

Agronomy, Soil Science and Plant Physiology

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Title: Systematic analysis and expression of Gossypium 2ODD superfamily highlight the roles of GhLDOXs responding to alkali and other abiotic stress in cotton

Author: Tiantian Jiang, Aihua Cui, Yupeng Cui, Ruifeng Cui, Mingge Han, Yuexin Zhang, Yapeng Fan, Hui Huang, Xixian Feng, Yuqian Lei, Xiaoyu Liu, Kesong Ni

Imprint: BMC Plant Biology volume 23, Article number: 124 (2023)

Abstract: 2-oxoglutarate-dependent dioxygenase (2ODD) is the second largest family of oxidases involved in various oxygenation/hydroxylation reactions in plants. Many members in the family regulate gene transcription, nucleic acid modification/repair and secondary metabolic synthesis. The 2ODD family genes also function in the formation of abundant flavonoids during anthocyanin synthesis, thereby modulating plant development and response to diverse stresses.

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Title: Potential of Leaf Extract of Miracle Plant (*Moringa oleifera* L.) As Seed Priming Agent and Foliar Fertilization of Cotton (*Gossypium hirsutum* L.)

Author: Bushra Urooj Panhwar, Abdullah Keerio

Imprint: RADS Journal of Biological Research and Applied Sc. Volume 13 (2),
December 2022

Abstract: A key desire of a farmer is to produce a higher yield with low inputs. Through proper nutrient management, potential yield can be picked but mostly cotton is not grown with balanced nutrition. In this scenario, seed priming and foliar fertilizers have the advantage of quick plant responses. Therefore, a cost-effective, farmers-friendly, and full of nutrients supplement should be considered. Moringa is known as a miracle plant and its role as a seed priming agent and foliar spray has been observed in many other crops.

Title: Cotton Growth Modelling Using UAS-Derived DSM and RGB Imagery.

Author: Vasilis Psiroukis , George Papadopoulos , Aikaterini Kasimati , Nikos Tsoulas and Spyros Fountas

Imprint: Remote Sens. 2023, 15, 1214. <https://doi.org/10.3390/rs15051214>

Abstract: Modeling cotton plant growth is an important aspect of improving cotton yields and fiber quality and optimizing land management strategies. High-throughput phenotyping (HTP) systems, including those using high-resolution imagery from unmanned aerial systems (UAS) combined with sensor technologies, can accurately measure and characterize phenotypic traits such as plant height, canopy cover, and vegetation indices. However, manual assessment of plant characteristics is still widely used in practice. It is time-consuming, labor-intensive, and prone to human error. In this study, we investigated the use of a data-processing pipeline to estimate cotton plant height using UAS-derived visible-spectrum vegetation indices and photogrammetric products. Experiments were conducted at an experimental cotton field in Aliartos, Greece, using a DJI Phantom 4 UAS in five different stages of the 2022 summer cultivation season. Ground Control Points (GCPs) were marked in the field and used for georeferencing and model optimization. The imagery was used to generate dense point clouds, which were then used to create Digital Surface Models (DSMs), while specific Digital Elevation Models (DEMs) were interpolated from RTK GPS measurements. Three (3) vegetation indices were calculated using visible spectrum reflectance data from the generated orthomosaic maps, and ground coverage from the cotton canopy was also calculated by using binary masks. Finally, the correlations between the indices and crop height were examined. The results showed that vegetation indices, especially Green Chromatic Coordinate (GCC) and Normalized Excessive Green (NExG) indices, had high correlations with cotton height in the earlier growth stages and exceeded 0.70, while vegetation cover showed a more consistent trend throughout the season and exceeded 0.90 at the beginning of the season.

Title: Analysis of the Effects of Climate Change on Cotton Production in Maharashtra State of India using Statistical Model and GIS Mapping .

Author: Anirup Sengupta and Mohanasundari Thangavel

Imprint: Caraka Tani: Journal of Sustainable Agriculture, 38(1), 000-000, 2023

Abstract: Cotton is a prominent cash crop cultivated for fiber, edible oil and oil cake. A global environmental issue, like climate change, alters weather parameters necessary for the healthy growth and development of cotton plants, affecting fiber quality and economic yield. The study aims to illustrate the evidence of climate change in Maharashtra and assess its impact on the production of cotton in this region. The study was conducted in the state of Maharashtra, India. Geographic information system (GIS)-based models were created based on the vector data (geopolitical boundaries of the state and Maharashtra Districts) and the corresponding raster attributes (meteorological data) to examine the changes in the patterns of distribution of temperature, rainfall and severity of drought (Standardized precipitation index-SPI) over the study period (1990 to 2015). Further, a statistical multiple linear regression model was developed using district-wise data on yield and climatic parameters obtained from International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) to estimate the relationship between the dependent variable (yield of cotton) and the independent variables (annual rainfall and annual mean temperature). GIS modeling and mapping provide evidence of changes in the spatial distribution of rainfall and temperature. Although the regression analysis seems weak, it is acceptable for natural systems because natural systems are complex and often highly variable, making it difficult to create a perfect model. The multiple linear regression model shows that such changes in climatic parameters have a significant negative impact on the economic yield of cotton.

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Title: Effect of sulphur on growth, yield and seed quality of Bt cotton hybrid

Author: Sankat KB, Pawar SL, Ramani HR and Patel MM

Imprint: The Pharma Innovation Journal 2023; 12(2): 2468-2471

Abstract : Field experiments were conducted during kharif season of 2018, 2019 and 2020 to investigate the effects of different sulphur application rates (0, 30, 40, 60, 80 and 100 kg/ha) on the yield and yield parameters of cotton (*Gossypium hirsutum* L.) in the South Gujarat under irrigated condition. Sulphur levels were found to significantly influence number of bolls, seed cotton yield and lint yield. Seed oil content although increased with sulphur levels but failed to produce any significant difference. With respect to sulphur content in cotton seed and stalk was found to influence significantly due to sulphur levels. Application of sulphur significantly influenced the uptake of sulphur by seed, stalk and total uptake. Significant increase in sulphur content in soil was observed at both the depths due to application of gypsum.

Title: The Na⁺/H⁺ antiporter GbSOS1 interacts with SIP5 and regulates salt tolerance in *Gossypium barbadense*

Author: Fu-Chun Xu , Mei-Juan Wang , Ya-Wei Guo , Jie Song , Wei Gao , Lu Long

Imprint: Plant Science, Volume 330, May 2023, 111658

Abstract: Cotton is a globally cultivated economic crop and is a major source of natural fiber and edible oil. However, cotton production is severely affected by salt stress. Although Salt Overly Sensitive 1 (SOS1) is a well-studied Na⁺/H⁺ antiporter in multiple plant species, little is known about its function and regulatory mechanism in cotton. Here, we cloned a salt-induced *SOS1* from sea-island cotton. Real-time quantitative PCR analysis revealed that *GbSOS1* was induced by multiple stresses and phytohormones. Silencing *GbSOS1* through virus-induced gene silencing significantly reduced cotton resistance to high Na⁺ but mildly affected Li⁺ tolerance. On the other hand, overexpression of *GbSOS1* enhanced salt tolerance in yeast, *Arabidopsis*, and cotton largely due to the ability to maintain Na⁺ homeostasis in protoplasts. Yeast-two-hybrid assays and bimolecular fluorescence complementation identified a novel protein interacting with GbSOS1 on the plasma membrane, which we named SOS Interaction Protein 5 (SIP5). We found that the *SIP5* gene encoded an unknown protein localized on the cell membrane. Silencing *SIP5* significantly increased cotton tolerance to salt, exhibited by less wilting and plant death under salt stress. Our results revealed that GbSOS1 is crucial for cotton survival in saline soil, and SIP5 is a potentially negative regulator of SOS1-mediated salt tolerance in cotton. Overall, this study provides a theoretical basis for elucidating the molecular mechanism of *SOS1*, and a candidate gene for breeding salt-tolerant crops.

Title: Manipulation of plant growth stimulants on plant morphology, phenology, and disease incident of *Gossypium hirsutum* L. under various thermal regimes

Author: Muhammad Sarwar, Muhammad Farrukh Saleem, Basharat Ali, Muhammad Sagir, Muhammad Bilal Tahir

Imprint: *Arabian Journal of Geosciences* **volume 16**, Article number: 170 (2023)

Abstract: Different environmental conditions affect the phenology and insect/disease incidence in cotton crop. Studies on modulatory role of plant growth stimulants on cotton phenology, insect/disease incidence, and the bolls opening under various

thermal regimes/sowing dates under field conditions are lacking. In this study, different growth stimulants, e.g., hydrogen peroxide (H₂O₂-30 ppm), salicylic acid (SA-50 ppm), *moringa* leaf extract (MLE-30 times diluted), and ascorbic acid (AsA-70 ppm), were applied at squaring, flowering, and boll formation. June/late thermal regime showed higher incidence of CLCV, insect-infected bolls, and unopened bolls than April/early and May/normal sowing dates. Among the biostimulants, foliar spray of H₂O₂ and SA (averaged across) reduced the incidence of CLCV, cotton boll worms, and unopened bolls by 25%, 30%, and 29% in June thermal regime than water-treated plants of respective sowing date. April thermal regime took more days for the accumulation of required growing degree days for all phenological components, i.e., days to squaring, flowering, boll split, boll maturation period, and node number for first fruiting branch, while June thermal regime took less days to initiate these phenological stages. Foliar spray of H₂O₂ and SA (averaged across) increased earliness at squaring and flowering by 12% and 7%, respectively under April thermal regime while MLE and AsA delayed earliness. The results indicate that exogenous application of SA and H₂O₂ could improve cotton phenology but reduce the insect and disease incidence under field conditions.

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Title: Phosphorus Availability Affects the Photosynthesis and Antioxidant System of Contrasting Low-P-Tolerant Cotton Genotypes .

Author: Mirezhatijiang Kayoumu, Asif Iqbal, Noor Muhammad , Xiaotong Li , Leilei Li , Xiangru Wang , Huiping Gui , Qian Qi , Sijia Ruan , Ruishi Guo , Xiling Zhang Meizhen Song and Qiang Dong

Imprint: Antioxidants 2023, 12, 466. [https:// doi.org/10.3390/antiox1202046](https://doi.org/10.3390/antiox1202046)

Abstract: Phosphorus (P) is an essential macronutrient, and an important component of plant metabolism. However, little is known about the effects of low P availability on P absorption, the photosynthetic electron transport chain, and the antioxidant system in cotton. This study used cotton genotypes (sensitive FJA and DLNTH and tolerant BX014 and LuYuan343) with contrasting low-P tolerance in a hydroponic experiment under 15 µM, 50 µM, and 500 µM P concentrations. The results showed that low P availability reduced plant development and leaf area, shoot length, and dry weight in FJA and DLNADH, compared to BX014 and LuYuan343. The low P availability decreased the gas-exchange parameters such as the net photosynthetic rate, transpiration rate, and stomatal conductance, and increased the intercellular CO₂ concentration. Chlorophyll a fluorescence demonstrated that the leaves' absorption and trapped-energy flux were largely steady. In contrast, considerable gains in absorption

and trapped-energy flux per reaction center resulted from decreases in the electron transport per reaction center under low-P conditions. In addition, low P availability reduced the activities of antioxidant enzymes and increased the content of malondialdehyde in the cotton genotypes, especially in FJA and DLNTDH. Moreover, low P availability reduced the activity of PEPC and generated a decline in the content of ATP and NADPH. Our research can provide a theoretical physiological basis for the growth and tolerance of cotton under low-P conditions

Crop Protection

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Title: The cotton miR530-*SAP6* module activated by systemic acquired resistance mediates plant defense against *Verticillium dahlia*.

Author :

Guang Hu , Bingting Wang , Pei Jia , Pan Wu , Chengzhe Lu , Yunjiao Xu , Linfang Shi , Feiyan Zhang , Naiqin Zhong , Aimin Chen , Jiahe Wu

Imprint: Plant Science, Volume 330, May 2023, 111647

Abstract: Many cotton miRNAs in root responding to *Verticillium dahliae* infection have been identified. Conversely, the miRNAs in leaf distantly responding to this fungal infection from roots via systemic acquired resistance (SAR) remain to be explored. Here, we constructed two groups of leaf sRNA libraries in cotton treated with *V. dahliae* via root-dipped method at 7- and 10-day post inoculation. Analysis of high-throughput sRNA sequencing identified 75 known and 379 novel miRNAs, of which 41 miRNAs significantly differentially expressed in fungal treatment plant leaves compared to the mock treatment at two time points. Then we characterized the cotton miR530-*SAP6* module as a representative in the distant response to *V. dahliae* infection in roots. Based on degradome data and a luciferase (LUC) fusion reporter analysis, ghr-miR530 directedly cleaved *GhSAP6* mRNA during the post-transcriptional process. Silencing of ghr-miR530 increased plant defense to this fungus, while its overexpression attenuated plant resistance. In link with ghr-miR530 function, the knockdown of *GhSAP6* also decreased the plant resistance, resulting from down-regulation of SA-relative gene expression including *GhNPR1* and *GhPR1*. In all, these results demonstrated that there are numerous miRNAs in leaf distantly responding to *V. dahliae* infection in roots mediate plant immunity.

Title: Molecular Genetic Basis of Lab- and Field-Selected Bt Resistance in Pink Bollworm.

Author: Jeffrey A. Fabrick, Xianchun Li, Yves Carrière and Bruce E. Tabashnik

Imprint: Insects 2023, 14(2), 201; <https://doi.org/10.3390/insects14020201>

Abstract: The pink bollworm, *Pectinophora gossypiella*, is one of the most damaging pests of cotton worldwide. Cotton has been genetically engineered to produce insect-killing proteins from the bacterium *Bacillus thuringiensis* (Bt) to control major lepidopteran pests, including the pink bollworm. The Bt proteins in genetically engineered crops are not toxic to people, other vertebrates, or most beneficial insects. Advantages of Bt crops can include pest suppression, improved yields, increased farmer profits, and decreased use of conventional insecticides. In the United States, Bt cotton, sterile moth releases, and other tactics were used to eradicate the pink bollworm. For more than 20 years, Bt cotton has been effective against pink bollworm in China. However, the benefits of Bt crops are reduced when pests evolve resistance, as exemplified by pink bollworm resistance to Bt cotton in India. For each of the two Bt proteins used widely in Bt cotton, the genetic basis of resistance is similar between resistance selected in the lab versus the field, regardless of the country of origin. The results suggest that lab selection can be useful for identifying genes likely to be important in field-evolved resistance to Bt crops and that differences in management practices among countries caused different outcomes.

Title: Symptomatology of leaf spot disease of cotton caused by *Curvularia lunata* (Wakker) Boedijn .

Author: S H Joshi, J R Pandya and D H Chaudhary

Imprint: The Pharma Innovation Journal 2023; 12(1): 363-365

Abstract: The *Curvularia* leaf spot is the most important and destructive disease of cotton. The research was conducted to prove *Curvularia lunata* as an Incitant of *Curvularia* leaf spot of cotton. Infected leaves with typical symptoms were subjected to isolation and purification. As a result, brown to brownish-black fungal colonies were

found. The morphological study was carried out by using microscope, the spores of fungus found slightly curved or straight; mycelium was septate and brown to black in colour, and conidia was found 25-27×8-10 µm in size. The pathogenic nature of incitant was proved and typical symptoms such as small, brown to black in coloured spots were observed. Further, re-isolated pure culture resembled with original culture on the basis of their cultural characteristics. Hence it is identified as *Curvularia lunata* (Wakker) Boedijn - an Incitant of *Curvularia* leaf spot of cotton.

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Title: Assessment of Extension Interventions for Management of PBW for Enhancing Cotton Production through Frontline Demonstrations among Cotton Growers in Khammam District of Telangana .

Author: B. Raja Madhu Shekar , J. Hemanth Kumar , K. Ravikumar , V. Chaitanya and R. Uma Reddy

Imprint: International Journal of Bio-resource and Stress Management December 2022, 13(12):1471-1481

Abstract: Frontline Demonstrations were conducted at Krishi Vigyan Kendra, Wyrā, Khammam district, Telangana, India during kharif (June–December) from 2019, 2020 and 2021 in different villages of Khammam district. Total 30 demonstrations were laid out on farmers' fields in the district. The main objective was management of PBW with various technological interventions. The study revealed that 70.00% of the respondents had high school or above education, 46.67% of the respondents had more than 10 years of experience in farming, 100.00% gap was observed on use of pheromone traps and Trichogamma cards. The average yield recorded was 2207 kg ha⁻¹ in demonstration plot, a 22.75% increase over farmer's practice (1808 kg ha⁻¹). The technology gap under 3 year FLD programme was 1043 kg ha⁻¹, extension gap was 399 kg ha⁻¹ with a technology index of 32.09%. The demonstrated plots gave higher gross returns, net return with higher benefit cost ratio when compared to farmer's practice. In present study efforts were also made to study the impact of FLDs on horizontal spread which increased by 221.42%, adoption levels by 130.60%. The study also revealed that there was significant increase in knowledge level of the farmers due to frontline demonstrations, a significant and positive relationship existed between age of the respondent, education, farm size, farming experience, trainings received and extension contacts with yield of cotton.

Title: Characterization, expression, and functional analysis of TRPV genes in cotton aphid, *Aphis gossypii* Glover

Author:

Haixiang Lv , Yongsheng Yao , Xuchao Li , Xiwu Gao , Jianhong Li , Kangsheng Ma

Imprint: Comparative Biochemistry and Physiology Part C: Toxicology & Pharmacology, Volume 267, May 2023, 109582

Abstract: Transient receptor potential vanilloid (TRPV) channels have been found to be the molecular target of afidopyropen, a novel insecticide that is highly effective in controlling *Aphis gossypii* Glover in the field. However, the TRPV genes of *A. gossypii* has not yet been characterized. In this study, two TRPV genes of *A. gossypii* (*AgNan* and *AgIav*) were cloned and their expression levels were determined by quantitative real-time PCR (RT-qPCR). The deduced amino acids of *AgNan* and *AgIav* contain all conserved domains of TRPV and share very high amino acid identity with other insect TRPVs. *AgNan* and *AgIav* expressed in all developmental stages and their expression can be induced by afidopyropen in a dose- and time-dependent manner. Moreover, we found that silencing of *AgNan* and *AgIav* by RNA interference resulted in a significant mortality increase of adult *A. gossypii* compared to the control, which was even higher than 93 % at five days after feeding with ds*AgIav*, suggesting that knockdown of *AgNan* and *AgIav* have great effects on the survival of *A. gossypii*. The results of this study would be helpful for determining the reasonable use of afidopyropen in the integrated pest management programs of *A. gossypii* and provide useful information for further functional study of TRPVs in insects.

Title: Evaluation of Beauveria bassiana metabolite pretreated with silica nanoparticles against the cotton leafworm, *Spodoptera littoralis* (Boisd.)

Author: Hatem, M. Al-Shannaf ; Gamal, H. Rabie ; Rabab, A. Metwally ; Hala, Sh. Azab

Imprint: Bulletin of Faculty of Science, Zagazig University (BFSZU))) e-ISSN: 1110-1555 Volume-2023, Issue-1, pp-181-191

ABSTRACT : Plant herbivorous insects are danger to the agricultural production of crops. Insecticides resulted in habitat destruction due to high toxicity and resistance. Hence, the development of alternatives to such insecticides is a sustainable approach to supreme crop production with the least damage is a crucially prerequisite. As a result, the current study was carried out to evaluate the potential effect of arbuscular mycorrhizal (AM) fungi along with *Beauveria bassiana* silica nanoparticles (Si NPs) as a new approach to protect cotton (*Gossypium hirsutum* L.) against *Spodoptera littoralis*. AM and non-AM inoculated cotton plants were infested with *S. littoralis* and then treated with metabolites of *B. bassiana* Si NPs or Chlorpyrifos.

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Title: A simple technique for continuous rearing of cotton aphid, *Aphis gossypii* Glover

Author: Y. Venkanna & Sachin S. Suroshe

Imprint: International Journal of Tropical Insect Science (2023)

Abstract: Cotton aphid, *Aphis gossypii* Glover is a cosmopolitan pest which causes huge damage by sucking a vital content of plants, it also transmit viral diseases in various field and horticultural crops. Due to development of resistance to insecticides and the environmental hazard it poses, more emphasis is being directed on biological control of cotton aphid. Continuous rearing of host insects is a key in biological control experiments. Of late, potted cotton plants are being extensively used for the rearing of cotton aphids. This method is cumbersome and requires more time and space. The other methods viz., rearing on excised cotton leaves and artificial diet are not suitable for rearing in large numbers. Hence, the present studies were aimed to find out an easy and reliable method for rearing. A simple rearing technique based on a host, *Hibiscus cannabinus* L. of Malvaceae family, is found effective for continuous rearing of cotton aphids throughout the year. Here, we assessed the developmental periods and population change of aphids as temperature dependent parameters. Among the different temperatures tested, 24 °C is found most suitable to produce nymphs and wingless adults in large numbers. For the production of winged adults, rearing at 27 °C is observed most suitable. This technique has certain advantages as it requires less space, is easy to maintain, incurs less cost and ensures clear visibility of all the instars for counting. This technique would help researchers in continuous rearing of *A. gossypii* for use in biological control and other studies.

Plant Genetics and Breeding

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Title: Exploiting genetic diversity in enhancing phenotypic plasticity to develop climate-resilient cotton.

Author: Zulfiqar Ali, Hira Maryam, Muhammad Abu Bakar Saddique & Rao Muhammad Ikram

Imprint: Genetic Resources and Crop Evolution (2023)

Abstract: Larger emissions of greenhouse gases in the atmosphere and climatic variability are the primary constraints responsible for biotic and abiotic stresses. Whilst, in cotton germplasm resources, beneficial alleles have the potential if exploit in developing climate-resilient cultivars which are well-adapted to environmental conditions. Thus, the utilization of variability among *Gossypium* species upsurges the possibility of long-term persistence of cotton crop. The narrow genetic base of modern cultivars poses a major challenge to crop improvement and utilizing crop wild relatives is one of the most promising approach to widen the genetic diversity among cultivars. This review article meets the status of genetic diversity of *Gossypium* species, with an exploration of crop wild relatives as a potential source to improve tolerance against biotic and abiotic stresses. We summarized the current breakthrough in the field of genomics and phenomics platforms and discussed the utilization of recent reference genomes of cotton and assemblies of its wild relatives. Moreover, elaborated the computational means of information to further exploitation of wild resources and cultivated species in the next generation editing tools. We foresee that the integrated use of various technologies will be crucial for cotton improvement in current climate change scenarios. Thus, breeders can use the rich diversity from landraces and the cultivated cotton species to prioritize the selection of agronomically important traits.

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Title: Detecting Cotton Leaf Curl Virus Resistance Quantitative Trait Loci in *Gossypium hirsutum* and iCottonQTL a New R/Shiny App to Streamline Genetic Mapping.

Author: Ashley N. Schoonmaker, Amanda M. Hulse-Kemp, Ramey C. Youngblood

Imprint: Plants 2023, 12(5), 1153; <https://doi.org/10.3390/plants12051153>

Abstract: Cotton leaf curl virus (CLCuV) causes devastating losses to fiber production in Central Asia. Viral spread across Asia in the last decade is causing concern that the virus will spread further before resistant varieties can be bred. Current development depends on screening each generation under disease pressure in a country where the disease is endemic. We utilized quantitative trait loci (QTL) mapping in four crosses with different sources of resistance to identify single nucleotide polymorphism (SNP) markers associated with the resistance trait to allow development of varieties without the need for field screening every generation. To assist in the analysis of multiple populations, a new publicly available R/Shiny App was developed to streamline genetic mapping using SNP arrays and to also provide an easy method to convert and deposit genetic data into the CottonGen database. Results identified several QTL from each cross, indicating possible multiple modes of resistance. Multiple sources of resistance would provide several genetic routes to combat the virus as it evolves over time. Kompetitive allele specific PCR (KASP) markers were developed and validated for a subset of QTL, which can be used in further development of CLCuV-resistant cotton lines.

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Title: Genomic identification of cotton SAC genes branded ovule and stress-related key genes in *Gossypium hirsutum*.

Author: Ma Shuya, Liu Le, Shi Huiyun, Gu Yu, Li Yujun, and Ghulam Qanmber

Imprint: Front Plant Sci. 2023; 14: 1123745.

Abstract: SAC genes have been identified to play a variety of biological functions and responses to various stresses. Previously, SAC genes have been recognized in animals and *Arabidopsis*. For the very first time, we identified 157 SAC genes in eight cotton species including three diploids and five tetraploids with 23 SAC members in *G. hirsutum*. Evolutionary analysis classified all cotton SAC gene family members into five distinct groups. Cotton SAC genes showed conserved sequence logos and WGD or segmental duplication. Multiple synteny and collinearity analyses revealed gene family expansion and purifying selection pressure during evolution. *G. hirsutum* SAC genes showed uneven chromosomal distribution, multiple exons/introns, conserved protein motifs, and various growth and stress-related *cis*-elements. Expression pattern analysis revealed three *GhSAC* genes (*GhSAC3*, *GhSAC14*, and *GhSAC20*) preferentially expressed in flower, five genes (*GhSAC1*, *GhSAC6*, *GhSAC9*, *GhSAC13*, and *GhSAC18*) preferentially expressed in ovule and one gene (*GhSAC5*) preferentially expressed in

fiber. Similarly, abiotic stress treatment verified that *GhSAC5* was downregulated under all stresses, *GhSAC6* and *GhSAC9* were upregulated under NaCl treatment, and *GhSAC9* and *GhSAC18* were upregulated under PEG and heat treatment respectively. Overall, this study identified key genes related to flower, ovule, and fiber development and important genetic material for breeding cotton under abiotic stress conditions.

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Title: Genome-Wide Characterization of the SAMS Gene Family in Cotton Unveils the Putative Role of *GhSAMS2* in Enhancing Abiotic Stress Tolerance.

Author: Joseph Wanjala Kilwake, Muhammad Jawad Umer

Imprint: Agronomy 2023, 13(2), 612; <https://doi.org/10.3390/agronomy13020612>

Abstract: The most devastating abiotic factors worldwide are drought and salinity, causing severe bottlenecks in the agricultural sector. To acclimatize to these harsh ecological conditions, plants have developed complex molecular mechanisms involving diverse gene families. Among them, S-adenosyl-L-methionine synthetase (SAMS) genes initiate the physiological, morphological, and molecular changes to enable plants to adapt appropriately. We identified and characterized 16 upland cotton SAMS genes (*GhSAMSs*). Phylogenetic analysis classified the *GhSAMSs* into three major groups closely related to their homologs in soybean. Gene expression analysis under drought and salt stress conditions revealed that *GhSAMS2*, which has shown the highest interaction with *GhCBL10* (a key salt responsive gene), was the one that was most induced. *GhSAMS2* expression knockdown via virus-induced gene silencing (VIGS) enhanced transgenic plants' susceptibility to drought and salt stress. The TRV2:*GhSAMS2* plants showed defects in terms of growth and physiological performances, including antioxidative processes, chlorophyll synthesis, and membrane permeability. Our findings provide insights into SAMS genes' structure, classification, and role in abiotic stress response in upland cotton. Moreover, they show the potential of *GhSAMS2* for the targeted improvement of cotton plants' tolerance to multiple abiotic stresses.

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Title: Comparative analysis of genome sequences of the two cultivated tetraploid cottons, *Gossypium hirsutum* (L.) and *G. barbadense* (L.)

Author:

Qingying Meng , Jiaqi Gu , Zhongping Xu , Jie Zhang , Jiwei Tang , Anzhou Wang , Ping Wang , Zhaowei Liu

Imprint: Industrial Crops and Products, Volume 196, June 2023, 116471

Abstract: With innovations in sequencing technology and the progress of high-performance computing systems, it is now relatively straightforward to sequence and assemble complex genomes. Many genomes from multiple cotton species have been released in recent years, with the highly homozygous standard genetic lines of two cultivated allotetraploid cottons, *i.e.*, *Gossypium hirsutum* TM-1 and *G. barbadense* 3-79, assembled multiple times by different research groups using diverse sequencing technologies. The assembly quality among these genomes is variable, even between multiple accessions or versions of the same species, which can generate both confusion in choosing the appropriate genome for genetic analysis and obstacles when comparing results among the different reference genomes. Accordingly, an assessment of the many cotton genome sequences is necessary to facilitate both choice of genome sequence and comparisons between different versions or species. Here we comprehensively assess and compare genome assembly accuracy, completeness, and contiguity for nine *G. hirsutum* assemblies and four *G. barbadense* assemblies using multiple analysis strategies with the same criteria. We identify centromeric regions and several large-scale inversions among genomes from the same accession, indicating structural errors introduced during sequence ordering and orientation in *G. hirsutum* and *G. barbadense* genome assembly. Gene relationships between annotations from multiple genomes are defined within and across species, and the results are available at the Cotton Paralogs Groups Search website (<https://ihope.shinyapps.io/cottonParalogs/>), a convenient resource for converting gene ids and comparing annotations between different genome versions. This study comprehensively assesses and compares assembly quality among multiple versions of the two cultivated tetraploid cotton species with different assembly strategies, illustrating the challenges of sequencing and assembling complex genomes and providing a resource for cotton genomics.

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Title: Genome-Wide Identification and Characterization of the PPO Gene Family in Cotton (*Gossypium*) and Their Expression Variations Responding to *Verticillium* Wilt Infection.

Author: Shuhan Yang, Qun Ge, Yuzhen Shi

Imprint: Genes , Volume 14 , Issue 2 , [10.3390/genes14020477](https://doi.org/10.3390/genes14020477)

Abstract: Polyphenol oxidases (PPOs) are copper-binding metalloproteinases encoded by nuclear genes, ubiquitously existing in the plastids of microorganisms, plants, and animals. As one of the important defense enzymes, PPOs have been reported to participate in the resistant processes that respond to diseases and insect pests in multiple plant species. However, PPO gene identification and characterization in cotton and their expression patterns under *Verticillium* wilt (VW) treatment have not been clearly studied. In this study, 7, 8, 14, and 16 PPO genes were separately identified from *Gossypium arboreum*, *G. raimondii*, *G. hirsutum*, and *G. barbadense*, respectively, which were distributed within 23 chromosomes, though mainly gathered in chromosome 6. The phylogenetic tree manifested that all the PPOs from four cotton species and 14 other plants were divided into seven groups, and the analyses of the conserved motifs and nucleotide sequences showed highly similar characteristics of the gene structure and domains in the cotton PPO genes. The dramatically expressed differences were observed among the different organs at various stages of growth and development or under the diverse stresses referred to in the published RNA-seq data. Quantitative real-time PCR (qRT-PCR) experiments were also performed on the GhPPO genes in the roots, stems, and leaves of VW-resistant MBI8255 and VW-susceptible CCRI36 infected with *Verticillium dahliae* V991, proving the strong correlation between PPO activity and VW resistance. A comprehensive analysis conducted on cotton PPO genes contributes to the screening of the candidate genes for subsequent biological function studies, which is also of great significance for the in-depth understanding of the molecular genetic basis of cotton resistance to VW.

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Title: First Report on the Genetic Diversity of Populations of *Gossypium barbadense* L. and *Gossypium hirsutum* L. in the Amazonian Native Communities, Cusco-Peru.

Author: Luis Morales-Aranibar Francisca Elena Yucra Yucra, Carlos Genaro Morales Aranibar

Imprint: Plants 2023, 12(4), 865; <https://doi.org/10.3390/plants12040865>

Abstract: The genus *Gossypium* has important ethnobotanical and economic value for Amazonian Native Communities (A.N.C.). However, little research has been undertaken on the distribution and genetic diversity of cotton populations maintained in the Peruvian rainforest. This work aims to present the first report on the genetic diversity of *Gossypium* spp. populations in the A.N.C. of the province of La Convención, Cusco-Peru. The methodology was based on exploring, collecting, identifying, and characterizing the *Gossypium* populations present in the A.N.C. Twenty-six descriptors were evaluated (9 quantitative and 17 qualitative), and with this information,

distribution, correlation, and principal component (PC) analyses were carried out. As a result, plants of two species [*G. barbadense* L. (44 samples) and *G. hirsutum* L. (19 samples)], one variety [*G. barbadense* var. *brasiliensis* (75 samples)], and three previously unidentified variations (9 samples) were identified. Altogether, 147 samples were collected. *G. barbadense* var. *brasiliensis*, which was always found in association with other economic crops within an altitude range of 338 to 1086 m, was the most predominant (51%), distributed in eleven A.N.C. and always in small plots (up to 2 ha). *G. barbadense* L. was cultivated between 397 and 1137 m of altitude in eight A.N.C. in plots of up to 3 ha in marginal lands. *G. hirsutum* L., with a smaller distribution (13%), was found between 334 and 497 m of altitude in only three communities; this species is cultivated in marginal areas throughout the year. The variability found for the first two PCs when considering the quantitative and qualitative descriptors was high (74.7%) and moderate (48.2%), respectively. When combining all the descriptors, the analysis showed that the first two PCs accounted for 51.8% of the total variability of the data. The PCs of the two types of data and their combination confirmed that the three populations found were grouped. The nine undefined samples were close to or intermediate between the described ones, showing that these samples may be the result of spontaneous crosses; as such, these samples need to be better evaluated with other tools for further definition. The information obtained shows that in the A.N.C. of Cusco-Peru, there is variability conserved by the inhabitants, who have been able to maintain and use these genotypes, even from their Amazonian indigenous ancestry, and the environment has been able to generate variability among the species, as will be highlighted in future works.

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Title: Mapping of quantitative trait loci controlling cotton leaf curl disease resistance in upland cotton.

Author: Muhammad N. Sattar, Muhammad Javed, Syed B. Hussain, Muhammad Babar, Peng W. Chee, Zafar Iqbal, Muhammad Munir, Sallah A. Al-Hashedi

Imprint: Plant Breeding, First published: 22 February 2023,
<https://doi.org/10.1111/pbr.13084>

Abstract: Cotton leaf curl disease (CLCuD) is a major threat to cotton production in Asia and Africa. Using marker-assisted breeding can be the best sustainable approach to tackle CLCuD. Identification of new QTLs in the indigenous cotton germplasm is necessary to combat CLCuD. The current study was designed to construct a genetic linkage map of bi-parental F2:F3 populations developed from highly tolerant MNH-886 and highly susceptible S-12 cotton cultivars. One hundred seven CLCuD-associated

simple sequence repeat (SSR) marker alleles were identified as polymorphic and three new QTLs were found on chromosomes C11, C19 and C21. Two QTLs on chromosomes C11 and C19 were detected in both F2 and F3 populations in the region flanked by SSR markers CIR316 and BNL4094, and BNL285 and BNL3348, respectively. Whereas, one QTL on chromosome C21 was detected in the region flanked by SSR markers JESPR158 and JESPR135 in both F2 and F3 generations. The CLCuD-associated QTLs identified in this study can help fine-tune the molecular mapping of the QTLs on the cotton genome against CLCuD.

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Title: Estimating the combining ability and genetic parameters for growth habit, yield, and fiber quality traits in some Egyptian cotton crosses

Author: M.S. Abdel-Aty, F. A. Sorour, W. M. B. Yehia, H. M. K. Kotb, Ahmed M. Abdelghany, Sobhi F. Lamloom, Adnan Noor Shah & Nader R. Abdelsalam

Imprint: *BMC Plant Biology* volume 23, Article number: 121 (2023)

Abstract: It is crucial to understand how targeted traits in a hybrid breeding program are influenced by gene activity and combining ability. During the three growing seasons of 2015, 2016, and 2017, a field study was conducted with twelve cotton genotypes, comprised of four testers and eight lines. Thirty-two F1 crosses were produced in the 2015 breeding season using the line x tester mating design. The twelve genotypes and their thirty-two F1 crosses were then evaluated in 2016 and 2017. The results demonstrated highly significant differences among cotton genotypes for all the studied traits, showing a wide range of genetic diversity in the parent genotypes. Additionally, the line-x-tester interaction was highly significant for all traits, suggesting the impact of both additive and non-additive variations in gene expression. Furthermore, the thirty-two cotton crosses showed high seed cotton output, lint cotton yield, and fiber quality, such as fiber length values exceeding 31 mm and a fiber strength above 10 g/tex. Accordingly, selecting lines and testers with high GCA effects and crosses with high SCA effects would be an effective approach to improve the desired traits in cotton and develop new varieties with excellent yield and fiber quality.

Fiber and Fiber Technology

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Title: Yield and fiber quality traits of cotton (*Gossypium hirsutum* L.) cultivars analyzed by biplot method

Author: Mustafa Yaşar

Imprint: Journal of King Saud University - Science, Volume 35, Issue 4, June 2023, 102632

Abstract: Cotton is a vital fiber crop fulfilling global demands for raw materials in the textile sector. Therefore, high-yielding cultivars with superior-quality traits are desired at regional scales. The high-yielding cultivars can be selected by determining their responses to various environmental conditions at different locations over a short or long period. Genotypes, environment, and year significantly alter seed cotton yield and fiber quality. Therefore, determining the response to various environmental conditions is necessary for selecting high-yielding cultivars with superior fiber quality.

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Title: Co-expression networks regulating cotton fiber initiation generated by comparative transcriptome analysis between fiberless XZ142FLM and *GhVIN1i*

Author: Jun Li , Yong-Ling Ruan , Fan Dai , Shuijin Zhu , Tianzhen Zhang

Imprint: Industrial Crops and Products, Volume 194, April 2023, 116323

Abstract: Cotton produces natural fiber as crucial raw material for textile industry and thus is economically one of the most important crops worldwide. Currently the mechanisms that control fiber initiation on ovules are still not well understood. In this study, we performed comparative transcriptome analysis between the natural fiberless mutant XZ142FLM and transgenic fiberless line *GhVIN1i* generated by RNAi silencing of *GhVIN1* to identify molecular regulatory networks controlling fiber initiation. It was found that XZ142FLM and *GhVIN1i* shared many common differentially expressed genes (DEGs) in ovules during fiber initiation, and their respective DEGs were enriched in several identical pathways related to fiber initiation. Many reported fiber initiation or elongation related genes including *GhMML3*, *GhVIN1*, *GhMYB25*, *GhHD-1*, *GhHOX3* exhibited similar expression patterns in XZ142FLM and *GhVIN1i* during fiber initiation, suggesting similar mechanisms of fiber initiation operating in the two

fiberless lines, which was further verified by comparative temporal expression pattern analysis between TM-1/XZ142FLM and Coker 312/*GhVIN1i*. Co-expression regulatory networks for controlling fiber initiation were constructed for XZ142FLM and *GhVIN1i*, respectively, which centered on *GhMML3* or *GhVIN1* with many known fiber initiation/elongation related genes. Several transcription factors and hub genes were identified in the co-expression networks generated, which may facilitate future research in identification of novel candidate genes regulating fiber initiation and elongation. Overall, the results obtained in this study shed light on the regulatory networks mediated by *GhMML3* and *GhVIN1* for controlling fiber initiation in cotton.

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Title: Brassinosteroids regulate cotton fiber elongation by modulating very-long-chain fatty acid biosynthesis .

Author: Zuoren Yang, Zhao Liu, Xiaoyang Ge, Lili Lu, Wenqiang Qin, Ghulam Qanmber, Le Liu, Zhi Wang, Fuguang Li

Imprint: The Plant Cell, koad060, <https://doi.org/10.1093/plcell/koad060>

Abstract: Brassinosteroid (BR), a growth-promoting phytohormone, regulates many plant growth processes including cell development. However, the mechanism by which BR regulates fiber growth is poorly understood. Cotton (*Gossypium hirsutum*) fibers are an ideal single-cell model in which to study cell elongation due to their length. Here we report that BR controls cotton fiber elongation by modulating very-long-chain fatty acid (VLCFA) biosynthesis. BR deficiency reduces the expression of 3-ketoacyl-CoA synthases (*GhKCSs*), the rate-limiting enzymes involved in VLCFA biosynthesis, leading to lower saturated VLCFA contents in *pagoda1* (*pag1*) mutant fibers. In vitro ovule culture experiments show that BR acts upstream of VLCFAs. Silencing of *BRI1-EMS-SUPPRESSOR 1.4* (*GhBES1.4*), encoding a master transcription factor of the BR signaling pathway, significantly reduces fiber length, whereas *GhBES1.4* overexpression produces longer fibers. *GhBES1.4* regulates endogenous VLCFA contents and directly binds to BR RESPONSE ELEMENTS (BRREs) in the *GhKCS10_At* promoter region, which in turn regulates *GhKCS10_At* expression to increase endogenous VLCFA contents. *GhKCS10_At* overexpression promotes cotton fiber elongation, whereas *GhKCS10_At* silencing inhibits cotton fiber growth, supporting a positive regulatory role for *GhKCS10_At* in fiber elongation. Overall, these results uncover a mechanism of fiber elongation through crosstalk between BR and VLCFAs at the single-cell level.

Title: Quantitative effects of heat stress on fiber related and agronomically important parameters in cotton. (*Gossypium hirsutum* L.)

Author: HUSSAIN S , ASLAM MZ , YOUSAF MI, IQBAL J , BUKHARI MSJ , ALI F , ASHFAQ M , QAMAR MJ , FAROOQ MR , HAFEEZ Z , AKHTAR I , SHAH SWH

Imprint: Biol. Clin. Sci. Res. J., Volume, 2023: 210

Abstract: Climate change is one of the biggest problems for growing crops in a sustainable way around the world. At the cotton research station in Bahawalpur, this experiment aimed to assess and classify cotton genotypes under conditions of heat stress. The study was done using RCBD with three replications. The distance between plants was 30 cm, and the distance between rows was kept at 75 cm. For key plant and fiber quality traits, data were taken from ten fully guarded plants and chosen randomly. Under conditions of heat stress, ANOVA showed that there were highly significant differences among the plant traits that were studied. The correlation coefficient analysis showed that seed cotton yield has a positive correlation with plant height ($r = 0.46$), plant population per hectare ($r = 0.33$), sympodial branches per plant ($r = 0.27$), number of bolls per plant ($r = 0.27$) and nodes per plant ($r = 0.27$) but a negative relationship with staple length ($r = -0.35$). The multivariate statistical methods of principal component and cluster analysis were used to describe cotton genotypes. Principal component analysis and cluster analysis showed that the most productive and heat-tolerant cotton genotypes were BH-200, BH-254, CIM-600, and BH-341. Also, BH-284 seemed more resistant to CLCuV than the other genotypes. So, rigorous, large-scale, and multilocation testing must be done on these cotton genotypes and plant traits to make cotton genotypes that can handle heat and CLCuV.

Title: Evaluating the effects of defoliant spraying time on fibre yield and quality of different cotton cultivars.

Author: Liyuan Wang, Yongsheng Deng, Fanjin Kong, Bing Duan, Muhammad Saeed

Imprint: The Journal of Agricultural Science , First View , pp. 1 - 12,
DOI: <https://doi.org/10.1017/S0021859623000151>

Abstract: Chemical defoliant are widely used in cotton (*Gossypium* L.) to accelerate leaf abscission and boll maturation, as well as, to facilitate mechanical harvesting. The current study was conducted to determine the interactive effect of cotton cultivars and spraying time of defoliant on defoliation, boll opening, fibre yield and quality. An experiment was performed with four cultivars and three defoliant spraying time during 2019 and 2020 in split plot design with three replications. At harvest, the defoliation and boll opening rate of all treatments after spraying defoliant was 94.6 and 85.4%, while the blank control (water) was 73.9 and 79.1%, respectively. After spraying defoliant, the effects of defoliation rate, boll opening rate, fibre yield and quality were different among cultivars, indicating that different cultivars had different responses to defoliant. Among them, L7619 was the most sensitive to defoliant, with the average defoliation rate of 95.6% and a seed cotton yield reduction of 882.9 kg/ha. Among the different time of applications, late spraying (17 September, B3) of defoliant recorded the highest defoliation rate (97.3%), boll opening rate (89.8%), seed cotton yield (3991 kg/ha) and steadily increased the fibre strength by 0.59 cN/tex compared with the control. Late spraying of defoliant had little or even no adverse effect on the remaining fibre quality traits (length, uniformity, micronaire and elongation). In general, these results suggested that the appropriate time for spraying defoliant can be determined based on the sensitivity of the cotton cultivar, the weather conditions at the field and the harvest time.

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Title: A brassinosteroid transcriptional regulatory network participates in regulating fiber elongation in cotton.

Author: Le Liu , Guoquan Chen , Shengdong Li , Yu Gu , Lili Lu , Ghulam Qanmber Venugopal Mendu , Zhao Liu , Fuguang Li and Zuoren Yang

Imprint: Plant Physiology 2023: 00: 1–16 <https://doi.org/10.1093/plphys/kiac590>

Abstract: Brassinosteroids (BRs) participate in the regulation of plant growth and development through BRI1-EMS-SUPPRESSOR1 (BES1)/ BRASSINAZOLE-RESISTANT1 (BZR1) family transcription factors. Cotton (*Gossypium hirsutum*) fibers are highly elongated single cells, and BRs play a vital role in the regulation of fiber elongation. However, the mode of action on how BR is involved in the regulation of cotton fiber elongation remains unexplored. Here, we generated GhBES1.4 over expression lines and found that overexpression of GhBES1.4 promoted fiber elongation, whereas silencing of GhBES1.4 reduced fiber length. DNA affinity purification and sequencing (DAP-seq) identified 1,531 target genes of GhBES1.4, and five recognition motifs of GhBES1.4 were identified by enrichment analysis. Combined analysis of DAP-seq and RNA-seq data of GhBES1.4-OE/RNAi provided mechanistic insights into GhBES1.4-mediated regulation of cotton fiber development. Further, with the

integrated approach of GWAS, RNA-seq, and DAP-seq, we identified seven genes related to fiber elongation that were directly regulated by GhBES1.4. Of them, we showed Cytochrome P450 84A1 (GhCYP84A1) and 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (GhHMG1) promote cotton fiber elongation. Overall, the present study established the role of GhBES1.4-mediated gene regulation and laid the foundation for further understanding the mechanism of BR participation in regulating fiber development.

Plant Biotechnology

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Title: Genome-Wide Identification and Evolutionary Analysis of Gossypium YTH Domain-Containing RNA-Binding Protein Family and the Role of GhYTH8 in Response to Drought Stress.

Author: Wei Hao, Weipeng Wang, Xiangfen Xiao, Jiali Sun

Imprint: Plants 2023, 12(5), 1198; <https://doi.org/10.3390/plants12051198>

Abstract: YTH domain-containing proteins are one kind of RNA-binding protein involved in post-transcriptional regulation and play multiple roles in regulating the growth, development, and abiotic stress responses of plants. However, the YTH domain-containing RNA-binding protein family has not been previously studied in cotton. In this study, a total of 10, 11, 22, and 21 YTH genes were identified in *Gossypium arboreum*, *Gossypium raimondii*, *Gossypium barbadense*, and *Gossypium hirsutum*, respectively. These *Gossypium* YTH genes were categorized into three subgroups by phylogenetic analysis. The chromosomal distribution, synteny analysis, structures of *Gossypium* YTH genes, and the motifs of YTH proteins were analyzed. Furthermore, the cis-element of GhYTH genes promoter, miRNA targets of GhYTH genes, and subcellular localization of GhYTH8 and GhYTH16 were characterized. Expression patterns of GhYTH genes in different tissues, organs, and in response to different stresses were also analyzed. Moreover, functional verifications revealed that silencing GhYTH8 attenuated the drought tolerance in the upland cotton TM-1 line. These findings provide useful clues for the functional and evolutionary analysis of YTH genes in cotton.

Title: Selection Procedures for Improving Some Economic Characters and Correlated Responses in Cotton (*Gossypium barbadense* L.) Cross

Author: Heba Hussien Elsayed Hamed , Soad H. Hafez , Ashraf Ebrahim Ismail Darwesh , Maamoun Ahmed Abdel-Moneam

Imprint: Plant Cell Biotechnology and Molecular Biology, Page 1-16
DOI: 10.56557/pcbmb/2023/v24i1-28091

Abstract: A study was done at Sakha Agricultural Research Station Farm, Kafr El-Sheikh, Egypt during 2019-2021 growing seasons. The study aimed at assessing the efficacy and usability of various selection procedures, determining the effectiveness of selection for superior families and estimating the response to selection. The materials utilized for selection of promising families in early segregating generations included F₂, F₃ and F₄ generations of Giza 94 × S106 cotton cross.. Findings revealed better F₄ means than the F₃ and F₂ means for all studied characters due to the selection procedures used. High heritability values were recorded for most studied characters. Significant desirable correlations were noticed between seed cotton yield with lint yield, bolls/plant, lint/seed, seeds/boll and boll weight. Canonical discriminant analysis among F₃ families showed that the first five canonical functions accounted for 100% of total variances. While first canonical discriminant function represented 46% of the total variance among genotypes with the greatest Eigen value and prevailed by great loading from most yield characters and micronaire reading. Ten of the selection indices surpassed direct selection in improving lint yield. The highest actual advance in lint yield for F₃ obtained from selection index comprising lint yield/plant in addition to bolls/plant, seeds per boll and lint per seed. In F₄ generation, the maximum actual gains were obtained for most yield traits with indices involved lint yield/plant and seeds/boll with lint/seed. Most of the selected families in F₄ scored high values for almost all the studied characters and surpassed the corresponding means of selected families in F₃ and F₂ generations; these selected families might be used to improve cotton yield and fiber quality in breeding programs.

Title: Identification and Characterization of Phycocyanin Family Genes in Cotton Genomes.

Author: Muhammad Bilal Tufail, Muhammad Yasir, Dongyun Zuo

Imprint: Genes 2023, 14(3), 611; <https://doi.org/10.3390/genes14030611>

Abstract: Phycocyanins (PCs) are a class of plant-specific blue copper proteins that have been demonstrated to play a role in electron transport and plant development. Through analysis of the copper ligand residues, spectroscopic properties, and domain architecture of the protein, PCs have been grouped into four subfamilies: uclacyanins (UCs), stellacyanins (SCs), plantacyanins (PLCs), and early nodulin-like proteins (ENODLs). The present study aimed to identify and characterise the PCs present in three distinct cotton species (*Gossypium hirsutum*, *Gossypium arboreum*, and *Gossypium raimondii*) through the identification of 98, 63, and 69 genes respectively. We grouped PCs into four clades by using bioinformatics analysis and sequence alignment, which exhibit variations in gene structure and motif distribution. PCs are distributed across all chromosomes in each of the three species, with varying numbers of exons per gene and multiple conserved motifs, and with a minimum of 1 and maximum of 11 exons found on one gene. Transcriptomic data and qRT-PCR analysis revealed that two highly differentiated PC genes were expressed at the fibre initiation stage, while three highly differentiated PCs were expressed at the fibre elongation stage. These findings serve as a foundation for further investigations aimed at understanding the contribution of this gene family in cotton fibre production.

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Title: Assessing the biotechnological potential of cotton type-1 and type-2 diacylglycerol acyltransferases in transgenic systems

Author : Jay Shockey , Prasad Parchuri , Gregory N. Thyssen , Philip D. Bates

Imprint: Plant Physiology and Biochemistry, Volume 196, March 2023, Pages 940-951

Abstract: The chemical and physical properties of vegetable oils are largely dictated by the ratios of 4–6 common fatty acids contained within each oil. However, examples of plant species that accumulate from trace amounts to >90% of certain unusual fatty acids in seed triacylglycerols have been reported. Many of the general enzymatic reactions that drive both common and unusual fatty acid biosynthesis and accumulation in stored lipids are known, but which isozymes have evolved to specifically fill this role and how they coordinate *in vivo* is still poorly understood. Cotton (*Gossypium* sp.) is the very rare example of a commodity oilseed that produces biologically relevant amounts of unusual fatty acids in its seeds and other organs. In this case, unusual cyclopropyl fatty acids (named after the cyclopropane and cyclopropene moieties within the fatty acids) are found in membrane and storage glycerolipids (e.g. seed oils). Such fatty acids are useful in the synthesis of lubricants, coatings, and other types of valuable industrial feedstocks. To characterize the role of cotton acyltransferases in cyclopropyl fatty acid accumulation for bioengineering applications, we cloned and characterized type-1 and

type-2 diacylglycerol acyltransferases from cotton and compared their biochemical properties to that of litchi (*Litchi chinensis*), another cyclopropyl fatty acid-producing plant. The results presented from transgenic microbes and plants indicate both cotton DGAT1 and DGAT2 isozymes efficiently utilize cyclopropyl fatty acid-containing substrates, which helps to alleviate biosynthetic bottlenecks and enhances total cyclopropyl fatty acid accumulation in the seed oil.

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Title: Genome-Wide Identification, Characterization and Experimental Expression Analysis of CNGC Gene Family in *Gossypium*.

Author: Lei Chen, Wenwen Wang, Hailun He, Peng Yang, Xiaoting Sun, and Zhengsheng Zhang

Imprint: Int. J. Mol. Sci. 2023, 24(5), 4617; <https://doi.org/10.3390/ijms24054617>

Abstract: Cyclic nucleotide-gated ion channels (CNGCs) are channel proteins for calcium ions, and have been reported to play important roles in regulating survival and environmental response of various plants. However, little is known about how the CNGC family works in *Gossypium*. In this study, 173 CNGC genes, which were identified from two diploid and five tetraploid *Gossypium* species, were classified into four groups by phylogenetic analysis. The collinearity results demonstrated that CNGC genes are integrally conservative among *Gossypium* species, but four gene losses and three simple translocations were detected, which is beneficial to analyzing the evolution of CNGCs in *Gossypium*. The various cis-acting regulatory elements in the CNGCs' upstream sequences revealed their possible functions in responding to multiple stimuli such as hormonal changes and abiotic stresses. In addition, expression levels of 14 CNGC genes changed significantly after being treated with various hormones. The findings in this study will contribute to understanding the function of the CNGC family in cotton, and lay a foundation for unraveling the molecular mechanism of cotton plants' response to hormonal changes.

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Title: NMR-Based Metabolomics: A New Paradigm to Unravel Defense-Related Metabolites in Insect-Resistant Cotton Variety through Different Multivariate Data Analysis Approaches.

Author: Anam Amin Shami, Muhammad Tayyab Akhtar, Muhammad Waseem Mumtaz

Imprint: Molecules 2023, 28(4), 1763; <https://doi.org/10.3390/molecules28041763>

Abstract: Cotton (*Gossypium hirsutum*) is an economically important crop and is widely cultivated around the globe. However, the major problem of cotton is its high vulnerability to biotic and abiotic stresses. It has been around three decades since the cotton plant was genetically engineered with genes encoding insecticidal proteins (mainly Cry proteins) with an aim to protect it against insect attack. Several studies have been reported on the impact of these genes on cotton production and fiber quality. However, the metabolites responsible for conferring resistance in genetically modified cotton need to be explored. The current work aims to unveil the key metabolites responsible for insect resistance in Bt cotton and also compare the conventional multivariate analysis methods with deep learning approaches to perform clustering analysis. We aim to unveil the marker compounds which are responsible for inducing insect resistance in cotton plants. For this purpose, we employed ¹H-NMR spectroscopy to perform metabolite profiling of Bt and non-Bt cotton varieties, and a total of 42 different metabolites were identified in cotton plants. In cluster analysis, deep learning approaches (linear discriminant analysis (LDA) and neural networks) showed better separation among cotton varieties compared to conventional methods (principal component analysis (PCA) and orthogonal partial least square discriminant analysis (OPLSDA)). The key metabolites responsible for inter-class separation were terpinolene, α-ketoglutaric acid, aspartic acid, stigmasterol, fructose, maltose, arabinose, xylulose, cinnamic acid, malic acid, valine, nonanoic acid, citrulline, and shikimic acid. The metabolites which regulated differently with the level of significance $p < 0.001$ amongst different cotton varieties belonged to the tricarboxylic acid cycle (TCA), Shikimic acid, and phenylpropanoid pathways. Our analyses underscore a biosignature of metabolites that might involve in inducing insect resistance in Bt cotton. Moreover, novel evidence from our study could be used in the metabolic engineering of these biological pathways to improve the resilience of Bt cotton against insect/pest attacks. Lastly, our findings are also in complete support of employing deep machine learning algorithms as a useful tool in metabolomics studies.

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Title: Freezing transcriptome analysis showed that *GhZAT10* regulates freezing tolerance through a partially CBF-dependent pathway in upland cotton (*Gossypium hirsutum* L.)

Author:

Pengzhen Li , Minxuan Wang , Yuqing Zhou , Qidi Wu , Yanhui Shen , Ziqian Cui , Rui

da Liu , Ruihua Liu , Qian Shen , Jing Chen , Siping Zhang , Shaodong Liu , Huijuan Ma , Chaoyou Pang , Changwei Ge

Imprint: Environmental and Experimental Botany, Volume 208, April 2023, 105263

Abstract: Cotton is an important economic crop worldwide, which is mainly distributed in the tropics and subtropics; therefore, it is highly sensitive to low temperatures. *ZAT* and *CBF* play important roles in plant growth and stress responses. However, few studies have investigated the role of these genes in freezing tolerance of cotton, and the interaction between these two remains unclear. In this study, KN27-3 cotton with strong freezing tolerance was selected from 17 cotton varieties. RNA-sequencing analysis showed that KN27-3 cotton presented 6747 differentially expressed genes (DEGs), which were mostly upregulated at the early time points after the treatments. Weighted gene co-expression network analysis and Gene Ontology enrichment analysis showed that various DEGs were involved in plant abiotic stress resistance, including *SRK2I*, *ELF3*, *WRKY70*, and *TPS6*. Moreover, 31 early upregulated transcription factors, including *CBF* and *ZAT*, were identified after 15 min of freezing treatment. Such significant upregulation at the early stage suggested that *GhCBF4* (*Gh_A12G2357*) and *GhZAT10* (*Gh_D05G2011*) play important roles in cotton freezing stress. Virus-induced gene silencing indicated that *GhCBF4*- and *GhZAT10*-silenced plants exhibit significant freezing-sensitive phenotypes. Biofilm interferometry and dual luciferase experiments showed that *GhCBF4* regulated transcription by directly binding to a CRT/DRE motif within the *GhZAT10* promoter. In summary, *GhZAT10* and *GhCBF4* regulated plant freezing tolerance, and *GhZAT10* expression was at least partially regulated by *CBF*. These findings expand our current understanding of the mechanisms underlying *GhZAT10*- and *GhCBF4*-mediated freezing stress reactions in cotton, thereby establishing a foundation for further research on the molecular mechanisms underlying cotton freezing tolerance.

Seed Science and Technology

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Title: Genome-wide association study identifies GhSAL1 affects cold tolerance at the seedling emergence stage in upland cotton (*Gossypium hirsutum* L.)

Author: Qian Shen, Siping Zhang, Changwei Ge, Shaodong Liu, Jing Chen, Ruihua Liu, Huijuan Ma, Meizhen Song & Chaoyou Pang

Imprint: Theoretical and Applied Genetics **volume 136**, Article number: 27 (2023)

Abstract: Cotton can undergo low-temperature stress at the seedling emergence stage, which adversely affects growth and yield; however, the regulatory mechanism underlying cold tolerance remains nebulous. Here, we analyze the phenotypic and physiological parameters in 200 accessions from 5 ecological distributions under constant chilling (CC) and diurnal variation of chilling (DVC) stresses at the seedling emergence stage. All accessions were clustered into four groups, of which Group IV, with most germplasms from the northwest inland region (NIR), had better phenotypes than Groups I-III under the two kinds of chilling stresses. A total of 575 significantly associated single-nucleotide polymorphism (SNP) were identified, and 35 stable genetic quantitative trait loci (QTL) were obtained, of which 5 were associated with traits under CC and DVC stress, respectively, while the remaining 25 were co-associated. The accumulation of dry weight (DW) of seedling was associated with the flavonoid biosynthesis process regulated by Gh_A10G0500. The emergence rate (ER), DW, and total length of seedling (TL) under CC stress were associated with the SNPs variation of Gh_D09G0189 (GhSAL1). GhSAL1^{HapB} was the elite haplotype, which increased ER, DW, and TL by 19.04%, 11.26%, and 7.69%, respectively, compared with that of GhSAL1^{HapA}. The results of virus-induced gene silencing (VIGS) experiment and determination of metabolic substrate content preliminarily illustrated that GhSAL1 negatively regulated cotton cold tolerance through IP₃-Ca²⁺ signaling pathway. The elite haplotypes and candidate genes identified in this study could be used to improve cold tolerance at the seedling emergence stage in future upland cotton breeding.