



GLEANINGS IN COTTON RESEARCH

FEBRUARY 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: Impact of CROPSAP Scheme on Cotton Growers: A Probit Regression Approach.

Author: Prachi D. Undirwade, R.V. Chavan and S.V. Bharti

Imprint: Biological Forum – An International Journal 15 (11): 599-601(2023)

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 Jalna district of Maharashtra state purposively on the basis of 2nd highest area under cotton crop. Multistage sampling technique was used for selection of district, tehsils and villages. Total sample size was 160 where 80 was beneficiary and 80 non-beneficiary cotton growers. Probit regression model was fitted to assess the impact of CROPSAP scheme on beneficiary and non-beneficiary cotton growers. CROPSAP provide a larger canvas for pest management implementation in term of technological use, number of stakeholders, number of crops, area covered, skill imparted and employment generated. The pest affected area across cotton is implemented with scientifically based pest management practice across Maharashtra state of jalna district. In view of limited time, resources, the study is restricted to certain variables which may have influences on impact of Crop Pest Surveillance and advisory project on farmers. Application of only recommended pesticides at right dosages using proper application equipment and technique have brought in judicious use of chemical and reduces the occupational hazards. 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 X₂ (spacing) was significant at 1 per cent level, X₄ (plant protection under CROPSAP) was also significant at 1 per cent level, and factor X₆ (Yield) significant at 10 per cent level. Hence this result indicated that the above significant factors are greatly influenced on farmers towards adoption of the CROPSAP scheme. Our result show that the CROPSAP scheme is helpful to increase the income level of cotton growers and it is also helpful in future to increase the income level and reduce losses of crops which are affected by insect/ pest.

2

Title: Comparing the influence of natural farming on cotton (*Gossypium hirsutum*) yield and economics with integrated and organic farming.

Author: M, Monicaa, Krishnan , R., Sunitha , R. , Sanbagavalli , S. , Manickam , S. , Senthil , A. , Sangeetha, S. P.

Imprint: Journal of Applied and Natural Science; Vol 15 No 3 (2023); 1268 - 1275

Abstract: Cotton, a vital global cash crop, influences the economy and sustainability. Natural farming is a cost-effective, eco-friendly method. This study examines Natural Farming's effects on cotton yield and the economics of cotton compared to Integrated and organic farming. Field experiments were conducted during 2021-22 and 2022-23 at Tamil Nadu Agricultural College, Coimbatore. The experiment consisted of eight treatments, laid out in Randomized Block Design and replicated thrice. The treatments consist of control (T1), various Indian Natural farming practices including Beejamirit as a seed treatment, Ghanajeevamirit as basal, Jeevamirit with irrigation water, crop residue mulch, intercropping with pulses (T2 to T5), Organic farming practices (T6), Integrated crop management (ICM) practices with organic pest control.

3

Title: Knowledge level of cotton growers about recommended cotton production practices.

Author: PB Raviya, LK Mokariya and KP Vaghasiya

Imprint: The Pharma Innovation Journal 2023; SP-12(12): 2365-2366

Abstract: Cotton is one of the most important fiber and cash crop of India and plays a dominant role in the industrial and agricultural economy of the country. It provides the basic raw material (cotton fibre) to cotton textile industry. Cotton in India provides direct livelihood to 6 million farmers and about 40 -50 million people are employed in cotton trade and its processing. Cotton farming sustains small and marginal farmers across numerous states, especially in Maharashtra, Gujarat, and Andhra Pradesh. It provides income and stability to rural communities. A study was conducted in Junagadh district of Gujarat state. Four villages from three random talukas were selected. Ten cotton growers from each village and make a sample of 120 cotton growers who having highest area under cotton cultivation. Three fifth (60.00 percent) of the respondents had medium level knowledge group followed by 21.66 percent and 18.34 percent.

4

Title: The Strategic Importance of Cotton Production for the World and Türkiye

Author: Songül Akın

Imprint: Published: 10 January 2024, DOI: 10.5772/intechopen.114084 FROM THE EDITED VOLUME, Best Crop Management and Processing Practices for Sustainable Cotton Production by Dr. Songül Gürsoy and Dr. Songül Akın

Abstract: Cotton can be grown in a wide variety of geographical regions worldwide. It is a valuable crop as it contributes positively to the economy of the regions and countries with its wide range of use, added value and employment opportunities. Beyond its being just an agricultural commodity, cotton has strategic importance for Türkiye where there have been ideal regions for cultivation. Growing interest in natural fiber and rising living standards increase the demand for cotton. In this study, in addition to the general information on cotton crops and their cultivation, explanations and interpretations were made on production and trade particularly in Türkiye and trade generally in the world for this crop based on the recent cotton production and trade data.

5

Title: Influence of Integrated Nutrient Management (INM) Practices on Soil Quality Indicators and Indices under Cotton (*Gossypium Spp.*) + Black Gram (*Vigna Mungo* (L.) Hepper) and Green Gram (*Vigna Radiata* (L.) R. Wilczek) + Rabi Sorghum (*Sorghum Bicolor* (L.) Moench) Inter Cropping Systems in Rainfed Vertisols of Western India.

Author: K.L. Sharma, Munna Lal, A.K. Indoria, Ch. Chandra Sekhar, Vinod Kumar Singh

Imprint: Communications in Soil Science & Plant Analysis, <https://doi.org/10.1080/00103624.2024.2303124>

Abstract: A field experiment was conducted to study the effect of seven predominant integrated nutrient management (INM) practices on soil quality indicators and indices under two inter-cropping systems, namely cotton + black gram and green gram + rabi sorghum, at the All-India Coordinated Research Project for Dryland Agriculture (AICRPDA), Parbhani Center, located in Central and Western Maharashtra, India. The INM practices include F1: Farmyard Manure (FYM) @ 5 t ha⁻¹; F2: Gliricidia @ 3t ha⁻¹ (semi dried leaves + very soft upper twigs); F3: Recommended dose of fertilizer (RDF); F4: 25% RDF + FYM @ 2.5 t ha⁻¹; F5: 25% RDF + Gliricidia @ 1.5 t ha⁻¹ (semi dried leaves + very soft upper twigs); F6: Control with rotation and F7: Absolute control without rotation. The order of overall performance of the INM treatments, in terms of mean Soil Quality Index (SQI), across both the cropping systems studied was: F1 (2.59) > F4 (2.55) > F5 (2.52) > F2 (2.49) > F3 (2.40) > F6 (2.12) > F7 (2.04). In case of

Cotton + black gram system, the predominant soil parameters which emerged as key soil quality indicator, along with their percent contribution toward soil quality index, were: organic C (21%), available Mn (21%), labile C (20%), dehydrogenase activity (DHA) (19%), pH (5%), available S (5%), mean weight diameter of soil aggregates (MWD) (5%) and available K (4%). However, in case of green gram + rabi sorghum system, labile C (24%), available K (23%), available Mn (23%), microbial biomass C (MBC) (21%) and available S (9%) were found to be the key soil quality indicators in the black soil under study. The common indicators for the two cropping systems studied under these Vertisol soils were: available K, available S, available Mn and Labile carbon (LC). Thus, these indicators assume great significance in managing the Vertisol soils under study. The methodology followed and the results of the present study will be immensely useful to different stakeholders in conducting such future studies and managing and improving soil quality under different inter-cropping systems in Vertisols.

6

Title: DREB transcription factors are crucial regulators of abiotic stress responses in *Gossypium* spp.

Author: Bello Sadau, Zhixin Liu, Vincent Ninkuu, Liping Guan, Xuwu Sun

Imprint: Plant Stress, Volume 11, March 2024, 100350

Abstract: Plants are adversely affected by abiotic stress conditions such as heat, drought, cold, and salinity. The physiological determinants of cotton stress tolerance and its processes were investigated to mitigate the effect of abiotic stress on cotton growth and development. The *DEHYDRATION-RESPONSIVE ELEMENT BINDING* protein (*DREB*) transcription factors are stress-responsive and regulate the expression of downstream stress-inducible genes, leading to subsequent resistance to several abiotic stressors. Advanced omics technologies have recently improved our understanding of the complex molecular events of cotton that precede abiotic stress responses. We highlight the central abiotic stress resistance mechanisms in cotton, elaborating on the identified and unidentified regulatory variables. The evolutionary relationship between *DREB* transcription factors (TFs), divided into six subtypes in *Gossypium hirsutum*, *Gossypium raimondii*, and *Arabidopsis thaliana*, was reviewed. Moreover, the evolutionary antecedents, conserved motifs, and gene structure of the cotton *DREB* gene family have been discussed. This review offers an in-depth perspective on the contribution of *DREB* TFs to cotton tolerance to abiotic stress conditions, such as cold, drought, salt, heat, and heavy metals. Overall, this review identified essential genes in *Gossypium* spp and other species that could hasten applied studies toward their engineering into plants to mitigate abiotic stress.

Title: Effect of foliar application of 6-benzylaminopurine and pix on growth characteristics and yield of delayed transplanting cotton (*Gossypium hirsutum* L.)

Author: Dariush Saadati , Matin Jami Moeini , Mohammad Armin

Imprint: Crop Sc.Res. in Arid Regions, [10.22034/CSRAR.2023.391000.1333](#)

Abstract: Cotton (*Gossypium hirsutum* L.) is the most widely used natural fiber and the most important dual-purpose industrial plant in the world. Delayed transplanting of cotton using early cultivars is one of the effective methods to increase the cultivated area and increase the production of this strategic crop. Plant growth regulators can be effective in the source-sink balance in different plants and are progressively used to increase yield in many plants. Cytokinins are one of the most important plant growth regulators, which increase cell division and differentiation, reduce the effect of terminal dominance, increase leaf surface development, increase the number of lateral branches, increase mobility of nutrients, prevent chlorophyll decomposition, and prevent aging. Growth regulators containing mepiquat chloride, such as pix, reduce vegetative growth in cotton by preventing the synthesis of gibberellic acid. Controlling the growth of cotton as a result of the use of pix, allocates the photosynthetic assimilates to the fruit organs and growing bolls, which increases the weight of the bolls.

Title: Impact of salinity stress on cotton and opportunities for improvement through conventional and biotechnological approaches

Author: Muhammad Tanees Chaudhary, Sajid Majeed, Iqrar Ahmad Rana, Zulfiqar Ali, Yinhua Jia, Xiongming Du, Lori Hinze & Muhammad Tehseen Azhar

Imprint: BMC Plant Biology Review, [Open access](#), [Published: 02 January 2024](#), Volume 24, article number 20, (2024)

Abstract: Excess salinity can affect the growth and development of all plants. Salinization jeopardizes agroecosystems, induces oxidative reactions in most cultivated plants and reduces biomass which affects crop yield. Some plants are affected more than others, depending upon their ability to endure the effects of salt stress. Cotton is moderately tolerant to salt stress among cultivated crops. The fundamental tenet of plant breeding is genetic heterogeneity in available germplasm for acquired characteristics. Variation for salinity tolerance enhancing parameters (morphological, physiological and biochemical) is a pre-requisite for the development of salt tolerant cotton germplasm followed by indirect selection or hybridization programs. There has been a limited success in the development of salt tolerant genotypes because this trait depends on several factors, and these factors as well as their interactions are not completely understood. However, advances in biochemical and molecular techniques

have made it possible to explore the complexity of salt tolerance through transcriptomic profiling. The focus of this article is to discuss the issue of salt stress in crop plants, how it alters the physiology and morphology of the cotton crop, and breeding strategies for the development of salinity tolerance in cotton germplasm.

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Title: Differential Responses of Bacterial Communities in Rhizosphere and Bulk Soils of Cotton to Long-Term Amelioration Practices Based on Freezing Saline Water Irrigation and Plastic Mulching in a Coastal Saline Soil

Author: Xiaogai Wang, Luming Wang, Zhenhua Yu, Yinping Tian

Imprint: Agronomy 2024, 14(1), 103; <https://doi.org/10.3390/agronomy14010103>

Abstract: Soil amelioration in coastal saline areas plays an important role in alleviating land resource shortages, improving regional ecological environments, ensuring food security, and promoting economic development. Plastic mulching (M) and the combination of freezing saline water irrigation and plastic mulching (WIM) are successful amelioration practices that dramatically reduce the salinity of surface soil and facilitate plant growth in coastal saline soil. However, the bacterial responses that are closely related to these amelioration practices in coastal saline soil remain poorly understood. In this study, bacterial richness and diversity, community composition, and potential ecological functions in the rhizosphere and bulk soils of cotton in M and WIM treatments, along with a control treatment, were investigated using high-throughput sequencing in a coastal saline field. The results showed that both the M and WIM treatments increased bacterial richness and alpha diversity, which were in general significantly higher in bulk soil than in rhizosphere soil. Non-metric multidimensional scaling and the Bray–Curtis dissimilarity analysis revealed that the bacterial community in rhizosphere soil was assembled far from those in the control and bulk soils and behaved more specifically in rhizosphere soil than in bulk soil. The relative abundances of most of the dominant phyla showed opposite trends of variation in bulk and rhizosphere soils compared to those in control soil in both M and WIM treatments; in particular, the specific bacterial groups of Proteobacteria and Actinobacteria decreased in bulk soil but significantly increased in rhizosphere soil. Functional groups of chemoheterotrophy, aerobic chemoheterotrophy, and nitrate reduction were predominant in rhizosphere rather than bulk soil, according to the Functional Annotation of Prokaryotic Taxa. These findings improve the understanding of the mechanism of bacterial responses to amelioration practices M and WIM in coastal saline soils and provide valuable information for the development of amelioration techniques based on agricultural practices and soil microbiome to enhance plants' adaptability to saline soil in the future.

10

Title: Drone agrotechnology's for cotton (*Gossypium hirsutum* L.) pest and diseases management in Western of Burkina Faso.

Author: Adama ZONGO, Oumar BADINI, Emile KABORE, Adama TRAORE, Sylvestre SAWADOGO and Mahamadou SAWADOGO

Imprint: World Journal of Advanced Research and Reviews, 2023, 20(03), 1212–1222

Abstract: Drone technologies, also known as "unmanned aerial vehicles" (UAVs) or "unmanned aerial systems" (UAS), have a wide range of applications, including mapping, land-use planning, crop/infrastructure damage assessment, fertilizer spraying and precision crop protection. However, its use is still very limited in the agricultural sector in Africa in general and in Burkina Faso in particular. This study was initiated to explore the potential of UAVs for optimizing cotton yields through monitoring and phytosanitary efficiency. To this end, phytosanitary treatments and monitoring of vegetation status using multispectral drone imagery were carried out on cotton. The experimental sample consisted of four (04) cotton fields in four (04) locations. Phytosanitary treatments and aerial photography were respectively carried out using a DJI AGRAS T16 spray drone and a DJI Phantom 4 Multispectral drone. Phytosanitary treatment with DJI AGRAS T16 drone resulted in savings of 32.41% in treatment duration, 23.58% in water, 1% in pesticides and 10.5% in labor compared with manual spraying, but did not have a positive impact on boll yields due to jassid populations attack. The RGB and NDVI vegetation indices generated by photogrammetric processing of multispectral images acquired by drone enabled us to perceive phytosanitary state of cotton plants during their development cycle. Information provided by these vegetation indices and by this study in general can be used to improve the efficiency of phytosanitary treatments against cotton pests and diseases.

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Title: Population Dynamics of Sucking Insect Pest and Predator, *Chrysoperla carnea* in Transgenic Bt Cotton and Non Bt Cotton Varieties.

Author: Qadeer Ahmed Soomro, Mubasshir Sohail , Riffat Sultana , Niaz Hussain Khuhro and Raza Muhammad Memon

Imprint: Pakistan J. Zool., pp 1-6, 2023. DOI: <https://dx.doi.org/10.17582/journal.pjz/20211231101251>

Abstract: Transgenic Bt cotton, initially introduced to combat bollworm infestations, inadvertently resulted in increased populations of sucking pests such as *Thrips tabaci*, *Bemisia tabaci*, and *Amerasia devastans* in Bt cotton fields. The heavy reliance on indiscriminate pesticide application to control these pests has detrimental effects on natural fauna. This study aimed to explore the efficacy of natural enemies as an alternative to pesticides for managing sucking pests in different varieties of Bt cotton. Field experiments were conducted on various Bt cotton varieties, including Super NIAB-602, Super NIAB-992, Super NIAB-3701, Super NIAB-886, Super NIAB-142, NIABt-102, IR-443, NIA-Bt-100, IR-1513, IRNIBGE-1524, and the non-transgenic Bt variety Sadori. Population densities of *A. devastans*, *T. tabaci*, *B. tabaci*, and the predator *Chrysoperla carnea* were recorded on the upper, middle, and lower leaves of twenty plants in each group. Results revealed that Super NIAB-142 exhibited the highest population of *A. devastans* (10.00 ± 0.57), followed by NIABt (8.00 ± 0.57). Likewise, Super NIAB-602 demonstrated the highest population of *T. tabaci* (7.66 ± 0.33), with IR-1513 ranking second (6.66 ± 0.88). For *B. tabaci*, Super NIAB-142 displayed the highest population (10.00 ± 0.57), closely followed by Super NIAB-602 (8.00 ± 1.15). Conversely, Sadori exhibited the lowest populations of *A. devastans*, *T. tabaci*, and *B. tabaci*, with values of 0.33 ± 0.33 , 1.00 ± 0.57 , and 1.0 ± 0.57 , respectively. Additionally, Super NIAB-142 showcased significantly higher populations of *C. carnea* eggs, larvae, and adults (0.54 ± 0.0 , 0.44 ± 0.01 , and 0.38 ± 0.05), followed by Super NIAB-602. In contrast, Sadori displayed the lowest populations of *C. carnea* eggs, larvae, and adults (0.07 ± 0.01 , 0.16 ± 0.01 , and 0.06 ± 0.06). These findings underscore the potential of utilizing natural enemies, particularly *C. carnea*, as a viable method for managing sucking pests in transgenic Bt cotton, thereby reducing the excessive dependence on pesticides.

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Title: Cotton (*Gossypium* spp.) pest management in the era of next-generation sequencing: A review.

Author: Julie Rebecca Joseph Mathari, Habeeb Shaik Mohidee

Imprint: Journal of Applied Biology & Biotech. Published: Dec 15, 2023, I: 10.7324/JABB.2023.149697

Abstract: Cotton, as a cash crop, has huge economic importance. The high prevalence of pests, illnesses, weed pressure, the evolution of herbicide-resistant weeds, salinity, soil degradation, and climate anomalies such as droughts, floods, and heatwaves all limit cotton output around the world. Strategies like integrated pest management are employed to control the pest population across major cotton-producing countries. This method is effective as it aids in pest management and saves farmers a significant amount of money on pesticide purchases. Biotechnological advances have led to the

development of Bt crops, which underwent a series of modifications according to the needs of farmers. Pyramid Bt and the effectiveness of RNA interference technology have been highlighted here. Also advances in the field of genomics have helped us understand plant-pest interaction. The following review is an overview of advancements in the field of cotton pests' management and the role of genomics and other bioinformatics approaches to better understand the effective management of pests with the least effect on the ecosystem. There is a rising need to develop methods to achieve Sustainable Development Goals (SDGs) aimed at sustainable development. Developments in the field of cotton research for SDGs have also been discussed here.

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Title: Transcriptomic datasets of Verticillium wilt resistant and non-resistant *Gossypium barbadense* varieties during pathogen inoculation

Author: Xianpeng Xiong, Cong Sun, Bin Chen, Jie Sun, Cong Fei & Fei Xue

Imprint: Scientific Data volume 11, Article number: 11 (2024)

Abstract: Cotton is a significant cash crop and the primary source of natural fiber globally. Among the numerous diseases encountered in cotton production, Verticillium wilt is one of the most serious, caused by the pathogen *Verticillium dahliae* (*V. dahliae*). Unfortunately, there are no effective targeted methods to combat this disease. Genomic resources for Verticillium wilt resistance primarily exist in *Gossypium barbadense* (*G. barbadense*). Regrettably, there have been limited transcriptomic comparisons between *V. dahliae*-resistant and -susceptible varieties of *G. barbadense* due to the scarcity of susceptible resources. In this study, we conducted a transcriptome analysis on both *V. dahliae*-resistant and -susceptible varieties of *G. barbadense* at the 0, 12, 24 and 48 hours after *V. dahliae* inoculation. This comparative transcriptome analysis yielded high-quality data and offered new insights into the molecular mechanisms underlying cotton's resistance against this destructive pathogen.

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Title: Gene Expression in Response to Cotton Leaf Curl Virus Infection in *Gossypium Hirsutum* under Variable Environmental Conditions

Author: Iqra REHMAN, Beenish AFTAB, Muhammad BILAL SARWAR, Bushra RASHID, Qurban ALI, Muhammad Umair Majid, Sameera HASSAN, Muhammad AZAM ALI

Imprint: Genetika, Vol 49, No.3, 1115-1126.

Abstract: Cotton Leaf Curl Disease (CLCuD) is one of the threatening constrains of cotton production in Pakistan for which no adequate remedy is available until now. Local variety of *Gossypium hirsutum* (FH-142) was grown in field and infected

naturally by CLCuV under variable range of temperature and humidity. Plants showed thickening of veins in lower leaf surface at 34°C and 60% relative humidity at 15days post infection (dpi) and curling of leaf margins at 33°C with 58% relative humidity at 30dpi. Remarkable leaf darkening was observed with reduced boll formation at 45dpi at 26°C and 41% relative humidity. Enation developed, severe thickening and curling of leaves intensified and plants showed dwarf growth at 60dpi at 24°C with 52% relative humidity. PCR amplification of Rep associated gene confirmed the presence of CLCuD-associated begomovirus in the infected samples. Quantitative RT-PCR confirmed the amplification and differential expression of a number of pathogen stress responsive genes at different levels of temperature and humidity. This observation predicts that Cotton Leaf Curl Virus (CLCuV) interacts with several host genes that are upregulated to make plants susceptible or suppress other genes to overcome host defense responses.

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Title: Natural regulation of *Helicoverpa armigera* larvae by hymenopteran parasitoids in northern Cameroon: Is there scope for application of conservation biological control in cotton agroecosystems?

Author: Pierre J. Silvie, Eric Gozé, Gérard Delvare, Théodore Lawe Djague, Noé Socrates Doké

Imprint: Crop Protection, Volume 178, April 2024, 106583

Abstract: The conservation biological control (CBC) concept has been explored through research conducted in northern Cameroon on larval parasitism of *Helicoverpa armigera*, a major cotton pest, on different host plants year round, from early September 2008 to late December 2014. A total of 47,152 caterpillars were reared over the 6-year period. They were found regularly present on crops such as cotton and okra and on wild plants, including *Corynandra viscosa* and *Hyptis* spp. The overall percentages of nematode- and disease-infected caterpillars were very low (1.05% and 2.92%, respectively). Diptera species accounted for less than 0.1% of the parasitoids that had emerged from caterpillars. Total hymenopteran parasitism was 10.5%, and varied markedly depending on the host plants. Nine Hymenoptera species were identified, with *Meteorus laphygmarum* being the dominant one (almost 80% of all 2698 adult parasitoids obtained after rearing), followed by *Schoenlandella variegata* (16.42%) and *Charops spinitarsis* (<2%). Out of this total, 35%, 28% and 25% of the adults were obtained respectively on *C. viscosa*, cotton and *Hyptis* spp., i.e. < 5% on all other host plants. The analysis conducted on 237 collections showed that, after adjusting for year and month effects, a highly significant difference was found between the parasitism rates observed on the different host plant species. The plants most suitable for *H. armigera* parasitism were *Acantospermum hispidum*, *C. viscosa* and *Hyptis* spp. The proportion of *M. laphygmarum* among emerged hymenoptera was highest on *C. viscosa*, medium on cotton and *Hyptis* spp. and lowest on *L. esculentum*. Future studies that

could be carried out are outlined in the discussion with the aim of facilitating the transfer of parasitoids from caterpillars present on one plant species to those infesting cotton crops.

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Title: Microbial Influencers and Cotton Leaf Curl Disease (CLCuD) susceptibility: A network perspective.

Author: Rhea Aqueel, Ayesha Badar, Umer Zeeshan Ijaz

Imprint: Research Square, DOI: <https://doi.org/10.21203/rs.3.rs-3857920/v1>

Abstract: Biotic stresses such as plant viruses e.g. Cotton Leaf Curl Virus (CLCuV) can alter root-associated and leaf-associated microbial diversity in plants. There are complex ecological dynamics at play with each microbe contributing to multitude of biotic and abiotic interactions thus deciding the stability of the plant's ecosystem in response to disease. Deciphering these networks of interactions is a challenging task. The inferential research in microbiome is also at a nascent stage, often constrained by the underlying analytical assumptions as well as the limitations with respect to the depth of sequencing. There is also no real consensus on which network-wide statistics to identify the influential microbial players in a network. Guided by latest developments in network science, particularly, recently published metrics such as Integrated View of Influence (IVI), and some other centrality measures, in this study, we provide an exposé of the most influential nodes in the rhizospheric and phyllospheric microbial networks of the Cotton Leaf Curl Disease (CLCuD) susceptible, partially tolerant, and resistant cotton varieties.

PLANT GENETICS AND BREEDING

17

Title: Genomic and co-expression network analyses reveal candidate genes for oil accumulation based on an introgression population in Upland cotton (*Gossypium hirsutum*).

Author: Ma J , Jia B , Bian Y , Pei Wi, Song J ,Wu M , Wang W

Imprint: TAG. Theoretical and Applied genetics. Theoretische und Angewandte Genetik, 17 Jan 2024, 137(1):23, <https://doi.org/10.1007/s00122-023-04527-3>

Abstract: Integrated QTL mapping and WGCNA condense the potential gene regulatory network involved in oil accumulation. A glycosyl hydrolases gene

(GhHSD1) for oil biosynthesis was confirmed in Arabidopsis, which will provide useful knowledge to understand the functional mechanism of oil biosynthesis in cotton. Cotton is an economical source of edible oil for the food industry. The genetic mechanism that regulates oil biosynthesis in cottonseeds is essential for the genetic enhancement of oil content (OC). To explore the functional genomics of OC, this study utilized an interspecific backcross inbred line population to dissect the quantitative trait locus (QTL) interlinked with OC. In total, nine OC QTLs were identified, four of which were novel, and each QTL explained 3.62-34.73% of the phenotypic variation of OC. The comprehensive transcript profiling of developing cottonseeds revealed 3,646 core genes differentially expressed in both inbred parents. Functional enrichment analysis determined 43 genes were annotated with oil biosynthesis processes. Implementation of weighted gene co-expression network analysis showed that 803 differential genes had a significant correlation with the OC phenotype. Further integrated analysis identified seven important genes located in OC QTLs. Of which, the GhHSD1 gene located in stable QTL qOC-Dt3-1 exhibited the highest functional linkages with the other network genes. Phylogenetic analysis showed significant evolutionary differences in the HSD1 sequences between oilseed- and starch- crops. Furthermore, the overexpression of GhHSD1 in Arabidopsis yielded almost 6.78% higher seed oil. This study not only uncovers important genetic loci for oil accumulation in cottonseed, but also provides a set of new candidate genes that potentially influence the oil biosynthesis pathway in cottonseed.

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Title: Genetic Diversity and Association Analysis of Salt Tolerance in Asiatic Cotton (*Gossypium Arboreum*) With Molecular Markers.

Author: Tussipkan Dilnur, Pan Zhaoe, Gong Wenfang, Dai Panhong, Manabayeva Shuga¹, and Du Xiongming

Imprint: Eurasian Journal of Applied Biotechnology. №.4, 2023

Abstract: *Gossypium arboreum* possesses favorable characteristics that are profitable for developing elite cotton cultivars. This study analyzed genetic diversity and identifies marker-trait association analysis related to salt tolerance using SSR markers for 215 accessions of *G. arboreum*. The salt tolerance-related traits like germination rate, fresh weight, stem length, water content, chlorophyll content, electric conductivity, and MDA of the accessions were identified using 150 mM NaCl for 7 days of seedling growth. Two hundred fifteen accessions were categorized mainly into four groups based on the comprehensive index of salt tolerance. Twenty-four accessions were classified as highly tolerant to salt treatment (>2.5). The natural population was classified into 3 main groups by phylogenetic analysis. The classifications of phylogenetic analysis were largely congruent with the breeding history and ecological region. Twenty-two strong marker-trait associations were obtained with strict significant P value i.e. $P < 0.01$ and

four makers including NAU1023, NAU1099, JESPR222, and NAU2783 were significantly related to salt tolerance. The marker NAU2783 was highest associated ($P=1.98E-12$) with relative electric conductivity, and with the highest phenotype variation of 20.87%. Some markers are significantly associated with more than two traits. MUSS020 was significantly ($P<0.01$) related with relative fresh weight, and relative MDA, NAU1375 was associated with relative fresh weight and relative stem length, while NAU3468 was significantly associated with relative fresh weight, relative germination rate, and relative water content. The strong marker-trait association results might provide insights for marker-assisted selecting salt-tolerant varieties and will be useful for future cotton breeding programs.

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Title: Development of *Gossypium hirsutum*-*Gossypium raimondii* introgression lines and its usages in QTL mapping of agricultural traits

Author: Liang Wang , Nijiang Ai , Zechang Zhang , Chenhui Zhou , Guoli Feng, Sheng Cai , Ningshan Wang , Liuchun Feng

Imprint: Journal of Integrative Agriculture, Available online 14 January 2024

Abstract: *Gossypium raimondii* ($2n=2x=26$, D_5), an untapped wild species, is the putative progenitor of the D-subgenome of *G. hirsutum* ($2n=4x=52$, AD_1), an extensively cultivated species. Here, we developed a *G. hirsutum* (recipient)-*G. raimondii* (donor) introgression population to exploit favorable QTLs/genes and mapped potential quantitative trait loci (QTLs) from wild cotton species. The introgression population consists of 256 lines with an introgression rate of 52.33% of the genome *G. raimondii*. The range of introgression segment length was 0.03-19.12 Mb, with an average of 1.22 Mb. The coverage of total introgression fragments was 386.98 Mb from *G. raimondii*. Further genome-wide association analysis (Q+K+MLM) and QTL mapping (RSTEP-LRT) identified 59 common QTLs, including 14 stable QTLs and 6 common QTL (co-QTL) clusters, and one hotspot of MIC. The common QTLs for seed index showed all positive additive effects, while the common QTLs for boll weight were all negative additive effects, indicating that the linkage between seed index and boll weight could be broken. QTLs for lint percentage showed positive effect and could be beneficial for improving cotton yield. Most QTLs for fiber quality had negative additive effects, implying these QTLs were domesticated/improved in *G. hirsutum*. A few fiber quality QTLs showed positive additive effects, which could be used to improve cotton fiber quality. These introgression lines developed would be useful for molecular marker-assisted breeding and facilitate us to map QTLs precisely for mining desirable genes from the wild species *G. raimondii* to improve cultivated cotton in future via a design-breeding approach.

Title: Genetic Variability in Advance Lines of Upland Cotton For With in Boll Yield Components

Author: Sar Rauf, Muhammad Talha Shafique, Muhammad Yasir Salem, Muhammad Ans Hussain and Muhammad Mubashir Asim

Imprint: Trends in Biotechnology and Plant Sciences Volume 2, No. 1, 50-61

Abstract: Cotton (*Gossypium hirsutum* L.) is an important fiber crop all over the world as well as in Pakistan. But the production of cotton crop is low due to biotic and abiotic factors. As boll is the basic determinant for yield in cotton crop, therefore a study on within boll yield parameters was carried out using 24 cotton bulk and 2 check varieties to check their variability for within boll components. The experiment was performed in the research area of the department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The genotypes were seeded in two replications following a randomized complete block design. Data were recorded at maturity for different traits including seed cotton yield, number of seeds per boll, boll weight, seed index, lint index, seed mass per boll, lint mass per boll, GOT%, seed volume, seed density, seed surface area and fiber related traits. Data were subjected to analysis of variance to check significance among different genotypes. Genotypes were significantly different. Basic statistical values like maximum or minimum value, standard error of mean and variance were calculated. Seed cotton yield, number of seeds per boll, boll weight, seed index, lint index, seed mass per boll, GOT %, seed volume, seed density, fiber length, fiber fineness and fiber strength showed high heritability with higher genetic advance. The genotype PB-132 performed best for most of the parameters including GOT %, lint index, lint mass per seed and seed density. The findings of the current study revealed the potential of different bulks of cotton for the development of high yielding varieties. This information may be used to devise breeding strategies to enhance cotton production and variety development.

Title: Cotton variety 14r913b2xf

Inventor: ROBERT E. McGOWEN

Current Assignee: Monsanto Technology LLC

Abstract: The invention relates to the novel cotton variety designated 14R913B2XF. Provided by the invention are the seeds, plants, plant parts and derivatives of the cotton variety 14R913B2XF. Also provided by the invention are methods of using cotton variety 14R913B2XF and products derived therefrom. Still further provided by the invention are methods for producing cotton plants by crossing the cotton variety

14R913B2XF with itself or another cotton variety and plants and seeds produced by such methods.

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Title: Recent Advances in Genetic Improvement of Cotton.

Author: Kajal Verma, Pooja Sharma, Kanchan Tripathi, Reena Yadav & Surendra Pratap Singh

Imprint: Genetic Engineering of Crop Plants for Food and Health Security pp 69–99
First Online: 06 January 2024

Abstract: Cotton (*Gossypium* spp.) has an important role in the world economy because of cotton fiber. Cotton fiber is a valuable resource for the textile industry, developed from epidermal ovule cells. Among the 50 species, four (*Gossypium hirsutum*, *Gossypium barbadense*, *G. herbaceum*, and *Gossypium arboretum*) are cultivated for fiber production. Over 90% of cotton worldwide comes from Upland cotton (*Gossypium hirsutum*). The genetic improvement of cotton has been ongoing for centuries, but recent advances in genetic engineering and genomics have made this process faster and more efficient. This chapter focuses on the genetic improvement approaches adopted in enhancing cotton fiber quality and yield. Cotton has been the most exploited crop through genetic engineering tools due to the establishment of robust transformation and regeneration protocols. It also harbors the recent updates on the genetic enhancement of cotton through biotechnological interventions for biotic (pest and disease resistance) and abiotic stress (drought, climate resilience, etc.) management and cotton fiber development. It also discusses the role of epigenetics in improving the quality and yield of cotton fiber. Recent technological advances in cotton production have included CRISPR-Cas9, RNA interference (RNAi), marker-assisted selection (MAS), genomic selection, and genetically modified cotton, which have improved productivity, sustainability, and profitability. Information pertaining to the exploitation of the male sterility system in cotton is also detailed in this chapter. In a nutshell, this chapter provides an overview of the recent advancements, impact, strategies, and trends toward sustainable crop improvement of cotton through genetic modification regimes.

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Title: Global gene expression profile and functional analysis reveal the conservation of reproduction-associated gene networks in *Gossypium hirsutum*.

Author: Sarah Muniz Nardeli, Luis Willian Pacheco Arge, Sinara Artico, Stéfanie Menezes de Moura, Diogo Antonio Tschoeke, Fernanda Alves de Freitas Guedes, Maria Fatima Grossi-de-Sa, Adriana Pinheiro Martinelli & Marcio Alves-Ferreira

Imprint: Plant Reproduction , (2024)

Abstract: Cotton (*Gossypium hirsutum* L.) is the world's most extensively cultivated fiber crop. However, its reproductive development is poorly characterized at the molecular level. Thus, this study presents a detailed transcriptomic analysis of *G. hirsutum* at three different reproductive stages. We provide evidence that more than 64,000 genes are active in *G. hirsutum* during flower development, among which 94.33% have been assigned to functional terms and specific pathways. Gene set enrichment analysis (GSEA) revealed that the biological process categories of floral organ development, pollen exine formation, and stamen development were enriched among the genes expressed during the floral development of *G. hirsutum*. Furthermore, we identified putative *Arabidopsis* homologs involved in the *G. hirsutum* gene regulatory network (GRN) of pollen and flower development, including transcription factors such as *WUSCHEL* (*WUS*), *INNER NO OUTER* (*INO*), *AGAMOUS-LIKE 66* (*AGL66*), *SPOROCTELESS/NOZZLE* (*SPL/NZZ*), *DYSFUNCTIONAL TAPETUM 1* (*DYT1*), *ABORTED MICROSPORES* (*AMS*), and *ASH1-RELATED 3* (*ASHR3*), which are known crucial genes for plant reproductive success. The cotton MADS-box protein-protein interaction pattern resembles the previously described patterns for *AGAMOUS* (*AG*), *SEEDSTICK* (*STK*), *SHATTERPROOF* (*SHP*), and *SEPALLATA3* (*SEP3*) homolog proteins from *Arabidopsis*. In addition to serving as a resource for comparative flower development studies, this work highlights the changes in gene expression profiles and molecular networks underlying stages that are valuable for cotton breeding improvement.

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Title: Genetic Diversity, Population Structure, and Genome-Wide Association Study of Seven Agronomic Traits in 273 Diverse Upland Cotton Accessions.

Authors: Yajun Liang; Juyun Zheng; Junduo Wang; Zhaolong Gong; Zhiqiang Li; Ling Min; Zeliang Zhang; Zhiwei Sang; Yanying Qu; Xueyuan Li; Quanjia Chen

Imprint: Phyton (0031-9457), 2023, Vol 92, Issue 12, p3345

Abstract: Upland cotton (*Gossypium hirsutum*) is the most important plant producing natural fibers for the textile industry. In this study, we first investigated the phenotypic variation of seven agronomic traits of 273 diverse cotton accessions in the years 2017 and 2018, which were from 18 geographical regions. We found large variations among the traits in different geographical regions and only half of the traits in either years 2017 or 2018 followed a normal distribution. We then genotyped the collection with 81,612 high quality SNPs. Phylogenetic tree and population structure revealed a diverse genetic structure of the core collection, and geographical diversification was an important factor, but account for part of the variances of genetic diversification. We then performed genome-wide association study for the seven traits in the years 2017 and 2018, and the average values of each trait in the two years, respectively. We

identified a total of 19 significant marker-trait associations and found that Pollen Ole e 1 allergen/ extension could be the candidate gene associated with the fall-off cotton bolls from the last three branches. In addition, large variations were observed for the heritability of traits in the years 2017 and 2018. These results provide new potential candidate genes for further functional validation, which could be useful for genetic improvement and breeding of new cotton cultivars with better agronomic performances.

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Title: Yield and Plant Characteristics of 200 Different Cotton (*Gossypium* spp.) Genotypes.

Author: Fatih Killı , Tahsin Beycioglu

Imprint: International Journal of Scientific Engineering and Science Volume 7, Issue 12, pp. 49-56, 2023. I

Abstract– The experiment was conducted to determine the yield and plant characteristics (plant height, number of sympodial branches, boll number, seed cotton weight, 100-seed weight, seed cotton yield and seed yield,) of two-hundred different cotton (*Gossypium* spp.) genotypes in Kahramanmaras (Türkiye) conditions using a randomized complete block design with four replications in 2018 and 2019. At the end of the study, it was determined that there were statistically significant differences among the cotton genotypes for all investigated characteristics. Results of two year average showed that plant height, number of sympodial branches, boll number, seed cotton weight,, 100-seed weight, seed cotton yield and seed yield for cotton genotypes ranged between 53.10 - 110.50 cm, 4.2 - 12.0 no. plant-1 , 4.5 - 18.3 no. plant-1 , 2.0 - 6.4 g, 7.7 - 13.5 g, 1290 - 6230 kg ha⁻¹and 880 - 406 kg ha⁻¹ , respectively. As a result of the study, AzGR-11835 and NIA-UFAQ for seed cotton yield had the highest value.

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Title: Genetic Nature of Fertility Type in Cotton Hybrids.

Author: Malokhat Khalikova , Elmira Matyakubova, Turgun Uzokov, and Sayyora Soriyeva

Imprint: BIO Web of Conferences, 020 (2024) MSNBAS2023 82 31
<https://doi.org/10.1051/bioconf/20248202031>

Abstract: Studies have been conducted to evaluate the genetic potential of cotton species and to develop disease and pest resistant cotton varieties from them. The significance of the level of leaf hairiness in the representatives of the *Gossypium* L. family in tolerance to sucking pests, spider mite, aphid, was studied. Resources were obtained to measure or qualitatively assess leaf hairiness, transfer the hairiness marker

for pest tolerance into the genome of *G. hirsutum* L., and create cultivars with a combination of tolerance and economic traits. In the C2 plants of the combinations obtained by cross-breeding the wild-type ridges with twisting hairiness with the analyzer L-001 line, separation of the hairiness character was noted, its ratio was 3:1 according to the phenotype (1:2:1 according to the genotype). This separation in second-generation hybrids indicates that the feather shape trait is monogenic in nature.

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Title: Genome-wide identification and expression profiling of photosystem II (*PsbX*) gene family in upland cotton (*Gossypium hirsutum* L.).

Author: Raza Irum, Parveen Abida, Ahmad Adeel, Hu Daowu, Pan Zhaoe, Ali Imran & Du Xiongming

Imprint: Journal of Cotton Research Volume 7, article number 1, (2024)

Abstract: Photosystem II (*PSII*) constitutes an intricate assembly of protein pigments, featuring extrinsic and intrinsic polypeptides within the photosynthetic membrane. The low-molecular-weight transmembrane protein *PsbX* has been identified in *PSII*, which is associated with the oxygen-evolving complex. The expression of *PsbX* gene protein is regulated by light. *PsbX*'s central role involves the regulation of *PSII*, facilitating the binding of quinone molecules to the Qb (*PsbA*) site, and it additionally plays a crucial role in optimizing the efficiency of photosynthesis. Despite these insights, a comprehensive understanding of the *PsbX* gene's functions has remained elusive.

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Title: GhVOZ1-AVP1 module positively regulates salt tolerance in upland cotton (*Gossypium hirsutum* L.)

Author: Boying Lian, Aimin Wu, Hongmei Wu, Xiaoyan Lv, Mengxi Sun, Yiran Li, Zhengying Lu, Shiyun Li

Imprint: International Journal of Biological Macromolecules, Volume 258, Part 2, February 2024, 129116

Abstract: Vascular Plant One-zinc Finger (VOZ) transcription factor can respond to a variety of abiotic stresses, however its function in cotton and the molecular mechanisms of response to salt tolerance remained unclear. In this study, we found that *GhVOZ1* is highly expressed in stamen and stem of cotton under normal conditions. The expression of *GhVOZ1* increased significantly after 3 h of salt treatment in three-leaf staged upland cotton. Overexpressed transgenic lines of *GhVOZ1* in *Arabidopsis* and upland cotton were treated with salt stress and we found that *GhVOZ1* could respond positively to salt stress. GhVOZ1 can regulate *Arabidopsis Vacuolar Proton Pump Pyrophosphatase (H⁺-PPase) gene (AVP1)* expression through specific binding to GCGTCTAAAGTACGC site

on *GhAVP1* promoter, which was examined through Dual-luciferase assay and Electrophoretic mobility shift assay (EMSA). *AVP1* expression was significantly increased in *Arabidopsis* with *GhVOZ1* overexpression, while *GhAVP1* expression was decreased in virus induced gene silenced (VIGS) cotton plants of *GhVOZ1*. Knockdown of *GhAVP1* expression in cotton plants by VIGS showed decreased superoxide dismutase (SOD) and peroxidase (POD) activities, whereas an increased malondialdehyde (MDA) content and ultimately decreased salt tolerance. The *GhVOZ1*-*AVP1* module could maintain sodium ion homeostasis through cell ion transport and positively regulate the salt tolerance in cotton, providing new ideas and insights for the study of salt tolerance.

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Title: Molecular Genetic Phylogeny of *Gossypium* L Specimens

Author: Abrorjon Kurbonov , Feruza Mamedova, and Viktor Avtonomov

Imprint: BIO Web of Conferences, 010 (2024) MSNBAS2023 82 13
<https://doi.org/10.1051/bioconf/20248201013>

Abstract: In the article, the phylogenetic tree of kinship of unique samples created at the Scientific Research Institute of Cotton Selection, Seeding and Cultivation Agrotechnologies and stored in the collection was compiled using molecular markers. 185 primer pairs from TMB, JESPR, GH, NAU, BNL and CIR collections were used, 45 of which turned out to be polymorphic, which allowed to identify 96 polymorphic loci, 20 of which were unique. Phylogenetic analysis of cotton samples based on genotyping using SSR markers divided the samples into 5 different groups. Namangan-34 and Namangan-102 varieties were the most distant from the remaining samples, and these varieties did not differ from each other. Varieties L-175_276 and C-4727 also formed a separate cluster, sample 13 and Sultan variety are related and also form a separate cluster, sample 4 and variety C-7934 also belong. The remaining 29 samples were not significantly different from each other and formed a large cluster, which is called their narrow genetic base.

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Title: Phosphatidic acid interacts with an HD-ZIP transcription factor GhHOX4 to influence its function in fiber elongation of cotton (*Gossypium hirsutum*).

Author: Wang NN , Ni P , Wei YL , Hu R , Li Y , Li XB

Imprint: The Plant Journal for Cell and Molecular Biology, 07 Jan 2024, <https://doi.org/10.1111/tpj.16616> PMID: 38184843

Abstract: Upland cotton, the mainly cultivated cotton species in the world, provides over 90% of natural raw materials (fibers) for the textile industry. The development of cotton fibers that are unicellular and highly elongated trichomes on seeds is a delicate and complex process. However, the regulatory mechanism of fiber development is still largely unclear in detail. In this study, we report that a homeodomain-leucine zipper (HD-ZIP) IV transcription factor, GhHOX4, plays an important role in fiber elongation. Overexpression of GhHOX4 in cotton resulted in longer fibers, while GhHOX4-silenced transgenic cotton displayed a "shorter fiber" phenotype compared with wild type. GhHOX4 directly activates two target genes, GhEXLB1D and GhXTH2D, for promoting fiber elongation. On the other hand, phosphatidic acid (PA), which is associated with cell signaling and metabolism, interacts with GhHOX4 to hinder fiber elongation. The basic amino acids KR-R-R in START domain of GhHOX4 protein are essential for its binding to PA that could alter the nuclear localization of GhHOX4 protein, thereby suppressing the transcriptional regulation of GhHOX4 to downstream genes in the transition from fiber elongation to secondary cell wall (SCW) thickening during fiber development. Thus, our data revealed that GhHOX4 positively regulates fiber elongation, while PA may function in the phase transition from fiber elongation to SCW formation by negatively modulating GhHOX4 in cotton.

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Title: Genome-wide identification of the key Kinesin genes during fiber and boll development in upland cotton (*Gossypium hirsutum* L)

Author: Hong Zhu, Jianzhong Xu, Kanbing Yu, Jianfei Wu, Huifang Xu, Shubin Wang & Tianwang Wen

Imprint: Molecular Genetics & Genomics Volume 299, article number 2, (2024)

Abstract: Kinesin is a kind of motor protein, which interacts with microtubule filaments and regulates cellulose synthesis. Cotton fiber is a natural model for studying the

cellular development and cellulose synthesis. Therefore, a systematic research of Kinesin gene family in cotton (*Gossypium* spp.) will be beneficial for both understanding the function of Kinesin protein and assisting the fiber improvement. Here, we aimed to identify the key Kinesin genes present in cotton by combining genome-wide expression profile data, association mapping, and public quantitative trait loci (QTLs) in upland cotton (*Gossypium hirsutum* L.). Results showed that 159 Kinesin genes, including 15 genes of the Kinesin-13 gene subfamily, were identified in upland cotton; of which 157 Kinesin genes can be traced back to the diploid ancestors, *G. raimondii* and *G. arboreum*. Using a combined analysis of public QTLs and genome-wide expression profile information, there were 29 QTLs co-localized together with 28 Kinesin genes in upland cotton, including 10 Kinesin-13 subfamily genes. Genome-wide expression profile data indicated that, among the 28 co-localized genes, seven Kinesin genes were predominantly expressed in fibers or ovules. By association mapping analysis, 30 Kinesin genes were significantly associated with three fiber traits, among which a Kinesin-13 gene, *Ghir_A11G028430*, was found to be associated with both cotton boll length and lint weight, and one *Kinesin-7* gene, *Ghir_D04G017880* (*Gh_Kinesin7*), was significantly associated with fiber strength. In addition, two missense mutations were identified in the motor domain of the Gh_Kinesin7 protein. Overall, the Kinesin gene family seemingly plays an important role in cotton fiber and boll development. The exploited Kinesin genes will be beneficial for the genetic improvement of fiber quality and yield.

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Title: Synergistic interplay of redox homeostasis and polysaccharide synthesis promotes cotton fiber elongation

Author: Xuehan Tian , Mengyuan Ji , Jiaqi You , Yuqi Zhang , Keith Lindsey , Xianlong Zhang , Lili Tu

Imprint: The Plant Journal (2023) doi: 10.1111/tpj.16615

Abstract: Cell polarity is the foundation of cell development and tissue morphogenesis. The investigation of polarized growth provides opportunities to gain profound insights into morphogenesis and tissue functionality in organisms. Currently, there are still many mysteries surrounding the mechanisms that regulate polarized cell growth. Cotton fiber cells serve as an excellent model for studying polarized growth, and provide important clues for unraveling the molecular mechanisms, signaling pathways, and regulatory networks of polarized growth. In this study, we characterized two functional genes, GhMDHAR1AT/DT and GhDHAR2AT/DT with predominant expression during fiber elongation. Loss of function of both genes contributed to a significant increase in fiber length. Transcriptomic data revealed up-regulated expression of antioxidant genes in CRISPR mutant lines, along with delayed expression of secondary wall-related genes and temporally prolonged expression of primary wall-

related genes. Experimental evidence demonstrated that the increase in GSH content and glutathione peroxidase (GPX) enzyme activity led to enhanced total antioxidant capacity (T-AOC), resulting in reduced H₂O₂ levels, which contributed to the extension of fiber elongation stage in CRISPR mutant lines. Moreover, the increased polysaccharide synthesis in CRISPR mutant lines was found to provide an abundant supply of raw materials for fiber cell wall elongation, suggesting that synergistic interplay between redox homeostasis and polysaccharide synthesis in fiber cells may facilitate cell wall remodeling and fiber elongation. This study provides valuable insights for deciphering the mechanisms of cell polarized growth and improving cotton fiber quality.

PLANT BIOTECHNOLOGY

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Title: HLS1 promotes apical hook formation by regulating YUCCA8 and GH3.17 expression differently in the inner and outer side of the hook in cotton.

Author: Xiangqiang Kong, Jingyuan Zhou, Xue Li, Cuimei Liu, Jinfang Chu, Hui Zhang, Hezhong Dong

Imprint: Physiologia Plantarum First published: 03 January 2024, <https://doi.org/10.1111/ppl.14148>

Abstract: *HOOKLESS1 (HLS1)* plays an indispensable role in apical hook development by promoting asymmetric auxin distribution in the hook. However, the precise mechanisms by which *HLS1* regulates the differential gene expression in the inner and outer sides of the apical hook to promote this asymmetric auxin distribution remains unknown. The inner and outer sides of the cotton apical hook were separated for gene sequencing to search for differently expressed auxin-related genes. Then, the *GhYUCCA8* and *GhGH3.17* genes, which are highly expressed in the inner and outer side, respectively, as well as *GhHLS1*, were silenced by the SSA-VIGS method to study their interaction and function on auxin asymmetric distribution and hook formation. The hook formation was inhibited in the VIGS-*GhHLS1*, VIGS-*GhYUCCA8* and VIGS-*GhGH3.17* seedlings. Silencing *GhHLS1* decreased the expression of *GhYUCCA8* on the inner side but increased the expression of *GhGH3.17* on the outer side of the apical hook, which weakened the auxin asymmetric distribution in the hook. Our results indicated that the high expression of *GhHLS1* in the inner side caused high expression of *GhYUCCA8* and *GhGH3.17* in the inner and outer side of the apical hook, respectively,

which caused the gradient of free auxin between the inner and outer side and ultimately promoted apical hook formation.

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Title: Enhancement of Yield and Quality of Cotton (*Gossypium Hirsutum* L.) through Different Molecular Markers

Author: ABBAS A, REHMAN AU, ARSHAD A, RAZA GM, UMAR M, BUKHARI MS

Imprint: J. Phys. Biomed. Biol. Sci., Volume, 3: 19

Abstract: Cotton (*Gossypium hirsutum* L.) is a member of the Malvaceae family and the *Gossypium* genus, which contains 50 different species. Only four of these species, however, are commercially farmed. This study aims to evaluate the genetic diversity of wild and cultivated cotton gene pools, as well as QTL mapping and marker-assisted selection activities in cotton genetics. Various marker-based approaches, including RAPD, ISSR, AFLP, SSR, and SNP analysis, have been used to investigate genetic diversity, genotype correlations, and map saturation in cotton. These technologies have also assisted genome-wide association studies (GWAS) and the finding of quantitative trait loci (QTLs). Furthermore, novel approaches such as linkage disequilibrium, association mapping, and genomic selection are applied to classic ideas such as genetic variation, QTL mapping, and marker-assisted selection (MAS). These genomic technologies can boost cotton productivity and meet global demand for high-yielding, high-quality cotton fiber by incorporating additional omics resources.

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Title: Identification and characterization of circular RNAs involved in the fertility stability of cotton CMS-D2 restorer line under heat stress.

Author: Ruijie Wang, Meng Zhang, Hui Wang, Liangliang Chen, Xuexian Zhang, Liping Guo, Tingxiang Qi, Huini Tang, Kashif Shahzad, Hailin Wang,

Imprint: BMC Plant Biology volume 24, Article number: 32 (2024)

Abstract: Background- As a vital type of noncoding RNAs, circular RNAs (circRNAs) play important roles in plant growth and development and stress response. However, little is known about the biological roles of circRNAs in regulating the stability of male fertility restoration for cytoplasmic male sterility (CMS) conditioned by *Gossypium harknessii* cytoplasm (CMS-D2) cotton under high-temperature (HT) stress.

Results: In this study, RNA-sequencing and bioinformatics analysis were performed on pollen grains of isonuclear alloplasmic near-isogenic restorer lines NH [N (Rf₁rf₁)] and SH [S(Rf₁rf₁)] with obvious differences in fertility stability under HT stress at two environments. A total of 967 circRNAs were identified, with 250 differentially expressed

under HT stress. We confirmed the back-splicing sites of eight selected circRNAs using divergent primers and Sanger sequencing. Tissue-specific expression patterns of five differentially expressed circRNAs (DECs) were also verified by RT-PCR and qRT-PCR. Functional enrichment and metabolic pathway analysis revealed that the parental genes of DECs were significantly enriched in fertility-related biological processes such as pollen tube guidance and cell wall organization, as well as the Pentose and glucuronate interconversions, Steroid biosynthesis, and N-Glycan biosynthesis pathways. Moreover, we also constructed a putative circRNA-mediated competing endogenous RNA (ceRNA) network consisting of 21 DECs, eight predicted circRNA-binding miRNAs, and their corresponding 22 mRNA targets, especially the two ceRNA modules circRNA346-miR159a-MYB33 and circRNA484-miR319e-MYB33, which might play important biological roles in regulating pollen fertility stability of cotton CMS-D2 restorer line under HT stress.

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Title: Molecular-genetic and cytogenetic analyses of cotton chromosome introgression from *Gossypium barbadense* L. into the genome of *G. hirsutum* L. in BC2F1 hybrids

Author: M.F. Sanamyan, Sh.U. Bobokhujayev, Sh.S. Abdukarimov, O.G. Silkova

Imprint: PLANT GENETICS Original article Вавиловский журнал генетики и селекции. 2023;27(8):958-970 DOI 10.18699/VJGB-23-110

Abstract: Substitution lines of the cotton *Gossypium hirsutum* L. involving chromosomes of the tetraploid species *G. barbadense* L., *G. tomentosum* Nutt. ex Seem., and *G. mustelinum* Miers ex Watt. are a valuable source for breeding, increasing the genetic diversity of *G. hirsutum*. The substitution of certain *G. hirsutum* L. chromosomes with *G. barbadense* chromosomes affect fibre elongation, fibre yield, fibre strength, and micronaire. To increase the efficiency of creating lines, it is necessary to study the nature of the introgression of alien chromosomes into the *G. hirsutum* L. genome. As a result of molecular genetic analysis of BC2F1 hybrids obtained from crossing monosomic lines of the cotton *G. hirsutum* from the cytogenetic collection of Uzbekistan with monosomic backcross hybrids BC1F1 *G. hirsutum* × *G. barbadense* on the same chromosomes, genetic differences between the hybrids in the profile of chromosome-specific microsatellite SSR markers were found. The predominant introgression of chromosomes 4, 6 and 12 of the At -subgenome and 22 of the Dt -subgenome of *G. barbadense* was revealed, while chromosomes 2 and 7 of the At -subgenome and 18 of the Dt -subgenome of *G. barbadense* were characterized by elimination. Among them, chromosomes 7 of the At -subgenome and 18 of the Dt -subgenome of *G. barbadense* were eliminated in the first backcross generation. In this work, two lines, CS-B06 and CS-B07, from the American cytogenetic collection with a putative substitution involving chromosomes 6 and 7 of the At -subgenome were analysed. The presence of only

polymorphic alleles from the species *G. hirsutum* and the absence of polymorphic alleles from the species *G. barbadense* were revealed, which showed the absence of substitution involving these chromosomes. BC2F1 hybrids with monosomy for both *G. barbadense* and *G. hirsutum* chromosomes were characterized by regular pairing of chromosomes and high meiotic indexes. However, many hybrids were characterized by a decrease in pollen fertility. Two hybrids with monosomy for chromosome 7 of the At -subgenome of *G. hirsutum* and chromosome 6 of the At -subgenome of *G. barbadense* had the greatest reduction in pollen viability (70.09 ± 1.57 and 75.00 ± 1.66 %, respectively). Thus, this work shows a specific feature in the introgression of individual chromosomes of the cotton species *G. barbadense* into the cotton *G. hirsutum* genome.

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Title: The *EIN3/EIL-ERF9-HAK5* transcriptional cascade positively regulates high-affinity K⁺ uptake in *Gossypium hirsutum*.

Author: Shuang Xiao, Doudou Yang, Fangjun Li, Xiaoli Tian, Zhaohu Li

Imprint: New Phytologist, First published: 02 January 2024, <https://doi.org/10.1111/nph.19500>

Abstract: High-affinity K⁺ (HAK) transporters play essential roles in facilitating root K⁺ uptake in higher plants. Our previous studies revealed that GhHAK5a, a member of the HAK family, is crucial for K⁺ uptake in upland cotton. Nevertheless, the precise regulatory mechanism governing the expression of *GhHAK5a* remains unclear. The yeast one-hybrid screening was performed to identify the transcription factors responsible for regulating *GhHAK5a*, and ethylene response factor 9 (GhERF9) was identified as a potential candidate. Subsequent dual-luciferase and electrophoretic mobility shift assays confirmed that GhERF9 binds directly to the *GhHAK5a* promoter, thereby activating its expression. Silencing of *GhERF9* decreased the expression of *GhHAK5a* and exacerbated K⁺ deficiency symptoms in leaves, also decreased K⁺ uptake rate and K⁺ content in roots. Additionally, it was observed that the application of ethephon (an ethylene-releasing reagent) resulted in a significant upregulation of *GhERF9* and *GhHAK5a*, accompanied by an increased rate of K⁺ uptake. Expectedly, GhEIN3b and GhEIL3c, the two key components involved in ethylene signaling, bind directly to the *GhERF9* promoter. These findings provide valuable insights into the molecular mechanisms underlying the expression of *GhHAK5a* and ethylene-mediated K⁺ uptake and suggest a potential strategy to genetically enhance cotton K⁺ uptake by exploiting the *EIN3/EILs-ERF9-HAK5* module.

Title: A novel single nucleotide mutation of TFL1 alters the plant architecture of *Gossypium arboreum* through changing the pre-mRNA splicing.

Author: Ji Liu, Pengfei Miao, Wenqiang Qin, Wei Hu, Zhenzhen Wei, Wusi Ding, Huan Zhang & Zhi Wang

Imprint: Plant Cell Reports, Volume 43, article number 26, (2024)

Abstract: Growth habit is an important agronomic trait that plays a decisive role in the plant architecture and crop yield. Cotton (*Gossypium*) tends to indeterminate growth, which is unsuitable for the once-over mechanical harvest system. Here, we identified a determinate growth mutant (*dt1*) in *Gossypium arboreum* by EMS mutagenesis, in which the main axis was terminated with the shoot apical meristem (SAM) converted into flowers. The map-based cloning of the *dt1* locus showed a single nucleotide mutation from G to A at the 201st positions in *TERMINAL FLOWER 1* (*GaTFL1*), which changed the alternative RNA 5' splice site and resulted in 31 amino acids deletion and loss of function of *GaTFL1*. Comparative transcriptomic RNA-Seq analysis identified many transporters responsible for the phytohormones, auxin, sugar, and flavonoids, which may function downstream of *GaTFL1* to involve the plant architecture regulation. These findings indicate a novel alternative splicing mechanism involved in the post-transcriptional modification and *TFL1* may function upstream of the auxin and sugar pathways through mediating their transport to determine the SAM fate and coordinate the vegetative and reproductive development from the SAM of the plant, which provides clues for the *TFL1* mechanism in plant development regulation and provide research strategies for plant architecture improvement.

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Title: Transcriptional patterns and histone modification signatures reveal dehydration memory behaviour in seedlings of *Gossypium hirsutum*.

Author: Shibin He, Penghui Zhang, Yuehua Wang, Rui Zheng, Yaqian Li, Hui Cheng

Imprint: Environmental and Experimental Botany, Available online 19 January 2024, 105663

Abstract: In nature, plants often experience recurring stress conditions. Some plants have evolved a memory response, which shows an enhanced reaction upon subsequent stress. However, whether cotton (*Gossypium hirsutum* L.) exhibits dehydration stress memory and the underlying mechanisms have remained unclear. Here, we characterized the responses to recurring dehydration stress in cotton seedlings from physiological changes, gene expression patterns and histone modification levels. Our results showed that short-term dehydration stress memory could develop in cotton seedlings. Transcriptome analysis identified 602 transcriptional dehydration memory genes (DMGs), and these genes could be divided into four distinct response patterns. A homology analysis indicated that conservation and species-specific memory responses existed between cotton and other plants. Chromatin immunoprecipitation - qPCR results revealed that the transcriptional behaviour of [+ / +] memory genes was related to the retention of increased H3K4me3 levels during the recovery stage and that H3K4me3 could act as a memory mark at the [+ / +] dehydration memory genes in cotton. A virus-induced gene silencing assay indicated that the histone demethylase gene *GhJM17-A/D* may participate in the transcriptional behaviour of [+ / +] memory genes in cotton. These results will improve the understanding of the mechanisms of formation and maintenance of dehydration stress memory in plants and will be useful for the improvement of cotton and other crops.

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Title: Seed lipid composition as a breeding target to improve cold germination ability in upland cotton (*Gossypium hirsutum*).

Author: Lakhvir Kaur

Imprint: A Dissertation In Plant and Soil Science Submitted to the Graduate Faculty of Texas Tech University in Partial Fulfillment of the Requirements for the Degree of DOCTOR OF PHILOSOPHY, December, 2023

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Title: Unsaturated fatty acids improve germination of upland cotton (*Gossypium hirsutum*) under cold stress

Author: LAKHVIR KAUR, Junghyun Shim, Dick Auld, Rosalyn B. Angeles-Shim

Imprint: Front. Plant Sci., Sec. Plant Abiotic Stress, Volume 15 - 2024 | doi: 10.3389/fpls.2024.1286908

Abstract: The level of fatty acid unsaturation in seeds is one of the major determinants of cold germination ability, particularly in oilseeds. The presence of cis double bonds in unsaturated fatty acids creates bends that lowers their melting temperatures compared to saturated fatty acids. Unsaturated fatty acids with low melting points mobilize faster at low temperatures providing seeds with sufficient energy for germination. To investigate the effects of fatty acid unsaturation on the ability of cotton seeds to germinate under cold conditions, four recombinant inbred lines (RILs) of cotton with unique fatty acid profiles were evaluated using a set of developmental and biochemical assays at 12°C (critically low temperature), 15°C (cardinal minimum temperature) and 30°C (optimum temperature). The RILs with higher unsaturation/saturation ratios registered robust germination performance, lower solute leakage, and optimum water uptake rates under cold stress. Imbibition at 30°C for 8 hours before cold exposure significantly improved the germination of cold sensitive genotypes, indicating that the first few hours of water uptake are critical for cold stress. Whole seed lipidome profiling of all the genotypes specifically associated cold germination ability with higher unsaturation levels of phospholipids during early imbibition. The presence of cis double bonds in phospholipids creates kinks that maintain the fluidity of cell membranes under low temperature. Membrane flexibility under cold conditions is essential for facilitating key germination events including membrane organization and respiration. The current results highlight the importance of fatty acid composition in cold germination ability of upland cotton.

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Title: Improving Cotton Cool Test Result Consistency Within and Among Laboratories.

Author: Miranda Smidt, Tim Gutormson, Lauren Shearer

Imprint: SoDak Labs November 22, 2023

Abstract: The cotton cool test is an established vigor test in the Seed Vigor Testing Handbook (Association of Official Seed Analysts, 2009) that has been used in seed testing for over 60 years. Typically, seeds are placed in an inner chamber (a plastic bag) enclosing vertically positioned rolled towels or acrylic “crisper” boxes with horizontally positioned rolled towels. If the temperature inside the inner chamber begins to exceed 18°C as set by the outer chamber, then the seeds accumulate more growing degree days

(heat units) in the seven-day test duration. Standardization of an outer chamber that maintains $18^{\circ}\text{C} \pm 0.5^{\circ}\text{C}$ has been achieved; however, temperature control in the inner chamber has yet to be refined and could be a significant source of error among laboratories. Evaluation of seedlings states that a normal is considered any seedling having a combined hypocotyl and root length of 4 cm or greater, emphasizing the importance of temperature maintenance for consistent growth. Inconsistencies in cotton cool test results have been known for years, and this study's objectives are: 1) to better understand "seed" and "experimental" sources of variation; 2) to compare the "outer" and "inner" chamber model used for Accelerated Aging test for relevance to the Cool Test standardization; and 3) implement the measurement of Growing Degree Days (GDDs) as an additional tool to evaluate the uniformity of laboratory inner and outer chambers regimes during the seven day 18°C test period and compare accumulated GDDs to average germination result responses. The overall study goal is to minimize the experimental error contribution to test result variation among laboratories to provide the cotton seed end user more consistent quality data.

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Title: Rheology of Cottonseed (*Gossypium hirsutum*) oil Used as Biodegradable Lubricant.

Author: Ioana Stanciu

Imprint: Orient. J. Chem., Vol. 39(6), 1696-1699 (2023)

Abstract: Vegetable oils are often associated with well-known varieties like sunflower, olive, and corn. However, there are lesser-known options worth exploring to appreciate their distinct qualities. One such overlooked oil is cottonseed oil, derived from the Malvaceae cotton family plant. In a recent study, we delved into the rheological behavior of cottonseed oil. Similar to many vegetable oils, it exhibits a non-Newtonian behavior, making it a viable alternative to mineral oils. The rheological analysis was conducted using the Brookfield RVDV III Ultra Rheometer, with shear rates incrementally increasing.

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Title: Crossing and Setting of Hybrid Seeds in the Creation of Chromosome-Substituted Cotton Lines g. *Hirsutum* l.

Author: Marina Sanamyan , and Shukhrat Bobokhujayev

Imprint: BIO Web of Conferences, 020 (2024) MSNBAS2023 82 34
<https://doi.org/10.1051/bioconf/20248202034>

Abstract: A comparative study of the indicators of crossability and setting of hybrid and backcross seeds F1, F1BC1, F1BC2, obtained from crossings of monosomic and

monotelodisomic lines of cotton *G.hirsutum* L. with the donor line Pima 3-79 of the species *G.barbadense* L. and aneuploid backcross hybrids, was found to be a linear decrease of these indicators in some hybrids, as well as their increase, as well as the alternation of indicators of crossability and setting in different hybrid generations. The study of chromosome conjugation in hybrid monosomic F1 obtained from crossing monosomic lines with the donor line Pima 3-79 of the species *G. barbadense* L., as well as backcross monosomic F1BC1, F1BC2 with the replacement of specific chromosomes of the cotton genome, revealed normal chromosome conjugation with the formation of 25 bivalents and one univalent of different size in all studied PMCs in most hybrids. Key words: crossability, hybrid seed setting, monosomic lines, backcrossing, chromosome conjugation, cotton, *G.hirsutum* L.