

Agronomy, Soil Science and Plant Physiology

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Title: The morphological diversity of pollen in the genus *Gossypium*

Author: CAI Xiaoyan, HOU Yuqing, MUHAMMAD Umer Jawad

Imprint: Journal of Cotton Research volume 6, Article number: 6 (2023)

Abstract: Plant pollen has diverse morphological characteristics that can be consistently passed down from generation to generation. Information on pollen morphology is thus immensely important for plant classification and identification. In the genus *Gossypium*, however, in-depth research on pollen morphology is lacking, with only few reports on limited cotton species. To evaluate the diversity of pollen in *Gossypium*, we therefore conducted a comprehensive analysis of the pollen morphology of 33 cotton species and varieties using scanning electron microscopy.

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Title: Mineral-Solubilizing Bacteria-Mediated Enzymatic Regulation and Nutrient Acquisition Benefit Cotton's (*Gossypium hirsutum* L.) Vegetative and Reproductive Growth

Author: Iqra Ahmad, Maqshoof Ahmad

Imprint: Microorganisms 2023, 11(4), 861; <https://doi.org/10.3390/microorganisms11040861>

Abstract: Many farmers' incomes in developing countries depend on the cultivation of major crops grown in arid and semi-arid regions. The agricultural productivity of arid and semi-arid areas primarily relies on chemical fertilizers. The effectiveness of chemical fertilizers needs to improve by integration with other sources of nutrients. Plant growth-promoting bacteria can solubilize nutrients, increase plant nutrient uptake, and supplement chemical fertilizers. A pot experiment evaluated the promising plant growth-promoting bacterial strain's effectiveness in promoting cotton growth, antioxidant enzymes, yield, and nutrient uptake. Two phosphate solubilizing bacterial strains (*Bacillus subtilis* IA6 and *Paenibacillus polymyxa* IA7) and two zinc solubilizing bacterial strains (*Bacillus* sp. IA7 and *Bacillus aryabhatai* IA20) were coated on cotton seeds in a single as well as co-inoculation treatments. These treatments were compared with uninoculated controls in the presence and absence of recommended chemical fertilizer doses. The results showed the co-inoculation combination of *Paenibacillus polymyxa* IA7 and *Bacillus aryabhatai* IA20 significantly increased the number of bolls, seed cotton yield, lint yield, and antioxidants activities, including superoxide

dismutase, guaiacol peroxidase, catalase, and peroxidase. Co-inoculation combination of *Bacillus subtilis* IA6 and *Bacillus* sp. IA16 promoted growth attributes, including shoot length, root length, shoot fresh weight, and root fresh weight. This co-inoculation combination also increased soil nutrient content. At the same time, *Paenibacillus polymyxa* IA7 + *Bacillus aryabhatai* IA20 increased nutrient uptake by plant shoots and roots compared.

3

Title: Fruiting patterns impact carbon accumulation dynamics in cotton

Author : Lorraine B. Pabuayan , James P. Bordovsky , Katie L. Lewis, Glen L. Ritchie

Imprint: Field Crops Research, Volume 295, 1 May 2023, 108892

Abstract: Cotton (*Gossypium spp.*) boll distribution captures important aspects of fruit development and adaptation over a long period of time. However, due to its complex fruiting habit, it is possible that the boll distribution patterns may not accurately identify the level of sink strength with respect to fruiting locations. Plant and box mapping data collected from producer fields in Georgia in 2009 (Burke and Colquitt, 5 cultivars) and from experimental fields in Texas from 2011 to 2013 (Halfway and Lubbock, 18 cultivars) were analyzed to determine the actual level of carbon sink strengths with respect to the center of mass end-of-season and to gain a better understanding of the regulation of carbon accumulation within a plant. Results showed that the end-of-season boll distribution obscures the level of sink strength in the middle of the plant. The node cohort-center of sink strength was determined to be above the node cohort-center of mass end-of-season when cotton plants were grown under a high-yielding and indeterminate growing condition. On the other hand, the node cohort-center of sink strength was located below the node cohort-center of mass under a determinate situation and low-yielding environment. This difference in the level of sink strength may have been a low risk-taking strategy by the plant to survive under a limiting-environment by partitioning resources toward early-produced fruit at the expense of later-produced fruit. These carbon accumulation dynamics quantify the propensity of cotton plants to shift production toward a conservative strategy of earlier fruiting under conditions that encourage determinate growth and toward additional risk when growing conditions favor growth, relative to the final boll distribution.

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Title: Genetic regulation of nitrogen use efficiency in *Gossypium* spp.

Author: Ninkuu V, Liu Z, Sun X

Imprint: Plant, Cell & Environment, 20 Mar 2023, DOI: [10.1111/pce.14586](https://doi.org/10.1111/pce.14586)

Abstract: Cotton (*Gossypium* spp.) is the most important fibre crop, with desirable characteristics preferred for textile production. Cotton fibre output relies heavily on nitrate as the most important source of inorganic nitrogen (N). However, nitrogen dynamics in extreme environments limit plant growth and lead to yield loss and pollution. Therefore, nitrogen use efficiency (NUE), which involves the utilisation of the 'right rate', 'right source', 'right time', and 'right place' (4Rs), is key for efficient N management. Recent omics techniques have genetically improved NUE in crops. We herein highlight the mechanisms of N uptake and assimilation in the vegetative and reproductive branches of the cotton plant while considering the known and unknown regulatory factors. The phylogenetic relationships among N transporters in four *Gossypium* spp. have been reviewed. Further, the N regulatory genes that participate in xylem transport and phloem loading are also discussed. In addition, the functions of microRNAs and transcription factors in modulating the expression of target N regulatory genes are highlighted. Overall, this review provides a detailed perspective on the complex N regulatory mechanism in cotton, which would accelerate the research toward improving NUE in crops.

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Title: The cotton pectin methyl esterase gene GhPME21 functions in microspore development and fertility in *Gossypium hirsutum* L.

Author: Yihan Xu, Yanhua Jiang, Junye Jiao, Hongli Zheng,

Imprint: Plant Molecular Biology (2023)

Abstract: Pectin widely exists in higher plants' cell walls and intercellular space of higher plants and plays an indispensable role in plant growth and development. We identified 55 differentially expressed genes related to pectin degradation by transcriptomic analysis in the male sterile mutant, ms1. A gene encoding pectin methylesterase (GhPME21) was found to be predominantly expressed in the developing stamens of cotton but was significantly down-regulated in ms1 stamens. The tapetal layer of GhPME21 interfered lines (GhPME21i) was significantly thickened compared to that of WT at the early stage; anther compartment morphology of GhPME21i lines was abnormal, and the microspore wall was broken at the middle stage; Alexander staining showed that the pollen grains of GhPME21i lines differed greatly in volume at the late stage. The mature pollen surfaces of GhPME21i lines were deposited with discontinuous and broken sheets and prickles viewed under SEM. Fewer pollen tubes

were observed to germinate in vitro in GhPME21i lines, while tiny of those in vivo were found to elongate to the ovary. The seeds harvested from GhPME21i lines as pollination donors were dry and hollow. The changes of phenotypes in GhPME21i lines at various stages illustrated that the GhPME21 gene played a vital role in the development of cotton stamens and controlled plant fertility by affecting stamen development, pollen germination, and pollen tube elongation. The findings of this study laid the groundwork for further research into the molecular mechanisms of PME's involved in microspore formation and the creation of cotton male sterility materials.

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Title: Research Cotton Mechanisation in Asian Countries

Author: Israilov Sardorbek Sandjarovich

Imprint: International Journal of Biological Engineering and Agriculture Volume 2, No 3 | Mar - 2023

Abstract: Cotton Harvesters has proven to be a promising approach for cotton harvesting in India and developing countries. However challenges still remain in its implementation in India though considerable progress has been made in recent years. Developed countries have 100% mechanized cotton picking. With increasing labor charges and its unavailability, mechanization has gained pace in Indian agriculture sector. This review paper provides an overview of cotton harvesters and its various types. It also covers the anatomy of cotton plant, production, and its importance in Indian economy. Indian cropping pattern are studied in detail and various mechanism discussed and their pros and cons are evaluated in this paper.

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Title: Potassium Losses in Runoff from Cotton Production Fields.

Author: M. B. Daniels, M. Fryer, S. B. Fernandes, N. A. Slaton, A.N. Sharpley, P. Webb, L. Riley, J. Burke, L. G. Berry, T. Roberts, B. Robertson

Imprint: Agronomy Journal <https://doi.org/10.1002/agj2.21335>

Abstract: K loss in runoff represents a potential financial concern since fertilizer-K is routinely applied to sustain optimal crop K nutrition and yield potential. Our research objectives were to quantify and characterize the soluble-K loss in runoff from fields used for continuous cotton (*Gossypium hirsutum* L.) production while determining if time of year (growing season vs non growing season, type of hydrological event (irrigation vs rainfall) and cover crops influence K loss in runoff. Field-scale, edge-of-field monitoring of runoff water and its soluble-K concentration was performed on 10

site years in southeastern Arkansas across three production seasons. The mean K loss in surface runoff per event was 0.98 kg ha⁻¹ across all sites and events (n = 304). The relationship between loss of K mass to runoff volume was positive and significantly correlated (P<0.0001) when both variables were transformed by the natural logarithm. K loss during the growing season was significantly higher (P<0.001) in the cotton growing season whereas K loss resulting from runoff events generated irrigation or rainfall was not significant. Additionally, losses from fields with cover crops were significantly larger (P<0.05) than from fields without covers. Cumulative annual-K loss, between annual fertilizer-K applications, averaged 32.2 kg K ha⁻¹ across all site-years representing a significant economic loss to replace the lost K with fertilizer. This study illustrates the increased risk of K losses on poorly drained soils in the Southeastern United States. Runoff-K loss represents a significant amount of K that requires additional research on how to mitigate these losses.

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Title: Revisiting the Culture of Cotton in the Past: Historical Cultivation Practices, Farmers Decision Making, Intensification of Production.

Author: Ray, A

Imprint: South Asian History, Culture and Archaeology, 2: 2, pp. 229-242

Abstract: The cultivation of cotton and production of cotton textiles have been a well-entrenched culture and it has supported the economy of the Indian subcontinent since historic times. The subcontinent attained excellence in textile production relying on high-quality and decentralized cotton production, elegant workmanship, efficient and locally-evolved tools, and intergenerational knowledge of dyeing, stitching, and printing. The glory began to fade with the introduction of exotic species and the saga of decline continued thereafter. Here, I revisited the historic cotton cultivation that fed the production of diverse cotton textiles catering to local and global consumers. It revealed a broad range of local varieties grown almost throughout the country in a range of agro-ecosystems. The different quality of cotton supplied the raw material to manufacture very simple, coarse to elegant and extravagant textiles of myriad kinds. A review of historic texts also showed that farmers have exercised various practices like multi-cropping, crop rotations, and cultivating extensively or intensively contingent on available capital and resources, over the centuries. These demonstrate their ability to adopt measures to mitigate risk and underscore the primacy of farmers in decision-making. The cultivation of cotton began to change responding to various socio-economic factors and intensification of production, especially in the twentieth century, was one of the drivers underlying such change. In summarising, I show the apparent contrast between some critical dimensions of the past and present cultivation practice and shed light on a part of the agricultural history of cotton and its change.

Title: Effects of cultivar and nitrogen application rate on lint, seed, oil, and protein yields of field-grown cotton

Author: Ved Parkash, John L. Snider, Aaron Bruce, Alessandro Ermanis, Gurpreet Virk, Navneet Kaur, Guy Collins, Kent D. Chapman

Imprint: Crop Science , <https://doi.org/10.1002/csc2.20938>

Abstract: Cotton (*Gossypium hirsutum* L.) is not only the dominant fiber crop grown worldwide, but it is also an important source of plant-based oil and protein. Previous research has documented a significant effect of cotton cultivar and nitrogen application individually on lint yield and seed composition, but very limited studies have evaluated the lint, seed, oil, and protein yield responses of cultivars with different seed mass and composition to a broad range of N application rates. The objective of this study was to evaluate the lint, seed, oil, and protein yield responses of cultivars with different seed mass and composition to N application rates (0–168 kg N ha⁻¹) for field-grown cotton. A field experiment was conducted in Tifton, GA, USA during the 2019 and 2020 growing seasons that included six cultivars and six N application rates. Cultivar significantly affected seedcotton, lint, seed, and seed reserve yields in both growing seasons. Lint yield did not follow identical trends as seed yield mainly due to cultivar variation in lint percent. Similarly, protein and oil yield were influenced by cultivar variation in seed composition. Seedcotton, seed, protein, and oil yields continually increased with increases in N application from 0 to 168 kg N ha⁻¹, whereas for lint yield, all fertilized treatments produced comparable yields that were significantly higher (68%) than the 0 kg N ha⁻¹ treatment. We conclude that variability in the distribution of photosynthates to fiber and seed as well as seed oil and protein composition can significantly alter trends in fiber, seed, and seed component yields in response to cultivar or N application rates for field-grown cotton.

Crop Protection

Title: Transmission efficiency of Cotton leaf curl Khokhran virus / Cotton leaf curl Multan betasatellite complex by two whitefly cryptic species in Pakistan.

Author: Muhammad Afzal, Shafqat Saeed, Hasan Riaz, Muhammad Ishtiaq & M. Habib ur Rahman

Imprint: International Journal of Tropical Insect Science (2023)

Abstract: Cotton leaf curl disease (CLCuD) is a major constraint in the production of cotton crop across the Africa and Asia which is caused by a complex of begomoviruses (family Geminiviridae). Cotton leaf curl Khokhran virus and associated Cotton leaf curl Multan betasatellite (CLCuKoV/CLCuMB) complex are important agents of CLCuD which transmitted by whiteflies of the Bemisia tabaci species complex. Information regarding the transmission efficiency of CLCuKoV/CLCuMB by whitefly cryptic species is seriously lacking in Pakistan, therefore present study is conducted for comparison of transmission efficiency of CLCuKoV/CLCuMB by two characterized whitefly cryptic species (Asia II-1 and Asia II-5). Whitefly cryptic species were reared separately on Nicotiana benthamiana plants infected with CLCuKoV/CLCuMB for 24 or 48 h and these infected whitefly cryptic species were transferred to un-infected cotton and alternative host plants for 24 or 48 h. The first experiment results showed that Asia II-1 was able to transmit CLCuKoV/CLCuMB with high efficiency in cotton and bitter gourd plants as compared to the Asia II-5 while other host plants did not develop symptoms. Further in the second experiment results revealed that Asia II-1 was able to transmit CLCuKoV/CLCuMB with high efficiency from symptomatic bitter gourd to cotton plants as compared to Asia II-5 which did not show symptoms of transmission. Infection symptoms were confirmed by visual inspection after 30 days and PCR analysis. We found the percentage of virus infection symptoms in alternate host plants differed between two whitefly cryptic species due to varying transmission efficiencies. This research finding advances our understanding to explore the whitefly cryptic species involved in the transmission of CLCuD and will aid in the development of management strategies for control of whitefly cryptic species and CLCuD transmission in Pakistan.

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Title: Validation of IPM module for pink bollworm, Pectinophora gossypiella on Bt cotton .

Author: MV Variya, MF Acharya, AM Bharadiya and DV Patel

Imprint: The Pharma Innovation Journal 2023; 12(3): 3488-3491

Abstract : Validation of IPM module and farmer practices revealed that the range of percent rosette flower by pink bollworm during 2020-21 was 0.79 to 2.32 percent and 5.45 to 6.50 percent recorded from 50 to 65 DAS in IPM module and farmer practices, respectively. The percent green boll damage was 2.18 to 2.60 percent and 11.24 to 15.9 percent record from 120 to 150 DAS in IPM module and farmer practices, respectively. During 2021-22 percent of the rosette flowers by pink bollworm was 0.67 to 1.97 percent and 5.37 to 6.13 percent recorded from 50 to 65 DAS in IPM module and farmer

practices, respectively. The percent green boll damage was 1.98 to 2.23 percent and 10.83 to 16.20 percent recorded from 120 to 150 DAS in IPM module and farmer practices, respectively. Also seed cotton yields during 2020-21 & 2021-22 were recorded at 3321kg/ha and 3455 kg/ha in the IPM module, respectively.

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Title: Pink bollworm *Pectinophora gossypiella* (Saunders), a destructive pest of cotton: A review

Author: NK Bhute, CS Patil, KV Deshmukh, RS Wagh and NK Medhe

Imprint: The Pharma Innovation Journal 2023; 12(3): 2036-2042

Abstract: Cotton, the important cash crop, globally known as “King of Fibre” offers an important natural fabric material to the world has been a point of fascination. Since it is grown as major cash crop in India, appears to have been the center of an important cotton industry as early as 1500 BC. Besides serving as a source of natural fiber, it is also an oilseed crop, providing raw material to the oil and textile industries, playing dominant role in the economic and social status of the people. Amongst the various factors responsible for low yields, the losses due to pests assume significant importance as cotton crop is a heaven for insects. A total of 1326 species of insects have been recorded on cotton throughout the world. The pest spectrum of cotton crop is quite complex comprising of several species of the insects. However, main losses in cotton production are due to its susceptibility to about 162 species of insect pests. The sucking pests and bollworm complex account for a considerable yield loss up to 36.2 per cent. Chemical insecticides, are being used extensively for control of these insect pests. After the introduction of Bt cotton the use of pesticides minimized and the problem of bollworms was solved, but from last few years, pink bollworm has developed resistance against Bt toxins. Worldwide, pink bollworm has become economically the most notorious pest of cotton. Among the bollworms, pink bollworm poses greater threat to the cotton in recent past and has known to cause loss in normal opening of bolls, loss in oil content, seed cotton yield and damage locules. The authors tried here to collect the information about its distribution and origin, seasonal incidence, life history, nature of damage, symptoms, different management tools including IPM strategies. This information will helpful to the scientists to plan their research on pink bollworm which is the most destructive pest of cotton.

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Title: Deep Learning Models for Cotton Leaf Disease Detection with VGG-16.

Author: Awad Bin Naeem , Biswaranjan Senapati , Alok Singh Chauhan , Sumit Kumar Juan Carlos Orosco Gavilan , Wael M. F. Abdel-Rehim

Imprint: INTELLIGENT SYSTEMS AND APPLICATIONS IN ENGINEERING IJISAE, 2023, 11(2), 550–556

Abstract: Cotton, potatoes, tomatoes, and chilies are the principal crops exported from Pakistan. Cotton is produced in greater quantities in India, China, and the US than in Pakistan. Eighty percent of all public oil is made up of cotton. Like other crops, it is being attacked by viruses, which lowers production and reduces economic revenue. There is misinformation on how illness diagnosis and care affect a region's ability to produce more. In this research, deep convolutional neural networks (CNN) were trained to recognize three forms of cotton leaf disease using a transform learning approach (Cotton leaf curl virus, fusarium wilt, bacterial blight). This study's main goal was to develop a single framework that could handle the challenging process of finding, identifying, and diagnosing cotton leaf disease. Additionally, to improve their performance on datasets of healthy and allergic cotton leaves, bigger weight parameter optimization using the Adam and RMSProp optimizers was explored. When compared to the other DL meta-architectures, Inception-VGG-16 trained with the feature extractor showed the greatest mean average accuracy. The recommended method was found to be new since it distinguished between leaf types that were healthy and those that were unhealthy. Using the DL approach to accurately identify cotton leaf disease would help to avoid the adverse effects of dietary management issues. On photos of cotton leaves, the trained model recognizes and labels the four classes (Cotton leaf curl virus, bacterial blight, fusarium wilt, healthy).

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Title: Isolation of Actinomycetes from *Arachis hypogaea* L. and *Gossypium herbaceum* L. for Screening Antibacterial and Antifungal Activities

Author: J. S. Mehta a , Kunal N. Odedra a and B. A. Jadeja a

Imprint: Microbiology Research Journal International Volume 33, Issue 1, Page 17-23, 2023;

Abstract: The principal objective of the present study was to check the antimicrobial activity of Actinomycetes isolated from soil samples collected from the fields of *Arachis hypogaea* L. and *Gossypium herbaceum* L. against different plant pathogenic strains. Various soil samples were isolated from fields located near the Junagadh district, Gujarat, India. Isolation was followed by a serial dilution process which was later plated on Actinomycete Isolation Agar (AIA) media. Potential colonies were subjected to screening, purification, and storage in glycerol stock. Morphological and Biochemical characterization of the isolates was performed. Isolated candidates were subjected to extraction for the production of the antimicrobial compound. The antimicrobial activity of the purified extract of isolates was tested. Total 30 actinomycete isolates were

evaluated for antagonistic activity against pathogenic microorganisms. Isolates C-25, C-15, and G-1 showed the best results in the decreasing order of their potency against fungal pathogens, and C-5, C-25, C-14, and C-13 showed the best results in decreasing order of potency against bacterial pathogens. 3 isolates inhibited all 4 test fungi. 10 isolates inhibited 3 test fungi. 11 isolates inhibited 2 test fungi. 6 isolates did not inhibit any test fungi. 4 isolates show potent inhibition. 15 inhibited *Macrophomina*. C-10 showed a 1 cm inhibition zone & G-1 showed a 0.8 cm zone of inhibition. 12 isolates gave 0.2-0.6 cm zone and 15 isolates gave negative results against *Macrophomina*. C-10 showed a very potent zone of inhibition of 0.7 cm. 9 isolates showed a 0.1-0.5 cm zone of inhibition. 20 isolates did not show inhibition against *Fusarium*. 1 isolate C-11(a) gave the 1cm potent zone of inhibition. 15 isolates gave the 0.7-0.2cm inhibition of the growth. 14 isolates gave negative results against *Alternaria* fungus. From these results, it was concluded that isolates had antibacterial and antifungal activities and could be used in the development of new antibiotics for pharmaceutical or agricultural purposes.

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Title: Comparative transcriptome analysis of interspecific CSSLs reveals candidate genes and pathways involved in verticillium wilt resistance in cotton (*Gossypium hirsutum* L.)

Author: Youzhong Li , Xinyu Zhang , Zhongxu Lin , Qian-Hao Zhu

Imprint: Industrial Crops and Products, Volume 197, July 2023, 116560

<https://doi.org/10.1016/j.indcrop.2023.116560>

Abstract: *Verticillium wilt* (VW), known as the ‘cancer’ of cotton, is a vascular disease of cotton caused by *Verticillium dahliae*, which seriously affects the yield and quality of cotton. Upland cotton (*Gossypium hirsutum*, Gh) has good yield but low resistance to VW, while Sea-island cotton (*G. barbadense*, Gb) has excellent resistance to VW and good fiber quality but low yield. Creating chromosome segment substitution lines (CSSLs) from progeny of interspecific cross between Gh and Gb is a way to combine the superior traits of Gh and Gb to breed cotton varieties with high yield and fiber quality as well as good disease resistance. In this study, a CSSL population derived from Emian22 (Gh) × 3-79 (Gb) was subject to disease assay in multiple environments to identify VW-resistant CSSLs. The two CSSLs (M20 and M34) showing stable VW-resistance in different assay conditions together with the VW susceptible parent Emian22 were selected for comparative transcriptome analysis to identify genes associated with cotton response to *V. dahliae* infection. Significant transcriptome changes were found to occur at each time point (24, 48, and 72 h) after *V. dahliae* infection in all three lines. Gene ontology (GO) analysis of the DEGs identified in each line revealed enriched terms shared by the three lines or unique to each line. Based on gene expression trend analysis, the DEGs identified in M20, M34, and Emian22 were

clustered into 8, 8, and 7 cluster, respectively, with one unique to Emian22 and one unique to both M20 and M34. Weighted gene co-expression network analysis (WGCNA) identified 8 modules significantly related to cotton response to *V. dahliae* infection, especially the cyan module with 22 hub genes, including two genes (*Ghi_D02G10111* and *Ghi_A03G10581*) encoding probable protein phosphatase 2. Suppressing the expression level of *Ghi_D02G10111* (*GhPP2C52*) by virus-induced gene silencing led to the reduction of VW-resistance, implying *GhPP2C52* being a positive regulator of VW-resistance. In addition, genes of the ABA and Ca^{2+} signaling pathways were found to be associated with the response of cotton plants to *V. dahliae* infection. The findings of the study revealed the molecular difference between the VW-resistant and VW-susceptible cotton lines. Combining the genetic mapping results of the same population, the results of this study will facilitate cloning and molecular characterization of the genes responsible for VW-resistance observed in M20 and M34 and finally accelerate breeding VW-resistant cotton varieties through marker assisted selection and gene editing.

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Title: EFFICACY OF SEED TREATMENT CHEMICALS AGAINST SUCKING PESTS OF Bt COTTON

Author: PARMAR P.R. , BHANDERI G.R., DESAI H.R. AND PATEL R.D

Imprint: International Journal of Agriculture Sciences ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 15, Issue 1, 2023, pp.-12153-12156

Abstract: The present investigation was carried out during Kharif 2021 at the Main Cotton Research Station, Navsari Agricultural University, Surat. Seven treatments viz., carbosulfan 25 DS at 60 g kg⁻¹ seed, imidacloprid 70 WG at 3 g kg⁻¹ seed, imidacloprid 48 FS at 8 ml kg⁻¹ seed, imidacloprid+hexaconazole 20 FS at 2 ml kg⁻¹ seed, thiamethoxam 30 FS at 10 ml kg⁻¹ seed, thiamethoxam 70 WS at 4 g kg⁻¹ seed and chlorantraniliprole 9.3 SC+lamba cyhalothrin 4.6 CS (13.9 ZC) at 2.5 ml kg⁻¹ as chemicals for seed treatment were tested for their efficacy against key sucking pests. In general, imidacloprid 70 WG at 3 g kg⁻¹ seed was found most effective and economical against sucking pests whereas, thiamethoxam 30 FS at 10 ml kg⁻¹ seed proved next effective treatment. As far as duration of protection is concerned, imidacloprid 70 WG provided best protection up to 58 days against aphid and leafhopper, 65 days against thrips and 72 days against whitefly as well as mealybug populations whereas thiamethoxam 30 FS stood next to provide protection up to 51 days against aphid and leafhopper and up to 72 days for thrips, whitefly and mealybug populations. The combination product chlorantraniliprole 9.3 SC+lamba cyhalothrin 4.6 CS (13.9 ZC) was found less effective to above treatments and provided protection up to 30 days against thrips, 51 days against aphid and leafhopper, 58 days against whitefly and 72 days

against mealybug and more or less comparable to untreated control. The seed treatment of imidacloprid 70 WG at 3 g kg⁻¹ seed was registered highest seed cotton yield (21.69 q ha⁻¹) and highest germination percentage (90.67%).

Plant Genetics and Breeding

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Title: Role of Molecular Breeding Tools in Enhancing the Breeding of Drought-Resilient Cotton Genotypes: An Updated Review

Author: Adnan Rasheed, Long Zhao, Ali Raza

Imprint: Water 2023, 15(7), 1377; <https://doi.org/10.3390/w15071377>

Abstract: Drought stress is an inevitable factor that disturbs the production of plants by altering morphological, physiological, biochemical, and molecular functions. Breeding for drought tolerance requires a complete understanding of the molecular factors controlling stress-responsive pathways. The plant responds to drought stress by adopting four mechanisms: avoidance, escape, tolerance, and recovery. Traditional plant-breeding tools have been employed to increase tolerance in cotton, but the complexity of drought tolerance has limited the use of these breeding methods. The plant adopts several key strategies against drought stress, such as activating the signaling network and activating molecular factors. Cotton breeders have been engaged in elucidating the molecular mechanisms of drought tolerance in cotton using significant molecular tools such as quantitative trait loci (QTL) mapping, transcription factor (TFs) analysis, transcriptome analysis, genome-wide association studies (GWAS), genetic engineering, and CRISPR/Cas9. Breeders have studied the functional description of genes and the interacting pathways accountable for controlling drought tolerance in cotton. Hundreds of genes/QTL have been identified, and many have been cloned for drought tolerance in cotton; however, a complete understanding of these traits still needs more study. This review presents a detailed overview of molecular tools, their application for improving drought tolerance in cotton, and their prospects. This review will help future researchers to conduct further studies to develop drought-tolerant cotton genotypes that can thrive under conditions of water scarcity.

Title: Line × Tester Analysis for Yield and Quality Traits under Salinity Stress in Cotton (*Gossypium barbadense* L.)

Imprint: Egyptian Journal of Agronomy,

DOI: 10.21608/agro.2023.189662.1358

Author: Ezzat Elsayed Mahdy ; Hamdy Mahrous Mohamed; Mohamed Gamal Housein; Mohammed Abdelaziz Sayed

Abstract: The issue of salinity tolerance in crops has received a great amount of attention recently in Egypt, especially under the climate change phenomenon. The main objective of this experiment was to study the gene action that controls yield and quality traits of Egyptian cotton under normal and saline soil. Nine lines were crossed to three testers in a line × tester mating design. The 27 crosses and their parents were evaluated under normal and saline soil conditions in the seasons of 2018 and 2019 using a randomized complete block design with three replicates. Both additive (s^2_A) and dominance (s^2_D) variances were higher under normal soil than under salinity stress conditions for all the analyzed characteristics. Under normal soil, the ratio s^2_A/s^2_D was less than unity for seed cotton yield/plant (SCY/p), number of bolls (NB/p), number of seeds (NS/b), boll weight (BW), lint yield (LY/p), and lint%. s^2_D was not significant for seed index (SI), lint index (LI), days to the first flower (DFF), plant height (PH), and upper half-mean length (UHML). Under normal soil and based on the mean performance the cross (*Giza90* × *Aus* × *Giza85*) × *Giza95* was the best one for SCY/p, LY/p, NB/p, BW, SI and NS/b, and *Ashmouni* × *Giza90* × *Aus* × *Giza83* for lint%, *Dandara* × *Giza90* × *Aus* × *Giza83* for LI, *Ashmouni* × *Giza90* × *Aus* × *Giza83* for DFF, *Giza85* × *Giza95* for UHML. *Giza95*, *Giza90* and *Giza90* × *Aus* × *Giza83* were the best combiners in all the analyzed traits. These crosses can be used to develop new lines for the two environments.

Title: Genome-wide identification and expression analysis of DREB family genes in cotton.

Author: Jiuchang Su, Shanglin Song, Yiting Wang, Yunpeng Zeng, Tianyu Dong, Xiaoyang Ge

Imprint: BMC Plant Biology volume 23, Article number: 169 (2023)

Abstract: Dehydration responsive element-binding (DREB) transcription factors are widely present in plants, and involve in signalling transduction, plant growth and development, and stress response. DREB genes have been characterized in multiple species. However, only a few DREB genes have been studied in cotton, one of the most important fibre crops. Herein, the genome-wide identification, phylogeny, and expression analysis of DREB family genes are performed in diploid and tetraploid cotton species.

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Title: Functional characterization of the *GhNRT2.1e* gene reveals its significant role in improving nitrogen use efficiency in *Gossypium hirsutum*.

Author: Xinmiao Zhang, Jiajia Feng, Ruolin Zhao, Hailiang Cheng, Javaria Ashraf, Qian Wang

Imprint: PeerJ 11:e15152 <https://doi.org/10.7717/peerj.15152>

Abstract: Background -Nitrate is the primary type of nitrogen available to plants, which is absorbed and transported by nitrate transporter 2 (NRT2) at low nitrate conditions. Methods-Genome-wide identification of *NRT2* genes in *G. hirsutum* was performed. Gene expression patterns were revealed using RNA-seq and qRT-PCR. Gene functions were characterized using overexpression in *A. thaliana* and silencing in *G. hirsutum*. Protein interactions were verified by yeast two-hybrid and luciferase complementation imaging (LCI) assays.

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Title: Association and path analysis studies for yield contributing and fibre quality traits in the F₁ population of *Gossypium hirsutum* L.

Author: Subhasini Selvaraj, Rajeswari S,

Imprint: Environment Conservation Journal <https://doi.org/10.36953/ECJ.13812409>

Abstract: The present investigation on correlation and path analysis studies helps to study the relationship among the yield and yield contributing traits along with the quality parameters. The observations were taken in the F₁ population of 35 hybrids along with lines (7 lines) and testers (5 testers) for the traits *viz.* plant height (cm), number of sympodial branches per plant, the number of bolls per plant, boll weight

(g), lint index (g), single cotton yield per plant (g), ginning outturn (%), upper half mean length (cm), elongation percent (%) and micronaire value (μg per inch). The results revealed that seed cotton yield per plant had strong and positive association with the traits namely number of sympodial branches per plant (0.646), number of bolls (0.633) and boll weight (0.652). Path analysis study revealed that number of sympodial branches per plant (1.5396), boll weight (0.6285), lint index (1.3526) and upper half mean length (0.3392) had high direct positive effects on single plant yield and indirect very high positive effects through the traits *viz.*, number of sympodial branches per plant *via.*, number of bolls per plant (1.5125) and boll weight (1.0121). Hence selection based on these traits that are positively associated and direct positive effect with the yield would produce the best outcome in the genotypes in further breeding programmes.

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Title: *Gossypium purpurascens* genome provides insight into the origin and domestication of upland cotton

Author : Yu Cheng , Chujun Huang , Yan Hu

Imprint: Journal of Advanced Research, Available online 24 March 2023

Abstract: Allotetraploid upland cotton (*Gossypium hirsutum* L.) is native to the Mesoamerican and Caribbean regions, had been improved in the southern United States by the mid-eighteenth century, was then dispersed worldwide. However, a Hainan Island Native Cotton (HIC) has long been grown extensively on Hainan Island, China.

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Title: Estimation of Combining Ability for Within-Boll Yield Components in Upland Cotton (*Gossypium hirsutum*).

Author: Bano, Mishal; Shakeel, Amir; Waqar-ul-Haq; Khalid, Muhammad Nouman; Ahmad, Nadia Hussain; Sharif, Muhammad Sajid; Kanwal, Sadia; Bhutta, Muhammad Asim; Bibi, Amna; Amjad, Ifrah

Imprint: Sarhad Journal of Agriculture . Mar2023, Vol. 39 Issue 1, p174-181. 8p.

Abstract: In this study, three varieties Tarzon-05, FH-342, and VH-329 were crossed in line \times tester fashion with three testers CIM-595, CRS-2, and BS-80 during the 2021–2022. The F1 hybrids and their parents were planted in the fields, Plant Breeding and Genetics department, University of Agriculture Faisalabad using two replications

with randomized complete block design (RCBD). Results of ANOVA revealed that all the genotypes were highly significant for most of the plant height, sympodial branches/plant, monopodial branches/plant, first fruiting nodes, number of bolls per plant, boll weight, number of seeds per boll, seed cotton yield/plant, lint index, lint percentage, seed index, seed density, seed volume, fiber fineness, fiber strength, and fiber length. For plant height, fibre strength, and seed density, Tarzon-05 stood out among the lines as a very effective general combiner. For the number of bolls per plant, the number of sympodial and monopodial branches, the number of nodes on the first fruiting branch, seed cotton yield and the lint percentage, VH329 demonstrated good general combining ability. For boll weight, the FH-342 was proven to be an effective combiner. CIM-595 stood out among the testers as a good general combiner in terms of number of bolls per plant, monopodial branches, number of first fruiting branch node, seed cotton yield, and lint%. For fibre fineness, BS-80 was identified to be a good general combiner. A good specific combining ability was shown by the F1 hybrids Tarzon-05×BS-80 for plant height and fibre length, VH-329×CIM-595 for the quantity of bolls per plant, VH-329×BS-80 for the quantity of sympodial branches per plant and Tarzon-05×CRS-2 for the quantity of monopodial branches per plant and fibre strength. For the number of nodes for first fruiting branch, boll weight, fibre length, and seed cotton yield/plant, VH-329×CRS-2 was determined to be a good specific combiner, and FH-342×CIM-595 shown good specific combining ability for seed density and fibre strength. For seed volume, all of the parents and their hybrids displayed non-significant GCA and SCA values. All attributes, with the exception of seed index, were governed by non-additive gene action. The information related to GCA, SCA and gene action obtained from this research will be helpful for plant breeders in future breeding programs.

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Title: Genome-Wide Investigation and Co-Expression Network Analysis of SBT Family Gene in *Gossypium*.

Author: Tianxi Xue, Lisen Liu, Xinyi Zhang

Imprint: Int. J. Mol. Sci. 2023, 24(6), 5760; <https://doi.org/10.3390/ijms24065760>

Abstract: Subtilases (SBTs), which belong to the serine peptidases, control plant development by regulating cell wall properties and the activity of extracellular signaling molecules, and affect all stages of the life cycle, such as seed development and germination, and responses to biotic and abiotic environments. In this study, 146 *Gossypium hirsutum*, 138 *Gossypium barbadense*, 89 *Gossypium arboreum* and 84 *Gossypium raimondii* SBTs were identified and divided into six subfamilies. Cotton SBTs are unevenly distributed on chromosomes. Synteny analysis showed that the members of SBT1 and SBT4 were expanded in cotton compared to *Arabidopsis thaliana*.

Co-expression network analysis showed that six *Gossypium arboreum* SBT gene family members were in a network, among which five SBT1 genes and their *Gossypium hirsutum* and *Arabidopsis thaliana* direct homologues were down-regulated by salt treatment, indicating that the co-expression network might share conserved functions. Through co-expression network and annotation analysis, these SBTs may be involved in the biological processes of auxin transport, ABA signal transduction, cell wall repair and root tissue development. In summary, this study provides valuable information for the study of SBT genes in cotton and excavates SBT genes in response to salt stress, which provides ideas for cotton breeding for salinity resistance.

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Title: Evaluation of Some Promising Cotton Genotypes and Commercial Variety for Yield, Quality and Bacterial Blight Resistance

Author: Maria Abdalla , Salim Kafi a , A. M. Mustafa a and W. M. B. Yehia

Imprint: Asian Journal of Biotechnology and Genetic Engineering Volume 6, Issue 1, Page 12-19, 2023;

Abstract: Ten cotton genotypes were evaluated (*Gossypium Barbadense* L) for seed cotton yield, better quality and bacterial blight resistance. in the Agricultural Research Corporation, ARC at the Gezira Research Station, Gezira State, Wad Medani, Sudan.in seasons 2012/2013 and 2013/2014, The experiment was laid in a randomized complete block design (RCBD) with four replications. The results indicated that 94-B-2 line has an average seed cotton yield advantage of 19% over Barakat90, mean seed cotton yield 2219 compare to 1868 for Barakat-90, with fiber length of 35.1, micronaire value of 3.7 and fiber strength of 37.5 better than Barakat-90. It gave 52% of its yield in the first pick compared to 44 for Barakat-90. It has a GOT of 34% compared to 32.6 for Barakat-90. It recorded disease incidence and disease severity of 0.58 and 38.8%, respectively compared to 0.72 and 51.8 for Barakat-90. Hence this line emerged as a new candidate with new traits: higher seed cotton yield, earliness of maturity, resistance to bacterial blight, higher GOT and better fiber characteristics is better than the commercial cotton cultivar Barakat-90.

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Title: Transcriptome and Metabolome Profiling Unveil Pigment Formation Variations in Brown Cotton Lines (*Gossypium hirsutum* L.)

Author: Yin-Ping Lv, Gang Zhao, Yong-Fei Xie, Anane Gideon Owusu

Imprint: Int. J. Mol. Sci. 2023, 24(6), 5249; <https://doi.org/10.3390/ijms24065249>

Abstract: Naturally brown colored cotton (NBCC) is becoming increasingly popular due to its natural properties of coloration. However, poor fiber quality and color fading are key issues that are hindering the cultivation of naturally colored cotton. In this study, based on transcriptome and metabolome of 18 days post-anthesis (DPA), we compared the variations of pigment formation in two brown cotton fibers (DCF and LCF), with white cotton fiber (WCF) belonging to a near-isogenic line. A transcriptome study revealed a total of 15,785 differentially expressed genes significantly enriched in the flavonoid biosynthesis pathway. Furthermore, for flavonoid biosynthesis-related genes, such as flavonoid 3'5'-hydroxylase (F3'5'H), anthocyanidin synthase (ANS), anthocyanidin reductase (ANR), chalcone synthase (CHS), dihydroflavonol 4-reductase (DFR), and chalcone isomerase (CHI), their expressions significantly increased in LCF compared with DCF and WCF. Moreover, transcription factors MYB and bHLH were significantly expressed in LCF and DCF. Most flavonoid-related metabolites (myricetin naringenin, catechin, epicatechin-epiafzelechin, and epigallocatechin) were found to be more highly up-regulated in LCF and DCF than WCF. These findings reveal the regulatory mechanism controlling different brown pigmentation in cotton fibers and elucidate the need for the proper selection of high-quality brown cotton fiber breeding lines for promising fiber quality and durable brown color pigmentation.

Fiber and Fiber Technology

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Title: Fiber-specific increase of carotenoid content promotes cotton fiber elongation by increasing abscisic acid and ethylene biosynthesis

Author: Jianyan Zeng, Dan Yao, Ming Luo, Lingli Ding, Yi Wang, Xingying Yan, Shu'e Ye, Chuannan Wang, Yiping Wu, Jingyi Zhang, Yaohua Li, Lingfang Ran, Yonglu Dai, Yang Chen

Imprint: The Crop Journal, Available online 31 March 2023

Abstract: Cotton fiber is a raw material for the global textile industry and fiber quality is essential to its industrial application. Carotenoids are plant secondary metabolites that may serve as dietary components, regulate light harvesting, and scavenge reactive oxygen species. Although carotenoids accumulate predominantly in rapidly elongating cotton fibers, their roles in cotton fiber development remain poorly understood. In this study, a fiber-specific promoter *proSCFP* was applied to drive the expression of GhOR1^{Del}, a positive regulator of carotenoid accumulation, to upregulate the carotenoid level in cotton fiber *in planta*. Fiber length, strength, and fineness were increased in *proSCFP:GhOR1^{Del}* transgenic cotton and abscisic acid (ABA) and ethylene contents were increased in elongating fibers. The ABA downstream regulator

GhbZIP27a stimulated the expression of the ethylene synthase gene *GhACO3* by binding to its promoter, suggesting that ABA promoted fiber elongation by increasing ethylene production. These findings suggest the involvement of carotenoids and ABA signaling in promoting cotton fiber elongation and provide a strategy for improving cotton fiber quality.

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Title: CELL LINES, VARIETIES, AND METHODS FOR IN VITRO COTTON FIBER PRODUCTION

Author: PAREZ KARI (US), DODDS DAVID (US), ELBL PAULA (US)

Document Type and Number: WIPO Patent Application WO/2022/155456

Kind Code:A1

Abstract: The present disclosure provides in vitro methods for producing cotton fiber, including methods using cotton cells that include and express one or more selected genes.

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Title: FIBER LENGTH AND QUALITY INDICATORS IN COTTON VARIETIES

Author: Anisa Barotova Razzakovna , Xurramov Asilbek Abdusamat o'g'li

Imprint: JOURNAL OF AGRICULTURE & HORTICULTURE International scientific journal, Tashkent State Agrar University student ,
<https://doi.org/10.5281/zenodo.7747930>

Abstract: Quantitative characteristics of cotton include many important economic characteristics - fiber length, quantity, boll size, etc. To evaluate such signs, it is necessary to measure, weigh, count them. A variation series is generated based on these measurements. Quantitative traits are polygenic, that is, the development of the same trait is determined not by a pair of genes, but by several genes acting in the same way. Keywords: *Gossypium hirsutum*, *Gossypium barbadense*, method, cotton, varieties, plant, cultivar, fiber, maturity; micronaire, fiber, length, color grade, database, regional, climatic. Introduction. Cotton fiber length is an essential parameter for the cotton industry and cotton research. However, differences between industry- and laboratory-scale ginning may lead to inconsistencies between research and industry results for measured length. Seedcotton from farms is processed in large industry-scale gins, while researchers typically use small laboratory-scale gins. The proposed method successfully reduces the differences in fiber length parameters between these two types of ginning. Only one new step is needed before assessing fiber quality in lint from a laboratory-scale gin to simulate the processing effect of an industry-scale gin.

Title: Genome scale analysis of 1-aminocyclopropane-1-carboxylate oxidase gene family in *G. barbadense* and its functions in cotton fiber development

Author: Yousaf, S., Rehman, T., Tabassum, B

Imprint: *Sci Rep* 13, 4004 (2023). <https://doi.org/10.1038/s41598-023-30071-7>

Abstract: A class of proteins, 1-aminocyclopropane-1-carboxylate oxidase (ACO), is required in the final step of production of ethylene from its immediate precursor 1-aminocyclopropane-1-carboxylic acid (ACC). Despite the crucial and regulatory role of ACO gene family in the fiber development, it has not been thoroughly analyzed and annotated in *G. barbadense* genome. In the present study, we have identified and characterized all isoforms of ACO gene family from genomes of *Gossypium arboreum*, *G. barbadense*, *G. hirsutum* and *G. raimondii*. Phylogenetic analysis classified all ACO proteins into six distinct groups on the basis of maximum likelihood. Gene locus analysis and circos plots indicated the distribution and relationship of these genes in cotton genomes. Transcriptional profiling of ACO isoforms in *G. arboreum*, *G. barbadense* and *G. hirsutum* fiber development exhibited the highest expression in *G. barbadense* during early fiber elongation. Moreover, the accumulation of ACC was found highest in developing fibers of *G. barbadense* in comparison with other cotton species. ACO expression and ACC accumulation correlated with the fiber length in cotton species. Addition of ACC to the ovule cultures of *G. barbadense* significantly increased fiber elongation while ethylene inhibitors hindered fiber elongation. These findings will be helpful in dissecting the role of ACOs in cotton fiber development and pave a way towards genetic manipulations for fiber quality improvement.

Title: Raman spectroscopic assessment of fibers and seeds of six cotton genotypes .

Author: Zhongqi He , Sunghyun Nam , David Fang

Imprint: *Agric Environ Lett.* 2023;8:e20102. [wileyonlinelibrary.com/journal/ael2](https://doi.org/10.1002/ael2.20102) 1 of 5
<https://doi.org/10.1002/ael2.20102>

Abstract: Raman spectroscopy (RS) is a vibrational spectroscopy. This work reported the RS spectral characteristics of fiber and seed of six cotton (*Gossypium* sp.) genotypes differing in fiber length. While the RS spectra of fiber samples were dominated by the cellulose-related peaks, the spectra of cottonseed samples were featured by the bands related to oil, protein, carbohydrate, and lignin components. Principal component analysis (PCA) revealed that the first two principal components (PCs) accounted for >87% of the total variation of the two types of samples. The PC1 versus PC2 plot

classified the six fiber samples into three groups, but their cottonseeds into four groups. This experimental evidence implied the possibility of RS combined with PCA for rapid fiber phenotyping of cotton as well as for evaluating cottonseed nutrient information.

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Title: Phenomics and transcriptomics analyses reveal deposition of suberin and lignin in the short fiber cell walls produced from a wild cotton species and two mutants

Author: Hee Jin Kim ,Yongliang Liu,Gregory N. Thyssen,Marina Naoumkina,James Frelichowski

Imprint: PLOS One March 9, 2023, <https://doi.org/10.1371/journal.pone.0282799>

Abstract: Fiber length is one of the major properties determining the quality and commercial value of cotton. To understand the mechanisms regulating fiber length, genetic variations of cotton species and mutants producing short fibers have been compared with cultivated cottons generating long and normal fibers. However, their phenomic variation other than fiber length has not been well characterized. Therefore, we compared physical and chemical properties of the short fibers with the long fibers. Fiber characteristics were compared in two sets: 1) wild diploid *Gossypium raimondii* Ulbrich (short fibers) with cultivated diploid *G. arboreum* L and tetraploid *G. hirsutum* L. (long fibers); 2) *G. hirsutum* short fiber mutants, Ligon-lintless 1 (*Li*₁) and 2 (*Li*₂) with their near isogenic line (NIL), DP-5690 (long fibers). Chemical analyses showed that the short fibers commonly consisted of greater non-cellulosic components, including lignin and suberin, than the long fibers. Transcriptomic analyses also identified up-regulation of the genes related to suberin and lignin biosynthesis in the short fibers. Our results may provide insight on how high levels of suberin and lignin in cell walls can affect cotton fiber length. The approaches combining phenomic and transcriptomic analyses of multiple sets of cotton fibers sharing a common phenotype would facilitate identifying genes and common pathways that significantly influence cotton fiber properties.

Plant Biotechnology

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Title: The cotton protein GhIQD21 interacts with GhCaM7 and modulates organ morphogenesis in Arabidopsis by influencing microtubule stability.

Author: Xing Li, Li Wang, Yupeng Cui, Chen Liu, Yujie Liu, Lili Lu & Ming Luo

Imprint: Plant Cell Reports (2023)

Abstract: Calcium ion (Ca^{2+}) and the calcium sensor calmodulin play crucial roles in the growth and development of plants. GhCaM7, a calmodulin in upland cotton (*Gossypium hirsutum* L.), is highly expressed in cotton fiber cells during the rapid elongation period and plays an important role in fiber cell development. In this study, we screened for GhCaM7-interacting proteins and identified GhIQD21, which contains a typical IQ67-domain. GhIQD21 was preferentially expressed at the fiber rapid elongation stage, and the protein localized to microtubules (MTs). Ectopic expression of GhIQD21 in *Arabidopsis* resulted in shorter leaves, petals, siliques, and plant height, thicker inflorescences, and more trichomes when compared with wild type (WT). Further investigation indicated that the morphogenesis of leaf epidermal cells and silique cells was altered. There was less consistency in the orientation of cortical microtubules in cotyledon and hypocotyl epidermal cells. Furthermore, compared with WT, transgenic seedling hypocotyls were more sensitive to oryzalin, a MT depolymerization drug. These results indicated that GhIQD21 is a GhCaM7-interacting protein located in MTs and that it plays a role in plant growth and potentially cotton fiber development. This study provides a foundation for further studies of the function and regulatory mechanism of GhIQD21 in fiber cell development.

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Title: Sequence Characteristics and Expression Analysis of the Gene Encoding Sedoheptulose-1,7-Bisphosphatase, an Important Calvin Cycle Enzyme in Upland Cotton (*Gossypium hirsutum* L.)

Author: Maoni Chao, Genhai Hu, Jie Dong, Yu Chen, Yuanzhi Fu, Jinbao Zhang Qinglian Wang

Imprint: Int. J. Mol. Sci. 2023, 24(7), 6648; <https://doi.org/10.3390/ijms24076648>

Abstract: Sedoheptulose-1,7-bisphosphatase (SBPase, EC 3.1.3.37) is a key enzyme in the plant Calvin cycle and one of the main rate-limiting enzymes in the plant photosynthesis pathway. Many studies have demonstrated that the SBPase gene plays an important role in plant photosynthetic efficiency, yield, and stress responses; however, few studies have been conducted on the function and expression of the GhSBPase gene in upland cotton. In this study, our results showed that the coding sequence (CDS) of GhSBPase gene was 1182 bp, encoding a protein with 393 amino acids. The GhSBPase protein had adenosine monophosphate (AMP) binding site and a FIG (FBPase/IMPase/glpX) domain, and had six Cys residues and a CGGT(A/Q)C motif that were involved in redox regulation in plants. Evolutionarily, the GhSBPase protein clustered into the dicotyledon subgroup and was most closely related to the tomato SISBPase protein. Western-blot analysis further indicated that

the GhSBPase gene was indeed the gene encoding the SBPase protein in upland cotton. The GhSBPase protein was localized in chloroplast, which was consistent with its function as a key enzyme in photosynthesis. The GhSBPase gene was specifically highly expressed in leaves, and its expression level was significantly lower in a yellow-green leaf mutant than in the wild type. Moreover, the GhSBPase expression was in response to drought, salt, high- and low-temperature stress, and exhibits different expression patterns. The GhSBPase promoter had the cis-acting elements in response to abiotic stress, phytohormone, and light. In addition, the GhSBPase expression was positively correlated with the chlorophyll fluorescence parameters, suggesting that changes in the expression of the GhSBPase had potential applicability in breeding for enhanced cotton photosynthetic efficiency. These results will help to understand the function of the GhSBPase gene in photosynthesis and the adaptability of plants to external stress and provide important gene information for the high-yield breeding of crops in the future.

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Title: Engineering of cry genes “*Cry11* and *Cry1h*” in cotton (*Gossypium hirsutum* L.) for protection against insect pest attack.

Author: Abdul Razzaq, Arfan Ali, Sara Zahid, Arif Malik, Li Pengtao, Wankui Gong

Imprint: Archives of Phytopathology and Plant Protection , Volume 56, 2023 - Issue 5

Author: Cotton is white gold and contributes significantly to the economy of the countries. The process of evolution of resistance in various cotton insects directly affects the life of people. Among the cotton insect pests, pink bollworm (*Pectinophora gossypiella*) and army bollworm (*Spodoptera litura*) have turned out to be destructive. The development of seed using gene stacking approach has tremendously reduced the applications of agrochemicals making the technology greener for society. A gene cassette containing *Cry11* and *Cry1H* genes was constructed. The cassette was cloned into the pCAMBIA2300 plant expression vector using the CAMV3-35S promoter. The construct was transformed into cotton line FBS-222 using the shoot apex-cut *Agrobacterium*-mediated transformation method. The expression of the *Cry* genes was 3-fold higher in transgenic than the non-transgenic cotton plants using qRT-PCR. Finally, the insect bioassay with transgenic cotton showed 90% mortality against pink bollworms and 80% against cotton army bollworms. The results demonstrate the development of seeds using the gene pyramiding approach is an effective strategy to control insect pest attacks.

Title: Transformation and expressional studies of *GaZnF* gene to improve drought tolerance in *Gossypium hirsutum*

Author: Fatima Batool, Sameera Hassan, Saira Azam, Zunaira Sher, Qurban Ali

Imprint: *Scientific Reports* volume 13, Article number: 5064 (2023)

Abstract: Drought stress is the major limiting factor in plant growth and production. Cotton is a significant crop as textile fiber and oilseed, but its production is generally affected by drought stress, mainly in dry regions. This study aimed to investigate the expression of Zinc finger transcription factor's gene (*GaZnF*) to enhance the drought tolerance in *Gossypium hirsutum*. Sequence features of the *GaZnF* protein were recognized through different bioinformatics tools like multiple sequence alignment analysis, phylogenetic tree for evolutionary relationships, Protein motifs, a transmembrane domain, secondary structure and physio-chemical properties indicating that *GaZnF* is a stable protein. CIM-482, a local *Gossypium hirsutum* variety was transformed with *GaZnF* through *Agrobacterium*-mediated transformation method with 2.57% transformation efficiency. The integration of *GaZnF* was confirmed through Southern blot showing 531 bp, and Western blot indicated a 95 kDa transgene-GUS fusion band in transgenic plants. The normalized real-time expression analysis revealed the highest relative fold spatial expression of cDNA of *GaZnF* within leaf tissues at vegetative and flowering stages under drought stress. Morphological, physiological and biochemical parameters of transgenic cotton plants at 05- and 10-day drought stress was higher than those of non-transgenic control plants. The values of fresh and dry biomass, chlorophyll content, photosynthesis, transpiration rate, and stomatal conductance reduced in *GaZnF* transgenic cotton plants at 05- and 10-day drought stress, but their values were less low in transgenic plants than those of non-transgenic control plants. These findings showed that *GaZnF* gene expression in transgenic plants could be a valuable source for the development of drought-tolerant homozygous lines through breeding.

Title: Co-overexpression of *RCA* and *AVP1* in cotton substantially improves fiber yield for cotton under drought, moderate heat, and salt stress conditions

Author: Jennifer Smith , Inosha Wijewardene , Yifan Cai

Imprint: *Current Research in Biotechnology*, Volume 5, 2023, 100123

<https://doi.org/10.1016/j.crbiot.2023.100123>

Abstract: Abiotic stresses such as drought, heat, and salt are major causes of crop failure and are the main challenges that we face in agriculture. Genetic engineering has been successful in controlling harmful insects and conferring herbicide resistance, but has yet to produce similar results in reducing damages caused by abiotic stresses. It was previously shown that overexpression of *AVP1* that encodes a vascular H⁺-pyrophosphatase in *Arabidopsis* could increase drought and salt tolerance and overexpression of *RCA* that encodes Rubisco activase in *Larrea tridentata* could increase heat tolerance in transgenic plants. It was therefore hypothesized that co-overexpression of *AVP1* and *RCA* would make transgenic plants more tolerant to all three stresses simultaneously. Indeed, this hypothesis was confirmed in *Arabidopsis*. To test if this result could be duplicated in an actual crop, *AVP1* and *RCA* were co-overexpressed in cotton. The results from this study indicated that *RCA/AVP1* co-overexpressing cotton plants produced 50% and 96% higher seed fiber yield than wild-type cotton under combined drought and salt stresses and combined drought and heat stresses, respectively. Furthermore, *RCA/AVP1* co-overexpressing cotton plants showed a 6.5-fold increase in net photosynthetic rates under heat stress as well as having much higher V_{max} rates under multiple stress conditions. Results from two field studies showed that *RCA/AVP1* co-overexpressing cotton plants had 90% and 66–75% increase in seed fiber yield in comparing to wild-type cotton under dryland conditions. This study proves that co-overexpression of *AVP1* and *RCA* can improve cotton's fiber yield in a dryland agricultural region, and this approach could increase other crops' yield in arid and semiarid regions of the world.

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Title: Fine mapping and candidate gene analysis of *qFL-A12-5*: a fiber length-related QTL introgressed from *Gossypium barbadense* into *Gossypium hirsutum*

Author: Xianghui Xiao, Ruixian Liu, Juwu Gong, Pengtao Li, Ziyin Li, Wankui Gong,

Imprint: Theoretical and Applied Genetics volume 136, Article number: 48 (2023)

Abstract: Fiber length is a key determinant of fiber quality in cotton, and it is a key target of artificial selection for breeding and domestication. Although many fiber length-related quantitative trait loci have been identified, there are few reports on their fine mapping or candidate gene validation, thus hampering efforts to understand the mechanistic basis of cotton fiber development. Our previous study identified the *qFL-A12-5* associated with superior fiber quality on chromosome A12 in the chromosome segment substitution line (CSSL) MBI7747 (BC₄F_{3:5}). A single segment substitution line (CSSL-106) screened from BC₆F₂ was backcrossed to construct a larger segregation population with its recurrent parent CCRI45, thus enabling the fine mapping of 2852 BC₇F₂ individuals using denser simple sequence repeat markers to narrow the *qFL-A12-5* to an 18.8 kb region of the genome, in which six annotated genes were identified in *Gossypium hirsutum*. Quantitative real-time PCR and comparative analyses led to the

identification of *GH_A12G2192* (*GhTPR*) encoding a tetratricopeptide repeat-like superfamily protein as a promising candidate gene for *qFL-A12-5*. A comparative analysis of the protein-coding regions of *GhTPR* among Hai1, MBI7747, and CCRI45 revealed two non-synonymous mutations. The overexpression of *GhTPR* resulted in longer roots in *Arabidopsis*, suggesting that *GhTPR* may regulate cotton fiber development. These results provide a foundation for future efforts to improve cotton fiber length.

Seed Science and Technology

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Title: A mutant cotton *fatty acid desaturase 2-1d* allele causes protein mistargeting and altered seed oil composition.

Author: Jay Shockey, Matthew K. Gilbert & Gregory N. Thyssen

Imprint: *BMC Plant Biology* volume 23, Article number: 147 (2023)

Abstract: Previous studies, including those from our laboratory, identified pima accessions containing approximately doubled levels of seed oil oleic acid, compared to standard upland cottonseed oil. Here, the molecular properties of a fatty acid desaturase encoded by a mutant allele identified by genome sequencing in an earlier analysis were analyzed. The mutant sequence is predicted to encode a C-terminally truncated protein lacking nine residues, including a predicted endoplasmic reticulum membrane retrieval motif. We determined that the mutation was caused by a relatively recent movement of a Ty1/*copia* type retrotransposon that is not found associated with this desaturase gene in other sequenced cotton genomes. The mutant desaturase, along with its repaired isozyme and the wild-type A-subgenome homoeologous protein were expressed in transgenic yeast and stably transformed *Arabidopsis* plants. All full-length enzymes efficiently converted oleic acid to linoleic acid. The mutant desaturase protein produced only trace amounts of linoleic acid, and only when strongly overexpressed in yeast cells, indicating that the missing C-terminal amino acid residues are not strictly required for enzyme activity, yet are necessary for proper subcellular targeting to the endoplasmic reticulum membrane.

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Title: Dirigent gene editing of gossypol enantiomers for toxicity-depleted cotton seeds

Author: Jia-Ling Lin, Xin Fang, Jian-Xu Li, Zhi-Wen Chen

Imprint: Nature Plants volume 9, pages605–615 (2023)

Abstract: Axial chirality of biaryls can generate varied bioactivities. Gossypol is a binaphthyl compound made by cotton plants. Of its two axially chiral isomers, (–)-gossypol is the bioactive form in mammals and has antispermatogenic activity, and its accumulation in cotton seeds poses health concerns. Here we identified two extracellular dirigent proteins (DIRs) from *Gossypium hirsutum*, GhDIR5 and GhDIR6, which impart the hemigossypol oxidative coupling into (–)- and (+)-gossypol, respectively. To reduce cotton seed toxicity, we disrupted GhDIR5 by genome editing, which eliminated (–)-gossypol but had no effects on other phytoalexins, including (+)-gossypol, that provide pest resistance. Reciprocal mutagenesis identified three residues responsible for enantioselectivity. The (–)-gossypol-forming DIRs emerged later than their enantiocomplementary counterparts, from tandem gene duplications that occurred shortly after the cotton genus diverged. Our study offers insight into how plants control enantiomeric ratios and how to selectively modify the chemical spectra of cotton plants and thereby improve crop quality.

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Title: Seed Priming Improves Germination, Yield, and Water Productivity of Cotton Under Drought Stress

Author: Khalequzzaman, Hayat Ullah, Sushil Kumar Himanshu, Noor-E-Tajkia Islam, Rujira Tisarum, Suriyan Cha-um & Avishek Datta

Imprint: Journal of Soil Science and Plant Nutrition (2023)

Abstract: The deleterious effects of drought stress on cotton (*Gossypium hirsutum* L.) could be mitigated through seed priming. The objective of this study was to assess the effects of various seed priming materials on cotton under different soil moisture levels and to compare the effectiveness of these priming materials in mitigating the detrimental effects of water-deficit stress. A polyhouse experiment comprising six seed priming treatments (priming with salicylic acid [SA] at 100 mg L⁻¹, silicon [Si] at 1 mM, potassium nitrate [KNO₃] at 5 g L⁻¹, proline [PRO] at 100 mg L⁻¹, glycine betaine [GB] at 100 mg L⁻¹), hydropriming, and non-primed control) under three soil moisture levels (50, 75, and 100% field capacity [FC]) was carried out. The results revealed a significant decrease in all evaluated parameters with reducing soil moisture levels (44–58% reduction in boll number per plant, 25–50% reduction in seed cotton yield, 18–41% reduction in lint index, 6–21% reduction in leaf relative water content, and 18–53% reduction in net photosynthetic rate at 50% FC in comparison to 100% FC) across seed priming treatments. However, there was up to a 9-fold increase in free proline concentration at 50% FC in comparison to 100% FC across seed priming treatments.

Plants raised from KNO₃- and GB-primed seeds outperformed all other treatments and caused a significant increase in germination-related traits and other evaluated parameters. There were 54, 36, and 125% higher shoot dry matter, seed cotton yield, and net photosynthetic rate, respectively, of KNO₃-primed plants over the control plants (non-primed) at 50% FC, and 31, 11, and 79% higher single boll weight, leaf greenness, and membrane stability index, respectively, of GB-primed plants over the control (non-primed) at 50% FC. Priming cotton seeds with KNO₃ at 5 g L⁻¹ or GB at 100 mg L⁻¹ can be recommended as a promising technique for growing cotton under water-scarce environments.

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Title: CORRELATION STUDIES AMONG SEED VIGOUR TRAITS AND YIELD IN DIFFERENT SEED LOTS OF G. HIRSUTUM L. COTTON

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Abstract: Cotton is immensely important fibre crop of India having great role in economy. The quality seed is foundation for achieving desired production targets. Therefore, an experiment was conducted to assess the seed vigour traits in cotton (*Gossypium hirsutum* L.) and its association with seed cotton yield to predict the seed potential at Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth Akola, Maharashtra (India) during the 2018- 2019 with seven genotypes of *G. hirsutum* cotton viz., AKH-13-55, AKH-13-81, AKH-14-59, AKH-14-12, AKH-13- 92, AKH-13-26 and AKH-13-51. The analysis of six vigour traits in laboratory along with fifteen yield and yield contributing traits in field with objectives to estimate the mean performance of seed vigour traits in cotton and to assess the correlation between seed vigour traits and yield contributing characters. Genotypes viz., AKH-14-12 and AKH-13-26 exhibited superiority for all six vigour traits, as well as found top ranking for most of yield contributing traits. Correlation coefficient analysis revealed that all six seed vigour parameters were significantly correlated with all fifteen yield and it's contributing traits in positive direction except ginning outturn and oil content which exhibited non significant association. The positive and highly significant correlation were recorded in between seed cotton yield per plant and all six vigour traits viz., germination per cent ($r=0.623^{**}$), root length ($r=0.871^{**}$), shoot length ($r=0.516^{*}$), seedling dry weight ($r=0.754^{**}$), seed vigour index-I ($r=0.905^{**}$) and seed vigour index-II ($r=0.757^{**}$). Hence, utilization of seed vigour traits is possible and effective for the prediction of yield potential in cotton along with planting value of seed lot.

Title: Priming with sodium nitroprusside and hydrogen peroxide increases cotton seed tolerance to salinity and water deficit during seed germination and seedling development.

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Abstract: A major difficulty in cotton crops is high-quality seed production, which interferes with plant vigor and establishment. Techniques such as seed physiological conditioning have been reported due to their ability to improve stress tolerance in seeds and plants. Considering this, we carried out this research to evaluate the use of signaling molecules to increase cotton plant stress tolerance. Seeds were conditioned on aerated solutions of indoleacetic acid (100 μM), hydrogen peroxide (100 μM), chitosan (0.75 mM), melatonin (0.2 mM), sodium nitroprusside (100 μM), and pure water (hydropriming), at 20 °C for 24 h. Then seeds were washed with running water and dried in an oven with forced air circulation at 25 °C for 24 h. Treated seeds or nontreated seeds were placed to germinate under salinity (10 dS m⁻¹ NaCl) and water deficit by using polyethylene glycol (PEG 6000) at - 0.6 MPa, and with nonstressed condition (water). The solutions mentioned were used to moisten the Germitest® paper roll at 2.5 times its weight. We also analyzed the activity of the enzymes superoxide dismutase, catalase, and ascorbate peroxidase, as well as the content of proline, hydrogen peroxide, and lipid peroxidation. Physiological conditioning with signaling molecules effectively improved cotton seed germination under stress, especially to hydrogen peroxide and sodium nitroprusside, which resulted in better performance on the parameters of germination and seedling growth. As stress conditions induced oxidative stress, as observed by lipid peroxidation, we found that physiological conditioning improved the seed antioxidant system, with hydrogen peroxide and sodium nitroprusside resulting in better performance. Our results highlighted the potential of sodium nitroprusside and hydrogen peroxide as inducers of stress tolerance in cotton.

