

Title: AI-Assisted Image Analysis and Physiological Validation for Progressive Drought Detection in a Diverse Panel of *Gossypiumhirsutum* L

Author: Vito Renó, Angelo Cardellicchio, Ben C. Romanjenko

Imprint: Front. Plant Sci., Sec. Plant Abiotic Stress, Volume 14 - 2023 | doi: 10.3389/fpls.2023.1305292

Abstract: Drought detection, spanning from early stress to severe conditions, plays a crucial role in maintaining productivity, facilitating recovery, and preventing plant mortality. While handheld thermal cameras have been widely employed to track changes in leaf water content and stomatal conductance, research on thermal image classification remains limited due mainly to low resolution and blurry images produced by handheld cameras. In this study, we introduce a computer vision pipeline to enhance the significance of leaf-level thermal images across 27 distinct cotton genotypes cultivated in a greenhouse under progressive drought conditions. Our approach involved employing a customized software pipeline to process raw thermal images, generating leaf masks, and extracting a range of statistically relevant thermal features (e.g., min and max temperature, median value, quartiles, etc.). These features were then utilized to develop machine learning algorithms capable of assessing leaf hydration status and distinguishing between well-watered (WW) and dry-down (DD) conditions. Two different classifiers were trained to predict the plant treatment – random forest and multilayer perceptron neural networks – finding 75% and 78% accuracy in the treatment prediction, respectively. Furthermore, we evaluated the predicted vs. true labels based on classic physiological indicators of drought in plants, including volumetric soil water content, leaf water potential, and chlorophyll a fluorescence, to provide more insights and possible explanations about the classification outputs. Interestingly, mislabeled leaves mostly exhibited notable responses in fluorescence, water uptake from the soil, an/or leaf hydration status. Our findings emphasize the potential of AI-assisted thermal image analysis in enhancing the informative value of common heterogeneous datasets for drought detection. This application suggests widening the experimental settings to be used with deep learning models, designing

future investigations into the genotypic variation in plant drought response and potential optimization of water management in agricultural settings.

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Title: Cotton Monocultures and Reorganizing Socioecological Life in Telangana, India

Author: Andrew Flachs

Imprint: Journal of Ethnobiology <https://doi.org/10.1177/02780771231221645>

Abstract: Five hundred years of desire for cotton has reshaped landscapes, built global economic commodity chains, and devalued human life in the name of producing cheap clothing. Since 2001, cotton monocultures in South India have also reorganized genetic codes, continuing centuries of work to maintain the socioecological possibility of extractive agricultural production. This paper combines ethnographic and ethnobiological research in Telangana, India, to center cotton's role in organizing socioecological life for an agrarian world including farmers, farmworkers, plants, soils, buyers, weeds, and animals. Mutually exclusive systems of genetically modified Bt and organic cotton production offer a range of possible organizations of labor, aspiration, reciprocity, and labor. While historically situated in plantation inequalities, cotton production can also make unexpected room for socioecological relationships outside extractive monoculture.

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Title: The Supply of Macro- and Microelements to Cotton Plants at Different Distances from a Fertilizer Production Factory.

Author: Andrey Litvinovich, Anton Lavrishchev

Imprint: Agronomy , Volume 13 , Issue 12 , 10.3390/agronomy13123063

Abstract: Environmental pollution from industrial factories via air deposition is an urgent problem worldwide. Phosphate fertilizers, derived from rock phosphate, are characterized by the presence of potentially toxic elements, such as Zn, Co, Pb, Ni, Cr, Mn, Fe, and Cu, which are dispersed in the form of solid dust-like materials from the pipes of the factory. This study aimed to investigate the effects of airborne industrial emissions on the chemical and biochemical compositions of cotton grown in the immediate vicinity of a fertilizer factory in Uzbekistan. The composition of airborne dust deposited on the plants, the chemical composition of the cotton leaves before and after washing, as well as that of above- and below-ground plant organs, and their protein contents were determined. The concentrations of macro- and microelements in

the leaves and roots were determined using an atomic absorption spectrophotometer. The fluorine contents in the leaves and in the roots were determined using a fluorine-selective electrode. The radius of dispersion of industrial emissions in the air was best described by measuring the fluorine contents in washed and unwashed cotton leaves. The relationships among P, K, Mg, Ca, S, F, and Mn in plant roots and leaves as a function of distance from the pollutant source were analyzed. Based on the fluorine contents in washed and unwashed cotton leaves, the two following zones of technogenic pollution were distinguished: the zone < 5 km from the factory, with high technogenic pollution, and the zone > 5 km from the factory, with moderate technogenic pollution. It was found that the resistance of cotton to air pollution from industrial emissions is determined by the ability of cotton plants to neutralize toxic compounds by increasing the influx of alkaline earth metals into the affected tissues. This study showed the possibility of growing cotton at a distance of >5 km from the fertilizer factory. It is strongly recommended to analyze the chemical composition of plants located in a highly polluted zone only after the dust particles have been washed off of the plant's surface. Despite the resilience of cotton to industrial pollution, the monitoring of areas identified as pollution zones is recommended.

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Title: Development of a cotton fiber quality simulation module and its incorporation into cotton crop growth and development model: GOSSYM

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Imprint: Computers and Electronics in Agriculture Volume 21 Issue C Sep 2023 <https://doi.org/10.1016/j.compag.2023.108080>

Abstract: GOSSYM is a mechanistic, process-level cotton crop simulation model. It can simulate the growth and development of cotton under different environmental and management conditions and provide information on crop growth and development, various stresses, and yield. The current model version does not have the capability of simulating cotton fiber quality. Cotton fiber quality is as significant as fiber quantity. In this study, a cotton fiber quality simulation module is developed and integrated into GOSSYM. The functional relationships between the fiber quality and the major factors influencing fiber quality (temperature, water, and nutrient status) are established based on the temperature, water, and nutrient-controlled sunlit soil plant atmospheric research (SPAR) chamber experiments. In the developed model, the potential fiber quality in terms of four major fiber quality indices (fiber length, fiber strength, micronaire, and uniformity) is estimated based on the temperature function, and actual fiber quality indices are determined by reducing potential quality as a function of water and nutrient status in the crop. The newly developed model's fiber quality modeling capabilities are demonstrated using illustrative examples from a case study. Illustrated

examples analyze the effect of different temperatures, nitrogen fertilizer application rates, irrigation, planting date, and atmospheric carbon dioxide concentrations on fiber quality indices. Simulation results are discussed by correlating them with underlying processes (growth and development, water, and nitrogen status), literature data, and functional relationships incorporated into the fiber quality module in GOSSYM. The model has demonstrated a reasonable simulation of fiber quality. The developed model can be a valuable tool for accurate cotton fiber quality simulations, lint yield production, fiber quality optimization, and making policy decisions under varying environmental and management conditions.

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Title: Characterization of water-deficit tolerance in Upland cotton (*Gossypium hirsutum* L.) assessing morphological, biochemical, molecular and yield attributes.

Author: Muhammad Saeed, Muhammad Naeem, Alia Javed, Shagufta Perveen

Imprint: Acta Physiologiae Plantarum, Volume 46, article number 13, (2024)

Abstract: Upland cotton (*Gossypium hirsutum* L.) is an important crop in the world due to its natural fiber production. As a result of climate change, its production is affected due to frequent occurrence of water-deficit conditions during its growth period. Five cotton varieties, namely FH-114, FH-142, FH-152, CIM-473 and CIM-496 were evaluated under limited irrigation conditions to characterize water-deficit tolerance. The data were recorded for plant height, content of biochemical parameters (carotenoid, chlorophyll, wax, proline) and seed cotton yield per plant. The plant material was genotyped with 23 highly polymorphic simple sequence repeats markers. The cotton varieties, CIM-473 and FH-142, with higher content of carotenoid, chlorophyll, epicuticular wax, and proline maintained sustained vegetative growth and development due to osmoregulation; optimal photosynthesis and photochemical efficiency; and maintenance of balance in the C/N metabolism and energy homeostasis; which resulted in better seed cotton yield (> 30% than the drought susceptible varieties) under limited irrigation conditions. Significant associations of simple sequence repeat DNA markers with plant height, carotenoid content, chlorophyll content, wax content, and seed cotton yield were identified. Especially, the DNA markers BNL1153 (chromosome 25) and BNL3031 (chromosome 9) might be the markers flanking the genes involved in the biosynthesis of proteins/enzymes (such as Late Embryogenesis Abundant proteins; chaperones; antioxidants; L-ascorbate peroxidase; enzymes in the ABA, proline, carotenoids and epicuticular wax biosynthesis) catalyzing the metabolic pathways leading to water-deficit tolerance in cotton and thus would be valuable resources for molecular breeding programs to develop water-deficit-tolerant cotton cultivars.

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Title: Exploring 65 years of progress in cotton nutrient uptake, efficiency and partitioning in the USA.

Author: Jagdeep Singh , Audrey V. Gamble , Steve Brown , Todd B. Campbell , Johnie Jenkins , Jenny Koebernick , Paul C. Bartley III , Alvaro Sanz-Saez

Imprint: Field Crops Research, Volume 305, 1 January 2024, 109189

Abstract: Cotton is a vital crop worldwide, and as increases in population and changes in climate occur, it is critical for breeders to continue to improve lint yields. One area to further investigate is how nutrient uptake and nutrient use efficiencies have changed through time to develop future management and breeding strategies.

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Title: Genome-wide identification and expression analysis of salinity stress-related protein kinase in cotton.

Author: Shafeeq Ur Rahman, Anzhen Qin, Muhammad Shehzad, Muhammad Zain, Sher Muhammad Shahzad, GhulamYasin, Khalid Ali Khan

Imprint: Agronomy Journal 20 November 2023, <https://doi.org/10.1002/agj2.21512>

Abstract: Salinity stress is a worldwide problem that damages crop growth and development. As a principal regulatory component in eukaryotic cells, protein kinase is key to regulating crop tolerance to salinity stress. However, it is still unclear about the responses of protein kinase to salinity stress across different upland cotton species in China. This study was conducted to evaluate the functional expression of protein kinase genes in three cotton species (*Gossypiumhirsutum*, *Gossypiumraimondii*, and *Gossypium arboretum*) under salinity stress. A total of 134 genes that encode the protein kinase were recognized in cotton species. The results indicated that 67 genes belonged to *G. hirsutum*, 34 genes belonged to *G. arboretum*, and 33 genes belonged to *G. raimondii*, respectively. Protein kinase genes were unequally distributed on the chromosomes of the three cotton species. Based on the syntenic analysis, 58 protein kinase genes were duplicated in *G. hirsutum*, *G. raimondii*, and *G. arboretum*. The results of synonymous (Ks), non-synonymous (Ka), and Ka/Ks values for orthologous genes showed that the top ten *G. hirsutum* protein kinase genes were mostly expressed. Co-expression network analysis of protein kinase genes confirmed their function in improving crop tolerance to salinity stress for different cotton species. It was concluded that protein kinase genes were stress-inducible and were linked to stress-responsive miRNAs in

cotton species. The findings can be used for breeding new salt-tolerant cotton varieties in China.

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Title: Optimal row spacing configuration to improve cotton yield or quality is regulated by plant density and irrigation rate

Author: Wenqing Zuo, Baojian Wu, Yuxuan Wang, Shouzhen Xu,

Imprint: Field Crops Research, Volume 305, 1 January 2024, 109187

Abstract: Conventional high-density planting of machine-picked cotton in Xinjiang is associated with poor light distribution and low fiber quality. The objective of this study was to assess how different row spacing configurations, irrigation rates, and planting densities impact cotton photosynthetic production and fiber quality. Methods

We conducted a 3-year field experiment in Shihezi, Xinjiang, China, to evaluate the impact of different row spacing configurations and irrigation amounts on cotton photosynthesis and fiber quality. The four row spacing configurations used were: RS₆₆₊₁₀H (high-density with 66 +10 cm spacing), RS₆₆₊₁₀L (low-density with 66 +10 cm spacing), RS₇₆H (high-density with 76 cm spacing), and RS₇₆L (low-density with 76 cm spacing). Additionally, two irrigation amounts were tested: MD-T₃ (mulch drip irrigation with three tapes on one film) and MD-T₂ (mulch drip irrigation with two tapes on one film). We measured and compared the distribution of cotton canopy leaves, light, canopy apparent photosynthesis, reproductive organs and fiber quality among these groups. Results The results showed that RS₆₆₊₁₀H had a higher lint yield than RS₇₆L under MD-T₂, with an increase of 5.4–7.1%. This can be attributed to the higher fraction of photosynthetically active radiation, canopy apparent photosynthesis (CAP), and boll biomass in RS₆₆₊₁₀H between the full boll and boll opening stages. The maximum lint yield (3227–3580 kg ha⁻¹) was obtained in RS₆₆₊₁₀H under MD-T₃. Interestingly, RS₇₆L had a similar lint yield to RS₆₆₊₁₀H under MD-T₃, mainly due to the middle and lower canopy having higher leaf area index (LAI) values ranging from 1.8 to 2.1. This resulted in increased CAP and cotton boll biomass of the middle and lower canopy compared to RS₆₆₊₁₀H during the full boll to boll opening stage. Under MD-T₃, RS₇₆L also exhibited longer fiber length in the middle and lower canopy (30.2–32.0 mm and 31.6–33.3 mm, respectively) compared to RS₆₆₊₁₀H, with a difference of 3.2–3.8% and 5.6–6.5%. Furthermore, RS₇₆L demonstrated higher fiber strength in the middle and lower canopy (31.4–32.7 cN tex⁻¹ and 33.2–33.9 cN tex⁻¹, respectively) compared to RS₆₆₊₁₀H, with a difference of 2.6–6.2% and 5.9–6.8%. Maintaining an LAI of around 2.0 during the transition from full boll to boll opening stage optimized canopy architecture and enhanced photosynthetic productivity. Conclusion Under adequate irrigation, RS₇₆L could be a suitable replacement for RS₆₆₊₁₀H in order to improve cotton fiber quality by optimizing leaf-boll spatial distribution. This study provides guidance for selecting the appropriate row spacing configuration under different water conditions. RS₆₆₊₁₀H is

recommended for increasing yield under water-deficient conditions, while RS₇₆L is suitable for improving fiber quality under adequate irrigation.

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Title: Enhancing cold and drought tolerance in cotton: a protective role of *SikCOR413PM1*

Author: Mei Wang, Lepeng Wang, Xiangxue Yu, Jingyi Zhao, Zhijia Tian, Xiaohong Liu, Guoping Wang, Li Zhang & Xinyong Guo

Imprint: BMC Plant Biology, [Published: 18 November 2023](#), volume 23, Article number: 577 (2023)

Abstract: The present study explored the potential role of cold-regulated plasma membrane protein *COR413PM1* isolated from *Saussureainvolucrata* (Matsum. & Koidz) (*SikCOR413PM1*), in enhancing cotton (*Gossypium hirsutum*) tolerance to cold and drought stresses through transgenic methods. Under cold and drought stresses, the survival rate and the fresh and dry weights of the *SikCOR413PM1*-overexpressing lines were higher than those of the wild-type plants, and the degree of leaf withering was much lower. Besides, overexpressing *SikCOR413PM1* overexpression increased the relative water content, reduced malondialdehyde content and relative conductivity, and elevated proline and soluble sugar levels in cotton seedlings. These findings suggest that *SikCOR413PM1* minimizes cell membrane damage and boosts plant stability under challenging conditions. Additionally, overexpression of this gene upregulated antioxidant enzyme-related genes in cotton seedlings, resulting in enhanced antioxidant enzyme activity, lowered peroxide content, and reduced oxidative stress. *SikCOR413PM1* overexpression also modulated the expression of stress-related genes (*GhDREB1A*, *GhDREB1B*, *GhDREB1C*, *GhERF2*, *GhNAC3*, and *GhRD22*). In field trials, the transgenic cotton plants overexpressing *SikCOR413PM1* displayed high yields and increased environmental tolerance. Our study thus demonstrates the role of *SikCOR413PM1* in regulating stress-related genes, osmotic adjustment factors, and peroxide content while preserving cell membrane stability and improving cold and drought tolerance in cotton.

Title: Transcriptomic analysis reveals the beneficial effects of salt priming on enhancing defense responses in upland cotton under successive salt stress

Author: Mian Faisal Nazir, Baojun Chen, Muhammad Jawad Umer, Zareen Sarfraz, Zhen Peng

Imprint: Physiologia Plantarum, 13 November 2023, <https://doi.org/10.1111/ppl.14074>

Abstract: Priming-mediated stress tolerance in plants stimulates defense mechanisms and enables plants to cope with future stresses. Seed priming has been proven effective for tolerance against abiotic stresses; however, underlying genetic mechanisms are still unknown. We aimed to assess upland cotton genotypes and their transcriptional behaviors under salt priming and successive induced salt stress. We pre-selected 16 genotypes based on previous studies and performed morpho-physiological characterization, from which we selected three genotypes, representing different tolerance levels, for transcriptomic analysis. We subjected these genotypes to four different treatments: salt priming (P0), salt priming with salinity dose at 3-true-leaf stage (PD), salinity dose at 3-true-leaf stage without salt priming (0D), and control (CK). Although the three genotypes displayed distinct expression patterns, we identified common differentially expressed genes (DEGs) under PD enriched in pathways related to transferase activity, terpene synthase activity, lipid biosynthesis, and regulation of acquired resistance, indicating the beneficial role of salt priming in enhancing salt stress resistance. Moreover, the number of unique DEGs associated with *G. hirsutum purpurascens* was significantly higher compared to other genotypes. Coexpression network analysis identified 16 hub genes involved in cell wall biogenesis, glucan metabolic processes, and ribosomal RNA binding. Functional characterization of *XTH6* (*XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE*) using virus-induced gene silencing revealed that suppressing its expression improves plant growth under salt stress. Overall, findings provide insights into the regulation of candidate genes in response to salt stress and the beneficial effects of salt priming on enhancing defense responses in upland cotton.

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Title: The BEL1-like transcription factor GhBLH5-A05 participates in cotton response to drought stress.

Author: Jing-Bo Zhang , Yao Wang , Shi-Peng Zhang

Imprint: The Crop Journal, Available online 15 November 2023

Abstract: Drought stress impairs crop growth and development. BEL1-like family transcription factors may be involved in plant response to drought stress, but little is known of the molecular mechanism by which these proteins regulate plant response and defense to drought stress. Here we show that the BEL1-like transcription factor GhBLH5-A05 functions in cotton (*Gossypiumhirsutum*) response and defense to drought stress. Expression of *GhBLH5-A05* in cotton was induced by drought stress. Overexpression of *GhBLH5-A05* in both *Arabidopsis* and cotton increased drought tolerance, whereas silencing *GhBLH5-A05* in cotton resulted in elevated sensitivity to drought stress. GhBLH5-A05 binds to *cis* elements in the promoters of *GhRD20-A09* and *GhDREB2C-D05* to activate the expression of these genes. GhBLH5-A05 interacted with the KNOX transcription factor GhKNAT6-A03. Co-expression of GhBLH5-A05 and GhKNAT6-A03 increased the transcription of *GhRD20-A09* and *GhDREB2C-D05*. We conclude that GhBLH5-A05 acts as a regulatory factor with GhKNAT6-A03 functioning in cotton response to drought stress by activating the expression of the drought-responsive genes *GhRD20-A09* and *GhDREB2C-D05*.

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Title: Drone agrotechnology's for cotton (*Gossypiumhirsutum* L.) Protection against pest and diseases in Western of Burkina Faso

Author: Adama ZONGO, OumarBADINI , Emile KABORE

Imprint: Research Square: November 14th, 2023 DOI: <https://doi.org/10.21203/rs.3.rs-3496812/v1>

Abstract: Background: Drone technologies, also known as "unmanned aerial vehicles" (UAVs) or "unmanned aerial systems" (UAS), have a wide range of applications, including mapping, landuse planning, crop/infrastructure damage assessment, fertilizer spraying and precision crop protection. However, its use is still very limited in the agricultural sector in Africa in general and in Burkina Faso in particular. Results: This study was initiated to explore the potential of UAVs for optimizing cotton yields through monitoring and phytosanitary efficiency. To this end, phytosanitary treatments and monitoring of vegetation status using multispectral drone imagery were carried out

on cotton. The experimental sample consisted of four (04) cotton fields in four (04) locations. Phytosanitary treatments and aerial photography were respectively carried out using a DJI AGRAS T16 spray drone and a DJI Phantom 4 Multispectral drone. Phytosanitary treatment with DJI AGRAS T16 drone resulted in savings of 32.41% in treatment duration, 23.58% in water, 1% in pesticides and 10.5% in labor compared with manual spraying, but did not have a positive impact on boll yields due to jassid populations attack. The RGB and NDVI vegetation indices generated by photogrammetric processing of multispectral images acquired by drone enabled us to perceive phytosanitary state of cotton plants during their development cycle. Conclusion: Information provided by these vegetation indices and by this study in general can be used to improve the efficiency of phytosanitary treatments against cotton pests and diseases

CROP PROTECTION

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Title: Sublethal concentrations of thiamethoxam induce transgenerationalhormesis in cotton aphid, *Aphis gossypii* Glover

Author: HinaGul, Ali Güncan, Farman Ullah, XinyuanNing, Nicolas Desneux & Xiaoxia Liu

Imprint: CABI Agriculture and Bioscience , Published: 20 November 2023, volume 4, Article number: 50 (2023)

Abstract: In agro ecosystems, insects have to compete with chemical insecticides, which are frequently present at sublethal concentrations. The exposure of insects to these modest stresses is now well-established to generate hormesis effects, which has implications for controlling insect pests. In this study, we assessed the sublethal effects of thiamethoxam on the biological parameters of *Aphis gossypii* Glover (Hemiptera: Aphididae), adults (F₀) and subsequent transgenerational impacts, i.e., on the progeny (F₁ generation), using an age stage, two-sex life table analysis. Results showed that thiamethoxam exhibited high toxicity against adult *A. gossypii* with the LC₅₀ of 0.313 mg L⁻¹ after 48 h exposure. The LC₅ and LC₁₀ of thiamethoxam considerably reduced the adult cotton aphids (F₀) longevity and fecundity, while the reproductive days were reduced only at LC₁₀. The pre-adult stage was decreased, while the adult longevity,

total longevity, and fecundity were significantly extended in F₁ aphids after exposure of F₀ aphids to the sublethal concentrations of thiamethoxam. Moreover, the key demographic parameters such as intrinsic rate of increase, finite rate of increase and reproductive days were significantly increased, while mean generation time and total prereproductive were significantly reduced in the progeny. No significant effects were observed on the net reproductive rate. Taken together, these results showed that the sublethal concentrations of thiamethoxam affect the directly exposed aphids (F₀) while causing transgenerationalhormetic effects on the F₁ generation of *A. gossypii*. In conclusion, our research showed that thiamethoxam has both sublethal and transgenerational effects on cotton aphids; it could be effective in IPM programs targeting this key pest.

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Title: Cotton Leaf Curl Disease Suppression by Interspecies Microbiome Transplantation

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Imprint: Preprint from Research Square, 20 Nov 2023, <https://doi.org/10.21203/rs.3.rs-3621901/v1>

Abstract: Begomovirus , the causative agent of the Cotton Leaf Curl Disease (CLCuD), has been corrupting cotton yield, quality, and production throughout the world since its first outbreak in 1912. The cotton crop, the “white gold” of Pakistan, has been plucked by various biotic stresses including Cotton Leaf Curl Virus (CLCuV), amounting the production loss of the crop to almost half in the past ten years. Although several breeding attempts have been made to develop cotton lines tolerant to CLCuD, the mutation rate of CLCuV remains too high to allow permanent tolerance to any developed cultivar. In this study, the plant microbiome is proposed as a favorable environmental and economy friendly alternative to induce CLCuD suppression in the CLCuD-susceptible specie *Gossypiumhirsutum*. The study employed the microbiome of the naturally immune diploid species of cotton, *Gossypiumarboreum* , as a hub of diverse bacterial community. Both the rhizospheric and phyllosphericmicrobiotas of *G. hirsutum* (PFV1 and PFV2) and *G. arboreum* (FDH228) species with varying tolerance levels to CLCuD were isolated. The rhizospheric and phyllosphericmicrobiotas were termed as Microbial Fractions (MFs) and were transplanted to young *G. hirsutum* and *G. arboreum* seedlings, with null microbiota development, through soil drench method. Salicylic Acid (SA), a known plant phytohormone with defense-inducing properties, was also applied to a positive control group through foliar spray method. Results Most prominent CLCuD suppression was recorded through disease incidence assays in *G. hirsutum* varieties transplanted with rhizospheric MFs successively from FDH228

(RMF), PFV1 (pRMF) and PFV2 (SMF). The phyllospheric MFs also suppressed CLCuD but to a lesser extent as compared to rhizospheric MFs. The findings laid by disease incidence assays have been further supported with IlluminaMiSeq 16S rRNA gene sequence analysis for microbial diversity of the MF samples and corresponding associated pathways. The results strongly demonstrate distinct bacteriomes of the cotton species governed by relative CLCuD tolerance levels. Conclusions A strong practical foundation is laid to present the role of plant microbiome in CLCuD suppression and remains the first attempt to elucidate this against a viral disease. Microbiome transplantation can contribute to the advancement of sustainable agriculture.

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Title: Transmission of Pathogenic Fungi from Seeds to Seedlings in Cotton (*GossypiumHirsutum* L.)

Author: AMINA KHATUN , SHAMIM SHAMSI AND MA BASHAR

Imprint: Dhaka Univ. J. Biol. Sci. 32(2): 225-232, 2023 (July) DOI: <https://doi.org/10.3329/dujbs.v32i2.67681>

Abstract: Cotton seeds of susceptible variety CB10 were inoculated with nine pathogenic fungi viz., *Aspergillusflavus*, *A. niger*, *A. tamarii*, *Colletotrichumgloeosporioides*, *Curvularialunata*, *Fusariumnivale*, *F. moniliforme*, *Mucor* sp. and *Rhizoctoniasolani*. Seedlings were grown in water agar test tube and in earthen pots. In water agar test, *R. solani* showed the highest percentage of seed to seedling transmission (35.27%) which was followed by *F. moniliforme* (31.29%) and *A. niger* showed the lowest (8.03%) transmission. Germination percentage of control seeds was 90.32% whereas in pathogen inoculated seeds it varied from 58.33 to 89.07%. The seedling mortality percentage was highest in *R. solani* (46.68%) and lowest in *C. gloeosporioides* (18.67%). Germination percentage of control seeds in pot was 99% whereas in pathogen inoculated seeds it varied from 43.37 to 84.34%. The seedling mortality percentage was highest in *F. moniliforme* (48.28%) and lowest in *A. niger* (19.64%). Percentage of seed to seedling transmission of fungi varied from 17.85% (*A. niger*) to 46.56% (*F. moniliforme*).

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Title: Population dynamics of major sucking insect pests infesting Bt. cotton (*Gossypiumhirsutum* L.) and their natural enemies .

Author: SarojJat, MK Mahla, Deepak Kumar Saini and S Ramesh Babu

Imprint: The Pharma Innovation Journal 2023; SP-12(12): 17-22

Abstract: The experiment on “Population dynamics of major sucking insect pests infesting Bt. cotton (*Gossypiumhirsutum* L.) and their natural enemies” was carried out at Agronomy Farm, Rajasthan College of Agriculture, MaharanaPratap University of Agriculture and Technology, Udaipur during kharif, 2019. The population of aphids reached its peak during the 40th SMW (49.20 aphids/plant). The peak population of jassids (30.25 jassids/plant) and whiteflies (32.40 whiteflies/plant) was recorded during the 34th SMW and 31st SMW, respectively. The peak population of thrips (41.60 thrips/plant) was recorded during the 36th SMW. Whereas, the peak population of mealybugs (26.00 mealybugs/10 cm twig) was recorded during the 37th SMW. The correlation coefficient study reveals that the population of jassids, aphids, whiteflies, thrips and mealybugs was positively correlated with mean temperature, relative humidity and total average rainfall, and the population of these pests was found significantly positive with the relative humidity.

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Title: Cotton (*GossypiumHirsutum* L.) Yield Losses Linked To Boll Rot In The Sudano-Sahelian Zone Of Mali .

Author: SorySissoko, ElhadjiMamoudouKassambara , Mariam Traoré , GassiréBayoko , DaoudaMaiga And MamadouOumarDiawara

Imprint: IOSR Journal of Environmental Science, Toxicology and Food Technology (IOSR-JESTFT) e-ISSN: 2319-2402,p- ISSN: 2319-2399.Volume 17, Issue 12 Ser. 1 (December 2023), PP 29-37

Abstract: Cotton (*Gossypiumhirsutum* L.) is an important cash crop in Mali's national economy, contributing around 19% of gross domestic product (GDP). Yield depends on various factors, including the high (healthy) number of bolls in the field. The aim of this study was to assess the effect of boll rot on seed cotton yield. The experiment was conducted at the Finkolo station (11° 22' North, 5° 51' West) in Mali in 2020 and 2021. The plant material consisted of eight varieties of cotton planted in a Randomized Complete Block Design (RCBD) with eight replications. The results of this experiment showed no significant interaction between varieties and the total number of rotten bolls per hectare, the percentage of rotten bolls, seed cotton yield and yield loss due to boll rot. This suggests that boll rot is not a varietal problem but an environmental concern. In addition, the number of rotten bolls increased when the annual average rainfall, temperature (max and min), maximum humidity, number of plants per hectare, and seed cotton yield increased. This experiment revealed an average yield loss of around 100 kg per hectare of cotton planted in the area. As the area is one of Mali's major cotton production basins, the loss observed is too high on the scale of the area planted in

particular and the country in general. It is important to take appropriate precautions to preserve the bolls in the fields in years of high rainfall and high temperatures, and to guarantee a good harvest.\

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Title: Variability in bacterial endophytes in leaves of transgenic Bt and non-Bt cotton crop varieties and their role in suppression of bacterial leaf blight pathogen *X. a. pv. malvacearum* and the incited disease reaction .

Author: Suresh GovindaraoBorkar , A. N. Bhosale and Ajayasree T. S.

Imprint: World Journal of Advanced Research and Reviews, 2023, 20(02), 626–636

Abstract: Microbial epiphytes and endophytes are an integral part of the plant system and are known to play various roles in crop growth and crop health management. The transgenic crop plays an important role in crop pest management, however, environmentalists and ecologists have reservations about the cultivation of these crops. Whether the transgenic Bt cotton and non-Bt cotton vary in their microbial habitat ecology is not yet studied. In the present investigations, the leaf endophytic bacteria were detected in the leaves of both transgenic Bt and non-Bt cotton hybrids. However, there were differences in the endophytic bacterial types and their population densities i.e. bacterial colony-forming units (cfu) in the leaves of Bt and non-Bt cotton varieties. At least ten different leaf endophytic bacteria were detected from two cotton varieties i.e. RCH-2 and Bunny (of transgenic Bt and non-Bt versions). A maximum of four types of leaf endophytic bacteria was present in RCH-2 Bt cotton leaves. The population density of leaf endophytic bacteria ranged from 50 cfu/leaf to 5×10^3 cfu/leaf and varied with individual leaf endophyte and cotton variety. These bacterial leaf endophytes were observed to inhibit or suppress the growth of bacterial leaf blight pathogen *Xanthomonas axonopodis* pv. *malvacearum* (Xam) under in-vitro test. Leaf endophyte no.7 was more effective followed by leaf endophyte no.4 in suppressing the Xam population and population of other endophytes in the interaction studies. Interaction of leaf endophytes and Xam in cotton leaves suggested that endophytes of transgenic Bunny-Bt were effective on Xam in transgenic Bunny–Bt hybrid only and so these changed the induction of susceptible water-soaking disease reaction into hypersensitive browning resistance reaction (HR). However, these endophytes of Bt-cotton were not effective in the non-Bt version in changing the susceptible reaction of Xam into an HR reaction. This indicated that the endophytes of the respective Bt and non-Bt crops were able to change the susceptible reaction of Xam into a hypersensitive one in their respective host, indicating that the use of leaf endophytes can be effective in their own habitat crop as a biocontrol agent against Xam. The specificity of leaf endophytes has to be considered in biological disease management programs.

Title: The Investigation of Effect of Bacteria in Biological Control of Red Spider Mite (*Tetranychus* spp.) and Plant Yield Parameter in Cotton (*Gossypiumhirsutum* L.).

Author: SefaÇELİK ,Göksel TOZLU , Recep KOTAN

Imprint: YuzuncuYil University Journal of Agricultural Sciences, Volume: 33, Issue: 4, 31.12.2023

Abstract: The purpose of this study was to assess the usability of two bacterial strains, namely *Bacillus subtilis* PA1 and *Paenibacillusazotofixans* PA2, for the biological control of red spider species, and their effects on plant quality and yield in cotton under field conditions. The experiments were conducted at three different locations with multiple replications. As a control, a commercial preparation containing Lambda-Cyhalothrin as the active ingredient was used. The obtained results from the study revealed that the application of the bioagent formulation led to a significant decrease in the density of *Tetranychus* spp. at different biological stages, ranging from 59.22% to 61.07%, when compared to the control group. Additionally, several important plant growth parameters showed remarkable improvements. The number of fruit branches increased by 130.20%, plant crown diameter by 88.16%, plant height by 40.15%, the number of flowers by 21.25%, the number of wood branches by 18.13%, the average number of cocoons by 126.53%, and cocoon weights by 54.65% significantly across all three trial parcels. The successful implementation of the bacterial application for pest control had a positive impact on cotton yield. Bulk cotton yield increased by 80.03%, and fiber yield increased by 82.17%. Consequently, the bacterial formulation containing these two bacteria demonstrated its potential as a biopesticide in cotton cultivation, effectively controlling pests while also playing a crucial role in enhancing productivity. Overall, the study suggests that using the bioagent formulation consisting of *Bacillus subtilis* PA1 and *Paenibacillusazotofixans* PA2 could be an effective and environmentally friendly approach for pest control in cotton farming, leading to increased productivity.

Title: Phylogenetic and recombination analysis of Begomoviruses associated with Cotton leaf curl disease and *in silico* analysis of viral-host protein interactions

Author:Heena Jain, Inderjeet Singh, Shiwani Chahal, Ramandeep Kaur, Priyanka Siwach

Imprint: Microbial Pathogenesis, Volume 186, January 2024, 106504

Abstract: Cotton leaf curl disease (CLCuD), caused by numerous begomoviruses (BGVs), is a highly disastrous disease in cotton crops worldwide. To date, several efforts have shown limited success in controlling this disease. CLCuD-associated BGVs (CABs) are known for their high rate of intra and interspecific recombinations, which raises an urgent need to find an efficient and conserved target region to combat disease. In the present study, phylogenetic analysis of selected 11 CABs, along with associated alphasatellites, and betasatellites revealed a close evolutionary relationship among them. Recombination analysis of 1374 isolates of CABs revealed 54 recombination events for the major players of CLCuD in cotton and the Cotton leaf curl Multan virus (CLCuMuV) as the most recombinant CAB. Recombination breakpoints were frequent in all regions except C2 and C3. C3-encoded protein, known as viral replication enhancer (REn), promotes viral replication by enhancing the activity of replicase (Rep) protein. Both proteins were found to contain significantly conserved domains and motifs. The identified motifs were found crucial for their interaction with host protein PCNA (Proliferating cell nuclear antigen), facilitating viral replication. Interruption at the REn-PCNA and Rep-PCNA interactions by targeting the identified conserved motifs is proposed as a prospect to halt viral replication, after suitable experimental validation.

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Title: Characterizing the diversity of oomycetes associated with diseased cotton seedlings in Alabama

Author: Oluwakemisola Olofintila, Kathy S. Lawrence, and Zachary Albert Noel

Imprint: Plant Disease Published Online: 17 Dec 2023 <https://doi.org/10.1094/PDIS-06-23-1159-RE>

Abstract: Many oomycete species are associated with the seedlings of crops, including upland cotton (*Gossypium hirsutum* L.), leading to annual threats. The diversity of oomycete species in Alabama needs to be better understood since the last survey of oomycetes associated with cotton in Alabama was twenty years ago, before significant updates to taxonomy and improvements in identification of oomycetes using molecular tools. Our current study aimed to identify oomycetes associated with Alabama cotton seedlings, correlate diversity with soil edaphic factors, and assess virulence toward cotton seed. Thirty symptomatic cotton seedlings were collected independently from 25 fields in 2021 and 2022 two to four weeks after planting. Oomycetes were isolated by plating root sections onto a semi-selective medium. The internal transcribed spacer region was sequenced to identify the resulting isolates. A seed virulence assay was conducted in vitro to verify pathogenicity. Three hundred and forty-seven

oomycete isolates were obtained representing 36 species. Northern Alabama soils had the richest oomycete communities and a greater silt and clay concentration than sandier soils in the central and southern coastal plains. *Globisporangium irregulare* and *Phytophthora nicotianae* were consistently recovered from cotton roots in both years. *Globisporangium irregulare* was pathogenic and recovered from all Alabama regions, whereas *P. nicotianae* was pathogenic but recovered primarily in areas with lower sand content in northern Alabama. Many oomycete species have not been previously reported in Alabama or the southeastern United States. Altogether, this knowledge will help facilitate effective management strategies for cotton seedling diseases caused by oomycetes in Alabama and the U.S.

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Title: Effect of Verticillium Wilt on the Antioxidant System and Formation of Iron Nanoparticles in Cotton Genotypes

Author: Amrahov, N. R.; Allahverdiyev, V. Y.; Agharzayeva, Y. I.; Mammadova, R. B.; Omarova, S. N.; Khudayev, F. A.; Nasibova, A. N.; Shoaib, M.; Khalilov, R. I.; Mammadov, Z. M.

Imprint: JAPS: Journal of Animal & Plant Sciences, 2023, Vol 33, Issue 6, p1322

Abstract: The effect of a highly virulent fungus *Verticillium dahliae* Kleb. VD-11, with non-defoliating strain on polyphenol oxidase (PPO) and the antioxidant enzymes, such as guaiacol peroxidase (POX) and superoxide dismutase (SOD), was studied in double haploid cotton variety-Pima 3-79 (*Gossypium barbadense* L.), highly inbred line TM-1 (*Gossypium hirsutum* L.), as well as in genotypes CS B-15 and GS B-22, created by the substitution of one chromosome of TM-1 with the chromosome 15 and 22 of Pima 3-79 respectively. The treatment of plants with the pathogen led to an increase in the activity of PPO approximately 1.2 times in the case of TM-1 and CS B-15. However, these changes were insignificant in the case of Pima 3-79 variety, whereas the activity of the enzyme in the case of CS B-22 was decreased apparently. Similar effects were also obtained for POX. After inoculation, the activity of SOD in all genotypes, except CS B-15, was increased. On the contrary, the activity of SOD was decreased in the case of CS B-15 genotype. It was found that plant infection with the pathogen leads to a change in the concentration of free radicals, which, in turn, affects the activity of antioxidant enzymes. The fungal infection also led to the creation of new paramagnetic centers and nanophase crystal-like iron oxide particles in roots, but not in leaves.

Title: Decoding the guardians of cotton resilience: A comprehensive exploration of the β CA genes and its role in *Verticilliumdahliae* resistance

Author: Mengying Yang, Muhammad JawadUmer, Heng Wang, Jiale Han, Jiangping Han, Qiankun Liu, JieZheng, XiaoyanCai, YuqingHou, YanchaoXu, Yuhong Wang,

Imprint: PhysiologiaPlantarum, First published: 21 December 2023, <https://doi.org/10.1111/ppl.14113>

Abstract: Plant Carbonic anhydrases (Cas) have been shown to be stress-responsive enzymes that may play a role in adapting to adverse conditions. Cotton is a significant economic crop in China, with upland cotton (*Gossypiumhirsutum*) being the most widely cultivated species. We conducted genome-wide identification of the β CA gene in six cotton species and preliminary analysis of the β CA gene in upland cotton. In total, 73 β CA genes from six cotton species were identified, with phylogenetic analysis dividing them into five subgroups. *GH* β CA proteins were predominantly localized in the chloroplast and cytoplasm. The genes exhibited conserved motifs, with motifs 1, 2, and 3 being prominent. *GH* β CA genes were unevenly distributed across chromosomes and were associated with stress-responsive cis-regulatory elements, including those responding to light, MeJA, salicylic acid, abscisic acid, cell cycle regulation, and defence/stress. Expression analysis indicated that *GH* β CA6, *GH* β CA7, *GH* β CA10, *GH* β CA15, and *GH* β CA16 were highly expressed under various abiotic stress conditions, whereas *GH* β CA3, *GH* β CA9, *GH* β CA10, and *GH* β CA18 had higher expression patterns under *Verticilliumdahliae* infection at different time intervals. In *Gossypiumthurberi*, *Gth* β CA1, *Gth* β CA2, and *Gth* β CA4 showed elevated expression across stress conditions and tissues. Silencing *GH* β CA10 through VIGS increased *Verticillium* wilt severity and reduced lignin deposition compared to non-silenced plants. *GH* β CA10 is crucial for cotton's defense against *Verticilliumdahliae*. Further research is needed to understand the underlying mechanisms and develop strategies to enhance resistance against *Verticillium* wilt.

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Title: Genetic Diversity Evaluation of Some Upland Cotton Genotypes (*Gossypiumhirsutum* L.) By Cluster Analysis.

Author: Zakariya Bader Fathi Al-Hamdany, Khalid Mohammed. Dawod. Al-Zubaidy, Abdullah Moayad Omar

Imprint: Journal of Medical and Industrial Plant Sciences, 2023, Volume, Issue, Pages 74-82

Abstract: The study included ten genotypes of upland cotton, in 2022 at Rahmani-yah (Mosul) using a randomized complete block design with three replications, it was analyzed statistically to identify the nature of the differences between the genotypes. The stages of the cluster analysis showed that the genotypes were distributed in eight groups, the first, second, fourth, fifth, sixth and seventh included one genotype for each of them, respectively COKER310, MONTANA, SPERO, LACHATA, CANDIA and EDESSA, indicating the variation between it and the other genotypes, which is due to the variation in their genetic origin, which was thus reflected on their performance, while the other groups included two genotypes each. It is concluded from the results of the cluster analysis that there is a strong convergence between the pairs of genotypes W888 with IK259, and FLASH with BA440, because they have the least Euclidean distances, and this necessitates avoiding crossing between them, while the highest distance between the genotypes COKER310 and FLASH, was an indication of high genetic variation between them and other genotypes, that may be due to the difference in their genetic origin or to their possession of preferred main genes that the other genotypes lack, which encourages their inclusion in crosses with genotypes that showed distinguished genetic heterogeneity, to take advantage of the phenomenon of heterosis and the segregations that result from it.

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Title: Performances of F3 and F4 Bulk Populations in Cotton (*Gossypiumhirsutum* L.) .

Author: ŞerifeBALCI ,Volkan Mehmet ÇINAR , Aydın ÜNAY

Imprint: YuzuncuYil University Journal of Agricultural Sciences, Volume: 33, Issue: 4, 31.12.2023

Abstract: The experiment was laid out in 2020 to compare the performance of thirty-seven F3 and F4 multi-parental bulk populations of cotton, including comparative cultivars, and to assess the heritability of traits studied. The differences within generations were significant for seed cotton yield, ginning outturn, fiber quality, and nep fragments. The mean fiber strength of the F4 generation showed significant performance compared with F3. The broad sense heritability was high for ginning outturn, fiber length, and fiber strength. The normal distribution for F3 and F4 generations due to non-significant skewness and kurtosis values indicated that there were no epistatic effects on the heritability of traits studied. Eight F4 lines were selected for transfer to F5 generation according to optimization in terms of desired traits.

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Title: Genome-wide analysis of SET domain genes and the function of *GhSDG51* during salt stress in upland cotton (*Gossypiumhirsutum* L.)

Author: HongliangJian, Fei Wei, Pengyun Chen, Tingli Hu, XiaolanLv, Bingqin Wang

Imprint: *BMC Plant Biology* volume 23, Article number: 653 (2023)

Abstract: Cotton, being extensively cultivated, holds immense economic significance as one of the most prominent crops globally. The SET (Su(var), E, and Trithorax) domain-containing protein is of significant importance in plant development, growth, and response to abiotic stress by modifying the lysine methylation status of histone. However, the comprehensive identification of SET domain genes (SDG) have not been conducted in upland cotton (*Gossypiumhirsutum* L.). **Results** A total of 229 SDGs were identified in four *Gossypium* species, including *G. arboretum*, *G. raimondii*, *G. hirsutum*, and *G. barbadense*. These genes could distinctly be divided into eight groups. The analysis of gene structure and protein motif revealed a high degree of conservation among the SDGs within the same group. Collinearity analysis suggested that the SDGs of *Gossypium* species and most of the other selected plants were mainly expanded by dispersed duplication events and whole genome duplication (WGD) events. The allopolyploidization event also has a significant impact on the expansion of SDGs in tetraploid *Gossypium* species. Furthermore, the characteristics of these genes have been relatively conserved during the evolution. *Cis*-element analysis revealed that *GhSDGs* play a role in resistance to abiotic stresses and growth development. Furthermore, the qRT-PCR results have indicated the ability of *GhSDGs* to respond to salt stress. Co-expression analysis revealed that *GhSDG51* might co-express with genes associated with salt stress. In addition, the silencing of *GhSDG51* in cotton by the virus-

induced gene silencing (VIGS) method suggested a potential positive regulatory role of *GhSDG51* in salt stress.

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Title: Comprehensive analysis of MAPK gene family in *Gossypium hirsutum* and functional characterization of GhMPK31 in regulating defense response to insect.

Author: Fuqiu Wang, Sijia Liang, Guanying Wang, Qiongqiong Wang

Imprint: Research Square <https://doi.org/10.21203/rs.3.rs-3623274/v1>

Abstract: Mitogen activated protein kinases (MAPKs) are a crucial class of protein kinases, which play essential role in various biological processes in plants. Upland cotton (*G. hirsutum*) is the most widely cultivated cotton species with high economic value. To gain a better understanding of the role of the MAPK gene family, we conducted a comprehensive analysis of MAPK gene family in cotton. In this study, a total of 55 GhMPK genes were identified from the whole genome of *G. hirsutum*. Through an investigation of the expression patterns under diverse stress conditions, we discovered that the majority of GhMPK family members demonstrated robust responses to abiotic stress, pathogen stress, and pest stress. Furthermore, the overexpression of GhMPK31 in cotton leaves led to a hypersensitive response (HR)-like cell death phenotype and impaired the defense capability of cotton against herbivorous insects. Transcriptome and metabolomics data analysis showed that overexpression of GhMPK31 enhanced the expression of H₂O₂-related genes and reduced the accumulation of defensive related metabolites. The direct evidence of GhMPK31 interacting with GhRBOHB (H₂O₂ generating protein) were found by Y2H, BiFC and LCI. Therefore, we propose that the increase of H₂O₂ content caused by overexpression of GhMPK31 resulted in HR-like cell death in cotton leaves while reducing the accumulation of defensive metabolites, ultimately leading to a decrease in the defense ability of cotton against herbivorous insects. This study provides valuable insights into the function of MAPK genes in plant resistance to herbivorous insects.

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Title: Evaluation of Cotton Genotypes through the Selection Index Technique

Author: Abdullah Moayad Omar

Imprint: IOP Conf. Ser.: Earth Environ. Sci. 1259 012095

Abstract: Eight upland cotton genotypes introduced from different origins (BA440, FLASH, EDESSA, SPERO, IK259, W888, MONTANA and CANDIA) in addition to the two local cultivars (Coker 310 and Lachata) were cultivated on April 22 and 23, 2022 in the Rahmaniyah region at levels (0, 1, 2, and 3 g/liter). I) of nano-chelated NPK 20-20-20 under drip irrigation conditions, and using a randomized complete block design with three replications, in order to evaluate it by creating multiple selection indices and to estimate the expected increase in seed cotton yield. The results of the analysis of variance for the studied traits (seed cotton yield, plant height, number of fruiting per plant, number of bolls per plant, average boll weight, seed index, and lint index) showed that the mean square of genotypes and levels of nano-fertilizer and their interaction was highly significant for all traits except seed index in case of nanofertilizer levels. The selection index that included the two traits of plant height and number of bolls per plant was characterized by a high increase in efficiency compared to direct selection of the seed cotton yield, indicating the importance of selection by adopting the selection index for several traits. This selection index in the current study was considered the best due to its high efficiency, and by adopting it in evaluating the genotypes, it was found that the highest mean of the index was 7.689 for the CANDIA genotype, with a significant difference from most other genotypes, followed by the FLASH and BA440 genotypes. The sequence of local varieties adopted in the study (Coker 310 and Lachata) in terms of performance was 10 and 7, respectively. It appeared that six introduced genotypes were superior to the best local cultivars (Lachata), and all introduced genotypes were higher than the least performing local variety (Coker 310).

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Title: In vivo maternal haploid induction system in cotton

Author: Lu Long , Ya-Mei Feng , Shen-Zhai Shang

Imprint: PLANT PHYSIOLOGY 2023: 00: 1-4, Received July 24, 2023. Accepted October 27, 2023. Advance access publication November 18, 2023

Abstract: Upland cotton (*Gossypium hirsutum*, AADD genome) is a leading economic crop that provides approximately 83% of the raw materials for the global textile industry. Upland cotton has a relatively higher fiber yield than other *Gossypium* species, but lower fiber quantity and resistance to various stresses. Owing to the limited germplasm of upland cotton, introgression of desired traits from sea-island cotton or wild cotton to improve the fiber quality and adaptability to the external environment is the most commonly used strategy in cotton breeding (Yang et al. 2023). The conventional breeding reliance on selfing or backcrossing requires several generations for the fixation of recombinant haplotypes, which is a time-consuming and cost-prohibitive approach, and therefore greatly hampers the breeding of elite cultivars of

cotton. Doubled haploid technology, which provides homozygous lines within 2 generations, has been utilized in many crops and greatly shortens the breeding process. Haploid breeding of cotton has also received much attention since the 1970s. However, owing to the tremendous difficulty in producing haploid inducer lines, little progress has been made.

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Title: Nature of Combining Abilities and Genetic Interpretation for Some Quantitative Traits in Egyptian cotton

Author: M. D.H. Dewdar

Imprint: Bull. Fac. Agric., Cairo Univ., 62: 418- 424 (2011)

Abstract: This investigation was conducted with the objective of approaching an efficient parental choice of cotton cultivars in the breeding program for developing superior cultivars for high yielding and good fiber quality. Five Egyptian cotton genotypes were crossed in a diallel pattern, i.e. in all possible combinations, excluding reciprocals in season 2009. In the summer 2010, field evaluation experiment of 15 entries (5 parents and 10 F₁ , s) was undertaken. The data revealed that there were noticeable differences between the parental genotypes for their positive significant general combining ability (GCA) effects for most studied traits. In general, the magnitude of GCA mean squares was mostly greater than SCA mean squares expressed as GCA/SCA ratio, indicated that the magnitude of additive and additive x additive genetic effects were considerable in the inheritance of all characters rather than non-additive effects, except for boll number, where the effects were mainly non-additive. The parental genotype Giza 83 (P₄) superseded all other parents for GCA effect and showed the highest GCA effects for lint yield and was also in the 2nd rank for seed cotton yield. Giza 81 (P₃) had maximum GCA effects for seed cotton yield followed by Giza 85 (P₂) for boll number. Furthermore, Giza 75 (P₁) was in the 1st rank by having maximum GCA effects for fiber strength and showed desirable negative GCA effects for fiber fineness, revealing that these parental genotypes could be considered as good combiners in breeding program for developing high yielding genotypes. Out of 10 hybrids, five hybrid combinations, i.e. P₁ x P₂, P₁ x P₃, P₁ x P₄, P₁ x P₅ and P₄ x P₅ showed desirable specific combining ability and heterotic effects for most of the studied traits.

Title: The properties of “Khurmo” variety of cotton.

Author: ZakirRajabovPulatovich

Imprint: Texas Journal of Agriculture and Biological Sciences, Volume 22

Abstract: "China and India (about 23% of the total production), the USA (about 16.5%), Brazil (about 8%) and Uzbekistan are the leading countries in the production of raw cotton. in turn, it produces about 3 percent of the world's cotton."

2. Creating cotton varieties that fully meet the requirements of the textile industry in the world and are resistant to various biotic and abiotic factors is one of the urgent issues of today. Scientists of the world are conducting research on the creation of high-yield varieties of cotton that are resistant to various pests and diseases, have high fiber yield and quality, are suitable for mechanized harvesting, and are suitable for different soil and climatic conditions. Despite this, in recent years there has been a decline in cotton production around the world, and according to experts, the reason for this is unfavorable weather conditions, water shortages and pest problems. As a solution to these problems, scientists are achieving high results in the field of agriculture using innovative methods of selection, i.e. marker-based selection (MAS) and biotechnological methods such as RNA interference. In our republic, two types of cotton, medium fiber (*Gossypiumhirsutum* L.) and fine fiber (*G. barbadense* L.), are grown in cotton fields. Although fine-fiber cotton varieties are characterized by high fiber quality, cotton varieties belonging to this type are adapted to a hot climate and are grown only in our southern regions. At the same time, yield and fiber output are somewhat lower than those of medium fiber cotton varieties. "Medium-fiber cotton varieties, which supply more than 95 percent of the world's cotton fiber share, are distinguished from other cotton varieties by their productivity and high fiber output.

Title: Improvement of qualitative and quantitative traits in cotton under normal and stressed environments using genomics and biotechnological tools: A review

Author: Aarti Gupta , Manoj Kumar , Baohong Zhang, Maharishi Tomar , Amandeep Kaur Walia, Prince Choyal

Imprint: Plant Science, Available online 2 December 2023, 111937

Abstract: Owing to the increasing demand for high-quality and high fiber-yielding cotton (*Gossypium* spp.), research into the development of stress-resilient cotton

cultivars has acquired greater significance. Various biotic and abiotic stressors greatly affect cotton production and productivity, posing challenges to the future of the textile industry. Moreover, the content and quality of cottonseed oil can also potentially be influenced by future environmental conditions. Apart from conventional methods, genetic engineering has emerged as a potential tool to improve cotton fiber quality and productivity. Identification and modification of genome sequences and the expression levels of yield-related genes using genetic engineering approaches have enabled to increase both the quality and yields of cotton fiber and cottonseed oil. Herein, we evaluate the significance and molecular mechanisms associated with the regulation of cotton agronomic traits under both normal and stressful environmental conditions. In addition, gossypol is a toxic phenolic compound in cottonseeds, limiting their consumption by animals and humans. In this article, we also review studies that investigated the reduction of gossypol levels in cottonseeds.

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Title: Genome-Wide Identification and Preliminary Functional Analysis of *BAM* (β -Amylase) Gene Family in Upland Cotton

Author: Yanlong Yang, et.al

Imprint: *Genes* 2023, 14(11), 2077; <https://doi.org/10.3390/genes14112077>

Abstract: The β -amylase (*BAM*) gene family encodes important enzymes that catalyze the conversion of starch to maltose in various biological processes of plants and play essential roles in regulating the growth and development of multiple plants. So far, *BAMs* have been extensively studied in *Arabidopsis thaliana* (*A. thaliana*). However, the characteristics of the *BAM* gene family in the crucial economic crop, cotton, have not been reported. In this study, 27 *GhBAM* genes in the genome of *Gossypium hirsutum* L (*G. hirsutum*) were identified by genome-wide identification, and they were divided into three groups according to sequence similarity and phylogenetic relationship. The gene structure, chromosome distribution, and collinearity of all *GhBAM* genes identified in the genome of *G. hirsutum* were analyzed. Further sequence alignment of the core domain of glucosyl hydrolase showed that all *GhBAM* family genes had the glycosyl hydrolase family 14 domain. We identified the *BAM* gene *GhBAM7* and preliminarily investigated its function by transcriptional sequencing analysis, qRT-PCR, and subcellular localization. These results suggested that the *GhBAM7* gene may influence fiber strength during fiber development. This systematic analysis provides new insight into the transcriptional characteristics of *BAM* genes in *G. hirsutum*. It may lay the foundation for further study of the function of these genes.

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Title: From genes to fields: Environmental compatibility of herbicide tolerant transgenic cotton

Author: Kamran Shehzad Bajwa , Muhammad Qayyum Rao, Sarfraz Kiani , Farooq Ahmad

Usman Ali , Abdul

Imprint: Industrial Crops and Products, Volume 209, March 2024, 117903

Abstract: Here are several enticing reasons to use genetic engineering to develop transgenic cotton plants with economically relevant new traits. The use of transgenic cotton to protect crops from biotic stressors like weeds may prove to be a cost-effective solution. **Objectives:** The development of herbicide-resistant cotton variants is the primary motivation for gene transfer in this crop. In the current study, we conducted a battery of experiments on the herbicide-tolerant cotton variety MNH-786 to investigate its expression patterns and environmental adaptation. **Material and methods:** The 35S promoter controls the expression of the codon-optimized Cp4-EPSPS gene that is present in this variety. Several different molecular approaches, such as polymerase chain reaction (PCR), Florescent In-Situ Hybridization analysis, and enzyme-linked immunosorbent assay (ELISA), are used to confirm the presence of transgenic cotton plants. The glyphosate spray assay was performed using molecular analysis, employing a dosage of 2000 ml per acre. The suitability of transgenic and non-transgenic cotton plants in four unique environments – the Multan, Vehari, Bahawalpur, and Faisalabad Districts of Punjab province, Pakistan was assessed using a comparative comparison. A gene x environment interaction (GEI) biplot was used to analyze the correlation between genes and their environments.

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Title: Transcriptome Analysis Revealed that GhPP2C43-A Negatively Regulates Salinity Tolerance in an Introgression Line from a Semi-Wild Upland Cotton.

Author: Changjiang Cui, Liuchun Feng, Chenhui Zhou, Hui Wan and Baoliang Zhou

Imprint: Plant & Cell Physiology, 1-17 (2023)

Abstract: Salt damage is a major threat to sustainable cotton production owing to the limited arable land in China, which is mainly occupied by the production of staple food crops. Salt-stress-tolerant cotton varieties are lacking in production, and the mechanisms underpinning salt stress tolerance in cotton remain enigmatic. Here, DM37, an intraspecific introgression line from *Gossypiumhirsutum* race yucatanense acc TX-1046 into the *G. hirsutum* acc TM-1 background, was found to be highly tolerant to salt stress. Its seed germination rate and germination potential were significantly higher than those of the recipient TM-1 under salt stress. Physiological analysis showed that DM37 had a higher proline content and peroxidase activity and lower Na⁺/K⁺ ratios at the seedling stage, which is consistent with a higher seedling survival rate after durable salt stress. Furthermore, comparative transcriptome analysis revealed that responsive patterns to salt stress in DM37 were different from those in TM-1. Weighted correlation network analysis demonstrated that co-expression modules associated with salt stress in DM37 also differed from those in TM-1. From this analysis, GhPP2C43-A, a phosphatase gene, was found to exhibit negative regulation of salt stress tolerance verified by virus-induced gene silencing and the generation of transgenic *Arabidopsis*. Gene expression showed that GhPP2C43-A in TM-1 was induced by durable salt stress but not in DM37, probably attributable to a variation in the cis-element in its promoter, thereby conferring different salt stress tolerance. These results provide new genes/germplasms from semi-wild cotton in salt-stress-tolerant cotton breeding, as well as new insight into the mechanisms underpinning salt stress tolerance in cotton.

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Title: Identification, evolution, and expression of GDSL-type Esterase/Lipase (GELP) gene family in three cotton species: a bioinformatic analysis

Author: LishengDuan, Fei Wang, HaitaoShen, ShuangquanXie, Xifeng Chen, QuanliangXie, Rong Li, Aiping Cao & Hongbin Li

Imprint: *BMC Genomics* volume 24, Article number: 795 (2023)

Abstract: GDSL esterase/lipases (GELPs) play important roles in plant growth, development, and response to biotic and abiotic stresses. Presently, an extensive and in-depth analysis of *GELP* family genes in cotton is still not clear enough, which greatly limits the further understanding of cotton *GELP* function and regulatory mechanism. **Results:** A total of 389 *GELP* family genes were identified in three cotton species of *Gossypiumhirsutum* (193), *G. arboreum* (97), and *G. raimondii* (99). These *GELPs* could be classified into three groups and eight subgroups, with the *GELPs* in same group to have similar gene structures and conserved motifs. Evolutionary event analysis showed that the *GELP* family genes tend to be diversified at the spatial dimension and certain conservative at the time dimension, with a trend of potential continuous expansion in the future. The orthologous or

paralogous *GELPs* among different genomes/subgenomes indicated the inheritance from genome-wide duplication during polyploidization, and the paralogous *GELPs* were derived from chromosomal segment duplication or tandem replication. *GELP* genes in the A/D subgenome underwent at least three large-scale replication events in the evolutionary process during the period of 0.6–3.2 MYA, with two large-scale evolutionary events between 0.6–1.8 MYA that were associated with tetraploidization, and the large-scale duplication between 2.6–9.1 MYA that occurred during diploidization. The cotton *GELPs* indicated diverse expression patterns in tissue development, ovule and fiber growth, and in response to biotic and abiotic stresses, combining the existing *cis*-elements in the promoter regions, suggesting the *GELPs* involvements of functions to be diversification and of the mechanisms to be a hormone-mediated manner.

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Title: *MORPHOLOGICAL PROPERTIES OF COTTON PHYB RNAI LINES OBTAINED THROUGH SOMATIC EMBRYOGENESIS*

Author: M.S. Ayubov, A.N. Yusupov, B.O. Mamazhonov, N.S. Obidov, L.K. Kamalo

Imprint: Современная биология и ..., 2023

Abstract: The goal of the study is to control the flowering process by inhibiting the functions of the *PHYB* genes that are responsible for cotton flowering using synthetic RNAi duplexes.

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Title: Single-Cell Transcriptome Atlas and Regulatory Dynamics in Developing Cotton Anthers.

Author: Yanlong Li, Huanhuan Ma, Yuanlong Wu, Yizan Ma, Jing Yang, Yawei Li, Dandan Yue, Rui Zhang, Jie Kong, Keith Lindsey, Xianlong Zhang, and Ling Min

Imprint: Adv. Sci. News, 2023, 2304017 DOI: 10.1002/advs.202304017

Abstract: Plant anthers are composed of different specialized cell types with distinct roles in plant reproduction. High temperature (HT) stress causes male sterility, resulting in crop yield reduction. However, the spatial expression atlas and regulatory dynamics during anther development and in response to HT remain largely unknown. Here, the first single-cell transcriptome atlas and chromatin accessibility survey in cotton anther are established, depicting the specific expression and epigenetic landscape of each type of cell in anthers. The reconstruction of meiotic cells, tapetal cells, and middle layer cell developmental trajectories not only identifies novel expressed genes,

but also elucidates the precise degradation period of middle layer and reveals a rapid function transition of tapetal cells during the tetrad stage. By applying HT, heterogeneity in HT response is shown among cells of anthers, with tapetal cells responsible for pollen wall synthesis are most sensitive to HT. Specifically, HT shuts down the chromatin accessibility of genes specifically expressed in the tapetal cells responsible for pollen wall synthesis, such as QUARTET 3 (QRT3) and CYTOCHROME P450 703A2 (CYP703A2), resulting in a silent expression of these genes, ultimately leading to abnormal pollen wall and male sterility. Collectively, this study provides substantial information on anthers and provides clues for heat-tolerant crop creation.

SEED SCIENCE AND TECHNOLOGY

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Title: Mepiquat chloride priming confers the ability of cotton seed to tolerate salt by promoting ABA-operated GABA signaling control of the ascorbate–glutathione cycle

Author: Qi Qian, Wang Ning, RuanSijia, Muhammad Noor, Zhang Hengheng

Imprint: Journal of Cotton Research , Volume 6, article number 24, (2023)

Abstract:Ensuring that seeds germinate and emerge normally is a prerequisite for cotton production, esp. in areas with salinized soil. Priming with mepiquat chloride (MC) can promote seed germination and root growth under salt stress, but its mechanism has not been fully elucidated. In this study, physiological and biochemical experiments revealed that MC-priming promotes the tolerance of cotton seeds to salt stress by increasing the ability of antioxidant enzymes related to the ascorbate–glutathione (AsA-GSH) cycle to scavenge reactive oxygen species (ROS).

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Title: Effects of cultivar, storage period, and seed-borne fungi on aflatoxin content of cotton seeds

Author: Kamel A. Abd-Elsalam Marian M. Habeeb

Imprint: Summa Phytopathol. 49 • 2023 • <https://doi.org/10.1590/0100-5405/257388>

Abstract: Non-sterilized seeds from three commercial cultivars of cotton (*Gossypium barbadense* L.) were examined for qualitative and quantitative estimates of seed-borne fungi. The observed fungi were *Aspergillus* sp.1, *Aspergillus* sp.2, *Penicillium* sp., *A. flavus*, *Alternaria* sp., *A. niger*, *Fusarium* sp., *Rhizopus* sp. and *A. ochreous*. According to the quantitative estimates, *A. niger* (36.02%), *A. flavus* (19.29%) and *Penicillium* sp. (16.74%) were the most predominant fungi isolated from the seeds. Other fungi occurred at frequencies ranging from 0.21% to 10.44%. Analysis of variance showed that each aflatoxin type (A) and cotton cultivar (V) was a significant source of variation in the seed aflatoxin content, while storage period (P) was a nonsignificant source of variation. The first-order interactions A×V and A×P were always nonsignificant sources of variation. In general, aflatoxin B₁ content was greater than that of B₂. Two regression models, derived from stepwise multiple regression analysis, were constructed to describe the effects of the isolated fungi (independent variables or predictors) on aflatoxin content (dependent variables). The first one-variable model (R² = 34.8%) was used to predict B₁ content, while the second five-variable model (R² = 98.2%) was used to predict B₂ content. It is worth noting that species of the genus *Aspergillus* alone accounted for 53.6% of the total variation in B₂ content. In conclusion, cottonseed is susceptible to infection with toxigenic fungi that can be harmful during storage. The study demonstrated the deleterious impacts of *A. flavus* and aflatoxins on the assessed seed quality measures, highlighting the need to monitor toxigenic fungi and their aflatoxins. The findings of this study might aid in the development of techniques for reducing aflatoxins in oily seeds.

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Title: Synthesis and Assessment of Physicochemical Attributes of Biodiesel Obtained from Cottonseed (*Gossypium arboretum* L.) Oil

Author: Bikash Parajuli, Dhruva Prasad Poudya, Manoj Kumar Tharu

Imprint: International Journal of Innovative Science and Research Technology, Volume 8, Issue 11, November - 2023

Abstract:- Biodiesel manufacture is one of the advanced and technical areas for researchers as it is conquering the world because of petroleum shortage and increasing rate together with the environment friendly nature. Biodiesel define as the mono-alkyl esters of fatty acids prepared through trans-esterification reaction. The use of biodiesel is increasing rapidly worldwide due to its positive impact on diesel engines, combustion processes, and pollution formation. Biodiesel is a well-known derivative of long-chain fatty acids that can be obtained from renewable sources such as vegetable oils or animal fats. It can be effectively used in diesel engines. The process of preparing biodiesel from raw materials, such as cottonseed oil, involves the trans-esterification of fat, followed by biodiesel characterization testing. Cottonseed oil, non-edible oil, was

chosen as the raw material for this experiment, as it does not contribute to food versus fuel conflict. Methanol was used as a catalyst in the trans-esterification process for biodiesel preparation. However, the optimum conditions for biodiesel production are suggested in this paper, a maximum of 77% biodiesel was produced with 20% methanol in presence of 0.5% sodium hydroxide. Furthermore, after the preparation of biodiesel, for its identification, numbers of test was done and the prepared biodiesel was verified.

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Title: Comprehensive study on influence of maturity duration and position of boll formation on seed quality in Asiatic Cotton (*Gossypium arboreum*)

Author: Debashis Paul , V. Santhy, Amarpreet Singh, Rishi Kumar

Imprint: Research Square, DOI: <https://doi.org/10.21203/rs.3.rs-3542876/v1>

Abstract: Asiatic/Desi cotton (*G. arboreum*) is in demand in the North zone due to its higher price, tolerance to major sucking insects and better suitability under Cotton-Mustard Cropping system. The production of vigorous seeds in desi cotton is still a major challenge and, the present study was formulated to address this issue. An experiment with nine varieties in RBD was conducted for two years (2020-21 and 2021-22) to ascertain the influence of maturity duration and boll position on seed quality parameters in cotton. The tagged bolls for each genotype were harvested separately from bottom (up-to 40 cm), middle (41–80 cm) and top position (more than 80 cm of plant height) at 140 days after sowing (DAS), 150 DAS, 160 DAS and 170 DAS respectively, and the seeds obtained after ginning were used for conducting experiments. Genotype, picking time, plant stratum and their interaction influenced the seed physiological parameters significantly. The highest mean germination (%) was observed in the seeds picked at 140 DAS (83.72%) followed by 150 DAS (83.14%) after which a significant decline in germination (%) was noticed. Significantly ($P < 0.05$) higher Seed vigour index-I (SV-I) & SV-II was noted in the seeds harvested during 140 DAS (2027.77 & 1435.44) to 150 DAS (2158.11 & 1254.21). A gradual decrease in terms of seed vigour parameters after 150 DAS suggested picking of matured bolls during 140 to 150 (DAS) for obtaining seeds with better quality in desi cotton.

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Title: Exogenous γ -Aminobutyric Acid Can Improve Seed Germination and Seedling Growth of Two Cotton Cultivars under Salt Stress

Author: Zhiduo Dong, JianHuang, Tong Qi

Imprint: Plants 2024, 13(1), 82; <https://doi.org/10.3390/plants13010082>

Abstract: Excessive salt content in soil has adverse effects on cotton production, especially during the germination and seedling stages. γ -aminobutyric acid (GABA) is an important active substance that is expected to improve the resistance of plants to abiotic stresses. This study focused on two cotton cultivars (*Gossypium hirsutum* L.: Tahe 2 and Xinluzhong 62) and investigated the impact of exogenous GABA (0, 1, 2, 3, and 4 mM) on seed germination, seedling growth, and related morphological, physiological, and biochemical indicators under salt stress (150 mMNaCl). The results showed that salt stress significantly reduced the germination rate and germination index of cotton seeds (decreased by 20.34% and 32.14% for Tahe 2 and Xinluzhong 62, respectively), leading to decreased seedling height and biomass and causing leaf yellowing. Salt stress induced osmotic stress in seedlings, resulting in ion imbalance (marked reduction in K^+/Na^+ ratio) and oxidative damage. Under salt stress conditions, exogenous GABA increased the germination rate (increased by 10.64~23.40% and 2.63~31.58% for Tahe 2 and Xinluzhong 62, respectively) and germination index of cotton seeds, as well as plant height and biomass. GABA treatment improved leaf yellowing. Exogenous GABA treatment increased the content of proline and soluble sugars, with varying effects on betaine. Exogenous GABA treatment reduced the Na^+ content in seedlings, increased the K^+ content, and increased the K^+/Na^+ ratio (increased by 20.44~28.08% and 29.54~76.33% for Tahe 2 and Xinluzhong 62, respectively). Exogenous GABA treatment enhanced the activities of superoxide dismutase and peroxidase, and reduced the accumulation of hydrogen peroxide and malondialdehyde, but had a negative impact on catalase activity. In conclusion, exogenous GABA effectively improved cotton seed germination. By regulating osmoprotectant levels, maintaining ion homeostasis, and alleviating oxidative stress, GABA mitigated the adverse effects of salt stress on cotton seedling growth.

FIBER AND FIBER TECHNOLOGY

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Title:CELL LINES, VARIETIES, AND METHODS FOR IN VITRO COTTON FIBER PRODUCTION
Document Type and Number:United States Patent Application 20230399668, Kind Code:A1

Inventors:Bueno, Luciano Luiz, Elbl, Paula Maria , Dodds, David, Tewari, Anant,
De Sousa, Luz Leticia Silveira

Application Number:18/033957, **Publication Date:**12/14/2023

Abstract:The present disclosure provides in vitro methods for producing cotton fiber, including methods using cotton varieties that were discovered to be particularly amendable for use in the presently disclosed in vitro methods of cotton fiber production.

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Title: Dissecting the major genetic components underlying cotton lint development.

Author: Yali Sun, Yuman Yuan, Shoupu He, Warwick Stiller, Iain Wilson, Xiongming Du, Qian-Hao Zhu

Imprint: GENETICS, 2023, iyad219 <https://doi.org/10.1093/genetics/iyad219>

Abstract: Numerous genetic loci and several functionally characterized genes have been linked to determination of lint percentage (lint%), one of the most important cotton yield components, but we still know little about the major genetic components underlying lint%. Here, we first linked the genetic loci containing MYB25-like_At and HD1_At to the fiberless seed trait of 'SL1-7-1' and found that MYB25-like_At and HD1_At were very lowly expressed in 'SL1-7-1' ovules during fiber initiation. We then dissected the genetic components involved in determination of lint% using segregating populations derived from crosses of fuzzless mutants and intermediate segregants with different lint%, which not only confirmed the HD1_At locus but identified the HD1_Dt locus as being the major genetic components contributing to fiber initiation and lint%. The segregating populations also allowed us to evaluate the relative contributions of MYB25-like_At, MYB25-like_Dt, HD1_At, and HD1_Dt to lint%. Haplotype analysis of an Upland cotton (*Gossypium hirsutum*) population with 723 accessions (including 81 fuzzless seed accessions) showed that lint% of the accessions with the LP allele (higher lint%) at MYB25-like_At, MYB25-like_Dt, or HD1_At was significantly higher than that with the lp allele (lower lint%). The lint% of the Upland cotton accessions with 3 or 4 LP alleles at MYB25-like and HD1 was significantly higher than that with 2 LP alleles. The results prompted us to propose a strategy for breeding high-yielding cotton varieties, i.e. pyramiding the LP alleles of MYB25-like and HD1 with new lint% LP alleles without negative impact on seed size and fiber quality.

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Title: Pattern of Transgressive Segregants for Fibre Quality Traits in Segregating Populations derived from an intra-hirsutum cross in Cotton (*Gossypium hirsutum* L.)

Author: Revanasiddayya, J.M. Nidagundi, B. Fakrudin, P.H. Kuchanur, Yogeesh L.N., S. G. Hanchinal, T.C. Suma and Gururaj Sunkad

Imprint: Biological Forum – An International Journal 15(2): 1217-1223(2023)

Abstract: One of the challenge in plant breeding is retrieving and identifying most potential transgressivesegregants in segregating population. The present study was aimed at understanding the pattern of transgressivesegregants (TS) for fibre quality traits in different segregating population's viz., F2, B1F2, B2F2 and F3 derived from an intra-hirsutum cross in upland cotton. Among the four populations, number of TS were found to be highest in F2 population followed by F3, B2F2 and B1F2 population for UHML and micronaire value owing to their population size while pattern of superiority was F2>F3>B1F2>B2F2 for fibre strength. When TS were estimated using different methods viz., parental lines (P1 and P2), mid-parental value, F2 population mean and standard checks (BGDS-1063 and BGDS-1033), number of TS were found to be the highest over check BGDS-1063 in F2(70 (2.4 %)) followed by F3(16 (2.1 %)), B1F2 (2 (0.5 %)) and B2F2 (9 (2.3 %)) populations for UHML and fibre strength while for micronaire value, their number were more over F2 population mean compared to other methods. The segregants viz., RAH1-F2-10 (33.79 mm), RAH1-F3-47 (32.64 mm), RAH1-B1F2-39 (30.51 mm) and RAH1-B2F2-30 (31.98 mm) were identified as the most potential transgressivesegregants for UHML in F2, F3, B1F2 and B2F2 populations, respectively. The present study concluded that the pattern in number of transgressivesegregants varies in different segregating populations (F2, F3, B1F2 and B2F2) according to differences in population size and method of estimation. Most potential transgressivesegregants for fibre quality traits are identified with can be used to derive superior homozygous lines for the concerned trait.

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Title: Role of Transcription Activity of WRKY Transcription Factor in Cotton Fiber Initiation and Elongation .

Author: Sainath K, Eshwar, Hemanth S, Spoorthi S R and Rohit Kumar

Imprint: VigyanVarta an International E-Magazine for Science Enthusiasts Vol. 4, Issue 11

Abstract: Cotton known as "King of fibre" and "White gold" is a globally vital crop used for soft clothing. Its cultivation spans over 50 countries with major producers including the USA, India, China, the Middle East and Australia. Cotton deriving from species like *G. arboreum*, *G. herbaceum*, *G. hirsutum* and *G. barbadense* dominates textile production due to its ecofriendliness. Cotton fibre development involves complex biological processes influenced by genetic factors and transcription factors (TFs) crucial for regulating elongation. Cotton flowering leads to boll formation containing seeds encased in fibres. Ethylene hormone significantly impacts fibre elongation. Specific TFs notably WRKY factors, play essential roles in cotton fibre development regulating genes associated with fibre growth and quality. Studies identified WRKY genes' significance in initiation, elongation and maturation phases, showing their regulatory functions.

GhWRKY16, a fibre-specific TF positively influences fibre initiation and elongation binding to gene promoters and enhancing fibre development in cotton.

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Title: A novel seed balling technology and its effect on cotton emergence, yield and fiber quality

Author: Zhangshu Xie,^{1,2} Chengxuan Zhou,^{1,2} Xuefang Xie

Imprint: Italian Journal of Agronomy, VOL. 18 NO. 3 (2023)

Abstract: Cotton is a *Gossypium* plant of the Malvaceae family. It is an economic crop known as “white gold”, and the Yangtze River Basin is an important planting area in China. As global agriculture mechanizes, the direct seeding mode has gradually replaced the traditional seedling-transplantation mode in China. The new direct planting of cotton seedlings following rape or wheat harvest achieved initial success and has been widely applied in southern China (Xiao et al., 2009; Zou et al., 2021). However, there are still some problems with this method, such as the difficulty of growing a seedling out of each seed, resulting in low yield and poor fiber quality. Hunan Province, the main cotton production region in the Yangtze River Basin, suffers from cold spells every late spring that cause plant losses during cotton planting. Low temperatures and heavy rain lead to more cotton diseases and later seed emergence, severely restricting the yield of direct seeded cotton following rape harvest (Li et al., 2013).

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Title: View Of Valuable Agricultural Characters In F1 Plants Of Medium Fiber Cotton Gen Collection Lines.

Author: Xayitova Shaxlo Davlatovna

Imprint: Texas Journal of Multidisciplinary Studies ISSN NO: 2770-0003
<https://zienjournals.com> Date of Publication: 14-11-2023

Abstract: Today, cotton (*Gossypium* L.), which is one of the main branches of agriculture in the world, is being paid special attention to increase the quality of valuable economic traits, especially the fiber quality, and to improve the efficiency of their genetic potential with initial sources that are genetically resistant to various stress factors, diseases and pests. One of the urgent issues is the expansion of the priority directions for the perspective of cotton production and the creation of productive cotton varieties that are competitive in the world and have high fiber quality.

Therefore, it is important to study the inheritance of valuable economic traits in cotton gene collection lines and to create and establish resources. Fiber length and fiber output

is a quantitative trait, which appears under the influence of polygenic genes and is also significantly influenced by external factors. According to the data, the inheritance of the long fiber trait in F1 hybrids was observed mainly in dominant, super-dominant and intermediate states. [3]. The ratio of fiber weight to raw cotton weight depends on the amount and weight of fibers in the seed. [2]. In the inheritance of the fiber index, the high fiber index is completely dominant over the low fiber index, when the high fiber index lines with relatively the same indicators are crossed, the trait increases in F1 compared to the parental indicators. One of the main economic indicators of the productivity of cotton, which has an intermediate position compared to the parent forms, is the weight of 1000 seeds. High-quality and large-sized seeds can be grown under favorable agrotechnical conditions

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Title: EB1C forms dimer and interacts with protein phosphatase 2A (PP2A) to regulate fiber elongation in upland cotton (*Gossypiumhirsutum*)

Author: Haoming Mao, Li Wang, Yanwen Wang, Pan Feng, Jikun Song

Imprint: International Journal of Biological Macromolecules, Volume 256, Part 2, January 2024, 128036

Abstract: Cotton is the most economically important natural fiber crop grown in more than sixty-five countries of the world. Fiber length is the main factor affecting fiber quality, but the existing main varieties are short in length and cannot suit the higher demands of the textile industry. It is necessary to discover functional genes that enable fiber length improvement in cotton through molecular breeding.

In this study, overexpression of *GhEB1C* in *Arabidopsis thaliana* significantly promotes trichomes, tap roots, and root hairs elongation. The molecular regulation of *GhEB1C* involves its interactions with itself and GhB'ETA, and the function of *GhEB1C* regulation mainly depends on the two cysteine residues located at the C-terminal. In particular, the function activity of *GhEB1C* protein triggered with the regulation of protein phosphatase 2A, while silencing of *GhEB1C* in cotton significantly influenced the fiber protrusions and elongation mechanisms., Further, influenced the expression of MYB-bHLH-WD40 complex, brassinosteroids, and jasmonic acid-related genes, which showed that transcriptional regulation of *GhEB1C* is indispensable for cotton fiber formation and elongation processes. Our study analyzed the brief molecular mechanism of *GhEB1C* regulation. Further elucidated that *GhEB1C* can be a potential target gene to improve cotton fiber length through transgenic breeding.