GLEANINGS IN COTTON RESEARCH

MARCH 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.

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

We duly thank The Director, Dr Y G Prasad, 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: Simulation modeling of cotton yield responses to management strategies under climate change: insights from DSSAT.

Author: Mohil Pourebrahimi Foumani, Xinhua Yin, Joshua S. Fu, & Cheng-En Yang

Imprint: Journal of Plant Nutrition https://doi.org/10.1080/01904167.2025.2462702

Abstract: Forecasting cotton response to management strategies under climate change is considered an advanced tool for future planning to ensure global fiber security. An existing data set from a long-term cotton field experiment (39 years) at The University of Tennessee Institute of Agriculture Research and Education Center in Jackson was used for this project. This experiment consists of the complete combinations of two tillage systems (no-tillage and conventional tillage), and four nitrogen (N) application rates of 0, 30, 60, and 90 lb acre−1. In this study, climate change impacts on cotton yield responses to management strategies were assessed using the DSSAT model for three projected periods (2030, 2040, and 2050) under the Representative Concentration Pathway 8.5 (RCP8.5). Results were compared with the baseline scenario of 1986–2018. As temperatures rise and rainfall decrease continuously from 2030 to 2050, the trend of cotton yield decreases more pronounced in 2050 compared to 2040 and 2030. Under future climate change, lint yield will suffer severe damage from no or low N application, and intensive conventional tillage. There will be greater need that apply a high N rate to cotton under no-till production than conventional tillage. Overall, a combination of 60 to 90 lb acre−1 and no-tillage will be warranted to mitigate the negative effects of changing climate on lint yield. In conclusion, results from the DSSAT model provide management strategies on cotton for the future under changing climates. The best management system for future cotton production will be 90 lb acre−1 under no-tillage.

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Title: Effect of Supplemental Irrigation at Different Irrigation Levels on Cotton Yield and Water Use Efficiency at Werer, Middle Awash, Ethiopia.

Author: Fikadu Robi, Jemal Mohammed , Tesema Mitiku , Kebede Nanesa , Nigussie Abebe and Wondimu Tolcha

Imprint: Proceedings of Completed Research Activities by the Soil and Water Management Research Directorate Volume II, 2023 Ethiopian Institute of Agricultural Research

Abstract: A terminal dry spell is one of the main limiting factors for cotton productions. Therefore, this study was conducted to assess the effects of supplemental irrigation at various levels on cotton yield and water use efficiency at Werer, Middle Awash, Ethiopia, during the 2018, 2019 and 2021 cropping seasons. Cotton was sown in a randomized complete block design layout, comprising six treatments (No supplemental irrigation as a control, and 100%, 80%, 60%, 40%, and 20% of the crop evapotranspiration), replicated three times. The result indicated that the highest average cotton seed yield (3,252 kg/ha) was obtained with 80% supplementary irrigation application. A water use efficiency of 0.87 kg/m3 was attained when 80% of the crop evapotranspiration was provided as supplementary irrigation. The application of supplemental irrigation in the area improved cotton yield and water productivity during seasons characterized by limited and erratic rainfall.

3

Title: Maximizing Cotton Yield and Quality: The Interplay of Canopy Structure and Planting Density.

Author: Samuel Klutse , Gideon Boabeng Duncan , Isaac Akomaning , Muhammad Faisal , Ahmad Iqbal, Muhammad Wajahat Rasool , Pootchy Jasmin Belizaire , Emmanuel Botchway , Muhammad Khizar Hayat , B. A. Ouma

Imprint: World News of Natural Sciences 59 (2025) 413-429

Abstract: Cotton, a globally significant cash crop, demands optimized cultivation practices to ensure sustainable yields and superior fiber quality. This study underscores the critical role of canopy management and planting density in achieving these objectives. By strategically manipulating canopy architecture through techniques such as pruning and chemical topping, growers can significantly enhance light penetration and nutrient distribution within the cotton plant. These practices contribute to improved boll development, increased boll number, and enhanced boll weight, ultimately boosting overall yield. Furthermore, it emphasizes the importance of planting density in optimizing light interception and microclimate conditions within the canopy. Higher planting densities generally lead to increased light interception, which positively impacts photosynthesis and subsequent yield. However, it is crucial to find the optimal balance as excessive density can negatively impact boll weight and fiber quality. The complex interplay between canopy management and planting density is evident in their influence on various physiological parameters. Canopy temperature, water-use efficiency, and nitrogen uptake are significantly affected by these factors. By carefully managing canopy structure and plant spacing, growers can create favorable microclimatic conditions for cotton growth and development. In nut shells, highlights the need for a holistic approach to cotton cultivation, emphasizing the integration of canopy management and planting density strategies. By optimizing these factors, farmers can improve resource utilization, enhance yield, and maintain fiber quality, thereby contributing to the sustainability and profitability of cotton production.

4

Title: Yield maximization of Bt. cotton by integrated crop management techniques.

Author: SP Bhagat, NK Medhe, SS Ilhe, NJ Danawale, NK Bhute, PS Bodake and MR Patil

Imprint: International Journal of Research in Agronomy 2024; SP-7(11): 395-399

Abstract: A field experiment entitled, "Yield maximization of Bt. cotton by integrated crop management techniques" was caried out during kharif, 2023 at Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra (India). The experiment was laid out in Randomized Block Design (RBD) with three replications and nine treatments. The results of present investigation revealed that, yield and yield contributing characters of Bt. cotton were significantly influenced by different treatments. Treatment T1 i.e., wider spacing (90 cm × 90 cm) recorded significantly maximum lint weight boll-1 (1.36 g), seed weight boll-1 (2.64 g), boll weight (4.00 g), number of green (unopened) bolls plant-1 (2.60), number of picked bolls plant-1 (45.09) and seed cotton yield plant-1 (180.36 g). The highest seed cotton yield (4162 kg ha-1) and stalk yield (6202 kg ha-1) were recorded with treatment T9 (Cotton in closer spacing + Detopping at 100 cm height + Pruning of monopodia at 45 DAS + Two sprays of Mepiquat chloride @ 25 g a.i. at 45 and 60 DAS). The quality parameters viz., ginning percentage (%), lint index (%), micronaire value (µg inch-1), tensile strength (g tex-1), 2.5% span length (mm) and uniformity ratio (%) were not influenced significantly due to different treatments. Treatment T9 (Cotton in closer spacing + Detopping at 100 cm height + Pruning of monopodia at 45 DAS + Two sprays of Mepiquat chloride @ 25 g a.i. at 45 and 60 DAS) recorded highest cost of cultivation (₹ 1,27,328), gross monetary returns (₹ 2,81,780), net monetary returns (₹ 1,54,452) and B:C ratio (2.21) than rest of all treatments.

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Title: Socio-economic Status of CROPSAP Scheme of Cotton Growers.

Author: P.D. Undirwade, R.V. Chavan and Tukaram B. Munde

Imprint: International Journal of Theoretical & Applied Sciences, 16(1): 46-49(2024)

ABSTRACT: In the present study the socio-economic characteristics of beneficiary and non-beneficiary cotton growers have been assessed. It may prove beneficial to know socio-economic characteristics of the CROPSAP scheme of cotton cultivators as well as their knowledge about CROPSAP scheme of cotton. The increasing yield of fibre is a big challenge around the globe especially for researchers. This was based mainly on primary data which was collected through personal interview method with the help of pre-tested schedules. An investigation was conducted in the Jalna district of Maharashtra purposively based on 2nd highest area under cotton crop. Multistage sampling technique was used for selection of district, tehsils and villages. Total sample size was 160 where 80 were beneficiary and 80 non-beneficiary cotton growers. Data was analyzed with the help of Descriptive statistics, was used to calculate the socioeconomic level of cotton growers using mean, frequency, and percentage. Beneficiary cotton growers are more educated than non-beneficiary cotton growers. Both beneficiary and non-beneficiary cotton growers were middle age group (41.25 per cent) and (43.75 per cent) respectively. Both the growers have agriculture was the main occupation. The benefit of CROPSAP scheme for farmers is reduces the extra application of insecticides and pesticides hence saving the cost and increasing the status of farmers. The benefit of this scheme is that the problems are sorted according to their severity from the respondents' perspective.

6

Title: Study of critical crop-weed competition in cotton (Gossypium hirsutum L.) under south Gujarat conditions.

Author: JB Vasave, MS Dudhat, HM Patel, HM Virdia, RR Sisodiya, Munira S Mandiwala and VT Parmar

Imprint: International Journal of Research in Agronomy 2025; 8(1): 363-367

Abstract: The field experiment was conducted at College Farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari during 2020-21 and 2021-22. To Study of critical crop-weed competition in cotton (Gossypium hirsutum L.) under south Gujarat condition. There were twelve different critical crop weed competition treatments and randomized block design with three replications. The treatment W6 (Weed free up to harvest) was recorded significantly higher plant height (cm), number of sympodial branches per plant, number bolls per plant, boll weight (g), seed cotton yield and stalk yield during both the years and in pooled results. Significantly maximum weed control efficiency and minimum weed index was also recorded under the weed free up to harvest treatments (W6) during both the years and in pooled results. The treatments W5 (Weed free up to 75 DAS), W4 (Weed free up to 60 DAS) and W7 (Weedy up to15 DAS) effective proved for higher plant height, number of sympodial branches per plant (cm), number bolls per plant, boll weight (g), seed cotton yield and stalk yield, weed control efficiency (%) and weed index (%). The treatment

W12 (Weedy up to harvest) recorded lower growth parameters, yield attributes and yields parameters, weed index and weed control efficiency during both the years and in pooled results. Weed index during 2020-21 (40.40%), 2021-22 (43.13%) and in pooled results (41.77%) were recorded under treatment W12 (Weedy up to harvest) it indicates the percentage reduction in seed cotton yield due to heavy weed infestation compared to a weed-free plot.

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Title: Burkholderia sp. AQ12-mediated Molecular Adjustments Assist Growth of Salt-stressed Cotton (Gossypium hirsutum L.) By Modulating Biochemical Status and Nutrient Acquisition Patterns.

Author: Sidra Batool, Sijal Fatima, Uzma Qaisar, Muhammad Shahid & Muhammad Sohail Akram

Imprint: Journal of Soil Science and Plant Nutrition , Published: 03 February 2025

Abstract: Soil salinity negatively modulates plant growth and physio-biochemical attributes. The present study deciphered the Burkholderia sp. AQ12-mediated responses in cotton plants. Methods Seeds of FH-941 (salt sensitive) and FH-326 (tolerant) genotypes were inoculated using AQ12 or water. Half of the both (inoculated and un-inoculated) received no salt while other received salt/NaCl stress. The raised plants were analyzed for various bio-chemical indicators. Results In presence of salt stress, chlorophyll (chl) a content (24.68 mg g−1 FW) in FH-941 was 11.3% and 8.6% less in comparison to its control group and chl a content in FH-326, respectively. FH-941 exhibited a higher oxidant response as indicated by 8.69 and 25.54 μmol g−1 FW malondialdehyde (MDA) and hydrogen peroxide (H_2O_2), respectively. A balanced catalase (CAT) and peroxidase (POD) activity across all treatments particularly under salt stress (23.82 and 40.98 U mg−1 protein, respectively) was recorded in FH-326 indicating its potential to cope NaCl induced oxidative injury. Further, FH-326 exhibited 17.58 mg g−1 DW root K^+ associated with balanced expression of NHX1 and HAK5. A higher expression of HKT1 but reduced expression of NHX1, SOS1 and HAK5 indicted poor salt tolerance by FH-941. However, AQ12 inoculation resulted in optimum chl a (28.66 mg g−1 FW), chl b (13.93 mg g−1 FW), MDA (6.89 μmol g−1 FW), H_2O_2 (20.11 μmol g−1 FW) content in FH-941 resulting in better growth in saline soil. Conclusions The findings highlighted the biochemical and molecular basis of salt tolerance in cotton and signify the importance of AQ12 inoculation for cotton cultivation in saline soils.

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Title: Selection of Accurate Irrigation System Based on Root Anatomy In Cotton (Gossypium Hirsutum L. Cv. Stoneville 468) Cultivation.

Author: Tuylu, G. İ.

Imprint: Applied Ecology and Environmental Research 23(1):1115-1127.

Abstract. In the study it was aimed to figure out the accurate irrigation system conditions for cotton cultivation. So how cotton root tissues respond to different irrigation applications was examined under different conditions created by applying different irrigation water levels and using Drip Irrigation System and Subsurface Drip Irrigation System. Finally, the effects of two irrigation systems on cotton root anatomy were compared and optimum irrigation conditions were determined for both systems. In irrigation period of 2015 cotton was cultivated. Four different irrigation water levels were applied to cotton by two irrigation systems. Anatomical studies were performed by using paraffin method and light microscopy in 2016. It was anatomically determined that the optimum irrigation condition was 25% limited- irrigation under Drip Irrigation System Condition while it was 50% limited- irrigation under Subsurface Drip Irrigation System Condition. The effects of the two systems on development of the periderm tissue, which is one of the cotton root tissues, were different under drought and water stress conditions. Under both conditions, xylem vessels developed an anatomically similar response when the roots of cotton were exposed to the amount of irrigation water which was more than or less than 25% of the optimum irrigation water requirement.

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Title: Transport of Nitrate, Phosphate and Potassium in Vadose Zone with Varying Rainfall Scenarios for a Semi-arid Cotton Growing Region of South India.

Author: Deepak Kumar, P. Vijay Kumar, Pankaj Kumar Gupta & Suri L. Naidu

Imprint: Navigating the Nexus , Chapter First Online: 02 February 2025 pp 275–295, Part of the book series: Water Science and Technology Library ((WSTL,volume 102))

Abstract: In terms of farm fertilizer Consumption, India is the world's second largest country after China. Reducing fertilizer use cannot be considered a viable option, since optimizing food output was the highest priority for the population's food and nutritional protection. Nitrogen, Phosphorous and Potassium fertilizers are farm fertilizers and are in great demand in Indian agriculture. This study investigated the effect of rainfall dynamics on farm fertilizer transport for rainfed Cotton Crop in Semi-arid Region in the Raichur district of South India. The solute transport and reaction parameters were assessed at the depths of 50, 100 and 150 cm of soil column. Hydrus-1D and Hydrus-2D software has been used for modelling transport of fertilizer in vadose zone. Rainfall data from 2015 to 2020, Soil data, Crop data, Soil hydraulic parameters, and Solute data has been used for this study. Results suggested that solute transport for average actual precipitation, 20% decreased precipitation and 20%

increased precipitation at 150 cm depth of soil column was 0.000109, 0.00000000424, 0.000371 mmol cm−3 for nitrogen fertilizer, 0, 0, 0.00000014 mmol−3 for phosphorous fertilizer and 0, 0, 0.0000000329 mmol−3 respectively for potassium fertilizer. From this, it can be inferred that increased precipitation caused solutes to move more quickly than usual. Therefore, it can be concluded that due to climate change, changes in rainfall patterns and increased rainfall intensity might lead to excessive leaching of agricultural fertilizers into the vadoze zone and groundwater.

10

Title: Morphological characteristic extraction of unopened cotton bolls using image analysis and geometric modeling methods.

Author:Cheng Cao, Pei Yang, Chaoyuan Tang, Fubin Liang, Jingshan Tian, Yali Zhang, Wangfeng Zhang

Imprint: Computers and Electronics in Agriculture, Volume 232, May 2025, 110094

Abstract: Extracting cotton boll phenotypic parameters from imaging data is a prerequisite for intelligently characterizing boll growth and development. However, current methods relying on manual measurements are inefficient and often inaccurate. To address this, we developed a cotton boll phenotypic parameter extraction program (CPVS), a tool designed to estimate the morphological characteristics of unopened cotton bolls from images. CPVS integrates semi-automatic data extraction with advanced algorithms to calculate length, width, volume, and surface area. Length and width estimation algorithms were developed using a custom “Fixed” image set, which links pixel dimensions to actual measurements. Volume and surface area models were based on shape classification using a custom “Random” image set, trait correlations, and measured data. Testing showed strong performance, with R^2 values of 0.880 and 0.769 and root mean square error (RMSE) values of 0.173 and 0.188 for length and width, respectively. The volume model achieved an R^2 of 0.91 and an RMSE of 1.76, while surface area models had R^2 values of 0.76 and RMSEs of 2.37 and 2.41. These results indicate that CPVS is a robust tool, providing theoretical and practical support for efficient, accurate characterization of cotton boll morphology.

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Title: Enhanced coordination of photosynthetic functions among cotton boll–leaf systems to maintain boll weight under high-density planting.

Author:Minzhi Chen , Yinhua Yan , Fubin Liang , Jinyu An , Yuxuan Wang , Jingshan T ian , Yali Zhang , Chuangdao Jiang , Wangfeng Zhang

Imprint: European Journal of Agronomy, Volume 165, April 2025, 127540

Abstract: High planting density curtails the boll number per plant more significantly than the single boll weight, yet it is hard to estimate the boll weight from single-leaf photosynthesis with increasing boll abscission. We speculated that high plant density may lead to coordination among photosynthetic organs to maintain boll weight. Therefore, cotton (*Gossypium hirsutum* L.) yield formation, the photosynthetic characteristics of the leaves and boll–leaf system were studied under various plant densities. The results showed that the boll number per plant or boll number per boll–leaf system decreased more greatly than the boll–leaf system number per plant with increasing plant density. Leaf area, single leaf photosynthetic rate, and CO_2 assimilation of the boll–leaf system all gradually decreased with the increase of plant density. There was a significant positive linear correlation between integrated CO_2 assimilation of the boll–leaf system and boll biomass per boll–leaf system. After girdling treatment, the boll biomass of the boll–leaf system decreased more greatly compared with non-girdling treatment with increasing plant density. Moreover, the girdling/non-girdling of boll biomass per boll–leaf system reached 0.8–1.0 at 19–25 plants m^{-2}. The removal of the lower-canopy bolls caused a significant increase in the boll biomass of the upper canopy, and the biomass per boll at high densities (>25 plants m^{-2}) increased more greatly than at low densities. Therefore, the rapid decrease in CO_2 assimilation of the boll–leaf system resulted in a decreased boll number per boll–leaf system as plant density increased (<25 plants m^{-2}). Under high densities (>25 plants m^{-2}), the boll biomass not only depends on the photosynthetic rate of the corresponding boll–leaf system, but also on the coordination of photosynthetic functions among adjacent cotton boll–leaf systems. Optimal planting density (19–25 plants m^{-2}) means that the assimilate production and utilization of the boll–leaf system can be balanced. At this density, the coordination of boll number and boll weight is conducive to maximizing the yield per plant and unit ground area.

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Title: Silencing of GhSHP1 hindered flowering and boll cracking in upland cotton.

Author: Wenjuan Xu, Qi Ma, Jisheng Ju, Xueli Zhang, Wenmin Yuan, Han Hai, Caixiang Wang, Gang Wang, Junji Su

Imprint: Front. Plant Sci. , 25 February 2025, Sec. Plant Breeding, Volume 16 - 2025 | https://doi.org/10.3389/fpls.2025.1558293

Abstract: The opening of cotton bolls is an important characteristic that influences the precocity of cotton. In the field, farmers often use chemical defoliants to induce cotton leaves to fall off earlier, thus accelerating the cracking of cotton bolls. However, the molecular mechanism of cotton boll cracking remains unclear. We identified ten *AGAMOUS* subfamily genes in upland cotton. Three pairs of *Gossypium hirsutum* AG subfamily genes (*GhAGs*) were amplified via tandem duplication. The promoters of the *GhAGs* contained a diverse array of *cis*-acting regulatory elements related to light responses, abiotic stress, phytohormones and plant growth and development. Transcriptomic analyses revealed that the expression levels of *GhAG* subfamily genes were lower in vegetative tissues than in flower and fruit reproductive organs. The qRT−PCR results for different tissues revealed that the *GhSHP1* transcript level was highest in the cotton boll shell, and *GhSHP1* was selected as the target gene after comprehensive analysis. We further investigated the functional role of *GhSHP1* using virus-induced gene silencing (VIGS). Compared with those of the control plants, the flowering and boll cracking times of the *GhSHP1*-silenced plants were significantly delayed. Moreover, the results of paraffin sectioning at the back suture line of the cotton bolls revealed that the development of the dehiscence zone (DZ) occurred later in the *GhSHP1*-silenced plants than in the control plants. Furthermore, at the same developmental stage, the degree of lignification in the silenced plants was lower than that in the transformed plants with empty vector. The expression of several upland cotton genes homologous to key *Arabidopsis* pod cracking genes was significantly downregulated in the *GhSHP1*-silenced plants. These results revealed that *GhSHP1* silencing delayed the flowering and cracking of cotton bolls and that the cracking of cotton bolls was delayed due to effects on DZ development. These findings are highly important for future studies of the molecular mechanism of cotton boll cracking and for breeding early-maturing and high-quality cotton varieties.

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Title: Comparative Analysis of Floral Transcriptomes in Gossypium hirsutum (Malvaceae).

Author: Alexander Nobles, Jonathan F. Wendel, and Mi-Jeong Yoo

Imprint: Plants 2025, 14(4), 502; https://doi.org/10.3390/plants14040502

Abstract: Organ-specific transcriptomes provide valuable insight into the genes involved in organ identity and developmental control. This study investigated transcriptomes of floral organs and subtending bracts in wild and domesticated Gossypium hirsutum, focusing on MADS-box genes critical for floral development. The expression profiles of A, B, C, D, and E class genes were analyzed, confirming their roles in floral organ differentiation. Hierarchical clustering revealed similar expression patterns between bracts and sepals, as well as between petals and stamens, while carpels clustered with developing cotton fibers, reflecting their shared characteristics. Beyond MADS-box genes, other transcription factors were analyzed to explore the genetic basis of floral development. While wild and domesticated cotton showed similar expression patterns for key genes, domesticated cotton exhibited significantly higher expression in carpels compared to wild cotton, which aligns with the increased number of ovules in the carpels of domesticated cotton. Functional enrichment analysis highlighted organ-specific roles: genes upregulated in bracts were enriched for photosynthesis-related GO terms, while diverse functions were enriched in floral organs, supporting their respective functions. Notably, A class genes were not significantly expressed in petals, deviating from the ABCDE model, which warrants further analysis. Lastly, the ABCDE class genes exhibited differential homoeolog expression bias toward each subgenome between two accessions, suggesting that the domestication process has influenced homoeolog utilization despite functional constraints in floral organogenesis.

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Title: Effect of Critical Crop Weed-Competition in Cotton (Gossypium hirsutumL.)

Author: J. B. Vasave, M. S. Dudhat , Munira S. Mandiwala , H. M. Patel , R. R. Sisodiya , V. T. Parmar , S. S. Sonavane , V. D. Patel and P. A. Patil

Imprint: International Journal of Plant & Soil Science , Volume 37, Issue 1, Page 418-426, 2025;

Abstract: The field experiment was conducted at College Farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari during 2020-21 and 2021-22. Study of critical crop-weed competition in cotton (Gossypium hirsutum L.) under south Gujarat condition. The treatment W6 (Weed free up to harvest) were recorded significantly higher plant height at harvest, number of sympodial branches per plant, seed cotton weight (g/plant), stalk weight at harvest (g/plant) and seed cotton yield (kg/ha) during 2020-21, 2021-22 and in pooled results. But treatment (W6) was statistically at par with the treatments W5 (Weed free up to 75 DAS), W4 (Weed free up to 60 DAS) and W7 (Weedy up to 15 DAS) in both the years and in pooled results. The magnitude of increase in seed cotton yield with weed free up to harvest treatment (W6) over weedy up to harvest treatment (W12) were to the tune of 67.82, 75.90 and 71.87% higher during 2020-21, 2021-22 and in pooled results. Number of monopodial branches per plant was found non-significant results in both the individual years and in pooled results. Significantly minimum total least nutrient depletion (Nitrogen, phosphorus and potassium) by weed was recorded under the treatment W6 (Weed free up to harvest), value were nitrogen 0.27, 0.23 and 0.25 per cent, phosphorus 0.07, 0.06 and 0.06 per cent, potassium 0.38, 0.32 and 0.35 per cent during both individual years and in pooled results, respectively. But it remained at with the treatments W5, W4 and W7. Whereas, total highest nutrient depletion was recorded under the treatment W12 (Weedy up to harvest), value were nitrogen 13.34, 11.35 and 12.34 per cent, phosphorus 3.01, 2.73 and 2.87 per cent, potassium 14.37, 12.19 and 13.28 per cent during 2020-21, 2021-22 and in pooled results, respectively .

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Title: Ghβ-LCY1 influences metabolism and photosynthetic in *Gossypium hirsutum.*

Author:Yanmin Qian, Yaping Wang , Yu Zhang , Zongyan Chu , Mengxin Shen, Cheng Zhang , Lihua Huang, Zhihua Yang, Kaiwen Ren , Yuanyuan Shi , Tingting Jiao , Baoting Yang, Qiuyue Meng, Yuchen Miao, Jinggong Guo

Imprint: Plant Science, Volume 353, April 2025, 112417

Abstract: Carotenoids are metabolites of isoprene, which are crucial roles for plant growth and response to abiotic stress. Lycopene β-cyclase (β-LCY) is a key protease in the synthesis pathway of plant carotenoid, playing an important role in the carotenoid metabolism and synthesis pathway. However, the function of β-LCY is almost unknown in cotton (*Gossypium spp.*). In this study, we cloned the *A* and *D* genomes of *β-LCY1* from upland cotton (*Gossypium hirsutum*), designated as *Ghβ-LCY1A* and *Ghβ-LCY1D*. We found that *Ghβ-LCY1A* and *Ghβ-LCY1D* were highly expressed in the cotton leaves and localized in the chloroplasts, respectively. The bacterial pigment complementarity experiment showed that Ghβ-LCY1 has the activity of β-LCY in *Escherichia coli*. The virus-induced gene silencing (VIGS) analysis exhibited that *Ghβ-LCY1* silencing cotton plants resulted in a spotted phenotype on the leaves and sepals, slow growth, and stunted plant growth in upland cotton. Additionally, the content of chlorophyll, carotenoids, antheranthun, zeaxanthin, violaxanthin and ABA, were significantly decreased. Under normal light intensity, the chloroplast ultrastructure of leaves in *Ghβ-LCY1* silencing cotton plants was abnormal, and their photosynthesis (leaf absorptance, Fv/Fm) and non-photochemical quenching (NPQ) were significantly lower than control cotton plants, and this difference was enhanced after high light treatment. Taken together, our results indicate that Ghβ-LCY1 plays an important role in carotenoids metabolism, photosynthesis and participates in plant growth and light protection in cotton.

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Title: Characterization and functional analysis of CONSTANS-like 3 involved in photoperiodic flowering of *Gossypium hirsutum.*

Author:Zhangqiang Song , Han Zhao, Xin Wang , Miaomiao Ren , Ao Pan , Yu Chen , Jingxia Zhang , Tao Lu , Juan Cao , Furong Wang , Jun Zhang

Imprint: Plant Physiology and Biochemistry, Volume 221, April 2025, 109643

Abstract: The CONSTANS-like (COL) family plays a pivotal role in regulating plant photoperiodic flowering pathways. Although several COLs have been characterized in *Arabidopsis*, their functions in cotton lack clarity. Here, *GhCOL3*, a gene of the COL family in cotton (*Gossypium hirsutum*), was cloned and characterized. GhCOL3 is located in the nucleus, and *GhCOL3* was expressed in young leaves, hypocotyls, and flower organs and exhibited obvious circadian rhythms under long-day conditions. Overexpressing of *GhCOL3* heterogeneously in *Arabidopsis thaliana* led to delayed flowering, whereas silencing of *GhCOL3* in cotton using the virus-induced gene silencing system led to earlier flowering, suggesting a negative regulatory role of *GhCOL3* in plant flowering. Transcriptome analysis and expression detection showed that *bHLH38*, *bHLH100*, *bHLH101*, and *BBX31* were significantly upregulated in *GhCOL3* heterogeneous overexpression lines, whereas the expression of *FT* was downregulated. Moreover, the expression of *GhbHLH38*, *GhBBX31*, and *GhFT* were significantly affected in the *GhCOL3*-silenced line, thus laying the foundation for elucidating the regulatory mechanism of GhCOL3 in cotton flowering.

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Title: REVOLUTIONIZING COTTON HARVESTING: A COMPARATIVE STUDY OF MODIFIED AND EXISTING KNAPSACK COTTON PICKER.

Author: B.M. Khanpara, R.K. Kathiria, T.D. Mehta , N.B. Bharad , N.B. Parmar and Ravina Parmar

Imprint: Plant Archives Vol. 25, Special Issue (ICTPAIRS-JAU, Junagadh) Jan. 2025 pp. 193-199

Abstract: Cotton is a major fibre crop in India, accounting for 33% of global cultivation, yet its harvesting process remains predominantly manual, resulting in labour-intensive and time-consuming operations. This study compares an existing knapsack cotton picker, a modified knapsack cotton picker and traditional manual harvesting methods. The modified picker, with improved design for better cotton flow, achieved a higher picking capacity of 7.62 kg/h, surpassing the existing picker at 6.06 kg/h and manual methods at 3.72 kg/h. Both mechanical pickers exhibited high picking efficiency, with the modified picker achieving 95.79% and the existing picker 95.71%, compared to 96.93% for manual picking. The modified picker produced cotton of higher quality, as indicated by superior span length, uniformity ratio and fibre strength, compared to both the existing picker and manual harvesting. However, the modified picker exhibited a drawback of higher trash content (8.13%) relative to the existing picker (6.33%) and manual picking (3.59%). Despite this, the modified picker significantly reduced harvesting time by 51.44% and lowered costs by 14.86% compared to manual methods. Although, it had higher energy consumption, the modified picker still offered a net realization 3.27% greater than manual picking. These findings suggest that the modified knapsack cotton picker, despite its higher trash content, is a viable option for increasing the efficiency and cost-effectiveness of cotton harvesting, particularly in labour-constrained regions.

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Title: Harnessing multivariate insights coupled with susceptibility indices to reveal morpho-physiological and biochemical traits in heat tolerance of cotton.

Author: Tahira Luqman, Manzoor Hussain & Muhammad Kashif Riaz Khan

Imprint: *BMC Plant Biology* volume 25, Article number: 126 (2025)

Abstract: Cotton is essential for the global textile industry. However, climate change, especially extreme temperatures, threatens sustainable cotton production. This research aims to identify breeding strategies to improve heat tolerance and utilize stress-resistant traits in cotton cultivars. This study investigated heat tolerance for 50 cotton genotypes at the seedling stage by examining various traits at three temperatures (32 °C, 45 °C and 48 °C) in a randomized plot experiment. Analysis of variance revealed significant differences among the genotypes for all the studied traits. Morphological traits, including root and shoot length, fresh and dry root, and shoot weights, were adversely affected by heat stress. Chlorophyll contents declined significantly, indicating impaired and compromised photosynthetic efficiency. Biochemical assays underlined the elevated activities of antioxidant enzymes superoxide dismutase (SOD), peroxidase (POD), total free amino acids (TFA), total soluble sugars (TSS), proline content and declined production of total soluble proteins (TSP), which is indicative of oxidative stress. Physiological traits such as photosynthetic rate and cell membrane stability% decreased severely under stress conditions. The first five PCs under control and the first six PCs under stresses depicted eigenvalues > 1 and presented 72.96%, 76.11%, and 77.93% of total cumulative variability under control, T1 and T2, respectively. Cell membrane stability, a potential marker for heat tolerance, showed a strong positive correlation with total soluble sugars (TSS) and root length (RL) under extreme stress. Based on clustering, the genotypes were classified into four groups. Stress susceptibility indices indicated that NIAB-545 and FH-142 are promising genotypes for developing heat tolerance breeding strategies in cotton.

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Title: Metabolomics Provide New Insights into Mechanisms of *Wolbachia*-Induced Plant Defense in Cotton Mites.

Author: Xinlei Wang, Sha Wang, Qianchen Wei, Kedi Zhao, Feng Liu and Yiying Zhao

Imprint: 17 February 2025, doi: 10.20944/preprints202502.1205.v1

Abstract: Endosymbiotic bacteria play a significant role in the co-evolution of insects and plants. However, whether they induce, activate, or inhibit host plant defense responses remains unclear. In this study, non-targeted metabolomic sequencing was performed on cotton leaves infested with *Wolbachia*-infected and uninfected spider mites using parthenogenetic backcrossing and antibiotic treatment methods. A total of 55 differential metabolites were identified, which involved lipids, phenylpropanoids and polyketides. KEGG pathway enrichment analysis revealed seven significantly enriched metabolic pathways. Among them, flavonoid and flavonol biosynthesis, glycerophospholipid metabolism, and ether lipid metabolism showed extremely significant differences. In *Wolbachia* infected cotton leaves, the flavonoid biosynthesis pathway was significantly upregulated, including quercetin and myricetin, suggesting that the plant produces more secondary metabolites to enhance its defense capability. Glycerophosphocholine (GPC) and sn-glycerol-3- phosphoethanolamine (PE) were significantly downregulated, suggesting that *Wolbachia* may impair the integrity and function of plant cell membranes. The downregulation of lysine and the upregulation of L-malic acid indicated that *Wolbachia* infection may shorten the lifespan of spider mites. At various developmental stages of the spider mites, *Wolbachia* infection increased the expression of detoxification metabolism related genes, including gene families such as cytochrome P450, glutathione S-transferase, carboxylesterase, and ABC transporters, thereby enhancing the detoxification capability of the host spider mite. This study provides a theoretical basis for further elucidating the mechanisms by which endosymbiotic bacteria induce plant defense responses and expands the theoretical framework of insect-plant co-evolution.

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Title: Population build-up of natural enemies in cotton habitat after insecticidal applications at farmer’s field.

Author: Khyali Ram, Dalip Kumar, Deepika Kalkal, Ravi Kant, Bhupender Singh, Pavitra Kumari and Vivek Kumar Saini

Imprint: International Journal of Biology Sciences 2025; 7(1): 105-109

Abstract: Genetically modified (GM) cotton crop extensively cultivated in tropical and sub-tropical regions worldwide. An experiment was conducted twice in crop season at five different locations to record the relative toxicity and build-up of natural enemies after application of different insecticide at farmers' fields. During the first application of insecticides, emamectin benzoate 50 SG + flonicamid 50 SG (0.42 ladybird beetle, 0.84 green lacewing, 2.11 spiders, 0.29 yellow paper wasp/plant and 4.98% nymphal parasitization of whitefly) favoured to build up more compared to dinotefuran 20 SG + imidacloprid 70 WG treated plots (0.34 ladybird beetle, 0.57 green lacewing, 1.44 spiders, 0.17 yellow wasp per plant and 4.52% whitefly nymph parasitization). In pursuit of second application, average build-up in flonicamid 50 WG + imidacloprid 200 SL i.e., 0.49 ladybird beetle, 0.49 green lacewing, 1.64 spiders, 0.24 yellow paper wasp/plant and 3.93% nymphal parasitization of whiefly observed on lower side, while in flonicamid 50 WG + thiamethoxam 30 FS recorded 0.57 ladybird beetle, 0.73 green lacewing, 1.81 spiders, 0.37 yellow wasp/plant and 4.17% nymphal parasitization exhibited to favour more of numbers of natural enemies. Thus, while selecting an insecticide for the management of a target pest, negative effects on natural enemies, it's survival and growth, reproduction and changes in behaviour must be kept in mind.

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Title: Induction by caterpillars of stored and emitted volatiles in terpene chemotypes from populations of wild cotton (*Gossypium hirsutum*).

Author: Marine Mamin, Mary V. Clancy, Galien Flückiger, Teresa Quijano-Medina, Biiniza Pérez-Niño, Luis Abdala-Roberts, Ted C. J. Turlings & Carlos Bustos-Segura

Imprint: *BMC Plant Biology* volume 25, Article number: 127 (2025)

Abstract: Upland cotton (*Gossypium hirsutum*) plants constitutively store volatile terpenes in their leaves, which are steadily emitted at low levels. Herbivory leads to a greater release of these stored volatiles. Additionally, damaged plants increase the accumulation of volatile terpenes in their leaves and begin to synthesize and emit other terpenes and additional compounds. This has been well characterised by cultivated *G. hirsutum*, but little is known about volatile production in response to herbivory in wild populations. We investigated how damage by a generalist herbivore species, the beet armyworm (*Spodoptera exigua*), affects leaf-stored and emitted volatiles in wild *G. hirsutum* plants and compared the responses of two known chemotypes. Wild cotton plants were grown in a greenhouse from seeds collected from four distinct locations covering sixteen populations, along the Yucatan coast (Mexico), from where this cotton species originates. We assessed whether the differences in leaf terpene profiles between the two chemotypes persisted upon herbivory, in leaves and in headspace emissions, and whether these chemotypes also differed in the production and release of herbivory-induced volatiles. In addition to chemotypic variation, we further investigated intraspecific variation in the volatile response to herbivory among genotypes, populations, and the four geographic regions.

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Title: Monitoring and biochemical characterization of resistance against commonly used insecticides in cotton jassid, *Amrasca biguttula* (Ishida) from Punjab, Pakistan

Author: Sikandar Hussain, Shoaib Freed, Afifa Naeem, Muhammad Sheraz Shah, Muhammad Zeeshan Nazar & □ Muhammad Waqas Sumra

Imprint: International Journal of Tropical Insect Science, Published: 29 January 2025

Abstract: Amrasca biguttula, commonly known as the cotton jassid, is a major sap-sucking pest of cotton, which causes chlorosis, leaf curling, and hopper burn leading to the stunted plant growth and reduced yield. However, over-reliance on insecticide to manage this pest contributes to resistance development and raises environmental concerns. Insecticidal and biochemical assays were carried out from nine districts of Pakistan to monitor resistance of commonly used insecticides against A. biguttula. The field resistance levels recorded were 10.31-41.23-fold to profenofos, 10.07-83.57-fold to chlorpyrifos, 8.70-30.02-fold to bifenthrin, 4.56-26.24-fold to deltamethrin, 56.28-218.16-fold to imidacloprid, 5.70-23.30-fold to fipronil, 2.99-18.26-fold to clothianidin, 4.66-25.43-fold to chlorfenapyr, and 5.33-44.51-fold to carbosulfan as compared to the susceptible population. Elevated levels of acid and alkaline phosphatases were recorded as 43.18 and 45.25 µmol/min/mg protein in clothianidin and deltamethrin treated population, respectively. In the case of esterases the highest activity i.e., 63.79 µmol/min/mg protein was noted in carbosulfan exposed population. Maximum level of glutathione S-transferase was recorded as 21.99 µmol/min/mg protein in fipronil treated population. Clothianidin treated population showed increased level of acetyl cholinesterase i.e., 46.22 µmol/min/mg. Increased activities of detoxification enzymes can possibly be the cause of resistance development against insecticides. Integrated pest management techniques including cultural practices, avoiding excessive and repeated use of insecticides can aid in the management of A. biguttula.

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Title: A New Host Record for Cotton Leaf Curl Gezira Virus (CLCuGeV) Infecting Common Bean, (Phaseolus vulgaris) Plants in Egypt.

Author: Aly M. Abdel-Salam* and Doaa Z. Soliman

Imprint: Egypt. Acad. J. Biolog. Sci., 17(1):53-68 (2025)

Abstract: Cotton leaf curl disease is a major threat to cotton production in Africa. Some bean plants in Giza governorate, Egypt, exhibited symptoms including stunting, mottling, leaf curling, rugosity, vein enlargement, and pod malformation. Immunocapture polymerase chain reaction (IC-PCR) using antisera for CLCuGeV and degenerate primers for begomoviruses indicated the presence of a begomovirus in infected bean plants. Analysis of the coat protein (CP) (V1 gene) of this virus indicated the presence of CLCuGeV, which was given a GenBank accession number of OQ676568.CLCuGeV-EG: Bean isolate had the highest pairwise sequence identity (PSI) of nucleotide/amino acids (Nt/AA) with an isolate from okra (USA: MN027199 [97.9/98.7]), respectively. Furthermore, CLCuGeVEG:Bean had >94% PSI of Nt/AA CP sequences with other CLCuGeV-EG isolates from okra (Egypt:AY036010, FJ030878 [97.5/98.7]), pepper (Egypt:MK947932 [97.5/98.7]), melon (Egypt:MK947933 [97.5/98.7]), Cucumissp. (Egypt: JX416187 [97.5/98.6]), cotton (Egypt:FJ030874 [97.3/97.7]), squash (Egypt:FJ030879 [97.3/-]), and other CLCuGeV isolates from Israel (KT099132 [97.7/98.1]), Jordan (GU945265 [97.5/98.7]), Pakistan (FR751145, FR751145 [97.1/97.5]), and Iran (MZ911854 [96.6/97.5]). A phylogenetic tree based on AA sequences of CPs revealed two major clusters of CLCuGeV isolates. The first cluster involved CLCuGeV isolates from the above-mentioned countries in addition to Oman, the United Arab Emirates, and Cameron. The second cluster circumvented the CLCuGeVs from Madagascar, Burkina Faso, Niger, Sudan, and Saudi Arabia. CLCuGeV from Tanzania clustered alone; suggesting that Tanzania is one of the Sahel-region countries where CLCuGeV originated. To our knowledge, this is the first report of CLCuGeV-EG:Bean naturally infecting P. vulgaris (Fabaceae) in Egypt. The P. vulgaris infection with CLCuGeV widens the host range of this virus and increases its biological and molecular diversity.

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Title: Synergistic effects of Rhizobium, Bacillus and Arbuscular Mycorrhizal fungi on enhancing cotton growth.

Author: Sultana T, Kumar Pindi P.

Imprint: Iran J Microbiol. 2025;17(1):180-193.

Abstract: Background and Objectives: Telangana district is renowned for its prominence in cotton production, a crop vital to the livelihoods of local farmers. For years, synthetic fertilizers have been relied upon to bolster yields, but escalating costs have shifted focus towards biofertilizers as a cost-effective and sustainable alternative. Materials and Methods: A microbial consortium comprising *Rhizobium* sp. PKS, *Bacillus* sp. PU-7, and *Funneliformis mosseae* AMF was employed. Microbial identification was performed using 16S rRNA gene sequencing. Biochemical evaluations of consortium-inoculated plants included measurements of protein, sugar, proline, and chlorophyll levels, along with IAA quantification.

Results: A consortium of *Bacillus* sp. PU-7, *Rhizobium* sp. Pks [NCBI OK663003, NCMR-MCC4960], and *Funneliformis mosseae* enhanced Mahyco cultivar growth. Treatment increased plant height, fresh and dry weight, and improved biochemical profiles (reduced proline, elevated IAA, protein, chlorophyll, and sugars). Soil field trials were undertaken in four cotton-producing regions of Mahabubnagar region confirmed for efficacy, with deep black soil promoting phytohormone synthesis (IAA-917.66 ± 2.51) and light black soil (IAA- 802 ± 2) enhancing plant growth. Conclusion: Given these outcomes, the application of the tested bioinoculants and AMF spores is suggested as an effective strategy to enhance cotton development and yield in the soils of Mahabubnagar, potentially revolutionizing the district's agricultural practices.

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Title: Fatty Acid ABCG Transporter *GhSTR1* Mediates Resistance to *Verticillium dahliae* and *Fusarium oxysporum* in Cotton.

Author:Guanfu Cheng, Xiuqing Li, W. G. Dilantha Fernando, Shaheen Bibi, Chunyan Liang, Yanqing Bi, Xiaodong Liu, and Yue Li

Imprint*: Plants* 2025, *14*(3), 465; https://doi.org/10.3390/plants14030465

Abstract: Verticillium wilt and Fusarium wilt cause significant losses in cotton (*Gossypium hirsutum*) production and have a significant economic impact. This study determined the functional role of *GhSTR1*, a member of the ABCG subfamily of ATP-binding cassette (ABC) transporters, that mediates cotton defense responses against various plant pathogens. We identified *GhSTR1* as a homolog of *STR1* from *Medicago truncatula* and highlighted its evolutionary conservation and potential role in plant defense mechanisms. Expression profiling revealed that *GhSTR1* displays tissue-specific and spatiotemporal dynamics under stress conditions caused by *Verticillium dahliae* and *Fusarium oxysporum*. Functional validation using virus-induced gene silencing (VIGS) showed that silencing *GhSTR1* improved disease resistance, resulting in milder symptoms, less vascular browning, and reduced fungal growth. Furthermore, the *AtSTR1* loss-of-function mutant in *Arabidopsis thaliana* exhibited similar resistance phenotypes, highlighting the conserved regulatory role of *STR1* in pathogen defense. In addition to its role in disease resistance, the mutation of *AtSTR1* in *Arabidopsis* also enhanced the vegetative and reproductive growth of the plant, including increased root length, rosette leaf number, and plant height without compromising drought tolerance. These findings suggest that *GhSTR1* mediates a trade-off between defense and growth, offering a potential target for optimizing both traits for crop improvement. This study identifies *GhSTR1* as a key regulator of plant–pathogen interactions and growth dynamics, providing a foundation for developing durable strategies to enhance cotton's resistance and yield under biotic and abiotic stress conditions.

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Title: PR-proteins Mediated Disease Resistance in Cotton Genotypes against Cotton Leaf Curl Disease Upon Pretreatment with Salicylic Acid and β-aminobutyric Acid.

Author: Archana Kumari, M.K. Sangha, Om Prakash Raigar and Dharminder Pathak

Imprint: Indian Journal of Ecology (2025) 52(1): 95-102 DOI: https://doi.org/10.55362/IJE/2025/4462

Abstract: Cotton leaf curl disease, caused by the and transmitted by whitefly, is a major concern for cotton growers. This study Geminivirus observed the effect of resistance-inducing chemicals (RICs); salicylic acid (SA) and β-aminobutyric acid (BABA), on pathogen-related proteins, total soluble protein, disease incidence, and disease index. Both elicitors were applied @ 250 µM using two methods: seed priming (once) and foliar spray (thrice at 5, 19, and 33 days after germination) on three cotton cultivars showing differential responses: F1378 (susceptible), LH2076 (moderately resistant), and FDK124 (resistant). The activities of proteins such as chitinase (PR-3), β-1,3-glucanase (PR-2), peroxidase (PR-9), and total soluble protein were estimated at 7, 21, and 35 days after germination. These resistance-inducing chemicals work via systemic acquired resistance, an eco-safe technique providing long-term protection. Our results revealed that SA and BABA significantly increased PR-proteins' activities viz. chitinase, β-1,3-glucanase, peroxidase and total soluble protein content compared to the controls. Furthermore, treated plants showed a remarkable reduction in cotton leaf curl disease incidence and index compared to untreated plants. The higher activity of PR-proteins might be responsible for the decreased disease incidence and index in cotton cultivars. In addition, β-1,3-glucanase and chitinase negatively correlated with disease incidence and index, strongly indicating PR-proteins' role in the plant defense mechanism. A comparison between modes of elicitor treatment indicates seed priming to be the most effective as seed treatment given once sustained its effect up to 35 DAG whereas foliar spray in general gave better results. Although both elicitors seemed at par in their effectiveness, economy-wise SA will be the preferred elicitor. Therefore, SA treatment is suggested as an effective and eco-safe method to induce resistance against cotton leaf curl disease.

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Title: Quantitative analysis of pathogenesis-related protein expression in *Gossypium hirsutum* L. to elicitor-induced resistance against cotton leaf curl disease and predicted in-silico protein-protein interactions.

Author :Muhammad Fahad Khan , Syed Atif Hasan Naqvi , Adnan Iqbal , Seth Alan Steichen, Amjad Ali , Rana Muhammad Amir Gulzar , Judith K. Brown , Ummad Ud Din Umar

Imprint: Physiological and Molecular Plant Pathology, Volume 137, May 2025, 102611

Abstract: Systemic acquired resistance (SAR) can offer an effective management strategy for plant diseases. Pathogenesis-related (PR) gene expression was investigated in *Gossypium hirsutum* plants in response to SAR induced by the exogenous application of salicylic acid, jasmonic acid, and benzothiadiazole as elicitors, followed by inoculation with *Cotton leaf* curl *Multan virus* (CLCuMuV). Expression of cotton, PR genes encoded on multiple loci were determined by qPCR. Primers were designed based on sequence regions conserved in each group of aligned gene targets in the annotated *Gossypium hirsutum* reference genome assembly. While designing primers for gene expression analysis, the copy number variation (CNV) was mitigated using bioinformatics and alignment tools to craft primers specific to their target genes. Gene expression of pathogenesis-related proteins such as PR1, PR4, PR5, β 1,3 glucanase, and chitinase was quantified by qPCR. In silico protein interactions were predicted between the five PR and begomoviral proteins using Phyre 2. The results indicated that all the PR genes were expressed on the 2nd date of analysis. The exogenous benzothiadiazole (BTH) application significantly increased all PR gene expression and suppressed the virus infection. The application of BTH after virus inoculation significantly enhanced systemic acquired resistance, which indicates that virus infection initially triggered SAR, and subsequent application of elicitor, i.e., BTH, further facilitated the signal transduction for the expression of PR genes. In silico interactions predicted significant interactions between CLCuMuV coat protein (AV1) gene and Chitinase, PR1, PR5, whereas the replication-associated gene, AC1, interacted with PR1. Results indicate that cotton PR genes suppress the CLCuMuV infection in *G. hirsutum* plants. The identified PR genes could be exploited to enhance resistance through genetic transformation in cotton plants to control CLCuMuV.

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Title: Patterns of phenotypic variation in Gossypium turneri: a wild cotton with a restricted distribution in Sonora, Mexico.

Author: Karla Fabiola Yescas-Romo, Corina Hayano-Kanashiro & Francisco Molina-Freaner

Imprint: Genetic Resources and Crop Evolution Published: 11 February 2025

Abstract: Crop wild relatives (CWR) represent important genetic resources for crop improvement. Gossypium turneri, a wild cotton species with a restricted distribution in the Sonoran Desert of northwestern Mexico, has been identified as a potential breeding resource for cotton improvement. While several agronomically important traits have been previously identified through limited observations from only one location within its range, phenotypic variation in this xerophytic species has not been thoroughly studied. This study aimed to describe the pattern of phenotypic variation in floral and leaf traits along the three known populations of G. turneri and identify traits of agronomic interest. Leaves and flowers through its distribution range were collected and quantitative and qualitative attributes were analyzed. Phenotypic variation in flowers and leaves was predominantly found among individuals within populations, with a smaller proportion occurring between populations, likely due to the species' restricted distribution. Interpopulation variation in leaf traits was probably influenced by differences in local rainfall, whereas flower traits exhibited minimal interpopulation variation, likely due to similarities in pollinator composition. Some traits of interest for cotton improvement were identified, such as polymorphic bracts and production of anthers without pollen among flowers. This desert-adapted wild cotton offers valuable traits with potential for adaptation of cultivated cotton to water- and heat-stressed environments.

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Title: Impact of environments on combining ability and heterosis in cotton (Gossypium hirsutum L.).

Author: Mundakochi Meera, Alagesan Subramanian, Nallathambi Premalatha, Narayanan Manikanda Boopathi, Dhashnamurthi Vijayalakshmi, Krishnamoorthy Iyanar, Ramalingam Thangapandian & Santosh Ganapati Patil

Imprint: The Nuckeus, 2025Pu February 2025

Abstract: Heterosis breeding in cotton is predominantly adopted owing to the predominance of non-additive gene action for most traits. However, a few researchers have reported the occurrence of additive gene action. Therefore, assessing the combining ability associated with parents and the heterosis of the corresponding hybrids across environments is crucial for determining the consistency of gene action, since there is a paucity of such information in cotton. The current study examines the general combining ability (GCA) of parents, specific combining ability (SCA), and heterosis of the hybrids across environments. Thirty hybrids developed by crossing six lines and five testers in Line × Tester (L × T) mating fashion were evaluated in a randomized block design across three environments. The analysis focused on seed cotton yield per plant, number of sympodia per plant, number of bolls per plant, seed index, and upper half mean length. The results indicated that non-additive gene action predominated in individual environments. However, additive gene action was detected in a few traits, on a pooled basis, possibly due to the influence of differential experimental environments on gene action. The significance of GCA × environment was limited, hence opting for the selection of parents on a pooled basis for the majority of traits could be possible. However, significant SCA × environment interaction and varied *sca* effects across environments suggested that the selection of trait and environment-specific combinations must be adopted. Overall, the line TVH002 and the tester CO14 were identified as good combiners while, the crosses exhibited differential performance for environments.

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Title: Analysis of Mitochondrial Sequence Deletion in the *atp9* 5′UTR Region and Design of Molecular Markers in Cotton (*Gossypium* spp.).

Author: Wanlin Kang, Lanlan Zhang, Zhiyu Li, Yuzhu Fang, Jinglong Yang, Yan Song, Shining Liu, Xiao Zhang, Rui Zhang

Imprint: Plant Breeding, First published: 06 February 2025, https://doi.org/10.1111/pbr.13261

Abstract: Cotton (*Gossypium*) is the most important fibre crop in the world, consisting of 45 diploid and 7 tetraploid cotton species. These cotton varieties are valuable for breeding, but their molecular identification methods still need further study. We identified an insert/deletion site (AATTT) at the *atp*9 5′UTR region in the mitochondrial genome of cotton, which could be used to distinguish different cotton species. In this study, the target fragments of 33 cotton species (29 diploid and 4 tetraploid species) were amplified by PCR, and the PCR products potentially containing an *Eco*R I restriction site were subsequently digested and analyzed. The sequencing results revealed that 27 out of 33 cotton species lacked ‘AATTT’ sequences, while six cotton species (*G. longicalyx*, *G. hirsutum*, *G. barbadense*, *G. tomentosum*, *G. mustillinum* and *G. darwinii*) were found to possess the sequences. Additionally, 39 SNPs were found in this region, and specific molecular markers for *G. stocksii*, *G. bickii* and E-genome were developed, respectively. The comparative analysis of mitochondrial sequences from diploid and tetraploid cotton species elucidated their genetic diversity and evolutionary relationships, and species-specific markers were able to discriminate among these species, thereby provided a foundation for more targeted use of wild genetic resources in cotton improvement and efforts to ensure their conservation.

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Title: Development of a set of monosomic alien addition lines from Gossypium raimondii in Gossypium hirsutum toward breeding applications in cotton.

Author: Zhenzhen Xu, Xiaoxi Lu, Wenjie Ding, Wei Ji, Wuzhimu Ali, Heyang Wang, Shan Meng, Qi Guo, Peng Xu, Xianglong Chen, Liang Zhao, Huan Yu & Xinlian Shen

Imprint: BMC Plant Biology , Published: 05 February 2025, Volume 25, article number 150, (2025)

Abstract: Gossypium raimondii Ulbr is a diploid wild cotton (2n = 26, D5D5) that originated in west-central Peru of South America and possesses desirable characteristics that are absent in the Upland cotton G. hirsutum. Many beneficial genes were lost from G. hirsutum in the process of domestication, leading to a narrowed genetic base and greater vulnerability to biotic and abiotic stresses. This genetic base can be expanded through distant hybridization using the superior genes of G. raimondii. Results In this study, putative hexaploid F1 plants of G. hirsutum - G. raimondii were generated by interspecific hybridization. Analysis of its mitotic metaphase plates revealed the presence of 78 chromosomes, with each of the six chromosome-specific fluorescence in situ hybridization (FISH) probes (3D5, 5D5, 6D5, 7D5, 9D5, and 10D5) of G. raimondii exhibiting bright and distinct signals on its respective pair of chromosomes. Then, the fertile hexaploid F1 plants were continuously backcrossed with G. hirsutum and a set of G. hirsutum - G. raimondii monosomic alien addition lines (MAALs) were developed using SSR markers in successive backcrosses and self-crossing from BC2F1 to BC4F2. These MAALs were confirmed by chromosome-specific anchored SSRs and FISH. This set of MAALs exhibited abundant variation in morphological traits, agronomic characteristics, yield, and fiber quality traits, as well as in drought and salt resistance at seedling stage. Notably, MAAL_9D5 and MAAL_10D5 demonstrated excellent fiber length (FL), fiber uniformity (FU), fiber strength (FS), micronaire value, and fiber elongation (FE); At seeding stage, MAAL_8D5, MAAL9D5, MAAL_10D5, MAAL_12D5, and MAAL_13D5 showed salt resistance potential; while MAAL_1D5, MAAL_3D5, MAAL_4D5, MAAL_7D5, MAAL_8D5, MAAL_12D5, and MAAL_13D5 exhibited drought resistance potential. These MAALs will provide important genetic bridge materials for gene transfer from G. raimondii as well as for the study of Gossypium species genomes and their evolution. Conclusions A set of Gossypium hirsutum - Gossypium raimondii MAALs were developed, and they showed abundant variation in morphological, agronomic, yield, and fiber quality traits, as well as in drought and salt resistance at seedling stage.

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Title: Unravelling the Genetic Divergence and Trait Association for Yield and

Its Component Traits among Germplasm Lines in Cotton, (Gossypium hirsutum L.)

Author: Channabasava , J. M. Nidagundi , Gurumurthy S , P. H. Kuchanur , G. Y. Lokesh , M. Lakshmikanth and M. K. Meena

Imprint*: Journal of Experimental Agriculture International, Volume 46, Issue 7, Page 731-738, 2024.*

Abstract: The current study was focused on unravelling the genetic basis for seed cotton yield and yield attributing traits with an emphasis on isolating most potential germplasm accessions. A set of 192 cotton germplasm accessions were evaluated in augmented design for two seasons (2022 and 2023) in two different environments. The observations on yield and yield attributing traits were recorded at the time of harvest and advanced for essential statistical analysis. The results of correlation analysis indicated the presence of significant and positive correlation between seed cotton yield with number of sympodia per plant, number of bolls per plant, lint yield, boll weight and lint index, indicating selection for these traits indirectly enhance the seed cotton yield. While diversity analysis categorized germplasm accessions into eight different clusters. The results indicated the existence of adequate genetic diversity among the germplasm lines which can be exploited to manifest higher magnitude of heterosis through hybridization of genotypes belonging to different clusters.

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Title: Genome-wide identification of SERKs in four *Gossypium* species. reveals *GhBAK1* potentially promotes cotton defoliation.

Author:Ning Qin , Yuan Tian, Abdul Rehman , Xinli Ma , Xiaoyang Wang , Xiangru Wa ng , Zhen Peng, Zhaoe Pan , Shoupu He , Xiongming Du , Hongge Li

Imprint: Industrial Crops and Products, Volume 226, April 2025, 120681

Abstract: Cotton (*Gossypium* spp.) holds significant global industrial importance as a **primary** textile fiber crop. Using chemical defoliants to speed up the shedding of leaves before machine harvesting is a necessary agricultural practice in cotton production. Somatic Embryogenesis Receptor Kinases (SERKs) have been reported to play roles in plant organ abscission. Still, *SERK* genes have not been fully studied in cotton, and whether cotton *SERK* genes respond to defoliant-induced abscission remains unknown. This study explores the biological roles of the *SERK* gene family in four cotton species (*G. arboreum*, *G. raimondii*, *G. barbadense*, and *G. hirsutum*), identifying 14,13, 22 and 26 SERK proteins, respectively. Phylogenetic analysis revealed three subfamilies of SERKs in cotton, with high homology within the subfamily suggesting similar biological functions among different cotton varieties. Expression profiling demonstrated distinct patterns of *GhSERK* genes in response to defoliant treatment in upland cotton. Functional studies demonstrated that *GhSERK2–2* encoding brassinosteroid insensitive 1-associated kinase 1 (BAK1) plays a crucial positive role in leaf abscission, as evidenced by its upregulation following defoliant treatment and its involvement in brassinosteroid (BR) signaling pathways. Additionally, a hormone crosstalk network was constructed to elucidate the interactions between *SERK* genes and phytohormones in the defoliation process. These findings enhance our understanding of the functional diversity of *SERK* genes and their potential applications in improving cotton production efficiency

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Title: A computational analysis revealed BES1 transcription factor and ß-amylase as crosstalk elements in Upland cotton species (*Gossypium* sp.).

Author: Villamar-Torres R.O., Mestanza Uquillas C.A., Chévez-Vera H.D., Heredia-Pinos M.R., Viot C., Jazayeri S.M.

Imprint: 2024. *Scientia Agropecuaria*, 15 (3): p. 449-
460.DOI: 10.17268/sci.agropecu.2024.033

Abstract: Cotton is a resilient and multipurpose crop, meeting major of the world's textile needs while also yielding byproducts like edible oil and animal feed. Starch plays a crucial role in cotton fabric production. It enhances fabric strength by forming a protective film around cotton fibers, making them more resistant to wear and tear. BES1 (brassinosteroid insensitive 1) is a key regulator in brassinosteroid signaling. It controls thousands of target genes involved in development processes. Interestingly, two ß-amylase proteins (BAM7 and BAM8) are part of the BES1 family, despite their primary function as ß-amylases. ß-Amylase (BAM) and BES1 are two gene families with functional and regulatory roles in controlling shoot growth and development by mediating brassinosteroid effects. They share similar domains and participate in various biological processes, tolerance and responses to stresses like salt and drought. In a computational analysis comparing Arabidopsis and Gossypium species, BAM and BES1 were characterized. BES1 genes were grouped into four clusters based on the comparison of the two species. Two clusters corresponded to BAM7 and BAM8, while the other two clusters were associated with BES1. The conserved nucleotide domain sequence is GCTGGATGG. Short tandem repeats include TG and TTG, which can serve as molecular markers. BES1 is specifically linked to cellulose and fiber production and holds promise as a candidate for plant selection and breeding in Gossypium (cotton).

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Title: Genome-wide identification of *CA* genes in cotton and the functional analysis of *GhaCA4-D*, *GhβCA6-D* and *GhγCA2-D* in response to drought and salt stresses.

Author:Runrun Sun , Yuanyuan Wang, Ruihao Zhu , Lijie Li , Qianhui Xi , Yunpeng Dai , Jiahui Li , Yuanyuan Cao, Xinlei Guo , Xiaoping Pan, Qinglian Wang , Baohong Zhang

Imprint: International Journal of Biological Macromolecules, Volume 304, Part 2, April 2025, 140872

Abstract: Carbonic anhydrases (CAs) are critical metalloenzymes, widely exist in organisms, which involve in many physiological processes, including response to adverse environmental conditions. Although *CA* genes have been comprehensively identified and analyzed in numerous plants, there are a few reports in cotton. Therefore, we conducted exhaustive research for *CA* genes from two tetraploid cotton species and their ancestral species. A total of 138 *CA* genes were found, and 45 of them belonged to *Gossypium hirsutum*. Phylogenetic relationships and sequences analysis showed that *CA* genes were categorized into three distinct subtypes: α-type, β-type and γ-type. The exon numbers of β-type members were highly variable. Various types of *cis*-elements, including drought inducibility, were identified in *CA* genes, suggesting that *CA* genes might be involved in the regulation of drought stress response. qRT-PCR was applied to assess the gene expression level in various tissues under drought stress. The results indicated that the expression levels of *GhaCA4-D*, *GhβCA1-A*, *GhβCA1-D*, *GhβCA3-D* and *GhβCA6-D* were significantly higher in leaves than that in stems and roots. The expression of *GhaCA4-A*, *GhaCA8-A*, *GhaCA4-D*, *GhβCA3-D*, *GhβCA6-D* and *GhγCAL1-D* was significantly upregulated in roots at severe drought treatment. The functions of *GhaCA4-D*, *GhβCA6-D* and *GhγCA2-D* were analyzed using virus-induced gene silencing (VIGS) technology. Compared to the controls, *GhγCA2-D*-

silenced upland cotton seedlings were more sensitive to salt stress. However, the drought tolerance of *GhaCA4-D* and *GhβCA6-D* silenced plants was significantly decreased. Stomatal density, width and area were significantly higher in TRV:*GhβCA6-D* compared to TRV:00 inoculated plants. *GhaCA4-D* silenced plants were susceptible to oxidative stress, and silencing *GhaCA4-D* induced leave cell death. Our results will assist to make clear the regulatory mechanism of *CA* genes under abiotic stress.

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Title: Genome-wide analysis of the *FKBP* gene family and the potential role of *GhFKBP 13* in chloroplast biogenesis in upland cotton.

Author: Jianguang Liu, Zhao Geng, Guiyuan Zhao, Mengzhe Li, Zetong An, Hanshuang Zhang & Yongqiang Wang

Imprint: *BMC Genomics* volume 26, Article number: 125 (2025)

Abstract: In plants, FK506-binding proteins (FKBPs) have been shown to participate in various biological processes such as photosynthetic system reaction, stress response, and growth and development. However, the roles of *FKBPs* in cotton are less well known. Results In this study, we investigated *FKBP* family genes on a genome-wide scale in four *Gossypium* species. A total of 147 *FKBP* genes were identified from these four *Gossypium* species and placed into three classes based on phylogenetic analysis. Collinearity analysis indicated that whole-genome duplication events and segmental duplication events were the main sources of gene amplification during the evolution of *FKBP* genes. Conserved motif, expression profiles and cis-acting elements prediction of the *GhFKBPs* analysis revealed that *GhFKBP*s were differentially expressed in different tissues and under abiotic stress. qRT-PCR analysis showed that some *GhFKBPs* were predominantly expressed in leaves. The analysis of cis-acting elements prediction revealed that MYB, MYC and ERE related binding sites in the promoters of *GhFKBP* genes were the most abundant. Furthermore, the composition and distribution of these cis-acting elements exhibited differences between homologous *GhFKBP* gene pairs. Silencing of *GhFKBP13* in cotton resulted in disruption of chloroplast structure and starch metabolism disorders. Conclusions Taken together, 147 *FKBP* family genes in four *Gossypium* species are comprehensively characterized, and *GhFKBP13* play a critical role in chloroplast biogenesis in upland cotton.

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Title: In vitro culture and profiling of secondary metabolites in naturally colored cotton (Gossypium hirsutum L.

Author: Onur Aydın & Neslihan Turgut Kara

Imprint: Plant Cell, Tissue and Organ Culture (PCTOC) , 05 February 2025, Volume 160, article number 46, (2025)

Abstract: The cotton (*Gossypium* spp.) plant, which is the leading source of plant-based textile fiber, is also an economically valuable resource for agriculture and many other industries. Some cotton varieties may also have fibers in brown, green and tan tones, aside from the common white. Cotton with this type of fiber development is called 'Naturally Colored Cotton' (NCC). Various applications were performed here, including callus induction and propagation, root suspension cultures, and the analysis of secondary metabolite profiles in *in vitro* grown roots and callus tissues of NCC (*Gossypium hirsutum* L. Sarıgelin variety). Studies on callus culture have revealed multiple plant growth regulator (PGR) concentrations and combinations with high success rates for callus induction from NCC hypocotyl explants. Among the concentrations tested, MS medium containing 1.0 mg/L IAA and 0.5 mg/L Kinetin was the most effective combination for callus induction. Rooted shoots were successfully propagated from cotyledonary nodes. Following HPLC analyses of white cotton roots, NCC roots, and callus tissues grown *in vitro* revealed both varieties to be rich in phenolic sources such as flavonoids and anthraquinones. Plant tissue culture practices on NCC provide substantial source materials for future biotechnological applications. Therefore, this study is expected to provide valuable data, enabling further research to be conducted on naturally colored cotton.

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Title: Insights into the Role of *GhTAT2* Genes in Tyrosine Metabolism and Drought Stress Tolerance in Cotton.

Author: Teame Gereziher Mehari, Jungfeng Tang, Haijing Gu, Hui Fang, Jinlei Han, Jie Zheng, Fang Liu, Kai Wang, Dengbing Yao, Baohua Wang

Imprint: *Int. J. Mol. Sci.* 2025, *26*(3), 1355; https://doi.org/10.3390/ijms26031355

Abstract: *Gossypium hirsutum* is a key fiber crop that is sensitive to environmental factors, particularly drought stress, which can reduce boll size, increase flower shedding, and impair photosynthesis. The aminotransferase (AT) gene is essential for abiotic stress tolerance. A total of 3 *Gossypium* species were analyzed via genome-wide analysis, and the results unveiled 103 genes in *G. hirsutum*, 47 in *G. arboreum*, and 53 in *G. raimondii*. Phylogenetic analysis, gene structure examination, motif analysis, subcellular localization prediction, and promoter analysis revealed that the *GhAT* genes can be classified into five main categories and play key roles in abiotic stress tolerance. Using RNA-seq expression and KEGG enrichment analysis of *GhTAT2*, a coexpression network was established, followed by RT-qPCR analysis to identify hub genes.

The RT-qPCR results revealed that the genes *Gh_A13G1261*, *Gh_D13G1562*, *Gh_D10G1155*, *Gh_A10G1320*,and *Gh_D06G1003* were significantly upregulated in the leaf and root samples following drought stress treatment, with *Gh_A13G1261* identified as the hub gene. The *GhTAT2* genes were considerably enriched for tyrosine, cysteine, methionine, and phenylalanine metabolism and isoquinoline alkaloid, tyrosine, tryptophan, tropane, piperidine, and pyridine alkaloid biosynthesis. Under drought stress, KEGG enrichment analysis manifested significant upregulation of amino acids such as L-DOPA, L-alanine, L-serine, L-homoserine, L-methionine, and L-cysteine, whereas metabolites such as maleic acid, p-coumaric acid, quinic acid, vanillin, and hyoscyamine were significantly downregulated. Silencing the *GhTAT2* gene significantly affected the shoot and root fresh weights of the plants compared with those of the wild-type plants under drought conditions. RT-qPCR analysis revealed that *GhTAT2* expression in VIGS-treated seedlings was lower than that in both wild-type and positive control plants, indicating that silencing *GhTAT2* increases sensitivity to drought stress. In summary, this thorough analysis of the gene family lays the groundwork for a detailed study of the *GhTAT2* gene members, with a specific focus on their roles and contributions to drought stress tolerance.

SEED SCIENCE AND TECHNOLOGY

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Title: EVALUATING THE STABILITY OF SEED COTTON YIELD AND ITS KEY COMPONENTS OVER ENVIRONMENTS.

Author: C.J. Rajani and M.G. Valu

Imprint: Plant Archives Vol. 25, Special Issue (ICTPAIRS-JAU, Junagadh) Jan. 2025 pp. 405-412

Abstract: The stability analysis for seed cotton yield and its attributing traits was performed as per Eberhart and Russell (1966) in 45 crosses developed through line x tester mating design (nine lines and five testers) along with 14 parents grown under three dates of sowing (environments) E1 , E2 and E3 . The stability analysis indicated significant differences among the genotypes (G) and environments (E) indicating variable response of different genotypes for various traits under varied environmental conditions. The G × E interaction was significant for most traits, except for plant height and boll weight, when tested against pooled error. When considering the combined effect of E + (G × E), significant impacts were observed across all traits against pooled error and pooled deviation. A very high proportion of total variance was accounted for the environment (linear) component. This indicated that environments created by various sowing dates were justified and had mostly linear effect. The stability parameters viz., overall mean (X), regression coefficient (bi) and deviation from regression (S2di) revealed that, top five crosses identified on the basis of seed cotton yield per plant viz., GJHV-522 × GJHV-503, GJHV-548 × GJHV-585, TCH-1828 × GJHV-503, GBHV-187 × GJHV-503 and GISV-365 × GJHV-503 were the most widely adapted and stable crosses for seed cotton yield per plant and its components. The parents, GBHV-187, GJHV-548 and GJHV-585 were identified as the stable genotypes for seed cotton yield and its components and hence, they may be utilized in breeding programmes for incorporation of stability in cotton.

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Title: Microbial-priming of seeds with plant growth-promoting rhizobacteria and arbuscular mycorrhizal fungi for improving cotton (Gossypium barbadense L.) growth, yield and water productivity under drought stress.

Author: Hossam S. El-Beltagi, Essam Abdelaziz El-Waraky, Mohamed M. El-Mogy, Mohamed Fathi El-Nady, Ahmed Mahmoud Ismail, Elsayed B. Belal, Mohammed I. Al-Daej, Nagwa Mohamed El-Khateeb, Lamy Hamed & Metwaly Mahfouz Salem Metwaly

Imprint: Biologia, Published: 31 January 2025

Abstract: Cotton is particularly vulnerable to water deficit stress, resulting in substantial reduction in both its growth and yield. Therefore, the aim of the present study was to assess the effectiveness of extending irrigation intervals (to every 30, 45 days) compared to well-irrigated plants (every 15 days). Additionally, in an effort to mitigate adverse effects of water deficit stress, cotton seeds and soil were inoculated with *Bacillus amyloliquifaciens*, *Funneliformis mosseae*, either individually or in combination. The study was conducted over two summer seasons in 2021, 2022. Results revealed that extending irrigation intervals had negative impact on mycorrhizal colonization, and various plant growth or productivity parameters, including, plant height, leaf area, dry weight per plant, number of fruiting branches and bolls per plant, lint percentage, seed index, seed yield, fiber quality. Furthermore, physiological, or biochemical characteristics, including chlorophyll pigments (chl.a, b and total) and leaf relative water content were adversely affected by prolonged irrigation intervals. Biopriming of cotton seeds with rhizobacteria that promotes plant growth and arbuscular mycorrhizal fungi was found to improve plant height, leaf area, plant dry weight, number of fruiting branches and bolls/plant, yield and yield component, chlorophyll pigments, as well as enhance efficiency of antioxidant enzyme activity (catalase, peroxidase and polyphenol oxidase), leaf total phenols and proline contents.

Biopriming cotton seeds presents hopeful strategy for boosting cotton yield, reducing effects of drought stress and fostering soil fertility.

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Title: Efficacy of certain insecticides against Thrips tabaci Lind in cotton seedlings at El-Gharbia Governorate, Egypt.

Author: Hazem Mohamed Amine , Fatma H. Hegazy , Hanaa Atef Nassem

Imprint: Journal of Sustainable Agric. & Environ Science10.21608/JSAES.2025.350303.1123

Abstract: Cotton (Gossypium barbadense L) crop have an important role in the national income of Egypt. Field experiments were achieved during 2023 at El- Gharbia Governorate, Egypt under field condition to evaluate the initial and residual effect of certain insecticides, which applied singly and mixed with Mineral oil or plant extract against Thrips tabaci during Seedling stages. Results showed that all tested compounds used separately induced the highest residual reduction against thrips. In the case when insecticides are applied alone, the mean of reduction in insect population varies between 44.31 to 80.37, while the initial effect of all tested compounds causes a moderate reduction giving from 45.49 to 69.15 against cotton Thrips. Also, the results obtained indicated that mineral oil and plant extract, when mixed with all tested compounds, caused a high level of reduction in insect population as initial and residual effect. mineral oil + Thiamethoxam caused the highest initial and residual reduction giving 88.76 and 89.09 respectively, while plant extract + Thiamethoxam caused the highest initial and residual reduction giving 84.41 and 82.42 respectively to cotton thrips. (control). Generally, we can said that all mixtures had potentiation effect which resulted in reducing thrips population (T. tabaci.) during seedling stage.

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Title: Identification of salt-resilient cotton genotypes using integrated morpho-physiological and biochemical markers at the seedling stage.

Author: Nimra Gul, Zafran Khan, Muhammad Yousaf Shani, Barira Shoukat Hafiza, Asif Saeed, Azeem Iqbal Khan, Amir Shakeel & Mehdi Rahimi

Imprint: *Scientific Reports* volume 15, Article number: 5276 (2025)

Abstract: Soil salinity drastically hinders cotton productivity (*Gossypium hirsutum*), and fiber quality. The current study evaluated morpho-physiological and biochemical responses of fifty cotton genotypes under different salinity levels (control, 12 dS/m, and 17 dS/m) at the seedling stage. The experiment was performed in a factorial complete randomized design with three replications. Significant genotype × treatment interactions were observed for most traits, including shoot length (SL), root length (RL), fresh and dry shoot weight (FSW, DSW), fresh and dry root weight (FRW, DRW), total soluble protein (TSP), proline content, and antioxidant enzymes. Severe salinity stress reduces shoot length (SL) and root length (RL) along with notable decreases in biomass and altered biochemical responses, including increased antioxidant activities and proline content, indicating stress adaptation. Moreover, PCA and Pearson's correlation analyses unveiled strong positive and negative correlations among studied attributes while MGIDI analyses assist in determining the salt-resilient cotton genotypes under applied treatments. The best-performing genotypes under control conditions were G_2, G_8, and G_{12}, while G_7, G_{43}, and G_{30} showed resilience under severe salinity stress. MGIDI effectively identified genotypes with outstanding salinity tolerance, such as G_2, G_{43}, G_{40}, and G_{26}, across all stress levels. This research assists in determining the salinity stress-tolerant cotton genotypes using morpho-physiological and biochemical parameters and MGIDI is used as a precise method for identifying salt-resilient cotton accessions.

FIBER AND FIBER TECHNOLOGY

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Title: Effect of Water Deficit and Sulfur Doses on Fiber Yield and Quality in Cotton .

Author: Berkant Ödemiş , Batuhan Akgöl , Deniz Can & Yaşar Akışcan

Imprint: International Journal of Innovative Approaches in Agricultural Research 2024, Vol. 8 (4), 336-353 https://doi.org/10.29329/ijiaar.2024.1109.6

Abstract: The study was carried out in the Eastern Mediterranean Region (Amik Plain) using the Carisma cotton variety with a randomized block design, split plots, and three replications. Various irrigation levels were implemented: full field capacity (I100), 66% (I66), 33% (I33), and non-irrigated (I0). Additionally, sulfur doses were applied as foliar sulfur at 150 ml da^{-1} (S1), 250 ml da^{-1} (S2), 350 ml da^{-1} (S3), and a control (S0). The impact of these treatments was evaluated based on factors such as fiber yield, evapotranspiration, leaf sulfur concentration, and fiber quality characteristics. Evapotranspiration (ET) ranged from 299 mm to 1096 mm in the first year and from 247 mm to 995 mm in the second year. In comparison to the control (K0), evapotranspiration slightly decreased with increasing sulfur doses in the first year but increased in the second year. Water restriction led to a reduction in both fiber yield and evapotranspiration in both years. Fiber yield decreased in the first year but increased in the second year with higher sulfur doses. The highest fiber yield was observed in the fully irrigated (I100) treatments in both years (227.2 kg da^{-1} and 230.2 kg da^{-1}). Among sulfur doses, the highest fiber yield was obtained with S0 (175.8 kg da^{-1}) in the first year and S1 (185.5 kg da^{-1}) in the second year. With an increase in water restriction, ginning percentage efficiency improved in the first year but displayed an inconsistent trend in the second year. The highest ginning percentage efficiency was achieved with the S2 dose in the first year and the S1 dose in the second year, on average. The effects of irrigation water deficit and sulfur doses on fiber quality varied by year. Water stress influenced the spinning consistency index, fiber fineness, fiber length, and fiber uniformity in both years. In the first year, short fiber content and fiber strength were affected, while in the second year, fiber elongation and fiber brightness showed significant changes. Sulfur doses had fewer effects on the parameters; in the first year, fiber fineness and yellowness were impacted, whereas in the second year, the spinning consistency index, fiber uniformity, short fiber content, and fiber strength were influenced.

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Title: Proteomics-based models of gene expression and cellular control of cotton fiber development.

Author: Youngwoo Lee, Pengcheng Yang , Heena Rani , Gideon Miller , Corrinne E Grove , Sivakumar Swaminathan , Olga A Zabotina , Jonathan F Wendel , Jun Xie , and Daniel B Szymanski

Imprint: bioRxiv preprint doi: https://doi.org/10.1101/2025.02.05.636703;

Abstract: The cotton textile industry is based on the material properties of terminally differentiated trichoblasts. Tens of thousands epidermal trichoblasts emerge from the seed coat and march through a reproducible developmental program that includes interconversion between cell-autonomous and tissuebased morphogenesis. Proteomic analyses of purified fibers provide a way to associate molecules with cellular processes that directly affect morphological transitions and material properties of the harvested cells. However, insufficient temporal sampling and poor protein coverage have limited the extent to which proteomic data predict control mechanisms. Here we quantified the subcellular proteomes of purified fibers daily over a 20-day interval that includes diverse modes of elongation and cell wall remodeling. Thousands of reliable protein abundance profiles were assigned to expression groups and tested for associations with a broad array of phenotypes. Integration of proteomic and RNA-sequencing data revealed distinct modes of transcriptional and post-transcriptional control. Collectively these datasets provide large-scale gene function predictions that can serve as a toolkit to engineer cotton material properties.

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Title: Two duplicated GhMML3 genes coordinately control cotton lint and fuzz fiber development .

Author: Rui Chen, Jun Zhang, Jun Li, Jinwen Chen, Fan Dai, Yue Tian, Yan Hu, Qian-Hao Zhu, Tianzhen Zhang

Imprint: PLANT COMMUNICATIONS, Available online 12 February 2025, 101281

Abstract: Cotton produces fuzz and lint two types of fibers. Cotton yield is determined by the number of epidermal cells that develop into lint fibers. Despite numerous studies, the genetic and molecular mechanisms controlling lint and fuzz fiber development remain elusive. Here, using the recessive naked seed or fuzzless-linted mutant (n_2NSM) in combination with gene editing and complement, we identified the recessive fuzzless gene *n_2* encodes an MML transcription factor, *GhMML3_D12*. Over-expressing *GhMML3_D12* in n_2NSM restored fuzz fiber development. Conversely, knocking out *GhMML3_D12* in wild-type cotton (J668) by CRISPR/Cas9 led to a fuzzless-linted phenotype. Interestingly, simultaneous editing of duplicated ***GhMML3****s* (*GhMML3_A12* and *GhMML3_D12*) resulted in plants with the fiberless (fuzzless-lintless) phenotype. Detailed investigation of the seed fiber phenotype of the segregating progeny derived from a cross between a fibreless mutant of *GhMML3* (#*mml3s*) created by gene editing and J668 not only identified progeny mimicking the natural fuzzless and fiberless mutants but also revealed that the duplicated *GhMML3_A12* and *GhMML3_D12* regulate the development of fuzz and lint fibers in a dosage-dependent manner. Comparative transcriptome and single cell RNA-seq illuminated *GhMML3* being the hub gene of the gene network regulating fiber initiation and early-stage elongation. The gene regulatory network revealed potential candidate genes and key regulators that may contribute to fiber initiation development. A model for lint and fuzz fiber development controlled by *GhMML3* is proposed. We also revealed that GhMML3_D12 protein can directly bind to the promoters of *GhHD-1* and *GhMYB25*, two key genes involved in fiber initiation, thereby activating their expression. The findings of this study provide fresh insights on the fundaments responsible for cotton fiber development.

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Title: Dimerization among multiple NAC proteins mediates secondary cell wall cellulose biosynthesis in cotton fibers.

Author: Feng Chen, Mengfei Qiao, Li Chen, Min Liu, Jingwen Luo, Yanan Gao, Mengyun Li, Jinglong Cai, Staffan Persson, Gengqing Huang, Wenliang Xu

Imprint: The Plant Journal, First published: 27 January 2025, https://doi.org/10.1111/tpj.17223

Abstract: Cotton fibers, essentially cellulosic secondary cell walls (SCWs) when mature, are the most important raw material for natural textiles. SCW cellulose biosynthesis determines fiber thickness and industrially important fiber quality parameters, such as fiber strength and fiber length. However, transcriptional regulatory networks controlling fiber SCW cellulose formation remain incomplete. Here, we identify eight NAC domain proteins (GhNACs) that are involved in fiber SCW cellulose synthesis. These eight GhNACs can form pairwise heterodimers that may act as dimers, or perhaps even as an octameric protein complex, to transactivate *GhCesA* expression. Moreover, heterodimerization of GhNACs can in different combinations synergistically activate *GhCesA* genes. Through our analyses of transcription factor—DNA and transcription factor—transcription factor interactions, we propose a multi-layered transcriptional regulatory network in which the regulation of SCW cellulose biosynthesis in cotton fiber is mediated by multiple NAC protein dimers. These findings enhance our understanding of the roles of NAC proteins in SCW formation and offer new insights into fiber-specific transcriptional regulatory mechanisms of cellulose synthesis.