GLEANINGS IN COTTON RESEARCH

MAY 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
Incharge Library

Chetali Rodge
Technical Officer (T5)

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AGRONOMY, SOIL SCIENCE AND PLANT PHYSIOLOGY

1

Title: Optimization of Nitrogen Fertilization Strategies for Drip Irrigation of Cotton in Large Fields by DSSAT Combined with a Genetic Algorithm.

Author: Zhuo Yu, Weiguo Fu
Imprint: *Appl. Sci.* 2025, *15*(7), 3580; https://doi.org/10.3390/app15073580

Abstract: This study presents a hybrid modeling framework synergizing process-based crop modeling with evolutionary optimization to reconcile yield sustainability with nitrogen management in arid cotton systems. Building upon the DSSAT-CROPGRO model's demonstrated superiority over pure machine learning approaches in simulating nitrogen–crop interactions (calibrated with multi-year phenological datasets), we develop a genetic algorithm-embedded decision system that simultaneously optimizes nitrogen use efficiency (NUE) and economic returns. Field validations across contrasting growing seasons demonstrate the framework's capacity to reduce nitrogen inputs by 15–20% while increasing profitability by 8–12% compared to conventional practices, without compromising yield stability. The tight coupling of mechanistic understanding with multi-objective optimization advances precision agriculture through two key innovations: (1) dynamic adaptation of fertilization strategies to both biophysical processes and economic constraints and (2) closed-loop integration of crop physiology simulations with evolutionary computation. This paradigm-shifting methodology establishes a new template for developing environmentally intelligent decision-support systems in water-limited agroecosystems.

2

Title: Effect of Organic, Inorganic and Natural Farming Practices on Microbial Activity at Rhizosphere in Cotton and Green gram Intercropping System.

Author: Sravani Arem, Chandrashekara C. P, Potdar M. P and Geeta D. Goudar

Imprint: Journal of Advances in Microbiology Volume 25, Issue 1, Page 8-16, 2025

Abstract: A field experiment was conducted during the kharif season 2021-22 at Natural Farming Project plot - E 131, Main Agricultural Research Station, UAS, Dharwad on clayey soils to study the effect of different farming practices and foliar application of different organic liquid manures on soil microbial activity of cotton+ greengram

rhizosphere. The results revealed that maximum number of microbial populations viz., Bacteria (18.50, 59.22 and 33.83 ×105 cfu g soil-1 (cfu {colony forming unit}), fungi (4.67, 4.61 and 3.67 ×104 cfu g soil-1), actinomycetes (11.72, 9.61 and7.17 ×103 cfu g soil-1), N2 fixers (12.61, 19.61 and 17.44 ×105 cfu g soil-1) and PSM´S (6.94, 14.83 and 13.11 ×105 cfu g soil-1) at harvest stage of green gram, at 90 DAS and harvest stage of cotton was significantly found in organic farming practices. Among liquid organic manures, foliar application of Jeevamrutha @100 % recorded higher number of bacteria (21.17, 61.67 and 35.83 ×105 cfu g soil-1), fungi (5.17, 6.17 and 5.17 ×104 cfu g soil-1), actinomycetes (12.83, 10.50 and 7.00 ×103 cfu g soil-1), N2 fixers (15.67, 21.33 and 18.50 ×105 cfu g soil-1) and PSM´S (8.50, 17.00 and 15.17 ×105 cfu g soil-1) at harvest stage of green gram, 90 DAS and harvest stage of cotton. When compared with recommended package of practices, foliar application of Jeevamrutha @100 % under organic farming practices recorded higher number of bacteria (26.33, 64.00 and 36.33 ×105 cfu g soil-1), fungi (5.67, 6.67 and 5.67 ×104 cfu g soil-1), actinomycetes (13.67, 11.00 and 8.00 ×103 cfu g soil-1) and PSM´S (9.33, 18.00 and 16.33 ×105 cfu g soil-1) at harvest stage of green gram, at 90 DAS and harvest stage of cotton than all other treatments. Foliar application of vermiwash 20% recorded highest N2 fixers (23.67 and19.67 ×105 cfu g soil-1) at 90 DAS and harvest stage of cotton.

3

Title: Photosynthetic mechanism of cotton under fluctuating light field planted with different densities.

Author: Zhangying Lei, Xilin Li, Youzhong Li, Tong Zhang, Xiaoming Li,

Yanlong Yang, Yali Zhang, Daohua He

Imprint: Industrial Crops and Products, Volume 228, June 2025, 120920

Abstract: Leaves, especially in the lower canopy, experience a complex and variable light condition that determines photosynthesis and biomass accumulation. However, the photosynthetic mechanism under fluctuating light filled remains controversial. We investigated leaf morphology, stomatal anatomy, gas exchange, chlorophyll fluorescence, proteomics, biomass, and yield in one field experiment (three plant densities of cotton) and two simulation experiments (light fluctuation frequency and intensity). Field experiment indicated that higher plant density significantly reduced light intensity but increased the frequency of light fluctuation in lower canopy, and this exerted a detrimental effect on leaf photosynthesis, biomass accumulation and yield. The simulation experiments revealed that increase in light intensity led to higher photosynthetic rate (A_N) and biomass supported by enhancing leaf area, chlorophyll content, maximum photochemical efficiency, and stomatal conductance and density. Under the same light intensity, higher frequency of light fluctuation had no impact on A_N and biomass owing to consistent trait variations regarding light harvesting and conversion, and carbon gain. Proteomic data also demonstrated that photosynthetic

capacity was mainly determined by light intensity under fluctuating light field. Consequently, this study emphasizes an appropriate improvement of light intensity plays a crucial role in enhancing photosynthetic productivity and cotton yield under fluctuating light fields planted with different densities.

4

Title: Latitude, Planting Density, and Soil Available Potassium Are the Key Driving Factors of the Cotton Harvest Index in Arid Regions.

Author: Xiaopeng Yang, Wanli Yu, Qve Li, Dongdong Zhong, Jiajing He, Hegan Dong

Imprint: Agronomy 2025, 15(3), 743; https://doi.org/10.3390/agronomy15030743

Abstract: The lint harvest index (HI) of cotton is the ratio of cotton lint yield to the total aboveground biomass of cotton, which is not yet clear in arid-zone cotton areas. In 2022–2023, large-scale sampling was carried out in Xinjiang, and the HI of different variety types of cotton in Xinjiang and their key drivers were clarified using methods such as random forest modeling (RFM) and structural equation modeling (SEM). The results show that the overall cotton HI in Xinjiang ranged from 0.276 to 0.333 and 0.279 to 0.328 for the Xinluzao (XLzao) variety types, and from 0.276 to 0.333 for the Xinluzhong (XLzhong) variety types. The results of the SEM analysis show that the latitude (−0.99) and planting density (0.50), in the climatic geography factors, and available potassium in soil (0.88), in the soil nutrient factors, have the greatest effects on the overall cotton HI in Xinjiang. The key driving factors of cotton HI were found to be different among different variety types. This study aimed to clarify the HI of different variety types of cotton in arid-zone cotton and to explore its key driving factors. This was undertaken in order to provide a theoretical basis for the accurate estimation of cotton and cotton straw yields in the arid zone.

5

Title: Assessment of Adoption Levels of Recommended Cotton Cultivation Practices in Jamnagar District.

Author: Parth Vaghasiya and Amitkumar Datta

Imprint: Asian Journal of Advances in Agricultural Research, Volume 25, Issue 4, Page 22-28, 2025;

Abstract: This study investigates the assess adoption level of cotton growers in the Jamnagar district, where cotton is a major cash crop that generally yields better returns than expected despite several factors hindering profitability. A multi-stage sampling technique was used to select 120 farmers from the Jamnagar district. Primary data was gathered through structured questionnaires. The adoption levels of recommended

cotton cultivation practices were analyzed by three point scale measure and categorized in low, medium and high adoption, revealing a mean adoption index of 18.02 with a standard deviation of 1.96. The results show that majority of farmers that is 57.50% had a medium level of adoption, while education playing a key role in influencing adoption of recommended practices among cotton growers. Effective pest initiation spraying, pink bollworm management, and fungal foliar disease control have been significant barriers. Enhanced on-field demonstrations and reinforced extension services for pest control will improve adoption, leading to higher yields and increased profitability in the region.

6

Title: Delving Into Phytochemical Analysis and Antioxidant Potential of Ethylacetate Leaf Extract of Gossypium Hirsutum Linn – A Research Article.

Author: Dr. Brijesh Kumar Nagwanshi, Dr. Arun Kumar, Dr Surabhi Verma, Dr. Nishant Saxena, Prof. Amitabh Pande, Neelu Mishra Ashok Kumar Yadav Prabhat Bhagat & Vishwanath Pradeep B

Imprint: SEEJPH Volume XXVI, S2,2025, ISSN: 2197-5248; Posted:03-02-25

Abstract: Gossypium hirsutum is an important plant with therapeutic properties; hence this study seeks to screen the leaf extract for its chemical composition and antioxidant activities to find possible natural sources of novel phytochemicals in pharmaceutical formulations. The qualitative and quantitative phytochemicals screening was conducted using standard procedure, the chemical composition was determined using gas chromatography mass spectrophotometer (GC/MS) while the antioxidant activities were determined using three assays, DPPH, ABTS and NOS. The qualitative phytochemical screening revealed the presence of saponin, alkaloid, phenol, tannin, phytate, steroids, terpenoids, flavonoids and proanthocyanidin. Alkaloid was conspicuously absent in the extract. The qualitative phytochemical screening revealed the presence of saponins, alkaloids, flavonoids, steroids, phytates, terpenoids and proanthocyanidin in different concentrations in which total phenol is the highest 552.64±35.30 mg/100g. In comparison, total saponin is the lowest 22.25±1.41 mg/100g. The GC/MS analysis revealed the presence of 24 compounds which include caryophyllene with the highest percentage composition 33.62%. The antioxidant activities of the extract revealed that the extract has moderate antioxidant activities with EC50 of 12.12, 6.01 and 5.01 mg/mL. In conclusion, the leaf extract demonstrated antioxidant properties suitable for exploration in new drug development.

7

Title: Deletion of GhSCY2D Causes Impaired Chloroplast Development and Temperature-Dependent Leaf Yellowing in Cotton (Gossypium hirsutum L.).

Author: Xiaokang Feng, Yanmei Ma, Qian Liang, Yanlong Jin, Xuefeng Wang, Jianhang Wang, Feng Liu, Xinyu Zhang, Dongnan Shao, Jie Sun, Qian-Hao Zhu4 , Fei Xue

Imprint: Plant, Cell & Environment, 2025; 1–16 16 1 of 16 https://doi.org/10.1111/pce.15476

Abstract: Leaf colour mutants play an important role in understanding chlorophyll metabolism and photosynthesis. In this study, we characterized a temperature-sensitive yellow leaf cotton mutant. Genome resequencing and comparison identified a 10.327 Kb deletion on the D12 chromosome (D12:670726-681053) in the mutant. The deletion region contains two annotated genes, GH_D12G0047 and GH_D12G0048. Investigations integrating gene mapping, comparative transcriptome analysis, gene annotation, virus-induced gene silencing and gene complementation, found deletion of GH_D12G0047 or GhSCY2D, a crucial constituent of the Sec2 complex essential for the function of chloroplasts, being responsible for the yellow leaf phenotype. The yellow leaf mutant had disrupted chloroplast structure and hindered chlorophyll synthesis when temperature was below 28°C but regained normal green leaf colour at 32°C. By analysing the transcriptome data and hormonal level changes of the mutant under conditions of 25°C and 32°C, it was found that the jasmonic acid signalling pathway and GhSCY2 work in concert to maintain the structural integrity of chloroplasts. The outcomes of the study reveal the indispensable role of GhSCY2 and jasmonic acid in sustaining chloroplast homoeostasis, providing new insights into the regulation of cotton leaf colour and paving the way for advancement in high photosynthetic efficiency breeding strategies.

8

Title: Reproductive Meristem (REM) family genes *GhREM1* and *GhREM5.4* act as potential regulators of temperature stress response in cotton.

Author:Roshan Zameer, Mushtaque Ali, AreejS. Jalal, Sajid Fiaz, KotbA. Attia, Cheng Li , Chengde Yu, Farrukh Azeem, Zhi-Fang Li

Imprint: Plant Physiology and Biochemistry, Available online 13 March 2025, 109767

Abstract: Cotton (*Gossypium* spp.) is considered a major cash crop in agriculture, food, and textile industries all over the world. The foremost focus of scientists and farmers is to meet global food security needs, but unfortunately, evolving weather conditions have significantly reduced the overall production. The latest genome sequence of *Gossypium*

hirsutum enables us to understand the molecular mechanisms and identify development-related and stress-responsive genes. The Reproductive Meristem (REM) gene family, a subfamily of B3 DNA-binding superfamily of transcription factors, is characterized in model plants including Arabidopsis and Chickpea, but no study reported in *G. hirsutum*. In the current study, 33 members of REM gene family were predicted and confirmed to possess the conserved REM-related domains in *G. hirsutum*. The phylogenetic analysis revealed that REM family members are divided into six sub-groups consistent with Arabidopsis, further confirming the evolutionary relationship across species. The pattern of introns, exons, and conserved motifs also indicated evolutionary conservation. Gene duplication analysis suggested segmental duplication as a reason for the expansion of REM gene family. RNA-seq and real-time qPCR assisted expression analysis in root, leaf and stem under multiple abiotic stresses (drought, salt, low and high temperature) collectively suggesting *GhREM1* and *GhREM5.4* as potential regulators under low and high temperature stress which is supported with the presence of temperature responsive *cis*-elements. Furthermore, GhREM1-OE and GhREM5.4-OE revealed the significant regulation of peroxidase (POD) under both low and high temperature stress, indicating the potential involvement in temperature tolerance. Green fluorescent protein GFP revealed that both genes were localized in the nucleus. Our findings elucidate the groundwork for co-regulatory relationship of REM genes and antioxidant activity in cotton under temperature stress.

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Title: Heat Stress Reduces Yield Through a Negative Effect on Radiation Use Efficiency during the Reproductive Phase in Cotton (Gossypium hirsutum L.) under Different Source Availabilities.

Author: Kelly Mercado Álvarez, H. Daniel Bertero, Marcelo J. Paytas and Edmundo L. Ploschuk

Imprint: Plant Ecophysiol. 2025, 1(1), 3

Abstract: Cotton is frequently exposed to high temperatures during the reproductive stage, which can negatively impact productivity. While previous research has shown that photosynthesis can decrease under heat stress, there is limited information on the effects of heat stress during the reproductive phase on crop variables such as radiation capture, use efficiency, and yield. This study aimed to: (i) assess the effect of heat stress on cumulative intercepted PAR radiation (IRcum), radiation use efficiency (RUE), harvest index (HI), and yield, and (ii) evaluate potential interactions between heat stress and source-sink relationships during the reproductive phase. Two field experiments were conducted, with heating treatments applied before and after flowering, and controls without temperature manipulation. In Experiment 1, two

genotypes with contrasting growth cycles were compared, while Experiment 2 examined intact versus defoliated plants. Heat stress significantly reduced yield and HI, particularly during post-flowering. Source reduction (defoliation) further reduced yield, independent of temperature. Although IRcum was unaffected by treatments, RUE dropped sharply under heat stress in intact plants and was similarly low in defoliated plants under both control and heated conditions. These results suggest that heat stress, especially during post-flowering, exacerbates the effects on cotton productivity by reducing both total plant dry weight and HI. The study highlights that the relationship between RUE and yield strongly depends on the specific limiting factors, such as heat stress or source restrictions.

CROP PROTECTION

10

Title: Biological Approaches to Sustainable Management of Fusarium Wilt in Cotton.

Author: Iqra Javed, Muhammad Arslan Khan, Hasan Riaz, Shafqat Saeed, Muhammad Sajid, Muhammad Bashair, Zulqarnain Abbas, Haider Ali, Munirah Abdullah Al-Dosary & Muhammad Bilawal Junaid

Imprint: Journal of Crop Health , Published: 21 March 2025, Volume 77, article number 69, (2025)

Abstract: Cotton (*Gossypium spp.*) is an annual shrub that provides valuable vegetable oil and natural fibers. Fusarium wilt, caused by *Fusarium oxysporum*, is one of the most devastating diseases that threaten sustainable cotton production. The present study was planned to check the response of *Trichoderma harzianum* formulation against Fusarium cotton wilt. *Trichoderma harzianum* formulation was prepared in combination with plant defense activators. The pot trials were conducted under a completely randomized design with three replicates. The growth and development of cotton plants were studied under different treatments, including control, fungicide, insecticide, and the application of the beneficial fungus *Trichoderma harzianum*. Results indicated that *T. harzianum* exhibited notable impacts over other treatments, showing significant growth improvement during the 7th and 8th weeks after sowing. The biocontrol agent effectively inhibited the growth of *F. oxysporum* mycelium, highlighting its potential as an efficient disease management tool. Furthermore, *T. harzianum* treatment induced increased activities of peroxidase (POD), hydrogen peroxide (H_2O_2), and superoxide dismutase (SOD), from 0.6–1.2 folds in cotton leaves. This enhancement of antioxidant defense mechanisms protected against oxidative damage and enhanced plant tolerance to pathogen attack. These findings revealed that *Trichoderma harzianum* has tremendous

potential as a sustainable and environmentally friendly method of managing Fusarium wilt in cotton. Implementing this biocontrol method can help the cotton industry remain sustainable and thrive, helping farmers' income and livelihoods. Further research is encouraged to elucidate the underlying mechanisms of *T. harzianum's* biocontrol activity and explore its implementation on a larger scale in cotton farming.

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Title: Evaluation of Appropriate Density of Natural Enemies for Release against Sucking Insects and Bollworms in Cotton Field.

Author: Mukhtar Umer, Abdul Ghani Lanjar, Tajwar Sultana Syed, Raza Muhammad Memon

Imprint: Planta Animalia, Volume 4, Issue 1. 165-173, DOI: 10.71454/PA.004.01.0082

Abstract: Cotton (*Gossypium hirsutum* L). is a major fiber crop being grown worldwide including Pakistan and known for its importance as cash crop of Pakistan. The present studies were conducted Evaluate the release of appropriate density of natural enemies in cotton field against sucking and bollworm insects to manage the population of major pests of cotton through bio-control agents in Sindh, Pakistan. The aim of the study was to use natural enemies effectively against insect pests of cotton crop with appropriate density. For this study, four different densities of Tricho-cards, Chrysoperla larvae and *Brumus suturalis* larvae were released at (5, 10 and 15 days) intervals in the cotton field. The results revealed that the releasing of Tricho-cards *and B. suturalis* at different intervals (days) and density had a very positive impact of the insect pests of cotton crops, especially on *B. tabaci, A. biguttula, P. gossypiella and E. vittella*. Releasing of Trichocard (500 eggs) + *Brumus suturalis* (40 larvae) at 5 days intervals found very effective in suppressing the population of *B. tabaci, A. biguttula, P. gossypiella* and *E. vittella*. Followed by Releasing of Tricho-card (1000 eggs) + *Brumus suturalis* (65 larvae) at 10 days interval which was effective against the population of *B. tabaci* and *A. biguttula*. All treatment showed different levels of effect as compared to control however maximum suppressing was observed in the blocks where Tricho-cards, Chrysoperla larvae and *Brumus suturalis* larvae were released at 5 days interval. but no impact of the treatment was seen on thrip population.

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Title: Toxicity of New Molecules against American Bollworm, *Helicoverpa Armigera* in Cotton.

Author: Poornima Viroopax Matti, Poornima M. Holeyannavar, Siddharuda. B. Patil and Rishi Kumar

Imprint: Plant Archives Vol. 25, Supplement 1, 2025 pp. 2133-2139

Abstract: Toxicities of new insecticides having novel modes of action along with conventional insecticides were evaluated against Helicoverpa armigera during 2021-2023 at ARS Dharwad. Profenofos 40%+Cypermethrin 4% EC @ 2.00 ml /ha showed most effective and offered lowest number of larvae of 0.34 per plant with reduction of 90.32 per cent, more of good, opened bolls (35.69/plant), bad opened bolls (6.42 per plant) with yield of 14.84q/ha followed by Cypermethrin 10% + Indoxcarb 10% @ 1.00 ml/lit shown significant control compared to individual formulations. Whereas Spinetoram 11.70SC @1.00 ml per lit proved to be promising treatment with 0.37 per plant (89.61% reduction) and also recorded 35.10 good, opened bolls, 6.84 bad opened bolls and yield of 13.94 q/ha. However, combi products resulted in relatively lowest coccinellids and Chrysoperla populations compared to individual formulations Spinetroam 11.7SC and Spinosad 45SC proving less hazardous.

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Title: 25 Years of Pesticidal Cry1Ab/Ac Fusion Proteins in Crop Protection: Advances in Bt Crop Development, Target Pest Management, Safety, Environmental Impact, and Regulatory Frameworks.

Author: Shuvobrata Majumder, Karabi Datta & Swapan K. Datta

Imprint: Journal of Crop Health, Published: 07 March 2025, Volume 77, article number 55, (2025)

Abstract: Cry (crystal) proteins from Bacillus thuringiensis (Bt) have been pivotal in integrated pest management (IPM) for lepidopteran insects. Genetically engineered Bt crops with cry genes are grown in 27 countries, significantly reducing pest infestations and chemical insecticide use. However, improper cultivation practices, such as repeated use of the same Bt crops over large areas, have led to insect adaptation to Cry proteins, raising global concern for crop protection. To combat this, plants expressing multiple Cry proteins, including fusion proteins like Cry1Ab/Ac, have been developed and extensively studied in crops such as rice (Oryza sativa), jute (Corchorus capsularis), chickpea (Cicer arietinum), and jatropha (Jatropha Curcas). Comprehensive biosafety analyses have confirmed the safety of Cry1Ab/Ac for non-target insects,

beneficial insects, soil microbes, water quality, and the environment. Food safety analyses have also validated its safety for human consumption. In 2009, China approved Cry1Ab/Ac rice lines Huahui-1 and Bt-Shanyou-63 for cultivation, and in 2018, the United States approved Bt-Shanyou-63 rice for human consumption. The large-scale adoption of Cry1Ab/Ac crops promises to reduce chemical pesticide use and increase farm profitability. This review highlights the advancements and applications of Cry1Ab/Ac fusion proteins in crop protection from 1998 to 2024, with a special focus on Bt (Cry1Ab/Ac) rice, emphasizing their potential to address key challenges in modern agriculture, ensuring food security, and promoting environmental sustainability.

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Title: Predicting select soil health genes using hyperspectral reflectance in nematode-infected and drought stressed greenhouse cotton.

Author: John P. Brooks, Martin J. Wubben, Renotta K. Smith, Josh Waldbieser, Sathishkumar Samiappan, Purushothaman Ramamoorthy, Raju Bheemanahalli

Imprint: Front. Soil Sci., 01 April 2025, Sec. Plant-Soil Interactions, Volume 5 - 2025 | https://doi.org/10.3389/fsoil.2025.1499491

Abstract: **Introduction:** Predicting, or correlating, soil microbiome metrics with above ground phenotypic plant measurements would enable rapid diagnosis of soil microbiome imbalances. Rapid plant measurements through remote sensing are a leading innovation in agriculture and have reduced the need for labor-intensive plant and soil measurements. In the current study we utilized cotton (*Gossypium hirsutum*) as a plant model whereby stress was induced by drought and root-knot nematode (RKN; *Meloidogyne incognita*) infection to induce a change in the soil microbiome which would be reflected as a plant phenotypic response. **Methods:** The experiment was a randomized complete block design with two cotton genotypes (RKN-susceptible or RKN-resistant) and four stress combinations. Rootzone samples were collected upon plant termination and quantified for five soil health genes: 16S rRNA, 18S rRNA, *ure*C, *pho*A, and *cbb*LR. Plant physiology, biomass, and remote sensing hyperspectral readings were previously reported. **Results and discussion:** Overall, RKN infection and plant genotype treatments had little effect on genes. Interestingly, drought stress increased most gene abundances, while plant physiological and biomass measurements decreased, indicating microbiome response to plant stress. Hyperspectral reflectance, through machine learning, accurately predicted the presence of drought stress with an area under the receiver operating characteristic curve value of 0.864. Furthermore, the readings were able to predict the abundance values for all genes except 18S rRNA within one standard deviation of ground truth levels. This study demonstrated that there are key plant characteristics that are registered via hyperspectral wavelengths which can be used to accurately predict soil health gene

abundance. While the use of hyperspectral readings and soil microbiome status to inform plant health and vice versa are still in their infancy, the current study provides us with future directions towards this end.

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Title: Effect of treated and untreated cotton fields with pesticides on the population fluctuations of the most important cotton pests and their associated insect predators.

Author; Ali A. El-Sayed ; Mohamed M. Nada; Adel E. Amer; and Hatem Fouad

Imprint; Egypt. J. Agric. Res., (2025) 103 (1) 72-87

Abstract: The cotton variety Gossypium barbadense was planted in experimental fields during the March (2022, 2023, and 2024) seasons, and the studies continued for five months. Field studies were carried out at El-Zagazig distract Sharkia Governorate to compare the effect of insecticide-treated and untreated cotton fields on average monthly numbers, the seasonal fluctuations of the most important cotton pests, and the common insect predators associated with cotton pests. The results showed that the treated and untreated cotton fields significantly affected the average monthly numbers of the four cotton pests Aphis gossypii, Bemisia tabaci, Spodoptera littoralis, and Pectinophora gossypiella and five associated common insect predators Chrysoperla carnea, Coccinella undecimpunctata, Scymnus spp., Orius spp. and Paederus alfierii during the three cotton seasons. Furthermore, the average monthly number of the four cotton pests and their accompanying predators in untreated cotton fields was greater than that of those treated with pesticides. The fluctuations of four insect pests in the treated and untreated cotton fields were recorded at 53 peaks; it was 24 peaks in the treated fields and 29 in the untreated fields. On the other hand, predators recorded 41 peaks; 18 were in treated fields and 23 in untreated fields. Thus, it is clear our study showed S. littoralis was the most common of the four pests, and *C. carnea* was the most common predator of the five predators in both treated and untreated cotton fields. Thus, the study recommended that preserving natural enemies is a key tactic in IPM.

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Title: Defense Responses Stimulated by Bacillus subtilis NCD-2 Through Salicylate- and Jasmonate-Dependent Signaling Pathways Protect Cotton Against Verticillium Wilt.

Author: Shaojing Mo, Weisong Zhao, Yarui Wei, Zhenhe Su, Shezeng Li, Xiuyun Lu

Imprint*: Int. J. Mol. Sci.* 2025, *26*(7), 2987; https://doi.org/10.3390/ijms26072987

Abstract: *Bacillus subtilis* NCD-2 demonstrates exceptional biocontrol potential against cotton Verticillium wilt. While previous studies have established its direct antifungal activity (e.g., inhibiting *Verticillium dahliae* mycelial growth and spore germination), our work reveals a novel mechanism: NCD-2 primes systemic resistance in cotton by activating plant immune-signaling pathways. Firstly, transcriptional profiling uncovered that NCD-2 triggers a defense response in roots analogous to *V. dahliae* infection, allowing cotton to maintain a more balanced state when confronted with pathogen attacks. Meanwhile, the mutant strains Δfen and Δsrf—defective in lipopeptide synthesis—also improved cotton resistance to Verticillium wilt by activating partially identical defense pathways in cotton roots. Furthermore, the application of lipopeptide compounds derived from NCD-2, particularly surfactin and fengycin, could enhance host resistance to *V. dahliae*. Using an RT-qPCR approach, we found that numerous resistance-related genes were induced by these lipopeptide compounds. The up-regulation of SA/JA pathway markers (e.g., *NPR1*, *ICS1*, *COI1*, and *LOX1*) revealed NCD-2's activation of plant immune signaling. Using virus-induced gene silencing (VIGS), we conclusively linked SA and JA signaling to NCD-2-induced defense priming. Silencing either pathway abolished resistance, highlighting their indispensable coordination. By bridging mechanistic insights and agricultural applicability, our work positions NCD-2 as a sustainable alternative to conventional fungicides, addressing both crop productivity and environmental health.

17

Title: Design of Precision Agriculture System using Automating Pink Bollworm Detection in Cotton Crops: AI based Digital Approach for Sustainable Pest Management.

Author: Kanchan J. Kakade; V. A More; Monica Shinde; Kavita Suryawanshi; Gopal U. Shinde

Imprint: IEEE Conference, 16-17 January 2025, **DOI:** 10.1109/ICAET63349.2025.10932187

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Title: Integrative GWAS and transcriptomics reveal GhAMT2 as a key regulator of cotton resistance to Verticillium wilt.

Author: Long Wang, Yonglin Yang, Jianghong Qin

Imprint: Front. Plant Sci., 25 April 2025, Sec. Plant Abiotic Stress, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1563466

Abstract: Introduction: Verticillium wilt, incited by the soilborne fungus Verticillium dahliae, is a severe threat to global cotton (Gossypium spp.) production, resulting in significant yield losses and reduced fiber quality.

Methods: To uncover the genetic and molecular basis of resistance to this devastating disease, we combined genome-wide association study (GWAS) and transcriptomic analyses in a natural population of 355 upland cotton accessions.

Results: GWAS identified a stable major-effect quantitative trait locus (QTL), qVW-A01-2, on chromosome A01, which harbors the candidate gene GhAMT2, encoding a high-affinity ammonium transporter. Transcriptomic profiling revealed that GhAMT2 was significantly upregulated at 12 hours post-inoculation with V. dahliae, coinciding with the activation of immune signaling pathways. Weighted Gene Co-expression Network Analysis (WGCNA) further linked GhAMT2 to critical defense pathways, including lignin biosynthesis, salicylic acid signaling, and reactive oxygen species (ROS) homeostasis, suggesting its role in cell wall reinforcement and systemic immune responses. Functional validation through virus-induced gene silencing (VIGS) confirmed that silencing GhAMT2 compromised disease resistance. In contrast, transgenic Arabidopsis plants overexpressing GhAMT2 exhibited enhanced resistance to V. dahliae, demonstrating its essential role in defense regulation.

PLANT BREEDING AND GENETICS

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Title: Mining Key Drought-Resistant Genes of Upland Co□on Based on RNA-Seq and WGCNA Analysis.

Author: Hu Zhang , Yu Tang , Yuantao Guo , Jinsheng Wang , Wenju Gao , Wen Zhang , Qingtao Zeng , Quanjia Chen and Qin Chen

Imprint: Posted Date: 26 March 2025, doi: 10.20944/preprints202503.2011.v1

Abstract: Cotton, as a globally important fiber crop, is significantly affected by drought stress during production. This study uses the drought-resistant variety Jin and the drought-sensitive variety TM-1 as test materials. Through multi-period drought stress treatments at 0d, 7d, 10d, 15d, and 25d, combined with dynamic monitoring of physiological indicators, RNA sequencing (RNA-Seq), and weighted gene co-expression network analysis (WGCNA), the molecular mechanism of co□on drought resistance is systematically analyzed. Dynamic monitoring of physiological indicators showed that

Jin significantly accumulated proline, maintained superoxide dismutase (SOD) activity, reduced malondialdehyde (MDA) accumulation, and delayed chlorophyll degradation. Transcriptome analysis revealed that Jin specifically activated 8,544 differentially expressed genes after stress, which were significantly enriched in lipid metabolism (α-linolenic acid, ether lipids) and secondary metabolic pathways. WGCNA identified co-expression modules significantly correlated with proline (r=0.81) and MDA (r=0.86) and selected the key hub gene *Gh_A08G154500* (WRKY22), which was expressed 3.2 times higher in Jin than in TM-1 at 15 days of drought stress. Functional validation suggested that WRKY22 may form a "osmotic regulation-membrane protection" co-regulatory network by activating proline synthesis genes (P5CS) and genes involved in the jasmonic acid signaling pathway. This study reveals, for the first time, the possible dual regulatory mechanism of WRKY22 in co□on's drought resistance, providing a theoretical basis for co□on drought-resistant breeding.

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Title: Cotton Genetic Resilience: Cytogenetic Tools for Biotic and Abiotic Stress Mitigation.

Author: Namala Sandeep, B. Surya Vardhan Reddy, Nerella Siri Madhuri, Rahul Singh

Imprint: International Journal of Plant & Soil Science Year: 2025DOI : 10.9734/ijpss/2025/v37i35346

Abstract: Cotton (Gossypium spp.) holds immense significance in the global economy due to its prized fiber, produced from the epidermal cells of the ovule. Among the approximately fifty cotton species, Gossypium arboreum, Gossypium herbaceum, Gossypium hirsutum, and Gossypium barbadense are primarily cultivated for fiber production. Of these, Gossypium hirsutum (Upland cotton) dominates global production, contributing to over 90% of the cotton used worldwide. Advancements in cotton cytogenetics have greatly enhanced fiber yield and quality, driven by the adoption of modern genomic and genetic engineering techniques. Innovations like CRISPR-Cas9, RNA interference (RNAi), and marker-assisted selection have improved cotton's tolerance to biotic and abiotic stresses, including pests and drought. These technologies have also enabled the refinement of fiber properties through epigenetic modifications. The development of male sterility systems has further streamlined breeding programs, accelerating genetic improvements in cotton. This analysis highlights the pivotal role of advanced cytogenetic and biotechnological tools in fostering the sustainable growth of cotton. The integration of these cutting-edge techniques marks a transformative era in cotton breeding, with promising prospects for improving fiber quality, enhancing stress resistance, and boosting overall crop performance. These advancements solidify cotton’s vital role in global agriculture and its potential for future innovation.

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Title: Role of molecular breeding in understanding salinity tolerance in cotton: limitations and perspectives

Author: Wang, S., Hou, M., Hassan, H., Abbas, F. M., Al Ahmad, Z. A., Qari, S. H., & Hanifah, N. A.

Imprint: *Notulae Botanicae Horti Agrobotanici Cluj-Napoca*, *53*(1), 14297. https://doi.org/10.15835/nbha53114297

Abstract: Cotton is a significant fiber crop globally and has a considerable share in many countries' gross domestic product (GDP). It is the most critical contributor to the textile industry and provides income to millions of farmers. Salt stress is abiotic stress, decreasing the cotton yield on a large area. Salt stress is a polygenic trait, and cotton's response to salt stress involves a complex gene pathway. Breeders have been breeding novel salt-tolerant cotton genotypes for decades to sustain their growth on salt-affected soils. In recent years, cotton breeders have employed several breeding tools like hybridization, backcrossing, and mass selection to develop tolerant genotypes. Still, due to several limitations, these techniques are being replaced by novel molecular breeding tools. With the advancement in molecular breeding, the speed to improve crop tolerance to salt stress has been increased. Quantitative trait loci (QTL) mapping, genome-wide association studies (GWAS), transcription factors (TFs) analysis, and transcriptome have identified several genomic regions for salinity tolerance in cotton. At the same time, genetic engineering and clustered regularly interspaced short palindromic repeats (CRISPR/Cas9) led to the development of salt-tolerant cotton cultivars. Genetic engineering is key in breeding transgenic cotton cultivars resistant to multiple abiotic stresses. CRISPR/Cas9, a new gene manipulation technique, is used to edit the genes for salt tolerance in cotton without any biological barrier. CRISPR/Cas9 could be a more powerful tool to manipulate the desired cotton genome against salinity tolerance. These research and breeding tools have been successfully used in genetic research and breeding for drought tolerance in cotton. This unique review presents a full overview of the use of different molecular tools and their role in enhancing salt tolerance in cotton. Using this information, cotton breeders can understand the salinity tolerance mechanism in cotton by choosing the most reliable genetic breeding tool.

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Title: Identification of the STY13 gene family across the entire genome and an analysis of the essential function of GhSTY13-12 in cotton's response to abiotic stress.

Author: Shaoliang Zhang, Huiyun Shan, Xiaopei Bo, Jiahui Li, Zili Liu,

Imprint: Functional & Integrative Genomics , Published: 26 March 2025, Volume 25, article number 74, (2025)

Abstract: Cotton is an important cash crop, and its yield and quality were affected by abiotic stresses. The serine/threonine protein kinase *STY13* gene, belonging to the protein kinase family, is one of the largest and most functionally diverse gene families, which is a critical regulatory molecule for cell function. In this study, we systematically identified and analyzed the *STY13* gene family in two major cultivated cotton species (*Gossypium hirsutum* and *Gossypium barbadense*) and their two ancestors (*Gossypium arboretum* and *Gossypium raimondii*). A total of 46, 50, 26 and 24 *STY13* genes were identified from these four species, respectively. Phylogeny analysis showed that cotton *STY13* genes (cotton STY protein kinase genes) could be classified into five groups. This gene family was evenly distributed on each chromosome in cotton. *STY13* genes contain light-responsive elements, stress-responsive elements, growth and developmental elements, and multiple gene and protein binding sites. Most motifs in the *STY13* proteins were conserved and had similar distribution patterns. However, there were some differences in specific motifs in different subfamilies. Gene expression analysis based on RNA-seq and qRT-PCR showed that *STY13* genes were responsive to abiotic stress. *GhSTY13-12* gene was located in cytoplasm. Silencing of the *GhSTY13-12* gene resulted in reduced leaf chlorosis, increased total antioxidant capacity, decreased malondialdehyde content, and enhanced drought and salt tolerance. These results provide a scientific basis for further research on the function of *STY13* in cotton and its application on cotton trait improvement.

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Title: Genome-wide identification and expression analysis of the *DnaJ* genes in *Gossypium hirsutum*.

Author:Pengyun Chen, Xianghui Xiao, Yunqing Li, Gu Lijiao, Yanli Zhang, Yanchun Pe ng, Xiao Han, Fei Wei

Imprint: Industrial Crops and Products, Volume 228, June 2025, 120904

Abstract: DnaJ proteins are considered critical players in enhancing plant resilience to environmental stresses, yet their identification and characterization in cotton remains largely unexplored. In this study, we systematically identified *DnaJ* genes in *Gossypium* species and conducted comprehensive phylogenetic and structural analyses. Our results suggest that polyploidy events significantly contributed to the expansion of *DnaJ* genes in *Gossypium* species. Furthermore, analysis of *cis*-elements revealed that *GhDnaJs* are involved in abiotic stress responses, indicating their potential role in the adaptive mechanisms of plants. RNA-seq and RT-qPCR analyses demonstrated that numerous *GhDnaJs* are upregulated in response to various abiotic stress conditions, such as *GhDnaJ94*. Subsequent VIGS experiments revealed

that *GhDnaJ94* positively regulates the drought stress in cotton. This study provides a detailed perspective on *GhDnaJs* in cotton, identifying potential genes that could be targeted to enhance plant resilience to abiotic stresses and offering valuable insights for future cotton breeding programs aimed at improving stress resistance.

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Title: Differential LTR-retrotransposon dynamics across polyploidization, speciation, domestication and improvement of cotton (Gossypium).

Author: Lucía Campos-Dominguez, Raúl Castanera, Corrinne E. Grover, Jonathan F. Wendel,

Imprint: https://doi.org/10.21203/rs.3.rs-6172192/v1, This work is licensed under a CC BY 4.0 License

Abstract: Transposable elements (TEs) are major components of plant genomes and major drivers of plant genome evolution. The cotton genus (Gossypium) is an excellent evolutionary model for polyploidization, speciation, domestication and crop improvement. Here, we implement genome and pangenome analyses to study in detail the dynamics of LTR-retrotransposons (LTR-RT) during the cotton evolution. Results- We show that some LTR-RT lineages amplified in tetraploid cotton compared to their diploid progenitors, whereas others stayed stable or amplified but were removed through solo-LTR formation. Using species-level pangenomes we show that only a few lineages (CRM, Tekay, Ivana and Tork) remained active after polyploidization and are still transposing. Tekay and CRM elements have re-shaped the centromeric and pericentromeric regions of tetraploid cottons in a subgenome specific manner, through new insertions but also selective eliminations through solo-LTR formation. On the other hand, Ivana and Tork have actively inserted within or close to genes. Finally, population-level analyses using the two pangenomes and data from 283 and 223 varieties of G. hirsutum and G. barbandense reveal changes in Transposon Insertion Polymorphism (TIP) frequencies accompanying domestication and improvement of both species, suggesting the possibility of selection on linked regions.

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Title: Construction of Gossypium hirsutum—Gossypium turneri chromosome segment introgression population for mapping new QTLs related to yield and fiber quality traits.

Author: Liang Wang, Chenhui Zhou, Mengfei Chen, Nijiang Ai, Guoli Feng, Ningshan Wang, Yu Chen & Baoliang Zhou

Imprint: Euphytica, Published: 24 March 2025, Volume 221, article number 46, (2025)

Abstract: Upland cotton is the most important natural fiber resource, but long-term excessive domestication and artificial selection has greatly impoverished its genetic diversity. Therefore, enriching the genetic diversity of upland cotton by transferring desirable genes from wild cotton is imperative. In this study, a *Gossypium hirsutum*–*Gossypium turneri* introgression population consisting of 253 lines was developed by molecular marker-assisted selection. The total introgression fragments covered 207.70 Mb (27.50%) of the *G. turneri* genome, with the introgression segment lengths ranging from 0.22 to 18.39 Mb and an average of 2.38 Mb. A total of 50 QTLs were identified using the stepwise regression (RSTEP-LRT) mapping method, forming 5 stable QTLs and 8 QTL clusters. Among these, 39 new QTLs were detected, with 17 favorable for improving fiber quality or yield. Constructing introgression lines could help retrieve favorable genes eliminated during domestication and artificial selection. Several positive QTLs (6/16) related to fiber quality were identified, which could potentially improve upland cotton. The introgression population developed in this study could be further utilized to mine favorable genes in *G. turneri* to enhance the overall quality of upland cotton in the future.

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Title: A telomere-to-telomere genome assembly of cotton provides insights into centromere evolution and short-season adaptation.

Author: Guanjing Hu, Zhenyu Wang, Zunzhe Tian, Kai Wang, Gaoxiang Ji, Xingxing Wang, Xianliang Zhang

Imprint: *Nature Genetics* volume 57, pages1031–1043 (2025)

Abstract: Cotton (*Gossypium hirsutum* L.) is a key allopolyploid crop with global economic importance. Here we present a telomere-to-telomere assembly of the elite variety Zhongmian 113. Leveraging technologies including PacBio HiFi, Oxford Nanopore Technology (ONT) ultralong-read sequencing and Hi-C, our assembly surpasses previous genomes in contiguity and completeness, resolving 26 centromeric and 52 telomeric regions, 5S rDNA clusters and nucleolar organizer regions. A phylogenetically recent centromere repositioning on chromosome D08 was discovered specific to *G. hirsutum*, involving deactivation of an ancestral centromere and the formation of a unique, satellite repeat-based centromere. Genomic analyses evaluated favorable allele aggregation for key agronomic traits and uncovered an early-maturing haplotype derived from an 11 Mb pericentric inversion that evolved early during *G. hirsutum* domestication. Our study sheds light on the genomic origins of short-season adaptation, potentially involving introgression of an inversion from primitively domesticated forms, followed by subsequent haplotype differentiation in modern breeding programs.

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Title: Identification and comparative analysis of flowering genes in the Sugar pathway from five *Gossypium* species.

Author: Lei-Ming Liu, Chuan-Bo Jiang, Yi-Lin Yang, Tian-Run Mei, Ruo-Fei Liu, Hai-Liang Liu, Xian-Zhong Huang

Imprint: Plant Gene, Volume 42, June 2025, 100500

Abstract: Flowering is a critical plant growth stage coordinated by internal and external factors. Changes to endogenous sugar levels can promote or inhibit flowering, but research on the regulation of flowering-related genes associated with the sugar pathway in cotton is limited. Here, a genome-wide study identified 165 flowering and sugar pathway-related genes in five cotton species: *Gossypium herbaceum*, *G. arboreum*, *G. hirsutum*, *G. barbadense*, and *G. raimondii*. The genes were phylogenetically classified into nine subfamilies and showed a high degree of conservation. Notably, no homologs of *INDETERMINATE DOMAIN 8* (*IDD8*), *SUCROSE-PROTON SYMPORTER 9* (*SUC9*), or *AGP GALACTOSYLTRANSFERASE 2* (*GALT2*) were identified. A synteny analysis provided evidence of varying degrees of gene expansion, and a selection pressure analysis indicated that the genes had undergone purifying selection, with *Ka*/*Ks* ratios of <1. The similarity among the genes identified in *G. herbaceum*, *G. arboreum*, and *G. raimondii* was higher than between these species and the allopolyploid cotton species, indicating the earlier divergence of these genes. A network analysis of protein interaction revealed *G. hirsutum* proteins to be associated primarily with sugar synthesis, transport, and metabolism. Yeast two-hybrid assays demonstrated that GhTPS1–1 and GhHXK1–1 can interact with GhPGI1–1. RNA-sequencing data for 46 genes from eight tissue-types in *G. hirsutum* revealed that most were highly expressed in stems and flowers. This study provides a comprehensive phylogenetic and network analysis of flowering-related genes in the sugar pathway across five *Gossypium* species, laying a foundation for future in-depth research on the functional mechanisms of these genes.

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Title: Screening of historical and current Upland and Pima cotton germplasm for resistance to Rhizoctonia solani.

Author: Jorge Garcia, Mauricio Ulloa, Robert B. Hutmacher & Margaret L. Ellis
Imprint: BMC Research Notes

Abstract: The fungus *Rhizoctonia solani* is an important seedling pathogen to many plant hosts including cotton (*Gossypium*). For multiple annual crops there have been relatively few screenings of germplasm conducted to identify potential sources of resistance to *R. solani*, and for cotton we have not been able to identify any recent germplasm screenings for resistance to this seedling pathogen. Therefore, the objective of this study was to screen historical as well as more recently developed Upland (*Gossypium hirsutum* L.) and Pima (*Gossypium barbadense* L.) cotton germplasm for resistance/susceptibility to *R. solani.* Results-The results of the *R. solani* screening found no significant differences among 85 Upland and 10 Pima cotton genotypes, which were all similarly susceptible to *R. solani* based on data for root rot and fresh root weight. While Upland and Pima cotton make up the majority of cotton grown worldwide, the lack of resistance identified in both historical and newer Upland and Pima germplasm suggests a pressing need for further exploration and selection of novel sources of resistance within the vast genetic diversity of different domesticated and wild cotton species.

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Title: Identification of Elite Alleles and Candidate Genes for the Cotton Boll Opening Rate via a Genome-Wide Association Study.

Author: Qi Ma, Xueli Zhang, Jilian Li, Xinzhu Ning, Shouzhen Xu

Imprint*: Int. J. Mol. Sci.* 2025, *26*(6), 2697; https://doi.org/10.3390/ijms26062697

Abstract: The boll opening rate (BOR) is an early maturity trait that plays a crucial role in cotton production in China, as BOR has a significant effect on defoliant spraying and picking time of unginned cotton, ultimately determining yield and fiber quality. Therefore, elucidating the genetic basis of BOR and identifying stably associated loci, elite alleles, and potential candidate genes can effectively accelerate the molecular breeding process. In this study, we utilized the mixed linear model (MLM) algorithm to perform a genome-wide association study (GWAS) based on 4,452,629 single-nucleotide polymorphisms (SNPs) obtained through whole-genome resequencing of a natural population of 418 upland cotton accessions and phenotypic BOR data acquired from five environments. A total of 18 SNP loci were identified on chromosome D11 that are stable and significantly associated with BOR in multiple environments. Moreover, a significant SNP peak (23.703–23.826 Mb) was identified, and a *GH-D11G2034* gene and favorable allelic variation (GG) related to BOR were found in this genomic region, significantly increasing cotton BOR. Evolutionary studies have shown that *GH-D11G2034* may have been subjected to artificial selection throughout the variety selection process. This study provides valuable insights and suggests that the *GH-D11G2034* gene and its favorable allelic variation (GG) could be potential targets for molecular breeding to improve BOR in upland cotton. However, further research is

needed to validate the function of this gene and explore its potential applications in cotton breeding programs. Overall, this study contributes to the advancement of genetic improvement in early maturity and has important implications for the sustainable development of the cotton industry.

PLANT BIOTECHNOLOGY

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Title: Transcriptome reveals Gafmt-1 and Gadlc-1–5 play positive roles in cotton resistance to Verticillium wilt.

Author: Jiale Chen, Susu Liu, Guoli Feng, Jianbo Gao, Ningshan Wang, Nijiang Ai & Baoliang Zhou

Imprint: Plant Cell Reports, Published: 18 March 2025, Volume 44, article number 76, (2025)

Abstract: Verticillium wilt (VW) caused by *Verticillium dahliae* is one of the most destructive diseases affecting cotton production and quality worldwide. Numerous resistance genes against the disease from tetraploid cultivated cotton ($2n = 4x = AADD = 52$) have been cloned and functionally analyzed to attempt to develop resistant varieties. However, VW continues to pose a significant threat to global cotton production due to the lack of cost-effective resistance genes to balance resistance and yield. Resistance genes from diploid cotton species such as *Gossypium arboreum* ($2n = 2x = AA = 26$) remain largely untapped, and their functions are unknown. Here, a resistant *G. hirsutum-G. arboreum* introgression line, DM10781, was employed to mine new resistance genes against *V. dahliae* from the diploid cotton species. We performed time-course transcriptome analysis on the RNA-seq data at 0, 4, 12, 24, 48, and 96 h post-inoculation. Weighted gene co-expression network analysis showed that nine differentially expressed genes (DEGs) caused by disease resistance have been identified. Among them, seven genes were found on the introgression segments from *G. arboreum* and suffered from virus-induced gene silencing in DM10781. Out of them, two genes were further overexpressing in Arabidopsis. The results indicated the two genes of *Gafmt-1* and *Gadlc-1–5* played positive roles in both cotton and Arabidopsis. Our study demonstrates that *G. arboreum* has the resistance genes to VW and can be used in future disease-resistance breeding, providing insights into the resistance of *Gafmt-1* and *Gadlc-1–5* against VW in cotton.

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Title: Genome-wide identification unravels the role of the arabinogalactan peptide (AGP) gene family in cotton plant architecture.

Author: Jungfeng Tang, Teame Gereziher Mehari, Dongmei Qian, Ruochen Li, Zhengyang Chen, Zitong Zhou, Yuchun Yan, Haodong Chen, Wei Wang & Baohua Wang

Imprint: Plant Cell Reports, Volume 44, article number 71, (2025)

Abstract: Arabinogalactan peptides are a class of hydroxyproline-rich proteins widely distributed in plants that participate in many life processes, including growth and development, cell division and even plant reproductive development. In this study, we identified 122 members of the AGP gene family via genome-wide identification in six cotton species. Through phylogenetic tree analysis, the AGP family was divided into six different subgroups. A core yet variable region composed of proline, hydroxyproline, serine, threonine, and alanine (PAST) was identified among these members. Furthermore, Ka/Ks analysis revealed that the AGP gene family underwent multiple fragment duplication events. Additionally, we analyzed the 1.5 kb upstream cis-acting elements of all upland cotton family members and identified numerous functional elements associated with growth and development, suggesting a close relationship among the family members. The results of RT–qPCR analysis revealed that the expression level of *Gohir.A08G240900* was significantly different among the four upland cotton varieties, with significant differences in plant height. Virus-induced gene silencing (VIGS) experiments revealed that the height of *Gohir.A08G240900* gene-silenced plants significantly decreased. The results revealed that *Gohir.A08G240900* may affect plant growth and development and may be a potential functional gene regulating cotton plant height.

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Title*: GhCTEF2* encodes a PLS-type PPR protein required for chloroplast development and plastid RNA editing in cotton.

Author:Huan He, Mengxue Cheng, Bowen Bao, Yanan Tian, Yating Zheng, Yuzhu Huo, Zengqiang Zhao, Zongming Xie, Jianing Yu, Peng He

Imprint: Plant Science, Volume 355, June 2025, 112478

Abstract: Cotton is a significant cash crop and serves as crucial raw material for the textile industry. The leaf, which is the site of photosynthesis in cotton plants, directly influences their growth and yield. Pentatricopeptide repeat (PPR) proteins are characterized by tandem 30–40 amino acid motifs. These proteins play a pivotal role in post-transcriptional regulation of organelle gene expression. In this study, we identified

GhCTEF2 as a PLS-type PPR protein and determined its subcellular localization within chloroplasts, highlighting its essential involvement in chloroplast development. Virus-induced gene silencing assays revealed that knockdown of the *GhCTEF2* gene resulted in macular phenotypes on cotton leaves and significantly reduced photosynthetic efficiency. Additionally, *GhCTEF2*-silenced plants exhibited incomplete chloroplasts with reduced thylakoids and grana structures. Furthermore, our findings showed that the downregulation of *GhCTEF2* reduced the transcription levels of PEP-dependent genes and significantly decreased the content of the chloroplast LHC II -T complex protein. Further studies showed that GhCTEF2 may interact with other editing factors to regulate the RNA editing process of *ndhB*, *accD,* and *rps18*. These findings offer valuable insights into future breeding strategies aimed at enhancing photosynthesis in cotton.

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Title: Differential miRNA expression and regulatory mechanisms in pigmentation and fiber development of white and brown cotton (Gossypium hirsutum).

Author: Sagar Prasad Nayak, Priti Prasad, Shafquat Fakhrah, Debashree Pattanaik, Sumit Kumar Bag & Chandra Sekhar Mohanty
Imprint: Functional & Integrative Genomics, 12 March 2025, Volume 25, article number 61, (2025)

Abstract: Cotton (*Gossypium hirsutum*) is a major global natural fiber crop used in the textile industry. Although white colored cotton remains the most popular form of cultivated cotton, colored varieties could replace chemically dyed fibers and provide more environmental friendly alternatives. In order to investigate the role of miRNAs in fiber color, we selected white and brown cotton varieties for comparative investigations. Through small RNA sequencing, a number of known miRNA families were discovered (74 in white cotton and 61 in brown cotton, with 44 shared) in which 11 miRNA families were significantly elevated in brown cotton variety. Functional enrichment and network analysis of target genes of these miRNAs revealed their regulatory role in secondary metabolite biosynthesis pathway, particularly the flavonoids pathway, which are known to be associated with fiber coloration. Pigmentation and developmental-related miRNA members such as miR396e-5p, miR167l, and miR1446 were also significantly enriched. Real-time PCR results suggest the regulatory role of miRNAs in these two cotton varieties. Furthermore, 30 and 25 novel miRNAs were also identified in white and brown cotton, respectively. Our findings also show miRNAs associated with fiber coloration and development through the intricate networks of miRNA and targets. Understanding these systems may provide novel insights on improving the fiber color and quality.

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Title: Simulation and experimental study on the seed filling performance of a split cotton seeder.

Author:Kezhi Li , Wenqing Cai , Binqiang Zhao , Bo Lu , Shufeng Li , Xiangdong Ni

Imprint: Biosystems Engineering, Volume 253, May 2025, 104128

Abstract: To enhance the seed-filling performance of the split-type cotton seed displacer, a force analysis of the cotton seed filling process and a coupling simulation analysis were conducted. Firstly, these analyses identified three key factors influencing the seed-filling performance: vibration frequency, negative air suction pressure, and seed content in the seed box. Secondly, single-factor simulation tests were carried out on the above three influencing factors, and the influence law of each single factor on the filling performance was obtained. Ultimately, by leveraging three evaluation indices, i.e. the qualification rate, the missed-seeding rate, and the re-seeding rate, a three-factor, five-level quadratic rotational orthogonal combination test was executed. This initiative was launched to formulate the mathematical models corresponding to each influencing factor, to analyse the underlying influence mechanisms of factor interactions on the qualification rate and missed-seeding rate, and to conduct parameter optimisation coupled with experimental verification. At the optimal simulated parameter combination of a vibration frequency of 81.69 Hz, air suction negative pressure of 2.24 kPa, and the seed content of the seed box of 51.19 %, the qualification rate was 92.4 %, the missed seeding rate was 3.4 %, and the reseeding rate was 4.2 %. This was verified by a bench test that gave a qualification rate of 92.3 %, the missed seeding rate was 3.6 %, and the reseeding rate was 4.1 %. The optimisation results were validated by the results of the bench test, which meets the agronomic requirements of cotton sowing.

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Title: Drought Resilience of Gossypium spp.: PEG-6000 Induced Responses at Germination and Seedling Stages.

Author: Sadettin Çelik, Gülay Zülkadir, Tahsin Beycioğlu

Imprint: DOI:10.20944/preprints202502.1988.v1

Abstract: This laboratory experiment was conducted in the Forestry Department of Bingöl University, Vocational School of Youth, in 2023. It aimed to investigate the responses of cotton genotypes to drought stress by creating osmotic pressure stresses of 0 MPa (control), -4 MPa, -6 MPa, -8 MPa, and -10 MPa using PEG 6000 chemical on the advanced lines SC32 and SC38, as well as the varieties Aşkabat 71 and May 505. Various parameters such as Root length (RL), Root Fresh Weight (RFW), Root Dry Weight (RDW), Shoot Length (SL), Shoot Fresh Weight (SFW), Shoot Dry Weight (SDW), Relative Water Content (RWC), Germination percent (GP), Vigor Seed Index (VSI), and Number of Lateral roots (NLRs) were measured. It was observed that as the severity of drought increased, the root system expanded in parallel. However, the plant's tolerance decreased with increasing drought severity. The genotypes SC32 and SC38, which were obtained from the breeding program for developing drought-tolerant varieties, exhibited high averages in almost all drought measurement parameters, demonstrating a high level of heterosis. As a conclusion, continuing the breeding program with these genotypes was found tolerant to contribute to the success of breeding. May 505 variety showed high tolerance to drought in terms of Relative Water Content (RWC), and it also exhibited promising results in other parameters compared to G. barbadense variety Aşkabat 71 and segregating population genotypes. May 505 variety showed a high germination rate and rapid germination, suggesting its potential use as a parent in both drought and early variety breeding programs.

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Title: SEEDSTICK Affects Seed Development by Mediating Cytokinin Levels in Cotton.

Author: Xiaohong Zhang, Yifan Li, Yunjie Ge, Yuhao Mao, Genhai Hu , Qifeng Ma, Eryong Chen

Imprint: Physiol Plant, . 2025 Mar-Apr;177(2):e70161. doi: 10.1111/ppl.70161.

Abstract: The SEEDSTICK transcription factor is important for flower and seed development, but the underlying molecular mechanisms remain unclear in cotton. In this study, we identified and cloned two STK homolog genes in upland cotton, an economically valuable cultivated crop. Phylogenetic and sequence analyses showed that the C-terminus of both GhSTKs had a conserved -DJJILHLG amino acid sequence and that GhSTK1 and GhSTK2 were very similar to GaAGL11 and GrAGL11, respectively. Quantitative real-time PCR analysis revealed that both GhSTKs were highly expressed in the ovules, and GUS activity was detected in the style and stigma. Subcellular localization experiments showed that GhSTK1 and GhSTK2 were localized to the nucleus. In Arabidopsis, the overexpression of GhSTK1 or GhSTK2 affected floral organ development and seed formation by increasing the transcript levels of the CKX genes and other genes related to floral development. Silencing both GhSTK1 and GhSTK2 increased the expression of GhFT and GhSHP and led to the earlier appearance

of cotton buds. Yeast two-hybrid and bimolecular fluorescence complementation assays indicated that the two GhSTK proteins could interact with the GhSEP3 and GhSEP4 proteins. The present results suggest that GhSTK1 and GhSTK2, which have different sequences and expression patterns, might be functionally redundant and influence the regulation of cotton bud and seed development.

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Title: Proteome-based investigation of seeds from two *Gossypium Hirsutum* L. Genotypes.

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

Imprint: South African Journal of Botany, Volume 180, May 2025, Pages 83-95
Abstract: Cotton is an important commercial crop regarding oil and fiber worldwide. It makes a significant contribution to the economy of Pakistan. The commercially significant cottonseed is used to produce oil, meal, linters, hulls, and other products. Heat stress is a major threat to cotton productivity, so there is a need to produce heat-resistant cotton crops to minimize yield losses. This proteomic study aims to identify and quantify differences in protein expression levels between heat-tolerant and heat-susceptible genotype seeds, providing insights into the molecular processes associated with heat stress tolerance by using LC-MS/MS analysis. We identified a total of 1807 proteins in heat-sensitive and 1564 in heat-tolerant genotypes. *Gossypium hirsutum,* L. seeds proteome exhibited the 44 significantly differentially expressed proteins that contributed to the understanding of heat tolerance-related biological processes occurring in the seeds during development. Protein functional classification showed that many identified proteins are involved in the metabolism of carbohydrates, lipids, amino acids, and energy production. In addition to these proteins, different peptidases, fiber-related proteins, and more than 100 heat tolerance-related proteins were also identified. This study provides understanding of the dynamics of the proteomes in two physiologically distinct cotton seeds that would help use heat-tolerant genotypes in future breeding programs.

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Title: Identification of favorable alleles from exotic Upland cotton lines for fiber quality improvement using multiple association models.

Author; Hrithik Mangla, Min Liu, Deepak Vitrakoti, Rama Vamsi Somala

Imprint: Front. Plant Sci., 16 April 2025, Sec. Plant Breeding

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Abstract: Upland cotton (Gossypium hirsutum) faces the challenge of limited genetic diversity in the elite or improved gene pool. To address this issue, we explored alleles contributed by five 'converted' exotic lines sampling most of the undomesticated botanical races of G. hirsutum, in BC1F2 and F3 populations. Joint analysis of all populations along with population-specific analyses identified 38 unique QTL for six different fiber quality traits. At 15 of these loci, DES56 or the elite allele improved upon all the exotics. For another 15, only a single of the five exotics improved upon the elite allele, suggesting the rare alleles that may not have been sampled in the cotton domestication or improvement. At the remaining 8 QTL, multiple exotic lines contributed the superior allele, suggesting that DES56 (and by extension the elite gene pool) has chronically poor alleles at these loci. Converted strains T1046, T326, and T063 showed the highest potential for contributions to cotton fiber quality breeding programs. Upper Half Mean Length and Fiber Strength showed multiple QTL regions affecting both traits simultaneously, while the Uniformity Index showed the smallest heritability values. The estimation of pairwise genetic distances for six parental lines indicates that DES56 has a higher genetic similarity with each exotic line than the exotic lines have with each other. Most of the detected QTL were 'minor' (explaining less than 10% of variance) supporting the implementation of genomic selection techniques to utilize the cumulative effects of most of these QTL distributed genome-wide. Finally, some regions were consistently unfavorable for exotic introgression such as on chromosomes A13 and D09, indicating the possible genome-wide haplotypes that may combine the benefits of a history of scientific breeding of the elite gene pool.

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Title: Variability in Cotton Fiber Quality under Innovated and Traditional Farming Systems.

Author:Muhammad Akbar Zardari, Lal Chand Mukwana, Nasir Shahzad Memon, Aijaz Ahmed Soomro, Touqeer Ahmed Shaikh, Reema Vistro, Medhia Hanif

Imprint: Research Journal for Social Affairs, 03 (02) 2025. 311-321

Abstract: The quality of fibers significantly impacts spinning efficiency, fabric durability, and overall market value in the industry. This study analyses the quality characteristics of cotton fibers produced by innovative and traditional farming methods, emphasizing the superior fiber properties attained through innovative cotton farming. The cultivation of cotton using advanced agricultural practices resulted in distinguished fiber qualities, attaining a spinning consistency index of 102.42, thereby ensuring improved processing and strong yarn development. The moisture content decreased to 6.05%, which improved fiber stability and reduced processing challenges. The micronnaire measurement of 5.05 µg/inch and a fiber maturity index of 0.899 were significantly increased, improving the overall fiber fineness, strength, and dye absorption characteristics. The mean length of 2.951 cm in the upper half is remarkable, ensuring longer and more durable fibers essential for high-quality textile production. The parameters of strength and elongation are essential in assessing yarn quality. The cotton obtained through advanced agricultural methods exhibited a fiber strength of 36.81 g/tex and an elongation of 6.81%, leading to increased tensile resistance and enhanced fabric durability. The brightness level (80.66 Rd) was significantly increased, while the yellowness (+b = 7.07) was decreased, leading to whiter, cleaner fibers preferred by premium textile manufacturers. Innovative farming practices resulted in a significant reduction in contamination levels, with a short fiber index of 4.88%, a trash count of 26.50 pieces per 100 grams of lint, and a minimal trash area of 1.05%. The enhancements yield a purer fiber, increasing its suitability for high-quality yarn manufacturing. The ginning out-turn of 37.63% was high, optimizing lint recovery and improving economic profitability. The results confirmed that advanced agricultural practices enhanced fiber length, strength, cleanliness, and yield, which are critical factors in the production of high-quality cotton textiles. Adopting these innovative practices can improve cotton status in global textile markets, establishing it as the preferred option for manufacturers in search of high-quality raw materials.

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Title: Genetic progress in cotton fiber yield and its components in Türkiye.

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Abstract: Understanding the genetic progress in yield and its components is crucial for the effective planning of future research. However, no study has been conducted to examine the genetic progress in yield and yield components of cotton varieties released in Türkiye. Objectives -In this context, the objectives of this study were to estimate the contribution of cotton breeding programs to the genetic improvement of fiber yield and its components in Türkiye, and moreover, to examine changes in yield components and their relationships with fiber yield. Methods- Ninety-eight cotton varieties released in Türkiye between 1964 and 2013 were evaluated in field experiments during the 2014 and 2015 growing seasons. Results- Fiber yields varied significantly among the varieties. Linear regression analysis revealed a highly significant positive relationship between fiber yield and the year of release ($P < 0.001$). Over the 50-year period from 1964 to 2013, cotton breeding programs achieved an annual increase of 1.07 % or 14.42 kg ha^{-1} . Additionally, fiber yield was positively correlated with the boll number (0.802) and the ginning percentage (0.536), while negatively correlated with plant height (-0.367) and seed index (-0.407). Conclusions- Improvement in fiber yield was mainly associated with an increase in the boll number and ginning percentage. Some key correlations were identified between fiber yield and its components. These relationships offer valuable insights into which traits can be enhanced concurrently in future breeding programs.

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Title: Impact of Species Differences on Cotton Fiber Characteristics and Dye-ability.

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Abstract: Gossypium barbadense and Gossypium hirsutum account for the vast majority of international cotton acreage. Therefore, the aim of this study is to compare the fiber quality of these cotton genotypes native to the Egyptian region with other cotton species grown worldwide to improve the understanding of cotton fiber quality and its applicability in different contexts of the textile industries. We conducted a comparative analytical study for a total of 14 cotton samples, 6 of G. barbadense (Egyptian cotton) and 8 of G. Hirsutum (Upland cotton). Fiber quality analyses of all cotton fiber samples were performed using the Uster high volume instrument (HVI) to determine fiber characteristics such as fiber length, uniformity, strength, elongation,

fineness, maturity, color, and trash. Also, fiber was chemically analyzed to determine the difference in chemical constituents such as ; α-cellulose %, reducing sugar %, wax %, moisture %, ash % of fibers, and seed oil content % of the seeds among the Gossypium hirsutum and Gossypium barbadense understudied samples. The dye ability of various cotton genotypes using orange reactive dye was measured, and all color measurements were analyzed. The data on fiber quality properties were analyzed. The results of fiber quality properties showed that characteristics of Gossypium barbadense have high quality compared to Gossypium hirsutum. Although G. barbadense cotton genotypes were superior to G. Hirsutum genotypes in the majority of fibers characteristics, both had good affinity to the reactive dye. Studying the differences between cotton fibers from Gossypium hirsutum and Gossypium barbadense is extremely important across scientific, industrial, and agricultural domains. The novelty lies in bridging fundamental science as genomics and biochemistry to the applied innovations across various fields, such as agriculture, textiles and sustainability.