

Agronomy, Soil Science and Plant Physiology

Title: Cover Cropping History Affects Cotton Boll Distribution, Lint Yields, and Fiber Quality

Author: Eric D. Billman, B. Todd Campbell

Imprint: Crop Science , <https://doi.org/10.1002/csc2.20931>

Abstract: There has been limited introduction of new cover crop species into cotton (*Gossypium hirsutum* L.) production within the last 30 years. Mounting evidence shows that traditional cover cropping species may be detrimental to cotton production, either by depleting soil fertility with crop removal, immobilizing minerals from high carbon residue, or excessive quantity of residue remaining at planting. The objective of this study was to determine the effects of growing a novel cover crop species, carinata (*Brassica carinata* A. Braun), as a winter annual cover crop for cotton rotation in the southeastern Coastal Plain. Over a two-year period, carinata, winter wheat (*Triticum aestivum* L.), and fallow covers were maintained over winter months, then rotated into cotton. Each year, seedcotton and lint yields were collected, along with subsamples for ginning and subsequent fiber quality analyses. Additionally, end-of-season plant mapping was conducted on plants from 1-m of row per plot to determine cover crop effects on boll formation, retention, and distribution, as well as canopy architecture. Results indicated that seedcotton and lint yield of cotton following carinata was greater than cotton following winter wheat, and lint yields of cotton following wheat were lower than cotton after fallow. Fiber quality was largely unaffected by preceding cover crop. End-of-season plant mapping indicated that cotton grown after carinata had more position 2 bolls, which correlated to greater lint yields. These results indicate that carinata can potentially serve as a new, more effective cover crop than winter wheat for cotton rotations in Coastal Plain soils.

Title: Association of profile of Bt. cotton growers and adoption of recommended package of practices

Author: PG Jambhule, DD Suradkar and RB Pendam

Imprint: The Pharma Innovation Journal 2023; 12(1): 2323-2329

Abstract: Study entitled “Adoption of recommended cultivation practices by the Bt. cotton growers” was undertaken in Warora, Bhadrawti and Chimur talukas in Chandrapur district of Vidarbha region of Maharashtra state. Ex-post facto research design was used for the same. The farmers growing Bt. cotton since last five years consecutively were identified and from each selected village 10 Bt. cotton growers as

respondents were selected randomly to constitute sample size of 120 respondents. The data from Bt. cotton growers were collected by personal interview method. Relatively higher proportion of Bt. cotton growers (36.66%) were in medium adoption level followed by (29.16%) were in low level of adoption of recommended package of practices whereas, 34.18 percent Bt. cotton growers who were in high level of adoption of recommended package of practices by Bt. cotton growers.

Title: Phenological impact in cotton crop affected by leaf reddening due to abiotic stress

Author: A Blesseena, RS Wagh and DA Raut

Imprint: The Pharma Innovation Journal 2023; 12(1): 2609-2613

Abstract: A field experiment was conducted during kharif 2020, at Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Ahmednagar (dist.), Maharashtra, India to evaluate the abiotic cause of major disorder i.e., leaf reddening in cotton plants. The main objective of study was on phenological responses of cotton plants studied using three different genotypes in three different irrigation environments and sown during three different intervals of time. Phenological parameters such as days for first square formation, days to 50% flowering and days for first boll opening were critically observed. The experiment was carried out in double split plot design, replicated thrice. Extra late sowing time, waterlogged environment and Bt hybrid i.e., Rashi 659 have taken more number of days for first square formation, days to 50% flowering and days for first boll opening.

Title: G.ARBOREUM L. AND G.HERBACEUM L. TYPES: HISTORY OF RESEARCH, NOW AND IN THE FUTURE

Author: Axmedov O.A., Xalikova M.B., Matyakubova E.U

Imprint: Journal of Pharmaceutical Negative Results | Volume 13 | Special Issue 10 | 2022 DOI: 10.47750/pnr.2022.13.S10.047

Abstract: Xindi growing in tropical and subtropical regions of Arabia, Africa and Asian countries-China (*G.arboreum* L.) and AfroAsia (*G.herbaceum* L.) wild, ruderal and cultural diploid goose species *Gossypium* L. forms the main part of the category. These species are one of the most ancient types of geese and show a number of valuable farm features in themselves. The researchers revealed the classification, origin, characteristics and prospects for genetic-selection use of these species

Title: Differential sensitivities of photosynthetic processes and carbon loss mechanisms govern N-induced variation in net carbon assimilation rate for field-grown cotton

Author: Ved Parkash, John L Snider, Henry Y Sintim, Lavesta C Hand, Gurpreet Virk, Amrit Pokhrel

Imprint: Journal of Experimental Botany, erad038, <https://doi.org/10.1093/jxb/erad038>

Abstract: Nitrogen (N) deficiency limits the net carbon assimilation rate (A_N), but the relative N sensitivities of photosynthetic component processes and carbon loss mechanisms remain relatively unexplored for field-grown cotton. Therefore, the objective of the current study was to define the relative sensitivity of individual physiological processes driving N deficiency-induced declines in A_N for field-grown cotton. Among the potential diffusional limitations evaluated, mesophyll conductance was the only parameter substantially reduced by N deficiency, but this did not affect CO_2 availability in the chloroplast. A number of metabolic processes were negatively impacted by N deficiency, and these effects were more pronounced at lower leaf positions in the cotton canopy. Ribulose biphosphate (RuBP) regeneration and carboxylation, A_N , and gross photosynthesis were the most sensitive metabolic processes to N deficiency, whereas photosynthetic electron transport processes, electron flux to photorespiration, and dark respiration exhibited intermediate sensitivity to N deficiency. Among thylakoid-specific processes, the quantum yield of PSI end electron acceptor reduction was the most sensitive process to N deficiency. It was concluded that A_N is primarily limited by Rubisco carboxylation and RuBP regeneration under N deficiency in field-grown cotton, and the differential N sensitivities of the photosynthetic process and carbon loss mechanisms contributed significantly to photosynthetic declines.

Title: Efficient land configurations and nutrient management in Bt cotton (*Gossypium herbaceum*)

Author: CH PRAGATHI KUMARI, K B SUNEETHA DEVI, K BHANU REKHA, S SRIDEVI and S NARENDER REDDY

Imprint: Indian Journal of Agricultural Sciences 93 (1): 67-72, January 2023/ Article <https://doi.org/10.56093/ijas.v93i1.109104>

Abstract: Field experiments were conducted during rainy (kharif) season, 2015 and 2016 to assess the impact of land configurations and nutrient management on Bt cotton (*Gossypium herbaceum* L.) at College Farm, College of Agriculture, Rajendranagar, Professor Jayashankar Telangana State Agricultural University, Hyderabad, Telangana.

Treatments consisted of four land configurations, viz. flat bed sowing, ridge and furrow, broad bed and furrow (BBF) and BBF laid with poly mulch as main plots and five nutrient management treatments in sub plots, viz. farmer's practice, 100% RDF-150:60:60 NPK kg/ha, 125% RDF, 100% RDF along with 25% N through farmyard manure and 100% RDF along with 25% N through pressmud laid out in triplicated strip plot design. Results revealed that yield attributes (bolls per plant and boll weight), seed cotton yield and field water use efficiency were significantly higher with BBF with poly mulch along with application of 100% RDF + 25% RDN through organics (pressmud or FYM) comparable to BBF laid with poly mulch and application of 125% RDF through inorganics. Soil moisture extraction by crop was higher from 0-15 cm and 15-30 cm depth in poly mulch + BBF over other land configurations.

Crop Protection

Title: Genome wide identification and evolutionary analysis of *vat* like NBS-LRR genes potentially associated with resistance to aphids in cotton

Author: U. Pirithiraj, M. Murugan, M. Jayakanthan, N. Manikanda Boopathi, V. alasubramani, N. Premalatha, S. Hari Ramakrishnan & S. Selva babu

Imprint: *Genetica* (2023)

Abstract: Nucleotide Binding Site - Leucine Rich Repeat (NBS-LRR) genes play a significant role in plant defense against biotic stresses and are an integral part of signal transduction pathways. *Vat* gene has been well reported for their role in resistance to *Aphis gossypii* and viruses transmitted by them. Despite their importance, *Vat* like NBS-LRR resistance genes have not yet been identified and studied in cotton species. This study report hundreds of orthologous *Vat* like NBS-LRR genes from the genomes of 18 cotton species through homology searches and the distribution of those identified genes were tend to be clustered on different chromosome. Especially, in a majority of the cases, *Vat* like genes were located on chromosome number 13 and they all shared two conserved NBS-LRR domains, one disease resistant domain and several repeats of LRR on the investigated cotton *Vat* like proteins. Gene ontology study on *Vat* like NBS-LRR genes revealed the molecular functions viz., ADP and protein binding. Phylogenetic analysis also revealed that *Vat* like sequences of two diploid species, viz., *G. arboreum* and *G. anomalum*, were closely related to the sequences of the tetraploids than all other diploids. The *Vat* like genes of *G. aridum* and *G. schwendimanii* were

distantly related among diploids and tetraploids species. Various hormones and defense related *cis*-acting regulatory elements were identified from the 2 kb upstream sequences of the *Vat* like genes implying their defensive response towards the biotic stresses. Interestingly, *G. arboreum* and *G. trilobum* were found to have more regulatory elements than larger genomes of tetraploid cotton species. Thus, the present study provides the evidence for the evolution of *Vat* like genes in defense mechanisms against aphids infestation in cotton genomes and allows further characterization of candidate genes for developing aphid and aphid transmitted viruses resistant crops through cotton breeding.

Title: Strigolactones positively regulate Verticillium wilt resistance in cotton via crosstalk with other hormones

Author: Feifei Yi, Guoyong An, Aosong Song, Kai Cheng, Jinlei Liu, Chenxiao Wang, Shuang Wu, Ping Wang, Jiaxuan Zhu, Zhilin Liang

Imprint: *Plant Physiology*, kiad053, <https://doi.org/10.1093/plphys/kiad053>

Abstract: Verticillium wilt caused by *Verticillium dahliae* is a serious vascular disease in cotton (*Gossypium* spp.). *V. dahliae* induces the expression of the *CAROTENOID CLEAVAGE DIOXYGENASE 7* (*GauCCD7*) gene involved in strigolactone (SL) biosynthesis in *Gossypium australe*, suggesting a role for SLs in Verticillium wilt resistance. We found that the SL analog *rac*-GR24 enhanced while the SL biosynthesis inhibitor TIS108 decreased cotton resistance to Verticillium wilt. Knock-down of *GbCCD7* and *GbCCD8b* genes in island cotton (*Gossypium barbadense*) decreased resistance, whereas overexpression of *GbCCD8b* in upland cotton (*Gossypium hirsutum*) increased resistance to Verticillium wilt. Additionally, Arabidopsis (*Arabidopsis thaliana*) SL mutants defective in *CCD7* and *CCD8* putative orthologs were susceptible, whereas both Arabidopsis *GbCCD7*- and *GbCCD8b*-overexpressing plants were more resistant to Verticillium wilt than wild-type (WT) plants. Transcriptome analyses showed that several genes related to the jasmonic acid (JA)- and abscisic acid (ABA)-signaling pathways, such as *MYELOCYTOMATOSIS 2* (*GbMYC2*) and *ABA-INSENSITIVE 5*, respectively, were up-regulated in the roots of WT cotton plants in responses to *rac*-GR24 and *V. dahliae* infection but down-regulated in the roots of both *GbCCD7*- and *GbCCD8b*-silenced cotton plants. Furthermore, *GbMYC2* suppressed the expression of *GbCCD7* and *GbCCD8b* by binding to their promoters, which might regulate the homeostasis of SLs in cotton through a negative feedback loop. We also found that *GbCCD7*- and *GbCCD8b*-silenced cotton plants were impaired in *V. dahliae*-induced reactive oxygen species (ROS) accumulation. Taken together, our results suggest that SLs positively regulate cotton resistance to Verticillium wilt through crosstalk with the JA and ABA-signaling pathways and by inducing ROS accumulation.

Plant Genetics and Breeding

Title: Comparative transmission genetics of introgressed chromatin in reciprocal advanced backcross populations in *Gossypium* (cotton) polyploids

Author: Jeevan Adhikari, Rahul Chandnani, Deepak Vitrakoti, Sameer Khanal,

Wiriyarat Ployaram & Andrew H. Paterson

Imprint: *Heredity* (2023)

Abstract: Introgression is a potential source of valuable genetic variation and interspecific introgression lines are important resources for plant breeders to access novel alleles. Experimental advanced-generation backcross populations contain individuals with genomic compositions similar to those resulting from natural interspecific hybridization and provide opportunities to study the nature and transmission pattern of donor chromatin in recipient genomes. Here, we analyze transmission of donor chromatin in reciprocal backcrosses between *G. hirsutum* and *G. barbadense*. Across the genome, recurrent backcrossing in both backgrounds yielded donor chromatin at slightly higher frequencies than the Mendelian expectation in BC₅F₁ plants, while the average frequency of donor alleles in BC₅F₂ segregating families was less than expected. In the two subgenomes of polyploid cotton, the rate of donor chromatin introgression was similar. Although donor chromatin was tolerated over much of the recipient genomes, 21 regions recalcitrant to donor alleles were identified. Only limited correspondence is observed between the recalcitrant regions in the two backgrounds, suggesting the effect of species background on introgression of donor segments. Genetic breakdown was progressive, with floral abscission and seed inviability ongoing during backcrossing cycles. Regions of either high or low introgression tended to be in terminal chromosomal regions that are generally rich in both genes and crossover events, with long stretches around the centromere having limited crossover activity resulting in relatively constant low introgression frequencies. Constraints on fixation and selection of donor alleles highlights the challenges of utilizing introgression breeding in crop improvement.

Title: Evaluation on Drought Resistance of Recombinant Inbred Lines of *Gossypium barbadense* L. at Flowering and Boll Stages.

Author: YANG Long, ZHAO Fuxiang, DUAN Yajie, CAI Yongsheng, ZHENG Kai, CHEN Qin, CHEN Quanjia, QU Yanying

Imprint: Xinjiang Agricultural Sciences, 2022, 59(12): 2861-2869.

Abstract: To provide raw materials for the improvement of drought-resistant cotton germplasm and breeding of high-quality stress-resistant varieties by constructing isolated populations of *Gossypium barbadense* L. and screening resistant and sensitive extreme materials, which provides a basis for future research on cotton drought resistance. **【Methods】** 71 strains of parents and Haihai recombinant inbred line populations were taken as experimental materials, the field was subjected to natural drought stress at the flowering and boll stage, and morphological indicators and yield-related indicators were measured. Meanwhile, variance analysis, principal component analysis, and clustering analysis were employed simultaneously to identify and evaluate the drought resistance of parents and RILs families. **【Results】** Principal component analysis of 7 traits could be divided into two comprehensive factors: plant morphology, yield-related traits per plant, and fiber yield-related traits; based on the comprehensive drought resistance measure (*D* value) for systematic clustering, the RILs materials were divided into four groups: more drought-sensitive type (28), drought-resistant type (26), drought-sensitive type (14) and strong drought-resistant type (3). When the drought resistance coefficient of each trait was used as the independent variable and the *D* value as the dependent variable for regression analysis, a multivariate linear model was obtained: $D \text{ value} = -0.771 + 0.089 \times DC \text{ Plant height} + 0.117 \times DC \text{ number of effective branches} + 0.132 \times DC \text{ number of bolls} + 0.343 \times DC \text{ effective number of bolls} + 0.338 \times DC \text{ single boll lint weight} + 0.230 \times DC \text{ Cotton yield per plant}$. **【Conclusion】** The strong drought-resistant materials HH-16, HH-61, HH-70 and the drought-sensitive materials HH-051 and HH-05 are screened out, which can be applied to the analysis of drought-related gene expression and the innovation of stress-resistant germplasm. The results of principal component analysis and multiple regression analysis show that the effective boll number, lint weight per boll and cotton yield per plant can be used as the main indicators for the identification of drought resistance of cotton inbred lines in the field.

Title: Genomic insights into the genetic basis of cotton breeding in China.

Author: Yiqian Li¹, Zhanfeng Si¹, Guoping Wang, Zhuolin Shi, Jinwen Chen, Guoan Qi, Shangkun Jin, Zegang Han, Wenhao Gao, Yue Tian, Yun Mao, Lei Fang, Yan Hu¹, Hong Chen, Xiefei Zhu and Tianzhen Zhang

Imprint: Molecular Plant (2023), <https://doi.org/10.1016/j.molp.2023.01.012>

Abstract: The excellent Upland cotton (*Gossypium hirsutum*) cultivars developed since 1949 have made a huge contribution to cotton production in China, the world's largest producer and consumer of cotton. However, the genetic and genomic basis for the improvements of these cotton cultivars remains largely unclear. In this study, we selected 16 Upland cotton cultivars with important historical status in Chinese cotton

breeding and constructed a multiparent, advanced generation, intercross (MAGIC) population comprising 920 recombinant inbred lines. A genome-wide association study using the MAGIC population identified 54 genomic loci associated with lint yield and fiber quality. Of them, 25 (46.30%) pleiotropic genomic loci cause simultaneous changes of lint yield and/or fiber quality traits, revealing complex trade-offs and linkage drags in Upland cotton agronomic traits. Deep sequencing data of 11 introduced ancestor cultivars and publicly available resequencing datasets of 839 cultivars developed in China during the past 70 years were integrated to explore the historical distribution and origin of the elite or selected alleles. Interestingly, 85% of these elite alleles were selected and fixed from different American ancestors, consistent with cotton breeding practices in China. However, seven elite alleles of native origin that are responsible for Fusarium wilt resistance, early maturing, good-quality fiber, and other characteristics were not found in American ancestors but have greatly contributed to Chinese cotton breeding and wide cultivation. Taken together, these results provide a genetic basis for further improving cotton cultivars and reveal that the genetic composition of Chinese cotton cultivars is narrow and mainly derived from early introduced American varieties.

Title: CHROMOSOME SEGMENT DERIVED FROM GOSSYPIUM ANOMALUM (G. ANOMALUM) GOSSYPIUM HIRSUTUM (G. HIRSUTUM), AND MOLECULAR MARKERS THEREOF

Document Type and Number:

United States Patent Application 20230037213

Kind Code:

A1

Abstract: A chromosome segment derived from *G. anomalum* leading to a lethal phenotype in *G. hirsutum*, and molecular markers thereof are provided. The chromosome segment A11-9 is derived from *G. anomalum*, is located on chromosome 11 of a *G. anomalum* genome, and is marked by 6 pairs of simple sequence repeat (SSR) markers: NAU5192, A11_175, JAAS3191, A11_243, JAAS3310, and A11_1193. With DNA of *G. anomalum* as a template, the 6 pairs of SSR markers are used together to amplify the DNA of *G. anomalum*, and a chromosome segment with target fragments of the 6 pairs of SSR markers is the *G. anomalum* chromosome segment A11-9. A single chromosome segment introgression line derived from *G. anomalum* with a lethal phenotype is obtained, and the development of the single chromosome segment introgression line provides an important material for promoting the fine mapping of a target gene and the subsequent map-based cloning

Title: COTTON VARIETY 14R913B2XF

Document Type and Number:

United States Patent Application 20230025689

Kind Code:

A1

Abstract:

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

Title: Genome-wide identification and characterization of polycomb repressive complex 2 core components in upland cotton (*Gossypium hirsutum* L.)

Author: Kai Cheng, Cangbao Lei, Siyuan Zhang, Qiao Zheng, Chunyan Wei, Weiyi Huang,

Minghui Xing, Junli Zhang, Xiangyu Zhang & Xiao Zhang

Imprint: *BMC Plant Biology* volume 23, Article number: 66 (2023)

Abstract: The evolutionarily conserved Polycomb Repressive Complex 2 (PRC2) plays a vital role in epigenetic gene repression by depositing tri-methylation on lysine residue K27 of histone H3 (H3K27me3) at the target loci, thus participating in diverse biological processes. However, few reports about PRC2 are available in plant species with large and complicated genomes like cotton.

Fiber and Fiber Technology

Title: Cotton green fiber promotes suberin synthesis interfering cellulose deposition in the secondary cell wall

Author :

Zhong Chen , Yaohua Li , Zhonghua Teng , Yue Zhang , Yong Liu , Qingwei Suo , Yi Wang , Jianyan Zeng , Aimin Liang , Qian Yan , Dexin Liu , Nian Liu , Nianjuan Fang , Haifeng Liu , Zhengsheng Zhang , Yuehua Xiao

Imprint: Industrial Crops and Products

Volume 194, April 2023, 116346

Abstract: Naturally green cotton (NGC) represents one of two commercialized naturally colored cottons, but its application is limited in the textile industry for inferior productivity and fiber quality of NGC cultivars. NGC fiber deposits substantial suberin at maturation, possibly related to fiber green coloration. The effects of suberin deposition on fiber development and fiber yield and quality are still to be elucidated. In the present study, the green fiber gene (*Lg*) in upland cotton (*Gossypium hirsutum* L.) was cloned using map-based method. It was found that *Lg* encoded an R2R3-MYB transcription factor, promoting suberin synthesis and deposition in cotton fiber via regulating multiple suberin structural genes. Suberin accumulated in green fibers continuously from the beginning of the secondary cell wall synthesis, along with significantly inhibited cellulose deposition, leading to dramatically decreased fiber strength and lint percentage. Our data demonstrated that suberin accumulation significantly interfered with cellulose deposition in fiber secondary cell wall, which conferred low yield and inferior fiber quality to green-fiber cottons.

Title: Studies on genetic parameters for yield, yield contributing and fiber quality characters in desi cotton (*Gossypium arboreum* L.)

Author: SL Kolhe, HV Kalpande and VN Chinchane

Imprint: The Pharma Innovation Journal 2022; 11(12): 5934-5936

Abstract: In the present investigation, fifty desi cotton (*Gossypium arboreum* L.) genotypes including six checks viz., AKA 7, AKA 8, JLA 794, JLA 505, PA 255 and PA 402 were studied to observe genetic variability, heritability and genetic advance for thirteen yield contributing and fiber quality characters. The analysis of variance revealed that the sufficient variability was present in the material for all the characters. The phenotypic coefficient of variation was higher than genotypic coefficient of variation. High estimates of GCV and PCV were observed for seed cotton yield per plant and moderate GCV and PCV for number of bolls per plant, plant height, lint index, seed index and boll weight. High heritability coupled with high genetic advance over mean was observed for the characters seed cotton yield per plant, number of bolls per plant, number of sympodia per plant, plant height and lint index indicating the presence of additive gene action in the inheritance of these traits. Whereas high heritability with moderate genetic advance was observed for fibre strength, fibre fineness, upper half mean length, seed index and boll weight.

Title: Heterosis study on yield, yield contributing and fibre quality traits in desi cotton (*Gossypium arboreum* L.)

Author: Yogesh Hottigodar, HV Kalpande and VN Chinchane

Imprint: The Pharma Innovation Journal 2023; 12(2): 491-495

Abstract : Eighteen hybrid combinations developed by crossing three lines and six testers in Line X Tester mating design were evaluated along with their parents including three checks with two replications in Randomised Block Design for seed cotton yield, yield contributing and fibre quality traits in desi cotton during kharif, 2021 at Cotton Research Station, Mahboob Baugh, VNMKV, Parbhani. Heterosis was estimated in relation to better parent (Heterobeltiosis) and standard checks (Standard heterosis). The magnitude of heterosis, heterobeltiosis and standard heterosis for all the characters in the current study was highly appreciable. Among eighteen crosses, the crosses showed the highest and desirable significant standard heterosis for various traits viz., cross PA 833 x JLA 505 for days to 50 per cent flowering; PA 904 x CNA 1032 for plant height, boll weight and ginning percentage; PA 899 x PA 740 for number of sympodial per plant; PA 833 x CNA 1032 for number of bolls per plant, seed cotton yield per plant, seed index and lint index; PA 904 x PA 785 for upper half mean length and fibre strength; PA 833 X AKA 7 for fibre fineness; PA 904 x AKA 7 for uniformity ratio over standard check PKVDH 1, PKV Suvarna and NACH 12, respectively. The crosses PA 899 x CNA 1032, PA 833 x CNA 1032 and PA 833 X AKA 7 for seed cotton yield and yield contributing traits, while crosses PA 904 x PA 785 and PA 833 X JLA 794 for fibre quality traits hold promise for further evaluation and commercial exploitation of heterosis.

Title: Delayed harvest time affects strength and color parameters in cotton fiber

Author: Gonzalo J. Scarpin, Antonela E. Cereijo, Pablo N. Dileo, H. Martin Winkler, Robertino J. Muchut, Fernando G. Lorenzini, Roxana A. Roeschlin, Marcelo Paytas

Imprint: Agronomy Journal ,<https://doi.org/10.1002/agj2.21295>

Abstract: Cotton (*Gossypium hirsutum* L.) is the most widely used natural fiber worldwide in the textile industry, thus maintaining or even improving fiber quality is essential to produce the best quality yarn and uniform fabrics. Final fiber quality properties are determined not only by genotypes or environmental conditions during crop development but can also be affected by other post-maturity factors, such as harvesting and ginning methods, and harvest time. The aim of this study is to associate

the different environmental factors that affect specific lint quality traits produced by a delay in harvest time, also assessing cultivar effect. This field study included 4 cotton cultivars evaluated at 7 different harvest times (manual harvested) for different quality parameters. Results indicate that prolonged exposure of cotton fiber to the environment affects lint percentage (LP), strength (Str), reflectance (Rd) and yellowness (+b). Str showed a decrease of 0.02 g tex^{-1} per day from defoliant application, while LP, Rd and +b presented different rates according to the season. No differences were obtained neither for length nor for fineness and maturity (micronaire) traits. In addition, the analysis of the results together with the climatic data recorded during the experiments indicated a negative correlation between Str, Rd, and +b with the number of rainy days, accumulated precipitation, and frost temperatures. Overall, this study establishes specific relationships between certain fiber characteristics and environmental conditions, being an important tool for crop management with regards to climate predictions that could help to make estimates of economic losses when the harvest is delayed.

Plant Biotechnology

Title: A Novel Tandem Zinc Finger Protein in *Gossypium hirsutum*, GhTZF2, Interacts with GhMORF8 to Regulate Cotton Fiber Cell Development

Author: Yang Li, Wei Xi, Jianfeng Hao, Li Zhang, Xingpeng Wen, Zhiguo Wu and Yuxian Zhu

Imprint: *Agronomy* 2023, 13(2), 519; <https://doi.org/10.3390/agronomy13020519>

Abstract: Arginine-rich Tandem Zinc Finger (RR-TZF) proteins make up a plant-specific superfamily that participates in plant development, while their roles in cotton fiber development remain to be explored. In this study, we identified an RR-TZF protein-coding gene, *GhTZF2*, containing two CCCH domains (C-X₇-C-X₅-C-X₃-H-X₁₆-C-X₅-C-X₄-C-X₃-H) and one RR domain at the N-terminus of the two CCCH domains, by comparing the differences of chromatin H3K4me3 modifications between wild-type upland cotton (WT) and the *fuzzless-lintless* mutant (*fl*) ovules. *GhTZF2* was highly expressed in ovule cells near anthesis, and multiple experiments revealed that *GhTZF2* could interact directly with GhMORF8. Homozygotic *GhTZF2*-knockout cotton lines produced significantly shorter fibers with thinner cell walls. Additionally, comparative transcriptome analysis confirmed that many differentially expressed transcripts contain adenine- and uridine-rich (AU-rich) elements (AREs) in their 3' untranslated regions (UTR). Together, this study indicated that *GhTZF2* may regulate

cotton fiber cell development through interacting with GhMORF8, or may be involved in mRNA turnover.

Title: Genome-wide identification and expression analysis of the cotton patatin-related phospholipase A genes and response to stress tolerance

Author: Yunxiao Wei, Zhili Chong, Chao Lu, Kaili Li, Chengzhen Liang, Zhigang Meng, Yuan Wang, Sandui Guo, Liangrong He & Rui Zhang

Imprint: *Planta* volume 257, Article number: 49 (2023)

Abstract: pPLA (patatin-related phospholipase A) is a key enzyme that catalyzes the initial step of lipid hydrolysis, which is involved in biological processes, such as drought, salt stress, and freezing injury. However, a comprehensive analysis of the pPLA gene family in cotton, especially the role of pPLA in the response to drought and salt tolerance, has not been reported so far. A total of 33 pPLA genes were identified in this study using a genome-wide search approach, and phylogenetic analysis classified these genes into three groups. These genes are unevenly distributed on the 26 chromosomes of cotton, and most of them contain a few introns. The results of the collinear analysis showed that *G. hirsutum* contained 1–5 copies of each pPLA gene found in *G. arboreum* and *G. raimondii*. The subcellular localization analysis of Gh_D08G061200 showed that the protein was localized in the nucleus. In addition, analysis of published upland cotton transcriptome data revealed that six *GhPLA* genes were expressed in various tissues and organs. Two genes (*Gh_A04G142100.1* and *Gh_D04G181000.1*) were highly expressed in all tissues under normal conditions, showing the expression characteristics of housekeeping genes. Under different drought and salt tolerance stresses, we detected four genes with different expression levels. This study helps to clarify the role of pPLA in the response to drought and salt tolerance.

Seed Science and Technology

Title: Cottonseed Oil: Physicochemical Attribute, Health Benefits and Applications

Author: Kanika Sharma, Ajinath Dukare, Sujata Saxena and Himanshu Shekhar Chaurasia

Imprint: Vigyan Varta An International E-Magazine for Science Enthusiasts Vol-4, Issue-12023

Abstract: Cotton plant is not only a source of fibre but it also provides around 4% of the world's vegetable oil supply. Cottonseed oil is obtained from the cottonseed after using various extraction methods such as solvent extraction, mechanical pressing of seeds, microwaveassisted extraction, ultrasound extraction and enzyme assisted extraction methods. Raw cottonseed oil is refined using various processes to eliminate the gossypol, a toxic compound present in cottonseed. But after refining, bleaching and deodorization, the gossypol content of CSO gets reduced to safe limit for human consumption and also the odor, color and flavor becomes suitable for cooking. It has various properties including cardio-protection, antiinflammatory and wound healing properties owing to high content of linoleic acid and tocopherols. Refined cottonseed oil has promising applications in food industries for frying and baking due to its high smoke point and stability. Furthermore it is considered as heart healthy oil because it contains more than 73% unsaturated fatty acids including approximately 52% linoleic acid and 21% oleic acid.

Title: Elucidating molecular characterization of chlorpyrifos and profenofos degrading distinct bacterial strains for enhancing seed germination potential of *Gossypium arboreum* L

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Imprint: *Environmental Science and Pollution Research* (2023)

Abstract: Chlorpyrifos (CP) and profenofos (PF) are organophosphate pesticides (OPs) widely used in agriculture and are noxious to both fauna and flora. The presented work was designed to attenuate the toxicity of both pesticides in the growth parameters of a cotton crop by applying plant growth-promoting rhizobacteria (PGPR), namely *Pseudomonas aeruginosa* PM36 and *Bacillus* sp. PM37. The multifarious biological activities of both strains include plant growth-promoting traits, including phosphate

solubilization; indole-3-acetic acid (IAA), siderophore, and HCN production; nitrogen fixation; and enzymatic activity such as cellulase, protease, amylase, and catalase. Furthermore, the molecular profiling of multi-stress-responsive genes, including *acdS*, *ituC*, *czcD*, *nifH*, and *sfp*, also confirmed the plant growth regulation and abiotic stress tolerance potential of PM36 and PM37. Both strains (PM36 and PM37) revealed 92% and 89% of CP degradation at 50 ppm and 87% and 81% at 150 ppm within 7 days. Simultaneously 94% and 98% PF degradation was observed at 50 ppm and 90% and 92% at 150 ppm within 7 days at 35 °C and pH 7. Biodegradation was analyzed using HPLC and FTIR. The strains exhibited first-order reaction kinetics, indicating their reliance on CP and PF as energy and carbon sources. The presence of *opd*, *mpd*, and *opdA* genes in both strains also supported the CP and PF degradation potential of both strains. Inoculation of strains under normal and OP stress conditions resulted in a significant increase in seed germination, plant biomass, and chlorophyll contents of the cotton seedling. Our findings indicate that the strains PM36 and PM37 have abilities as biodegraders and plant growth promoters, with potential applications in crop sciences and bioremediation studies. These strains could serve as an environmentally friendly, sustainable, and socially acceptable solution to manage OP-contaminated sites