



GLEANINGS IN COTTON RESEARCH

MARCH 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: Preliminary results of automatic cotton crops mapping using remote sensing data.

Author: Rinat Gulyaev , Azamat Sultonov , Ravil Yunusov , Damir Rafikov , Kamila Gulyaeva

Imprint: E3S Web of Conferences 486, 04009 (2024)
<https://doi.org/10.1051/e3sconf/202448604009>

Abstract: The paper presents the results of application of the method of automatic generation of representative and unbiased set for in-season cotton crop mapping, based on crop simulation model, previously parameterized using ground truth and satellite data. The method provided confident mapping of cotton fields without using actual ground-truth information or a prior information about their in-season phenology. Overall mapping accuracy calculated using relevant ground truth data for cotton fields has reached 95.6 %. Consideration of time series of NDVI values as a model of phase characteristics allowed using relatively simple criteria to identify typical representatives of the selected crop on the basis of analysis of their seasonal phenology and made it possible to build a reference sample for modeling and further classification.

2

Title: Integrated Pest Management Technology in Cotton in Parbhani District of Maharashtra State: An Economic Analysis.

Author: R. S. Ladane , S. H. Kamble , R. D. Shelke and P. A. Dive

Imprint: Journal of Scientific Research and Reports Volume 30, Issue 3, Page 172-176, 2024

Abstract: The present investigation pertinent to this study was conducted in Manwat and Parbhani tahasil of Parbhani district. For the present study 70 cotton growers who follow IPM technology were selected in consultation with KVK subject matter specialists, Officials of State Agriculture department and Extension Agronomists. Further the sample of 70 farmers were divided into three categories viz., Low adopters, medium adopters, high adopters, based on their levels of adoption. To assess extent of adoption of various IPM technology of cotton the concept of TAI was used According to the study, only 17.14 per cent respondents were high level of IPM technology adopters,

14.28 per cent have adopted IPM at low level while highest i.e. 68.57 per cent farmers had adopted IPM technology at medium level.

3

Title: Hydrogen Peroxide Alleviates Salt Stress Effects on Gas Exchange, Growth, and Production of Naturally Colored Cotton.

Author: Jackson Silva Nóbrega, Valéria Ribeiro Gomes, Lauriane Almeida dos Anjos Soares

Imprint: Plants 2024, 13(3), 390; <https://doi.org/10.3390/plants13030390>

Abstract: Cotton is one of the most exploited crops in the world, being one of the most important for the Brazilian Northeast. In this region, the use of irrigation is often necessary to meet the water demand of the crop. Water is often used from underground wells that have a large amount of salt in their constitution, which can compromise the development of crops, so it is vital to adopt strategies that reduce salt stress effects on plants, such as the foliar application of hydrogen peroxide. Thus, the objective of this study was to evaluate the effects of foliar application of hydrogen peroxide on the gas exchange, growth, and production of naturally colored cotton under salt stress in the semi-arid region of Paraíba, Brazil. The experiment was carried out in a randomized block design in a 5×5 factorial scheme, with five salinity levels of irrigation water – EC_w (0.3, 2.0, 3.7, 5.4 and 7.1 dS m⁻¹) – and five concentrations of hydrogen peroxide – H₂O₂ (0, 25, 50, 75 and 100 µM), and with three replicates. The naturally colored cotton ‘BRS Jade’ had its gas exchange, growth, biomass production, and production reduced due to the effects of salt stress, but the plants were able to produce up to the EC_w of 3.97 dS m⁻¹. Foliar application of hydrogen peroxide at the estimated concentrations of 56.25 and 37.5 µM reduced the effects of salt stress on the stomatal conductance and CO₂ assimilation rate of cotton plants under the estimated EC_w levels of 0.73 and 1.58 dS m⁻¹, respectively. In turn, the concentration of 12.5 µM increased water-use efficiency in plants subjected to salinity of 2.43 dS m⁻¹. Absolute and relative growth rates in leaf area increased with foliar application of 100 µM of hydrogen peroxide under EC_w of 0.73 and 0.3 dS m⁻¹, respectively. Under conditions of low water salinity (0.3 dS m⁻¹), foliar application of hydrogen peroxide stimulated the biomass formation and production components of cotton.

Title: Photosynthetic and Physiological Characteristics of *Gossypium hirsutum* L. x *Gossypium barbadense* L. Backcross Populations in Full Boll Stage.

Authors: LI Shengmei; PANG Bo; GENG Shiwei; SONG Wu; LI Hongmei; MA Maosen; ZHANG Ru; WANG Xinyan; GAO Wenwei

Imprint: Journal of Agricultural Science & Technology (1008-0864), 2024, Vol 26, Issue 1, p40

Abstract: In order to explore the photosynthetic characteristics and physiological basis of *G. hirsutum* x *G. barbadense* backcross cotton in the full boll stage, and to screen out light-efficiency germplasm resources in the progeny of island upland hybrid cotton, taking upland cotton 'Line 9' as the female parent and sea island cotton 'Xinhai 16' as the male parent, the BC₄F₂:₄ population consisting of 115 lines was constructed as the research object, and the photosynthetic and physiological traits under field conditions were measured to evaluate the breeding potential of progeny lines with the method of descriptive statistical, correlation, regression, principal component and cluster analyses. The results showed that 15 photosynthetic physiological traits had rich variation, with a coefficient of variation ranging from 8.96% to 51.09%, among which 9 traits with coefficients of variation of 20% or more including net photosynthesis rate, transpiration rate, water-use efficiency, intercellular CO₂ concentration, stomatal conductance, water vapor pressure deficit, malondialdehyde, soluble protein, and superoxide dismutase. Correlation analysis revealed that there was not only a significant internal correlation, but also a significant correlation between photosynthetic and physiological indicators, and soil and plant analyzer development (SPAD) significantly correlated with all 14 traits. Multiple stepwise regression analysis constructed the optimal regression equations for 10 photosynthetic physiological traits. By principal component analysis, 5 principal components were extracted and the cumulative contribution rate reached to 78.608%. Principal component 1(PC1) and PC4 were the effective basis for explaining the physiological indicators of the group, PC2, PC3 and PC5 were the effective basis for explaining group photosynthetic traits. The Ward. D hierarchical clustering method divided the population into 4 categories and the percentage of the group I, group II, group III and group IV to the total materials were 33.91%, 10.43%, 29.57% and 26.09%, and the 30 materials of the group IV had good comprehensive traits cotton, which could be used as high light-efficiency lines suitable for breeding needs. The results of the study provided a theoretical basis and material support for high light-efficiency breeding of cotton.

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Title: Effect of Chromium ions on the biochemical parameters of cotton plant, *Gossypium hirsutum* (L.)

Author: D. Ezhilvannan and P.S. Sharavanan

Imprint: Eco. Env. & Cons. 29 (January Suppl. Issue) : 2023; pp.

Author: The Cotton plant, *Gossypium hirsutum* (L.) treated different concentrations of chromium [Cr] ions (10, 25, 50, 75, 100 and 250 mgkg⁻¹) through soil for 60 days. At the end of the experiment, the biochemical parameters of the control and treated Cotton plant *G. hirsutum* (L.) such as chlorophyll a & b, total chlorophyll, total sugars, starch, amino acids, protein and proline were analyzed by standard procedures. Results were statistically analysed and the mean values between the groups were evaluated by Duncan post hoc with homogenous subset. In all the treated groups, the biochemical parameters were significantly reduced than control except 10mgKg⁻¹ which is representing the below critical concentration of the micronutrients, i.e., heavy metals. Our study evidenced that Cr levels in soil less than 10 mg Kg⁻¹ showed no impact on the chlorophyll, total sugars and amino acids in the cotton plants *Gossypium hirsutum* (L.) whereas higher concentrations of the Cr levels showed severe impact on the photosynthetic pigments (chief and total pigments) which resulted in the reduced food production (total sugars and starch) and sugar interconversion, finally the growth and metabolism of the cotton plant were severely altered.

6

Title: *Gossypium hirsutum* as a Study Species to Understand Plant Responses to Drought Stress.

Author: Student researcher: Sam Schafer, Senior

Imprint: Journal of Purdue Undergraduate Research: Volume 13, Fall 2023

Abstract: Throughout the past year of working with cultivated upland cotton (*Gossypium hirsutum* L.), it has been intriguing to learn how it can serve as a study species for understanding the effects of genotype and water stress on photosynthetic parameters. The goal of the project is to discover whether genotype and environment play a significant role in crop photosynthesis and to quantify any potential interaction between the two variables. Photosynthesis-CO₂ response (A/C_i) curves of 14 biogeographically diverse cotton accessions grown under controlled greenhouse

conditions were collected using a Li-COR 6800 Portable Photosynthesis System (Li-COR: Lincoln, Nebraska) and analyzed using R software. Broad-sense heritability (H^2) for maximum rate of rubisco carboxylation (V_{cmax}) and electron transport (J_{max}) were 0.575 and 0.686, respectively. Paired with a one-way ANOVA test, results suggested that photosynthetic parameters were not significantly affected by genotype. A subset of 4 cotton accessions were selected for a follow-up study. During the second experiment, a control group of replicates were maintained under well-watered conditions while another replicate group experienced a 75% reduction in irrigation for two weeks after flowering. Following the first week of treatment, a suite of physiological parameters were collected including plant height, number of developing bolls, number of healthy leaves, and number of buds. Results indicated significant differences between the two populations, which suggests a reduction in photosynthetic activity. A/C_i curves were collected at the two-week mark of drought treatment and are yet to be analyzed. Conclusions will be drawn based on the differences in photosynthetic performance between accessions from the first and second experiments.

7

Title: Utilization of Secondary Metabolites in Cotton Production.

Author: Ziming Yue, Te-Ming Tseng, K. Raja Reddy, Natraj Krishnan and Shien Lu

Imprint: FROM THE EDITED VOLUME, Best Crop Management and Processing Practices for Sustainable Cotton Production by Dr. Songül Gürsoy and Dr. Songül Akin, Published: 06 February 2024, DOI: 10.5772/intechopen.114098

Abstract: Cotton is the most critical fiber crop and one of the top three oilseed crops in the world. One pronounced feature of cotton is that it is rich in secondary metabolites, mainly including terpenoids, flavonoids, and phenolic acids. These secondary metabolites have various ecological roles, such as defense and signal transmission. With the concept of plant secondary metabolites becoming more and more evident in the mid-twentieth century, cotton secondary metabolites as natural phytoalexins were also established. Terpenoids are stored in pigment glands that are distributed almost all cotton plant surfaces or subsurfaces and defend cotton plants from chewing insects, pathogens, and other herbivores. Flavonoids are relevant to fiber quality and color and also play a role in mechanism in insect and pathogen resistance. Phenolic acids play a role in weed suppression and insect and pathogen resistance. There are several reviews on cotton secondary metabolites, and the most recent one was five years ago. They all focus on the metabolites themselves. None of them focus on applications in cotton production. This review started from browsing the abundant literature on cotton secondary metabolites, and then analyzing their potential application in cotton production. Finally, our recent findings were discussed in this chapter.

Title: Estimation of relative cell injury in response to heat stress in *Gossypium hirsutum* L.

Author: Iqbal, J., M. Hanif, N.H. Ahmad, A. Bibi, Z. Nisa and S. Kanwal.

Imprint: 2023. Sarhad Journal of Agriculture, 39(4): 952-956.

Abstract: Pakistan's main source of fiber is cotton. Both living (biotic) and non-living (abiotic) stimuli, including high temperatures, have a deleterious impact on its formation. The goal of the current study was to investigate the genetic foundation of upland cotton's heat tolerance. On the basis of CMT%, canopy temperature, seed cotton production, node number of first fruiting branch, days to first effective boll, heat index (HI), and heat tolerance index (HTI), fifty upland cotton genotypes were screened against high temperatures. Based on the traits utilized for screening, there were fifty genotypes with significant variation. Five heat-sensitive genotypes (Ali akbar-703, Ali akbar-708, IR-1524, Tarzan-1, CIM-598) and seven heat-tolerant genotypes (CIM-602, Cyto-178, MNH-1020, FH-142, MNH-1026, MNH-886 and IUB-222) were chosen. These selected heat tolerant genotypes can be utilized further in breeding program.

Title: Evaluating the impacts of long-term saline water irrigation on soil salinity and cotton yield under plastic film mulching: A 15-year field study.

Author: Junpeng Zhang , He Wang , Di Feng , Caiyun Cao , Chunlian Zheng , Hongkai Dang , Kejiang Li , Yang Gao , Chitao Sun

Imprint: Agricultural Water Management, Volume 293, 31 March 2024, 108703

Abstract: In the context of dwindling freshwater resources, it is imperative to comprehensively evaluate crop productivity and soil resource sustainability when considering the use of saline water for irrigation (SWI). This study aimed to investigate the effects of SWI on soil salinity variation and sustainability of flat sowing cotton (*Gossypium hirsutum* L.) through a comprehensive 15-year field experiment conducted in the North China Plain, encompassing six levels of irrigation water salinity (EC_{iw} of 1.3, 3.4, 7.1, 10.6, 14.1, and 17.7 $dS\ m^{-1}$, respectively). The results of the 15-year SWI revealed an increase in soil salinity within the cotton root zone, with increases of 5%, 20%, 39%, 67%, 116%, and 156%, respectively, observed across the six treatments. In treatments with higher EC_{iw} values (14.1 and 17.7 $dS\ m^{-1}$), salt accumulation extended to a depth of 3.0 m. Long-term SWI has a risk of causing soil sodicity and alkalinity. Sodium adsorption ratio (SAR) and pH in the treatments with $EC_{iw} \geq 7.1\ dS\ m^{-1}$ increased significantly ($P < 0.05$) after cotton harvest in the 15th year of continuous

SWI. Cotton yield performance exhibited a distinct response to varying levels of EC_{iw} . The treatment with an EC_{iw} of 3.4 dS m^{-1} yielded the highest average cotton yield of 3419 kg ha^{-1} , while cotton yields in treatments with an EC_{iw} of 14.1 and 17.7 dS m^{-1} were more than 13% and 20%, respectively, lower than the maximum yield ($P < 0.05$). The sustainability index of cotton yield was at its lowest (0.68) in the treatments with an EC_{iw} of 7.1 dS m^{-1} , with values between 0.72 and 0.75 in the other treatments. Additionally, long-term SWI resulted in changes in cotton quality, including a decrease in micronaire value and an increase in elongation index. A quadratic correlation analysis identified a threshold EC_{iw} of 6.8 dS m^{-1} for optimum cotton yield. In summary, it is recommended that the EC_{iw} should not exceed 6.8 dS m^{-1} to ensure the sustainability and safety of long-term SWI for cotton production in this research region.

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Title: GhUBC10-2 mediates GhGSTU17 degradation to regulate salt tolerance in cotton (*Gossypium hirsutum*).

Author: Yaru Sun, Zailong Tian, Dongyun Zuo, Qiaolian Wang, Guoli Song

Imprint: Plant Cell and Environment, 28 January 2024,
<https://doi.org/10.1111/pce.14839>

Abstract: Ubiquitin-conjugating enzyme (UBC) is a crucial component of the ubiquitin-proteasome system, which contributes to plant growth and development. While some UBCs have been identified as potential regulators of abiotic stress responses, the underlying mechanisms of this regulation remain poorly understood. Here, we report a cotton (*Gossypium hirsutum*) UBC gene, *GhUBC10-2*, which negatively regulates the salt stress response. We found that the gain of function of *GhUBC10-2* in both *Arabidopsis* (*Arabidopsis thaliana*) and cotton leads to reduced salinity tolerance. Additionally, *GhUBC10-2* interacts with glutathione S-transferase (GST) U17 (GhGSTU17), forming a heterodimeric complex that promotes GhGSTU17 degradation. Intriguingly, *GhUBC10-2* can be self-polyubiquitinated, suggesting that it possesses E3-independent activity. Our findings provide new insights into the PTM of plant GST-mediated salt response pathways. Furthermore, we found that the WRKY transcription factor GhWRKY13 binds to the *GhUBC10-2* promoter and suppresses its expression under salt conditions. Collectively, our study unveils a regulatory module encompassing GhWRKY13-GhUBC10-2-GhGSTU17, which orchestrates the modulation of reactive oxygen species homeostasis to enhance salt tolerance.

11

Title: Impact of Cropsap Scheme on Cotton Growers: A Probit Regression Approach.

Author: Vaishali G. Kogade, R. V. Chavan, S. V. Bharti

Imprint: MULTIOLOGIC IN SCIENCE, VOL. XIII, ISSUE XXXXVIII, Nov to Jan 2024

Abstract: In the present study economic impact of CROPSAP scheme on beneficiary and non-beneficiary cotton growers have been assessed. 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 Chhatrapati Sambhajanagar district of Maharashtra state purposively on the basis of 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. Probit regression model was fitted to access the impact of CROPSAP scheme on beneficiary and nonbeneficiary cotton growers. Probit model is a way to perform regression for binary outcome variable with two possibilities like beneficiary and non-beneficiary of cotton growers. In probit regression model factors like X4 (Plant protection under CROPSAP) and X6 (Yield) significant at 10 per cent and 5 per cent level respectively. This result indicates that the above significant factors are greatly influenced on cotton growers towards adoption of CROPSAP scheme.

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Title: High potential of cotton (*Gossypium hirsutum* L.) *Bacillus* isolates to promote plant growth.

Author: Thianny F. Carrelo Viana, Rodrigo Mattos S. Galeano, Gecele Matos Paggi

Imprint: Research Square, DOI: <https://doi.org/10.21203/rs.3.rs-3879877/v1>

Abstract: Cotton is socially and economically important worldwide. Notably, research on eco-friendly technologies that increase the sustainability of this production system is increasing. We explored the potential of bacterial strains isolated from cotton roots to promote plant growth. Bacteria were isolated from cotton roots by using a pasteurization method and cultivated on nutrient agar for strain purification and selection. The bacterial strains were subjected to in vitro tests to verify their ability to solubilize calcium phosphate, producing indole-3-acid acetic, siderophores, and cellulase. Potential strains were selected for the in vivo experiments in a greenhouse with cotton cultivars FM 985 and TMG 47. Treatments were conducted using 1 mL (10⁸ CFU/mL) of bacterial strain culture and a commercial inoculant, with nine replicates observed for 110 d. The plants were evaluated for physical, phytochemical, and macronutrient parameters. The physical parameters indicated a positive relationship between cultivars and microorganisms, increasing the height, fresh mass of the shoot, dry mass of fruits and roots, root volume and length, and number of leaves. Phytochemical parameters showed improvements in total sugars, ascorbate peroxidase,

phenolic compounds, free amino acids, total sugar, chlorophyll A, reducing sugars, flavonoids, catalase, and chlorophyll B. In conclusion, our results showed that our bacterial isolates from cotton roots had many biochemical features related to plant growth promotion and were able to promote the growth of cotton cultivars in a greenhouse experiment. Future research could conduct field tests to evaluate their use for improving cotton productivity on a large scale.

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Title: Uptake and effect of carboxyl-modified polystyrene microplastics on cotton plants.

Author: Wei Li , Junjie Zhao , Zhiqiang Zhang , Zhongying Ren, Xinyang Li , Ruoyu Zhang , Xiongfeng Ma

Imprint: Journal of Hazardous Materials, Volume 466, 15 March 2024, 133581

Abstract: Microplastics (MPs) have emerged as a significant global environmental concern, particularly within agricultural soil systems. The extensive use of plastic film mulching in cotton cultivation has led to the alarming presence of MP pollution in cotton fields. However, the uptake and effects of MPs on the growth of cotton plants are poorly understood. In this study, we conducted a comprehensive analysis of hydroponically cultured cotton seedlings at the phenotypic, transcriptional, and metabolic levels after exposure to carboxyl-modified polystyrene microplastics (PS-COOH). Treatment with three concentrations of PS-COOH (100, 300, and 500 mg/L) resulted in notable growth inhibition of treated plants and exhibited a dose-dependent effect. And, PS-COOH can invade cotton roots and be absorbed through the intercellular spaces via apoplastic uptake, with accumulation commensurate with treatment duration. Transcriptomic analysis showed significant up-regulation of genes associated with antioxidant activity in response to 300 mg/L PS-COOH treatment, suggesting the induction of oxidative stress. In addition, the PS-COOH treatment activated the phenylpropanoid biosynthesis pathway, leading to lignin and flavonoid accumulation, and altered sucrose catabolism. These findings illustrate the absorption and effects of MPs on cotton seedlings and offer valuable insights into the potential toxicity of MPs to plants in soil mulched with plastic film.

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Title: Foliar Benzoic Acid Triggered Agronomic, Physiological and Fiber Quality Traits of Cotton (*Gossypium hirsutum* L.) Under Heat Stress.

Author: Abdul Shakoor , Misbah Zulfqar , Ijaz Ahmad , Ali Sher , Muhammad Zafar , Muhammad Zeeshan , Waheed Arshad , Muhammad Arslan , Muhammad Rizwan Khurshid , Saima Naseer , Saba Saeed , Mustazhar Billah Zafar

Imprint: Journal of Xi'an Shiyou University, Natural Science Edition VOLUME 20
ISSUE 01 JANUARY 2024

Abstract: Heat stress at reproductive stages of cotton cause adverse effects on agronomic, physiological attributes and worsens the fiber quality of cotton. A field study was conducted to see the foliar spray of benzoic acid (BZA) could help to alleviate the negative effects of heat stress on agronomic, physiological quality traits of cotton. Two levels of heat treatment were assigned in the main plots, that was, H0 = no heat stress; H1 = heat stress imposed at squaring for the period of 7 days. Six levels of foliar spray of benzoic acid i.e. control, water spray, 0.25, 0.50, 0.75 and 1.00 mM were applied in each subplot during heat stress imposition. The crop was sown on 75 cm apart ridges and plant to plant distance was maintained at 30 cm. All other agronomic practices were kept normal and uniform. The standard procedures were adopted for recording the data on various cotton parameters. A remarkable decrease in agronomic, physiological and quality attributes was observed under heat stress compared to control. Foliar application of benzoic acid significantly improved agronomic, physiological and fiber quality. Conclusively, heat stress was more detrimental at squaring for one week than no heat stress for cotton crop in terms of the studied traits. Foliar BZA 0.75 mM is, therefore, recommended to mediate heat stress, due to its beneficial effect on agronomic, physiological and fiber related parameters of cotton.

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Title: Rapidly mining candidate cotton drought resistance genes based on key indicators of drought resistance

Author: Shiwei Geng, Wenju Gao, Shengmei Li, Qin Chen, Yang Jiao, Jieyin Zhao, Yuxiang Wang, Tingwei Wang, Yanying Qu & Quanjia Chen

Imprint: BMC Plant Biology volume 24, Article number: 129 (2024)

Abstract: Background- Focusing on key indicators of drought resistance is highly important for quickly mining candidate genes related to drought resistance in cotton. Results- In the present study, drought resistance was identified in drought resistance-related RIL populations during the flowering and boll stages, and multiple traits were evaluated; these traits included three key indicators: plant height (PH), single boll weight (SBW) and transpiration rate (Tr). Based on these three key indicators, three groups of extreme mixing pools were constructed for BSA-seq. Based on the mapping interval of each trait, a total of 6.27 Mb QTL intervals were selected on chromosomes A13 (3.2 Mb), A10 (2.45 Mb) and A07 (0.62 Mb) as the focus of this study. Based on the annotation information and qRT-PCR analysis, three key genes that may be involved in the drought stress response of cotton were screened: GhF6'H1, Gh3AT1 and GhPER55. qRT-PCR analysis of parental and extreme germplasm materials revealed that the

expression of these genes changed significantly under drought stress. Cotton VIGS experiments verified the important impact of key genes on cotton drought resistance. Conclusions- This study focused on the key indicators of drought resistance, laying the foundation for the rapid mining of drought-resistant candidate genes in cotton and providing genetic resources for directed molecular breeding of drought resistance in cotton.

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Title: Impact of Earliness, Flowering Time and Plant Design on Late Sown Cotton Production.

Author: Muhammad Rizwan Jamil Khan, Kalim Ullah, Muhammad Mohibullah Khan, Rashid Khan

Imprint: Research Square, DOI: <https://doi.org/10.21203/rs.3.rs-3962819/v1>

Abstract: Extremely diversified cropping environments prevails in most of the cotton growing areas of the country due to the prevailing rainfed conditions and thus cotton is cultivated over a prolonged period. This study examined the production and growth pattern of 8 cotton genotypes to find out the most effective strategies that could be transformed into breeding traits. Four experiments were conducted in 2018 and 2019 at two locations in Dera Ismail Khan to associate the 8 genotypes at 3 planting densities and two sowing dates. Various attributes like days to 1st flower opening, affective time of flowering, monopodial branches per plant, height of plant at the time of harvesting, ratio of height to node length of fruiting branch and average number of bolls retained at the 1st site of fruiting branch were investigated. Results revealed two ideotypes which performed better than the others. Genotype CIM-632 yielded better in late sowing-high plant density and regarded as by less growth of vegetative branches and early start of flowering, short flowering duration and less bolls retained at the 1st position of sympodia. Genotype CIM-663 and CIM343 performed outstandingly in early sowing-low plant density and regarded by more growth of vegetative branches, delayed flowering, lengthy flowering duration and more bolls retained at 1st position. Based on these attributes, a breeding scheme for these ideotypes is proposed with high heritability for flower opening, height of plant at the time of harvesting, ratio of height to node and fruiting branch length and medium heritability for monopodial branches, effective flowering time and bolls retained at 1st position of sympodia (fruit branch).

Title: A comprehensive review on *Gossypium hirsutum* resistance against cotton leaf curl virus.

Author: Sahar Nadeem, Syed Riaz Ahmed, Tahira Luqman, Daniel K. Y. Tan

Imprint: Front. Genet., 19 February 2024, Sec. Genomics of Plants and the Phytocoecosystem, Volume 15 - 2024 | <https://doi.org/10.3389/fgene.2024.1306469>

Abstract: Cotton (*Gossypium hirsutum* L.) is a significant fiber crop. Being a major contributor to the textile industry requires continuous care and attention. Cotton is subjected to various biotic and abiotic constraints. Among these, biotic factors including cotton leaf curl virus (CLCuV) are dominant. CLCuV is a notorious disease of cotton and is acquired, carried, and transmitted by the whitefly (*Bemisia tabaci*). A cotton plant affected with CLCuV may show a wide range of symptoms such as yellowing of leaves, thickening of veins, upward or downward curling, formation of enations, and stunted growth. Though there are many efforts to protect the crop from CLCuV, long-term results are not yet obtained as CLCuV strains are capable of mutating and overcoming plant resistance. However, systemic-induced resistance using a gene-based approach remained effective until new virulent strains of CLCuV (like Cotton Leaf Curl Burewala Virus and others) came into existence. Disease control by biological means and the development of CLCuV-resistant cotton varieties are in progress. In this review, we first discussed in detail the evolution of cotton and CLCuV strains, the transmission mechanism of CLCuV, the genetic architecture of CLCuV vectors, and the use of pathogen and nonpathogen-based approaches to control CLCuD. Next, we delineate the uses of cutting-edge technologies like genome editing (with a special focus on CRISPR-Cas), next-generation technologies, and their application in cotton genomics and speed breeding to develop CLCuD resistant cotton germplasm in a short time. Finally, we delve into the current obstacles related to cotton genome editing and explore forthcoming pathways for enhancing precision in genome editing through the utilization of advanced genome editing technologies. These endeavors aim to enhance cotton's resilience against CLCuD.

Title: IoT Innovations in Cotton Plant Disease Detection for Sustainable Agriculture.

Author: Dr. Jayashree Katti, Dr. Gulbakshee Dharmale, Dr. Swapnaja Amol Ubale, Mrs. Radha Deoghare, Shiv Havgirao Sutar

Imprint: International Journal of Intelligent Systems and Applications in Engineering IJISAE, 2024, 12(15s), 651-658

Abstract: Cotton, a crucial cash crop in the textile industry, faces significant threats from various diseases that can impact both yield and fiber quality. This research explores the integration of Internet of Things (IoT) innovations to revolutionize cotton plant disease detection, providing real-time monitoring and data-driven decision support for sustainable agriculture practices. The proposed system employs wireless sensor networks deployed in cotton fields, UAVs equipped with advanced imaging technology, and a centralized data processing platform. These components collect crucial environmental parameters, such as temperature, humidity, and soil moisture, alongside high-resolution images of the cotton crops. The dataset is then transmitted to a centralized platform where machine learning algorithms and analytics are applied for precise disease detection. Machine learning models, trained on diverse datasets containing images of cotton plants with various diseases, analyze incoming data to identify potential outbreaks promptly. Upon detection, the system triggers automated responses, such as notifying farmers or activating precision-targeted treatment protocols, minimizing environmental impact and optimizing resource usage. Implementation of this IoT-driven disease detection system not only enables early intervention but also contributes to sustainable agriculture by reducing reliance on broad-spectrum pesticides and optimizing yield. The collected data supports long-term trend analysis, offering insights into crop management practices and encouraging the adoption of precision agriculture. This research demonstrates the efficacy of IoT technologies in addressing critical challenges in cotton farming, providing a scalable and adaptable solution for sustainable agriculture. By presenting a comprehensive framework for disease detection and management, this study aims to contribute to the ongoing discourse on utilizing technological innovations for ensuring food and fiber security in an ever-changing agricultural landscape.

Title: Determination of Silicon Accumulation in Non-Bt Cotton (*Gossypium hirsutum*) Plants and Its Impact on Fecundity and Biology of Whitefly (*Bemisia tabaci*) under Controlled Conditions.

Author: Asim Abbasi , Muhammad Sufyan , Hafiza Javaria Ashraf , Qamar uz Zaman, Inzamam Ul Haq, Zahoor Ahmad, Ramish Saleem, Mohammad Rameez Hashmi, Mariusz Jaremko, Nader R. Abdelsalam and Rehab Y. Ghareeb

Imprint: Sustainability 2022, 14, 10996. <https://doi.org/10.3390/su141710996>

Abstract: Considering the resistance development-potential of whitefly (*Bemisia tabaci*) against control tactics with limited action mechanisms, the present study investigated the accumulation of two different silicon (Si) sources (SiO₂ and K₂SiO₃) in cotton plants. The tested dose rates (0, 200, and 400 mg/L) of both Si sources were applied directly to the soil or through foliar application on cotton leaves. Moreover, a laboratory bioassay was also conducted to evaluate the performance of applied Si sources against the oviposition preference and biology of *B. tabaci*. A significantly higher Si accumulation, reduction in oviposition preference, and prolonged developmental period of all nymphs and total life cycle of *B. tabaci* was observed in the case of foliar-applied silicon. Similarly, among Si sources, a significant decline in the number of oviposited eggs and delay in the developmental period of *B. tabaci* was observed in the case of SiO₂, followed by K₂SiO₃. Moreover, cotton plants subjected to SiO₂ treatments possessed higher Si contents in their leaves than K₂SiO₃ treated plants. The results further revealed that both Si sources showed promising results at their higher concentrations regarding the tested parameters of Si accumulation, fecundity, and developmental period of *B. tabaci*. Our results strongly suggest that among emerging pest control strategies in cotton plants lies the use of foliar application of Si, which can also be incorporated in different integrated pest management programs due to its safety for humans and beneficial insect fauna.

Title: Host Plant Resistance to Insects in Cotton.

Author: Lucy Egan, Qian-Hao Zhu, Iain Wilson & Warwick Stiller

Imprint: Plant Resistance to Insects in Major Field Crops pp 37–67First Online: 10 February 2024

Abstract: Across the globe, cotton production is limited by endemic and introduced insect pests. The incorporation of host plant resistance (HPR), defined as the ability of a plant to defend itself against targeted biotic stresses, has been a key breeding target for

many cotton breeding programs. The development of resistant cultivars provides a cost effective and environmentally sustainable solution for cotton growers. The key insect pests to cotton production include *Helicoverpa* spp., pink bollworm, *Spodoptera* spp., silverleaf whitefly, various plant and stink bugs, aphids, and thrips. Cotton plants have a range of native and genetically modified traits that confer HPR. However, breeding for HPR in cotton is a slow and complex process, with cultivar development commonly requiring more than 15 years to reach the market. Often, the incorporation of native HPR traits has a negative impact on yield and important agronomic characteristics, so it is not economically viable. Therefore, determining the value of a native HPR trait under multiple scenarios is a critical element for research and development investment. This chapter aims to review the major pests to cotton production and the current status of native HPR in commercial cultivars to each pest, outline the process of breeding for HPR in cotton, and discuss the economic value of HPR traits.

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Title: Cotton Health-Guard: AI-Enhanced Crop Health Assessment Through Image Classification.

Author: Manohar Kapse, Vinod Sharma, Jeanne Poulouse, N. Elangovan, Yogesh Mahajan

Imprint: Industrial Applications of Big Data, AI, and Blockchain, Copyright: © 2024 | Pages: 16, DOI: 10.4018/979-8-3693-1046-5.ch009

Abstract: Crop loss due to illness is the main issue that farmers deal with. The second issue is the delay in identifying which disorders to treat. Thus, the purpose of this study is to use the image classification technique to determine if the crop is healthy or sick. R software was used to implement picture categorization and machine learning techniques. The diseased leaf has been identified by the process of picture classification. In order to accomplish this, images of both healthy and diseased cotton crops were gathered from the fields. According to the study, the support vector machine algorithm is more accurate than other machine learning algorithms, which makes it suitable for real-time disease diagnosis and categorization.

22

Title: Estimation of yield losses due to pink bollworm, *Pectinophora gossypiella* (Saunders) on Bt cotton.

Author: KM Vora, Dr. YH Ghelani, BV Patoliya, Dr. MK Ghelani and NM Kachhadiya

Imprint: International Journal of Statistics and Applied Mathematics 2024; SP-9(1): 338-340

Abstract: The present research on “Estimate the yield losses due to pink bollworm, *Pectinophora gossypiella* (Saunders) infesting Bt cotton” was carried out at Village: Daliya, Ta. Gondal, Dist. Rajkot during Kharif, 2020-21. The results of experiment were revealed that the seed cotton yield of 2304.27 kg/ha were recorded from protected plots, while the seed cotton yield of 1478.73 kg/ha were recorded from unprotected plots. However, By providing protection with effective pesticides against pink bollworm 825.54 kg/ha yield loss can be saved and 35.83 per cent avoidable yield loss was recorded in protected plots over unprotected plots during kharif, 2020-21.

23

Title: Thrips composition in North Indian cotton agroecosystem: a single species or a species complex?

Author: Naveen Rao, Ram Karan Gaur, Satnam Singh, R. R. Rachana, Rishi Kumar, Suneet Pandher, Ramandeep Kaur, Sunita Yadav, Shashikant S. Udikeri & A. G. Srinivas

Imprint: Phytoparasitica, Volume 52, article number 11, (2024)

Abstract: Thrips have emerged as major sucking pests of American cotton *Gossypium hirsutum* L., limiting crop productivity through direct feeding and transmitting viral pathogens. Thrips have been long presumed to be a single species in cotton in northern India, with all the studies reporting it as onion thrips *Thrips tabaci* Lindeman (Thysanoptera: Thripidae). Even the majority of work from southern and central India reports it as the sole species in their studies conducted on pesticide efficacy, population dynamics, and host plant resistance etc. The present study entailed the sampling of cotton crop from 22 distinct locations representing the north-western, central, and southern zones of India using both morphological and molecular methods. The study reports the prevalence of a thrips species complex in cotton, which is dominated by melon thrips, *Thrips palmi* Karny (Thysanoptera: Thripidae), with the coexistence of other thrips species, viz., *T. tabaci*, *Scirtothrips* sp., (Thysanoptera: Thripidae) and common blossom thrips, *Frankliniella schultzei* Trybom (Thysanoptera: Thripidae). Our studies also throw light on the maiden reports of occurrence of orchid thrips, *Chaetanaphothrips orchidii* Moulton (Thysanoptera: Thripidae) and *Asprothrips bimaculatus* Michel & Ryckewaert (Thysanoptera: Dendrothripinae) thrips species in cotton from India. The genetic diversity analysis of *T. palmi* revealed the presence of cryptic species, and haplotyping showed the existence of 53 haplotypes globally, out of which two new haplotypes have been reported in the present study. The possible reasons for the change in cotton thrips composition from a single species to a complex

over the years have also been analyzed using historical and conventional population dynamics data gathered over the past 15 years, which categorically indicated that the invasion of new species over the previous years might be responsible for the change in the population structure of thrips in cotton.

24

Title: Studies on major insect pests of cotton and farmer perceptions in the Ghugus area of District Chandrapur, Maharashtra, India.

Author: Prajapati, S. K., & Kulkarni, R. R.

Imprint: Environment Conservation Journal. (2024)
<https://doi.org/10.36953/ECJ.26682646>

Abstract: A crucial crop in the world, cotton (*Gossypium hirsutum* L.), is frequently harmed by pests and illnesses. Chemical pesticides are frequently effective, but repeated use of these chemicals often results in pests developing greater insecticide resistance, fewer natural enemies, less natural control, and a deteriorated ecosystem. It has been widely used to implement the integrated pest management (IPM) strategy, which heavily emphasizes biological control. The present piece of work was carried out from January 2022 to December 2022 at different sites in the vicinity of the Ghugus area in Chandrapur district. In all, 10 species of insect pests of cotton from 9 families and 3 orders were recorded. The knowledge, perceptions and practices of farmers growing cotton under different pest management regimes were analyzed. The methods used were open and semistructured interviews using questionnaire with groups and individuals. In general, farmers had a poor understanding of the key concepts underlying alternative pest control systems. Pest damage was considered important and farmers were eager to share their knowledge, perceptions and practices in pest management. This study provides the foundation for the creation of a learning platform for future.

25

Title: Development, Design, and Application of Efficient siRNAs Against Cotton Leaf Curl Virus-Betasatellite Complex to Mediate Resistance against Cotton Leaf Curl Disease.

Author: Heena Jain, Ramandeep Kaur, Satish Kumar Sain & Priyanka Siwach

Imprint: Indian Journal of Microbiology, 2024

Abstract: Cotton leaf curl disease (CLCuD), caused by the Cotton leaf curl virus, is one of the most irrepressible diseases in cotton due to high recombination in the virus. RNA

interference (RNAi) is widely used as a biotechnological approach for sequence-specific gene silencing guided by small interfering RNAs (siRNAs) to generate resistance against viruses. The success of RNAi depends upon the fact that the target site of the designed siRNA must be conserved even if the genome undergoes recombination. Thus, the present study designs the most efficient siRNA against the conserved sites of the Cotton leaf curl Multan virus (CLCuMuV) and the Cotton leaf curl Multan betasatellite (CLCuMB). From an initial prediction of 9 and 7 siRNAs against CLCuMuV and CLCuMB, respectively, the final selection was made for 2 and 1 siRNA based on parameters such as no off-targets, good GC content, high validity score, and targeting coding region. The target sites of siRNA were observed to lie in the AC3 and an overlapping region of AC2-AC1 of CLCuMuV and β C1 of CLCuMB; all target sites showed a highly conserved nature in recombination analysis. Docking the designed siRNAs with the Argonaute-2 protein of *Gossypium hirsutum* showed stable binding. Finally, BLASTn of siRNA-target positions in genomes of other BGVs indicated the suitability of designed siRNAs against a broad range of BGVs. The designed siRNAs of the present study could help gain complete control over the virus, though experimental validation is highly required to suggest predicted siRNAs for CLCuD resistance.

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Title: First Infestation of an Exotic Crops Pest, *Amrasca biguttula* on Cotton *Gossypium hirsutum* L. in North Cameroon.

Author: Housseini Djida Jacques, Doké Noé Socrates, Yonki Bouladji, Théodore Lawe Djague, Adamou Moïse and Woïn Noé.

Imprint: International Journal of Plant & Soil Science Volume 36, Issue 3, Page 16-22, 2024.

Abstract: Cotton is a cash crop that actively contributes to the socio-economic development of the entire northern region of Cameroon. However, the production of this crop faces many constraints, including the pressure of bio-aggressors that cause significant damage and generate considerable losses for many producers. *Amrasca biguttula* is a feeding pest that was first reported in 2022 in a leafhopper sample collected in Djalingo, Benoue department, North region. The attacks of this atypical pest caused major damage on several cotton fields during the 2023 crop year. As a result several other outbreaks have been reported throughout most of the cotton zone. Adults average 2.82 ± 0.16 mm in length and are green, with two black dots near the tip of the forewing. Leafhopper samples collected at several sites showed the presence of *Amrasca biguttula* and this species alone represented 22% to 84% of the diversity of leafhopper populations on cotton. The month of August seems to be the propitious time

for the invasion of this new species, because it is during this period that it was mainly represented in the different leafhopper samples collected.

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Title: Evaluation of *BG*, *NPR1*, and *PAL* in cotton plants through Virus Induced gene silencing reveals their role in whitefly stress.

Author: Aiman Ehsan, Khurram Tanveer, Maryam Azhar,

Imprint: Gene, Volume 908, 25 May 2024, 148282

Abstract: Whitefly is one of the most hazardous insect pests that infests a wide range of host plants and causes huge damage to crop worldwide. In order to engineer plants resilient to whitefly stress, it is important to identify and validate the responsive genes by exploring the molecular dynamics of plants under stress conditions. In this study three genes *BG*, *NPR1*, and *PAL* genes have been studied in cotton for elucidating their role in whitefly stress response. Initially, insilico approach was utilized to investigate the domains and phylogeny of *BG*, *NPR1* and *PAL* genes and found out that these genes showed remarkable resemblance in four cotton species *Gossypium hirsutum*, *G. barbadense*, *G. arboreum*, and *G. raimondii*. In *BG* proteins the main functional domain was X8 belonging to glycohydro superfamily, in *NPR1* two main functional domains were *BTB_POZ* at N terminal and *NPR1_like_C* at C terminal. In *PAL* functional domain *PLN* was found which belongs to Lyase class I superfamily. The promoter analysis of these genes displayed enrichment of hormone, stress and stimuli responsive cis elements. Through Virus Induced Gene Silencing (VIGS), these genes were targeted and kept under whitefly infestation. Overall, the whitefly egg and nymph production were observed 60–70% less on gene down regulated plants as compared to control plants. The qPCR-based expression analysis of certain stress-responsive genes showed that in *BG* down regulated plants the elevated expression of these whitefly responsive genes was detected, in *NPR1* down regulated plants *JAZ1* and *HSP* were found up regulated, *ERF1* and *WRKY40* didn't show significant differential expression, while *MAPK6* was slightly down regulated. In *PAL* down regulated plants *ERF1* and *JAZ1* showed elevated expression while others didn't show significant alternation. Differential expression in gene down-regulated plants showed that whitefly responsive genes act in a complex inter signaling pathway and their expression impact each other. This study provides valuable insight into the structural and functional analysis of important whitefly responsive genes *BG*, *NPR1*, and *PAL*. The results will pave a path to future development of whitefly resilient crops.

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Title: An insight into the gene expression evolution in *Gossypium* species based on the leaf transcriptomes.

Author: Yuqing Wu, Rongnan Sun, Tong Huan, Yanyan Zhao, Dongliang Yu & Yuqiang Sun

Imprint: *BMC Genomics* volume 25, Article number: 179 (2024)

Abstract: Gene expression pattern is associated with biological phenotype and is widely used in exploring gene functions. Its evolution is also crucial in understanding species speciation and divergence. The genus *Gossypium* is a bona fide model for studying plant evolution and polyploidization. However, the evolution of gene expression during cotton species divergence has yet to be extensively discussed. Results Based on the seedling leaf transcriptomes, this work analyzed the transcriptomic content and expression patterns across eight cotton species, including six diploids and two natural tetraploids. Our findings indicate that, while the biological function of these cotton transcriptomes remains largely conserved, there has been significant variation in transcriptomic content during species divergence. Furthermore, we conducted a comprehensive analysis of expression distances across cotton species. This analysis lends further support to the use of *G. arboreum* as a substitute for the A-genome donor of natural cotton polyploids. Moreover, our research highlights the evolution of stress-responsive pathways, including hormone signaling, fatty acid degradation, and flavonoid biosynthesis. These processes appear to have evolved under lower selection pressures, presumably reflecting their critical role in the adaptations of the studied cotton species to diverse environments.

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Title: Genome-wide identification and expression analysis of autophagy-related genes (ATG) in *Gossypium* spp. reveals their crucial role in stress tolerance.

Author: Mamta Yadav, Garima Saxena, Rishi Kumar Verma, Mehar H. Asif, Vijay Pratap Singh

Imprint: *South African Journal of Botany*, Volume 167, April 2024, Pages 82-93

Abstract: Autophagy is an evolutionarily conserved process mediated by AuTophagy (ATG) genes, in which cellular components are degraded and recycled within vacuoles or lysosome. Yeast ATG was extensively studied; their homologs are reported in plants including *Arabidopsis*. However, they have not been reported in cotton. In the present study, the ATG cascade genes were studied in four *Gossypium* species, namely *G. hirsutum*, *G. arboreum*, *G. herbaceum*, and *G. raimondii*. A total of 40 *GhirATG*, 33 *GaATG*, 34 *GherbATG*, and 25 *GrATG* genes were identified in these species. These ATG sequences exhibited conserved ATG domains and other overlapping domains, including Ras, Pkinase, Snf7, WD40, Glyco_hydro_17, and bZIP_1, and were named based on their phylogenetic relationships with *Arabidopsis* ATGs. A phylogenetic analysis revealed evolutionary relationships among ATG genes among these species, as well as significant sub-clades indicating patterns of gene retention. Based on synonymous and non-synonymous substitutions, cotton groups diverged at different times from *Arabidopsis*. Gene structure analysis and chromosome localization showed exon-intron patterns and locations. Expression analysis of ATGs in different tissues during development and under stress conditions indicated their functional specificity. The ATG8 subclass genes were significantly expressed under abiotic stress conditions, indicating their role in stress response. In addition, qRT-PCR analysis of selected 12 *GhirATGs* in leaves treated with stress elicitors, MeJA, SA, NaCl, and PEG for varying time intervals showed a pattern of their significant upregulation. The findings contribute to our understanding of autophagy-related processes in cotton, including their potential role in stress response and development.

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Title: Estimation of mean performance of parents and their hybrids for yield related traits in *Gossypium hirsutum* L.

Author: Muhammad Naveed , Muhammad Nouman Khalid , Waseem Sabir , Muhammad Waqas Jamil , Muhammad Nasir , Muhammad Ilyas Khokhar , Shakira Jamil , Sajid Ur Rahman , Hafeez Ullah Raza , Abdul Latif Khan Tipu and Tariq Manzoor Khan

Imprint: Phytopathogenomics and Disease Control. 2023, 2(2):49-55

Abstract: Cotton (*Gossypium hirsutum* L.) is an important fiber crop and plays an important role in Pakistan's economy as a cash crop. Cotton crop is cultivated primarily for fiber. The main objective of all cotton breeders is the production of a new variety with high yield and fiber quality. The current experiment was conducted in the research area of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Crosses were made of four varieties AGC-999, IR-3701, VH-37 and AS01 by full Diallel mating design in the greenhouse during winter season. Evaluation of 12 crosses and 4 parental varieties were proceeded in the field during Kharif season of

2019 under RCBD (Randomized completely blocked Design) design with three replications. The data for agronomic characters and yield related traits as plant height, number of branches, number of bolls, number of nodes, seed cotton yield, ginning out turn, seed index and lint index was recorded. Mean data of seed cotton yield for all the genotypes indicated that the parent AS-01 provided the maximum yield (93.73 grams) among the parents while AGC-999 × IR-3701 had the maximum yield (82 grams) among the crosses. While VH-37, VH-37 × AS-01 and AS-01 × AGC-999 had the minimum value among parents and crosses respectively. These genotypes Keywords: Cotton, mean performance, seed cotton yield, hybrid.

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Title: Isolation and Functional Characterization of a Constitutive Promoter in Upland Cotton (*Gossypium hirsutum* L.)

Author: Yang Yang, Xiaorong Li, Chenyu Li, Hui Zhang

Imprint: Int. J. Mol. Sci. 2024, 25(3), 1917; <https://doi.org/10.3390/ijms25031917>

Abstract: Multiple cis-acting elements are present in promoter sequences that play critical regulatory roles in gene transcription and expression. In this study, we isolated the cotton FDH (Fiddlehead) gene promoter (pGhFDH) using a real-time reverse transcription-PCR (qRT-PCR) expression analysis and performed a cis-acting elements prediction analysis. The plant expression vector pGhFDH::GUS was constructed using the Gateway approach and was used for the genetic transformation of *Arabidopsis* and upland cotton plants to obtain transgenic lines. Histochemical staining and a β -glucuronidase (GUS) activity assay showed that the GUS protein was detected in the roots, stems, leaves, inflorescences, and pods of transgenic *Arabidopsis thaliana* lines. Notably, high GUS activity was observed in different tissues. In the transgenic lines, high GUS activity was detected in different tissues such as leaves, stalks, buds, petals, androecium, endosperm, and fibers, where the pGhFDH-driven GUS expression levels were 3–10-fold higher compared to those under the CaMV 35S promoter at 10–30 days post-anthesis (DPA) during fiber development. The results indicate that pGhFDH can be used as an endogenous constitutive promoter to drive the expression of target genes in various cotton tissues to facilitate functional genomic studies and accelerate cotton molecular breeding.

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Title: GhBRX.1, GhBRX.2, and GhBRX4.3 improve resistance to salt and cold stress in upland cotton.

Author: Wei Wei, Jisheng Ju, Xueli Zhang, Pingjie Ling, Jin Luo, Ying Li

Imprint: Front. Plant Sci., 09 February 2024, Sec. Plant Abiotic Stress, Volume 15 - 2024 <https://doi.org/10.3389/fpls.2024.1353365>

Abstract: Introduction: Abiotic stress during growth readily reduces cotton crop yield. The different survival tactics of plants include the activation of numerous stress response genes, such as BREVIS RADIX (BRX). Methods: In this study, the BRX gene family of upland cotton was identified and analyzed by bioinformatics method, three salt-tolerant and cold-resistant GhBRX genes were screened. The expression of GhBRX.1, GhBRX.2 and GhBRXL4.3 in upland cotton was silenced by virus-induced gene silencing (VIGS) technique. The physiological and biochemical indexes of plants and the expression of related stress-response genes were detected before and after gene silencing. The effects of GhBRX.1, GhBRX.2 and GhBRXL4.3 on salt and cold resistance of upland cotton were further verified. Results and discussion: We discovered 12, 6, and 6 BRX genes in *Gossypium hirsutum*, *Gossypium raimondii* and *Gossypium arboreum*, respectively. Chromosomal localization indicated that the retention and loss of GhBRX genes on homologous chromosomes did not have a clear preference for the subgenomes. Collinearity analysis suggested that segmental duplications were the main force for BRX gene amplification. The upland cotton genes GhBRX.1, GhBRX.2 and GhBRXL4.3 are highly expressed in roots, and GhBRXL4.3 is also strongly expressed in the pistil. Transcriptome data and qRT-PCR validation showed that abiotic stress strongly induced GhBRX.1, GhBRX.2 and GhBRXL4.3. Under salt stress and low-temperature stress conditions, the activities of superoxide dismutase (SOD), peroxidase (POD) and catalase (CAT) and the content of soluble sugar and chlorophyll decreased in GhBRX.1-, GhBRX.2- and GhBRXL4.3-silenced cotton plants compared with those in the control (TRV: 00). Moreover, GhBRX.1-, GhBRX.2- and GhBRXL4.3-silenced cotton plants exhibited greater malondialdehyde (MDA) levels than did the control plants. Moreover, the expression of stress marker genes (GhSOS1, GhSOS2, GhNHX1, GhCIPK6, GhBIN2, GhSnRK2.6, GhHDT4D, GhCBF1 and GhPP2C) decreased significantly in the three target genes of silenced plants following exposure to stress. These results imply that the GhBRX.1, GhBRX.2 and GhBRXL4.3 genes may be regulators of salt stress and low-temperature stress responses in upland cotton.

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Title: Characterization and gene expression analysis reveal universal stress proteins respond to abiotic stress in *Gossypium hirsutum*.

Author: Yunqing Li, Ao Zheng, Zhuang Li, Hu Wang, Jing Wang, Zhanghui Dong, Lina Yao, Xiao Han & Fei Wei

Imprint: BMC Genomics volume 25, Article number: 98 (2024)

Abstract: Universal stress proteins (USPs) are a class of stress-induced proteins that play a crucial role in biotic and abiotic stress responses. These proteins have previously been reported to participate directly in responses to various stress and protect plants against unfavorable environmental conditions. However, there is limited research on USPs in cotton, and systematic characterization of USPs in *Gossypium* species is lacking. In the present study, the USP genes in *Gossypium hirsutum* were systematically identified and classified into six distinct subfamilies. The expansion of USPs in *Gossypium* species is mainly caused by dispersed duplication and whole genome duplication. Notably, the USPs that have expanded through allotetraploidization events are highly conserved in the allotetraploid species. The promoter regions of GhUSPs contain a diverse range of cis-acting elements associated with stress response. The RNA-Seq analysis and RT-qPCR assays revealed a significant induction of numerous GhUSPs expressions in response to various abiotic stresses. The co-expression network of GhUSPs revealed their involvement in stress response. This study systematically analyzed the biological characteristics of GhUSPs and their response to abiotic stress. These findings serve as a theoretical basis for facilitating the breeding of cotton varieties in future research.

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Title: Characteristics of Quality Traits of Cotton Genetic Collection and Their Interrelation.

Author: A. K. Rakhimov

Imprint: SCIENCE AND INNOVATION INTERNATIONAL SCIENTIFIC JOURNAL
VOLUME 3 ISSUE 1 JANUARY 2024

Abstract: We discuss the problems of genetic qualitative traits of the cotton *G. hirsutum* L. The regularities of inheritance and splitting in F₂ in 23 variants of joint inheritance of 9 qualitative traits are determined and it is found that within the species *G. hirsutum* L., the presence of an anthocyanin spot at the base of flower petals is controlled by two non-allelic genes with complete dominance of the presence of an anthocyanin spot and joint inheritance and cleavage in F₂ of five variants of the sign "presence - absence" of an anthocyanin spot at the base of the petals of a flower with such signs as the shape of the leaf and bracts. Plant coloration, color of flower petals, "presence - absence" of leafy nectaries are observed both trigenous and tetragenous control. In the functioning of their genes, inter-allelic and non-allelic gene interactions (polymerization) are observed.

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Title: Identification and characterization of candidate genes for primary root length in Asiatic cotton (*Gossypium arboreum* L.)

Author: Daowu Hu, Zibo Zhao, Mian Faisal Nazir, Gaofei Sun, Zhen Peng, Yinhua Jia, Xiaoli Geng, Liru Wang, Zhaoe Pan, Hongge Li, Baojun Chen, Fenglei Sun, Shoupu He & Xiongming Du

Imprint: Theoretical & Applied Genetics, Volume 137, article number 52, (2024)

Abstract: Primary root elongation is an essential process in plant root system structure. Here, we investigated the primary root length (PRL) of 215 diploid cotton (*G. arboreum*) accessions at 5, 8, 10, 15 days after sowing. A Genome-wide association study was performed for the PRL, resulting in 49 significant SNPs associated with 32 putative candidate genes. The SNP with the strongest signal (Chr07_8047530) could clearly distinguish the PRLs between accessions with two haplotypes. *GamurG* is the only gene that showed higher relative expression in the long PRL genotypes than the short PRL genotypes, which indicated it was the most likely candidate gene for regulating PRL. Moreover, the *GamurG*-silenced cotton seedlings showed a shorter PRL, while the *GamurG*-overexpressed *Arabidopsis* exhibited a significantly longer PRL. Our findings provide insight into the regulation mechanism of cotton root growth and will facilitate future breeding programs to optimize the root system structure in cotton.

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Title: Screening cotton genotypes for their drought tolerance ability based on the expression level of dehydration-responsive element-binding protein and proline biosynthesis-related genes and morpho-physio-biochemical responses.

Author: Rujira Tisarum, Cattarin Theerawitaya, Patchara Praseartkul, Daonapa Chungloo, Hayat Ullah, Sushil Kumar Himanshu, Avishek Datta & Suriyan Cha-um

Imprint: Protoplasma, 20 February 2024

Abstract: Drought stress adversely affects growth, development, productivity, and fiber quality of cotton (*Gossypium hirsutum* L.). Breeding strategies to enhance drought tolerance require an improved knowledge of plant drought responses necessitating proper identification of drought-tolerant genotypes of crops, including cotton. The objective of this study was to classify the selected cotton genotypes for their drought tolerance ability based on morpho-physio-biochemical traits using Hierarchical Ward's cluster analysis. Five genotypes of cotton (Takfa 3, Takfa 6, Takfa 7, Takfa 84-4, and

Takfa 86-5) were selected as plant materials, and were grown under well-watered (WW; $98 \pm 2\%$ field capacity) and water-deficit (WD; $50 \pm 2\%$ field capacity) conditions for 16 days during the flower initiation stage. Data on morpho-physio-biochemical parameters and gene expression levels for these parameters were collected, and subsequently genotypes were classified either as a drought tolerant or drought susceptible one. Upregulation of *GhPRP* (proline-rich protein), *GhP5CS* (Δ^1 -pyrroline-5-carboxylate synthetase), and *GhP5CR* (Δ^1 -pyrroline-5-carboxylate reductase) in relation to free proline enrichment was observed in Takfa 3 genotype under WD condition. An accumulation of free proline, total soluble sugar, and potassium in plants under WD conditions was detected, which played a key role as major osmolytes controlling cellular osmotic potential. Magnesium and calcium concentrations were also enriched in leaves under WD conditions, functioning as essential elements and regulating photosynthetic abilities. Leaf greenness, net photosynthetic rate, stomatal conductance, and transpiration rate were also declined under WD conditions, leading to growth retardation, especially aboveground traits of Takfa 6, Takfa 7, Takfa 84-4, and Takfa 86-5 genotypes. An increase in leaf temperature ($1.1 - 4.0$ °C) and crop water stress index (CWSI > 0.75) in relation to stomatal closure and reduced transpiration rate was recorded in cotton genotypes under WD conditions compared with WW conditions. Based on the increase of free proline, soluble sugar, leaf temperature, and CWSI, as well as the decrease of aboveground growth traits and physiological attributes, five genotypes were categorized into two cluster groups: drought tolerant (Takfa 3) and drought susceptible (Takfa 6, Takfa 7, Takfa 84-4, and Takfa 86-5). The identified drought-tolerant cotton genotype, namely, Takfa 3, may be grown in areas experiencing drought conditions. It is recommended to further validate the yield traits of Takfa 3 under rainfed field conditions in drought-prone environments.

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Title: Advances and new insights in naturally colored cotton breeding and research.

Author: Tianwang Wen, Weigui Luo, Yuanxue Li, Zhongxu Lin

Imprint: Industrial Crops and Products, Volume 211, May 2024, 118252

Abstract: Cotton is the world's most important fiber crop, and naturally colored cotton (NCC) is an important kind of environmental friendly material. The NCC described here refers to that the cotton fiber itself can synthesize pigments and present colors. NCC has gone through domestication and traditional breeding era in history. Due to the bottlenecks faced by NCC such as low fiber yield, poor quality, narrow color spectrum and unstable color, coupled with the advent of the industrialization era, the practical application of NCC has entered into a trough period. However, NCC has the advantages of environmentally friendly, antimicrobial and flame retardant, and researchers gradually resume the study of colored cotton from the breeding and

physiological and biochemical perspectives. Especially with the arrival of the era of cotton functional genome, important research progresses have been made in the genetic study and genetic engineering of NCC. This study was focused on the metabolic pathways, genetic regulatory models and research highlights of NCC, which will provide new ideas for molecular design breeding of NCC, and realize the creation of high-yield, fine-quality and color-diverse NCC.

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Title: Genome-Wide and Expression Pattern Analysis of the DVL Gene Family Reveals GhM_A05G1032 Is Involved in Fuzz Development in *G. hirsutum*.

Author: Yang Jiao, Fuxiang Zhao, Shiwei Geng, Shengmei Li

Imprint: Int. J. Mol. Sci. 2024, 25(2), 1346; <https://doi.org/10.3390/ijms25021346>

Abstract: DVL is one of the small polypeptides which plays an important role in regulating plant growth and development, tissue differentiation, and organ formation in the process of coping with stress conditions. So far, there has been no comprehensive analysis of the expression profile and function of the cotton DVL gene. According to previous studies, a candidate gene related to the development of fuzz was screened, belonging to the DVL family, and was related to the development of trichomes in *Arabidopsis thaliana*. However, the comprehensive identification and systematic analysis of DVL in cotton have not been conducted. In this study, we employed bioinformatics approaches to conduct a novel analysis of the structural characteristics, phylogenetic tree, gene structure, expression pattern, evolutionary relationship, and selective pressure of the DVL gene family members in four cotton species. A total of 117 DVL genes were identified, including 39 members in *G. hirsutum*. Based on the phylogenetic analysis, the DVL protein sequences were categorized into five distinct subfamilies. Additionally, we successfully mapped these genes onto chromosomes and visually represented their gene structure information. Furthermore, we predicted the presence of cis-acting elements in DVL genes in *G. hirsutum* and characterized the repeat types of DVL genes in the four cotton species. Moreover, we computed the Ka/Ks ratio of homologous genes across the four cotton species and elucidated the selective pressure acting on these homologous genes. In addition, we described the expression patterns of the DVL gene family using RNA-seq data, verified the correlation between GhMDVL3 and fuzz development through VIGS technology, and found that some DVL genes may be involved in resistance to biotic and abiotic stress conditions through qRT-PCR technology. Furthermore, a potential interaction network was constructed by WGCNA, and our findings demonstrated the potential of GhM_A05G1032 to interact with numerous genes, thereby playing a crucial role in regulating fuzz development. This research significantly contributed to the

comprehension of DVL genes in upland cotton, thereby establishing a solid basis for future investigations into the functional aspects of DVL genes in cotton.

PLANT BIOTECHNOLOGY

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Title: Molecular characterization and expression pattern of Rubisco activase gene GhRCA β 2 in upland cotton (*Gossypium hirsutum* L.).

Author: Maoni Chao, Ling Huang, Jie Dong, Yu Chen, Genhai Hu, Qiufang Zhang, Jinbao Zhang & Qinglian Wang

Imprint: Genes and Genomics, 2024

Abstract: Rubisco activase (RCA) is a pivotal enzyme that can catalyse the activation of Rubisco in carbon assimilation pathway. Many studies have shown that RCA may be a potential target for genetic manipulation aimed at enhancing photosynthetic efficiency and crop yield. To understand the biological function of the *GhRCA β 2* gene in upland cotton, we cloned the coding sequence (CDS) of the *GhRCA β 2* gene and investigated its sequence features, evolutionary relationship, subcellular localization, promoter sequence and expression pattern. The bioinformatics tools were used to analyze the sequence features of GhRCA β 2 protein. Transient transformation of *Arabidopsis* mesophyll protoplasts was performed to determine the subcellular localization of the GhRCA β 2 protein. The expression pattern of the *GhRCA β 2* gene was examined by analyzing transcriptome data and using the quantitative real-time PCR (qRT-PCR).

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Title: GhRCD1 promotes cotton tolerance to cadmium by regulating the GhbHLH12-GhMYB44-GhHMA1 transcriptional cascade.

Author: Xi Wei, Menghan Geng, Jiachen Yuan, Jingjing Zhan , Lisen Liu

Imprint: Plant Biotechnology Journal (2024), pp. 1-20 doi: 10.1111/pbi.14301

Abstract: Heavy metal pollution poses a significant risk to human health and wreaks havoc on agricultural productivity. Phytoremediation, a plant-based, environmentally

benign, and cost-effective method, is employed to remove heavy metals from contaminated soil, particularly in agricultural or heavy metal-sensitive lands. However, the phytoremediation capacity of various plant species and germplasm resources display significant genetic diversity, and the mechanisms underlying these differences remain hitherto obscure. Given its potential benefits, genetic improvement of plants is essential for enhancing their uptake of heavy metals, tolerance to harmful levels, as well as overall growth and development in contaminated soil. In this study, we uncover a molecular cascade that regulates cadmium (Cd^{2+}) tolerance in cotton, involving GhRCD1, GhbHLH12, GhMYB44, and GhHMA1. We identified a Cd^{2+} -sensitive cotton T-DNA insertion mutant with disrupted GhRCD1 expression. Genetic knockout of GhRCD1 by CRISPR/Cas9 technology resulted in reduced Cd^{2+} tolerance in cotton seedlings, while GhRCD1 overexpression enhanced Cd^{2+} tolerance. Through molecular interaction studies, we demonstrated that, in response to Cd^{2+} presence, GhRCD1 directly interacts with GhbHLH12. This interaction activates GhMYB44, which subsequently activates a heavy metal transporter, GhHMA1, by directly binding to a G-box cis-element in its promoter. These findings provide critical insights into a novel GhRCD1- GhbHLH12-GhMYB44-GhHMA1 regulatory module responsible for Cd^{2+} tolerance in cotton. Furthermore, our study paves the way for the development of elite Cd^{2+} -tolerant cultivars by elucidating the molecular mechanisms governing the genetic control of Cd^{2+} tolerance in cotton.

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Title: Genome-wide identification of cotton *CrRLK1L* family genes and potential function of *GhCrRLK1L104* in cell elongation.

Author: Dongyun Zuo , Lijin Chen , Javaria Ashraf, Hailiang Cheng , Youping Zhang , Qiaolian Wang, Limin Lv , Shang Liu , Guoli Song

Imprint: Current Plant Biology, Volume 37, March 2024, 100325

Abstract: *Catharanthus roseus* receptor-like kinase 1-like (*CrRLK1L*) proteins play important roles in cell growth, plant morphogenesis, reproduction, hormone signaling, plant immunity and stress responses in Arabidopsis. However, not much information is available about their functions in cotton. We identified a total of 125, 73 and 71 full-length putative *CrRLK1L* genes in *G. hirsutum*, *G. arboreum* and *G. raimondii*, which are much greater than that of the other plants. The phylogenetic and gene structure analysis divided the cotton *CrRLK1L* genes into six major groups, among which only group I and II contained *AtCrRLK1Ls* of *Arabidopsis*. Genome collinearity analysis revealed large scale reciprocal translocations on chromosome 2 among Gossypium A genomes species, which led to uneven distribution of *CrRLK1L* genes on this chromosome. In addition, transcriptome data combined with qRT-PCR analysis showed some *GhCrRLK1Ls* were preferentially expressed in fibers during the specific stages of ovules or fibers development. Notably, *GhCrRLK1L104* was

highly expressed in fibers at 30 days post anthesis, and the GhCrRLK1L104::GFP fusion protein was located on the plasma membrane. Furthermore, overexpression of the *GhCrRLK1L104* gene in *Arabidopsis* increased the trichomes length of the rosette leaves, indicated its vital roles in cell elongation. These results provided a strong foundation to further explore the molecular mechanism of *CrRLK1L* genes in upland cotton in cell elongation, that can be used in future cotton breeding program.

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Title: Genome-wide Identification of the Cell Wall Related Gene GhGRP in *Gossypium hirsutum* L. and Its Role in Abiotic Stress.

Author: Wang D , Lu X , Zhang Y , Chen X , Zhao L , Wang J , Wang J , Han M , Fan Y , Wang S , Guo L , Yin Z , Rui C , Zhang H , Xu N , Wang Q , Sun L , Chen C , Ye W

Imprint: Preprint from Authorea Preprints, 31 Jan 2024, <https://doi.org/10.22541/au.170670935.52723515/v1> PPR: PPR797224

Abstract: GRP (glycine-rich protein) is characterized by glycine-rich and conserved motifs that include (Gly) N-X repeats. This superfamily is generally divided into five major subclasses. Although GRP has been found to be involved in the stress response in many model plants and nonmodel plant species, little is known about the key physiological processes and molecular mechanisms involved in these proteins. In this study, we identified and analyzed the GhGRP genes of five subgroups of *Gossypium hirsutum* for the first time. Our research showed that GRP overexpression could enhance the salt stress tolerance of *Arabidopsis thaliana* and cotton, which would play a very promising role in cotton genetic engineering breeding. The GRP gene had made some progress in rice, *Arabidopsis thaliana*, maize, tobacco and other plants. In cotton, only *Gossypium arboreum* and *Gossypium raimondii* had been analyzed and identified into subgroup IV [(#ref-0038)W. Yang et al., 2019), also known as the RB-GRP. VIGS and *Arabidopsis thaliana* overexpression experiments showed that the expression of GRP42 gene could indeed improve plant salt tolerance. The results of TEM showed that GRP42 gene might act on the cell wall of plant vascular tissue and played a supporting role.

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Title: The Silencing of GhPIP5K2 and GhPIP5K22 Weakens Abiotic Stress Tolerance in Upland Cotton (*Gossypium hirsutum*).

Author: Pingjie Ling, Jisheng Ju, Xueli Zhang

Imprint: Int. J. Mol. Sci. 2024, 25(3), 1511; <https://doi.org/10.3390/ijms25031511>

Abstract: Phosphatidylinositol 4-phosphate 5-kinases (PIP5Ks), essential enzymes in the phosphatidylinositol signaling pathway, are crucial for the abiotic stress responses and the overall growth and development of plants. However, the GhPIP5Ks had not been

systematically studied, and their function in upland cotton was unknown. This study identified a total of 28 GhPIP5Ks, and determined their chromosomal locations, gene structures, protein motifs and cis-acting elements via bioinformatics analysis. A quantitative real-time PCR (qRT-PCR) analysis showed that most GhPIP5Ks were upregulated under different stresses. A virus-induced gene silencing (VIGS) assay indicated that the superoxide dismutase (SOD), peroxidase (POD), and catalase (CAT) activities were significantly decreased, while malondialdehyde (MDA) content were significantly increased in GhPIP5K2- and GhPIP5K22-silenced upland cotton plants under abiotic stress. Furthermore, the expression of the stress marker genes GhHSFB2A, GhHSFB2B, GhDREB2A, GhDREB2C, GhRD20-1, GhRD29A, GhBIN2, GhCBL3, GhNHX1, GhPP2C, GhCBF1, GhSnRK2.6 and GhCIPK6 was significantly decreased in the silenced plants after exposure to stress. These results revealed that the silencing of GhPIP5K2 and GhPIP5K22 weakened the tolerance to abiotic stresses. These discoveries provide a foundation for further inquiry into the actions of the GhPIP5K gene family in regulating the response and resistance mechanisms of cotton to abiotic stresses.

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Title: Knockdown of the atypical protein kinase genes GhABC1K2-A05 and GhABC1K12-A07 make cotton more sensitive to salt and PEG stress.

Author: Caixiang Wang, Mei li Li, Dingguo Zhang, Xueli Zhang, Juanjuan Liu, Junji Su

Imprint: Journal of Integrative Agriculture, 2024

Abstract : Activity of bc1 complex kinase (ABC1K) is an atypical protein kinase (aPK) that plays a crucial role in plant mitochondrial or plastid stress responses, but little is known about the responses of ABC1Ks to stress in cotton (*Gossypium* spp.). Here, we verified 40 ABC1Ks in upland cotton (*Gossypium hirsutum* L.) and found that GhABC1Ks were unevenly distributed across 17 chromosomes. GhABC1K family members contained 35 paralogous gene pairs and were expanded by segmental duplication. The GhABC1K promoter sequences contained diversified cis-acting regulatory elements relevant to hormone or stress responses. The qRT-PCR results revealed that most GhABC1Ks were upregulated by exposure to different stresses. GhABC1K2-A05 and GhABC1K12-A07 expression was upregulated by at least three stress treatments. These genes were further functionally characterized by virus-induced gene silencing (VIGS). Compared with the controls, the GhABC1K2-A05- and GhABC1K12-A07-silenced cotton lines exhibited a higher malondialdehyde (MDA) content, lower catalase (CAT), peroxidase (POD) and superoxide dismutase (SOD) activities and reduced chlorophyll and soluble sugar contents under NaCl and PEG stress. In addition, the expression of stress marker genes (GhDREB2A, GhSOS1, GhCIPK6, GhSOS2, GhWRKY33, and GhRD29A) was significantly downregulated after

stress in the GhABC1K2-A05- and GhABC1K12-A07-silenced lines. The results indicate that knockdown of GhABC1K2-A05 and GhABC1K12-A07 make cotton more sensitive to salt and PEG stress. These findings can provide valuable information for intensive studies of GhABC1Ks in the responses and resistance of cotton to abiotic stresses.

SEED SCIENCE AND TECHNOLOGY

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Title: Comparative proteomic analysis of seed germination between allotetraploid cotton *Gossypium hirsutum* and *Gossypium barbadense*.

Author: Aishuake Huwanixi , Zhao Peng, Shenglan Li, Yutian Zhou, Sixian Zhao, Cuihong Wan

Imprint: Journal of Proteomics, Volume 297, 15 April 2024, 105130

Abstract: Seed germination, a key initial event in the plant life cycle, directly affects cotton yield and quality. *Gossypium barbadense* and *Gossypium hirsutum* gradually evolved through polyploidization, resulting in different characteristics, and this interspecific variation lacks genetic and molecular explanation. This work aimed to compare the proteomes between *G. barbadense* and *G. hirsutum* during seed germination. Here, we identified 2740 proteins for *G. barbadense* and 3758 for *G. hirsutum*. In the initial state, proteins in two cotton involved similar bioprocess, such as sugar metabolism, DNA repairing, and ABA signaling pathway. However, in the post-germination stage, *G. hirsutum* expressed more protein related to redox homeostasis, peroxidase activity, and pathogen interactions. Analyzing the different expression patterns of 915 single-copy orthogroups between the two kinds of cotton indicated that most of the differentially expressed proteins in *G. barbadense* were related to carbon metabolism. In contrast, most proteins in *G. hirsutum* were associated with stress response. Besides that, by proteogenomic analysis, we found 349 putative non-canonical peptides, which may be involved in plant development. These results will help to understand the different characteristics of these two kinds of cotton, such as fiber quality, yield, and adaptability.

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Title: Response of cotton (*Gossypium hirsutum* L.) seeding the ultra-narrow grooves and high population density.

Author: MARTINEZ-LARA, Filiberto, CHINO-CANTOR, Araceli, MARTÍNEZ-SÁNCHEZ, Itzcóatl and CIPRIANO-ANASTASIO, Juan

Imprint: Journal of Natural and Agricultural Sciences December 2023, Vol.10 No.27 15-21

Abstract: The cotton planting (*Gossypium hirsutum* L.) on narrow rows instead on conventional rows to 75 cm, show to be an alternative to increasing crop yield and to reduce production costs. The objective of this research was to study the effects of ultra-narrow rows and plant density on the biomass production and fiber quality. Three-row spacings and three plant densities were evaluated in the Comarca Lagunera, México. Ultra-narrow rows 50 and 35 cm, apart and conventional rows spaced to 75 cm, were used. The population densities were 80,000, 100,000 and 120,000 plants ha⁻¹. The conventional variety Fiber max 98 was used. The nine treatments were assigned to a randomized complete block design with three replications in a split plot arrangement. Row spacings were assigned to main plots and the population densities to subplots. Seedcotton and lint yield were evaluated in kg ha⁻¹, yield components (boll weight, lint percentage and seed index), fiber quality (length, resistance and fineness) and the plant growth indexes, leaf area index (LAI), net assimilation rate (NAR), crop growth rate (CGR), specific leaf area (SLA), leaf weight fraction (LWF) and leaf area ratio (LAR). Seed-cotton yield was different.

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Title: Exploring the impact of cadmium stress on morphophysiological traits and *GhPCS* gene expression in upland cotton seedlings.

Author: Yan , Xiang Wu , Juan Li , Ling Li

Imprint: South African Journal of Botany, Volume 167, April 2024, Pages 72-81

Abstract: Cadmium (Cd)-contaminated soil has seriously endangered the agricultural ecological environment, food security and human health. The large biomass, strong capacity of Cd accumulation, and non-edible properties of fiber are the characteristics of cotton, which make it unique in both agricultural production and the remediation of Cd pollution in soil. Phytochelatin synthase (PCS) is a key enzyme that catalyzes the synthesis of phytochelatin, and its gene expression is regulated by tissue development and Cd stress. In this experiment, the morphological and physiological characteristics of cotton seedlings were examined, and the *PCS* gene was cloned and its expression was analyzed in cotton leaves and roots under Cd stress. The results showed that Cd stress caused a decrease in the biomass of roots, stems and leaves of cotton seedlings, and the plants were slender and severely dehydrated, resulting in a decrease in the contents of glutamic acid (Glu), glycine (Gly) and cysteine (Cys), but a increase in the activity of superoxide dismutase (SOD), peroxidase (POD), catalase (CAT), ascorbate peroxidase

(APX), glutathione reductase (GR), and the content of malondialdehyde (MDA). The Cd contents of shoots and roots increased significantly, and the contents of Cu, Mn, Mg, K in shoots and Mn, Mg, K in roots decreased under Cd stress, while Cu in roots increased. A 1473 bp *GhPCS* gene was cloned, which can encode 491 amino acid residues. With the increasing Cd concentration and the extension of treatment time, the expression of *GhPCS* gene in leaves and roots showed dose and time effects. The expression of the *GhPCS* gene in cotton leaves increased to the highest at 48 h under 200 μM Cd, and reached a maximum at 24 h under 400 μM Cd, indicating that the *GhPCS* gene in leaves was rapidly and actively expressed in response to high concentration of Cd. The expression of *GhPCS* gene in roots was lower than that in leaves under different Cd concentrations, and reached the maximum at 48 h, indicating that the *GhPCS* gene in roots had relatively stable adaptability to Cd stress. And Cd stress improved the expression of *GhPCS* gene, especially in roots, which in turn increased the accumulation of Cd in shoots and roots. This study provides a theoretical basis for further research on the functional characteristics of the *GhPCS* gene and its molecular mechanism in cotton under Cd pollution in soil.

FIBER AND FIBER TECHNOLOGY

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Title: Gibberellin acid promotes single-celled fiber elongation through the activation of two signaling cascades in cotton.

Author: Peng He , Liping Zhu, Xin Zhou, Bin Jiang, Huiqin Wang, Guanghui Xiao

Imprint: Developmental Cell, February 14, 2024
DOI:<https://doi.org/10.1016/j.devcel.2024.01.018>

Abstract: The agricultural green revolution spectacularly enhanced crop yield through modification of gibberellin (GA) signaling. However, in cotton, the GA signaling cascades remain elusive, limiting our potential to cultivate new cotton varieties and improve yield and quality. Here, we identified that GA prominently stimulated fiber elongation through the degradation of DELLA protein GhSLR1, thereby disabling GhSLR1's physical interaction with two transcription factors, GhZFP8 and GhBLH1. Subsequently, the resultant free GhBLH1 binds to *GhKCS12* promoter and activates its expression to enhance VLCFAs biosynthesis. With a similar mechanism, the free GhZFP8 binds to *GhSDCP1* promoter and activates its expression. As a result, GhSDCP1 upregulates the expression of *GhPIF3* gene associated with plant cell

elongation. Ultimately, the two parallel signaling cascades synergistically promote cotton fiber elongation. Our findings outline the mechanistic framework that translates the GA signal into fiber cell elongation, thereby offering a roadmap to improve cotton fiber quality and yield.

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Title: The comparative transcriptome and co-expression of hub genes analysis for fiber development in RIL populations of upland cotton.

Author: Renhui Wei , Yike Zhong , Nan Xu , Pengtao Li

Imprint: Industrial Crops and Products, Volume 210, April 2024, 118130

Abstract: Upland cotton (*Gossypium hirsutum*) is one of the important crops to produce natural fiber, and fiber length (FL) and fiber strength (FS) are important fiber quality traits. In this study, we developed a population of recombinant inbred lines (RILs) with the parents 0-153 (P1, high fiber quality) and sGK9708 (P2, low fiber quality), which were constructed for detection of elite alleles. According to the RNA-seq data of P1, P2, 69307 (L1, high fiber quality) and 69362 (L2, low fiber quality), 350/90, 71/132, 214/120, 199/201, and 287/229 genes were differentially expressed (up-/down-regulated) in high quality fiber lines (P1 and L1) in contrary to low quality fiber lines (P2 and L2) at 5, 10, 15, 20 and 25 days post-anthesis (DPA), respectively. Short Time-series Expression Miner (STEM) analysis detected the presence of five expression profiles, Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) annotation were investigated to determine the functional differences between specific genes of profile 7 and 26. A total of 234 differentially expressed genes (DEGs) belong to quantitative trait locus loci (QTLs) controlling FL and FS. Co-expression network analysis revealed the presence of two modules which were associated with various stages of fiber development. The weighted gene co-expression network analysis (WGCNA) was also carried out to distinguish 13 hub genes in blue module and 24 hub genes in turquoise module. The alignment between quantitative real-time PCR and RNA-seq data gave the clue for guaranteeing reliability of selected candidate genes for further analysis. In this study, we combine the identified genes from FL and FS QTLs with the results of STEM, WGCNA and time-course analysis. In addition, six candidate genes

GH_A04G0817, GH_A05G0644, GH_A08G0267, GH_A11G0850, GH_D02G1011 and GH_D11G3494) were selected as candidate genes to improve cotton fiber quality.

Title: Variations in Fiber Length and Color Parameters of Four Varieties of Cotton (*Gossypium Hirsutum* L.) in Two Climatic Zones of Mali

Author: Sory Sissoko, Mariam Traoré, Elhadji Mamoudou Kassambara, Gassiré Bayoko, Daouda Maiga and Mamadou Oumar Diawara

Imprint: Journal of Biotechnology and Biochemistry (IOSR-JBB) ISSN: 2455-264X, Volume 10, Issue 1 Series 1 (Jan. – Feb. 2024), PP 06-10

Abstract: Varietal selection involves developing varieties that best satisfy the requirements of growers (better productivity in the field), the ginning industry (high fiber yield), and the spinning industry (good technological fiber characteristics). The price of cotton fiber is essentially linked to the characteristics of the fiber. When selecting cotton varieties, it is essential to be very attentive to the characteristics and variations of the fiber in different environments. The aim of this study is to investigate variations in the fiber length and color parameters of four cotton varieties of Mali. Four cotton varieties were tested in two different environments, the southern and northcentral zones of Mali, for variations in fiber length and color. The analysis showed a significant interaction between varieties and zones. The values of the parameters studied varied from one zone to another for the same variety. The best values for the Upper Half Mean Length (UHML) were obtained in the southern zone, while the uniformity index was better in the north-central zone. The colorimetry of all the varieties was good in the northcentral zone, with a good percentage reflectance value and low levels of fiber yellowing. Variability in fiber properties at the crop production level can be used to determine potential and genotype choice.

Title: Effect of Salicylic Acid Application on Cotton (*Gossypium Hirsutum* L.) Yield and Fibre Quality

Author: Rukiye KILIÇ and Çetin KARADEMİR

Imprint: Journal of Applied Life Sciences and Environment, <https://doi.org/10.46909/alse-564118> Vol. 56, Issue 4 (196) / 2023: 597-617

Abstract: This study was carried out to determine the effect of SA (salicylic acid) application on the yield, yield components, and fibre quality characteristics of cotton at different growth stages (squaring, flowering and squaring + flowering). The experiment was carried out at Siirt University, Faculty of Agriculture, Department of Field Crop's experimental area during the 2022 cotton growing season. The experimental design was

a split-plot design with four replications. The main plot and sub-plots consisted of SA applications [Control (0.0 mM), squaring (1.0 mM), flowering (1.0 mM), squaring (0.5 mM) + flowering (0.5 mM)] and varieties (MAY 455, Stoneville 468, Fiona), respectively. SA application and variety interactions were significant in terms of the first boll opening days and the number of nodes. There were significant differences between varieties, except for the number of monopodial branches, number of bolls, chlorophyll content value, normalised difference vegetation index value, and micronaire and fibre strength. The MAY 455 cotton variety had the highest values in terms of seed cotton yield (2993.1 kg ha⁻¹) plant height (62.14 cm), boll weight (6.51 g), seed cotton weight per boll (4.90 g), number of seeds per boll (29.46), number of nodes to first fruiting branch (8.65), fibre yield (1361.0 kg ha⁻¹) and 100-seed weight (8.82 g), while the Fiona variety came to the fore in terms of number of days to first boll opening (118.0 d), number of sympodial branches (7.56), number of nodes per plant (17.79), ginning percentage (46.45%), fibre length (828.52 mm) and fibre reflectance (82.18 Rd). There was a slight increase in yield (223.8 kg ha⁻¹) compared to the control. SA application may show different effects on each cotton variety, and the positive effect may increase by applying SA at different intervals.

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Title: Potential of Brown Cotton Fiber Development for Sustainable Textile Materials.

Author: Taufiq Hidayat RS, Nurindah, Dwi Adi Sunarto

Imprint: Proceeding Indonesian Textile Conference (International Conference) 3rd Edition Volume 1 2019 <http://itc.stttekstil.ac.id>

Abstract: The use of brown cotton fiber to meet fiber raw materials needs to be supported, because chemicals used for colouring in textile industry contributes to high pollution in the environment. The program for assembling brown cotton fiber varieties in Indonesia has begun in 2006. In 2018 three new superior varieties of brown cotton fiber were released, namely Bronesia 1, Bronesia 2 and Bronesia 3. This paper discusses the potential of brown cotton fiber as a textile raw material in Indonesia. The brown cotton fiber of Bronesia variety has the potential to produce 1011 kg/ha cotton fiber. Cotton fiber of Bronesia has fiber lengths ranging from 23-25 mm and has fiber strength between 21-23 g/tex. The uniformity fiber of brown cotton Bronesia is included in the high category, ranging from 83 - 84%. The brown cotton fiber of Bronesia has three color gradations, namely medium brown, light brown and dark brown. The brown cotton fiber of Bronesia has resistance to pest infestations, and can grow well on dry land. The brown cotton fiber of Bronesia has the potential to be used in the textile industry, especially the traditional weaving industry; therefore, it can support the sustainable textile industry. The purpose of this review is to discuss the opportunities for the use of

brown cotton fibers from Bronesia varieties in supporting the Indonesian textile industry.

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Title: Expression analysis of fiber-related genes for staple length in upland cotton (*Gossypium hirsutum* L.).

Author: Muhammad Nadeem, Muhammad Shahzad , Zulqurnain Khan , Umar Akram, Muhammad Hasnain , M. Ajmal Ali , Mohamed Soliman Elshikh

Imprint: Journal of King Saud University - Science, Volume 36, Issue 4, April 2024, 103119

Abstract: Cotton fibers, derived from the seed coat and used in the global textile industry for fabric production, are generally recognized as the predominant form of individual unicellular cells. The investigation of cellular proliferation and differentiation may be efficiently conducted by using cotton fiber production as a model system. Expression profiling techniques are very helpful to determine the tissue (stem and roots) and stage (0, 05, 10, 15 and 20 DPA) specific gene expression in cotton fiber. This profiling technique is helpful in the development of a new plant (variety) through transformation, resulting in the development of a new plant with desirable fiber characteristics. **Methods-** The expression profiling was carried out in upland cotton genotypes with variable staple length including: i) long staple length, ii) medium staple length and iii) short staple length) at five different days post anthesis (DPA) phases of fiber elongation (0, 5, 10, 15 and 20 DPA) through real-time PCR. Two internal controls (*ubiquitin* and *18sr RNA*) genes were used for data normalization. Current research has focused on genetic basis of fiber regulation and understanding the molecular basis of fiber development in upland cotton (*G. hirsutum* L.) genotypes ('CYTO-179', 'CIM-616' and 'CIM-707') with variable staple length medium, long and short respectively. The present work aimed to investigate the expression levels of three fiber genes, namely *PEPc*, *XTH*, and *GA-20 Oxidase*, throughout several developmental phases.

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Title: Fiber Quality Improvement of Upland Cotton (*Gossypium Hirsutum* L.) Through Interspecific Introgression.

Author: Samantha Jo Wan

Imprint: Master of Science (MS), University of Georgia, 12/2023

Abstract: Stagnation in fiber quality improvement created by the narrow genetic base of elite cotton germplasm has hindered long term improvement of upland cotton (*Gossypium hirsutum* L.). A closely related species, *G. barbadense*, has been successfully utilized as a source of novel alleles for fiber quality improvement of upland cotton. The obsolete germplasm line, Sealand 883, carries several fiber quality quantitative trait loci (QTLs) introgressed from *G. barbadense*. This research focuses on further validating the genetic effect of qFL-Chr.25, a QTL which improves fiber length profile of nearly-isogenic lines in four diverse genetic backgrounds tested. In addition, RNA-seq analysis identified three candidate genes (Ghir_D06G000180, Ghir_D06G000680 and Ghir_D06G000880) within the QTL region associated with the *G. barbadense* allele. The transcriptomic data along with fiber profile data provide valuable insight into fiber cell development as well as a new avenue for improved understanding of cross-species gene transferability in cotton.