



GLEANINGS IN COTTON RESEARCH

OCTOBER 2024



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Preface

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

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

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

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

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

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

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

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

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

Swati Dixit
Incharge Library

Chetali Rodge
Technical Officer (T5)

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1

Title: Insights into Cotton Regrowth and Management.

Author: Naveed S, Jones M, Campbell BT, Rustgi S

Imprint: Clemson (SC): Clemson Cooperative Extension, Land-Grant Press by Clemson Extension; 2024 Aug. LGP 1195. <https://lgpress.clemson.edu/publication/insights-into-cotton-regrowth-and-management/>.

Abstract: Cotton growers grapple with regrowth challenges post-defoliation, leading to diminished fiber quality and economic returns. Chemical treatments, while effective, depend on various factors such as growing season conditions, soil moisture, fertility, temperature, defoliant application timing, and harvest scheduling. By exploring molecular breeding approaches, the goal is to develop cotton genotypes that minimize or eliminate regrowth, complementing and reducing chemical treatments. This publication aims to provide cotton producers, researchers, Extension Agents, and specialists with insights into cotton regrowth genetics and physiology. For those who may need more of an introduction to the importance of cotton physiology and genetics, resources such as Ritchie et al.¹ and the Genetic Science Learning Center² will help build a baseline of knowledge for the content of this publication.

2

Title: Deficit Irrigation and High Planting Density Improve Nitrogen Uptake and Use Efficiency of Cotton in Drip Irrigation.

Author: Fengquan Wu, Qiuxiang Tang, Jianping Cui, Liwen Tian, Rensong Guo, Liang Wang, Tao Lin

Imprint: *Agronomy* 2024, 14(9), 1876; <https://doi.org/10.3390/agronomy14091876>

Abstract: The optimization of plant density plays a crucial role in cotton production, and deficit irrigation, as a water-saving measure, has been widely adopted in arid regions. However, regulatory mechanisms governing nitrogen absorption, transportation, and nitrogen use efficiency (NUE) in cotton under deficit irrigation and high plant density remain unclear. To clarify the mechanisms of N uptake and NUE of

cotton, the main plots were subjected to three irrigation amounts based on field capacity (Fc): (315 [W1, 0.5 Fc], 405 [W2, 0.75 Fc, farmers' irrigation practice], and 495 mm [W3, 1.0 Fc]). Subplots were planted and applied at three densities: (13.5 [M1], 18.0 [M2, farmers' planting practice], and 22.5 [M3] plants m⁻²). The results revealed that under low-irrigation conditions, the cotton yield was 5.1% lower than that under the farmer's irrigation practice. In all plant densities and years, the nitrogen uptake of cotton increased significantly with the increase in irrigation. However, excessive irrigation resulted in nitrogen accumulation and migration, mainly concentrated in the vegetative organs of cotton, which reduced the NUE by 9.2% compared with that under farmers' irrigation practice. Concerning the interaction between irrigation and plant density, under low irrigation, the nitrogen uptake of high-density planting was higher, and the yield of seed cotton was only 2.9% lower than that of the control (the interaction effect of farmers' irrigation × plant density), but the NUE was increased by 10.9%. Notably, with the increase in irrigation amount, the soil nitrate nitrogen at the 0–40 cm soil layer decreased, and high irrigation amounts would lead to the transfer of soil nitrate nitrogen to deep soil. With the increase in plant density, the rate of nitrogen uptake and the amount of nitrogen uptake increased, which significantly reduced the soil nitrate nitrogen content. In conclusion, deficit irrigation and high plant density can improve cotton yield and NUE. We anticipate that these findings will facilitate optimized agricultural management in areas with limited water.

3

Title: Comprehensive growth monitoring index using Sentinel-2A data for large-scale cotton production

Author :Huihan Wang , Qiushuang Yao, Ze Zhang , Shizhe Qin

Imprint: Field Crops Research, Volume 317, 1 October 2024, 109525

Abstract: Timely and accurate plant growth monitoring is crucial for precision crop management. Traditional remote sensing methods use a single agronomic parameter to evaluate crop growth status (GST), limiting accuracy. Objective: To develop a comprehensive growth monitoring index (CGMI) based on multiple parameters. Methods A two-year field experiment in the Mosuwan Reclamation Region of Xinjiang, China was conducted to collect parameter characterization data for cotton growth, including leaf area index, canopy chlorophyll content, above-ground biomass, and boll numbers, and their contributions and interrelationships in relation to yield were analyzed. Entropy and game theory weighting methods were used to establish the CGMI_{EWM} and CGMI_{GT}, and a sequential forward selection algorithm (SFS) was used to screen the most effective remote-sensing monitoring feature variables for the different reproductive stages. Partial least squares regression (PLSR), random forest (RF), and support vector regression (SVR) were used to develop an optimal model to comprehensively monitor cotton growth and draw a spatial distribution map. Results

CGMI_{EWM} and CGMI_{GT} could effectively reflect GST. The correlation between CGMI_{GT} and yield based on a game theory combination weighting method was significantly higher than that between yield and each agronomic parameter. The correlation between CGMI_{GT} and yield ($r = 0.75$) was slightly higher at the initial boll stage than that of CGMI_{EWM} ($r = 0.73$), whereas at the initial boll-opening stage, the correlation between CGMI_{GT} and yield ($r = 0.74$) was significantly higher than that of CGMI_{EWM} ($r = 0.63$). The weight coefficients used to construct the CGMI_{GT} exhibited stable performance in different years. Feature variables were selected to monitor the comprehensive growth of cotton at different stages based on the SFS algorithm. PLSR, RF, and SVR were used to estimate CGMI_{GT}. The RF algorithm had the best estimation performance in both the initial boll and initial boll-opening stages ($R^2 = 0.63$, root mean square error (RMSE) = 0.086, RE = 19.8 % vs. $R^2 = 0.56$, RMSE = 0.107, RE = 24.1 %). A comprehensive cotton growth distribution map in the Mosuwan Reclamation Region was drawn using the optimal model, and growth was comprehensively evaluated. Areas with good cotton growth were concentrated in the north, and there was a decreasing trend from north to south.

4

Title: Optimizing the impact of spray characteristics of hybrid drone on spray deposition in cotton crops.

Author: P Rajesh, A P Mohankumar, R Kavitha, B Suthaker, K Ganesan

Imprint: Current Science, August 2024, 127(3)

Article available in Library in Print form.

5

Title: Optimal drip irrigation leaching amount and times enhance seed cotton yield and its stability by improving soil chemical environment and source-sink relationship

Author: Chao Xiao, Fucang Zhang, Yi Li

Imprint: Field Crops Research, Volume 317, 1 October 2024, 109531

Abstract: The arid and semi-arid regions of northwest China play a pivotal role in the national cotton production. However, soil salinization poses a severe constraint on seed cotton yield in this region. Salt leaching by drip irrigation has become increasingly popular for ameliorating saline-alkali soils. Yet, the most effective approach for utilizing drip irrigation leaching to maximize cotton productivity remains uncertain. Methods: Over a three-year period, field experiments were performed to explore the effects of four leaching amounts (75, 150, 225, and 300 mm) and four leaching times (seedling stage, budding stage, flowering stage, and boll-setting stage as one, two, three and four

times) on soil-water dynamics, ion composition, source-sink relationships, seed cotton yield and its stability in saline-alkali cotton fields under drip irrigation. Results: The study revealed that soil moisture significantly fluctuated during the cotton growing seasons. Timely irrigation significantly boosted soil moisture content by 11.3 %-23.5 %. Soil salinity was lower at the early growth stages of cotton, but it gradually increased over time, peaking at the flowering and boll-setting stages. Appropriate leaching effectively mitigated soil salinity, particularly at the flowering stage, resulting in a reduction of salt accumulation by 13.9 %-32.7 %. As leaching amount increased, the relative content of Ca^{2+} increased, while K^{+} and Na^{+} contents gradually decreased, thereby reducing the relative content of harmful ions and leading to a decrease in SAR by 7.07 %-34.3 %. In terms of biomass, the W3 treatment exhibited the highest level, which was 1.68 %-25.4 % greater than that of the other treatments. Among the three years, the S3 and S4 treatments consistently produced the highest biomass, with increases of 12.66 %-35.25 % and a slight 0.85 % difference, respectively.

6

Title: Organic nutrient management in colour cotton.

Author: AG Kshirsagar, YD Charjan, RS Wankhade and SM Nage

Imprint: International Journal of Advanced Biochemistry Research 2024; SP-8(7): 807-813

Abstract : A field experiment was conducted at Agriculture Research Station, Achalpur, Dist. Amravati under Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during the season kharif 2022-23. The topography of the field was fairly uniform and levelled. The soil was medium black cotton belonging to order Vertisol. The number of picked bolls plant-1, boll weight (g), and seed cotton yield plant-1 (g), and lint yield plant-1 (g) along with seed cotton, lint and stalk yield of colour cotton hectare-1 of colour cotton was observed significantly higher with treatment T3 - Vermicompost @ 2.5 t ha⁻¹ + Sunhemp in 2:1 proportion at 60 cm spacing (Green manuring of sunhemp 40 DAS) + Jeevamrut 10% at 50 DAS over all other treatments. The seed cotton equivalent yield of colour cotton was observed significantly higher with treatment T6 - Vermicompost @ 2.5 t ha⁻¹ + Black gram in 2:1 proportion at 60 cm spacing (Mulching of black gram after picking of pods) + Jeevamrut 10% at 50 DAS (1775 kg ha⁻¹). The available NPK status and bacterial, fungal and Actinomycetes population in soil at flowering stage of colour cotton was significant with treatment T3 - Vermicompost @ 2.5 t ha⁻¹ + Sunhemp in 2:1 proportion at 60 cm spacing (Green manuring of Sunhemp 40 DAS) + Jeevamrut 10% at 50 DAS over all other treatments.

7

Title: Evaluation of Potassium Requirement through Polyhalite Multinutrient Fertilizer for Enhancement of Quality and Yield of Bt. Cotton Under Different Irrigation Levels in Inceptisol

Author: Amolic Utkarsha Viju (Reg. No.2019/21)

Imprint: A Thesis submitted to the Mahatma Phule Krishi Vidyapeeth Rahuri - 413 722, Dist. Ahmednagar Maharashtra, India In Partial Fulfillment of The Requirements For The Degree Of Doctor Of Philosophy (Agriculture) In Soil Science And Agricultural Chemistry

8

Title: Effect of AMF Strains on Growth and Nutrient Uptake of Bt and Non Bt Cotton from Arid Region of Western Maharashtra, India

Author: Vilas Vikram Kamble and Chandrakant Jagannath Khilare

Imprint: The Planta RBS: Vol.-2 Issue-1 (April) 2021: 507 - 515 (Research Book Series - www.pgrindias.in)

Abstract: Arid conditions are restriction factors for cultivation of crops in Western Maharashtra of India. AM fungi have successfully proved the ability to enhance growth and nutrient uptake in crops of monocotyledonous and dicotyledonous plants. However, the role of AM fungi in arid region and in BT and Non BT is less known. In this study, pot experiments were conducted to evaluate effects of AMF strains on BT RASI II and non BT, Varlaxmi varieties of *Gossypium herbaceum* Linn. a significant cash crop from Maharashtra. Both BT and non BT Cotton seedlings were inoculated with three AMF strains (*Funneliformis mosseae*, *Glomus fasciculatum* and *Glomus intraradices*). The results revealed that the three AMF strains exhibit positive effects on growth and nutrient uptake under normal conditions. The results evince that AMF inoculation is vital strategy for Cotton cultivation from arid zone of Maharashtra.

9

Title: Modeling Comprehensive Deficit Irrigation Strategies for Drip-Irrigated Cotton Using Aqua Crop.

Author: Yalong Du, Qiuping Fu, Pengrui Ai, Yingjie Ma, and Yang Pan

Imprint: Agriculture 2024, 14(8), 1269; <https://doi.org/10.3390/agriculture14081269>

Abstract: The development of a crop production strategy through the use of a crop model represents a crucial method for the assurance of a stable agricultural yield and the subsequent enhancement thereof. There are currently no studies evaluating the suitability of the AquaCrop model for the drip irrigation of *Gossypium barbadense* in Southern Xinjiang, which is the primary planting region for *Gossypium barbadense* in China. In order to investigate the performance of the AquaCrop model in simulating the growth of cotton under mulched drip irrigation, the model was locally calibrated and validated according to different irrigation thresholds during a key growth period of two years. The results of the simulation for total soil water (TSW), crop evapotranspiration (ET_c), canopy coverage (CC), aboveground biomass (Bio), and seed cotton yield demonstrated a high degree of correlation with the observed data, with a root mean square error (RMSE) of <11.58%. The Bio and yield simulations demonstrated a high degree of concordance with the corresponding measured values, with root mean square error (RMSE) values of 1.23 t ha^{-1} and 0.15 t ha^{-1} , respectively. However, the predicted yield declined in the verification year, though the prediction error remained below 15%. Furthermore, the estimated evapotranspiration (ET_c) value demonstrated a slight degree of overestimation. Generally, the middle and late stages of cotton growth led to an overestimation of the TSW content. However, the prediction error was less than 13.99%. Through the calculation of each performance index of the AquaCrop model, it is found that they are in the acceptable range. In conclusion, the AquaCrop model can be employed as a viable tool for predicting the water response of cotton to drip irrigation under mulched film in Southern Xinjiang. Based on 64 years of historical meteorological data, three years were selected as scenarios for simulation. Principal component analysis (PCA) showed that, in a local wet year in Southern Xinjiang, the irrigation quota was 520 mm, and the irrigation cycle was 6 days/time. In normal years, the irrigation quota was 520 mm, with an irrigation cycle of 6 days/time. In dry years, the irrigation quota was 595 mm, with an irrigation cycle of 10 days/time. This allowed for higher seed cotton yields and irrigation water productivity, as well as the maximization of cotton yields and net revenue in the arid oasis area of Southern Xinjiang.

10

Title: Enhanced cotton chlorophyll content estimation with UAV multispectral and LiDAR constrained SCOPE model.

Author: Puchen Yan, Yangming Feng, Qisheng Han

Imprint: International Journal of Applied Earth Observation and Geoinformation
Volume 132, August 2024, 104052

Abstract: Accurate and non-destructive estimation of leaf chlorophyll content (LCC) is crucial for optimizing cotton production. This study enhances the SCOPE model by integrating unmanned aerial vehicle (UAV)-derived multispectral data with leaf area index (LAI) from LiDAR data, significantly improving precision of LCC estimation, particularly during crucial growth stages of cotton. We construct and analyze three cost functions: COST1, which relies solely on spectral data; COST2, which incorporates direct LAI inputs; and COST3, which adjusts for LAI measurement uncertainties by combining spectral term with an error term representing the squared relative error between measured and model-estimated LAI. Our findings indicate that while COST1 establishes a baseline, COST2 and COST3 provide more accurate LCC estimations. COST3, validated against theoretical data, field-measured cotton datasets, and an additional maize dataset, proves most robust, maintaining consistent accuracy across all growth stages especially when considering input data uncertainties. This highlights the importance of integrating appropriate forms of LAI in cost functions to refine LCC estimation. Future research should focus on improving data acquisition quality and developing more advanced cost functions to advance LCC estimation further.

11

Title: Optimizing cotton growth in saline soil: Compound microbial agent modulates indigenous bacteria to enhance photosynthesis and vegetative-reproductive balance

Author : Xiao Zhao , Panpan Guo , Xiong Wu , Meng Zhu

Imprint: Industrial Crops and Products

Volume 221, 1 December 2024, 119286

Abstract: Salt-tolerant composite plant growth-promoting rhizobacteria (STC-PGPR) can alleviate salt stress, though its complexity makes its stability and mechanisms in indeterminate-growing crops unclear. We tested STC-PGPR on two cotton (*Gossypium hirsutum* L.) varieties (G1: Xinluzao 72, G2: Zhongmiansuo 49), with two microbial treatments (B1: none, B2: with STC-PGPR) and three salinity levels (S1: 0 g NaCl kg⁻¹, S2: 4 g NaCl kg⁻¹, S3: 8 g NaCl kg⁻¹). The pot experiment used a three-factor completely randomized design in a greenhouse, with NaCl mixed into the soil before transplanting. STC-PGPR (*Paenibacillus polymyxa* SC2, *Bacillus velezensis* DSYZ, *Lactobacillus casei* DY-3, and *Saccharomyces cerevisiae* DY-4) was applied 14 days post-transplant and during flowering and boll development. STC-PGPR was diluted with water and applied to the rhizosphere. Results showed that under S1, STC-PGPR increased G2's seed cotton dry matter accumulation (Sc) by 25.1 %. Under S2, STC-PGPR increased G1's boll dry matter accumulation (Bo) from 0.21 g to 7.7 g per pot. Other STC-PGPR treatments were less effective due to overdeveloped vegetative organs, highlighting the need for balanced vegetative and reproductive growth. High salinity reduced STC-PGPR effectiveness under S3. Random forest analysis identified crucial indicators regulated by STC-PGPR that significantly affected reproductive organ dry matter accumulation (P<0.001).

Bioinformatics and correlation analyses showed biomarkers enriched by STC-PGPR influenced these indicators, not STC-PGPR directly. In S1, G2B2's biomarkers enhanced stomatal conductance, increasing the net photosynthetic rate (Pn) and promoting dry matter accumulation. They also increased stem diameter and inhibited vegetative growth, enhancing transport and channeling energy to reproductive organs. In S2, G1B2's biomarkers reduced leaf thickness, increased chlorophyll content to enhance Pn, and extended the maturation period. This enabled cotton to accumulate more photosynthetic products and allocate them to reproductive organs. This study demonstrates that STC-PGPR enhances productivity under salt stress, providing insights for optimizing saline soil cultivation.

12

Title: Effect of Different Intercropping System on Yield and Economics of Bt Cotton Production System Under Vidarbha Conditions

Author: M.D. Koli, S.U. Nemade , A.G. Mhetre , S.K. Chavan , S.U. Kakade

Imprint: New Era Agriculture Magazine, Volume-3, Issue-2, July, 2024

Abstract: A field experiment was conducted to study “Multi-tier cropping system to enhance resource utilization, productivity and profitability of Bt cotton production system” at Cotton Research Unit, Dr. PDKV, Akola during kharif season of 2021- 22. The experiment was laid out in Randomized Block Design with nine treatments and three replications. The variety of cotton PDKV JKAL-116 Bt (BG-II) was used for sowing with 60-120-60 cm paired row spacing and intercrops like greengram (Kopergaon), blackgram (AKU -10-1), soybean (JS 9305), and pigeonpea (PKVTARA) genotypes were used for sowing. Experimental results revealed that sole Bt cotton registered significantly higher yield attributes as compared to other paired row planting of cotton with different intercrops. The seed cotton yield, lint yield, cotton stalk yield and biological yield per hectare was also recorded significantly higher in sole Bt cotton than the paired row planting of cotton with different intercrops. Among the various treatments, the planting of cotton with pigeonpea in (6:2) row pattern and cotton + greengram (1:1) being at par with sole Bt cotton in respect to seed cotton yield per plant. The paired row planting of Bt cotton with two rows of greengram registered significantly highest seed cotton equivalent yield followed by cotton + greengram intercropping system at 1:1 row proportion and being at par with sole Bt cotton in respect to seed cotton yield. On the basis of growth, yield and economics studies it could be concluded highest GMR, NMR and B:C ratio was registered in paired row planting of Bt cotton with two rows of greengram

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Title: Salinity, Verticillium Wilt Tolerance and Genetic Diversity Analysis of Upland Cotton Genotypes

Author: Shader Alizada, Kamila Aliyeva, Ruhangiz Mammadova, Orkhan Bayramli, Babak Shahmorad Moghanloo

Imprint: Advances in Biology & Earth Sciences Vol.9, No.2, 2024, pp.242-252
<https://doi.org/10.62476/abes9242>

Abstract. Cotton is one of the most economically important crops. Screening and **selection** salt-tolerant cotton genotypes using DNA molecular markers not only introduces tolerant cultivars valuable for hybridization and breeding programs, but also identifies DNA regions implicated in the salinity tolerance mechanism. Screening and selection of cotton genotypes resistant to salinity stress and Verticillium wilt disease using DNA molecular markers not only introduces tolerant cultivars valuable for hybridization and breeding programs, but also identifies DNA regions implicated in the tolerance mechanism. The lowest Disease Severity Index was recorded in AP-317 (0.37) and Tashkent-2 (0.32) varieties. A total of 63 bands were generated based on 12 ISSR primers, 50 of which were polymorphic. The highest PIC value was recorded for UBC841 (0.466). AP-317 of Azerbaijan origin and Kirqizistan-174 of Kyrgyzstan origin were the most distant (0.358) genotypes and at the same time showed high resistance to Verticillium wilt. The obtained results showed that ISSR markers were an effective tool for determining genetic variation and identification of cotton cultivars.

14

Title: Cotton Leaf Disease Based on Image Processing Using Deep Learning

Author: D. Menaga; B T Shri Roshan; S R Shri Vikaas

Imprint: 2024 *International Conference on Innovations and Challenges in Emerging Technologies (ICICET)*, Nagpur, India, 2024, pp. 1-8, doi: 10.1109/ICICET59348.2024.10616267

Abstract: One of the most important occupations in India is agriculture. Out of all the crops, cotton is the best and is crucial to the agricultural economy of the country. In India, 40-50 million people work in the cotton trade and processing, while six million

farmers directly depend on the crop. The cotton leaf disease has grown in importance over the last few decades, resulting in losses to crops, farming operations, and financial resources. To achieve this aim, we first need to acquire different images of cotton plants. We can use image processing techniques to analyze dead leaf images and extract features like color, texture, and other characteristics with the Deep CNN model's assistance. In addition to being less expensive and more straightforward, automatic disease detection supports machine vision, which offers image-based automated process control and inspection. To properly train the algorithm, we will be using a dataset of approximately 1752 (approximately 440 images in each class) images classified into different categories according to the diseases. This model will be developed using tools present in Anaconda such as Jupyter Notebook, Spyder etc. The results of this project will demonstrate whether using it in real-time applications is feasible and whether traditional or manual disease and pest identification could benefit from the use of IT-based solutions.

15

Title: Evaluation of new chemistry insecticides against sucking insect pests of cotton.

Author: Ullah, M.I., M. Hasnain, M. Luqman, H. Hussnain, M. Tauseef, A. Ahmad, M. Shahid, Q. Abbas, M. Hussain, A. Raza, M.M.A. Khan, M.K. Nadeem, S. Nadeem.

Imprint: *Sarhad Journal of Agriculture*, 40(3): 858-865.

DOI | <https://dx.doi.org/10.17582/journal.sja/2024/40.3858.865>

Abstract: An evaluation of the efficacy of many novel pesticides against important sucking pests on cotton in field situation was carried out in 2023 at the Cotton Research Station, Ayub Agriculture Research Institute (ARRI), Faisalabad. A number of the most notorious and destructive pests to cotton crops are sucking insects, including whitefly *Bemisia tabaci*, jassid, *Amrasca biguttula* and thrips, *Thrips tabaci*. About 28% of losses occur in cotton crops every year due to the attack of these insect pests. The major goal of chemical control, which includes using different pesticides is to reduce yield losses in cotton crops. In order to identify an insecticide that could efficiently manage these sucking insect pests of cotton, the toxicity a few selected insecticides in the field have been assessed in current study. Six insecticides, when used alone or in a combination viz. chlothianidin 200ml/acre, spirotetramate 250ml/acre, matrine 500ml/acre, flonicamid 80gm/acre, imidacloprid + acephate 500gm/acre and dinotefuran 100gm/acre were tested against sucking insect pests such as whiteflies, jassids and thrips on cotton under field conditions at AARI Faisalabad. The population of cotton sucking insect pests was counted prior to pesticide administration as well as on 1st, 3rd, and 7th days following pesticide application. The results of this study revealed that overall reduction percentage of flonicamid and dinotefuran after 1st, 3rd, and 7th days was 33.33, 46.79, and 71.15%, and 30.52, 44.16, and 69.48%, respectively against

jassid after first spray and second spray. The overall reduction percentage of whitefly flonicamid after 1st, 3rd, and 7th days was 22.20, 44.54, and 73.39%, respectively after first spray. the first spray against thrips, the mixture of Imidacloprid and Acephate reduced the maximum insect infestation from 16.33 to 6.79 per leaf, respectively. The overall reduction percent of Imidacloprid + Acephate after 1st, 3rd, and 7th days was 10.89, 9.78, and 6.79%, respectively.

16

Title: Seasonal Incidence of Sucking Pests and Their Correlation with Weather Parameters in Bt Cotton.

Author: Rabari, P. H.; Patel, P. S.; Jaiman, R. S.; Muralidharan, C. M.; Chaudhary, F. K.

Imprint: Journal of Experimental Zoology India, 2024, Vol 27, Issue 2, p2095

Abstract: In cotton ecosystem, number of insect pests simultaneously occur and cause enormous damage to crop. Hence, investigation on succession of sucking pests in Bt cotton cultivar was carried out during 2022 and 2023 at S. D. Agricultural University, Sardarkrushinagar, Gujarat, India. The order of sequential occurrence of pests in Bt cotton was jassid > thrips > whitefly > aphid. Maximum incidence of aphid was observed during 46th standard meteorological week (SMW) (32.30 aphids/3 leaves), while maximum jassids (18.90 jassids/3 leaves) were observed during 42nd SMW. The incidence of whitefly reached to peak level (4.56 whiteflies/3 leaves) during 43rd SMW, however the peak activity of thrips was noticed during 41st SMW (19.72 thrips/3 leaves). The relationship obtained clearly showed that aphid and jassid population exhibited negative and significant correlation with morning and evening relative humidity. The whitefly exhibited negative and significant correlation with morning relative humidity. Highly significant and positive influence on whitefly, thrips and jassid population was noticed with maximum temperature during the study period.

17

Title: Effects of Plastic Mulch Residue on Soil Fungal Communities in Cotton

Author: Wenyue Song, Hongqi Wu, Zequn Xiang, Yanmin Fan, Shuaishuai Wang

Imprint: *Agriculture* 2024, 14(8), 1365; <https://doi.org/10.3390/agriculture14081365>

Abstract: Plastic mulch plays a crucial role in agricultural production in arid and semi-arid regions, positively impacting crop yields, salt suppression, and seedling protection.

However, as the usage of plastic mulch extends over time, residue accumulation becomes a significant issue in these regions. To clarify the effects of plastic mulch residue on soil fungi, this study focused on three typical cotton-growing areas in Xinjiang. Using high-throughput sequencing technology, the study analyzed the changes in the fungal community structure and diversity in rhizosphere and non-rhizosphere soils across 27 cotton fields under three different levels of plastic mulch residue: 0–75 kg/ha, 75–150 kg/ha, and 150–225 kg/ha. The results indicated that Ascomycota and Basidiomycota were the dominant fungal phyla across all treatments. Increasing levels of plastic mulch residue reduced the fungal richness in the soil, with a greater effects observed on rhizosphere fungi compared to bulk soil fungi. The α -diversity of cotton rhizosphere fungi showed an increasing trend, followed by a decrease with increasing plastic mulch residue, in Aksu and Bazhou, peaking at 75–150 kg/ha. Conversely, in Changji, the α -diversity decreased with increasing plastic mulch residue. The α -diversity of non-rhizosphere fungi associated with cotton decreased with increasing plastic mulch residue. Plastic mulch residue significantly altered the soil fungal α -diversity and had a greater effects on rhizosphere fungi. Different levels of plastic mulch residue had varying effects on the β -diversity of rhizosphere and non-rhizosphere fungi, significantly influencing rhizosphere fungi in Aksu and Bazhou and non-rhizosphere fungi in Changji and Bazhou. Overall, different levels of plastic mulch residue exerted varying degrees of influence on the community composition and diversity of soil fungi associated with cotton, potentially reducing the fungal richness and altering the community structure with increasing residue levels.

18

Title: Efficacy of New Insecticides Against *Amrasca biguttula* in Odienné Cotton Cultivation.

Author: Dohouonan Diabate , Ehouman Jean Brice Ohoueu , Drissa Fondio & Yao Tano

Imprint: Journal of Agricultural Science; Vol. 16, No. 9; 2024

Abstract: *Amrasca biguttula* (Hemiptera: Cicadellidae) is a major pest of cotton in Côte d'Ivoire. It reduces cotton yield despite pesticide spraying. This study carried out to evaluate the efficacy of new insecticides against *A. biguttula* in Odienné farms. Ten cotton hectares were established for field trials in 2021-2022 and 2022-2023. Each hectare was divided into two equal parts treated with one control insecticide and with one insecticide tested, respectively. *A. biguttula* adults and cotton yield of each treatment was evaluated. The results showed that JACOBIELLA 350 EC@Pyridine 200 g/L + Diamine 150 g/L, INDOXAN DUO 225 EC@Indoxacarb 125 g/L + Acetamiprid 100 g/L, Zidane 30 W@Flonicamide 30 g/kg, STINGER 500 WG@Flonicamide 500 g/kg, FLASHROLE PLUS 175 O@Flubendiamide 100g/L+ Spirotetramate 75 g/L, NICOMEDE 500 W@Flonicamide 500 g/kg, Tsunamide 280 OD@Flonicamide 200 g/L +

Flubendiamide 80 g/L, FLOMID MAX® Flonicamide 250 g/kg + rzth 100 g/kg, CYCLODAN 42%® O,o-dimethyl s-phthalimidomethyl and GARANT 200 WG® Acetamiprid 100 g/L + Lambdacyhalothrin 100 g/L were effective against *A. biguttula*. Their reduction rate of *A. biguttula* on cotton plants were higher than 50%. CORONI 672EC®, Dangoro 112EC® and CYPALM P 336EC® reduction rate was lower than 50%. THIAN 175 O-TEQ®, THALIS 112EC®, ATTAKAN 344SC®, EMERIT 112EC® and Coxytrine 672EC® were not effective against *A. biguttula*. The highest yields were recorded with FLOMID MAX® (1805 kg/ha), CYCLODAN® 12% (1716 kg/ha) and ZIDANE 30W® (982 kg/ha). Flonicamid, pyridine and diamine, indoxacarb and acetamiprid can be used against *A. biguttula* in cotton crops.

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Title: Efficacy of *Trichogramma Evanescens* (Hymenoptera: Trichogrammatidae), Six Pesticides, and Their Combinations to Control *Pectinophora Gossypiella* (Lepidoptera: Gelechiidae) in Egyptian Cotton Fields

Author: Seham Mansour Ismail

Imprint: *Int. J. Adv. Biol. Biomed. Res.* 2023, 11(4):185-195

Abstract:

Background: Pink bollworm, *Pectinophora gossypiella* Saunders (Lepidoptera: Gelechiidae) is one of the most economically devastating pests of cotton globally. Chemical control is the first line of defense, but has become ineffective in reducing yield losses caused by this pest. New management strategies against pink bollworm is urgently needed.

Methods: Field evaluations were conducted using the six pesticides were tested in two cropping seasons at a single dose, corresponding to their maximum recommended field rate of cotton in Egypt either with or without the egg parasitoid *Trichogramma evanescens*, TE (Hymenoptera: Trichogrammatidae). Treatments were applied to plots of cotton in 27th and 20th of July, 2021 and 2022, respectively, against pink bollworm, and efficacy was calculated based on the plant damage caused by the larvae through the yield.

Results: The highest reduction in pink bollworm larval numbers along with the least boll damage were found in azadirachtin, chlorantraniliprole, or hexaflumuron + *T. evanescens* (TE) plots. During both years, it was observed that plots treated with biological control agent and some pesticides led to a significant increase in cotton yield. The parasitism rates were 28.88, 24.19, 23.66, and 20.13% in the plots treated with azadirachtin, hexaflumuron, chlorantraniliprol, and spinosad and only 2.80 and 1.57% in

the plots treated with lambda-cyhalothrin and profenofos versus 33.62% in the control plot, there was difference significantly among treatments ($p \leq 0.05$). These findings underscore the potential use of TE combined with pesticides (mainly azadirachtin) to control pink bollworm larvae.

Conclusion: The promising results were achieved when combined TE with azadirachtin, the combined treatment significantly decreased the population of the pink bollworm and crop damage.

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Title: A diagnostic guide for *Berkeleyomyces rouxiae* causing black root rot of cotton

Author: Duy Phu Le, Chi Phuong Thi Nguyen, Maria Manjarrez, and Daniele Giblot-Ducray

Imprint: APS Publication, Published Online:19 Aug 2024<https://doi.org/10.1094/PHP-05-24-0043-DG>

Abstract: Black root rot (BRR) is a major seedling disease of cotton in Australia. The disease is caused by *Berkeleyomyces rouxiae* (formerly known as *Thielaviopsis basicola*), which is morphological identical to *B. basicola*. In this diagnostic guide, we aim to share current work and understanding of the *B. rouxiae* in cotton in Australia. This guide includes a comprehensive signs and symptoms to allow correct identification of the disease in the field. Methods and tricks to isolate and purify the pathogen from soil and diseased cotton were also discussed. Additionally, available molecular approaches for accurate identification of *B. rouxiae* were summarized. Last but not least, methods to preserve and assess pathogenicity of *B. rouxiae* on cotton were also presented.

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Title: A new host record of *Alternaria argyroxiphii* on Upland cotton (*Gossypium hirsutum*).

Author: Chi Phuong Thi Nguyen, Duy Phu Le

Imprint: Crop Protection, Volume 186, December 2024, 106907

Abstract: For the first time, we isolated and identified *Alternaria argyroxiphii* on Upland cotton (*Gossypium hirsutum*) in Australia and elsewhere. A single-spored *A. argyroxiphii* isolate was obtained from diseased cotton leaves that exhibited small circular to enlarged and coalesced irregular necroses in the 2021–2022 cropping season in northwest New South Wales, Australia. We identified *A. argyroxiphii* based on its

large conidia with filiform beaks and sequences of the internal transcribed spacer (ITS), glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and calmodulin (CAL). These multigene sequences of the cotton-*A. argyroxiphii* were 100% identical to those of the type *A. argyroxiphii* isolate CBS 117222; thus, confirming the identity. On two-true-leaf cotton seedlings, *A. argyroxiphii* was able to incite necrotic symptoms resembling those observed in the field, and was reisolated and re-identified, thus, fulfilling Koch's postulates. This is the first record of *A. argyroxiphii* on Upland cotton.

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Title: The Increased aspartate levels in transgenic cotton (*Gossypium hirsutum* L.) lead to improved tolerance against whitefly (*Bemisia tabaci*, Gennadius)

Author: Ambreen Gul, Abdul Qayyum Rao, Mukhtar Ahmed, Ayesha Latif, Allah Bakhsh, Sehrish Iftikhar

Imprint: Physiol Plant, . 2024 Jul-Aug;176(4):e14491. doi: 10.1111/ppl.14491.

Abstract: The whitefly, a polyphagous insect pest feeding on nearly 1328 plant species, is a major threat to global cotton production and incurs up to 50% yield losses in cotton production in Pakistan. We investigated whether increased aspartate in phloem sap imparts whitefly toxicity and protects cotton plants from intense damage. The enzymatic step for aspartate production is carried through aspartate aminotransferase (AAT). In this study, we constitutively overexpressed the *Oryza sativa* cytoplasmic AAT (OsAAT2) under the CaMV35S promoter in *Gossypium hirsutum* cv. CIM-482. Real-time PCR analysis of the AAT transcripts revealed a 2.85- to 31.7-fold increase in mRNA levels between the different cotton lines. A substantial increase in the free-amino acid content of the major N-assimilation and transport amino acids (aspartate, glutamate, asparagine, and glutamine) was seen in the phloem sap of the transgenic cotton lines. The bioassay revealed that the two transgenic cotton lines with the highest free aspartate content in the phloem sap exhibited 97 and 94% mortality in the adult whitefly population and a 98 and 96% decline in subsequent nymph populations, respectively. There was also a significant change in the physiological behaviour of the transgenic cotton lines, with an increased net assimilation (A), gaseous exchange (Gs) and rate of transpiration (E). Improved morphological characteristics like plant height, total number of bolls and fiber yield were recorded in transgenic cotton lines. The AAT gene shows promise in mitigating whitefly infestations and enhancing the overall health and yield of cotton plants.

Title: Proteomic insights into the saliva and salivary glands of the cotton aphid, *Aphis gossypii* (Hemiptera: Aphididae).

Author: Shanmugasundram Pavithran, Marimuthu Murugan, Kalenahalli Yogendra, Jayakanthan Mannu, Balasubramani Venkatasamy, Hemalatha Sanivarapu, Sankarasubramanian Harish, Senthil Natesan & Dhanyakumar Onkarappa

Imprint: *Phytoparasitica*, Published: 23 August 2024, Volume 52, article number 73, (2024)

Abstract: The cotton aphid or melon aphid, *Aphis gossypii* Glover (Hemiptera: Aphididae), is a rising threat to cotton production. Aphids use needle-like stylets to puncture the plant epidermis, access the sieve tube, and ingest the plant phloem. Aphids release salivary proteins while feeding, allowing them to colonize host plants successfully. Aphid saliva consists of many constituents that facilitate the consumption of phloem sap upon partial digestion and modulate plant defense systems. The salivary proteomes of *A. gossypii* were studied using liquid chromatography-tandem mass spectrometry (LC-MS/MS), which resulted in the identification of 189 proteins in excised salivary glands and 95 proteins in artificial diet-fed aphid saliva, with 25 proteins commonly noticed in both proteomes. Several proteins, including CAH1711662.1, CAH1735943.1, PFF0380w, XP_027839681.2, CAH1714583.1, CAH1713131.1 and XP_027840117.2 remained unique and uncharacterized. Previously identified salivary proteins of insects, such as glucose dehydrogenase, Mp1, Mp58, peroxidase, heat shock protein (HSP), elongation factor, and aminopeptidases, were also found. The identified proteins were categorized into seven groups, viz., enzymes, cytoskeletal proteins, sheath proteins, calcium-binding proteins, transporter proteins, chromatin-, RNA-, and DNA-binding proteins, and miscellaneous proteins. Twenty-five proteins from diet-fed aphid saliva and 17 proteins in the salivary gland possessed signal peptides. This study's results offer a more detailed understanding of the salivary proteins of *A. gossypii* and provide the foundation for future functional studies on aphid-cotton interactions to develop new aphid control methods.

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Title: Multi-Omics analysis reveals the important role of indole-3-acetic acid homeostasis in male fertility of cotton.

Author: Tao Zhang, Li-hong Ma, Qian-hao Zhu, Xin-yu Zhang, Chu-yi Nie, Jingya Zhou, Jie Sun, Feng Liu

Imprint: Industrial Crops and Products, Volume 222, Part 1, 15 December 2024, 119480

Abstract: Auxin (Indole-3-acetic acid, IAA) is essential for anther development and male fertility, but little is known about its homeostasis in developing anthers due to its complex and diverse synthesis pathways. Here, we employed transcriptomic, targeted metabolomic, and amino acid analyses on a wild type (WT) cotton (*Gossypium hirsutum*) line SD98-6 and its nearly-isogenic male sterile (MS) line SD98-6A, to delve into the relationship between IAA and anther fertility. In WT anthers, IAA homeostasis was achieved mainly through self-synthesis, conjugate hydrolysis, and polar transport, and accumulation of IAA exhibited an inverted "U" pattern with the highest content observed at the tetrad stage. In MS anthers, no IAA accumulation was observed after the meiosis stage and the IAA content remained constantly low, mainly due to reduction of the substrates (phenylalanine and tryptophan) for IAA synthesis, and significantly decreased expression of the genes involved in IAA synthesis. Meanwhile, carbohydrate metabolism pathways directly contributing to IAA synthesis and synthesis of amino acids were malfunctioned in MS anthers based on the expression profile of the metabolic genes and content measurement. These results provide valuable insights into the IAA homeostasis in cotton anthers and imply that genes related to IAA homeostasis are potential targets for development of IAA-sensitive male sterile cotton lines.

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Title: Integrating RTM-GWAS and meta-QTL data revealed genomic regions and candidate genes associated with the first fruit branch node and its height in upland cotton.

Author: Junji Su, Dandan Li, Wenmin Yuan, Ying Li, Jisheng Ju, Ning Wang, Pingjie Ling, Keyun Feng & Caixiang Wang

Imprint: Theoretical and Applied Genetics, Volume 137, article number 207, (2024)

Abstract: The first fruit branch node (FFBN) and the height of the first fruit branch node (HFFBN) are two important traits that are related to plant architecture and early maturation in upland cotton. Several studies have been conducted to elucidate the genetic basis of these traits in cotton using biparental and natural populations. In this study, by using 9,244 SNP linkage disequilibrium block (SNPLDB) loci from 315 upland cotton accessions, we carried out restricted two-stage multilocus and multiallele genome-wide association studies (RTM-GWASs) and identified promising haplotypes/alleles of the four stable and true major SNPLDB loci that were significantly associated with FFBN and HFFBN. Additionally, a meta-quantitative trait locus (MQTL) analysis was conducted on 274 original QTLs that were reported in 27 studies, and 40 MQTLs associated with FFBN and HFFBN were identified. Through the integration of the RTM-GWAS and meta-QTL analyses, two stable and true major SNPLDBs (LDB_5_15144433 and LDB_16_37952328) that were distributed in the two MQTLs were identified. Ultimately, 142 genes in the two genomic regions were annotated, and three candidate genes associated with FFBN and HFFBN were identified in the genomic region (A05:14.64–15.64 Mb) via RNA-Seq and qRT-PCR. The results of virus-induced gene silencing (VIGS) experiments indicated that GhE6 was a key gene related to HFFBN and that GhDRM1 and GhGES were important genes associated with early flowering in upland cotton. These findings will aid in the future identification of molecular markers and genetic resources for developing elite early-maturing cultivars with ideal plant characteristics.

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Title: Translational Regulation of Duplicated Gene Expression Evolution in Allopolyploid Cotton.

Author: Guiling Fu, Haotian Luo, Juqing Jia, Mingming Hou and Guanqing Hu

Imprint: *Preprints.org* (www.preprints.org) | NOT PEER-REVIEWED | Posted: 20 August 2024 doi:10.20944/preprints202408.1407.v1

Abstract: Polyploidy, a prevalent event in plant evolution, drives phenotypic diversification and speciation. While transcriptional changes and regulation in polyploids have been extensively studied, the translational level impact remains largely unexplored. To address this gap, we conducted a comparative transcriptomic and translatomic analysis of cotton leaves from allopolyploid species *G. hirsutum* (AD1) and *G. barbadense* (AD2) relative to their model A-genome and D-genome diploid

progenitors. Our data revealed that while allopolyploidization significantly affects the transcriptional landscape, its impact on translation was relatively modest, evidenced by a narrower expression range and fewer expression changes in ribosome-protected fragments than in mRNA levels. Allopolyploid-specific changes commonly identified in both AD1 and AD2 were observed in 7,393 genes at either transcriptional or translational levels. Interestingly, the majority of translational changes exhibited concordant down-regulation in both ribosome-protected fragments and mRNA, particularly associated with terpenoid synthesis and metabolism. Regarding translational efficiency (TE), at least one-fifth of cotton genes exhibit translational level regulation, with a general trend of more down-regulation than up-regulation of TE. The magnitude of translational regulation was slightly reduced in allopolyploids compared to diploids, and allopolyploidy tends to have a more profound impact on genes and functional associations with ultra-low TE. Moreover, we demonstrated a reduced extent of homeolog expression biases during translation compared to transcription. In conclusion, our study provides insights into the regulatory consequences of allopolyploidy post-transcription, contributing to a comprehensive understanding of regulatory mechanisms of duplicated gene expression evolution.

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Title: Identification of QTNs and Their Candidate Genes for Boll Number and Boll Weight in Upland Cotton.

Author: Xiaoshi Shi, Changhui Feng, Hongde Qin, Jingtian Wang

Imprint: *Genes* 2024, 15(8), 1032; <https://doi.org/10.3390/genes15081032>

Abstract: Genome-wide association study (GWAS) has identified numerous significant loci for boll number (BN) and boll weight (BW), which play an essential role in cotton (*Gossypium* spp.) yield. The North Carolina design II (NC II) genetic mating population exhibits a greater number of genetic variations than other populations, which may facilitate the identification of additional genes. Accordingly, the 3VmrMLM method was employed for the analysis of upland cotton (*Gossypium hirsutum* L.) in an incomplete NC II genetic mating population across three environments. A total of 204 quantitative trait nucleotides (QTNs) were identified, of which 25 (24.75%) BN and 30 (29.13%) BW QTNs were of small effect (<1%) and 24 (23.76%) BN and 20 (19.42%) BW QTNs were rare (<10%). In the vicinity of these QTNs, two BN-related genes and two BW-related genes reported in previous studies were identified, in addition to five BN candidate genes and six BW candidate genes, which were obtained using differential expression analysis, gene function annotation, and haplotype analysis. Among these, six candidate genes were identified as homologs of Arabidopsis genes. The present study addresses the limitation of heritability missing and uncovers several new candidate

genes. The findings of this study can provide a basis for further research and marker-assisted selection in upland cotton.

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Title: Impacts of parental genomic divergence in non-syntenic regions on cotton heterosis

Author: Chujun Huang, Yu Cheng, Yan Hu, Xuemei Zhang

Imprint: Journal of Advanced Research, Available online 6 August 2024

Abstract: Heterosis has revolutionized crop breeding, enhancing global agricultural production. However, the mechanisms underlying heterosis remain obscure. Xiangzamian 2# (XZM2), a super hybrid upland cotton (*Gossypium hirsutum* L.) characterized by high-yield heterosis, has been developed and extensively planted in China. We conducted a systematic analysis of CRI12 and J8891, two parents of XZM2. We aimed to reveal the precise genetic information and the role of non-syntenic divergence in shaping heterosis, laying a foundation for advancing understanding of heterosis. We *de novo* assembled high-quality genomes of CRI12 and J8891, and further uncovered abundant genetic variations and non-syntenic regions between the parents. Whole-genome comparison, association analysis, transcriptomic analysis and relative identity-by-descent (rIBD) estimation were conducted to identify structural variations (SVs) and introgressions within non-syntenic blocks and to analyze their impacts on promoting heterosis. Parental genetic divergence increased in non-syntenic regions. Furthermore, these regions, accounting for only 16.71% of the total genome, contained more loci with significantly higher heterotic effects, far exceeding the syntenic background. SVs covered 97.26% of non-syntenic sequences and caused widespread gene expression differences in these regions, driving dynamic complementation of gene expression in the hybrid. A set of SVs were responsible for trait improvement and had positive effects on heterosis, contributing larger heritability than short variations. We characterized numerous parental-specific introgressions from *G. barbadense*. Specifically, a functional introgression segment within non-syntenic blocks introduced an elite haplotype, which significantly increased lint yield and enhanced heterosis. Our study clarified non-syntenic regions to harbor more loci with higher heterotic effects, revealed their importance in promoting heterosis and supported the crucial role of genetic complementation in heterosis. SVs and introgressions were identified as key factors responsible for non-syntenic divergence between the parents. They had important effects on gene expression and trait improvement, positively contributing to heterosis.

Title: Investigating the Combining Ability of Yield and Fiber Quality in Upland Cotton (*Gossypium hirsutum* L.)

Author: Sadia Farooq, Hadia Bilal, Zonera Arshad, Muhammad Ans Hussain and Kashif Ali¹

Imprint: TRENDS IN ANIMAL AND PLANT SCIENCES
<https://doi.org/10.62324/TAPS/2024.040>

Abstract: Cotton is an essential fiber crop across the world that has a vital role in the GDP of Pakistan as a source of fiber, vegetable oil, and livestock feed. Cotton crop is adversely affected by climate change due to which a significant decrease in yield has been observed over the last few years. The production of improved cotton cultivars is essential as the demand for crop yield and quality of fiber has increased with the increase in population. Combining ability helps to select parents with specific traits that interact favorably in hybrids, ensuring more controlled and targeted improvement. The primary goal of the present investigation is to assess the combining ability for yield and associated character of 8 parents (3 lines and 5 testers) and 15 crosses developed by the line \times tester analysis. Significant variations in yield and fiber properties were found by analysis of variance, indicating considerable genetic variability among parents. The GCA and SCA were computed for the yield and its related characters. All the studied traits were primarily governed by nonadditive types of gene action. The parents viz., S-9, Bahar-2017, MSDK, and AA-933 were identified as good general combiners. The hybrids, Bahar-2017 \times AA-933, FH-172 \times AA-933, MSDK \times FH-154 and MNH-992 \times NIAB777 were identified as best hybrids. The parents and their hybrids having high values of GCA and SCA respectively will provide a route for research programs to increase cotton yield.

Title: Hybridization Events in *Gossypium*: Impact on Crop Improvement.

Author: Guo Tianxia

Imprint: Cotton Genomics and Genetics, 2024, Vol. 15, No.
 Received: 01 Jan., 1970 Accepted: 01 Jan., 1970 Published: 09 Aug., 2024

Abstract: Cotton, derived from the genus *Gossypium*, holds significant importance in global agriculture. This study provides a comprehensive examination of the historical and modern practices of hybridization in *Gossypium*, detailing the genetic and genomic bases, techniques used, and associated challenges. We explore the impact of

hybridization on crop improvement, highlighting enhancements in yield, fiber quality, disease and pest resistance, and environmental stress tolerance. The study delves into molecular insights gained from hybridization events, emphasizing genomic analysis, key gene identification, and the role of epigenetics. Furthermore, we discuss the integration of biotechnology in hybrid cotton breeding, including genetic engineering, CRISPR applications, and synthetic biology approaches. Economic and ecological implications are analyzed, considering cost-benefit aspects, biodiversity impacts, and sustainability. The study concludes with future prospects, focusing on advances in genomic tools, potential new hybrid varieties, and ethical and regulatory challenges. This study aims to consolidate current knowledge and guide future research directions in the hybridization of *Gossypium*.

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Title: Genome-wide Identification and Bioinformatics Analysis of Cotton KCR Gene Family.

Author: Hongyuan Xi, Man Wu, Shoulin Hu

Imprint: International Journal of Biology & Life Sciences, DOI:

<https://doi.org/10.54097/apnzx171>

Abstract: 3-ketoacyl-CoA reductase (*KCR*) is a key enzyme gene in the biosynthesis pathway of ultra-long chain monounsaturated fatty acids. Combining the sequence of *KCR* protein in *Arabidopsis thaliana*, we conducted a whole-genome identification and systematic evolutionary study of the *KCR* gene in cotton, focusing on *Gossypium. arboreum*, *Gossypium. raimondii*, *Gossypium. barbadense*, *Gossypium. hirsutum*. We analyzed the expression pattern of the *KCR* gene in high oil and low oil materials using transcriptome data and quantitative real-time polymerase chain reaction (qRT-PCR). Four *KCR* genes were identified in *Gossypium arboreum*, four in Ramond cotton, eight in Sea *Gossypium barbadense*, and eight in *Gossypium hirsutum*. Systematic evolutionary analysis divided the cotton *KCR* gene family members into three branches, and all branches had similar conserved motifs. Some promoter regions of *Gossypium hirsutum KCR* genes contained light response and drought regulation elements, suggesting that the *Gossypium hirsutum KCR* gene family may play a role in stress response. Four genes were identified that showed significant expression differences in the 15 DPA of high oil and low oil seed development, indicating that *GhKCR* gene family members may be related to lipid synthesis metabolism. The evolutionary relationship and related functions of *KCR* gene family members in cotton were analyzed and predicted, which provided a preliminary theoretical basis for the study of *KCR* gene function in cotton.

Title: Event-specific loop-mediated isothermal amplification for living modified cotton MON88701, MON531, MON15985, MON88913, and COT102.

Author: Wonkyun Choi, A-Mi Yoon, Jun-Woo Lee, Hye Song Lim, Young Jun Jung & Jung Ro Lee

Imprint: Biotechnology and Bioprocess Engineering , Published: 12 August 2024

Abstract: *Gossypium hirsutum* L., commonly known as upland cotton, is cultivated globally for natural fiber, feed, and seed oil. To enhance agricultural productivity and quality, living modified (LM) cotton has been developed and utilized since the late 1990s. Due to environmental concerns, such as biodiversity risks associated with living modified organisms (LMOs), the Korean government, including the Ministry of Environment, has been conducting LMO natural environment monitoring and post-management projects. In this study, we developed a loop-mediated isothermal amplification (LAMP) assay to detect five specific LM cotton events (MON88701, MON531, MON15985, MON88913, and COT102), which were the most abundant volunteers observed from 2019 to 2021 in South Korea. The event-specific LAMP assays for the five LM cotton events were established with a 40-min reaction time using LAMP reaction buffer, *Bst* DNA polymerase, and event-specific primers. The limit of detection ranged from 0.01 to 1 ng/ μ L. The assays' specificity and sensitivity were validated through colorimetric changes, fluorescence intensity measurements, and conventional PCR. To demonstrate the practical application of the LAMP assays, we tested 22 LM cotton volunteers collected from the natural environment in 2021. Each LAMP assay event-specifically amplified the respective LM cotton volunteers. These results indicate that the developed LAMP assays are effective tools for the efficient management and detection of LM cotton in field surveys, supporting regulatory compliance and environmental monitoring efforts.

Title: A telomere-to-telomere cotton genome assembly reveals centromere evolution and a Mutator transposon-linked module regulating embryo development.

Author: Gai Huang, Zhigui Bao, Li Feng, Jixian Zhai, Jonathan F. Wendel, Xiaofeng Cao & Yuxian Zhu

Imprint: *Nature Genetics* volume 56, pages1953–1963 (2024)

Abstract: Assembly of complete genomes can reveal functional genetic elements missing from draft sequences. Here we present the near-complete telomere-to-telomere

and contiguous genome of the cotton species *Gossypium raimondii*. Our assembly identified gaps and misoriented or misassembled regions in previous assemblies and produced 13 centromeres, with 25 chromosomal ends having telomeres. In contrast to satellite-rich *Arabidopsis* and rice centromeres, cotton centromeres lack phased CENH3 nucleosome positioning patterns and probably evolved by invasion from long terminal repeat retrotransposons. In-depth expression profiling of transposable elements revealed a previously unannotated DNA transposon (MuTC01) that interacts with miR2947 to produce *trans*-acting small interfering RNAs (siRNAs), one of which targets the newly evolved *LEC2* (*LEC2b*) to produce phased siRNAs. Systematic genome editing experiments revealed that this tripartite module, miR2947-MuTC01-*LEC2b*, controls the morphogenesis of complex folded embryos characteristic of *Gossypium* and its close relatives in the cotton tribe. Our study reveals a *trans*-acting siRNA-based tripartite regulatory pathway for embryo development in higher plants.

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Title: Inheritance of Fiber Length in Cotton F1 Hybrids

Author: Abror Mamajonov

Imprint; International Journal of Genetic Engineering 2024, 12(4): 54-58 DOI: 10.5923/j.ijge.20241204.03

Abstract: The article presents the results of the research on the heredity, variability and dominance of fiber length in the F1 generation of cotton plants. *G.hirsutum* cultivars, *G.mustelinum* wild type and hexoploid T-85 line were crossed and step hybridized. In the inheritance of the fiber length in the F1 generation, the participation of the objects involved in reciprocal hybridization as the father or mother form does not have great importance in the inheritance and formation of the character. Among the F1 hybrids, fiber length is higher in F1 Kyzyl baraka x Ghalib, F1 Namangan-77 x T-85, F1 (Ghalib x Andijan-35) x T-85 and F1 (Namangan-77 x Andijan-35) x T-85 combinations, F1 *G.mustelinum* Miers ex Watt x Winner, F1 *G.mustelinum* Miers ex Watt x Namangan-77 and F1 (Ghalib x Namangan-77) x *G.mustelinum* Miers ex Watt combinations showed relatively low results.

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Title: Impact of elevated temperatures on the genetic and morpho-physiological traits of cotton genotypes cultivation.

Author: Aamir Ali Abro, Muhammad Qasim, Muhammad Usama Younas, Ijaz Ali, Mubashir Abbas, Noor Muhammad, Shiguftah Khalid, Junaid Ahmed, Umbreen Bibi, Muhammad Waqas, Sezai Ercisli,

Imprint: Genetic Resources and Crop Evolution , Published: 21 August 2024

Abstract: Heat stress poses a significant threat to cotton, affecting crucial developmental stages from fertilization to boll development and thereby reducing both yield and quality. As global climate change advances, the likelihood of severe heat waves increases, presenting a serious challenge to agricultural production and our ability to feed a growing population. Cotton's resilience to heat involves a suite of physiological and biochemical responses, including adjustments in water management and protective mechanisms at the cellular level, such as the synthesis of heat shock proteins (HSPs) and antioxidants. These adaptations are crucial for maintaining cellular integrity and overall plant health under thermal stress. Recent research highlighted specific proteins and enzymes within the plant that help combat stress-related damage. However, the exact molecular mechanisms facilitating these protective responses are not fully delineated. Further research is needed to identify and validate additional molecular mechanisms underlying the plant's response to heat stress. Additionally, exploring new breeding strategies for the development of more resilient cultivars. In addition, field trials and testing under real-world conditions will be essential to assess the effectiveness of the proposed strategies for mitigating the negative effects of heat stress on crop yields.

PLANT BIOTECHNOLOGY

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Title: Strigolactone-gibberellin crosstalk mediated by a distant silencer fine-tunes plant height in upland cotton.

Author: Zailong Tian, Baojun Chen, Hongge Li, Ai Zhang, Xiongming Du, Shoupu He

Imprint: Molecular Plant, August 21, 2024

Abstract: Optimal plant height is crucial in modern agriculture, influencing lodging resistance and facilitating mechanized crop production. Upland cotton (*Gossypium hirsutum*) is the most important fiber crop globally; however, the genetic basis underlying plant height remains largely unexplored. In this study, we conducted a genome-wide association study to identify a major locus controlling plant height (*PH1*) in upland cotton. This locus encodes *gibberellin 2-oxidase 1A* (*GhPH1*) and features a 1133-bp structural variation (*PAV^{PH1}*) located approximately 16 kb upstream. The presence or absence of *PAV^{PH1}* influences the expression of *GhPH1*, thereby affecting

plant height. Further analysis revealed that a gibberellin-regulating transcription factor (GhGARF) recognizes and binds to a specific CATTG motif in both the *GhPH1* promoter and PAV^{PH1}. This interaction downregulates *GhPH1*, indicating that PAV^{PH1} functions as a distant upstream silencer. Intriguingly, we found that DWARF53 (D53), a key repressor of the strigolactone (SL) signaling pathway, directly interacts with GhGARF to inhibit its binding to targets. Moreover, we identified a previously unrecognized gibberellin-SL crosstalk mechanism mediated by the GhD53-GhGARF-*GhPH1*/PAV^{PH1} module, which is crucial for regulating plant height in upland cotton. These findings shed light on the genetic basis and gene interaction network underlying plant height, providing valuable insights for the development of semi-dwarf cotton varieties through precise modulation of *GhPH1* expression.

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Title: Proteomic and Phosphoproteomic Analyses during Plant Regeneration Initiation in Cotton (*Gossypium hirsutum* L.)

Author: Haixia Guo, Jin Wang, Xuehui Huo, Xiwang Cui, Li Zhang, Xiushan Qi

Imprint: *Genes* 2024, 15(8), 1079; <https://doi.org/10.3390/genes15081079>

Abstract: Somatic embryogenesis (SE) is a biotechnological tool used to generate new individuals and is the preferred method for rapid plant regeneration. However, the molecular basis underlying somatic cell regeneration through SE is not yet fully understood, particularly regarding interactions between the proteome and post-translational modifications. Here, we performed association analysis of high-throughput proteomics and phosphoproteomics in three representative samples (non-embryogenic calli, NEC; primary embryogenic calli, PEC; globular embryos, GE) during the initiation of plant regeneration in cotton, a pioneer crop for genetic biotechnology applications. Our results showed that protein accumulation is positively regulated by phosphorylation during SE, as revealed by correlation analyses. Of the 1418 proteins that were differentially accumulated in the proteome and the 1106 phosphoproteins that were differentially regulated in the phosphoproteome, 115 proteins with 229 phosphorylation sites overlapped (co-differential). Furthermore, seven dynamic trajectory patterns of differentially accumulated proteins (DAPs) and the correlated differentially regulated phosphoproteins (DRPPs) pairs with enrichment features were observed. During the initiation of plant regeneration, functional enrichment analysis revealed that the overlapping proteins (DAPs-DRPPs) were considerably enriched in cellular nitrogen metabolism, spliceosome formation, and reproductive structure development. Moreover, 198 DRPPs (387 phosphorylation sites) were specifically regulated at the phosphorylation level and showed four patterns of stage-enriched phosphorylation susceptibility. Furthermore, enrichment annotation analysis revealed that these phosphoproteins were significantly enriched in endosomal transport and

nucleus organization processes. During embryogenic differentiation, we identified five DAPs-DRPPs with significantly enriched characteristic patterns. These proteins may play essential roles in transcriptional regulation and signaling events that initiate plant regeneration through protein accumulation and/or phosphorylation modification. This study enriched the understanding of key proteins and their correlated phosphorylation patterns during plant regeneration, and also provided a reference for improving plant regeneration efficiency.

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Title: Molecular traits of MAPK kinases and the regulatory mechanism of GhMAPKK5 alleviating drought/salt stress in cotton.

Author: Rui Ding, Junhua Li, Jie Wang, Yan Li, Wuwei Ye, Gentu Yan, Zujun Yin

Imprint: Plant Physiology, 2024, 00, 1-18 <https://doi.org/10.1093/plphys/kiae415>
Advance access publication 14 August 2024

Abstract: Mitogen-activated protein kinase kinases (MAPKKs) play a critical role in the mitogen-activated protein kinase (MAPK) signaling pathway, transducing external stimuli into intracellular responses and enabling plant adaptation to environmental challenges. Most research has focused on the model plant *Arabidopsis thaliana*. The systematic analysis and characterization of MAPKK genes across different plant species, particularly in cotton (*Gossypium hirsutum*), are somewhat limited. Here, we identified MAPKK family members from 66 different species, which clustered into five different sub-groups, and MAPKKs from four cotton species clustered together. Through further bioinformatic and expression analyses, GhMAPKK5 was identified as the most responsive MAPKK member to salt and drought stress among the 23 MAPKKs identified in *Gossypium hirsutum*. Silencing GhMAPKK5 in cotton through virus-induced gene silencing (VIGS) led to quicker wilting under salt and drought conditions, while overexpressing GhMAPKK5 in *Arabidopsis* enhanced root growth and seed germination under these stresses, demonstrating GhMAPKK5's positive role in stress tolerance. Transcriptomics and Yeast-Two-Hybrid assays revealed a MAPK cascade signal module comprising GhMEKK (mitogen-activated protein kinase kinase kinases)3/8/31-GhMAPKK5-GhMAPK11/23. This signaling cascade may play a role in managing drought and salt stress by regulating transcription factor genes, such as WRKYs, which are involved in the biosynthesis and transport pathways of ABA, proline, and RALF. This study is highly important for further understanding the regulatory mechanism of MAPKK in cotton, contributing to its stress tolerance and offering potential in targets for genetic enhancement.

Title: Cell wall-associated receptor kinase GhWAKL26 positively regulates salt tolerance by maintaining Na⁺ and K⁺ homeostasis in cotton.

Author: Siqi Gao, Zhiqiang Zhang, Yinghao Zhao, Xiaona Li

Imprint: Environmental and Experimental Botany

Volume 226, October 2024, 105926

Abstract: Cell wall-associated receptor kinases (WAKs/WAKLs), are a specialized class of plant receptor kinases essential for signaling during stress conditions. However, there has been no report on the involvement of WAKs/WAKLs in salt tolerance in cotton. In this study, we report the functional characterization of *GhWAKL26*, whose expression is induced by salt, with its levels increasing over time and with higher salt concentrations. In addition, the fusion protein of *GhWAKL26* and GFP was localized to the plasma membrane. In transgenic Arabidopsis, the dry weight, fresh weight, and root length were significantly higher than those of wild-type plants, indicating enhanced salt tolerance. While in *GhWAKL26*-silenced cotton seedlings, H₂O₂, O₂⁻, and MDA content were increased, and chlorophyll content was reduced under salt stress, displaying compromised salt tolerance. RNA-seq analysis revealed that the silencing of *GhWAKL26* resulted in the down-regulation of expression levels of certain ion transport-related genes under salt stress, concurrently leading to an increased Na⁺/K⁺ ratio in cotton seedlings. Overall, our findings indicate that *GhWAKL26* enhanced plant resistance to salt stress in cotton by regulating the balance of Na⁺ and K⁺ ions.

Title: N⁶-methyladenosine RNA modification regulates photoperiod sensitivity in cotton.

Author: Ying He, Zhanfeng Si, Gaofu Mei, Yu Cheng, Jun Zhang, Tao Jiang, Jiani Chen, Huifang Xiong

Imprint: *Plant Physiology*, kiae371, <https://doi.org/10.1093/plphys/kiae371>

Abstract: The methylation of N⁶-methyladenosine (m⁶A) involves writers, erasers, and readers, acting synergistically in posttranscriptional regulation. These processes influence various biological processes, including plant floral transition. However, the specific role of m⁶A modifications in photoperiod sensitivity in cotton (*Gossypium hirsutum*) remains obscure. To elucidate this, in this study, we conducted transcriptome-wide m⁶A sequencing during critical flowering transition stages in the photoperiod-

sensitive wild *G. hirsutum* var. *yucatanense* (*yucatanense*) and the photoperiod-insensitive cultivated cotton *G. hirsutum* acc. TM-1 (TM-1). Our results revealed significant variations in m6A methylation of 2 cotton varieties, with *yucatanense* exhibiting elevated m6A modification levels compared with TM-1 under long-day conditions. Notably, distinct m6A peaks between TM-1 and *yucatanense* correlated significantly with photoperiod sensitivity. Moreover, our study highlighted the role of the demethylase *G. hirsutum* ALKB homolog 5 (*GhALKBH5*) in modulating m6A modification levels. Silencing *GhALKBH5* led to a decreased mRNA level of key photoperiodic flowering genes (*GhADO3*, *GhAGL24*, and *GhFT1*), resulting in delayed bud emergence and flowering. Reverse transcription quantitative PCR analyses confirmed that silencing *GhADO3* and *GhAGL24* significantly downregulated the expression of the floral integrator *GhFT1*. Collectively, our findings unveiled a transcriptional regulatory mechanism in which *GhALKBH5*-mediated m6A demethylation of crucial photoperiodic flowering transcripts modulated photoperiod sensitivity in cotton.

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Title: In vitro regeneration of cotton (*Gossypium hirsutum* L.) cultivar KC3 with controlled phenolic secretion by using *Kappaphycus alvarezii* sulfated polysaccharide extract and plant growth regulators.

Author: Packiaraj Gurusaravanan, Sathasivam Vinoth, Rajkumar Vasanthkumar, Muthukrishnan Arun, Muthukrishnan Saradhadevi

Imprint: Plant Tissue Culture, Published: 31 July 2024

Abstract: An efficient and reproducible *in vitro* regeneration protocol was developed for elite cotton cultivar KC3 by using plant growth regulators (PGRs) in combination with seaweed polysaccharide (SP) extracts. The existence of polysaccharide in seaweed extract was confirmed by Fourier transform infrared spectroscopy (FT-IR) and carbon-13 (¹³C) nuclear magnetic resonance (NMR) spectroscopy analysis. The extracted SP extract efficacy was tested for *in vitro* plant regeneration. The maximum callus frequency (89.4%) was obtained from hypocotyl explant in the Murashige and Skoog (MS) medium supplemented with 4.0% glucose, 1.5 mg L⁻¹ thidiazuron (TDZ), 0.6 mg L⁻¹ 2,4-dichlorophenoxyacetic acid (2,4-D), and 30.0 mg L⁻¹ SP. Remarkably, PGR- and SP-fortified medium inhibits the phenolic excretion from the explants. The well-developed yellow green friable texture of callus was transferred to shoot initiation medium. MS medium fortified with 4.0% glucose, 2.0 mg L⁻¹ 6-(γ,γ -dimethylallylamino) purine (2iP), 1.0 mg L⁻¹ kinetin (KIN), 1.0 mg L⁻¹ 6-benzylaminopurine (BA), and 40.0 mg L⁻¹ SP has shown maximum response (85.2%), and it produced 9.5 shoots per callus. The elongated shoots were cultured on root induction medium which consists of Murashige and Skoog (MS) salts with indole-3-acetic acid (IAA), indole-3-butyric acid (IBA), 1-naphthaleneacetic acid (NAA), and SP. The results revealed that the maximum

number of roots (12.9 per shoot) with 8.6 cm in length was achieved on MS medium supplemented with 0.6 mg L⁻¹ IBA, combined with 30.0 mg L⁻¹ SP. Therefore, modified MS medium with natural bio-stimulant has more potential and is more reliable for *in vitro* regeneration of plants by neutralizing the effects of phenolic compounds secreted by the explants.

SEED SCIENCE AND TECHNOLOGY

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Title: Low temperature exposure influences nitrogen metabolism resulting in decreased Cry1Ac insecticidal endotoxin content in cotton seeds

Author: Yuan Chen, Shu Dong, Yuyang Dai, Xiang Zhang, Dehua Chen, Yinglong Chen & Zhenyu Liu

Imprint: *BMC Plant Biology* volume 24, Article number: 781 (2024)

Abstract: Sudden temperature drops, resulting from extreme weather events, often occur during the boll-setting period of cotton in Xinjiang, China, causing decreased expression of *Bacillus thuringiensis* (Bt) insecticidal proteins in cotton bolls. The precise threshold temperatures and durations that lead to significant changes in Cry1Ac endotoxin levels under low temperatures remain unclear. To address this, we investigated the effects of different temperatures and stress durations on Cry1Ac endotoxin levels in cotton bolls. In 2020–2021, two Bt transgenic cotton varieties, conventional Sikang1 and hybrid Sikang3, were selected as experimental materials. Various low temperatures (ranging from 16 to 20 °C) with different durations (12 h, 24 h and 48 h) were applied during the peak boll-setting period. Results As the temperature decreased, the Cry1Ac endotoxin content in the boll shell, fiber, and seed exhibited a declining trend. Moreover, the threshold temperature which caused a significant reduction in Cry1Ac endotoxin content increased with the prolonged duration of low-temperature stress. Among the components of cotton bolls, seeds were most affected by low-temperature stress, with the threshold temperature for a significant reduction in Cry1Ac endotoxin content ranging from 17 °C to 19 °C. Correlation analysis indicated that low temperatures led to a decrease in protein synthesis capacity and an increase in degradation ability, resulting in reduced Cry1Ac endotoxin content. Pathway analysis revealed that both free amino acid and peptidase had significant negative effects on Cry1Ac endotoxin content.

Title: Glycyrrhizin Acid Complexes in Cotton Under Salinity Conditions (*Gossypium barbadense* L.) Influence on Seed Fertility.

Author: Kushiev H.H, Djuraev T.A

Imprint: (2024). *Western European Journal of Modern Experiments and Scientific Methods*, 2(8), 1-8.

Abstract: Glycyrrhizin acid (GA): Supramolecular complexes of phytohormones (PH) (PH: indole-3-acetic acid (IAA); indole-3-butyric acid (IBA); naphthalene-1-acetic acid (NAA) and kinetin) (100 μ M) of cotton in laboratory conditions « Sultan » It was found that the intensity and amount of water-soaking dynamics of the variety seeds were significantly increased compared to the control, and the germination energy and germination level of the seeds were optimized under experimental salinity conditions (NaCl=200 mM). The obtained results show the high prospects of using supramolecular complexes of GA: phytohormones in agricultural practice to optimize the process of germination and development of plants under conditions of stress factors, including salinity.

FIBER AND FIBER TECHNOLOGY

Title: GhEXL3 participates in brassinosteroids regulation of fiber elongation in *Gossypium hirsutum*.

Author: Changsheng Zhang, Zhao Liu, Sheng Shu, Xinyang Li, Yujun Li, Le Liu, Li Liu, Xuwen Wang, Fuguang Li, Ghulam Qanmber, Zuoren Yang

Imprint: *Plant J*, . 2024 Aug 22., doi: 10.1111/tpj.16995. Online ahead of print.

Abstract: Cotton fiber (*Gossypium hirsutum*) serves as an ideal model for investigating the molecular mechanisms of plant cell elongation at the single-cell level. Brassinosteroids (BRs) play a crucial role in regulating plant growth and development. However, the mechanism by which BR influences cotton fiber elongation remains incompletely understood. In this study, we identified EXORDIUM-like (GhEXL3) through transcriptome analysis of fibers from BR-deficient cotton mutant pagoda 1

(pag1) and BRI1-EMS-SUPPRESSOR 1 (GhBES1.4, encoding a central transcription factor of BR signaling) overexpression cotton lines. Knockout of GhEXL3 using CRISPR/Cas9 was found to impede cotton fiber elongation, while its overexpression promoted fiber elongation, suggesting a positive regulatory function for GhEXL3 in fiber elongation. Furthermore, in vitro ovule culture experiments revealed that the overexpression of GhEXL3 partially counteracted the inhibitory effects of brassinazole (BRZ) on cotton fiber elongation, providing additional evidence of GhEXL3 involvement in BR signaling pathways. Moreover, our findings demonstrate that GhBES1.4 directly binds to the E-box (CACGTG) motif in the GhEXL3 promoter region and enhances its transcription. RNA-seq analysis revealed that overexpression of GhEXL3 upregulated the expression of EXPs, XTHs, and other genes associated with fiber cell elongation. Overall, our study contributes to understanding the mechanism by which BR regulates the elongation of cotton fibers through the direct modulation of GhEXL3 expression by GhBES1.4.

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Title: Deciphering the dynamic expression network of fiber elongation and the functional role of the *GhTUB5* gene for fiber length in cotton based on an introgression population of upland cotton.

Author: Jianjiang Ma , Liupeng Yang , Yuanyue Dang

Imprint: Journal of Advanced Research, Available online 4 August 2024

Abstract: Interspecific introgression between *Gossypium hirsutum* and *G. barbadense* allows breeding cotton with outstanding fiber length (FL). However, the dynamic gene regulatory network of FL-related genes has not been characterized, and the functional mechanism through which the hub gene *GhTUB5* mediates fiber elongation has yet to be determined. Coexpression analyses of 277 developing fiber transcriptomes integrated with QTL mapping using 250 introgression lines of different FL phenotypes were conducted to identify genes related to fiber elongation. The function of *GhTUB5* was determined by ectopic expression of two *TUB5* alleles in *Arabidopsis* and knockout of *GhTUB5* in upland cotton. Yeast two-hybrid, split-luciferase and pull-down assays were conducted to screen for interacting proteins, and upstream genes were identified by yeast one-hybrid, dual-LUC and electrophoretic mobility shift assays. The 32,612, 30,837 and 30,277 genes expressed at 5, 10 and 15 days postanthesis (dpa) were grouped into 19 distinct coexpression modules, and 988 genes in the MEblack module were enriched in the cell wall process and exhibited significant associations with FL. A total of 20 FL-QTLs were identified, each explaining 3.34–16.04 % of the phenotypic variance in the FL. Furthermore, several FL-QTLs contained 15 genes that were differentially expressed in the MEblack module including the tubulin beta gene (*TUB5*). Compared with the wild type, the overexpression

of *GhTUB5* and *GbTUB5* in *Arabidopsis* suppressed root cell length but promoted cellulose synthesis. Knockout of *GhTUB5* resulted in longer fiber lines. Protein-based experiments revealed that GhTUB5 interacts with GhZFP6. Additionally, *GhTUB5* was directly activated by *GhHD-ZIP7*, a homeobox-leucine zipper transcription factor, and its paralogous gene was previously reported to mediate fiber elongation. This study opens a new avenue to dissect functional mechanism of cotton fiber elongation. Our findings provide some molecular details on how *GhTUB5* mediates the FL phenotype in cotton.

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Title: The DUF579 proteins GhIRX15s regulate cotton fiber development by interacting with proteins involved in xylan synthesis.

Author: Mengyun Li, Feng Chen, Jingwen Luo, Yanan Gao

Imprint: The Crop Journal, Volume 12, Issue 4, August 2024, Pages 1112-1125

Abstract: Cotton provides the most abundant natural fiber for the textile industry. The mature cotton fiber largely consists of secondary cell walls with the highest proportion of cellulose and a small amount of hemicellulose and lignin. To dissect the roles of hemicellulosic polysaccharides during fiber development, four *IRREGULAR XYLEM 15* (*IRX15*) genes, *GhIRX15-1/-2/-3/-4*, were functionally characterized in cotton. These genes encode DUF579 domain-containing proteins, which are homologs of AtIRX15 involved in xylan biosynthesis. The four *GhIRX15* genes were predominantly expressed during fiber secondary wall thickening, and the encoded proteins were localized to the Golgi apparatus. Each *GhIRX15* gene could restore the xylan deficient phenotype in the *Arabidopsis irx15irx15l* double mutant. Silencing of *GhIRX15s* in cotton resulted in shorter mature fibers with a thinner cell wall and reduced cellulose content as compared to the wild type. Intriguingly, GhIRX15-2 and GhIRX15-4 formed homodimers and heterodimers. In addition, the GhIRX15s showed physical interaction with glycosyltransferases GhGT43C, GhGT47A and GhGT47B, which are responsible for synthesis of the xylan backbone and reducing end sequence. Moreover, the GhIRX15s can form heterocomplexes with enzymes involved in xylan modification and side chain synthesis, such as GhGUX1/2, GhGXM1/2 and GhTBL1. These findings suggest that GhIRX15s participate in fiber xylan biosynthesis and modulate fiber development via forming large multiprotein complexes.