

Agronomy, Soil Science and Plant Physiology

Title: Influence of Transgenic (Bt) Cotton on the Productivity of Various Cotton-Based Cropping Systems in Pakistan.

Author: Muhammad Waseem Riaz Marral , Fiaz Ahmad , Sami Ul-Allah, Atique-ur-Rehman , Shahid Farooq and Mubshar Hussain

Imprint: Agriculture 2023, 13, 276. <https://doi.org/10.3390/agriculture1302027>

Abstract: Cotton (*Gossypium hirsutum* L.) is an important fiber crop in Pakistan with significant economic importance. Transgenic, insect-resistant cotton (carrying a gene from *Bacillus thuringiensis* (Bt)) was inducted in the cotton-based cropping systems of Pakistan during 2002, and is now sown in >90% of cotton fields in the country. However, concerns are rising that Bt cotton would decrease the productivity of winter crops (sown after cotton), leading to decreased system productivity. This two-year field study determined the impacts of transgenic (Bt) and non-transgenic (non-Bt) cotton genotypes on the productivities of winter crops (i.e., wheat, Egyptian clover, and canola), and the overall productivities of the cropping systems including these crops. Four cotton genotypes (two Bt and two non-Bt) and three winter crops (i.e., wheat, Egyptian clover, and canola) were included in the study. Nutrient availability was assessed after the harvest of cotton and winter crops. Similarly, the yield-related traits of cotton and winter crops were recorded at their harvest. The productivities of the winter crops were converted to net economic returns, and the overall economic returns of the cropping systems with winter crops were computed. The results revealed that Bt and non-Bt cotton genotypes significantly ($p < 0.05$) altered nutrient availability (N, P, K, B, Zn, and Fe). However, the yield-related attributes of winter crops were not affected by cotton genotypes, whereas the overall profitability of the cropping systems varied among the cotton genotypes. Economic analyses indicated that the Bt cotton-wheat cropping system was the most profitable, with a benefit-cost ratio of 1.55 in the semi-arid region of Pakistan. It is concluded that Bt cotton could be successfully inducted into the existing cropping systems of Pakistan without any decrease to the overall productivity of the cropping system.

Title: Transcriptome analysis reveals the effect of grafting on gossypol biosynthesis and gland formation in cotton

Author: Kun Ye, Teng Teng, Teng Yang, Degang Zhao & Yichen Zhao

Imprint: *BMC Plant Biology* volume 23, Article number: 37 (2023)

Abstract: Gossypol is a unique secondary metabolite and sesquiterpene in cotton, which is mainly synthesized in the root system of cotton and exhibits many biological activities. Previous research found that grafting affected the density of pigment glands and the gossypol content in cotton.

Title: Evolution of Liquid Multinutrient Fertilizer for Hybrid Cotton

Author: Divya K. , R. K. Kaleeswari , D. Jeyanthi , D. Amirtham and K. Sankaranarayanan

Imprint: International Journal of Plant & Soil Science 34(20): 666-671, 2022; Article no.IJPSS.88408

Author: A field experiment was conducted to assess the effect of drip fertigation and foliar nutrition of liquid multi nutrient on growth, yield and quality parameters of hybrid cotton. Liquid fertilizer was formulated using micronutrient (Zn, Fe, Mn, B, Mo, Cu), Mg and S to meet the nutrient requirement of hybrid cotton. Field experiment was laid out in Randomized Block Design with three replications and seven treatments. Drip fertigation was applied with 100% recommended dose of fertilizer (RDF) through water soluble fertilizer and Liquid Multinutrient (LMN). Treatment that received 100% RDF + LMN fertigation and foliar nutrition of LMN recorded the highest growth parameters (plant height, Leaf Area Index and dry matter production), yield parameters like number of sympodial branches/plant, number of bolls/plant, boll weight, seed cotton yield and quality parameters like staple length and ginning out turn per cent and in addition to that foliar nutrition of LMN containing Mg alleviated the Mg deficiency to the tune of 52% which in turn increases the above parameters. Fertigation and foliar nutrition of LMN enhanced the nutrient uptake of hybrid cotton that would economize the cost of fertilizer input.

Title: The Factual Demand and the Possibility of Self-reliant in Cotton Cultivation in Bangladesh

Author: Faridul Islam Ovi and Rownak Jahan Shova

Imprint: Royal Journal of Research in Engineering and Technology 2022, Vol. 1, No. 1, pp. 19-35

Abstract: The Bangladeshi garment is playing significant role in the country's development from the last decades. Today the garment sectors are providing 82% of the

national export and count USD 30 billion revenues these numbers represent the sector as the most important manufacturing industry in Bangladesh. Cotton is the oldest and most important of the textile fibers. It is the back bone of the world's textile trade. Current survey shows that world production are about 25 million tones or 110 million bales annually, accounting for 2.5% of the world's arable land. Cotton is regarded as the golden arm for Bangladeshi textile because about 65% textile fabrics are made from cotton every day. Bangladesh requires 4-4.5 million bales (1 bale=217.7 kg or 480 pounds) of raw cotton which is slightly increasing. But Bangladesh is lack behind fulfilling the demand as Bangladesh are producing 1-2% of cotton requirement through the local production every year which is far behind the need. The remaining 98-99% requirement is fulfilled by the imported cotton mostly from Uzbekistan, India, USA, African countries, Turkmenistan, Australia etc. It is not possible to be self-reliant in raw cotton production as our raw cotton demand is very high and there is a land shortage for cotton cultivation but it can possible of production of initially 10 lac bales and finally 20 lac bales without hampering food production which is 50% of our national demand of raw cotton requirement and can save foreign currency of TK 11000 core per annum.

Title: Evolution of the Cotton Genus, *Gossypium*, and Its Domestication in the Americas.

Author: Christopher R. Viot & Jonathan F. Wendel

Imprint: Critical Reviews in Plant Sciences <https://doi.org/10.1080/07352689.2022.2156061>

Abstract: *Gossypium*, the cotton genus, includes ~50 species distributed in tropical and sub-tropical regions of all continents except Europe. Here we provide a synopsis of the evolutionary history of *Gossypium* and domestication of the American allopolyploid species, integrating data from fundamental taxonomic investigations, biogeography, molecular genetics, phylogenetic analysis, and archaeology. These diverse sources of information provide a temporal and phylogenetic perspective on diversification among the diploids and on polyploid formation, uncover multiple previously cryptic interspecific hybridizations, clarify and contribute to the taxonomy of the genus, and offer a firm foundation for understanding parallel domestications in Mesoamerica and South America, which led to the globally important cotton crop species *G. barbadense* and *G. hirsutum*. *Gossypium* thus offers a testimonial example of the importance and utility of fundamental botanical discovery combined with modern technological capabilities to generate genomic insights into evolutionary history. We also review the current state of our knowledge regarding the archaeological history of cotton domestication and diffusion in the Americas, a seemingly unlikely story entailing parallel domestication origins and parallel directional selection tracing to 8,000

(*G. barbadense*) and 5,500 (*G. hirsutum*) years ago, transforming two geographically isolated wild short-day perennial shrubs having small capsules and seeds covered by short, tan-colored epidermal trichomes into modern daylength-neutral annuals bearing abundant, fine, strong white fibers. This dual domestication was followed several millennia later by unintentional and more recently intentional interspecific introgression, as the two species came into contact following their initial domestication in different hemispheres. Thus, the cycle of species divergence and biological reunion was reiterated, this time at the allopolyploid level. Understanding this evolutionary history is vitally important to our understanding of the genomic architecture of the world's most important fiber plant and contributes substantially to our understanding of general biological principles.

Title: The Intervention of Multi-Omics Approaches for Developing Abiotic Stress Resistance in Cotton Crop Under Climate Change

Author; Muhammad Kashif Riaz Khan, Allah Ditta, Baohua Wang, Liu Fang, Zunaira Anwar, Aqsa Ijaz, Syed Riaz Ahmed & Sana Muhyuddin Kha

Title: Sustainable Agriculture in the Era of the OMICs Revolution pp 37–82 (Book by Springer)

Abstract: Cotton is regarded as an important cash crop in the world. The major contributors to the cotton crop are China, USA, India, Pakistan, and Brazil. Abiotic stress, especially drought, soil salinity, waterlogging, cold stress, and high-temperature, limits crop growth and thus reduces crop yield. Climate change has posed threat to world agriculture because of abiotic stress intensity. Just like other crops, cultivated cotton species especially tetraploids are susceptible to fluctuating environmental scenarios. These environmental factors interact with abiotic stresses concurrently, for instance, drought, salt, waterlogging, and extreme heat, thus resulting in a 50% decrease in cotton yield and a significant deterioration in lint quality. Multi-omics approaches include genomics, transcriptomics, proteomics, metabolomics, and phenomics; hence, these integrated studies on plants in response to abiotic stress and changing environment are capable of generating multi-pronged data that can solve the mystery going on within the cells in response to abiotic stresses. Integration, analysis, and decoding of multi-layered data can provide immense outcomes, and this knowledge can be implemented for the improvement of field crops more efficiently than conventional breeding alone. In the last few decades, various stress-related mechanism studies employing different omics approaches have been devised for the development of tolerant varieties. Nevertheless, functional genomics aids to understand the relationship between organism's genome and its phenotype under varying environmental conditions. Integrated multi-omics along with bioinformatics will pave

the way for more in-depth functional investigations of stress tolerance in plants by utilizing recent genetic information and will help to improve methodologies and techniques. This chapter will present the purpose of multi-omics approaches in producing multi-faceted data to give a better understanding of cellular mechanisms that curb abiotic stresses in plants under extreme external conditions.

Title: Integrative transcriptomic, metabolomic and physiological analyses revealed the physiological and molecular mechanisms by which potassium regulates the salt tolerance of cotton (*Gossypium hirsutum* L.) roots.

Author: FeiyanJu, JialiPang, LiyuanSun, JiajiaGu, ZhuoWang, XinyuWu

Imprint: Industrial Crops and Products, Volume 193, March 2023, 116177

Abstract: Cotton is a valuable industrial fiber-producing crop. However, soil salinization has brought serious yield and economic losses to cotton production. Appropriate application of potassium can improve the salt tolerance of crops and reduce salt damage, but the regulatory mechanism of potassium improves cotton adaptability to salt stress is still limited. In this study, transcriptome and metabolome analyses were performed on cotton roots treated with C (0 mM NaCl), S (150 mM NaCl) and SK (150 mM NaCl + 9.38 mM K₂SO₄), and verified by physiological indexes. The results showed that ion transport, hormone metabolism and reactive oxygen species (ROS) scavenging pathways played important roles in cotton root adaptation to salt stress. Salt stress caused oxidative damage and ion toxicity in cotton roots by disrupting hormone homeostasis and down-regulating the expression of potassium transporter and antioxidase-related genes. However, appropriate application of potassium alleviated the damage of salt stress on cotton by maintaining hormone and ion homeostasis and promoting the removal of ROS. In this study, the key biological pathways, regulatory genes and metabolites of potassium regulating cotton root adaptation to salt stress were determined, and the regulatory network diagram of gene metabolite interactions was constructed, which provides a new insight into the complex mechanism of potassium regulates salt adaptation in cotton and other crops, and will promote the progress of cotton genetic improvement and cultivation techniques.

Title: Impact of long-term integrated nutrient management on soil quality and productivity of cotton (*Gossypium* spp.) + greengram (*Vigna radiata*) intercropping system in vertisols under semi-arid agroecosystem

Author: Vijay Gabhane, Ashwini Chandel, Rajesh Patode & Pratik Ramteke

Imprint: Journal of Plant Nutrition <https://doi.org/10.1080/01904167.2022.2160750>

Abstract: Integrated nutrient management has potential to enhance soil quality and sustain agricultural productivity, however, such effects under cotton + greengram intercropping is not well understood in vertisols of Maharashtra, India. Therefore, a field study was conducted during 2016–2017 at the Research field of AICRP for Dryland Agriculture Akola, Maharashtra (India), on an ongoing long-term experiment initiated in 1987–1988 under cotton + greengram (1:1) intercropping system to find out how different nutrient management practices affect the soil quality (SQ) and cotton + greengram productivity. The eight treatments comprised of sole use of organics and chemical fertilizers, integration of organics with chemical fertilizers (INM) to partially substitute nitrogen, and a control treatment. The results after 30th cycle revealed that the partial substitution of N through FYM/gliricidia increased cotton and greengram yield over control. These treatments caused significant improvement in the soil physical and biological properties and also improved the soil fertility status, mainly soil organic carbon (OC) by 53%, available N (AN) by 25%, available P (AP) by 50%, and available K (AK) by 25% over control. The SQ assessment through principal component analysis (PCA) revealed that, in this semi-arid subtropical region, HC, OC, and CO₂ evolution can be viewed as important indicators of SQ for cotton + greengram intercropping system. Therefore, we concluded that, INM practice that encourages balanced fertilization must include FYM/gliricidia as part of the nutrient application package in this region to improve soil quality and sustain productivity of cotton + greengram intercropping system.

Crop Protection

Title: GhWRKY41 forms a positive feedback regulation loop and increases cotton defense response against *Verticillium dahliae* by regulating phenylpropanoid metabolism

Author: Shenghua Xiao, Yuqing Ming, Qin Hu¹, Zhengxiu Ye, Huan Si, Shiming Liu¹, Xiaojun Zhang, Weiran Wang, Yu Yu, Jie Kong, Steven J. Klosterman, Keith Lindsey, Xianlong Zhang, Alifu Aierxi, *, Longfu Zh

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Abstract: Despite the established significance of WRKY proteins and phenylpropanoid metabolism in plant immunity, how WRKY proteins modulate aspects of the phenylpropanoid pathway remains undetermined. To understand better the role of WRKY proteins in plant defense, we identified a cotton (*Gossypium hirsutum*) protein, GhWRKY41, that is universally and rapidly induced in three disease-resistant cotton cultivars following inoculation with the plant pathogenic fungus, *Verticillium dahliae*. We show that overexpression of GhWRKY41 in transgenic cotton and *Arabidopsis* enhances resistance to *V. dahliae*, while knock-down increases cotton more susceptibility to the fungus. GhWRKY41 physically interacts with itself and directly activates its own transcription. A genome-wide chromatin immunoprecipitation and high-throughput sequencing (ChIP-seq), in combination with RNA sequencing (RNA-seq) analyses, revealed that 43.1% of GhWRKY41-binding genes were up-regulated in cotton upon inoculation with *V. dahliae*, including several phenylpropanoid metabolism master switches, receptor kinases, and disease resistance-related proteins. We also show that GhWRKY41 homodimer directly activates the expression of GhC4H and Gh4CL, thereby modulating the accumulation of lignin and flavonoids. This finding expands our understanding of WRKY-WRKY protein interactions and provides important insights into the regulation of the phenylpropanoid pathway in plant immune responses by a WRKY protein.

Title: Status of whitefly (*Bemisia tabaci* Gennadius) population on Bt cotton in Marathwada region of Maharashtra under changing climate.

Author: AG Lad, RY Khandare and YB Matre

Imprint: The Pharma Innovation Journal 2022; 11(12): 3791-3795

Abstract: The research was conducted during kharif seasons of 2017-18, 2018-19 and 2019-2020 at Seven major cotton growing districts (viz. Parbhani, Hingoli, Nanded, Jalna, Aurangabad, Osmanabad & Beed) in Marathwada region of Maharashtra under Crop Pest Surveillance and Advisory Project (CROPSAP). The severity of whitefly population is becoming a major concern to transgenic cotton farmers. Keeping this in view scientific survey of white fly (*Bemisia tabaci* Gennadius) incidence on Bt cotton was carried out from last Three years (2017-18 to 2019-20), in Seven major cotton growing districts (viz. Parbhani, Hingoli, Nanded, Jalna, Aurangabad, Osmanabad & Beed) in Marathwada region of Maharashtra under Crop Pest Surveillance and

Advisory Project (CROPSAP) by using ICT tools and total 171 ETL based advisories were issued twice in a week to monitor the pest. On the basis of taluka wise roving survey, the district wise mean data stated that during 2017-18, Nanded district was severely infested by whiteflies (1.65) followed by Jalna (1.09) and Parbhani (0.70). During 2018-19, Jalna district recorded highest population of whitefly (1.02) followed by Parbhani (0.54) and Hingoli (0.42). Whereas during 2019-20, Parbhani district recorded highest population of whitefly (0.22) followed by Jalna (0.19) and Aurangabad (0.17). On the basis of three years survey data, the severity of whiteflies incidence was more during 2017-18.

Title: Evaluation of Pyriproxyfen 8% + Clothianidin 3.5 SE against Sucking Pests of Cotton.

Author: R.K. Kalyan¹ and Deepika Kalyan

Imprint: Biological Forum – An International Journal 14(4): 1126-1130(2022)

Abstract: The field trials to evaluate the bio-efficacy of different doses of Pyriproxyfen 8% + Clothianidin 3.5 SE as foliar spray against sucking pests of cotton were conducted at Agricultural Research Station-Borwat Farm, Banswara (Rajasthan) during Kharif 2016 and 2017. The results of the investigation revealed that the ready mix molecule of Pyriproxyfen 8% + Clothianidin 3.5 SE @ 1500 ml and 1250 ml ha⁻¹ were very effective in providing protection against sucking pests of cotton viz. whiteflies, jassids and thrips with highest mean seed cotton yield (1986 & 1831 kg ha⁻¹, respectively) and were statistically at par. The next best treatments were Diafenthiuron 50 WP @ 600 g ha⁻¹, followed by Clothianidin 50 WDG @ 50 g ha⁻¹. None of the treatments showed any symptoms of phytotoxicity.

Title: Characterization of Green Mentha pulegium (L.) oil Nanotechnology and Adverse Effect on Two Cotton Bollworms, Pectinophora gossypiella (Saund.) and Earias insulana (Boisd).

Author: Warda A. Z. El-Medany, Rania Mahmoud El-Shennawy and Mirvat Abdel-Samea Kandil

Imprint: Egypt. Acad. J. Biology. Sci., 14(2):235-248(2022)

Abstract: In our study, laboratory trials to determine the effectiveness of Mentha pulegium leaves essential oil nanoparticles against the pink Pectinophora gossypiella, and spiny bollworms (Saunders) Earias insulana, too. Gas mass spectrometry was used

to study *M. pulegium* spectroscopy (GC/ MS) for the identification of the chemical the makeup of essential oil. Large three active components were identified as D-Carvone (28.46%), Menthol (27.88%) and l-Menthone (15.92%) the oil constituent. The level of LC values, *P. gossypiella* exhibited more sensitivity to *M. pulegium* than *E. insulana* and simply lengthening the exposure period, the death rate increased. A significant percent of larval mortality and malformation were recorded (81.113 and 68.89%) in addition to a remarkable percent of pupal mortality and malformation reached 30.55 and 34.53%, with a significant reduction in adult emergence for *P. gossypiella* and *E. insulana*, respectively. Moreover, some histological deformations at the level of the cuticular layer of treated larvae of both insects as a result of *M. pulegium* treatment were also detected compared to the control check.

Title: New *Bacillus subtilis* Strains Isolated from *Prosopis glandulosa* Rhizosphere for Suppressing *Fusarium* Spp. and Enhancing Growth of *Gossypium hirsutum* L.

Author: Ali Abdelmoteleb, Lizbeth Moreno-Ramírez, Benjamín Valdez-Salas Mahmoud F. Seleiman, Salah El-Hendawy, Khalid J. Aldhuwaib, Majed Alotaibi, Daniel González-Mendoza

Imprint: *Biology* 2023, 12(1), 73; <https://doi.org/10.3390/biology12010073>

Simple Summary: *Fusarium* species can cause serious damage to agricultural crops. Due to the significant losses in crop production along with the harmful effects of the chemical control of plant diseases on human health and the environment, the use of biocontrol agents for the efficient control of *Fusarium* spp. is becoming an important issue. In the present study, three *bacillus subtilis* strains (LDA-1, LDA-2, and LDA-3) were examined for their potential to promote cotton growth and act as biocontrol agents against *Fusarium* spp. All *Bacillus* strains exhibited defensive effects in cotton plants against phytopathogenic *Fusarium* spp. The results suggest that the antagonism mechanism of *Bacillus* strains against phytopathogenic *Fusarium* spp. could be due to the ability of bacterial strains to produce lipopeptides and other molecules with antifungal activities. In conclusion, these *Bacillus subtilis* strains can be promised as biocontrol agents, especially in organic and sustainable agricultural systems, and can reduce the extensive use of toxic chemical pesticides in agricultural system.

Abstract: Rhizobacteria from desert plants can alleviate biotic stress and suppress plant diseases, and consequently can enhance plant growth. Therefore, the current study was performed to isolate and identify *Prosopis glandulosa*-associating rhizobacteria based on their antagonistic activity against *Fusarium* species and plant growth-promoting properties. Three bacterial isolates were identified as *Bacillus subtilis*: LDA-1, LDA-2, and LDA-3. The molecular analysis suggests the biosynthesis of the bacteriocins

subtilisin and subtilosin, as well as the lipopeptide iturin, by these strains. In addition, the antagonistic study by dual-culture assay showed a high efficacy of all *B. subtilis* strains against phytopathogenic fungi (*Fusarium nygamai*, *F. equiseti*, *F. solani*, *F. solani* ICADL1, and *F. oxysporum* ICADL2) with inhibition percentages ranging from 43.3 to 83.5% in comparison to the control. Moreover, atomic force microscopy (AFM) analysis showed significant differences in the cell wall topography of the *F. solani* ICADL1 among the treated mycelia and untreated control. As a result, these three *B. subtilis* strains were used as bioinoculants for cotton seedlings infected by *F. solani* ICADL1 in pot trials, and the results revealed that the bacterial inoculations as an individual or combined with *F. solani* ICADL1 significantly improved cotton root and stem length, lateral roots, indole acetic acid (IAA), and gibberellic acid (GA₃) contents, as well as increased antioxidants, flavonoids, and phenols in comparison to those obtained from healthy and infected control plants. In conclusion, the three bacterial strains of *B. subtilis* (i.e., LDA-1, LDA-2, and LDA-3) are considered promising tools as biocontrol agents for *F. solani* and cotton growth promoters, and consequently can be used as bio-fertilizer in sustainable agriculture systems.

Title: Physiological responses in genetically modified cotton and its isohybrid attacked by *Aphis gossypii* Glover (Hemiptera: Aphididae)

Author: Nermy Ribeiro Valadares, Marcus Alvarenga Soares, Evander Alves Ferreira, Veríssimo Gibran Mendes de Sá, Alcinei Místico Azevedo, Germano Leão Demolin Leite & José Cola Zanuncio

Imprint: *Arthropod-Plant Interactions* (2023)

Abstract: In Brazil, genetically modified cotton is increasing in most cultivated areas to manage insects, mainly Lepidoptera. Pests associated with cotton crops are diverse. *Aphis gossypii* Glover, 1877 (Hemiptera: Aphididae), one of the most important cotton pests, sucks photoassimilates from the phloem sap causing mold growth and damage to plant tissues. The interactions between Bt plants and non-target organisms and the impact of *A. gossypii* damage on these plants need further studies. Therefore, the objective was to evaluate the physiological stress caused by *A. gossypii* on Bt cotton and its isohybrid (same genetic background but not transgenic). The Bt cotton (Cotton Event 281-24-236/3006-210-23) and the isohybrid of this plant were planted in pots in a completely randomized design, as the treatments, with 30 replications in a greenhouse. The chlorophyll fluorescence parameters of the plants were evaluated by using a fluorometer. Regression models were adjusted for Bt cotton and the isohybrid, and the differences between treatments were evaluated through the model identity test. The photosynthetic parameters of Bt cotton and its isohybrid infested by this insect were similar.

Title: Effects of different crop rotations on the incidence of cotton *Verticillium* wilt and structure and function of the rhizospheric microbial community

Author: Weisong Zhao, Shezeng Li, Lihong Dong, Peipei Wang, Xiuyun Lu, Xiaoyun Zhang, Zhenhe Su, Qinggang Guo & Ping Ma

Imprint: *Plant and Soil* (2023)

Abstract: Cotton continuous cropping might cause the soil-borne disease *Verticillium* wilt in agricultural production. Crop rotation has been shown to be an effective method for controlling this disease. The objectives of this study were to evaluate the effects of cotton-maize rotation (CMR) and cotton-maize-broccoli residues rotation (CMBR) on incidence of cotton *Verticillium* wilt (CVW), soil microbial community structure and function.

Title: Analysis of PAT1 subfamily members in the GRAS family of upland cotton and functional characterization of *GhSCL13-2A* in *Verticillium dahliae* resistance

Author: Chen Chen, Li-Li Lu, Shu-Ya Ma, Yan-Peng Zhao, Na Wu, Wen-Jie Li, Li Ma, Xian-Hui Kong, Zong-Ming Xie & Yu-Xia Hou

Imprint: *Plant Cell Reports* (2023)

Abstract: *Verticillium* wilt (VW) is a devastating disease of upland cotton (*Gossypium hirsutum*) that is primarily caused by the soil-borne fungus *Verticillium dahliae*. Scarecrow-like (SCL) proteins are known to be involved in plant abiotic and biotic stress responses, but their roles in cotton defense responses are still unclear. In this study, a total of 25 GhPAT1 subfamily members in the GRAS family were identified in upland cotton. Gene organization and protein domain analysis showed that GhPAT1 members were highly conserved. *GhPAT1* genes were widely expressed in various tissues and at multiple developmental stages, and they were responsive to jasmonic acid (JA), salicylic acid (SA), and ethylene (ET) signals. Furthermore, *GhSCL13-2A* was induced by *V. dahliae* infection. *V. dahliae* resistance was enhanced in *Arabidopsis thaliana* by ectopic overexpression of *GhSCL13-2A*, whereas cotton *GhSCL13-2A* knockdowns showed increased susceptibility. Levels of reactive oxygen species (ROS) and JA were also increased and SA content was decreased in *GhSCL13-2A* knockdowns. At the gene expression level, *PR* genes and SA signaling marker genes were down-regulated and JA signaling marker genes were upregulated in *GhSCL13-2A* knockdowns. GhSCL13-2A was shown to be localized to the cell membrane and the nucleus. Yeast two-hybrid and luciferase complementation assays indicated that GhSCL13-2A interacted with GhERF5. In *Arabidopsis*, *V. dahliae* resistance was enhanced by *GhERF5* overexpression; in cotton, resistance was reduced in *GhERF5* knockdowns. This study revealed a positive role

of *GhSCL13-2A* in *V. dahliae* resistance, establishing it as a strong candidate gene for future breeding of *V. dahliae*-resistant cotton cultivars.

Plant Genetics and Breeding

Title: Genome-Wide Characterization and Functional Analysis of ABCG Subfamily Reveal Its Role in Cutin Formation in Cotton

Author: Xuehan Huo , Ao Pan , Mingyang Lei , Zhangqiang Song , Yu Chen , Xin Wang , Yang Gao , Jingxia Zhang , Shengli Wang , Yanxiu Zhao , Furong Wang and Jun Zhang

Imprint: Int. J. Mol. Sci. 2023, 24, 2379. <https://doi.org/10.3390/ijms24032379>

Abstract: ATP-binding cassette transporter G (ABCG) has been shown to be engaged in export of broad-spectrum compounds with structural differences, but little is known concerning its role in cutin formation of cotton (*Gossypium* spp.). In this study, we conduct a genome-wide survey and detected 69, 71, 124 and 131 ABCG genes within *G. arboreum*, *G. raimondii*, *G. hirsutum* and *G. barbadense*, separately. The above ABCGs could be divided into four groups (Ia, Ib, Ic, II). Some ABCG genes such as GhABCG15, whose homologous gene transports cuticular lipid in *Arabidopsis*, was preferentially expressed in the development of fiber. A weighted gene co-expression network analysis (WGCNA) demonstrated that GhABCG expression was significantly associated with the amount of 16-Hydroxypalmitate (a main component of cutin precursor) in cotton fibers. Further, silencing of GhABCG15 by virus-induced gene silencing (VIGS) in cotton generated brightened and crinkled leaves as well as reduced thickness of cuticle and increased permeability. Chemical composition analysis showed the cutin content in GhABCG15-silenced leaves had decreased while the wax content had increased. Our results provide an insight for better understanding of the role of the *Gossypium* ABCG family and revealed the essential role of GhABCGs in cotton cutin formation.

Title: Genome-wide characterization of the *SHORT INTER-NODES/STYLISH* and *Shi-Related Sequence* family in *Gossypium hirsutum* and functional identification of *GhSRS21* under salt stress.

Author: Chendong Sun, Li Yu, Shuojun Zhang, Qijuan Gu, and Mei Wang

Imprint: Front Plant Sci. 2022; 13: 1078083.

Abstract: Saline stress is a significant factor that caused crop growth inhibition and yield decline. SHORT INTERNODES/STYLISH (SHI/STY) and SHI-RELATED SEQUENCE (SRS) transcription factors are specific to plants and share a conserved RING-like zinc-finger domain (CX₂CX₇CX₄CX₂C₂X₆C). However, the functions of *SHI/STY* and *SRS* genes in cotton responses to salt stress remain unclear. In this study, 26 *GhSRSs* were identified in *Gossypium hirsutum*, which further divided into three subgroups. Phylogenetic analysis of 88 *SRSs* from 8 plant species revealed independent evolutionary pattern in some of *SRSs* derived from monocots. Conserved domain and subcellular location prediction of *GhSRSs* suggested all of them only contained the conserved RING-like zinc-finger domain (DUF702) domain and belonged to nucleus-localized transcription factors except for the *GhSRS22*. Furthermore, synteny analysis showed structural variation on chromosomes during the process of cotton polyploidization. Subsequently, expression patterns of *GhSRS* family members in response to salt and drought stress were analyzed in *G. hirsutum* and identified a salt stress-inducible gene *GhSRS21*. The *GhSRS21* was proved to localize in the nucleus and silencing it in *G. hirsutum* increased the cotton resistance to salt using the virus-induced gene silencing (VIGS) system. Finally, our transcriptomic data revealed that *GhSRS21* negatively controlled cotton salt tolerance by regulating the balance between ROS production and scavenging. These results will increase our understanding of the *SRS* gene family in cotton and provide the candidate resistant gene for cotton breeding.

Title: Genome-wide identification and expression reveal the involvement of the FCS-like zinc finger (FLZ) gene family in *Gossypium hirsutum* at low temperature

Author: JunDuo Wang¹, Zhiqiang Li, Yajun Liang, Juyun Zheng, Zhaolong Gong, Guohui Zhou, Yuhui Xu, Xueyuan Li

Imprint: PeerJ 11:e14690 <https://doi.org/10.7717/peerj.14690>

Abstract: FCS-like zinc finger (FLZ) is a plant-specific gene family that plays an important regulatory role in plant growth and development and its response to stress. However, studies on the characteristics and functions of cotton FLZ family genes are still lacking. This study systematically identified members of the cotton FLZ gene family based on cotton genome data. The cotton FLZ family genes were systematically analyzed by bioinformatics, and their expression patterns in different tissues and under low-temperature stress were analyzed by transcriptome and qRT-PCR. The *G. hirsutum* genome contains 56 FLZ genes distributed on 20 chromosomes, and most of them are located in the nucleus. According to the number and evolution analysis of FLZ

family genes, FLZ family genes can be divided into five subgroups in cotton. The *G. hirsutum* FLZ gene has a wide range of tissue expression types, among which the expression is generally higher in roots, stems, leaves, receptacles and calyx. Through promoter analysis, it was found that it contained the most cis-acting elements related to methyl jasmonate (MeJA) and abscisic acid (ABA). Combined with the promoter and qRT-PCR results, it was speculated that *GhFLZ11*, *GhFLZ25*, *GhFLZ44* and *GhFLZ55* were involved in the response of cotton to low-temperature stress. Taken together, our findings suggest an important role for the FLZ gene family in the cotton response to cold stress. This study provides an important theoretical basis for further research on the function of the FLZ gene family and the molecular mechanism of the cotton response to low temperature.

Title: Duplicate mutations of *GhCYP450* lead to the production of ms_5ms_6 male sterile line in cotton

Author: Yun Mao, Fan Dai, Zhanfeng Si, Lei Fang & TianZhen Zhang

Imprint: *Theoretical and Applied Genetics* **volume 136**, pages1-14 (2023)

Abstract: The utilization of male sterility in cotton plays a vital role in improving yield and fiber quality. A complete male sterile line (ms_5ms_6) has been extensively used to develop hybrid cotton worldwide. Using Zhongkang-A (ZK-A) developed by transferring *Bt* and ms_5ms_6 genes into the commercial cultivar Zhongmiansuo 12, the duplicate genes were map-based cloned and confirmed via the virus-induced gene silencing (VIGS) assays. The duplicate mutations of *GhCYP450* genes encoding a cytochrome P450 protein were responsible for producing male sterility in ms_5ms_6 in cotton. Sequence alignment showed that GhCYP450-Dt in ZK-A differed in two critical aspects from the fertile wild-type TM-1: GhCYP450-Dt has three amino acid (D98E, E168K, G198R) changes in the coding region and a 7-bp (GGAAAAA) insertion in the promoter domain; GhCYP450-At appears to be premature termination of *GhCYP450* translation. Further morphological observation and cytological examination of GhCYP450-silenced plants induced by VIGS exhibited shorter filaments and no mature pollen grains. These results indicate that *GhCYP450* is essential for pollen exine formation and pollen development for male fertility. Investigating the mechanisms of ms_5ms_6 male sterility will deepen our understanding of the development and utilization of heterosis.

Title: Quantitative Study of Cry1Ac Protein and Bioassay for *Helicoverpa armigera* at Different Development Stages of Upland Cotton (*Gossypium hirsutum* L.

Author: Khadim ,Wajid NazeerGhazi ,Muhammad Akbar Farzana Ashraf

Muhammad Idrees Khan

Imprint: VOL. 3 NO. 2 (2022): PAKISTAN JOURNAL OF BIOCHEMISTRY AND BIOTECHNOLOGY /

Abstract: Eight transgenic (*Cry1Ac* -endotoxin) genotypes and one non-GMO cotton (*Gossypium hirsutum* L.) variety were used in the investigation. *Cry1Ac* protein was expressed at various extents in several strains. In a greenhouse environment, sixty days after planting, the cry 1Ac gene's expression peaked. At 60 DAP, the variety Bt.CIM-598 (1.871 g/g) expressed the most toxin of any genotype. Throughout the cropping season, larvae of the *Helicoverpa armigera* were gathered from every section of the nation that produces cotton. *H. armigera* larvae that were captured in the field were raised on artificial feeds. There was a negative relationship between the DAP and the amount of *Cry1Ac* protein (-0.332). The greatest amount of death was seen when first-instar larvae consumed the leaves of 60 DAP plants. It was found that transgenic variants had a considerable effect on the percentage mortality of *H. armigera*. MNH-886 larvae showed the highest mortality percentage when fed on leaves that were harvested 30 DAP (days after planting). When larvae were fed on 60 and 90 DAP leaves on CIM-598 and IR-1524, the mortality rate was greater. However, AA-802 had the highest death rate when larvae were fed on 120 DAP leaves. The variety with the highest death rate was CIM-598. When *H. armigera* consumed 60 DAP leaves, the greatest overall mortality was noted. The plant-toxin interaction in cotton varied depending on a number of physiological changes in plants. Regardless of plant age or variety, the highest rate of mortality of *H. armigera* larvae was seen after feeding 48-hour of treatment or feeding.

Title: Determination of Gene Action and Heterosis In Diallel Crosses For The F1 And F2 Cotton Generations.

Author: H.S. Abd El Samad , A.A. El Hosary , M.E. El-Badawy , A.E.M. Eissa

Imprint: Annals of Agric. Sci., Moshtohor ISSN 1110-0419 Vol. 61(1) (2023),XXX – XXX

Abstract: Heterosis and gene action on oil%, and yield traits were determined in a 6x6 diallel cross of cotton without reciprocals and their F2 generation to define and select an efficient and prospective material for immediate use in hybridization programs to improve seed yield of cotton in Egypt. Parents, F1 and F2 were evaluated in a randomized complete block design (RCBD) with three replicates for yield traits in 2021 season. High significant mean squares for genotype, parents and crosses were showed for the studied traits in both generations. Significant heterosis in F1 generation was obtained for all studied traits. The desirable heterosis of relative to better parent varied from 5.36 to 25.29, 5.92 to 33, 2.3 to 5.89 and 1.14 to 7.38 in F1 generation for seed cotton yield, lint yield, seed index and oil%, respectively. The cross P2xP3 was the best cross for all studied traits heterosis. Mean squares for general (GCA) and specific (SCA) combining ability were significant for all studied traits. MS (GCA)/ MS (SCA) ratios displays the relative importance of additive and additive by additive gene action effects in their inheritance for seed cotton yield, lint yield , seed index and lint percentage in F1 generation and seed cotton yield and lint yield in F2 generation. P1 exhibited significant desirable g_i effect among all the tested parents for lint percentage, lint index and oil% in F1 and seed cotton yield , lint yield and oil % in F2. The cross P2xP3 showed significantly desirable SCA effects for most studied traits.

Title: Multivariate Analysis in Egyptian Cotton *Gossypium barbadense* L.

Author: Abdel-Hafez, G. A; H. M. Hammoud ; M. W. Kamara and A. Kh. Attiya

Imprint: J. of Plant Production, Mansoura Univ., Vol. 13 (12) : 889 -897, 2022

Abstract: Eleven parental cotton genotypes (*Gossypium barbadense* L.) and their 28F1hybrids were canvassed by Principal Components and Linkage Cluster analyses to identify the major characters which account for the variation in yield contributing traits. Analysis of variance revealed highly significant differences for genotypes, crosses, parents for all the studied traits. Parents vs. crosses were significant for most traits indicating the heterotic response. The first principal component contributed 41.9 %to the total variability and was mainly attributed to plant height, boll weight, seed cotton yield/plant, number of fruiting branches/plant, lint yield /plant, boll number and seed

index. The second PCs contributed 16.7 % to the total variability and were mainly due to fiber fineness, length and uniformity ratio and showed positive loadings with most characters. The PC3 and PC4 contributed 9.1 % and 7.9 % of the total variability and were mainly attributed to pressely index, earliness index, vegetative branches and days to flowering. The 11 cotton parental genotypes were grouped into four major clusters based on dissimilarity among them and sixteen contributed characters. The female parents (testers) Suvin, (Giza 88xOkre leaf), (Giza 85xOkre leaf) and 24202 were grouped into two wide clusters. The parental genotypes Giza 93 and (Giza 81xAustraly12) formed two wide clusters from the other parents and having wide dissimilarity coefficients compared with other parents. The 39 genotypes, 11 original parents and 28 F1 crosses, were grouped into 13 major clusters relative to dissimilarity among them.

Title: Stability Analysis of Asiatic Cotton (*Gossypium arboreum* L.) Genotypes with Respect to Seed Cotton Yield, GOT and Boll Weight under Multi Environmental Trials through GGE Biplot Analysis

Author: S. K. Verma, Debashis Paul, Amarpreet Singh, S. K. Sain

Imprint: Environment and Ecology 40 (4A) : 2282–2289, October–December 2022

Abstract: The GGE biplot is a useful visualization tool for accessing the performance of genotypes in different environments. In the present study, the 9 genotypes viz CISA 6-165, CISA 6-350, CISA 6-123, CISA 6-187, CISA 6-214, CISA 6-295, CISA 614-1, CISA 6-209, CISA 6-256 were tested under seven different environmental conditions. The genotypes were referred as G1 to G9, respectively. The seven different environmental conditions were cotton growing season 2010-11 to 2016-17 henceforth referred as E-1 to E-7, respectively. The aim of our study was to determine the stability of the genotypes in terms of seed cotton yield (SCY in kg/ha), Ginning Out Turn (GOT) and Boll Weight (g) under different environmental conditions through GGE Biplot stability analysis technique. In case of SCY all the environments formed only one mega environment (ME) for seed cotton yield. Only G1, G7, G8 and G9 were under the mega-environment performed better as compared to other genotypes but were not stable across the environments. Performance of a particular genotype was accessed by average environment coordination method and result showed that G7 was the highest performer followed by G8, G9 and G1. In case of GOT, two mega environments were formed and the genotypes G1, G5, G7 and G9 were better performers under E2, E4, E5, E6 and E7 (ME1). Other genotypes viz. G2, G3 and G6 were being best performer under ME2 (i.e. under E1 and E3) in term of GOT. The genotype G9 was best performer with higher average GOT and stability followed by G5 and G7. In case of Boll wt. the environments formed three mega environments in which G2, G3, G4 and G6 were best

performer under ME1 (E3, E4, E6 and E7), G7 and G8 performed better under E1 and E2 (ME2) and G1 and G9 were better performer under E5 (ME3). The genotype G6 when placed on GGE biplot showed its higher average yield with better stability in terms of boll weight followed by G8 and G7. In conclusion, genotype G7 (CISA 614-1) for seed cotton yield, genotype G9 (CISA 6-256) for GOT and genotype G6 (CISA 6-295) for Boll weight may be used for further breeding program for specific trait improvement.

Title: Screening of Different Cotton (*Gossypium* spp.) Genotypes for Yield and Yield Parameters

Author: Fatih Killı , Tahsin Beycioglu , Tülay Kan

Imprint: International Journal of Scientific Engineering and Science Volume 6, Issue 12, pp. 14-18, 2022. ISSN (Online): 2456-7361

Abstract— The experiment was conducted to determine the yield (seed cotton and seed) and yield parameters (plant height, number of sympodial branches, number of boll per plant, seed cotton weight per boll, number of seeds per boll, 100-seed weight and ginning outturn) of different twohundred cotton (*Gossypium* spp.) genotypes in east Mediterranean climatic conditions using a randomized complete block design with three replications in 2018 and 2019 growing seasons. It was determined that there were statistically significant differences among the cotton genotypes for all investigated characteristics. The results showed that plant height, number of sympodial branches, number of boll per plant, seed cotton weight per boll, number of seeds per boll, 100-seed weight, ginning outturn, seed cotton yield and seed yield ranged between 53.10-110.50 cm, 4.20-12.00 no. plant-1 , 4.50-18.30 no. plant-1 , 2.00-6.40 g, 18.00-40.00 no. boll-1 , 7.70-13.50 g, 26.70-45.50%, 1290.0-6230.0 kg ha⁻¹ and 880.0- 4060.0 kg ha⁻¹ , respectively. As a result, these variations of cotton genotypes can be evaluated in cotton breeding studies for specific purposes.

Fiber and Fiber Technology

Title: VARIABILITY STUDIES IN F2 POPULATION OF UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.) FOR YIELD AND FIBRE QUALITY TRAITS.

Author: S. SUBHASHINI*, K. KEERTHIVARMAN, DEBADATTA PANDA, L. ANANDA LEKSHMI AND BHIMIREDDY SUKRUTHA

Imprint: International Journal of Agriculture Sciences ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 14, Issue 12, 2022, pp.-11967-11970.

Abstract: The present experiment on F₂ population of MCU 5 x KC 3, CO 14 x KC 3, CO 14 x KC 2 and TCH 1828 x KC 2 was investigated for the variability studies thereby identifying the phenotypic (PCV), genotypic variations (GCV), heritability (h²) and genetic advance as percent of mean (GAM) present in the population. These estimates provide the knowledge of genes that are additive or non-additive in nature. Predicting the nature of gene action would help in formulating the successful breeding programmes for the respective populations under study. For majority of the characteristics, PCV and GCV had a high level of agreement, indicating that the observed variance might be mostly genetic. High heritability along with high genetic advance as percent of mean might be viewed as positive qualities that indicate additive gene activity which was found in the trait seed cotton yield per plant in all the four crosses taken under study and as a result, simple selection method is effective for improvement of such trait. For seed cotton yield associated and fibre quality parameters, moderate to high GCV, PCV, heritability, and genetic advance percent of mean values were found, indicating that these qualities could be passed to the progeny when hybridization was undertaken and phenotypic based selection was effective.

Title: Triallel Analysis for Ginning Outturn in Inter and Intra Specific Cotton Hybrids.

Author: Y. Prashanth , T. Pradeep , A. Sudarshanam , D. Saida Naik and B. Ramprasad

Imprint: Biological Forum – An International Journal 14(1): 147-150(2022)

ABSTRACT: Ginning outturn, is one of the economically important trait to enhance lint yield. It showed that high GOT % is good for devising strategy for fiber quality improvement also. Genetical improvement of this complex trait had created attention of conventional plant breeders, any plant breeding technique has to be decided based on the gene action involved for expression trait. Triallel analysis provides information on all types of gene actions viz., additive, dominance and epistatic components besides giving information on order of parents in three-way cross combinations for obtaining superior hybrids transgressive segregants. In the present study an attempt was made to obtain information on gene action controlling the trait ginning outturn of cotton in 60 inter and intra specific three way cross hybrids. The result revealed that, role of additive as well as non-additive gene action in the expression of this trait. Suggested, improvement would be possible by adopting special breeding methods like inter

mating in early segregating generations for two to three generations with step by step improvement followed by pedigree method of breeding or special breeding methods like biparental selection scheme and recurrent selection schemes.

Plant Biotechnology

Title: Flame resistant cotton lines generated by synergistic epistasis in a MAGIC population.

Author: Gregory N. Thyssen ,Brian D. Condon,Doug J. Hinchliffe,Linghe Zeng, Marina Naoumkina, Johnie N. Jenkins,Jack C. McCarty,Ruixiu Sui,Crista Madison, Ping Li,David D. Fang

Imprint: PLOS ONE Published: January 18, 2023

<https://doi.org/10.1371/journal.pone.0278696>

Abstract: Textiles made from cotton fibers are flammable and thus often include flame retardant additives for consumer safety. Transgressive segregation in multi-parent populations facilitates new combinations of alleles of genes and can result in traits that are superior to those of any of the parents. A screen of 257 recombinant inbred lines from a multi-parent advanced generation intercross (MAGIC) population for naturally enhance flame retardance (FR) was conducted. All eleven parents, like all conventional white fiber cotton cultivars produce flammable fabric. MAGIC recombinant inbred lines (RILs) that produced fibers with significantly lower heat release capacities (HRC) as measured by microscale combustion calorimetry (MCC) were identified and the stability of the phenotypes of the outliers were confirmed when the RILs were grown at an additional location. Of the textiles fabricated from the five superior RILs, four exhibited the novel characteristic of inherent flame resistance. When exposed to open flame by standard 45° incline flammability testing, these four fabrics self-extinguished. To determine the genetic architecture of this novel trait, linkage, epistatic and multi-locus genome wide association studies (GWAS) were conducted with 473k SNPs identified by whole genome sequencing (WGS). Transcriptomes of developing fiber cells from select RILs were sequenced (RNAseq). Together, these data provide insight into the genetic mechanism of the unexpected emergence of flame-resistant cotton by transgressive segregation in a breeding program. The incorporation of this trait into

global cotton germplasm by breeding has the potential to greatly reduce the costs and impacts of flame-retardant chemicals

Title: Establishment of an efficient cotton root protoplast isolation protocol suitable for single-cell RNA sequencing and transient gene expression analysis

Author: Ke Zhang, Shanhe Liu, Yunze Fu, Zixuan Wang, Xiubo Yang, Wenjing Li, Caihua Zhang, Dongmei Zhang & Jun Li

Imprint: *Plant Methods* volume 19, Article number: 5 (2023)

Abstract: Cotton has tremendous economic value worldwide; however, its allopolyploid nature and time-consuming transformation methods have hampered the development of cotton functional genomics. The protoplast system has proven to be an important and versatile tool for functional genomics, tissue-specific marker gene identification, tracking developmental trajectories, and genome editing in plants. Nevertheless, the isolation of abundant viable protoplasts suitable for single-cell RNA sequencing (scRNA-seq) and genome editing remains a challenge in cotton.

Title: GENETIC AND EXPRESSIONAL EVIDENCE DISPLAYS FUNCTIONAL DISTINCTION OF COTTON BASIC HELIX-LOOP-HELIX PROTEINS IN ARABIDOPSIS TRICHOME INITIATION

Author: ANH PHU NAM BUI

Imprint: Pak. J. Bot., 55(3): DOI: [http://dx.doi.org/10.30848/PJB2023-3\(23\)](http://dx.doi.org/10.30848/PJB2023-3(23))

Abstract: The cultivated tetraploid cotton species (AD genomes) were originated from two ancestral diploid species (A and D genomes). While the ancestral A-genome species produce spinnable fibers, the D-genome species do not. Cotton fibers are unicellular trichomes originating from seed coat epidermal cells, and currently there is an immense interest in understanding the process of fiber initiation and development. Current knowledge demonstrates that there is a great deal of resemblance in initiation mechanism between Arabidopsis trichome and cotton fiber. In this study, comparative functional studies between A genome and D-genome species in cotton by using Arabidopsis trichome initiation as a model was performed. Four cotton genes TTG3, MYB2, DEL61 and DEL65 were amplified from A-genome and D-genome species and transformed into their homolog trichomeless mutants Arabidopsis *ttg1*, *gl1*, and *gl3egl3*, respectively. Our data showed that the transgenic plants expressing TTG3 and MYB2 genes from A genome and D-genome species complement the *ttg1* and *gl1*

mutants, respectively. It was also discovered that complete absences of two functional basic helix loop helix (bHLH) proteins (DEL65/DEL61) in D- diploid species and one (DEL65) that is functional in A-genome species, but not from Dgenome species. This observation is consistent with the natural phenomenon of spinnable fiber production in A- genome species and absence in D-genome species. These results suggested that MYB2, TTG3 and DEL65, when expressed in Arabidopsis, regulated the regulatory network genes during the trichome initiation process.

Title: Genetic polymorphism detection in brazilian perennial cottons (*Gossypium* spp.) using an ISSR marker system and its application for molecular interspecific differentiation.

Author: Fernando dos Santos Araújo, Riselane de Lucena Alcântara Bruno, Nair Helena Castro Arriel, Everaldo Paulo de Medeiros, Liziane Maria de Lima, Mayara Andrade de Souza, Alberício Pereira de Andrade, Richeliel Albert Rodrigues Silva, Francival Cardoso Felix & Karialane da Silva Belarmino

Imprint: *Molecular Biology Reports* (2023)

Abstract: The semi-domesticated Brazilian perennial cotton (*Gossypium* spp.) germplasm is considered a source of variability for creating modern upland cotton varieties. Here we used Inter-simple Sequence Repeat (ISSR) markers to detect intra and interspecific genetic polymorphism in *Gossypium hirsutum* L. r. marie-galante and *Gossypium barbadense* L. and to use molecular data to assessing genetic diversity and molecular discrimination of these species.

Title: Weighted Gene Co-Expression Network Analysis Reveals Hub Genes for Fuzz Development in *Gossypium hirsutum*

Author: Yilei Long, Kaixiang Xu

Imprint: *Genes* 2023, 14(1), 208; <https://doi.org/10.3390/genes14010208>

Abstract: Fuzzless *Gossypium hirsutum* mutants are ideal materials for investigating cotton fiber initiation and development. In this study, we used the fuzzless *G. hirsutum* mutant Xinluzao 50 FLM as the research material and combined it with other fuzzless materials for verification by RNA sequencing to explore the gene expression patterns and differences between genes in upland cotton during the fuzz period. A gene ontology (GO) enrichment analysis showed that differentially expressed genes (DEGs) were mainly enriched in the metabolic process, microtubule binding, and other

pathways. A weighted gene co-expression network analysis (WGCNA) showed that two modules of Xinluzao 50 and Xinluzao 50 FLM and four modules of CSS386 and Sicala V-2 were highly correlated with fuzz. We selected the hub gene with the highest KME value among the six modules and constructed an interaction network. In addition, we selected some genes with high KME values from the six modules that were highly associated with fuzz in the four materials and found 19 common differential genes produced by the four materials. These 19 genes are likely involved in the formation of fuzz in upland cotton. Several hub genes belong to the arabinogalactan protein and GDSL lipase, which play important roles in fiber development. According to the differences in expression level, 4 genes were selected from the 19 genes and tested for their expression level in some fuzzless materials. The modules, hub genes, and common genes identified in this study can provide new insights into the formation of fiber and fuzz, and provide a reference for molecular design breeding for the genetic improvement of cotton fiber.

Title: Cotton promoters for controlled gene expression

Author: Ana LuizaAtella, Maria FatimaGrossi-de-Sá, MarcioAlves-Ferreira

Imprint: Electronic Journal of Biotechnology, [Volume 62](#), March 2023, Pages 1-12

Abstract: Cotton (*Gossypium hirsutum*) is one of the most important crops and is the main source of fiber for the textile industry, but its productivity is still hampered by several challenges, such as pests, diseases and abiotic stresses. This scenario has increased interest in achieving cotton events with greater productivity and sustainability through biotechnological approaches. An essential component of these strategies is the controlled expression of the gene of interest, suggesting that promoters are a key element. These promoters are generally divided into three types: constitutive, spatiotemporal, and inducible. However, to date, this diversity of promoter activity has not been as widely explored in cotton improvement. In this review, we provide an overview of cotton promoters that can be used to achieve fine-tuning of expression, facilitating decision-making and improving the ability to develop desirable traits in cotton plants. In addition, we present new approaches to identify promoters that may be useful for the development of new tools for cotton improvement.

Title: Silencing of *GhORP_A02* enhances drought tolerance in *Gossypium hirsutum*

Author: Sani Muhammad Tajo, Zhaoe Pan, Yinhua Jia, Shoupu He, Baojun Chen, Salisu Bello Sadau, Yusuf KM, Aboleri Adijat Ajadi, Mian Faisal Nazir, Umar Auta, Xiaoli Geng & Xiongming Du

Imprint: *BMC Genomics* volume 24, Article number: 7 (2023)

Abstract: *ORP* (Oxysterol-binding protein-related proteins) genes play a role in lipid metabolism, vesicular transferring and signaling, and non-vesicular sterol transport. However, no systematic identification and analysis of *ORP* genes have been reported in cotton.

Title: Genome wide identification of GDSL gene family explores a novel *GhirGDSL26* gene enhancing drought stress tolerance in cotton

Author: Jiajun Liu, Jiangna Liu, Heng Wang, Aziz Khan, Yanchao Xu, Yuqing Hou, Yuhong Wang

Imprint: *BMC Plant Biology* volume 23, Article number: 14 (2023)

Abstract: Current climate change scenarios are posing greater threats to the growth and development of plants. Thus, significant efforts are required that can mitigate the negative effects of drought on the cotton plant. GDSL esterase/lipases can offer an imperative role in plant development and stress tolerance. However, the systematic and functional roles of the GDSL gene family, particularly in cotton under water deficit conditions have not yet been explored.

Seed Science and Technology

Title: Transcriptome Profiling of *Gossypium anomalum* Seedlings Reveals Key Regulators and Metabolic Pathways in Response to Drought Stress

Author: Wei Ji, Huan Yu, Yixin Shangguan

Imprint: *Plants* 2023, 12(2), 312; <https://doi.org/10.3390/plants12020312>

Abstract: Drought stress is a key limiting factor for cotton (*Gossypium* spp.) growth, production, development, and production worldwide. Some wild diploid cotton species are remarkably tolerant of water deficit and constitute an important reservoir for understanding the molecular mechanisms of *Gossypium* spp. drought tolerance and improving cultivated upland cotton. Here, we utilized RNA-Seq technology to characterize the leaf transcriptomes of a wild African diploid cotton species, *Gossypium anomalum*, under drought stress. A total of 12,322 differentially expressed genes (DEGs) were identified after mapping valid clean reads to the reference genome of *G. anomalum*, of which 1243 were commonly differentially expressed at all stages of drought stress. These genes were significantly enriched for molecular functions Gene Ontology terms related to cytoskeleton, hydrolase activity, cellular redox, and binding. Additionally, a substantial proportion of enriched biological process terms concerned cell or subcellular processes, while most in the cellular components category concerned membrane function and photosynthesis. An enrichment analysis against the Kyoto Encyclopedia of Genes and Genomes showed the top significantly enriched pathways to be photosynthesis-antenna proteins, amino sugar and nucleotide sugar metabolism, starch and sucrose metabolism, MAPK signaling pathway, glutathione metabolism, and plant hormone signal transduction. The DEGs also exhibited interestingly significant enrichments for drought stress-induced tandemly repeated genes involved in iron ion binding, oxidoreductase activity, heme binding, and other biological processes. A large number of genes encoding transcription factors, such as MYB, bHLH, ERF, NAC, WRKY, and bZIP, were identified as playing key roles in acclimatizing to drought stress. These results will provide deeper insights into the molecular mechanisms of drought stress adaptation in *Gossypium* spp.

Title: A Preliminary Study on the Determination of Carpel Characteristics, Yield Losses and Free Fatty Acid Content of Seed under Pre-Harvest Precipitation in Cotton (*Gossypium hirsutum* L.)

Author: Serife BALCI1 Volkan Mehmet CINAR2 Aydın UNAY

Imprint: ANADOLU, J. of AARI ISSN: 1300-0225 (Print) E-ISSN: 2667-6087 (Online)
2022, 32 (2): 161-166 DOI: 10.18615/anadolu.1224464

ABSTRACT: Pre-harvest precipitation in some years in many cotton-growing regions may adversely affect cotton yield and quality. The effect of carpel characters of cultivars on fall out (ground losses) and free fatty acid of seed under different precipitation amounts were investigated. The experiment was arranged in a two-factor Randomized Complete Block Design with four replications. The precipitation x cultivar interaction for carpel depth, free acid content and fall out were significant. Fall out values were between 38.9 kg ha⁻¹ at 20 mm precipitation and 234.2 kg ha⁻¹ at 125 mm precipitation. The amount of fall out in all varieties was negatively affected by the increase in precipitation. Gloria cultivar with a wide carpel had the lowest yield losses on the ground.