



GLEANINGS IN COTTON RESEARCH

FEBRUARY 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. Abstract follows the citation.

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

The guidance provided by Dr H B Santosh, Senior Scientist in this venture is highly appreciated.

We duly thank The Director, Dr Y G Prasad for providing the inspiration and support for this publication.

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

*Swati Dixit
Incharge Library*

*Chetali Rodge
Technical Officer (T5)*

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1

Title: Effects of DPC on Plant Type Shaping of Cotton Under Different Plant Spacing Configurations.

Authors: ZHAI Menghua; SUN Minghui; LI Xuerui; XU Xinlong; GAO Haizhou; ZHANG Jusong

Imprint: Journal of Agricultural Science & Technology (1008-0864), 2024, Vol 26, Issue 12, p145

Abstract: Optimizing the configuration of row spacing and the dosage of 1,1-dimethyl-piperidinium chloride (DPC) in machine-picked cotton is an important means for constructing a reasonable individual and group structure for cotton and increasing yield. 'Yuanmian 11' was used as planting material and a split-plot experimental design was adopted. Under the condition of consistent density, the main plot was set with 2 plant row spacing configurations including 76 cm equal row spacing and (66 10) cm wide and narrow row spacing; the sub-plot was set with 4 doses of DPC, which were 270, 410, 550 and 690 g•hm⁻², respectively. The effects of different treatments on the growth rate of the main stem of cotton, plant structure, canopy characteristics and yield components were studied. The results showed that under the same DPC treatment, 76 cm equal row spacing mode increased the daily growth rate and internode length of the main stem of cotton, increased the angle of the lower fruit branches and the length of the upper fruit branches, reduced the length of the lower fruit branches and the angle of the upper fruit branches, and had a reasonable distribution of leaf area index in the vertical direction of the canopy, which improved the number of bolls per plant, single boll weight and seed cotton yield. Under the same planting mode, the daily growth rate of the main stem of cotton, the internode length of the main stem at various parts, and the length of the first fruit internode of the upper fruit branches were all inversely proportional to the dose of DPC. The angle of fruit branches at various parts increased first and then decreased with the increase of DPC dose. Increasing the dose of DPC could reduce the leaf area index of cotton to a certain extent. Based on the comparison and analysis of cotton plant type and yield in this experiment, it was recommended that cotton with 76 cm equal row spacing configuration mode should be sprayed with 550 g•hm⁻² DPC during the whole growth period, while cotton with (66 10) cm mode should be sprayed with 410 g•hm⁻² DPC to obtain an ideal yield. Above results provided a theoretical basis for the selection of plant row spacing configuration and the application of chemical control management measures for machine-picked cotton in Xinjiang.

2

Title: A lightweight weed detection model for cotton fields based on an improved YOLOv8n.

Author: Jun Wang, Zhengyuan Qi, Yanlong Wang & Yanyang Liu

Imprint: *Scientific Reports* volume 15, Article number: 457 (2025)

Abstract: In modern agriculture, the proliferation of weeds in cotton fields poses a significant threat to the healthy growth and yield of crops. Therefore, efficient detection and control of cotton field weeds are of paramount importance. In recent years, deep learning models have shown great potential in the detection of cotton field weeds, achieving high-precision weed recognition. However, existing deep learning models, despite their high accuracy, often have complex computations and high resource consumption, making them difficult to apply in practical scenarios. To address this issue, developing efficient and lightweight detection methods for weed recognition in cotton fields is crucial for effective weed control. This study proposes the YOLO-Weed Nano algorithm based on the improved YOLOv8n model. First, the Depthwise Separable Convolution (DSC) structure is used to improve the HGNetV2 network, creating the DS_HGNetV2 network to replace the backbone of the YOLOv8n model. Secondly, the Bidirectional Feature Pyramid Network (BiFPN) is introduced to enhance the feature fusion layer, further optimizing the model's ability to recognize weed features in complex backgrounds. Finally, a lightweight detection head, LiteDetect, suitable for the BiFPN structure, is designed to streamline the model structure and reduce computational load. Experimental results show that compared to the original YOLOv8n model, YOLO-Weed Nano improves mAP by 1%, while reducing the number of parameters, computation, and weights by 63.8%, 42%, and 60.7%, respectively.

3

Title: High plant density optimizes leaf stomatal traits for accelerating the stomatal response rate at the lower cotton canopy.

Author: Xilin Li, Xiaoming Li, Tong Zhang, Xiaofei Xue, Yunjing Dai, Zhangying Lei, Daohua He

Imprint: Crop Science, 28 December 2024, <https://doi.org/10.1002/csc2.21443>

Abstract: Plants are often exposed to fluctuating light from a few seconds to a few minutes due to cloud movements, mutual shading of leaves, and change in the angle of the sun. Slow stomatal response to fluctuating light leads to carbon loss, but the influence of planting density on light fluctuation frequency and on stomatal response and carbon gain has yet to be fully explored. To fill this knowledge gap, we investigated leaf morphology, stomatal anatomy and response rate, nitrogen content, biomass, and

yield under low density, moderate density, and high density (HD) of cotton cultivar (*Gossypium hirsutum* L.). The results showed that higher planting density significantly increased light fluctuation frequency at the lower canopy. Stomatal size significantly decreased with the increase in planting density, while total stomatal density was consistent. Stomatal density had greater plasticity of determining maximum stomatal conductance than stomatal size. Faster stomatal response rate to fluctuating light under HD was attributed to smaller and denser stomata in the abaxial leaf side. Therefore, cotton under HD treatment had faster photosynthetic induction rate under light induction, resulting in greater carbon gain. We conclude that faster stomatal response rate achieved by the optimization of stomatal anatomy, especially the abaxial side, plays a crucial role in obtaining more carbon gain, biomass, and yield under HD cotton field. This finding indicates that selecting varieties with rapid stomatal response traits and planting at appropriate densities may optimize fluctuating light use to achieve higher yields.

4

Title: Increasing exposure of cotton growing areas to compound drought and heat events in a warming climate.

Author: Shengli Liu , Wei Zhang, Tongtong Shi, Tong Li , Hui Li , Guanyin Zhou, Zhanbiao Wang , Xiongfeng Ma

Imprint: Agricultural Water Management, Volume 308, 1 March 2025, 109307

Abstract: Cotton (*Gossypium hirsutum* L.) is a critical source of natural fiber and cottonseed oil for humans, yielding substantial economic benefits globally. However, the susceptibility of cotton cultivation to compound drought and heat events (CDHEs) brings significant threats to cotton productivity. Despite this, a comprehensive assessment of global CDHE occurrence over cotton-growing areas and its potential impacts on cotton yields remains unresolved, hindering efforts to implement adaptive strategies to ensure global cotton productivity. To address this gap, we analyzed changes in mean temperature and soil moisture within global cotton-growing areas during their respective growing seasons, estimated the probability of CDHEs across multiple spatial scales via copula theorems, and examined the relationship between cotton yield anomalies and CDHEs in major cotton countries. Our results indicate increasing but divergent trends in mean temperature and soil moisture. Specifically, while most regions exhibit drying trends, India and Pakistan show significant wetting trends, with soil moisture increasing during the cotton growing season. The global average probability of CDHEs between 1961–1990 and 1991–2020 showed a more than threefold increase in severity, with such an increase occurring in approximately 61 % of cotton-growing areas due to comparable contributions from drying and warming trends. Furthermore, major cotton-producing countries exhibited similar CDHE trends, leading to a heightened probability of synchronous CDHE occurrences, except in

countries connected to India and Pakistan. Such occurrences of CDHEs are significantly related to cotton yield failures in major cotton-producing countries. Our findings emphasize the growing exposures of cotton-growing areas to CDHEs and highlight the urgent need for adaptive strategies to enhance the resilience of cotton production systems under changing climatic conditions.

5

Title: Genetic progress in cotton dry matter partitioning in Argentina.

Author: Gonzalo J. Scarpin, Pablo N. Dileo, H. Martin Winkler, Antonela E. Cereijo, Fernando G. Lorenzini, Robertino J. Muchut, Roxana A. Roeschlin, Carlos Acuña, Marcelo Paytas

Imprint: Industrial Crops and Products, Volume 225, March 2025, 120419

Abstract: The Argentinian cotton (*Gossypium hirsutum* L.) has exhibited a rate of genetic progress of $3.24 \text{ kg ha}^{-1} \text{ y}^{-1}$, resulting in an increase of 194.4 kg ha^{-1} of lint from 1965 to the present day. This improvement has been achieved alongside enhanced seed oil content without compromising lint quality. While previous studies have explored trends in cotton lint yield, lint quality, and other agronomic traits over time, no research in Argentina have focused specifically on genetic progress concerning aboveground biomass, morphological attributes, and mapping-related variables. This study aimed to: i) quantify and compare the levels of aboveground biomass, morphological and mapping-related variables in varieties utilized over the past 50 years in Argentina, and ii) estimate the genetic progress in these variables. Over a two-year period, 20 cotton cultivars were assessed across four different environments through different sowing dates. Several parameters were evaluated, including 11 biomass-related variables, six morphological-related factors, and six mapping-related traits at three different moment of cotton cycle: 50 (M1), 100 (M2), and 150 (M3) days after emergence. Significant differences were observed across genotypes, environments, and their interactions. Our findings revealed that variables such as leaf biomass (M2), reproductive branch biomass (M2, M3), first reproductive branch node (M1, M2), first reproductive branch height (M1, M2, M3), and global retention (M2) exhibited either increases or decreases on the rate of genetic progress. This study presents the first report on aboveground biomass values, morphological variables, and mapping-related parameters for Argentinian cotton. The information obtained from the work provides valuable insights into the dynamics of cotton biomass and related variables, contributing to the understanding of genetic improvement in Argentinian cotton cultivation.

6

Title: Stomata and Pollen Grains Studies of Cotton (*Gossypium hirsutum* L.) in Iraq.

Title: Stomata and Pollen Grains Studies of Cotton (*Gossypium hirsutum* L.) in Iraq.

Author: Chnar Najmaddin Fathulla, Bahar Jalal Mahmood

Imprint: Vol. 36 No. 6 (2024): Zanco Journal of Pure and Applied Sciences

Abstract: The *Gossypium hirsutum* genotypes were have been different types of stomata as anisocytic, paracytic, hemi-paracytic and tetracytic with presence in both surfaces, and found conjugated stomata. The stomata generally composed of two guard cells with ordinary epidermal cells, while some genotypes composed of one guard cell. The pollen grains were colporated, prolate, sub-prolate, and prolate-spheroidal in shaped with echinus orientation sculpture.

7

Title: Integrative physiological, biochemical, and proteomic analysis of the leaves of two cotton genotypes under heat stress.

Author: Asia Perveen, Sheheryar Sheheryar ,Fiaz Ahmad,Ghazala Mustafa,Arlindo Alencar Moura,Francisco A. P. Campos,Gilberto B. Domont,Umar Nishan,Riaz Ullah,Mohamed A. Ibrahim,Fábio C. S. Nogueira ,Mohibullah Shah

Imprint: Plos One, Published: January 9, 2025,
<https://doi.org/10.1371/journal.pone.0316630>

Abstract: Cotton (*Gossypium hirsutum* L.), a crucial global fibre and oil seed crop faces diverse biotic and abiotic stresses. Among these, temperature stress strongly influences its growth, prompting adaptive physiological, biochemical, and molecular changes. In this study, we explored the proteomic changes underscoring the heat stress tolerance in the leaves of two locally developed cotton genotypes, i.e., heat tolerant (GH-Hamaliya H_{tol}) and heat susceptible (CIM-789 H_{sus}), guided by morpho-physiological and biochemical analysis. These genotypes were sown at two different temperatures, control (35°C) and stress (45°C), in a glasshouse, in a randomized complete block design (RCBD) in three replications. At the flowering stage, a label-free quantitative shotgun proteomics of cotton leaves revealed the differential expression of 701 and 1270 proteins in the tolerant and susceptible genotypes compared to the control, respectively. Physiological and biochemical analysis showed that the heat-tolerant genotype responded uniquely to stress by maintaining the net photosynthetic rate (P_n) (25.2–17.5 $\mu\text{molCO}_2\text{m}^{-2}\text{S}^{-1}$), chlorophyll (8.5–7.8mg/g FW), and proline contents (4.9–7.4 $\mu\text{mole/g}$) compared to control, supported by the upregulation of many proteins involved in several pathways, including photosynthesis, oxidoreductase activity, response to

stresses, translation, transporter activities, as well as protein and carbohydrate metabolic processes. In contrast, the distinctive pattern of protein downregulation involved in stress response, oxidoreductase activity, and carbohydrate metabolism was observed in susceptible plants. To the best of our knowledge, this is the first proteomic study on cotton leaves that has identified more than 8000 proteins with an array of differentially expressed proteins responsive to the heat treatment that could serve as potential markers in the breeding programs after further experimentation.

8

Title: The impact of temperature on cotton yield and production in Xinjiang, China.

Author: Yongyan Zhao, Yumeng Zhu, Shouli Feng, Ting Zhao, Luyao Wang, Zhihong Zheng, Nijiang Ai & Xueing Guan

Imprint: *npj Sustainable Agriculture* volume 2, Article number: 33 (2024)

Abstract: Cotton production in Xinjiang is crucial to China's economy, but the region's cold climate poses challenges to cultivation. This study analyzes temperature data from 33 meteorological stations in Xinjiang (1981–2020) alongside cotton yield data to assess cold damage during key cotton growth stages. A comparison is made with cotton-producing counties in the U.S. southwest (Texas, Kansas, Oklahoma). Results show that Xinjiang has a shorter frost-free period (140–210 days) compared to the U.S. (235–300 days). The Pearson correlation coefficient indicates that spring cold damage (SpCD) during emergence stage significantly impacts yield. SpCD lasts 5–10 days in NXJ, 3–7 days in SXJ, and 3–4 days in the U.S. Severe cold damage, notably in 1996 and 2010, led to a 40% yield decline. To mitigate cold damage, breeding cold-tolerant cotton varieties and developing innovative cultivation technologies are critical for sustaining cotton production in Xinjiang.

9

Title: Physiological characterization of leaf-shape isolines of upland cotton.

Author: William W. Spivey, Ricardo St. Aime, Taylor Sherer, Paul Zimmerman, Vasu Kuraparthi, Sruthi Narayanan

Imprint: *Agronomy Journal*. 2025;117:e70005. [wileyonlinelibrary.com/journal/agj2](https://doi.org/10.1002/agj2.70005) 1 of 9 <https://doi.org/10.1002/agj2.70005>

Abstract: Four major leaf shapes exist in tetraploid cotton (*Gossypium hirsutum* L.): normal, sub-okra/sea-island, okra, and super-okra. The majority of upland cotton (*G. hirsutum*) varieties in the United States possess a normal leaf shape. However, the other three leaf shapes were reported to show a few production advantages such as

accelerated flowering rates, early maturity, reduced lint trash and boll rot, and increased pest resistance. In this study, we evaluated the leaf-shape isolines LA-213-okra, LA-213-normal, LA-213-super-okra, and LA-213-sub-okra for physiological traits related to yield and performance and identified the isolines associated with superior physiological mechanisms. During flowering stage, narrow leaf shape isolines, LA-213-okra and LA-213-super okra, showed 6%–19%, 0%–15%, and 3%–73% greater chlorophyll index, quantum efficiency of photosystem II, and photosynthetic rate, respectively, than the LA-213-normal and LA-213-sub-okra isolines. Further, the water use of LA213-super-okra was 12%–22% lower than that of the other three leaf shape isolines. With superior physiological performance, the okra and super-okra leaf shapes offer useful trait variation for cotton breeding and variety development.

CROP PROTECTION

10

Title: Response of Cotton Genotypes to Insect Pests Complex.

Author: Imran Nadeem, Qurban Ali , Muhammad Kamil Malik, Asad Aslam , Muhammad Faheem Akhtar , Sikander Ali , Muhammad Zubair , Kanwal Hanif , Muhammad Bilal bin Iqbal , Muhammad Jawad Saleem

Imprint: International Journal of Research Publication and Reviews, Vol 5, no 12, pp 5428-5431 December 2024

Abstract: Pakistan's agricultural sector has been the cornerstone of its economy in the past. It contributes more than 21% of GDP and employs approximately 63% of the rural population. Among the company's crops, cotton (*Gossypium hirsutum*) stands out as the main cash crop. climate change Insect outbreak and face important challenges such as water scarcity. which causes production to decrease This study assessed the resistance of 11 cotton genotypes to important insect pests. Including whiteflies, jassids, thrips, pink bollworms. and gray cotton worms using a completely random block design... We are in different genotype groups. We also assessed insect populations and invasion rates. The results indicate different levels of resistance. Some genotypes are more effective at resisting pest pressure. The findings highlight the potential of genetically modified cotton varieties to increase yields and reduce reliance on chemical pesticides. This will help promote sustainable agricultural practices in Pakistan.

11

Title: Seed-Borne Dissemination of the Cotton Bacterial Blight Pathogen Under Field Conditions and Strategies for Translational Resistance.

Author: Adepoju, Philip Oluwatowo

Imprint: University of Georgia ProQuest Dissertations & Theses, 2024. 31638696.

Abstract: The reemergence of cotton bacterial blight (CBB) caused by *Xanthomonas citri* pv. *malvacearum* (Xcm) after a multi-decade absence raises questions regarding the factors underlying its resurgence and possible reservoirs of the pathogen. This study investigated seed-borne transmission of Xcm under field conditions and explored genetic modifications strategies to enhance cotton resistance. Leave sample testing and genotyping of recovered isolates from field trials conducted over two growing seasons revealed that CBB-resistant cultivars can serve as inoculum sources for the disease. In our first genetic modification strategy, we attempt to introduce the AtEFR pattern recognition receptor (PRR) construct into cotton but genotyped 136 EFR candidate plants lack the transgene. In our second strategy to disrupt susceptibility gene expression by Xcm Transcriptionactivator-like (TAL) effectors, we introduced and confirmed mutations in GhTFIIA γ that can prevent the interaction between Xcm effector and host protein however, infertility of 2 lines with high edit efficiency hindered progress.

12

Title: Role of *Verticillium dahliae* effectors in interaction with cotton plants.

Author: Lingling Yang, Tingyuan Fu, Ruichen Sha, Guihuan Wei, Yuhe Shen, Zhen Jiao & Bing Li

Imprint: Phytopathology Research, Volume 7, article number 1, (2025)

Abstract: Cotton (*Gossypium* spp.) is grown worldwide owing to the vast economic value of its natural fiber. However, the widespread and destructive soilborne pathogen, *Verticillium dahliae*, causes Verticillium wilt, leading to severe yield losses and reduced fiber quality of cotton. The ability of *V. dahliae* to perceive and infect cotton determines the outcome of their interactions. *V. dahliae* employs diverse defense mechanisms to evade or suppress plant immunity, ultimately establishing a proliferation niche. Evading plant immunity by suppressing host recognition or successive immune signaling is a successful infection strategy employed by various microbial pathogens, posing a significant challenge to effectively utilizing host hereditary resistance genes in sustainable disease management. This review focused on summarizing “effectors” and the molecular mechanisms of various effectors on cotton

and the corresponding defense mechanisms in the plants. Furthermore, it highlighted the potential of effectors for engineering resistance cotton plants against *Verticillium* wilt, aiming to provide a reference for the creation of cotton disease-resistant germplasm resources by host genome editing and other methods.

13

Title: Efficacy of different insecticides against major sucking insect-pests infesting Bt cotton Rank.

Author: Dulera JG and Bagul GD

Imprint: International Journal of Advanced Biochemistry Research 2024; 8(9): 170-175

Abstract: A field experiment was conducted during kharif, 2023-2024 to evaluate the bio-efficacy of major sucking insect-pests infesting Bt cotton at regional research station, Anand agricultural university, Anand, Gujarat. Among evaluated different insecticides dinotefuran 20% SG, clothianidin 50% WDG and tolfenpyrad 15% EC were most effective in reducing leafhopper and aphid population while, acetamiprid 20% SP, spiromesifen 240 SC and afidopyropen 50 gL⁻¹ DC were most effective for whiteflies, whereas clothianidin 50% WDG, fipronil 5% SC and tolfenpyrad 15% EC significantly reduced thrips population. The highest cotton yield was recorded from the treatment dinotefuran followed by clothianidin and tolfenpyrad. Looking to the ICBR dinotefuran provided the highest return (1:11.34), followed by acetamiprid (1:10.29) and acephate (1:8.23).

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Title: Cotton stalk management and a cover crop produce minimal effects on cotton leafroll dwarf virus.

Author: Samuel Frazier, Steven M. Brown, Quentin D. Read, Alana L. Jacobson, Kassie Conner, Cesar Escalante, Kipling S. Balkcom

Imprint: Agronomy Journal. 2025;117:e70002. wileyonlinelibrary.com/journal/agj2 1 of 19 <https://doi.org/10.1002/agj2.70002>

Abstract: In 2017, cotton (*Gossypium hirsutum* L.) leafroll dwarf virus (CLRDV) was first reported in the United States. One CLRDV inoculum source includes the previous year's cotton stalks; hence, destroying cotton stalks could be effective for CLRDV management. However, tillage-intensive stalk destruction methods (SDMs) can degrade southeastern soils, but a cover crop may provide short-term benefits and reduce CLRDV incidence. Therefore, we examined three SDMs (Tillage, Pull, Mow) across two cover crop levels (no cover and rye [*Secale cereale* L.]/clover [*Trifolium incarnatum* L.]

mixture) and two cotton varieties to determine how cotton growth, soil penetration resistance (PR), and two CLRDV incidence sample times (pre-harvest and post-harvest) were affected across six environments during the 2021 and 2022 growing seasons. None of the SDMs affected any factors examined in this experiment, except soil PR and cotton yield. The Pull and Mow SDMs both increased soil PR compared to the Tillage SDM. An 8% yield increase (Pull > Mow) was observed, but the Tillage SDM yield did not differ from Pull or Mow SDMs. The rye/clover mixture also increased soil PR. Although cotton stands were 15% greater with no cover crop, subsequent cotton yield and fiber quality were minimally affected by cover crops. The rye/clover mixture increased post-harvest CLRDV incidence, and cotton yields were equal between cover crops. Pre-harvest CLRDV incidence probability was 0.23, but post-harvest CLRDV incidence probability was 0.71. Continuing to identify and evaluate cultural practices that reduce CLRDV incidence is imperative to prevent negative impacts.

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Title: Fungicide sensitivity in *Phymatotrichopsis omnivora*, causal agent of cotton root rot.

Author: Maxwell Sturdivant and Thomas Isakeit

Imprint: APS, Published Online: 2 Jan 2025 <https://doi.org/10.1094/PHP-11-24-0108-RS>

Abstract: Cotton root rot (CRR), caused by the soilborne fungus *Phymatotrichopsis omnivora*, is a disease that significantly impacts cotton production in much of Texas. Currently, the only economically feasible control measure is a flutriafol fungicide application at or near the time of planting, either as a Topguard Terra or Xyway LFR formulation. Although this control measure has been used for over a decade, there has not been an assessment of baseline sensitivity in *P. omnivora* populations to Topguard Terra, or an assessment of efficacy of newer fungicide products. In this study, growth inhibition of 11 isolates of *P. omnivora* from three different Texas locations were evaluated on agar in the presence of the fungicides Topguard Terra, Provysol (mefentrifluconazole), and Fontelis (penthioapyrad), as well as the technical grades of the active ingredients. The active ingredient concentrations of the trade formulations tested ranged from 0.001 – 100 µg/ml. The average concentration that inhibited growth by 50% (EC₅₀) was 6.13x10⁻⁴ µg/ml for flutriafol (Topguard Terra), 1.18x10⁻³ µg/ml for mefentrifluconazole (Provysol), and 0.26 µg/ml for penthiopyrad (Fontelis). These results indicate that Topguard Terra and Provysol are most effective in inhibiting *P. omnivora* hyphal growth in vitro, and that there is no evidence to date of reduced sensitivity to flutriafol fungicides in *P. omnivora* populations.

Title: Natural incidence pattern of cotton pink bollworm, *Pectinophora gossypiella* (Saunders) larval parasitoids across India.

Author: S. Rakhesh, S.S. Udikeri , V. Chinna Babu Naik and T. Prabhulinga

Imprint: J. Environ. Biol., 2025 Volume 46 Issue 1 January 2025 pp. 77-86 DOI: <http://doi.org/10.22438/jeb/46/1/MRN-5403>

Abstract: Aim: To identify natural incidence pattern of pink bollworm larval parasitoids across different cotton growing zones in India. Methodology: Green bolls of cotton were collected from farmers field across India encompassing Northern, Central and Southern regions of cotton cultivation. In total 59 locations were selected for sampling and from each cotton field, five hundred matured green bolls were collected, packed and transferred to laboratory at CICR, Nagpur. Dead/inactive larvae were placed individually in plastic tubes under controlled laboratory conditions to monitor parasitoid emergence. Percent parasitization and parasitoid emergence were calculated accordingly. Results: The pink bollworm larval recovery varied among locations, with the highest average recovery and parasitised larvae observed in the Northern zone (480.50 and 12.10 larvae). Additionally, the average parasitization rate was higher in the Northern cotton zone (2.46 %) compared to the Southern (2.16 %) and Central zones (1.70 %). In terms of parasitoids, the Southern zone exhibited the highest average number of *Bracon lefroyi* (9.17 ± 3.59) with a range of 3.0-17.0 parasitoids, while the Northern zone recorded the highest average number of *Apanteles angaleti* (9.70 ± 2.83) with a range of 6.0-15.0 parasitoids. Interpretation: The natural parasitization of pink bollworm larvae by *Bracon lefroyi* and *Apanteles angaleti* ranged from 0.43 to 4.33 per cent across various cotton-growing zones. This natural occurrence presents a hopeful strategy for controlling pink bollworm populations, potentially reducing the need for chemical interventions and minimizing crop damage.

Title: The Story of the Pink Bollworm, *Pectinophora gossypiella* (Saunders) on Cotton.

Author: Rakhesh S , Udikeri S S , Mahamed Ashiq and Akarsh S V

Imprint: Annual Research & Review in Biology Volume 39, Issue 12, Page 199-206, 2024.

Abstract: Cotton, a vital commercial fibre crop, is prone to heavy infestations by insect pests, with bollworms being the most damaging globally. *Helicoverpa armigera* and other Heliiothines have developed significant resistance to conventional insecticides, rendering cotton cultivation uneconomical in many regions by the mid-1990s. The introduction of Bt cotton, expressing Cry1Ac toxins, marked a breakthrough in

bollworm management, drastically reducing pesticide usage and increasing yields. However, resistance to Cry toxins, particularly Cry1Ac, emerged over time, as first reported in pink bollworm (*Pectinophora gossypiella*) in Gujarat, India, by 2010. Factors contributing to resistance include mutations in genes such as PgCad1, ABC transporters, and others. Additionally, declining toxin expression in Bt cotton hybrids and improper pest management practices exacerbate resistance. Integrated pest management strategies, such as timely sowing, field sanitation, pheromone traps, and mating disruption tools, have been recommended to mitigate resistance. Recent data show an increase PBW infestations in North India, which is being driven by factors like shorter cotton seasons and little prior exposure to Bt toxins. Studies focusing on genetic and phenotypic polymorphism in Indian PBW populations have emphasized the need for sustainable resistance management. Adopting dual-toxin Bt cotton (Cry1Ac + Cry2Ab) and stringent IRM strategies remain critical to preserving the efficacy of transgenic technology.

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Title: Establishing best practices for insect resistance management: a new paradigm for genetically engineered toxins in cotton expressing Mpp51Aa2.

Author: Dominic Reisig, Anders Huseth

Imprint: Journal of Economic Entomology, toae312, <https://doi.org/10.1093/jee/toae312>

Abstract: Debate over resistance management tactics for genetically engineered (GE) crops expressing insecticidal toxins is not new. For several decades, researchers, regulators, and agricultural industry scientists have developed strategies to limit the evolution of resistance in populations of lepidopteran and coleopteran pests. A key attribute of many of these events was insecticide resistance management (IRM) strategies designed around a presumed high-dose expression sufficient to kill 99.5% of exposed larvae for some of the main target pests in corn, *Zea mays* L. and cotton, *Gossypium hirsutum* L. In contrast, other target pests did not meet this high-dose criterion. Similarly, the recent release of ThryvOn cotton that expresses thysanopteran and hemipteran active Mpp51Aa2.834_16 toxin is not high dose, working on a combination of behavioral and sublethal effects to suppress populations. This unique mode of control has generated considerable uncertainty about what IRM strategies will be most effective to limit field-evolved resistance to this unique spectrum of pests. The goal of this manuscript is to present several knowledge gaps that exist in proposed Mpp51Aa2 IRM plans, focusing on its activity on thrips, *Frankliniella* spp. Addressing these gaps will be crucial to limit resistance and preserve the benefits that this technology may provide by alleviating reliance on conventional insecticides and seed treatments. Broadly, these considerations will be important for future GE events that are non-high dose but remain valuable components of a more holistic insect

management programs that integrate multiple tactics to reduce conventional insecticide use for challenging pests.

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Title: Divergent *Cotton leaf curl Multan betasatellite* and three different alphasatellite species associated with cotton leaf curl disease outbreak in Northwest India.

Author: Kajal Kumar Biswas ,Nenavath Balram ,Marimuthu Elangovan,Supratik Palchoudhury,Utpal Kumar Bhattacharyya,Halima Khatoon,Shilpi Aggarwal,Shruti Godara,Pradeep Kumar,Satish Kumar Sain,Rupesh Arora,Sibnarayan Datta

Imprint: Plos One, Published: January 9, 2025,
<https://doi.org/10.1371/journal.pone.0313844>

Abstract: Cotton leaf curl disease (CLCuD) is a major constraint for production of cotton (*Gossypium* sp.) in Northwest India. CLCuD is caused by a monopartite, circular ssDNA virus belonging to the genus *Begomovirus* in association with betasatellites and alphasatellites, and transmitted by a whitefly vector (*Bemisia tabaci*). To explore the genetic variability in betasatellites and alphasatellite associated with the CLCuD-begomovirus complex in Northwest India. A survey was conducted for successive three years of 2014 to 2016 and twig samples from symptomatic and healthy cotton plants randomly were collected. Total plant DNAs were isolated, subjected to rolling circle amplification (RCA), cloning and sequencing. Full-length genome of 12 betasatellites and 13 alphasatellites, those were obtained in the present study, were analyzed. Sequence analysis showed that all the present betasatellites shared 85–99 percent nucleotide identity (PNI) among themselves and 84–95 PNI with other members of *Cotton leaf curl Multan betasatellite* (CLCuMB) and fell into one genogroup along with CLCuMB. But in close observation the present betasatellites clustered into two phylogenetic subgroups under single CLCuMB. The present alphasatellites showed 72–100 PNI among themselves and fell under three alphasatellite species, *Gossypium Darwinii symptomless alphasatellite* (GDarSLA), *Cotton leaf curl Multan alphasatellite* (CLCuMA) and *Cotton leaf curl Burewala alphasatellite* (CLCuBuA). In the recombination analysis, all the present betasatellites and alphasatellites were found to be recombinants involving intra species recombination in betasatellite, and interspecies recombination in alphasatellite species. The present study indicated that the betasatellite and alphasatellite molecules associated with CLCuD-begomovirus complex in Northwest India are genetically diverse.

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Title: Evaluating the impact of biogenic nanoparticles and pesticide application in controlling cotton leaf curl virus disease (CLCuD) in cotton (*Gossypium hirsutum* L.)

Author: Ercişli S.

Imprint: Chemical and Biological Technologies in Agriculture, vol.10, no.11, pp.1-17, 2024 (SCI-Expanded)

Abstract: Background Cotton leaf curl virus disease (CLCuD) is one of the major concerns for cotton growers. The traditional approach to managing CLCuD involves the control of the vector (whitefly) population through the use of pesticides. This study compares the efficacy of zinc oxide, iron oxide, copper and silver nanoparticles with conventional pesticides. Nanoparticles dose was optimized by evaluating their phytotoxic threshold in our previous study. In this study, optimized doses of nanoparticles such as zinc oxide (100 ppm), iron oxide (50 ppm), copper (50 ppm) and silver nanoparticles (25 ppm) were applied in a field trial of cotton against cotton leaf curl virus disease (CLCuD). Morphological parameters (height of stem, monopodial branches, sympodial branches, staple length, boll weight and number of bolls), yield parameters (seed cotton yield and ginning outturn), chlorophyll content (chlorophyll a, chlorophyll b, carotenoids and total chlorophyll), biochemical parameters (superoxide dismutase (SOD), peroxidase (POD), ascorbate peroxidase (APX), catalase (CAT), hydrogen peroxide (H₂O₂) and electrolyte leakage) and disease parameters (reduction infection, disease severity and disease incidence) were determined in this study. Results The incidence of cotton leaf curl virus was confirmed by triple antibody sandwich-enzyme-linked immunosorbent assay (TAS-ELISA). The pesticide Imidacloprid significantly reduced the infection by 79.3%. However, in comparison to pesticide, application of nanoparticles also reduced the infection. ZnO NPs reduced the infection by 42.33%, FeO NPs by 41%, Cu NPs by 34.7%, and Ag NPs by 44.8%. Moreover, these nanoparticles also improved the plant growth parameters as compared to control treatment. ZnO NPs enhanced morphological, yield parameters, and chlorophyll content by 36%, 22%, and 29%, respectively. FeO NPs showed improvements by 38%, 21%, and 29%; Cu NPs 39%, 25%, and 29%; and Ag NPs 31%, 19%, and 18%, respectively. Conclusion Although treatment pesticide showed the least disease incidence compared to nanoparticles, nanoparticles are eco-friendly and safe as compared to pesticides. Farmers can apply these nanoparticles at their optimal thresholds through foliar application as an alternative to traditional pesticides. It is concluded that nanocomposites and hybrid modes may be used for managing CLCuD efficiently in the future.

Title: Exploring the differences in traits and genes between brown cotton and white cotton hybrid offspring (*Gossypium hirsutum* L).

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

Imprint: *Planta*, Volume 261, article number 35, (2025)

Abstract: Brown cotton and white cotton are two important raw materials used in the cotton fiber industry. Clarifying the differences in morphology, agronomic traits, and fiber pigments between these varieties can facilitate the implementation of corresponding cultivation and breeding techniques. Therefore, we obtained F₂ generation brown cotton plants through hybridization and compared them with their parents. In terms of agronomic traits, plant morphology and leaf shape were similar, but brown cotton presented more villi on the main stem. The first fruiting branch node was within the range of 4–6 cm, and the first fruiting branch node height was greater than that of TM-1, i.e., between 13.25 cm and 22.79 cm, with no difference compared with that of P26. The plant height was greater than that of the parents, and the number of bolls was essentially the same as that in TM-1 and greater than that in P26. The lint percentage and average fiber length were lower in TM-1 than in P26, and the seed index was greater than that in TM-1 and P26. Pigment measurements revealed that the chlorophyll a content in brown cotton during the boll stage was lower than that in white cotton, and the content of proanthocyanidin in the cotton fibers was greater in brown cotton than in white cotton. At 15 days after pollination, the highest content was 159.8 mg/g. To determine the differences in gene expression levels, we conducted transcriptome sequencing. Gene Ontology (GO) analysis revealed that the differentially expressed genes (DEGs) were enriched in pathways related to the cell wall and enzyme activity, whereas Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis revealed that the DEGs were enriched in flavonoid synthesis pathways. Transcription factor analysis revealed that the expression of the MYB3 transcription factor (Ghir_D07G002110) was higher in brown cotton, and bioinformatics analysis revealed that this gene has regulatory effects on the *CHS*, *CHI1*, and *F3H* genes.

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Title: Interspecific Hybridization between *Gossypium hirsutum* (American Cotton) and *Gossypium barbadense* (Egyptian Cotton) for Quality Improvement.

Author: Md Ruhul Kuddus Joha , Mst Tanjina Shahnaj Turin , Nusrat Jahan , Md.Naimur Rahman and Khalid Syfullah

Imprint: Asian Journal of Research in Crop Science Volume 10, Issue 1, Page 51-61, 2025

Abstract: Cotton (*Gossypium* spp.) is a globally important cash crop, valued for its fiber and economic contributions to the textile industry. This study investigated the variability, heritability, and genetic advance of yield-related traits in interspecific hybrids of American (*G. hirsutum*) and Egyptian (*G. barbadense*) cotton. Using a randomized complete block design, 28 hybrids were evaluated for traits such as seed cotton yield, plant height, bolls per plant, and boll weight. Significant genetic variability was observed among hybrids, with high heritability estimates for seed cotton yield (96.84%), plant height (93.51%), and bolls per plant (76.44%), coupled with moderate genetic advance, suggesting additive gene action. Regression analysis revealed that the number of bolls emasculated and pollinated significantly influenced total seed production, with coefficients of determination (R^2) of 0.5924 and 0.5102, respectively. The hybrid JA-08/A \times JA-12/203 demonstrated superior crossability (100%) and seed production, making it a promising candidate for breeding programs. These findings emphasize the potential for exploiting genetic variability and hybrid vigor to develop high-yielding and high-quality cotton varieties.

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Title: GhWRKY207 improves drought tolerance through promoting the expression of *GhCSD3* and *GhFSD2* in *Gossypium hirsutum*.

Author: Gaofeng Zhang, Weichao Li , Tong Han , Tianyi Huang , Lirong Sun , Fushun Hao

Imprint: Plant Science, Volume 352, March 2025, 112392

Abstract: Tryptophan-arginine-lysine-tyrosine (WRKY) transcription factors are essential regulators of drought tolerance in multiple plants. However, whether and how GhWRKY207 modulates cotton response to drought stress is unclear. In this study, we determined that *GhWRKY207* expression was high in leaves and induced by drought stress. The gene encoded a nuclear protein that had transcriptional activation activity. Silencing *GhWRKY207* by virus-induced gene silencing (VIGS) caused significant reduction in drought tolerance of cotton plants. Consistently, overexpression

of *GhWRKY207* in *Arabidopsis thaliana* wild type (WT) plants clearly enhanced their drought tolerance. Moreover, *GhWRKY207* VIGS plants had notably increased malondialdehyde (MDA) contents, electrolyte leakage percentages and O_2^- accumulation rates whereas *GhWRKY207* overexpression lines showed markedly decreased levels of the three parameters compared to their corresponding controls under water deficit conditions. Additionally, *GhWRKY207* enhanced superoxide dismutase (SOD) activity by directly activating the expression of *GhCu/Zn-SOD3* (*GhCSD3*) and *GhFe-SOD2* (*GhFSD2*) genes. Silencing *GhCSD3* or *GhFSD2* also markedly reduced drought tolerance of cotton plants. Taken together, these results suggest that *GhWRKY207* positively regulates drought tolerance by inducing the expression of *GhCSD3* and *GhFSD2* in *Gossypium hirsutum*.

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Title: Evaluation of Cotton Germplasm (*Gossypium* spp.) for Resistance to Endemic Diseases in the Southeast United States.

Author: Beasley, Edward Donald

Imprint: University of Georgia ProQuest Dissertations & Theses, 2024.

Abstract: Cotton (*Gossypium* spp.) is a globally important crop valued for both its lint fiber and seed, with significant economic impact in the United States. The *Gossypium* genus includes over fifty species, highlighting profound genetic diversity. Upland cotton, *G. hirsutum*, is the predominant species grown in the United States. In cotton breeding, phenotypic selection has heavily focused on traits like fiber quality and lint yield, which has led to a gradual decline in genetic diversity within cultivated gene pool. The decrease in genetic diversity has hampered breeding for disease resistance, emphasizing the need to incorporate diverse germplasm into breeding programs to maintain a robust cotton gene pool. This study evaluated a large diverse selection of germplasm for resistance to endemic diseases including fusarium wilt (*Fusarium oxysporum* f. sp. *vasinfectum*), target spot (*Corynespora cassiicola*), and areolate mildew (*Ramulariopsis* spp.). Multi-year screening identified valuable sources of disease resistance among elite breeding lines, obsolete varieties, and wild accessions. The results from this study offer new knowledge about cotton germplasm regarding sources of disease resistance in cotton, providing cotton breeders tools to enhance cotton resilience, and discovering genes related to pathogen resistance.

Title: Cobalt-60- Γ -Radiation Effect on Morpho-Yield and Earliness Traits in Colored Cotton (*Gossypium Hirsutum* L.).

Author: A. Azimov, J. Shavkiev, S. Nabiev, S. Khamdullaev, S. Pulatov , O. Omonov And Z. Rajabov

Imprint: SABRAO Journal of Breeding and Genetics 56 (6) 2248-2259, 2024

Abstract: Cotton plant is a valuable technical crop grown in various regions of the world. For assessing the five colored cotton (*Gossypium hirsutum* L.) genotypes, the yield contributing traits received ^{60}Co γ -ray irradiation at 0 (control), 100, 150, and 200 Gy. By treating colored cotton cultivars with 100 and 200 Gy rays, variations were visible in early maturity properties. An enhancement in bolls per plant were evident when treating the cream-colored cotton genotypes; however, a decrease occurred in the green-colored cotton genotype. Notably, the colored fiber genotypes treated with 200 Gy ray showed an increased number of bolls per plant. Colored fiber genotypes treated with 200 Gy ray caused a slight fiber elongation than with lower doses of 100 and 150 Gy and the control. The result further revealed cotton genotypes treated with 100 and 200 Gy rays positively affected the yield-contributing traits. The above properties can be beneficial in the selection and improvement of colored fiber cotton genotypes.

Title: Comparative analysis of inheritable and modified variations induced by gamma irradiation in the first and second generation of cotton varieties Ganja-160, Ganja-182 and Ganja-183.

Author: E.S. Jafarov , A.A. Tagiyev , I.Ch. Zeynalova ,M.Z. Velijanova , A.E. Jafarov

Imprint: International Journal of Biology and Chemistry 17, № 2 (2024)

Abstract: The main goal of the conducted research was to obtain cotton genotypes resistant to extreme environmental factors and various diseases, since high doses of γ -irradiation is a mutagenic factor. At the initial stage, before sowing, 1100 samples of plants whose seeds were treated with γ -rays in different doses were cultivated (in four parallel versions), the characteristics of the growing plants were studied, and the plants with changed signs were identified. At the end of the growing season, the raw cotton of 850 plants was collected by individual sampling and the transformed and untransformed plants in M1 were separated, their seeds were collected individually, stored and used for sowing as a family in the next planting (in M2). Changes in vegetation duration, main stem height, number of sympodial branches and number of

bolts per bush of both M1 and M2 lineages were evaluated as the main criteria for determining the effectiveness of the mutation. In addition, the main economic characteristics and quality indicators such as the productivity of a bush, fiber yield, and fiber length, mass of raw cotton per boll were determined. It became clear

that radiation can create certain changes in the first generation of all three varieties, some of which can be preserved in the second generation. In order to clarify whether the changes observed in the I and II generations are genetic (mutagenic) or just modification changes, the listed parameters are also planned to be studied in the next generations of plants.

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Title: Comparison of yarn properties of *Gossypium hirsutum* and naturally colored *Gossypium arboreum* cotton.

Author: Syeda Hafsa Hassan , Tanveer Hussain , Zulfiqar Ali , Habib Awais

Imprint: Mehran University of Engineering and Technology 2025, <https://doi.org/10.22581/muet1982.3153>, 2025, 44(1) 60-68

Abstract: Naturally colored cotton can be a highly sustainable alternative to conventional cotton which entails huge consumption of water, energy, and chemicals in scouring, bleaching and dyeing. The objective of this study was to investigate the yarn properties of one of the most commonly grown *Gossypium hirsutum* cotton and naturally colored *Gossypium arboreum* cotton grown in Pakistan. Eighteen different samples of ring-spun yarn were developed using the two cotton types, in three different yarn counts (Ne 16, Ne 20, Ne 24), each with three different twist multipliers (TM: 4.00, 4.25, 4.50). Different yarn properties of all yarn samples were investigated as per standard test methods. Result comparisons show that tenacity and elongation of conventional cotton yarns was about 42% and 10 % higher as compared to that of colored cotton respectively. Similarly, hairiness, CVm and total imperfections of colored cotton yarns were 11%, 25% and 320 % higher as compared to conventional cotton respectively. Comparative analysis reveals that although yarns made from *Gossypium hirsutum* cotton are superior in terms of strength, elongation and uniformity. However, the properties of naturally colored *Gossypium arboreum* cotton yarn are good enough for making different textile products which do not require too high mechanical strength and uniformity such as knitwear, woven casuals, and home textiles like bed linen and curtains. It seems that the natural color genes of cotton suppress its strength and fiber length properties which reduced yarn tenacity, and increased yarn unevenness, imperfections, and hairiness.

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Title: Evolutionary dynamics of mitochondrial genomes and intracellular transfers among diploid and allopolyploid cotton species.

Author: Jiali Kong, Jie Wang, Liyun Nie, Luke R. Tembrock, Changsong Zou, Shenglong Kan, Xiongfeng Ma, Jonathan F. Wendel & Zhiqiang Wu

Imprint: *BMC Biology* volume 23, Article number: 9 (2025)

Abstract: Plant mitochondrial genomes (mitogenomes) exhibit extensive structural variation yet extremely low nucleotide mutation rates, phenomena that remain only partially understood. The genus *Gossypium*, a globally important source of cotton, offers a wealth of long-read sequencing resources to explore mitogenome and plastome variation and dynamics accompanying the evolutionary divergence of its approximately 50 diploid and allopolyploid species. Results- Here, we assembled 19 mitogenomes from *Gossypium* species, representing all genome groups (diploids A through G, K, and the allopolyploids AD) based on a uniformly applied strategy. A graph-based mitogenome assembly method revealed more alternative structural conformations than previously recognized, some of which confirmed the mitogenome structure reported in earlier studies on cotton. Using long-read data, we quantified alternative conformations mediated by recombination events between repeats, and phylogenetically informative structural variants were noted. Nucleotide substitution rate comparisons between coding and non-coding regions revealed low mutation rates across the entire mitogenome. Genome-wide mapping of nuclear organellar DNA transfers (NUOTs) in *Gossypium* revealed a nonrandom distribution of transfers in the nuclear genome. In cotton, the fate of NUOT events varied, with mitochondrion-to-nucleus transfer (NUMT) predominantly retained as short fragments in the nuclear genome, with more plastid sequences integrated into the nucleus. Phylogenetic relationships inferred using different data sets highlighted distinct evolutionary histories among these cellular compartments, providing ancillary evidence relevant to the evolutionary history of *Gossypium*. Conclusions- A comprehensive analysis of organellar genome variation demonstrates complex structural variation and low mutation rates across the entire mitogenome and reveals the history of organellar genome transfer among the three genomes throughout the cotton genus. The findings enhance our general understanding of mitogenome evolution, comparative organellar and nuclear evolutionary rates, and the history of inter-compartment genomic integration.

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Title: Identification of the MAP4K gene family reveals GhMAP4K13 regulates drought and salt stress tolerance in cotton.

Author: Qing Zeng, Fanjia Peng, Junjuan Wang, Shuai Wang, Xuke Lu, Allah Bakhsh, Yan Li, Bobokhonova Zebinisso Qaraevna, Wuwei Ye, Zujun Yin

Imprint: *Physiol Plant*, . 2025 Jan-Feb;177(1):e70031. doi: 10.1111/ppl.70031.

Abstract: Mitogen-activated protein kinase kinase kinase (MAP4Ks) are a class of highly conserved serine/threonine-protein kinases in eukaryotes. They participate in the typical MAPK cascade system and various signal transduction pathways regulating biological processes in plants, during stressful conditions. To date, genome-wide identification of MAP4Ks in cotton has not been reported. In this study, 77 MAP4K genes were identified in four *Gossypium* species. Protein characteristics, gene structures, conserved motifs and gene expression analysis were carried out. Genome-wide or fragment duplication has played an important role in the expansion of the GhMAP4K. Promoter cis-acting elements and expression patterns indicated that GhMAP4Ks are related to plant hormones (ABA, MeJA, GA, IAA, SA) and various stresses (drought, hypothermia and wound). Overexpressing GhMAP4K13 in *Arabidopsis* showed higher stem length in response to drought and salt stress. The wilting degree in virus-induced GhMAP4K13 gene silenced plants was substantially greater than wild type plants under drought and salt stress. Transcriptomic analysis showed that most differentially expressed genes were involved in the MAPK signaling pathway, carbon metabolism and porphyrin metabolism. Additionally, transgenic *Arabidopsis* and VIGS cotton showed that GhMAP4K13 was positively responsive to drought and salt stresses. This study will play an important role in understanding the function of the MAP4K gene family in response to abiotic stress in cotton.

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Title: Unveiling the Role of *GhP5CS1* in Cotton Salt Stress Tolerance: A Comprehensive Genomic and Functional Analysis of *P5CS* Genes.

Author: Hui Fang, Xin Gao , Yunhao Wu , Ke Zhang , Ying Wu , Junyi Li , Dongmei Qian, Ruochen Li , Haijing Gu , Teame Gereziher Mehar , Xinlian Shen, and Baohua W

Imprint: Posted Date: 30 December 2024, doi: 10.20944/preprints202412.2514.v1

Abstract: Proline, a critical osmoregulatory compound, is integral to various plant stress responses. The *P5CS* gene, which encodes the rate-limiting enzyme in proline biosynthesis, known as Δ^1 -pyrroline-5-carboxylate synthetase, is fundamental to these stress response pathways. While the functions of *P5CS* genes in plants have been extensively documented, their specific roles in cotton remain inadequately characterized. In this study, we identified 40 *P5CS* genes across four cotton species with diverse sequence lengths and molecular weights. Phylogenetic analysis of 100 *P5CS* genes from nine species revealed three subgroups, with *Gossypium hirsutum* closely related to *Gossypium barbadense*. Collinearity analysis highlighted significant differences in collinear gene pairs, indicating evolutionary divergence among *P5CS* genes in tetraploid and diploid cotton. Exon-intron structures and conserved motifs correlated

with phylogenetic relationships, suggesting functional differentiation. Stress-responsive elements in *P5CS* promoters suggest involvement in abiotic stress. Expression analysis under salt stress revealed differential expression of *GhP5CS* genes, with *GhP5CS1* emerging as a potential key regulator. Virus-induced gene silencing confirmed the pivotal role of *GhP5CS1* in cotton's salt stress response, as evidenced by increased salt sensitivity in the silenced plants. This study enhances our understanding of the functional diversity and stress response mechanisms of *P5CS* genes in cotton.

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Title: Genetic Analysis of F1 And F2 Generations for Early Mature, Yield and Fibre Traits in Upland Cotton (*Gosypium Hirsutum* L.).

Author: Ghulam Murtaza Channa, Zahoor Ahmed Soomro And Tanweer Fatah Abro

Imprint: Pak. J. Bot., 57(3): DOI: [http://dx.doi.org/10.30848/PJB2025-3\(34\)](http://dx.doi.org/10.30848/PJB2025-3(34))

Abstract: The Current study was conducted to genetically analysis the F1 and F2 generation for early mature, yield and fibre traits in upland cotton. During the studied parents, F1 and F2 were highly significant confirming the presence of variation among the genotypes. The parents MNH-886 and CRIS-342 recorded with highest mean performance. In F1 and F2, generally, it could be concluded that the parent IR-3701 and MNH-886 were the best combiners for many traits. The Specific Combining Ability (SCA) effects showed the excellent combinations for direct and reciprocal crosses i.e. plant height MNH-886 x CRIS-342; for no. of nodes to first fruiting branch IR-3701 x CRIS-342; for no. of days to first square MNH-886 x Bakhtawar; no. of days to 1 st flower Bakhtawar x CRIS-342; for no. of sympodia plant-1 Bakhtawar x CRIS-342; for earliness index IR-3701 x Bakhtawar; for days to 1 st open bolls MNH-886 x Bakhtawar; Boll maturation period (BMP) Sindh-1 x CRIS-342; no. of boll at 90 days MNH-886 x Sindh-1; for no. of bolls plant-1 IR-3701 x CRIS-342; for seed yield plant-1 Sindh-1 x CRIS-342; for GOT% MNH-886 x IR-3701; staple length IR-3701 x Bakhtawar. Thus, these parents, and hybrids for selection of early and yield-related traits in later generations could be utilized to the improvement of yield-related traits in short duration seasons in the cotton breeding programs under variable weather conditions for maximizing cotton production.

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Title: Exogenous overexpression of the gland development genes *G_{l2}* and *G_{l3}* creates a glandless germplasm in cotton by repressing the expression of endogenous genes.

Author: Fuyi Duan , Xiubao Hu, Peng Wu

Imprint: Industrial Crops and Products, Volume 225, March 2025, 120484

Abstract: Cotton (*Gossypium hirsutum* L.) plants and seeds contain gossypol, a toxic compound that acts as a defense mechanism against pests and diseases but also limits the use of cottonseeds. This study aimed to investigate the mechanisms involved in the synthesis of gossypol in cotton and to create a promising germplasm material to conform to the Chinese cottonseed food safety standard (gossypol content below 0.02 %) in cottonseed. *Gl₂* or *Gl₃* was overexpressed in *Gossypium hirsutum* acc. Jin668 via the 35S promoter using the Agrobacterium-mediated method, and the gossypol content in different tissues of cotton decreased by 86.52~99.99 %. This glandless phenotype resulted from the transcriptional repression of endogenous *Gl₂* or *Gl₃* due to the overexpression of exogenous *Gl₂* or *Gl₃*. Additionally, four genes involved in pigment gland development were identified, and silencing these genes resulted in a significant ($P < 0.05$) decrease in gossypol content. Furthermore, the α GP seed-specific promoter was used to overexpress *Gl₂* or *Gl₃* in cottonseed plants, and a promising germplasm material was created in which the gossypol content, specifically in the seeds, decreased by 87 %. These results demonstrate that the overexpression of *Gl₂* or *Gl₃* in cotton represses the transcription of endogenous *Gl₂* or *Gl₃*, resulting in a glandless phenotype in cotton plants via effects on the genes involved in pigment gland development. Moreover, a new cotton germplasm line with reduced gossypol levels only in seeds was developed for potential utilization in the food industry.

PLANT BIOTECHNOLOGY

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Title: Transgenic Cotton Expressing dsAgCYP6CY3 Significantly Delays the Growth and Development of *Aphis gossypii* by Inhibiting Its Glycolysis and TCA Cycle.

Author: Wenting Kong, Tingting Li, Yuan Li, Lianjun Zhang, Jingang Xie, and Xiaoning Liu

Imprint: *Int. J. Mol. Sci.* 2025, 26(1), 264; <https://doi.org/10.3390/ijms26010264>

Abstract: In our previous research, we found that CYP6CY3 not only participates in the detoxification metabolism of neonicotinoid insecticides in cotton aphid but also affects their growth and development. However, how does transgenic cotton expressing dsAgCYP6CY3 affect the growth and development of cotton aphid? In this study, we combined transcriptome and metabolome to analyze how to inhibit the growth and development of cotton aphid treated with transgenic cotton expressing dsAgCYP6CY3-P1 (TG cotton). The results suggested that a total of 509 differentially expressed genes

(DEGs) were identified based on the DESeq method, and a total of 431 differential metabolites (DAMs) were discovered using UPLC-MS in the metabolic analysis. Additionally, multiple DEGs and DAMs of glycolytic and The tricarboxylic acid (TCA) cycle pathways were significantly down-regulated. Pyruvate carboxylase (PC), citrate synthase (CS), malate dehydrogenase (MDH) enzyme activities and pyruvate content were reduced in cotton aphid treated with TG cotton. In addition, TG cotton could significantly decrease the total sugar content from the body and honeydew in cotton aphid. The above results indicated that TG cotton inhibited glycolysis and the TCA cycle, and this inhibition is consistent with previous studies showing that cotton aphid fed on TG cotton showed significantly reduced body length and weight as well as delayed molting. These findings provide a new strategy for reducing the transmission of viruses by cotton aphid honeydew, preventing fungal growth, mitigating impacts on normal photosynthesis and improving cotton quality.

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Title: CRISPR/Cas9-mediated knockout of GhAMS11 and GhMS188 reveals key roles in tapetal development and pollen exine formation in upland cotton.

Author:Juxin Hao , Lingling Chen, Chenglong Zhao, Kaikai Qiao , Ningna Wang, Jin Wang , Zhe Wang, Qiyue Ma , Conghui Shi, Shuli Fan , Qifeng Ma

Imprint: International Journal of Biological Macromolecules, Volume 293, March 2025, 139362

Abstract: The *ABORTED MICROSPORES (AMS)* gene is crucial for tapetal cell development and pollen formation, but its role in Upland cotton (*Gossypium hirsutum*) has not been previously documented. This study identified *GhAMS11* as a key transcription factor, with its high expression specifically observed during the S4-S6 stages of another development, a critical period for tapetal activity and pollen formation. Subcellular localization confirmed that *GhAMS11* was located in the nucleus. CRISPR/Cas9 knockout of *GhAMS11* resulted in pollen in viability, with mutants displaying abnormal tapetal development and defective pollen exine formation. TUNEL assays highlighted *GhAMS11*'s involvement in proper tapetal programmed cell death (PCD). Additionally, *GhAMS11* was found to activate *GhMS188* expression, as demonstrated by dual-luciferase assays and EMSA assays, with their interaction confirmed through LCI assays, yeast two-hybrid assays and GST pull down assays. Deletion of *GhMS188* led to pollen sterility, grain collapse, and impaired pollen exine formation. Thus, this research identified the bHLH transcription factor *GhAMS11*, addressing a gap in *AMS* gene research in Upland cotton, and elucidated its key regulatory role in pollen development in cooperation with *GhMS188*.

Title: Characterization of the wall-associated kinase (WAK) gene family in *Gossypium barbadense* reveals the positive role of GbWAK5 in salt tolerance.

Author: Zhiqiang Zhang, Wenyu Ma, Haijuan Wang, Zhongying Ren, Yangai Liu, Kunlun He, Fei Zhang, Wuwei Ye, Wenqi Huo, Wei Li, Xiongfeng Ma & Daigang Yang

Imprint: Plant Cell Reports, Volume 44, article number 18, (2025)

Abstract: Soil salinization is one of the main factors restricting cotton production. Although the role of the wall-associated kinases (WAKs) in plants has been extensively studied, its response to salt stress in sea-island cotton (*Gossypium barbadense* L.) has not been reported. Here, we conducted a whole-genome analysis of the WAK gene family in *G. barbadense*, identifying a total of 70 GbWAK genes, which were classified into five clades. Segmental and tandem duplication events have contributed to the expansion of the GbWAK gene family. A large number of *cis*-acting elements were predicted in the GbWAK promoter region. Through RNA sequencing, 37 GbWAKs that potentially play a role in cotton's response to salt stress were screened out, among which 10 genes with sustained up-regulated expression were confirmed by quantitative real-time PCR (qRT-PCR). GbWAK5, a member of Clade II, was significantly up-regulated following NaCl treatment and exhibited a typical WAK structure. Subcellular localization indicated that GbWAK5 is localized on the plasma membrane. Virus-induced gene silencing (VIGS) experiments revealed that the knockdown of GbWAK5 resulted in more severe dehydration and wilting in plants compared to the control under NaCl treatment. RNA-seq analysis revealed that several ion transport-related genes were down-regulated in TRV:GbWAK5 plants under salt stress, while TRV:GbWAK5 plants accumulated more Na⁺ and exhibited a higher Na⁺/K⁺ ratio compared to TRV:00 plants. These results offer a comprehensive analysis of the *G. barbadense* WAK gene family for the first time, and conclude that GbWAK5 is a promising gene for improving cotton's resistance to salt stress.

Title: Impact of Seed Halopriming on Germination, Morphological Traits, and Cry1Ac Gene Expression in Bt Cotton (*Gossypium hirsutum*) .

Author: Wenqi Shi , Binyameen Bin Shafqat , Muhammad Arif , Ayesha Fazal Nawaz , Muhammad Amir Zia , Xu Ling , Dingli Hong , Ruhong Xu and Luhua Li

Imprint: Phyton, 2025DOI: 10.32604/phyton.2025.059315 ARTICLE Tech Science Press
Published Online: 06 January 2025

Abstract: Seed priming is an effective seed pretreatment technology that enhances germination and overall crop performance by optimizing seed hydration and metabolic processes before planting. Seed quality is a critical determinant of cotton (*Gossypium hirsutum*) crop performance, influencing germination, plant vigor, and yield. This study evaluates the effects of seed priming with potassium salts (1% and 2% KCl and K₂SO₄) on germination, morphological traits, and Cry1Ac gene expression in three Bt cotton cultivars (IUB-2013, NIAB-878B, FH142) as Cry1Ac enhance the pest resistance in Bt cotton and reduce the plant's dependence on chemical insecticides. Seeds were primed for six hours, air-dried, and sown in the field. Germination rates, plant height, number of bolls per plant, boll weight, seed cotton yield, and ginning outturn (GOT) were assessed at crop maturity. Cry1Ac gene expression was quantified to explore the influence of priming treatments on transgene activity. Results demonstrated that 1% K₂SO₄ priming significantly enhanced germination and yield-related traits, with Cry1Ac expression peaking in the IUB-2013 cultivar under 1% K₂SO₄ treatment. These findings suggest that potassium-based halopriming improves cotton seedling establishment and Bt gene expression. This study addresses the critical gaps in understanding the effects of seed halopriming on morphological traits, germination, and expression of the Cry1Ac gene in Bt cotton while providing a novel eco-friendly and cost-effective halopriming approach, offering the potential to improve cotton production.

Title: Effects of Phosphorus Stress on Root System of Different Cotton Varieties at Seedling Stage .

Author: ZHAOXiaozheng, GUO Wenwen,LIYing ,ZHANGJunling , QUYanying ,CHENQuanjia,ZHENGKai

Imprint: Seed Vol.43 No.01 Jan.2024

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Title: Genome-wide analysis of Class III peroxidase (PRX) family core genes and functional mechanism of GhPRXR1-A for seed development in *Gossypium hirsutum*.

Author:Liupeng Yang , Yudie Xia, Chunmei Fei , Kashif Shahzad , Miao Niu , Juanjuan Feng, Jianjiang Ma

Imprint: International Journal of Biological Macromolecules, Volume 295, March 2025, 139529

Abstract: *Class III peroxidases (PRXs)* play critical roles in plant growth and development by oxidizing various substrates with H₂O₂. Although many *PRXs* have been identified and their roles in biotic and abiotic stress responses have extensively investigated in plants. However, functional mechanisms of *PRXs* in seed development remain poorly understood. In this study, 14, 17, 9, and 13 *PRX* core genes were identified in *Gossypium hirsutum*, *Gossypium barbadense*, *Gossypium arboreum*, and *Gossypium raimondii*, respectively. Phylogenetic analysis categorized *PRXs* core genes of cotton into five groups. Six of the *GhPRX* genes co-localized with quantitative trait loci (QTLs) associated with oil or seed size, and *GhPRXR1-A* showed significant high expression levels in developing ovules. Heterologous overexpression of *GhPRXR1-A* in *Arabidopsis thaliana* resulted in a significant increase in thousand seed weight (Col-0: 0.015 ± 0.00085 g vs. OE-*GhPRXR1-A*: 0.022 ± 0.0019 g). In addition, molecular mechanism assays revealed that *GhPRXR1-A* is directly activated by *GhGATA1* and interacts with GhNFYC4, a transcription factor of the nuclear factor Y, C subunit family that has previously been reported to mediate seed development. Collectively, these findings suggest that *GhPRXR1-A* is a regulator of seed development in *Arabidopsis* and may have similar functional role in cotton seed contributing traits.

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Title: A Comparative Study of the Technological Characteristics of Cotton Fibers from Two Types of Gins in Côte d'Ivoire.

Author: Brou Julien Kouakou, Tièba Victor Ouattara, Koffi Christophe Kobenan, Kouadio Emmanuel N'Goran, Nogbou Ferdinand Amangoua, Malanno Kouakou, N'Guessan Maxime Kouame

Imprint: American Journal of Plant Sciences > Vol.16 No.1, January 2025

Abstract: Production of this crop is experiencing significant challenges, resulting in a decline in seed and fiber quality. To address this challenge, generations of high-performance cotton plants of the *Gossypium hirsutum* L. species have been developed and are currently being commercialized. This study evaluated the impact of gin types on the agro-industrial quality of cotton in Côte d'Ivoire. To this end, cotton from the G3, R1, and R2 generations was harvested, sampled, and ginned on machines with 10 and 170 saws in the localities of Ouangolodougou, Ferkessédougou, Korhogo, M'Bengué, Boundiali, Séguéla, and Mankono, as well as at the Centre National de Recherche Agronomique CNRA) in Bouaké. The results demonstrated that cotton fibers obtained from ginning on 10-saw machines exhibited superior quality compared to those from 170-saw machines. Fiber length, fiber length uniformity, and short fiber rate exhibited the highest deviations according to gin type. The use of 170-saw gins resulted in a notable decline in quality. Conversely, micronaire index, fiber tenacity and elongation, and reflectance remained consistent across machine types. These results will enable us to more effectively regulate and advise cotton-processing factories, which primarily utilize 170-saw gins to enhance agro-industrial quality in Côte d'Ivoire. Furthermore, these results will assist breeders in incorporating them into their processes to enhance the quality of the varieties they offer to farmers.

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Title: Intraspecific Competition in a Cotton Field (*Gossypium hirsutum* L.) and its Impact on Cotton Fiber Quality in Côte d'Ivoire.

Author: Brou Julien Kouakou, Koffi Christophe Kobenan, Yao Kouadio Jacques-Edouard, Kouadio Emmanuel N'goran, N'guessan Maxime Kouame, Nogbou Ferdinand Amangoua and Malanno Kouakou

Imprint: Asian Journal of Biology Volume 20, Issue 12, Page 164-171, 2024.

Abstract: Background: In Côte d'Ivoire, cotton growing is crucial to the economy of the savannah region, accounting for 1.7% of national GDP and 7% of exports. However, yields remain insufficient due to various factors such as climate change and non-compliance with good agricultural practices. Objectives: The general objective of this study was to evaluate the effects of sowing densities on the technological characteristics of cotton fibre. Methodology: The experiment was conducted at the Station de Recherche sur le Coton in Bouaké and at the observation posts (OP) of the cotton companies (Ivoire Coton and SECO). Nine levels were studied in this factor, numbered T1 to T9. The agronomic observations covered the estimation of seed cotton yield, determination of the Seed Index, seed health, seed germination level and fat extraction and determination of oil content. The data collected from the quality tests on cotton fibre and seed were subjected to an analysis of variance (ANOVA) using R.4.0.1 software. Results: The density applied at T6 (111,111 plants per hectare) improved yield compared with the other densities. In terms of seed germinability, seeds from the T6 treatment had the best germination rate (78.67%). The highest oil content was found in treatments T3 (16.17%) and T6 (16.28%), with good Seed Index and healthy seed rates. The final oleic acid content ranged from 6.3 to 11.29%.

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Title: Combining suitable brown lint color, fiber quality, and yield in F₂ cotton hybrids.

Author :Volkan Mehmet Çınar, Aydın Ünay

Imprint: Industrial Crops and Products, Volume 224, February 2025, 119674

Abstract: Naturally colored cotton is eco-friendly because its use in textiles does not require dyeing, and textiles made from colored cotton are the best for human health. Despite their many advantages, the low yields and unfavorable quality traits of colored cotton varieties limit extensive production. Therefore, F₁ and F₂ populations of interspecific (*Gossypium hirsutum* L. × *Gossypium barbadense* L.) and intraspecific (*Gossypium hirsutum* L.) cotton hybrids were examined to develop brown-colored cotton varieties with superior traits. Gelincik and Nazilli Deve Tüyü (NDT)-15 varieties (*Gossypium hirsutum* L.) with brown-colored lint were used as female parents. The male parents included Giza-75, Bahar-82 (*Gossypium barbadense* L.), Fiona, May-455, İpek-607 and Claudia (*Gossypium hirsutum* L.) varieties with white-colored lint. According to the line × tester mating design, 12 hybrid combinations were obtained. F₁ populations had higher yield and fiber length values than their parents and F₂ populations. F₂ populations had more unfavorable color values (L: whiteness, a*: red-green, and b*: yellow-blue) than their colored parents but were superior to F₁s. The ratio of general combination ability variance to specific combination ability variance was less than 1, indicating that yield, ginning out-turn, fiber quality, and color parameters were controlled by non-additive genes. In the biplot graph, color and fiber parameters are located in the opposite direction from yield, indicating that it is difficult to develop

colored cotton with high yield and fiber quality. Among the 960 F₂ single plants evaluated, ten plants were carefully selected according to the optimization of yield, fiber quality, and color values. Based on potential diallel crosses of the ten selected plants, it was decided to begin a recurrent selection with that population. Furthermore, it was determined that F₂ seeds of Nazilli DT-15 × İpek-607 and Gelincik × Giza-75 combinations may be successfully given to farmers.

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Title: Assessment of heterosis and combining ability for fibre yield, its contributing and quality traits in *Bt* BGII upland cotton (*Gossypium hirsutum* L.) .

Author: S. S. Deshmukh, K. S. Baig and Bhaarat Sharma

Imprint: Electronic Journal of Plant Breeding, <https://doi.org/10.37992/2024.1504.107>
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Abstract: Heterosis breeding is one of the most practical and accomplishing tool for cotton improvement. In this context 32 intra-specific hybrids derived from eight lines and four testers were evaluated on multi-location to assess heterosis and combining ability for seed cotton yield and its contributing traits. Significant heterosis was observed in the crosses NH-2260 BGII × NH-2236 BGII, NH-2202 BGII × NH-2289 BGII and NH-2224 BGII × NH-2289 BGII for seed cotton yield and yield contributing characters over a better parent and best check. Combing ability analysis suggested the preponderance of non-additive gene action for most of the studied traits. The line NH-2230 BGII and NH-2260 BGII were observed to be good general combiners for seed cotton yield and its contributing traits and the tester NH-2289 BGII was identified as the best general combiner for seed cotton yield and its contributing characters, ginning outturn, lint index. The hybrid NH-22105 BGII × NH-2236 BGII exhibited a significant positive SCA effect for seed cotton yield per plant.