthers suggests that the same pathway that governs yellow pigmentation influences heat tolerance. *PSY4* is a promising target for breeding stress-tolerant cotton varieties.

## 6

**Title**: Exogenous superoxide dismutase alleviates drought stress in cotton genotypes.

**Author**: Andrezza Maia de Lima, Francisco de Assis da Silva, Mirandy dos Santos Dias, Rennan Fernandes Pereira, Aline Dayanna Alves de Lima Marcelino, Daniela Duarte Barbosa, Maria de Fátima Caetano da Silva, José Jaime Vasconcelos Cavalcanti, Roseane Cavalcanti dos Santos, Pedro Dantas Fernandes

**Imprint**: Pesq. Agropec. Trop., Goiânia, v. 55, e82354, 2025

**Abstract**: In drought-tolerant plants, adverse effects caused by water deficit can be mitigated by antioxidant enzymes, which activate the plant's defense mechanisms. This study aimed to evaluate the mitigating effect of exogenous superoxide dismutase (SOD) supplementation on cotton plants subjected to drought stress. Four cotton genotypes (BRS Seridó, FM 966, FMT 705 and CNPA 7MH) were grown in a greenhouse and evaluated under the following treatments: control (daily irrigation), drought stress (plants subjected to 6 days without irrigation) and drought stress with exogenous SOD supplementation at concentrations of 11, 22 and 33 μg mL-1. The experimental design was a randomized block arrangement, in a 4 × 5 factorial scheme, with four replications. Plant growth, biomass accumulation and gas exchange parameters were evaluated. Overall, the exogenous SOD supplementation at 33 μg $mL^{-1}$ effectively mitigated the adverse effects of drought stress on cotton growth and gas exchange, with a more pronounced response observed for the drought-sensitive genotypes.

## 7

**Title**: Evaluation of Soil Quality and Balancing of Nitrogen Application Effects in Summer Direct-Seeded Cotton Fields Based on Minimum Dataset.

**Author**: Yukun Qin, Weina Feng, Cangsong Zheng, Junying Chen, Yuping Wang, Lijuan Zhang and Taili Nie

**Imprint**: Agronomy 2025, 15(8), 1763; https://doi.org/10.3390/agronomy15081763

**Abstract**: There is a lack of systematic research on the comprehensive regulatory effects of urea and organic fertilizer application on soil quality and cotton yield in summer direct-seeded cotton fields in the Yangtze River Basin. Additionally, there is a redundancy of indicators in the cotton field soil quality evaluation system and a lack of reports on constructing a minimum dataset to evaluate the soil quality status of cotton fields. We aim to accurately and efficiently evaluate soil quality in cotton fields and screen nitrogen application measures that synergistically improve soil quality, cotton yield, and nitrogen fertilizer utilization efficiency. Taking the summer live broadcast cotton field in Jiangxi Province as the research object, four treatments, including CK without nitrogen application, CF with conventional nitrogen application, N1 with nitrogen reduction, and N2 with nitrogen reduction and organic fertilizer application, were set up for three consecutive years from 2022 to 2024. A total of 15 physical, chemical, and biological indicators of the 0–20 cm plow layer soil were measured in each treatment. A minimum dataset model was constructed to evaluate and verify the soil quality status of different nitrogen application treatments and to explore the physiological mechanisms of nitrogen application on yield performance and stability from the perspectives of cotton source–sink relationship, nitrogen use efficiency, and soil quality. The minimum dataset for soil quality evaluation in cotton fields consisted of five indicators: soil bulk density, moisture content, total nitrogen, organic carbon, and carbon-to-nitrogen ratio, with a simplification rate of 66.67% for the evaluation indicators. The soil quality index calculated based on the minimum dataset (MDS) was significantly positively correlated with the soil quality index of the total dataset (TDS) ($R^2 = 0.904$, $p < 0.05$). The model validation parameters RMSE was 0.0733, nRMSE was 13.8561%, and the d value was 0.9529, all indicating that the model simulation effect had reached a good level or above. The order of soil quality index based on MDS and TDS for CK, CF, N1, and N2 treatments was CK < N1 < CF < N2. The soil quality index of N2 treatment under MDS significantly increased by 16.70% and 26.16% compared to CF and N1 treatments, respectively. Compared with CF treatment, N2 treatment significantly increased nitrogen fertilizer partial productivity by 27.97%, 31.06%, and 21.77%, respectively, over a three-year period while maintaining the same biomass, yield level, yield stability, and yield sustainability. Meanwhile, N1 treatment had the risk of significantly reducing both boll density and seed cotton yield. Compared with N1 treatment, N2 treatment could significantly increase the biomass of reproductive organs during the flower and boll stage by 23.62~24.75% and the boll opening stage by 12.39~15.44%, respectively, laying a material foundation for the improvement in yield and yield stability. Under CF treatment, the cotton field soil showed a high degree of soil physical property barriers, while the N2 treatment reduced soil barriers in indicators such as bulk density, soil organic carbon content, and soil carbon-to-nitrogen ratio by 0.04, 0.04, 0.08, and 0.02, respectively, compared to CF treatment. In summary, the minimum dataset (MDS) retained only 33.3% of the original indicators while maintaining high accuracy, demonstrating the model's efficiency. After reducing nitrogen by 20%, applying 10% total nitrogen organic fertilizer could substantially improve cotton biomass, cotton yield performance, yield stability, and nitrogen partial productivity while maintaining soil quality levels. This study also assessed yield stability and sustainability, not just productivity alone. The comprehensive nitrogen fertilizer management (reducing N + organic fertilizer) under the experimental conditions has high practical applicability in the intensive agricultural system in southern China.

## 8

**Title**: Comparative analysis of salt tolerance in cotton cultivars under saline water stress.

**Author**: D K Sahu, A Manikandan, D Blaise, P K Shukla, R S Deshmukh, C R Mundafale & V N Waghmare

**Imprint**: PLANT SCIENCE TODAY Vol x(x): xx–xx https://doi.org/10.14719/pst.6980

**Abstract**: Soil salinity imposes multiple stresses on cotton (Gossypium spp.) and the use of saline water for irrigation is common in coastal regions. However, the effects of borewell saline water (NaCl) on cotton cultivars remains underexplored. A pot experiment conducted during 2017- 2018 aimed to evaluate the morphological, biochemical and physiological responses of six cotton cultivars- G. herbaceum (G-Cot

25, Jayadhar), G. arboreum (Phule dhanwantry, Roja) and G. hirsutum (Suraj, LRA-5166) subjected to NaCl treatments (100, 150 and 200 mM) and a control. All cultivars exhibited a progressive decline in growth parameters with increasing salinity. Among them, Jayadhar and Suraj demonstrated the highest tolerance, maintaining superior growth and physiological performance under NaCl stress. Relative water content decreased significantly across all cultivars; however, G-Cot 25 and LRA-5166 retained higher water content under saline conditions. Biochemically, NaCl stress resulted in reduced levels of total chlorophyll and carotenoids, alongside an increase in protein content, suggesting adaptive responses to salinity. Jayadhar, Suraj and Phule Dhanwantry exhibited greater chlorophyll retention, indicating enhanced biochemical stability. Malondialdehyde (MDA) levels increased under salinity, signifying lipid peroxidation; however, Jayadhar and Suraj accumulated lower MDA levels, suggesting reduced oxidative damage. Proline content increased in all cultivars, with Jayadhar and Suraj showing the highest accumulation, reflecting improved osmotic adjustment. Activities of antioxidant enzyme including superoxide dismutase, catalase and peroxidase were significantly enhanced, particularly in G-Cot 25, Jayadhar and Phule dhanwantry respectively. These findings indicate that antioxidant defense mechanisms play a crucial role in mitigating oxidative damage by scavenging reactive oxygen species under saline conditions. Based on an integrative assessment, the G. herbaceum cultivar Jayadhar demonstrated the highest tolerance to salinity.

## 9

**Title**: Enhanced Efficiency Nitrogen Fertilizers Reduced Ammonia Emissions in Rainfed Cotton.

**Author**: Kulpreet Singh, Eajaz A. Dar, Satinderpal Singh, Akash Shah, Lakesh Sharma, Hardeep Singh

**Imprint**: Journal of Sustainable Agriculture and Environment, 2025; 4: e70084

**ABSTRACT**: Ammonia volatilization is a nitrogen (N) loss pathway with severe environmental impacts, such as ecosystem eutrophication and secondary particulate formation. Rainfed agricultural systems and sandy soils in the Florida panhandle provide ideal conditions for ammonia (NH3) losses. This study investigated the potential of enhanced efficiency nitrogen fertilizers (EENFs) to reduce NH3 losses under rainfed cotton production. The experiment was conducted in 2023 and 2024 using a randomised complete block design. The experiment included four fertilizers: urea (U), urea coated with urease inhibitor (U + NBPT), urea coated with urease and nitrification inhibitor (U + NBPT + DCD), and polymer-coated urea (PCU [41-0-0]) applied at rate of 102 kg N/ha. Our results indicate that cumulative NH3 emissions were 50%–87.5% higher under U than U + NBPT, U + NBPT + DCD, and PCU (41-0-0) in 2023. In 2024, U and U + NBPT had 83%–87% higher emissions than U + NBPT + DCD and PCU

(41-0-0). There was no significant effect of EENFs on lint yield compared to U. This study underscores the potential of EENFs to reduce NH3 losses under rainfed conditions.

## 10

**Title**: Petiole Sampling as a Tool for In-Season Nitrogen Management in Cotton.

**Author**: Akash Shah, Hardeep Singh, Lakesh Sharma, Ethan Carter, and Guilherme Morata

**Imprint**: SS-AGR-491 , https://doi.org/10.32473/edis-AG489-2025, This document is SS-AGR-491, a publication of the Department of Agronomy, UF/IFAS Extension. Original publication date June 2025. Visit the EDIS website at https://edis.ifas.ufl.edu for the currently supported version of this publication. © 2025 UF/IFAS. This publication is licensed under CC BY-NC-ND 4.0.

**Abstract**: Cotton (*Gossypium* spp.) is a major cash crop in the southeastern United States (U.S.). Among the three major essential macronutrients, nitrogen (N), phosphorus (P), and potassium (K), N is the most limiting macronutrient and is required in relatively large quantities in cotton production (Khan et al. 2017). N is a critical element influencing cotton growth, yield, and fiber quality. Therefore, N fertilization sufficiency and balance are major concerns for cotton growers (Hickey et al. 2024). Effective in-season N management is essential to maximize crop performance and minimize environmental impacts. One of the most popular methods for monitoring in-season N status is cotton petiole (the stalk that attaches the leaf blade to the main stem) nitrate-nitrogen (NO3-N) analysis (Bronson et al. 2021). This method involves the analysis of NO3-N concentration in the petiole during early crop growth stages through full flowering, which ultimately helps to manage N fertilization rates. This publication aims to guide cotton producers, Extension agents, crop advisors, and consultants on the correct method of petiole sampling for NO3-N analysis and interpretation of petiole NO3-N test results.

## 11

**Title**: A lightweighted densely connected network for insect-pest identification in cotton crop.

**Author**: Shalini Kumari, Sudeep Marwaha, Md. Ashraful Haque, Harsh Sachan, Chandan Kumar Deb, Shashi Dahiya, Alka Arora & P. R. Shashank

**Imprint**: Neural Computing and Applications, Published: 09 August 2025, Volume 37, pages 21459–21472, (2025)

**Abstract**: Cotton, popularly known as "White-Gold" in India, accounts for about 23% of global production and significantly contributes to the Indian economy. However, it is highly susceptible to the infestation of various harmful insect-pests, which can cause substantial crop damage and yield reductions of up to 40–50%. In this context, we developed a lightweighted densely connected deep learning model for identifying insect-pests of cotton crop using RGB images. We collected 5,559 images of insect-pest infested cotton crops under natural field conditions across Indian agricultural farms. However, for enhancing the training images and to minimize the risk of overfitting the model, we applied a variety of image augmentation methods, including flipping, rotation, zooming, etc. The proposed model, with 83 layers, including four dense blocks and three transition layers, achieved around 99.24% of classification accuracy having 15 s/epoch of training time, outperforming the other pretrained models. Furthermore, Grad-CAM visualization technique was used for demonstrating the model's effectiveness and efficiency in multiclass classification of cotton insect-pest images. This model offers a practical tool for farmers to manage pest infestations and improve cotton crop yield.

## 12

**Title**; Characterizing season-long floral trajectories in cotton with low-altitude remote sensing and deep learning.

**Authors**: Jeevan Adhikari, Daniel Petti, Deepak Vitrakot, Wiriyanat Ployaram, Changying Li, Andrew H. Paterson

**Imprint**; Plants People Planet. 2025;1–17.

**Abstract**: Societal Impact Statement Plant breeding is a critical tool for increasing the productivity, climate resilience, and sustainability of agriculture, but current phenotyping methods are a bottleneck due to the amount of human labor involved. Here, we demonstrate high-throughput phenotyping with an unmanned aerial vehicle (UAV) to analyze the season-long flowering pattern in cotton, subsequently mapping relevant genetic factors underpinning the trait. Season-long flowering is a complex trait, with implications for adaptation of perennials to specific environments. We believe our approach can improve the speed and efficacy of breeding for a variety of woody perennials. Summary • Many perennial plants make important contributions to agroeconomies and agroecosystems but have complex architecture and/or long flowering duration that hinders measurement and selection. Iteratively tracking productivity over a long flowering/fruiting season may permit the identification of genetic factors conferring different reproductive strategies that might be successful in different environments, ranging from rapid early maturation that avoids stresses, to late maturation that utilizes the full seasonal duration to maximize productivity. • In cotton, a perennial plant that is generally cultivated as an annual crop, we apply aerial imagery and deep learning methods to novel and stable genetic stocks, identifying genetic factors influencing the duration and rate of fruiting. • Our phenotyping method was able to identify 24 QTLs that affect flowering behavior in cotton. A total of five of these corresponded to previously identified QTLs from other studies. • While these factors may have different relationships with crop productivity and quality in different environments, their determination adds potentially important information to breeding decisions. With transfer learning of the deep learning models, this approach could be applied widely, potentially improving gains from selection in diverse perennial shrubs and trees essential to sustainable agricultural intensification.

## 13

**Title**: Memory of Water Stress in Cotton (*Gossypium Hirsutum* L.): Evaluating Physiological Responses and Yield Stability.

**Author**: Omolbanin Checkani, Elham Faghani, Mohammad Reza Dadashi, Hossein Ajam Nourouzi & Borhan Sohrabi

**Imprint**: Journal of Soil Science and Plant Nutrition , Volume 25, pages 6802–6819, (2025)

**Abstract**: Drought stress, as one of the major abiotic stresses, has been expanded by global warming, with negative effects on cotton seed potential, cotton fiber, plant growth and yield. Therefore, many plant species have activated a drought stress memory on the physiological and biochemical level to increase drought stress threshold by balancing carbohydrate and starch and reducing water loss. The experiment in this study was carried out to improve our understanding of water-shortage memory in cotton. Golestan cotton genotype was planted in the double and triple water-stress exposures using split-plot factorial design. There were four levels of water requirements (rain-fed, 33%, 66%, and 100% Field capacity (FC). Bioinformatics results showed that catalase enzyme (CAT) with regulatory elements and Abscisic acid regulatory element (ABRE) play a role in abiotic stresses. On the other hand, Stress Tolerance Indices (STI), Yield Stability Indices (YSI), glucose content of the leaves and early-maturity of the seeds in $S_{33}$ and starch content of $S_{23}$ were the highest among the corresponding indices resulted from other seed treatments. Among fiber quality traits, fiber length and fiber strength of seeds planted in the triple water-stress exposure were greater than those in the double water-stress exposure. In addition, seed reproduction under triple water-stress exposure at 33% field capacity (FC) demonstrated higher STI and YSI than under double water-stress exposure. This suggests that plants can develop stress memory to enhance drought tolerance by activating catalase and balancing starch and glucose concentrations. Therefore, advanced breeding techniques that focus on memory responses to water scarcity can help address the challenges associated with drought.

## 14

**Title**: Comparative Transcriptome and Volatile Metabolome Analysis of Gossypium hirsutum Resistance to Verticillium Wilt.

**Author**: Ni Yang, Chaoli Xu, Yajun Liang, Juyun Zheng, Shiwei Geng, Fenglei Sun, Shengmei Li, Chengxia Lai, Mayila Yusuyin, Zhaolong Gong, and Junduo Wang

**Imprint**: Genes 2025, 16(8), 877; https://doi.org/10.3390/genes16080877

**Abstract**: Background: In recent years, changes in climate conditions and long-term continuous cropping have led to the increased occurrence of Verticillium wilt in various cotton-growing regions, causing significant economic losses in cotton production. Research has shown that volatile substances are closely linked to plant disease resistance; however, studies on their roles in the response of cotton to Verticillium wilt, including their relationship with gene regulation, are limited. Methods: In this study, the transcriptomes and metabolomes of Xinluzao 57 (a highly susceptible Verticillium wilt variety) and 192,868 (a highly resistant Verticillium wilt variety) were sequenced at different time points after inoculation with Verticillium wilt. Results: A total of 21,911 commonly differentially expressed genes (DEGs) were identified within and between the materials, and they were clustered into eight groups. Significant annotations were made in pathways related to amino acids and anthocyanins. Metabolomics identified and annotated 26,200 volatile metabolites across nine categories. A total of 158 differentially accumulated metabolites (DAMs) were found within and between the materials; three clusters were identified, and the 10 metabolites with the most significant fold changes were highlighted. Weighted gene coexpression network analysis (WGCNA) revealed that 13 genes were significantly correlated with guanosine, 6 genes were correlated with 2-deoxyerythritol, and 32 genes were correlated with raffinose. Conclusions: Our results provide a foundation for understanding the role of volatile substances in the response of cotton to Verticillium wilt and offer new gene resources for future research on Verticillium wilt resistance.

## 15

**Title**: Genetic dissection of resistance to Fusarium wilt and Verticillium wilt based on vascular discoloration in diploid Asiatic cotton, *Gossypium arboretum.*

**Author**: Abdelraheem Abdelraheem, Yi Zhu, Chunda Feng, Salliana Stetina, Derek Whitelock, Terry Wheeler, Linghe Zeng & Jinfa Zhang

**Imprint**: Euphytica , Volume 221, article number 129, (2025)

**Abstract**: Fusarium wilt and Verticillium wilt (VW) diseases are two most destructive soil-borne fungal diseases and can only be managed most effectively through resistant cultivars. Genetic studies of resistance to the two diseases have been predominantly conducted based on foliar symptoms and there was no report on the genetic basis of the resistance based on vascular discoloration (VD) in cultivated diploid A genome cotton (*Gossypium arboreum*). In this study, we assessed root VD, stem VD, and disease incidence (DI) in 245 *G. arboreum* accession across repeated greenhouse tests to identify single nucleotide polymorphisms (SNPs) associated with the wilt resistance. Results showed that many diploid Asiatic accessions exhibited resistance to both wilt diseases, providing a valuable genetic resource for breeding cotton with host plant resistance. A genome-wide association study revealed 54 and 14 SNPs significantly associated with *Fusarium oxysporum* f. sp. *vasinfectum* race 4 and VW resistance, respectively. Notably, five SNPs exhibited pleiotropic effects, contributing to resistance against both pathogens in cotton with significantly lowering DI. Forty-three of these identified SNPs were novel, while others were previously reported in a different genetic background. Those findings highlight the importance of leveraging diploid species as a genetic resource and the subsequent introduction of these resistance alleles into elite tetraploid cotton breeding lines.

## 16

**Title**: Genome-wide identification of the cotton *FAR* gene family reveals GhFAR3 as a positive regulator of *Verticillium dahliae* resistance.

**Author**: Wenhan Cheng, Siqi Gao, Zhaojie He, Nurimanguli Aini, Zengqiang Zhao, Xianpeng Xiong, Ning Wang, Rui Chen & Keyun Feng

**Imprint**: BMC Plant Biology , Volume 25, article number 887, (2025)

**Abstract**: Although fatty acyl-CoA reductase (FAR) proteins are known to play essential roles in plant growth and development, their involvement in biotic and abiotic stress responses remains insufficiently characterized. In this study, we performed a comprehensive genome-wide analysis of 31 *FAR* genes across four cotton species (*Gossypium arboreum*, *G. raimondii*, *G. hirsutum*, and *G. barbadense*). Phylogenetic and synteny analyses classified these *FAR* genes into three distinct clades, with whole-genome duplication events contributing significantly to their expansion. Promoter cis-element analysis and transcriptome profiling revealed that while most *FAR* genes were downregulated under abiotic stress, many were notably upregulated in response to hormone treatments and *Verticillium dahliae* infection. Among them, *GhFAR3* showed strong induction upon pathogen challenge. Functional validation using virus-induced gene silencing (VIGS) demonstrated that silencing *GhFAR3* compromised resistance to *V. dahliae*, correlating with a marked reduction in suberin deposition in root tissues. These findings uncover a previously unrecognized role of *FAR*-mediated lipid metabolism in plant defense and establish *GhFAR3* as a key positive regulator of cotton resistance to *V. dahliae* through suberin biosynthesis in roots. This study provides novel insights into the integration of lipid biosynthesis and pathogen resistance pathways in cotton.

## 17

**Title**: Integrative identification of key genes governing *Verticillium* wilt resistance in *Gossypium* hirsutum using machine learning and WGCNA.

**Author**: Yufeng Lei, Jing Zhao, Siyuan Hou, Fufeng Xu, Chongbo Zhang, Dongchen Cai, Xiaolei Cao, Zhaoqun Yao, Sifeng Zhao

**Imprint**: Front. Plant Sci., 28 July 2025, Sec. Plant Pathogen Interactions, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1621604

**Abstract**: Introduction**:** *Verticillium* wilt, caused by *Verticillium dahliae*, is one of the most devastating diseases affecting global cotton (*Gossypium hirsutum*) production. Given the limited effectiveness of chemical control measures and the polygenic nature of resistance, elucidating the key genetic determinants is imperative for the development of resistant cultivars. In this study, we aimed to dissect the temporal transcriptional dynamics and regulatory mechanisms underlying *Gossypium hirsutum* response to *V. dahliae* infection. **Methods:** We employed a time-course RNA-Seq approach using the susceptible upland cotton cultivar Jimian 11 to profile transcriptomic responses in root and leaf tissues post-*V. dahliae* inoculation. Differentially expressed genes (DEGs) were identified, followed by weighted gene co-expression network analysis (WGCNA). To prioritize key candidate genes, we applied machine learning algorithms including LASSO, Random Forest, and Support Vector Machine (SVM). **Results and discussion:** A robust set of core genes involved in pathogen recognition (*GhRLP6*), calcium signaling (*GhCIPK6, GhCBP60A*), hormone response, and secondary metabolism (*GhF3′H*) were identified. Our findings provide novel insights into the spatiotemporal regulation of immune responses in cotton and offer valuable candidate genes for molecular breeding of *Verticillium* wilt resistance.

## 18

**Title**: Detection of a new race of Meloidogyne enterolobii in cotton crop, genetic diversity of races, and resistance in Gossypium spp.

**Author**: CAIO FELIPE DE BARROS SOUZA

**Imprint**: Thesis presented to the University of Brasília as a partial requirement for obtaining the title of Doctor in Phytopathology from the Graduate Program in Phytopathology 2024. Work carried out in collaboration with the Department of Phytopathology at the Institute of Biological Sciences of the University of Brasília and Embrapa Genetic Resources and Biotechnology, advised by Professor Juvenil Enrique Cares and Dra. Regina Maria Dechechi Gomes Carneiro, with the support of the National Council for Scientific and Technological Development – CNPq who provided the student grant and financial support by CNPq Universal Project (404948/2021-9).

**Abstract**: Meloidogyne incognita is a well-known root-knot nematode (RKN) species that infects cotton globally. Recently, new resistant cultivars to M. incognita were released in Brazil, being considered the best control strategy. Meloidogyine enterolobii, not historically considered a major threat to cotton production, has caught the attention due to recent reports in the United States and Brazil, causing severe damage in M. incognita cotton resistant cultivars, highlighting its potential as an epidemic RKN. In 2019, the first infection by M. enterolobii on resistant cotton (IMA 5801B2RF) was reported in Minas Gerais state, Brazil. Subsequently, in 2021 M. enterolobii was detected again in the municipality of São Desidério, western Bahia state, on the same resistant cotton cultivar. Another survey in cotton fields cultivated with resistant 'IMA 5801B2RF' from six municipalities in Bahia state (three different geographical origins) were identified by esterase phenotypes (EST) and SCAR markers as M. incognita, but M. enterolobii was not found again, confirming its possible restricted occurrence in western Bahia state. A bioassay with the resistant cotton cultivar in greenhouse conditions demonstrated robust reproduction of M. enterolobii (RF=12.8), but no reproduction of the field populations of M. incognita (FR.

## 19

**Title**: Population Trends of Sucking Pest on Various Cotton Varieties under Field Condition.

**Author**: Asadullah Gorchani, Jam Ghulam Mustafa Sahto, Sajjad Hussain Rind, Abdul waheed Solangi, Nadeem Ali, Ghulam Hussain Khoso, Naveed Ahmed Abbasi, Asadullah, Zamin Hussain Dahri, Dileep Kumar, Muhsin Ali, Deewan Kumar Suthar

**Imprint**: Planta Animalia, Volume 4, Issue 4. 123-130

**Abstract**: Sucking insect pests pose a major threat to cotton productivity by damaging foliage and reducing yield. This study aimed to assess the population trends of Thrips tabaci, Amrasca biguttula, and Bemisia tabaci on different cotton varieties under field conditions, and to evaluate the influence of weather factors to identify resistant varieties for integrated pest management (IPM). Four cotton varieties i.e., Koonj, Bakhtawar, Sindh-1, and Sami were sown during the kharif season using a randomized complete block design (RCBD) with three replications. Weekly pest observations were recorded by randomly selecting ten plants per variety and examining five leaves per plant (top, middle, and bottom). Data on weather parameters were collected from the Meteorological Institute, Agriculture Research Center, Tandojam. Results revealed significant differences in pest populations among the varieties. The population of all pests increased gradually, peaking in mid-July, followed by a decline toward early August. T. tabaci populations peaked between late June and mid-July, with the highest infestation observed on Koonj (12.06±0.21) and Bakhtawar (12.00±0.45), while Sindh-1 maintained consistently lower populations. A sharp decline in thrips density was recorded after mid-July across all varieties, with Sindh-1 showing the lowest final count (0.16 ± 0.68), indicating its potential resistance. A similar trend was observed for A. biguttula and B. tabaci, where Koonj and Bakhtawar recorded higher infestations (3.15±0.35, 3.05±0.30) (4.90±0.51, 5.00±0.53), and Sindh-1 showed comparatively lower pest population (1.00±0.07, 1.30±0.19). Overall, Koonj and Bakhtawar recorded the highest pest densities, while Sindh-1 consistently showed the lowest populations of all three sucking pests, indicating its relative tolerance. Sami maintained intermediate pest densities across all species. Correlation analysis revealed that temperature had a significant positive relationship with pest abundance, especially for B. tabaci ($r = 0.715$, $P < 0.001$), followed by T. tabaci ($r = 0.5$, $P < 0.001$) and A. biguttula ($r = 0.348$, $P < 0.001$). This indicates that higher temperatures favored an increase in pest populations. Wind velocity had no significant effect. These findings highlight the importance of varietal resistance and climatic factors in pest population dynamics and support the inclusion of resistant varieties like Sindh-1 in integrated pest management (IPM) programs

## 20

**Title**: Cotton GhXEGIP1 confers resistance to Verticillium dahliae by inhibiting of fungal VdEG1 and the salicylic acid signaling pathway.

**Author**Linying Gao, Xin Yan, Menghui Hu, Yang Liu, Ping Wang, Xiaoyang Ge, Fuguang Li, Yuxia Hou

**Imprint**: Plant Physiology and Biochemistry, Volume 229, Part A, December 2025, 110360

**Abstract**: Verticillium dahliae is a widespread and destructive soilborne fungus that causes vascular wilt disease, significantly reducing cotton (Gossypium hirsutum) yield and quality. Cotton's xyloglucan-specific endoglucanase inhibitor protein (GhXEGIP1) has demonstrated effectiveness against the fungal glycoside hydrolase VdEG1, a member of the glycoside hydrolase family 12. However, the mechanisms underlying GhXEGIP1's defense against V. dahliae remain unclear. This study provides evidence that GhXEGIP1 are instrumental in plant responses to V. dahliae infection. GhXEGIP1 interacts with and regulates the expression of VdEG1. Docking models and molecular dynamics simulations revealed that a conserved arginine residue in GhXEGIP1 penetrates VdEG1's active site, interacting with its catalytic glutamate, resulting in a stable inhibitor–enzyme complex with lower binding free energy compared to that of the other glycoside hydrolases. Ectopic expression and purification of GhXEGIP1 further revealed its inhibitory effect on VdEG1's hydrolytic activity. GhXEGIP1-silenced cotton exhibited increased fungal biomass accumulation and heightened susceptibility to V. dahliae, along with a disproportionate oxidative burst. Transgenic Arabidopsis plants expressing GhXEGIP1 under the CaMV 35S promoter demonstrated reduced VdEG1 activity, enhanced resistance to V. dahliae, and decreased disease symptoms, including chlorosis and wilting. These transgenic plants also showed enhanced xylem lignification, likely contributing to limiting V. dahliae spread. Further analysis suggested that GhXEGIP1 may be involved in the transcriptional activation of defense-related genes and participate in salicylic acid-mediated defense pathways. These findings suggest that GhXEGIP1 is a potential defense gene against V. dahliae in cotton.

## 21

**Title**: Field evaluation of germplasm lines of extra-long staple cotton (Gossypium barbadense) for tobacco streak virus resistance.

**Author**: Valarmathi Pandian & Amutha Mari

**Imprint**: Euphytica , 12 August 2025, Volume 221, article number 140, (2025)

**Abstract**: The necrosis disease caused by *tobacco streak virus* (TSV) is highly destructive. Conventional management practices for TSV includes cultural methods such as crop rotation, maintaining field sanitation, rogueing of infected plants, intercropping with non-host crops of short duration, eliminating weed hosts like *Parthenium* and insecticide application to control vectors. However, the most efficient and convenient approach to combat this devastating disease is to cultivate resistant varieties. TSV distribution in the germplasm of ELS cotton, *Gossypium barbadense*, appears to be significant. In a consecutive two-season screening at ICAR-Central Institute for Cotton Research (CICR), Regional Station, Coimbatore, a total of three hundred *G. barbadense* germplasm lines were screened under natural field conditions for TSV. Among them, fourteen germplasm lines were categorized as Resistant (R), twenty-two as Moderately Resistant (MR), one hundred and sixty-eight as Moderately Susceptible (MS), and ninety-four as Susceptible (S) lines. The identified fourteen resistant germplasm lines of *G. barbadense* can be valuable resources in breeding programs as donor parents to develop TSV-resistant lines. These findings highlight the critical role of TSV resistance in sustaining cotton productivity, especially in disease-prone regions. The strong association between resistance and yield-related traits such as boll number and plant vigour suggests that integrating TSV resistance into breeding programs can significantly enhance the development of high-yielding, disease-tolerant cotton cultivars. In addition, traits like plant height and sympodial branching can be effectively used as indirect selection criteria for identifying promising genotypes under TSV pressure. Utilizing these lines in breeding efforts can contribute to the development of resistant varieties against TSV.

## 22

**Title**: Bollworm Incidence in Cultivated Cotton Species.

**Author**: Buha P. P., Bhanderi G. R., Patel R. D., Desai H. R., Chaudhari S. G. , Chaudhary M. S.

**Imprint**: Journal of Scientific Research and Reports, 2025, 31 (8), pp.573-580. ⟨hal-05205892⟩

**Abstract**: Investigations on “Bollworms incidence in cultivated cotton species” were carried out at Main Cotton Research Station, Navsari Agricultural University, Surat (Gujarat) during the Kharif, 2024-25. The experiment was carried out under protected and unprotected condition as main treatment and four cultivated species viz., Gossypium hirsutum (G. Cot. 40), G. herbaceum (GN. Cot. 27), G. arboreum (GN. Cot. 29) and G. barbadense (GSB 39) as sub treatments. The mean population of pink bollworm was observed significantly lower under protected (0.80 larvae/5 plants) as compared to unprotected (1.69 larvae/5 plants) plots. The lowest population of american bollworm was recorded in protected (1.04 larvae/5 plants) than unprotected (1.60 larvae/5 plants) condition. The population of spotted bollworm was 0.29 and 0.60 larvae/5 plants in protected and unprotected condition, respectively. The incidence of tobacco caterpillar was highest in unprotected (0.80 larvae/5 plants) over protected (0.46 larvae/5 plants) plots. The damage to green bolls by pink bollworm (32.46%), american bollworm (7.68%), spotted bollworm (3.62%) and tobacco caterpillar (5.98%) were significantly higher in unprotected condition as compared to protected (8.78, 5.62, 2.41 and 4.22%, respectively). Population of pink bollworm was lower in GSB 39 (0.99 larvae/5 plants) followed by GN. Cot. 29 (1.11 larvae/5 plants) and GN. Cot. 27 (1.30 larvae/5 plants), while it was found highest in G. Cot. 40 (1.49 larvae/5 plants). The incidence of american bollworm was found the lowest in GSB 39 (0.92 larvae/5 plants) within all varieties. The GN. Cot. 29 (1.19 larvae/5 plants) and GN. Cot. 27 (1.40 larvae/5 plants) were showed lower incidence of american bollworm than the G. Cot. 40 (1.81 larvae/5 plants). The lowest spotted bollworm population was observed in GSB 39 (0.33 larvae/5 plants). The GN. Cot. 29 (0.40 larvae/5 plants) and GN. Cot. 27 (0.46 larvae/5 plants) were recorded larval population higher than the GSB 39 but lower than G. Cot. 40 (0.56 larvae/5 plants). The lowest population of tobacco caterpillar occurred in GSB 39 (0.44 larvae/5 plants) followed by GN. Cot. 29 (0.56 larvae/5 plant) and GN. Cot. 27 (0.67 larvae/5 plants). It was noted highest in G. Cot. 40 (0.82 larvae/5 plants). The boll damage by pink bollworm was found lower in GSB 39 (13.88%) followed by GN. Cot. 29 (17.36%) and GN. Cot. 27 (21.05%). G. Cot. 40 was notified highest per cent of boll damage (25.21%). The lowest boll damage due to american bollworm was found in GSB 39 (5.49%). The GN. Cot. 29 (6.22%), GN. Cot. 27 (6.89%) and G. Cot. 40 (7.98%)

were recorded higher boll damage than the GSB 39. The green boll damage due to spotted bollworm was observed lowest boll damage GSB 39 (2.15%) within all the varieties. Among different varieties, the lowest boll damage due to tobacco caterpillar was recorded in GSB 39 (4.04%) followed by GN. Cot. 29 (4.92%), GN. Cot. 27 (5.26%) and G. Cot. 40 (6.13%).

## 23

**Title**: Evaluation of Planting Dates Effect to Reduce the Risk of Cotton Leaf Curl Disease in Field Conditions.

**Author**: Nargis Shah, Jamal-U-Ddin Hajano, Manzoor Ali Abro and Abdul Mubeen Lodhi

**Imprint**: J. *Micro. Sci.* Vol. 4(2), 115-123, 2025 https://doi.org/10.38211/jms.2025.04.128

**Abstract**: Cotton leaf curl disease (CLCuD) is one of the most destructive diseases significantly constraining the growth and output of cotton. Despite cultivation of resistant genotype against CLCuD is emphasized and is easily adoptable strategy for managing the disease in cotton crop throughout the world. But due to unavailability of resistant sources and resistant breaking potential of the virus there is need to consider alternate management approaches for CLCuD management. Therefore, the aim of this study was to determine the effects of various sowing times of different cotton genotypes on CLCuD intensity. In a two-year field study four cotton genotypes such as Bt. CRIS-671, Bt.CRIS-673, CRIS-585 and CRIS-613 were evaluated at different planting dated i-e, 1st April, 15th April 1st May and 15th May in split plot randomized complete block design. CLCuD incidence, severity and vector population were assessed at 30-day intervals after sowing (DAS). Disease index and Area Under the Disease Progress Curve (AUDPC) were computed and statistically analyzed using LSD at $\alpha = 0.05$. Results indicated a significant difference among the various sowing dates during both years of the study. Infection due to CLCuD also varied significantly among genotypes. There was less disease incidence on 1st April planted cotton as compared to late sown cotton (1st & 15th May). Maximum CLCuD incidence 100% was recorded in late planting at 120 days after sowing in CRIS-613 and Bt. CRIS-713 both the year of study. Bt. CRIS-671 consistently exhibited lower disease severity and AUDPC values compared to other genotypes. The least severity was observed when Bt. CRIS-671 was sown on April 15th (S2). Significantly lower AUDPC values 360000 and 367550 were determined in Bt. CRIS-671 at 15th April (S2) during 2019 and 2020, respectively. In contrast, late sowing dates (May 15th, S4) resulted in higher disease severity and AUDPC values, especially in CRIS-613 and Bt. CRIS-673. Statistical analysis confirmed significant differences in disease progression across sowing dates and genotypes, highlighting the importance of optimal sowing dates for managing CLCuD. Whitefly populations were also lowest in Bt. CRIS-671 and Bt. CRIS-673 when sown early (April 1st and April 15th). From the present study it is concluded that early planting on 1st April resulted with minimum disease and is suggested for including in the disease management strategy.

## PLANT BREEDING AND GENETICS

### 24

**Title**: Cultivation of Oil-Producing Cotton Varieties.

**Author**: Xiaojing Yang, Tianze Zhang

**Imprint**: Molecular Soil Biology 2025, Vol.16, No.3, 114-125

**Abstract**: The main purpose of this study is to figure out how to make cottonseeds contain more oil and better oil quality. We started from several aspects, such as genetic improvement, molecular technology, field management and environmental factors. The study found that if we make full use of the genetic differences of different cotton varieties, combined with traditional breeding, gene markers and genetic engineering technology, we can effectively increase the content of cottonseed oil and make the fatty acid composition of the oil more reasonable. The management method in the field is also critical. For example, how much water is irrigated, how much fertilizer is applied, and how dense the cotton is planted, all of which will affect the yield of cottonseed and the quality of oil. We also found that if some specific genes (such as *GhSWEET42*) are expressed more, the cottonseed can grow larger and contain more oil. This is very helpful for future genetic breeding. The interaction between the environment and genes will also affect the stability and genetic effect of oil. This study provides theoretical support and practical methods for the future breeding of high-oil cotton varieties and the realization of large-scale production.

### 25

**Title**: Phylogenetic Relationships of Tetraploid Cotton Species (Gossypium L.) and Their Genetic Potential for Breeding Programs.

**Author**: Feruza U. Rafieva, Ozod S. Turaev, Abdulqahhor Kh. Toshpulatov,

**Imprint**: This is a preprint; it has not been peer reviewed by a journal. https://doi.org/10.21203/rs.3.rs-6959594/v1, This work is licensed under a CC BY 4.0 License

**Abstract**: Gossypium mustelinum Miers ex Watt is a rare, wild tetraploid cotton species native to northeastern Brazil, yet its phylogenetic relationships with cultivated cottons (G. hirsutum and G. barbadense) and its genetic potential for breeding remain largely unexplored. This study aimed to investigate the cross-compatibility and molecular phylogenetic relationships between G. mustelinum and several accessions of G. hirsutum, G. barbadense, and G. darwinii to assess its utility as a genetic resource for cotton improvement. Interspecific hybridizations resulted in 22 distinct F1 combinations, showing varied cross-compatibility and reciprocal differences suggesting cytoplasmic or unilateral incompatibility. Notably, the G. hirsutum subsp. glabrum var. marie-galante × G. mustelinum cross exhibited the highest complete seed set (87.2%), despite a low boll set. F1 and F2 hybrids demonstrated significant potential for improved fiber traits. For instance, the 'Beshqahramon' variety (G. hirsutum) × G. mustelinum F1 hybrid showed a high positive heterosis for fiber length (hp = 33.00), and its F2 population had a mean fiber length of 36.2 mm with 0.62 heritability. Similarly, the 'Beshqahramon' variety × G. mustelinum F2 combination yielded the highest mean fiber yield at 41.2% with 0.61 heritability. Molecular phylogenetic analysis using 47 polymorphic simple sequence repeat (SSR) markers revealed a close relationship between G. mustelinum and G. hirsutum subsp. paniculatum (genetic distance = 0.13), and G. hirsutum subsp. glabrum var. marie-galante (genetic distance = 0.17). G. barbadense accessions and G. darwinii formed a separate cluster. Our findings confirm the distinct phylogenetic position of G. mustelinum and highlight its significant potential as a genetic resource for cotton breeding, particularly for introgression of valuable traits like enhanced fiber length and yield into G. hirsutum. The identification of promising transgressive segregants with fiber lengths of 41.0–43.0 mm and fiber yields of 40.0–51.0% provides valuable germplasm for developing new long and medium-staple cotton varieties. Further genomic studies are warranted to fully characterize its genetic potential and overcome interspecific hybridization barriers.

## 26

**Title**: Determination of Combining Ability and Heterosis of Some Cotton Crosses.

**Author**: Adel H. Mabrouk, Mohab W. El-Shazly and Badeaa A. Mahmoud

**Imprint**: JSAES 2025, 4 (3), 23-31

**Abstract**: The present study was carried out at Sakha Agricultural Research Station, Cotton Research Institute, Agricultural Research Center, Egypt, during 2023 and 2024 seasons. The results showed highly significant mean squares due to the genotypes, parents, crosses, parents vs. crosses, lines, tester and line x tester for all studied traits, except Micronair reading for the crosses and boll weight for the testers. Three crosses had the best heterosis effect over both mid and better-parent (Giza 88 x 10229, Giza 96 x

10229 and Giza 96 x Suvine) for the most studied traits. The results also revealed that the lines Giza 86 and Giza 96 were significant desirable GCA effects, while the testers Karshenky and Australy 13 had significant desirable GCA effects for most studied traits. On the other side, the cross combinations Giza 88 x 10229, Giza 89 x Karshenky, Giza 89 x Suvin and Giza 86 x C.B.58 were significant desirable SCA effects for some studied traits. Proportion contribution of lines was higher than testers contribution and lines x tester interaction for all traits studied, except uniformity index for testers. Non-additive of genetic parameters was larger than additive genetic variance with respect to all studied traits. The highest broad sense heritability estimates was observed in case of seed index with values of 88.02% and the lowest was for boll weight with value of 57.68%, while for narrow sense heritability, it was ranged from 5.26% to 17.30% for upper half mean and lint cotton yield/plant, respectively. Generally, Giza 96 and Australy13 could be used in breeding programs for improving high yielding varieties, while Giza 96 and Suvine could be considered as excellent parents for breeding programs to produce new varieties characterized with best fiber properties.

## 27

**Title**: Combining Ability and Inheritance Studies in Diallel Crosses of the Pima Cotton (*Gossypium Barbadense* L.).

**Author**: N.E. Chorshanbiev, E.A. Pardaev, S.M. Nabiev, A.A. Azimov, J.Sh. Shavkiev, A.O. Quziboev, R.R. Egamberdiev, G.K. Diyorov, O.R. Ergashev, And T.Kh. Makhmudov

**Imprint**: SABRAO Journal of Breeding and Genetics 57 (3) 900-910, 2025 http://doi.org/10.54910/sabrao2025.57.3.3

**Abstract**: The following study comprised the combining ability in parental genotypes and the inheritance of yield-related traits in F1 hybrids of the Pima cotton (Gossypium barbadense L.). The cotton cultivars, Surkhon-9 and Termiz-32, were notably the high-level donor parental genotypes in seed cotton yield and play a vital role in the development of high-yielding cotton cultivars. In all cultivars (σ2si>σ2gi), the dominant role of non-additive variances was evident in managing the seed cotton yield. Study results showed the cultivar Termez-32 can become a donor parent in developing new cultivars with numerous bolls per plant. By comparing the GCA and SCA variances of cotton cultivars, the bolls per plant reflected the control of non-additive genes (σ2si>σ2gi) in cultivars Surkhon-9, Duru Gavhar, and Surkhon-10. In cultivars Termiz-32 and Bukhoro-7, the bolls per plant had the additive genes (σ2si.

## 28

**Title**: Path Coefficient Analysis in Upland Cotton (*Gossypium Hirsutum* L.).

**Author**: M.H. JARALLAH and J.J.J. ALNUAIMI

**Imprint**: SABRAO Journal of Breeding and Genetics 57 (3) 1215-1222, 2025

**Abstract**: The following study comprised an evaluation of 21 genotypes, which includes six parental genotypes and 15 half-diallel F1 hybrids, applying the path coefficient analysis. The experiment, carried out in 2022 on upland cotton, used a randomized complete block design (RCBD) with three replications at the Musayyib Technical College of Babylon Governorate, Iraq. Path coefficient analysis enabled researchers to divide the correlation coefficient into direct and indirect effects, determining the relative contribution of each trait to seed cotton yield. The correlation analysis showed the seed cotton yield had a significant positive correlation with traits, such as the boll number, weight, ginning outturn, and seed index. The path coefficient analysis disclosed the seed cotton yield had considerable and direct effects from the ginning outturn and boll number. Correlation coefficient estimates indicated the ginning outturn contribution reached 21.12%, with the said trait becoming useful as a selection criterion to improve seed cotton yield. The coefficient contributions of the seed index and boll number were 11.49% and 8.83%, respectively, and the rest of the effects were 39.92%. The results revealed that the coefficient of determination of traits holds the highest relative importance as a major component of seed cotton yield. Breeders can use these estimates as selection criteria to enhance seed cotton yield in future breeding programs.

## 29

**Title**: Phenotypic stability of new cotton lines (Gossypium hirsutum L.).

**Author**: Valentina Dimitrova and Minka Koleva

**Imprint**: Bulgarian Journal of Agricultural Science, 31 (No 3) 2025, 531–544

**Abstract**: The genotype × environment interaction and stability of 24 advanced cotton lines and the standard cultivar Chirpan-539 were studied during 2019-2021. The years of study appeared to be different ecological environments. To evaluate the stability, different stability methods were used: the stability variances (s2 i , S2 i ) of Shukla (1972), the ecovalence (W2 i ) of Wricke (1962) and the parameter YSi of Kang (1993). The regression coefficient (bi) and the deviation from regression (S2 di) (Eberhart & Russel, 1966) were calculated only for seed cotton yield. A cluster analysis was applied to group the genotypes by phenotypic stability for the studied traits. It was found that the tested cotton genotypes significantly interacted with the environmental (years) conditions in terms of seed cotton yield, boll weigt, fiber length and lint persentage, which required their stability to be studied. Given the estimates of the parameter YSi and the overall performance based on the variantces s2 i and S2 i, and the ecovalence W2 i , the most valuable lines for the selection programs with cotton were: for seed cotton yield – 678 and 654, combining yield and stability expressed by regression and variance methods, 705 and 724, with high YSi scores due to high yields, 692, responsive to favorable environments; for boll weight – 701, 581 and 678; for lint percentage – 661, 663 and 718 and for fiber length – 724, 721 and 583, showed high average level and high stability for the relevant traits. Complex breeding value, high average level and stability, for two traits simultaneously was found in lines: 678 – for seed cotton yield and boll weight; 701 – for boll weight and lint percentage; 581 – for boll weight and fiber length. Cluster analysis very well groups genotypes by phenotypic stability and contributes to their more efficient use in breeding programs. The lines distinguished as most valuable based on the analysis of research results, formed independent smaller groups.

## 30

**Title**: Host-induced gene silencing is an effective strategy to mitigate pre-harvest aflatoxin contamination in cotton.

**Author**: Monica A. Schmidt, Shanmukh S. Salimath, Hillary L. Mehl & Kent D. Chapman

**Imprint**: Discover Plants, Volume 2, article number 218, (2025)

**Abstract**: Cotton is a globally important crop that is susceptible to fungal infections. In cotton and other crops, fungal infections can result in mycotoxin contamination, crops being tainted with fungal-produced toxic secondary metabolites. Aflatoxins, a mycotoxin produced by some *Aspergillus* species, pose a critical health issue and result in major agricultural economic losses annually in cotton. RNA interference technology that is aimed to suppress gene expression in contaminating pathogens is known colloquially as host-induced gene silencing (HIGS). This engineering strategy has been demonstrated in other crops to be an effective means to reduce or eliminate aflatoxins. We transformed cotton plants with a strong constitutive RNAi gene expression cassette that targeted the suppression of the aflatoxin-biosynthetic gene *aflC*, which encodes for a critical polyketide synthase gene in *Aspergillus* species. The three transgenic RNAi cotton lines did not display any notable agronomic differences compared to the nontransgenic counterpart cotton plants. However, when challenged with an *Aspergillus* infection, all transgenic lines displayed significant reduction, up to 99% less, in the accumulation of aflatoxin. These results show that HIGS can play a significant role in the pre-harvest alleviation of aflatoxin in cotton and this strategy could contribute to the enhancement of both global food security and safety.

## 31

**Title**: Reticulate allopolyploidy and subsequent dysploidy drive evolution and diversification in the cotton family.

**Author**: Ren-Gang Zhang, Hang Zhao, Justin L. Conover, Hong-Yun Shang, De-Tuan Liu, Min-Jie Zhou, Xiong-Fang Liu, Kai-Hua Jia, Shi-Cheng Shao, Meng-Meng Li, Chong-Yang Jin, Yi-Hui Liu, Xiao-Yi Shen, Da-Wei Li, Martin A. Lysak, Jonathan F. Wendel, Xiao-Yang Ge & Yong-Peng Ma

**Imprint**: nature communications , Published: 12 August 2025

**Abstract**: Polyploidy and subsequent post-polyploid diploidization (PPD) are key drivers of plant genome evolution, yet their contributions to evolutionary success remain debated. Here, we analyze the Malvaceae family as an exemplary system for elucidating the evolutionary role of polyploidy and PPD in angiosperms, leveraging 11 high-quality chromosome-scale genomes from all nine subfamilies, including newly sequenced, near-to-telomere assemblies from four of these subfamilies. Our findings reveal a complex reticulate paleoallopolyploidy history early in the diversification of the Malvadendrina clade, characterized by multiple rounds of species radiation punctuated by ancient allotetraploidization (Mal-β) and allodecaploidization (Mal-α) events around the Cretaceous–Paleogene (K–Pg) boundary. We further reconstruct the evolutionary dynamics of PPD and find a strong correlation between dysploidy rate and taxonomic richness of the paleopolyploid subfamilies ($R^2 \geq 0.90$, $P < 1e\text{-}4$), supporting the “polyploidy for survival and PPD for success” hypothesis. Overall, our study provides a comprehensive reconstruction of the evolutionary history of the Malvaceae and underscores the crucial role of polyploidy–dysploidy waves in shaping plant biodiversity.

# PLANT BIOTECHNOLOGY

## 32

**Title**: Assessment of genetically modified cotton GHB614 × LLCotton25 for renewal authorisation under regulation (EC) No 1829/2003 (dossier GMFF-2024-21890).

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

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

**Imprint**: EFSA J, . 2025 Aug 7;23(8):e9572. doi: 10.2903/j.efsa.2025.9572

**Abstract**: Following the submission of dossier GMFF-2024-21890 under Regulation (EC) No 1829/2003 from BASF Agricultural Solutions Seeds US LLC, the Panel on Genetically Modified Organisms of the European Food Safety Authority was asked to deliver a scientific risk assessment on the data submitted in the context of the renewal of authorisation application for the herbicide-tolerant genetically modified cotton GHB614 × LLCotton25, for food and feed uses, excluding cultivation within the European Union. The data received in the context of this renewal application contained post-market environmental monitoring reports, an evaluation of the literature retrieved by a scoping review, a search for additional studies performed by or on behalf of the applicant and updated bioinformatics analyses. The GMO Panel assessed these data for possible new hazards, modified exposure or new scientific uncertainties identified during the authorisation period and not previously assessed in the context of the original application. Under the assumption that the DNA sequences of the events in cotton GHB614 × LLCotton25 considered for renewal are identical to the sequences of the originally assessed events, the GMO Panel concludes that there is no evidence in renewal dossier GMFF-2024-21890 for new hazards, modified exposure or scientific uncertainties that would change the conclusions of the original risk assessment on cotton GHB614 x LLCotton25.

## 33

**Title**: The Expression of Cry1ac in Gossypium Hirsutum Against Chewing Insects Via Agrobacterium Mediated Genetic Transformation.

**Abstract**: Babur Ali Akbar, Muhammad Awais Arshad, Muhammad Huzaifa Mahmood, Nadia Iqbal, Muhammad Faisal, Muhammad Umar, Saba Khan, Farwah Murtaza, Shah Rukh, Muhammad Usman Hayat and Hafiz Muhammad Aftab Ayoub

**Imprint**: J Agri Horti Res, 8(1), 01-10.

**Abstract** Cotton (Gossypium hirsutum), a crop of immense global economic importance, faces substantial yield and quality losses due to insect pests such as Spodoptera exigua and Pectinophora gossypiella. Conventional pesticide strategies are increasingly unsustainable owing to environmental concerns, economic inefficiencies, and pest resistance. This study investigates the potential of cry1Ac, a gene derived from Bacillus thuringiensis (Bt), in developing insect-resistant transgenic cotton. Utilizing Agrobacterium-mediated transformation, cry1Ac was introduced into cotton under the regulation of a wound-inducible promoter (AoPR1), enabling localized expression and mitigating ecological risks associated with constitutive expression. Molecular analyses confirmed successful gene integration and expression, while bioassays demonstrated enhanced resistance, with transgenic lines achieving 80–90% pest mortality compared to negligible effects in controls. Insights into resistance mechanisms, including mutations in pest cadherin genes such as PgCad1, were explored alongside emerging RNA interference (RNAi)-based approaches for resistance management. Field evaluations corroborated the effectiveness of transgenic cotton in controlling target pests, while also identifying challenges posed by non-target pest adaptations and climatic variability. This research underscores the significance of wound-inducible promoters and integrative pest management strategies, offering a sustainable framework for developing resilient cotton varieties capable of addressing evolving pest pressures.

## 34

**Title**: Comprehensive identification of cotton EPF/EPFL receptors and functional characterization of the GhEPFL1-1-GhER1 module in drought tolerance.

**Author**: Shichang He, Huijian Sun, Qing Chen, Yanlong Yang, Zixin Zhou, Saiwen Chang, Shuaiqi Lu, Zhencai Liang, Julan Yang & Xiao fei

**Imprint**: BMC Plant Biology , Published: 11 July 2025, Volume 25, article number 901, (2025)

**Abstract**: The development of stomatal lineage cells in terrestrial plants is tightly regulated by epidermal patterning factors (EPFs/EPFLs) and their downstream receptors, including ERECTA, TOO MANY MOUTHS (TMM), and SOMATIC EMBRYOGENESIS RECEPTOR KINASEs (SERKs). These components form co-receptor complexes that activate the MAPK signaling cascade, playing critical roles in stomatal development, stress responses, and signal transduction. However, the EPF–ERECTA–TMM signaling network remains largely unexplored in cotton (*Gossypium* spp.). In this study, we performed a genome-wide identification and characterization of the *EPF/EPFL*, *ERECTA*, *TMM*, and *SERK* gene families in four cotton species (*G. hirsutum*, *G. barbadense*, *G. arboreum*, and *G. raimondii*), identifying 135 *EPF/EPFL*, 18 *ERECTA*, 6 *TMM*, and 90 *SERK* genes. Bioinformatics analyses—including gene collinearity, protein domain structure, cis-regulatory elements, and protein–protein interaction predictions—revealed functional divergence and stress-related regulatory potential across these families. Expression profiling in *G. hirsutum* indicated that several candidate genes, such as *GhEPFL1-1*, *GhER1*, and *GhSERK17*, are responsive to abiotic stresses. To validate these computational predictions, functional assays were conducted. Virus-induced gene silencing (VIGS) of *GhEPFL1-1*, *GhER1*, and *GhSERK17* led to increased stomatal density and reduced drought tolerance, confirming their roles in stress adaptation. Furthermore, luciferase complementation imaging in *Nicotiana benthamiana* demonstrated direct interactions between *GhEPFL1-1* and *GhER1*, and co-receptor complex formation with *GhSERK17*, consistent with molecular docking simulations. Collectively, this study lays a theoretical foundation for further exploration of the EPF/EPFL-mediated peptide-receptor signaling pathway in cotton and its potential application in breeding for stress resilience.

## 35

**Title**: Genome-wide characterization of *WHIRLY* genes in cotton identifies *GhWHY1-D* as a negative regulator of salt and drought stress responses.

**Author**: Shichang He, Huijian Sun, Yuguo Li, Qing Chen, Julan Yang & Fei Xiao

**Imprint**: Genetic Resources and Crop Evolution, Published: 12 August 2025

**Abstract**: WHIRLY (WHY) transcription factors are plant-specific DNA-binding proteins implicated in diverse biological processes, including organelle genome stability, development, and abiotic stress responses. However, the *WHY* gene family has not been comprehensively characterized in cotton. In this study, we identified 12 *WHY* genes across four *Gossypium* species (*G. hirsutum*, *G. barbadense*, *G. arboreum*, and *G. raimondii*), with conserved gene numbers reflecting whole-genome duplication events. Phylogenetic and structural analyses classified these genes into two major subfamilies (WHY1-like and WHY2-like), exhibiting conserved exon–intron structures and subgroup-specific motif compositions. Promoter cis-element analysis revealed distinct enrichment patterns related to stress, hormones, and light responsiveness, suggesting differential regulatory potentials. Expression profiling showed spatiotemporal divergence among *WHY* members; notably, *GhWHY1-D* was significantly downregulated under drought and salt stress. Virus-induced gene silencing of *GhWHY1-D* led to enhanced salt and drought tolerance, characterized by increased antioxidant enzyme activities, reduced ROS accumulation, and improved osmotic regulation. Protein–protein interaction predictions and 3D structural modeling further supported functional divergence between WHY1 and WHY2 subfamilies. Together, these findings provide the first integrative evolutionary and functional overview of the *WHY* gene family in cotton and identify *GhWHY1-D* as a key negative regulator of abiotic stress tolerance, with potential application in stress-resilient cotton breeding.

## 36

**Title**: Melatonin Mediates Methylglyoxal Homeostasis and Autophagy During Seed Germination Under Polyethylene Glycol-Induced Drought Stress in Upland Cotton.

**Author**: Deepika Dake , Laha Supriya , Amarjeet Kumar , Padmaja Gudipalli
**Imprint**: Physiol Plant, 2025 Jul-Aug;177(4): e70380.  doi: 10.1111/ppl.70380.

**Abstract**: Methylglyoxal (MGO), a toxic byproduct of glycolysis, acts as a signaling molecule at low levels, but its overaccumulation during drought stress disrupts redox balance and accelerates cell death in plants. Contrarily, melatonin maintains redox balance, particularly during stress. The redox status and MGO levels might differ in drought-sensitive and drought-tolerant varieties, so shall the melatonin's effect. This present study evaluated the effect of melatonin priming on MGO detoxification and autophagy during seed germination under polyethylene glycol (PEG)-induced drought stress in drought-sensitive (L-799) and drought-tolerant (Suraj) varieties of upland cotton. Melatonin priming increased endogenous melatonin content, reduced MGO accumulation and advanced glycation end-products (AGEs) and downregulated the expression of MGO biosynthesis genes in L-799 under stress. The expression and activities of glyoxalases and nonglyoxalases were upregulated, showing melatonin's effectiveness in MGO detoxification. Additionally, melatonin priming upregulated TPI1, PGK5, and PK1 expressions and downregulated HK3 expression, allowing better conversion of glucose to pyruvate, leading to reduced MGO in L-799. The downregulated expression of necrosis-related genes with reduced cell death in L-799 shows the potential of melatonin priming in maintaining cell viability under stress. Furthermore, the upregulated expression of SnRK1.1 and SnRK2.6 genes and the KIN10 protein levels confirmed improved autophagy in melatonin-primed L-799 under stress, as evidenced by enhanced autophagy markers (ATGs, MDC-stained bodies, lipidated-ATG8). Despite lowered ABA, melatonin-mediated MGO homeostasis likely activated MAPK6, thus inducing autophagy independent of ABA in stressed plants. Conversely, Suraj seedlings showed a limited response to melatonin priming under stress possibly owing to its inherent stress tolerance and higher endogenous melatonin. Overall, this study illustrates melatonin's role in regulating MGO homeostasis and autophagy under drought stress in cotton.

## 37

**Title**: 4D label-free proteomics reveals that lignin and gossypol biosynthesis are enhanced in the roots of cotton (*Gossypium hirsutum* L. cv. TM-1) seedlings after fifteen-days exposure to silver nanoparticles.

**Author**: Yuanhao Ding, Ping Li, Wenjie Lai, Yalan Li, Sihui Huang, Qiuping Zhong

**Imprint**: Plant Stress, Volume 17, September 2025, 100970

**Abstract**: Silver nanoparticles (AgNPs), the most extensively used nanomaterials, are inevitably released into the environment, yet their toxicological effects on plants remain not fully elucidated. To address a gap in the literature regarding the effects of AgNPs on cotton (*Gossypium hirsutum* L. cv. TM-1), a 15-days exposure experiment was conducted using AgNPs (10 mg/L), along with $Ag^+$ (0.4 mg/L $AgNO_3$) serving as a mock control and water as the control (CK). Compared to the $Ag^+$and CK groups, the roots of cotton seedlings exposed to AgNPs showed noticeable browning with significant reductions in biomass and root length. To explore the protein-level changes in cotton root response to AgNPs, a 4D label-free proteomics analysis was performed on the AgNPs, $Ag^+$, and CK groups. Finally, 1588 differentially expressed proteins (DEPs) unique expressed in the AgNPs-treated group, which were primarily enriched in lignin and gossypol biosynthesis pathways, as revealed by GO (Gene Ontology) and KEGG (Kyoto Encyclopedia of Genes and Genomes) analyses. Subsequent phloroglucinol staining and quantification confirmed an increased lignin biosynthesis, while LC-MS examination demonstrated elevated gossypol production in cotton roots following AgNPs exposure. Furthermore, roots from a glandless cotton mutant (*CCRI12gl*, lacking gossypol) were significant shorter than those of its wide-type counterpart (CCRI12, glandular, containing gossypol) after AgNPs treatment, suggesting that gossypol enhances cotton tolerance to AgNPs. Additionally, parallel reaction monitoring (PRM) technology validated that the expression levels of proteins involved in lignin and gossypol biosynthesis were consistent with the findings of the 4D label-free proteomics analysis. This study provides new insights into the mechanisms of plant responses to AgNPs exposure and offers a fundamental reference for investigating the toxicity of nanometal in crops.

## 38

**Title**: pseudo-GhFAD2-1 Is a lncRNA Involved in Regulating Cottonseed Oleic and Linoleic Acid Ratios and Seed Size in Gossypium hirsutum.

**Author**: Haihong Chen, Yanjun Li, XianPeng Xiong, Xuan Liu, Fei Xue, Jie Sun, Qian-Hao Zhu, Feng Liu

**Imprint**: Plant Biotechnology Journal, 2025; 0:1–23 https://doi.org/10.1111/pbi.70291

**Abstract**: Long non-coding RNAs (lncRNAs), defined as transcripts >200nt without protein-coding capacity, play crucial regulatory roles in plant growth and development. While numerous lncRNAs exist in plants including cotton (Gossypium spp.), few are functionally characterised. G.hirsutum serves as both a premier fibre crop and significant oil source, where fatty acid desaturase 2 (GhFAD2-1) is a key gene for the synthesis of polyunsaturated fatty acids in cottonseed. In this study, we confirmed that the GhFAD2-1 located on the D subgenome generated a tightly linked homologous copy through a tandem duplication event. Due to sequence divergence in the promoter and gene body following the duplication event, this homologous sequence was identified as a long non-coding RNA (lncRNA) and designated as pseudo-GhFAD2-1 (pGhFAD2-1). Knocking out pGhFAD2-1 increased linoleic acid content and reduced seed size, whereas over-expressing pGhFAD2-1 had opposite effects. pGhFAD2-1 interacts with histone deacetylase GhHDT1 and 40S ribosomal protein GhRPS12, transcriptionally recruiting GhHDT1 to suppress GhFAD2-1 expression and translationally inhibiting GhFAD2 protein synthesis by competitively binding RPS12 with GhFAD2-1 mRNA, ultimately disrupting cottonseed fatty acid biosynthesis. The impact of pGhFAD2-1 on seed size seems to be achieved through the ABA biosynthesis and signalling pathways via GhHDT1, with an increasing level of ABA leading to smaller seeds. The results expand our knowledge on the origin, function and regulatory mechanism of plant lncRNAs and provide new targets and pathways for genetic manipulation of cottonseed oil and seed size.

## FIBER AND FIBER TECHNOLOGY

### 39

**Title**: Weaving the wild: harnessing the potential of cotton relatives for superior fibre quality.

**Author**: M. Sakthipriya, A. Subramanian, N. Premalatha, S. Marimuthu & N. Chitra

**Imprint**: Genetic Resources and Crop Evolution, Published: 10 July 2025, Volume 72, pages 9147–9164, (2025)

**Abstract**: Cotton fibre plays a crucial role in yarn-based industries. With advancements in spinning technologies and the growing need for better quality fibre, attempts are being made for continuous production of superior fibre without compromising the yield. Cultivated cotton germplasms have lost their superior fibre quality traits during the process of domestication. It is imperative to understand the different traits possessed by various wild germplasms for their introgression through conventional and molecular breeding technologies to transfer superior fibre quality traits into the cultivated cotton. This review covers the exploitation of cotton wild relatives for introgression of genes for fibre quality into cultivated germplasm.

## 40

**Title**: GA suppresses the conversion from α-linolenic acid to JA through the GhGAI1-GhMYC3-GhLOX3 module to promote cotton fiber elongation.

**Author**:Xi Zhu, Qingwei Suo, Bo Ding, Jianyan Zeng, Yang Yang, Yumei Yang, Rongyu Hu, Linzhu Jiang, Silu Li, Huiming Zhang, Yi Wang, Mi Zhang, Yan Pei, Lei Hou

**Imprint**: Plant Science, Volume 360, November 2025, 112716

**Abstract**: Cotton fibers are essential raw materials for the textile industry and serve as a classical model for studying cell elongation. During the elongation phase, cotton fibers accumulate significant amounts of linolenic acid, which is an essential component of cell membranes and a key precursor for jasmonic acid (JA) biosynthesis. Although JA is known to play a critical role in fiber development, the regulatory mechanisms governing the conversion of linolenic acid to JA remain largely unknown. Our study compared linolenic acid metabolism in elongating cotton fibers with that in roots and seed coats. We discovered that JA biosynthesis from linolenic acid is specifically suppressed in elongating fibers. We further identified gibberellin as a key regulator of linolenic acid metabolism through a DELLA protein-mediated pathway. Specifically, high levels of gibberellin in rapidly elongating fibers promote the degradation of the DELLA protein GhGAI1. This degradation facilitates the interaction between GhJAZ3 and GhMYC3, a transcriptional factor of the lipoxygenase gene, *GhLOX3*, ultimately inhibiting JA biosynthesis. Our findings illuminate how gibberellin precisely balances JA suppression with high linolenic acid accumulation to drive rapid fiber elongation, offering promising targets for enhancing cotton fiber quality.

## 41

**Title**: Comparison of Fiber Quality Parameters in Cotton (Gossypium hirsutum L.) Varieties.

**Author**: Berna Büyükdereli , Fatih Kıllı

**Imprint**: Journal of Scientific and Engineering Research, 2025, 12(6):90-96

**Abstract**: This study was conducted to examine the fiber quality characteristics of 16 different cotton varieties belonging to Gossypium hirsutum L. Important quality parameters such as seed cotton yield, fiber length, fineness, strength, short fiber ratio, fiber length uniformity index, fiber elongation, and yellowness were evaluated. In terms of seed cotton yield, ES2, BA-440, and Harem-1 were among the highest-yielding varieties. ES2 achieved the highest average yield in 2018 (469.67 kg/da) and remained among the top performers in 2019 (407.19 kg/da). Similarly, BA-440 showed high yield in both years (398.30 and 366.38 kg/da), and Harem-1, despite a slight decrease in 2019, maintained relatively high performance. These results, supported by a high determination coefficient ($R^2 = 0.854$), indicate significant yield differences among varieties, mainly due to their response to environmental factors such as climate and soil conditions. Regarding fiber quality, SC2009 had the highest fiber length and should be preferred for commercial production. Fiber fineness, a parameter that directly affects quality, was lower (indicating coarser fibers) in ES2 and PG-2018. In terms of fiber strength, Lima, LYDIA, and SC2009 stood out with higher values, making them suitable for producing durable, high-quality fabrics, while ES1 had lower strength. NAZ07 and ES1 showed higher short fiber ratios, although this parameter generally does not significantly impact overall quality. SC2079 and BA119, with high fiber length uniformity index values, may provide more stable and high-quality results in yarn production. ES2 and Harem-1 also showed high fiber elongation, which is important for producing durable and flexible yarns. BA119 and ES2, with high yellowness values, indicate good brightness and suitability for yarn production, while LYDIA and Carisma, having high greyness values, could be preferred for manufacturing brighter and more visually appealing fabrics. Varieties, which have high greyness values, offer brighter and higher-quality fabrics and can be preferred.

## 42

**Title**: Harnessing GhGRDP1 natural variation for enhanced cotton seed yield: a rhamnose-dependent strategy in breeding.

**Author**:Yongyan Zhao, Hongyu Wu, Ting Zhao, Shengcai Huang, Yupeng Hao, Yidan Chen, Shouli Feng, Luyao Wang, Yumeng Zhu, Kai Huang, Jin Han, Yiqian Li

**Imprint**: Journal of Advanced Research, Available online 27 July 2025

**Abstract**: Breeding high-yield crops has long been a fundamental goal in global agriculture, with seeds serving as the essential vehicle to achieve this aim. Therefore, understanding the regulatory mechanisms of seed size is critical for ensuring food security. Objectives Our study focused on the natural variation, molecular regulatory mechanism and functional evolution of yield trait-related gene *GhGRDP1*, identified through GWAS and eQTL analyses in upland cotton natural population. Methods Population resequencing and phenotypic data analysis were combined with

competitive Allele Specific PCR, degradome, GUS staining assays, and qPCR revealed the natural variation, evolutionary history and geographic origins of *GhGRDP1*. Using CRISPR-Cas9 gene editing and plant transformation techniques, GRDP1 transgenic plants of cotton, rice and *Arabidopsis* were generated to unravel its conserved role in seed regulation. Co-IP, pull down, BiFC, LCI and enzyme activity assays were used to explore the molecular mechanism of GhGRDP1. The evolution of GRDP1 was understood through phylogenetic analysis and protein structure prediction, segmental interaction and enzyme activity assays. Results A 1-bp deletion in the eighth exon of *GhGRDP1* initiates the nonsense-mediated mRNA decay (NMD) mechanism, causing variations in seed index (SI) and lint percent (LP) among cotton populations. This variant, unique to *Gossypium hirsutum*, originated from specific races and was strongly selected during domestication. *GhGRDP1* positively regulates seed size and weight without compromising fiber quality, correlating with osmolyte accumulation in ovules. GhGRDP1 interacts with UDP-L-rhamnose synthase (GhRHM1) *in vivo* and *in vitro,* functioning as an activator of GhRHM1 enzymatic activity involved in cell wall composition. Notably, GRDP1 evolved a short glycine-rich domain (sGRD) on C-terminal throughout core angiosperms, playing a conserved role in seed development across both monocots and eudicots. Conclusion These findings significantly advance understanding the genetic basis of phenotypic variation in cotton seed yield, providing valuable targets for high-yield crop breeding.

### 43

**Title**: Characterization and Seed Priming Effect of Plant Growth Promoting Bacteria Isolated from Wild Cotton Rhizosphere.

**Author**: Moanaro Ong, Rajkumar B. K., Preeti R Parmar, H. R RRamani, Meet Dobariya, Diya Patel, Dukare Nikhil

**Imprint**: *Archives of* Current *Research International*, 2025, 25 (7), pp.837-849. ⟨hal-05187751⟩

**Abstract**: The present investigation was undertaken to explore the untapped potential of the rhizospheric bacteria associated with wild cotton, *Gossypium aridum*. All the 13 isolated rhizospheric bacterial isolates were screened for ten parameters comprising plant growth promoting (potash, phosphorus and zinc solubilization; IAA and GA3 production) and plant protection (chitinase, cellulase, and protease production; siderophore and HCN production). Four rhizospheric bacteria viz., NAU-RPM-4, NAU-RPM-9, NAU-RPM-1 and NAU-RPM-11 of wild cotton species recorded statistically significant plant growth and protection activities and thus chosen to study their seed priming effect on early cotton seedling growth of cultivated cotton (G. hirsutum). Bacterial isolate NAU-RPM-1 and NAU-RPM-11 significantly improved the growth parameters such as germination percent, shoot length, root length, fresh weight of shoot, dry weight of shoot, fresh weight of root, dry weight of root and root-shoot ratio as compared to absolute control. However, seed biopriming with NAU-RPM-4 and NAU-RPM-9 isolates also improved the early seedling growth parameters but this improvement was comparable to control. NAU-RPM-1 and NAU-RPM-11 were further characterized using 16S rDNA technique and preliminary identified as Enterobacter mori NAU-RPM-1 and Bacillus cereus NAU-RPM-11, respectively. Our results highlight the importance of rhizosphere bacteria isolated from wild cotton species (*G. aridum*) in improving the growth and resilience of cultivated cotton, especially in the context of utilizing PGPR for long-term sustainable agricultural practices.