GLEANINGS IN COTTON RESEARCH

AUGUST 2025

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Preface

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Information literacy is the ability to find, evaluate, organize, use, and communicate information in all its various formats, most notably in the acquisition of knowledge. The diversity of news sources thus makes the internet a source of information and knowledge.

Gleanings in Cotton Research *is an attempt made by the Library to scan, collect, edit and present, ongoing research in Cotton using the information available on the Internet in a concise manner.*

Articles related to Cotton subject area are represented by Agronomy, Soil Science, Plant Physiology, Genetics, Biotechnology, Crop Protection, Seed Technology, and Fiber Technology.

The information collected is arranged under these broad subject headings. The Title of the research paper is followed by the Imprint, wherein Names of the authors and Journal are given. Names of the journals are followed by year of publication, volume number, issue number in brackets and inclusive pages. The DOI (Digital Object Identifier) wherever applicable is also mentioned. The abstract follows the citation.

Information has been mainly retrieved from Google Scholar, Science Direct and GAIN website.

We duly thank The Director, Dr V. N. Waghmare, for providing inspiration and support for this publication.

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Title: Three Essays on the Economic Impact of Climate Variability, Cropping Systems, and Sustainability in Cotton Production.

 Author: Oluwaseun Samuel Oduniyi

Imprint: A Dissertation In Agricultural and Applied Economics Submitted to the Graduate Faculty of Texas Tech University in Partial Fulfillment of the Requirements for the Degree of Doctor of Philosophy, May, 2025

Abstract: In the first chapter of the dissertation, we investigate the economic impact of various cropping systems and irrigation levels on the management of Verticillium wilt in cotton production. Conducted at the Texas A&M AgriLife Helms research farm, the experimental design utilized 24 different treatments across a circular field historically affected by Verticillium wilt since 2007. This paper analyzes data collected from 2014 to 2021, focusing on Gross Margin Analysis, Fixed-Effects Model with Absorbed Treatment Effects and profit efficiency using Stochastic Frontier Analysis (SFA). Results indicate that cropping systems involving continuous cotton with a wheat cover and varying irrigation levels significantly influence yield and profitability. Particularly, systems under 1.5 inches of irrigation in conventional tillage with beds demonstrated the highest yield and economic returns. Sensitivity analysis on loan rates further emphasized the financial viability of specific cropping systems. The study concludes that strategic management of water resources and selection of appropriate cropping systems can substantially mitigate the effects of Verticillium wilt and enhance profitability in cotton production, providing a valuable guide for optimizing agricultural practices in similar environments.

The second chapter provides insight on the impact of climate change on cotton production through an in-depth analysis on the specific effects of heat stress on cotton yield characteristics. This study aimed to fill that gap by conducting a meta-analysis to assess the impact of heat stress on key cotton yield parameters, including lint yield, boll weight, boll number, boll retention, and seed yield. A systematic search across databases including ScienceDirect, Scopus, Web of Science, Google Scholar, and PubMed yielded 62 articles, of which 43 were included in the meta-analysis. Using the Open MEE software, a Random Effects Model (REM) was applied to generate pooled effect estimates at a 95% confidence interval, and subgroup analysis was also performed. The results indicated an overall reduction in all cotton yield parameters due to heat stress. In addition to agronomic effects, the study quantified the economic impact of heat stress, estimating a revenue loss of $2.20 per acre loss for U.S. cotton producers. These

findings emphasize the need for adaptive strategies, such as heat-tolerant cotton varieties, improved irrigation management, and climate-resilient policies to mitigate economic losses. Consequently, the study recommends further investigation into the long-term economic consequences of heat stress on cotton lint yield, particularly in the U.S.

The third chapter of the dissertation examines the impact of rising temperatures using a multilevel regression model applied to historical climate and yield data (1980–2018) from key cotton-growing regions. The analysis examines how maximum and minimum temperatures, precipitation, and growing degree days influence yield at different growth stages. Results show that a 1°C increase in maximum temperature during the flowering stage (TmaxGS2) reduces cotton yield by 5.5%, leading to revenue losses of up to $219 per acre. Conversely, higher precipitation during critical growth periods increases yield by 183 lb/acre, partially offsetting heat stress effects. Given these findings, adaptation strategies are essential. We recommend the development of heat-tolerant cotton varieties, improved irrigation management, and expanded financial support programs, including climate-based crop insurance. Additionally, optimizing plant timing and adopting precision agricultural practices can help mitigate yield losses. These measures will strengthen the resilience of cotton farming against escalating climate risks, ensuring long-term sustainability. This study provides valuable insights for farmers, policymakers, and researchers working to safeguard cotton production in a changing climate.

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Title: Profitability and comparative economic analysis of hybrid and local cotton cultivation in Kushtia district, Bangladesh.

Author: Nabila Hossain, Sagira Khatun, Ayesha Mahbub Rumana and Md. Masudul Hassan

Abstract: Cotton plays a key role in the national economy, generating direct and indirect employment in the Agricultural and Industrial sectors. The textile and clothing industries constitute Bangladesh's economy's most significant manufacturing sub-section. This study analyzes the profitability and economic feasibility of hybrid and indigenous cotton growing in the Kushtia district of Bangladesh, a substantial area for cotton production. The analysis employs a structured survey of 60 smallholder farmers; 30 growing hybrid varieties and 30 growing local types to assess financial outcomes via gross return, gross margin, net return, and benefit-cost ratio (BCR). The findings indicate that hybrid cotton production has much greater economic returns, with a gross return of Tk. 455,000 per hectare and a benefit-cost ratio (BCR) of 2.18, in contrast to Tk. 340,500 and a BCR of 1.65 for local varieties. Although hybrid farming incurs marginally elevated total expenses (Tk. 208,400 compared to Tk. 205,846), its enhanced yield and reduced input inefficiencies result in superior profitability. Research underscores the capacity of hybrid cotton to augment rural income, while advocating

investment in research, training, and extension services to facilitate equitable and environmentally sustainable adoption. These findings are crucial for policymakers seeking to enhance cotton sector production and diminish Bangladesh's reliance on cotton imports.

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Title: Integrative use of biochar and bio stimulants improves cadmium detoxification and yield in cotton.

Author:
S. Osman, Yan Gao, Zhicheng Luo, Khadiga Alharbi, Emadeldeen Rashwan, Alaa El-Dein Omara, Emad M. Hafez

Abstract: Dealing with abiotic stress is a challenge to maintaining sustainable agricultural productivity, especially for the dual stress of soil salinity and heavy metal contamination. A field experiment was conducted in a completely randomized factorial design to assess the combined effects of biochar (BC), plant growth-promoting microorganisms (PGPM), and seaweed extract (SWE) in mitigating cadmium (Cd) toxicity while promoting cotton growth in saline soils. The study included eight treatments: control (CK), single applications of SWE, PGPM, or BC, dual applications of BC + SWE, BC + PGPM, and PGPM + SWE, and a triple application (BC + PGPM + SWE). Results showed that the BC + PGPM + SWE treatment significantly improved soil quality by reducing the Na and Cd bioavailability by 31 % and 34 %, respectively, while enhancing soil organic matter, microbial biomass carbon, and soil enzymatic activity. Antioxidant defense mechanisms in cotton leaves were significantly induced, as indicated by enhanced activity of SOD, APX, DHAR and GR from 1.8-folds in SOD to 3.4-folds the control in GR. Multivariate analysis revealed that enzymatic and non-enzymatic antioxidants of the ascorbate-glutathione cycle seemed to play a key role in oxidative stress mitigation with maintenance of redox homeostasis and chelation of Cd, resulting in a reduction of 18 % and 56 % in Cd translocation factors from root to shoot, and from shoot to bolls, which contributing to a 65 % increase in cotton seed yield. This study demonstrates an integrative approach to enhancing the resilience of the soil and its productivity, thereby offering a scaling-up, eco-friendly strategy toward sustainable agriculture in degraded and stress-prone ecosystems.

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Title: Biochar impact on soil properties and soil solution nutrient concentrations under cotton production.

Author: Ramandeep Kumar Sharma, Gurbir Singh, Amrinder Jakhar

Abstract: Intensive tillage and unsustainable agricultural practices adversely impact soil health and the long-term sustainability of crop production in humid subtropics. Biochar, a soil amendment, can be used to improve soil properties and agricultural productivity. A field experiment evaluated the impact of biochar application rates (B) (0, 10, 20, and 40 Mg ha^{-1}) on soil properties and soil solution chemistry under rainfed cotton (*Gossypium hirsutum* L.) production systems in the Lower Mississippi Delta from 2020 to 2022. An application of 40 Mg ha^{-1} of biochar significantly reduced bulk density and increased water content in 0–15 cm compared to other rates and depths. Biochar increased aggregate stability compared to the control in the topsoil layer for aggregate fractions of size 0.5–1 mm and 1–2 mm in 2021. Biochar application at 20 and 40 Mg ha^{-1} reduced NO_3-N concentration in soil by 63 % and 53 %, respectively, compared to the control at a 0–15 cm depth in 2021. Biochar applications reduced soil solution NO_3^--N losses 49 %–87 % and 42 %–102 % during the fallow period compared to the control at a 46 and 81 cm depth, respectively. Biochar also reduced the soil solution PO_4^{3-}-P concentration 14 %–39 % compared to the control in the fallow period. Biochar improved soil properties while reducing nutrient losses in the soil solution and has the potential to be an alternative soil amendment strategy for sustainable cotton production.

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Title: Transitioning from Traditional to Integrated Crop Management: Advancing Cotton Production Practices.

Author: Aditya Ashok Pise; Vipin Jain; Adelin Parinita; Ashok Sampat Pise

Abstract: Cotton, a critical crop for the global agricultural economy, faces growing challenges due to traditional farming practices that rely heavily on chemical inputs, inefficient resource usage, and environmental degradation. This study explores the transition from Traditional Crop Management (TCM) to Integrated Crop Management (ICM) as a sustainable alternative, leveraging artificial intelligence (AI) and machine learning (ML) technologies. ICM incorporates a holistic approach, integrating precision agriculture, biological pest control, optimized resource usage, and soil health management practices. By utilizing AI and ML models to analyze data from experimental fields under similar environmental conditions, this research evaluates the economic, agronomic, and environmental impacts of transitioning to ICM in cotton farming. Key metrics such as crop yield, resource usage, soil health, and biodiversity are assessed, with AI-driven insights providing actionable recommendations for improving sustainability. The findings aim to support farmers and policymakers in making informed decisions to promote sustainable cotton production, addressing the environmental and economic challenges of the industry.

Title: Coupling effects of silicon and calcium foliar application and potassium soil fertilization on growth and yield production of cotton plants under drought stress conditions.

Author: Hossam S. El-Beltagi, Essam Abdelaziz El-Waraky, Mohammed I. Al-Daej, Kholoud Ahmed El-Naqma

Abstract: Drought significantly affects cotton production, decreasing both yield and fiber quality. This study investigated how foliar applications of calcium (Ca) or silicon (Si), along with varying potassium (K) levels in the soil, can improve drought tolerance in cotton. The foliar treatments involved calcium nitrate at 4 g/L or silicon oxide at 1 ml/L, combined with 106.6 and 160 kg K_2SO4 ha^{-1} as soil fertilizer. These treatments were compared to potassium-only applications, with irrigation intervals of 30 days during the 2021 and 2022 growing seasons. The 160 kg K_2SO4 ha^{-1} treatment notably improved plant growth, including increased plant height, dry weight, leaf area, and the number of fruiting branches, compared to the 106.6 kg K_2SO4treatment. It also enhanced chlorophyll content, antioxidant enzyme activity, leaf phenol and proline levels, and relative water content (RWC). Additionally, the 160 kg K_2SO4 ha^{-1} treatment improved yield-related traits, such as the number of open bolls, lint percentage, seed index, and fiber quality, including fiber length, strength, and micronaire. The number of open bolls, lint percentage, and seed index increased by 2.38%, 1.71%, and 1.68% in the first season, and by 4.29%, 1.57%, and 1.38% in the second season, respectively. The combination of Ca or Si foliar applications with K treatments further enhanced plant growth, chlorophyll, antioxidant activity, RWC, seed index, boll weight, and fiber quality. These treatments also raised nutrient levels of N, P, K, Ca, and Si compared to the control. Overall, combining Ca or Si sprays with 160 kg K_2SO4 effectively mitigated drought stress and improved cotton growth and productivity.

Title: Isolation and Screening of Phosphate and Potash Solubilizing Bacteria from Rhizosphere Soil of Maize and Cotton.

Author: Alish Kiruba Victoriya, Sasidharan Satheesh Kumar, Shubhiksha Rajesh, Deepika Muthusamy, Sabari Rani Ganesh Moorthy, and Kishore Devendran

Abstract: The availability of soil fertility and growth of plants mainly depends on the interaction of microorganisms with soil nutrients. However, Phosphorus and potassium are indeed essential nutrients for plant growth, but they are often present in the soil as insoluble forms. A microorganism plays a critical role in nutrient mobilization, hence

reducing the reliance on chemical fertilizers. The objective of this research is to isolate and screen Phosphate-Solubilizing Bacteria (PSB) and Potash-Solubilizing Bacteria (KSB) from the rhizospheric soil of maize (Zea mays) and cotton (Gossypium herbaceum). 38 different colonies of distinct bacteria were isolated and then screened using Pikovskaya's agar and Aleksandrow's agar. Through morphological identification and biochemical characterization, there were 14 isolates with the same morphology as well as 24 unique isolates. Out of them, 12 strains could solubilize phosphate, 10 could dissolve potassium, and 8 could perform both activities simultaneously. The two highest isolates for phosphate-solubilizing efficiency and the three best for potassium dissolution were found by measuring zones of solubilization on agar plates. Those isolates were characterized based on their 16S r RNA sequencing. This research clearly indicates that soil microorganisms play an important role in the availability of nutrients to plates and provides a way for this dependence on chemical fertilizers to decrease.

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Title: L-Tryptophan Blended Novel Organic Potassium Fertilizer Developed from fruit and vegetable waste Enhanced Cotton Growth and Yield.

Author: Shah, Z.- ul-H., Kubar, K. A., Talpur, N. A., Jamali, I. A., Arain, J. A., & Rajpar, I.

Abstract: Organic plant nutrition has been considered cost effective and environmentally benign, since it utilizes cheap and frequently available harmful organic waste material by converting into useful products. This study was conducted in cotton crop (cv. SAU-1) to test the efficacy of a novel potassium (K) enriched, L-tryptophan blended organic fertilizer, developed from fruit and vegetable waste. This field experiment was laid out in a randomized complete block design, involving the single and integrated application of six varying doses of inorganic and novel organic K fertilizers, i.e. 00-00 (control), 30-00, 00-30, 30-30, 60-00, 00-60 kg K ha^{-1}, with three repeats. The crop received recommended doses of nitrogen (N) and phosphorus (P) (160-80 kg ha^{-1}, respectively). Overall, K fertilization showed a significant enhancement in stem diameter, number of sympodia, number of bolls, seed cotton yield (86.4, 61.5, 84, 78%, respectively), and the accumulation of N, P and K (74, 75 and 264%, respectively). The results revealed that L-tryptophan blended novel organic K fertilizer integrated with equal amounts of inorganic K fertilizer (30-30 kg ha^{-1}) enhanced seed cotton yield and nutrient accumulation more than any other treatment. The correlation analysis suggested that K nutrition positively influenced nutrient accumulation, especially K, in cotton plants, which in turn, promoted its various growth traits and ultimately led to increased seed yield. We conclude that the integrated application of inorganic K fertilizer with K-enriched, L-tryptophan blended novel organic fertilizer in equal amounts (30 kg K ha^{-1} each) enhance cotton growth, seed cotton yield, and improves nitrogen, phosphorus and potassium accumulation and use. Further experiments are warranted to validate these results.

Title: Opportunistic keystone diazotrophs from co-occurrence networks drive biological nitrogen fixation in peanut/cotton intercropping systems.

Author: Shijie Zhang, Yingchun Han , Guoping Wang , Lu Feng, Yaping Lei, Shiwu Xiong, Beifang Yang , XiaoyuZhi, Minghua Xin, Yahui Jiao, Xiaofei Li, Yabing Li1, Zhen Jiao

Abstract: Legume-based intercropping enhances a symbiotic biological nitrogen fixation (BNF); however, the underlying mechanisms remain unclear, including the roles of soil keystone diazotroph taxa with varying niche breadths. A field experiment was conducted to evaluate soil BNF variations between rhizosphere and bulk soils in peanut/cotton intercropping systems and monocultures. BNF activities were measured by nitrogen fixation rates, nitrogenase activity, and nifH gene abundance. Phylogenetic null models, cooccurrence networks, and niche breadth analysis were applied to investigate the roles of diazotrophic keystone taxa and their ecological niches. Rhizosphere soils exhibited 7.8–125.5% higher BNF potentials than bulk soils, whereas intercropping systems showed 11.6–323.0% increases over monocultures for nitrogen fixation rate, nitrogenase activity, and nifH gene abundance (all P complex and interconnected communities in intercropping and rhizosphere soils that were dominated by opportunistic diazotrophs (78.8–85.9%), followed by specialists (10.2–18.5%) and generalists (1.38–3.80%). Keystone taxa, including opportunists such as Azoarcus, Azohydromonas, and Steroidobacter, and generalists like Pseudomonas and Azotobacter, correlated positively with microbial biomass carbon and nitrate nitrogen, contributing to enhanced BNF. Peanut/cotton intercropping enhances BNF by selectively enriching the keystone diazotrophic taxa with varying ecological roles, particularly opportunists and generalists. Such targeted intercropping strategies can optimize BNF, improve soil fertility, and promote sustainable agricultural production.

Title: Algal Biomass from Wastewater Treatment Stimulates Cotton (Gossypium hirsutum) Growth and Gene Regulation.

Author: Anh Quynh Nguyen, Waqar Ahmad, Ram Ray, Xiaonan Shan, Abdul Latif Khan & Venkatesh Balan

Abstract: Microalgae, phototrophic organisms, have been used for environmental bioremediation, including wastewater treatment. Algae have been tested for the promotion of plant growth. However, little has been known about re-using algae from wastewater treatment facilities as bio stimulants for non-edible crops. This study assessed the beneficial effects of algal pallets on cotton crops. The biochemical and

nutrient compositions of microalgae biomass (AB) were identified where essential nutrients, endogenous phytohormone content (salicylic acids > auxins > gibberellins), and biochemical content (crude protein > fat > fiber). Different AB concentrations were formulated to test the benefits for cotton (*Gossypium hirsutum*) plant growth and compared them with commercial fertilizer and untreated controls. AB and its combination (AB + NPK) significantly increased shoot length, root length, shoot biomass, and root biomass compared to the control. Oxidative stress enzymes and biochemicals significantly increased with catalase (~ 1.8-fold), superoxide dismutase (~ 2.3-fold), and phenolic content (1.2-fold) higher in AB-treated plants compared to control. Polyphenol oxidase and ascorbate peroxidase were not active in the treatments. Dehydration (dehydration responsive element binding-*GhDREB* and 9-Cis-epoxycarotenoid dioxygenase-*GhNCED1*) and stress (heat shock protein gene-*GhHSP101*) responses genes were respectively 2.2, ~ 2.8, and 2.4 times up-regulated in cotton plants during AB treatments comparing controls. In conclusion, the current findings show that algae, after wastewater treatment, could be recycled and reused to improve plant growth and help reduce the negative impact of synthetic fertilizers.

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Title: Genetic Association of Plant Physiological Parameters with Agronomically Important, Yield-Related Traits in American Cotton (Gossypium Hirsutum L.).

Author: Muhammad Younas, Muhammad Zafar, Muhammad Kashif Munir, Babar Hussain Babar, Ali Hassan Malik, Waseem Sabir, Ghulam Mustfa Siddiqui, Javed Iqbal, Muhammad Tauseef

Abstract: Cotton (*Gossypium hirsutum* L.) productivity in semi-arid regions like Pakistan is severely constrained by water scarcity and heat stress. With an average yield of 570.99 kg/ha, Pakistan lags behind major cotton-producing countries such as China (1,992 kg/ha), emphasizing the urgent need for identifying climate-resilient, high-yielding genotypes. Objective: To evaluate the physiological and yield-related performance of ten elite cotton genotypes under semi-arid conditions, and to identify superior candidates for breeding programs to improve cotton yield. Methods: A field trial was conducted at the Cotton Research Station, Bahawalpur, using a Randomized Complete Block Design (RCBD) with three replications. Ten cotton genotypes (BH-188, BH-226, BH-291, BH-403, BH-407, BH-410, BH-423, BH-563, BH-184, and CIM-600) were assessed for physiological traits including photosynthetic rate, stomatal conductance, and transpiration rate, as well as yield-related parameters such as boll weight, number of sympodial branches, and seed cotton yield. Statistical analyses

included ANOVA, Pearson correlation, Principal Component Analysis (PCA), and cluster analysis to determine genotypic variation and trait associations. Results: ANOVA revealed highly significant genotypic differences ($p \leq 0.01$) for most traits: seed cotton yield (F = 2.89245), photosynthetic rate (F = 15.793), and sympodial branches (F = 7.4963). Correlation analysis demonstrated strong positive relationships between yield and sympodial branches (r = 0.75*) and boll weight (r = 0.25). PCA showed that the first two principal components (PC1 = 33%, PC2 = 21.6%) explained 54.6% of the total variation, primarily influenced by yield and physiological traits. Cluster analysis grouped genotypes into three distinct clusters, with Cluster 1 (BH-188, BH-226, BH-410) exhibiting the highest yield (4.56 t/ha), driven by superior photosynthetic rate (30.33 μmol m^{-2} s^{-1}) and sympodial branching (21.66). Conclusion: This study highlights BH-226 and BH-410 as promising candidates for breeding programs to enhance cotton yield under semi-arid conditions. Their superior physiological efficiency and yieldrelated traits present viable solutions to overcoming productivity challenges in water-stressed environments. These genotypes can be pivotal in developing climate-resilient cotton varieties tailored to Pakistan's agro-climatic conditions.

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Title: Interactive effects of tillage, legumes and nitrogen on soil health and cotton-wheat productivity.

Author: Hafiz Muhammad Waleed Iqbal, Abdul Ghaffar, Muhammad Naveed Afzal, Khuram Mubeen, & Tanveer ul Haq

Abstract: Deteriorating soil health is one of the major constraints to achieving higher yields in the cotton-wheat cropping system. Conservation agriculture and optimum nitrogen fertiliser can improve natural resource usage and crop profitability. A two-year field experiment (2019–2021) conducted under the bed & furrow planting method involving two tillage systems (no – tillage; NT and conventional tillage; CT), different legumes (soybean, mungbean and mash bean) and two nitrogen levels (recommended nitrogen; NL_1 = 222, 133 kg ha^{-1} and 15% reduced nitrogen; NL_2 = 189, 113 kg ha^{-1}) for both cotton and wheat crops. The results indicated that soil organic matter and microbial population under cotton + mungbean-wheat with NT + NL_1 were 14.4%, 8% and 1.8% higher than sole cotton-wheat with CT + NL_1. Moreover, a significant increase was observed in wheat grain yield (1.31–7.48%) during 2019–2021, respectively under cotton + mungbean-wheat compared to the sole cotton-wheat cropping system. However, the highest cotton yield (2437–3037 kg ha^{-1}) was during 2019–2021 under sole cotton-wheat compared to other treatments. The maximum benefit-cost ratio was under CT + NL_1 with the cotton + mungbean-wheat crop system. In conclusion, the best

cropping system in terms of soil health was NT with cotton + mungbean-wheat, while, crop yield and cost-benefit ratio were increased under $CT + NL_1$ with the cotton + mungbean-wheat cropping system.

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Title: Antioxidant Potential of Aqueous and Hydroalcoholic Extracts of Gossypium hirsutum L.

Author: Luciene Ferreira de Lima, Adrielle Rodrigues Costa, Carlos Vinicius Barros Oliveira, Antônia Eliene Duarte, Cícera Norma Fernandes Lima, Damiana Gonçalves de Sousa Freitas, Severino Denicio Gonçalves de Sousa

Abstract: Plant extracts serve as a reservoir of bioactive phytochemicals applicable in various domains, with Gossypium hirsutum L. encompassing constituents such as terpenes, phenolic compounds, and flavonoids, all exhibiting notable antioxidant properties, as well as metal-reducing capabilities, alongside potential toxicity. These compounds are distributed throughout the seeds, capsules, goblets, leaves, stems, flowers, and roots of the plant. To assess these potential activities, this study investigated the antioxidant capacity of the extracts by neutralizing free radicals and iron ions. Aqueous and hydroalcoholic extracts from the leaves and roots (AERG, HERG, AELG, and HELG) were prepared and subsequently dried using spray drying techniques. Following this, evaluations of the antioxidant potential were conducted utilizing the DPPH method (1,1-diphenyl-2-picrylhydrazyl), while the reducing and chelating capacities of iron ions ($Fe2+$ and $Fe3+$) were determined by measuring the intensity of the orange complex formed with 1,10-phenanthroline and free $Fe2+$ in the control supernatant and extracts. The hydroalcoholic extracts exhibited antioxidant activity comparable to that of ascorbic acid ($IC50$ 46.30 μg/mL), effectively donating electrons to stabilize free radicals, demonstrating a higher percentage of efficacy than their aqueous counterparts from G. hirsutum. Nevertheless, the chelation and reduction assays for the iron extracts did not demonstrate significant chelation or oxidation of iron. It was concluded that the extracts displayed a mild antioxidant action; thus, conducting further tests with various metals would be beneficial to ascertain their reducing or chelating potential.

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Title: Multimodal Deep Learning Models in Precision Agriculture: Cotton Yield Prediction Based on Unmanned Aerial Vehicle Imagery and Meteorological Data.

Author: Chunbo Jiang, Xiaoshuai Guo, Yongfu Li, Ning Lai, Lei Peng and Qinglong Geng

Abstract: This study investigates a multimodal deep learning framework that integrates unmanned aerial vehicle (UAV) multispectral imagery with meteorological data to predict cotton yield. The study analyzes the impact of different neural network architectures, including the CNN feature extraction layer, the depth of the fully connected layer, and the method of integrating meteorological data, on model performance. Experimental results show that the model combining UAV multispectral imagery with weekly meteorological data achieved optimal yield prediction accuracy (RMSE = 0.27 t/ha; R^2 = 0.61). Specifically, models based on AlexNet (Model 9) and CNN2conv (Model 18) exhibited superior accuracy. ANOVA results revealed that deeper fully connected layers significantly reduced RMSE, while variations in CNN architectural complexity had no statistically significant effect. Furthermore, although the models exhibited comparable prediction accuracy (RMSE: 0.27–0.33 t/ha; R^2: 0.61–0.69 across test datasets), their yield prediction spatial distributions varied significantly (e.g., Model 9 predicted a mean yield of 3.88 t/ha with a range of 2.51–4.89 t/ha, versus Model 18 at 3.74 t/ha and 2.33–4.76 t/ha), suggesting the need for further evaluation of spatial stability. This study underscores the potential of deep learning models integrating UAV and meteorological data for precision agriculture, offering valuable insights for optimizing spatiotemporal data integration strategies in future research.

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Title: Evaluating Variation among Selected Cotton Genotypes for Growth, Yield and Boron-Use-Efficiency.

Author: Saeed Akhter Malik, Javed Ahmed Shah, Saibrina Sethar, Nazia Rais, Reema Vistro and Vishandas Suthar

Abstract: Boron (B) plays significant roles in the growth, development, yield and quality of cotton. However, there exists a very narrow gap between plant deficiency and toxicity limits of B. We conducted this field study, following a thrice replicated randomized complete block split-plot design (main: B levels and sub: genotypes), to evaluate the growth, yield, and boron-use-efficiency of five cotton genotypes (Sohni, Chandi, Reshmi, Qalandri and CRIS-443) of Sindh under deficient (0 kg B ha-1) and adequate (2.0 kg B ha-1) levels of soil applied B (Borax, 11.5% B). The crop also received a blanket dose of 120-60-60 kg NPK ha-1. The soil used was clay loam, alkaline in nature (pH: 8.2), slightly saline (EC: 1.7dS m-1), while low in organic matter (0.79%) and diluted HCl-B (0.42 mg kg-1). Both the sources of variance (B and cotton genotypes) (G) significantly (p <0.001) affected all the traits. Cotton genotypes significantly differed for their B accumulation. Boron × genotypes interaction significantly (p <0.05) affected the number of bolls and seed cotton yield. Qalandari produced maximum number of sympodia, bolls, seed cotton yield, and accumulated maximum B concentration under both the levels of B. Sohni had maximum ginning out turns and B accumulation under both B levels. Reshmi produced maximum boll weight under both conditions. Qalandari appeared to be a potential genotype to perform both under low and high B input

agriculture, being the most efficient-responsive genotype. We concluded that the adequate B nutrition significantly affects most of the growth traits and seed yield of cotton genotypes, though independent of boron accumulation. Hence, a wide range of cotton genotypes may be involved in exploiting their variation for B accumulation in quest of identifying B-use-efficient cotton genotypes

CROP PROTECTION

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Title: Cotton Flea hopper Herbivory on Cotton Squares Induces Plant Volatile Emissions that Repel Conspecifics.

Author: Malek A. Alwedyan, Anjel M. Helms, John M. Grunseich & Michael J. Brewer

Abstract: The cotton fleahopper, *Pseudatomoscelis seriatus*, is a piercing-sucking insect that feeds on several plant species, including squares (pre-floral buds) of upland cotton, *Gossypium hirsutum*, causing square abscission and yield reductions. Current control of cotton fleahoppers relies on pesticide applications, but there is growing interest in using chemical ecology to develop more sustainable methods for integrated pest management. Herbivore foraging behavior is often mediated by plant-produced volatile organic compounds (VOCs), which can serve as attractants or repellants during host-plant selection. This study aimed to evaluate the influence of cotton fleahopper herbivory on VOC emissions from cotton squares under field conditions and to investigate the behavioral responses of conspecific insects to these VOCs. Using dynamic headspace sampling, we identified seven VOCs emitted from cotton squares, with three compounds emitted in higher abundance following cotton fleahopper herbivory: (E)-β-ocimene, (E)-β-caryophyllene, and (E)-β-farnesene. The total emission of VOCs from squares with cotton fleahopper herbivory was greater than non-damaged (control) cotton squares. Using dual choice olfactometer assays, we found that adult cotton fleahoppers preferred VOCs from non-damaged squares compared to VOCs from squares with conspecific herbivory. Furthermore, cotton fleahoppers were attracted to synthetic (E)-β-ocimene but repelled by synthetic (E)-β-caryophyllene or the combination of (E)-β-ocimene and (E)-β-caryophyllene. Our findings suggest that cotton VOCs influence cotton fleahopper foraging, and that compounds identified in this

study have potential for development as lures or repellants to use in integrated pest management.

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Title: Residual-resistance effect of two known QTLs in cotton genotypes on *Meloidogyne enterolobii* reproduction.

Authors: Caio F. de Barros Souza, Nelson Dias Suassuna, Vanessa S. Mattos, Ana L. Porto Cruz, Juvenil E.

Abstract: *Meloidogyne enterolobii* is not described as a major concern in cotton production, but a new race of this nematode, recently reported in Brazil and the USA, can cause damage to this important crop. Genetic resistance is a promising approach to manage root-knot nematodes (RKN). This study aims to identify in cotton germplasm sources of resistance to *M. enterolobii* that exhibit resistance to *M. incognita*. In this study, 18 accessions including *Gossypium hirsutum* (Upland cotton), *G. barbadense* (Pima cotton), interspecific hybrids, and *G. arboreum* were examined for their susceptibility or resistance to *M. enterolobii*. The experiment involved eight plants of each genotype under glasshouse conditions and was repeated at two different times. The inoculations were made with 10 000 *M. enterolobii* eggs and, after a period similar to field conditions (120 days), the following variables were evaluated: gall index, egg mass index, total number of eggs (g root)$^{-1}$ and the reproduction factor (RF). The susceptible control, 'FM 966', displayed high reproduction factor (RF: 86.88-102.20) in both experiments, indicating the aggressiveness of the *M. enterolobii* cotton population (race 2). Upland genotypes and Upland×Pima hybrids exhibited resistance levels ranging from moderate partial resistant (MPR) to partial resistant (PR), and all *G. barbadense* genotypes were classified as susceptible, except 'Tanguis' and 'Pima California', which were MPR. The *Gossypium arboreum* genotype was considered susceptible in both experiments. Despite the virulence of *M. enterolobii* race 2, some cotton genotypes used in our experiments with RKN resistance QTLs (quantitative trait loci, *qMi-C11* and *qMi-C14*) demonstrated a significant partial resistance (*ca* 80%) in reducing the final high nematode population after 120 days of inoculation. Our study highlights the importance of selecting residual resistance effect to *Meloidogyne* spp. on cotton after more nematode cycles to show the final nematode population reduction to mitigate the impact of *M. enterolobii* on the cotton crop.

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Title: Phenology and monitoring of lepidopteran pests in cotton agroecosystems of Beshariq district, Fergana Valley.

Author: A.Yoqubov, A.Samijonov

Abstract: The cotton (*Gossypium spp.*) agroecosystems in Besharik district of the Fergana Valley are vulnerable to infestation by several Lepidoptera species, including *Helicoverpa armigera*, *Spodoptera litura*, and *Agrotis segetum*. This study, carried out during the 2023–2024 growing season, aimed to assess the diversity, population dynamics, and seasonal activity of major lepidopteran pests under regional agro-climatic conditions. Field surveys, pheromone traps, and mercury vapor light traps were used to monitor pest populations, supported by soil sampling and meteorological data analysis. Results demonstrated distinct temporal population peaks for each species, with *H. armigera* showing the highest activity during flowering and boll development stages, *S. litura* in late summer, and *A. segetum* during early seedling stages. Pest abundance was strongly influenced by environmental variables, particularly temperature and humidity. The integration of pheromone and light trap data provided robust insights into species phenology and highlighted the importance of implementing region-specific, ecologically based integrated pest management (IPM) strategies to sustain cotton production in the Fergana region.

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Title: Overexpressing *CrSMT* disrupts the growth and development of herbivorous insects by changing the composition of sterols in cotton.

Author: Guoqing Lu, Yuntao Liu, Wenfang Guo, Peilin Wang, Lida Han, Xiaofeng Su, Hongmei Cheng, Huiming Guo

Abstract: Herbivorous insects cause substantial losses in cotton production worldwide. To resolve insect resistance and environmental pollution challenges, an innovative and eco-friendly strategy for pest management is needed. Insects acquire sterols from dietary sources because they cannot endogenously synthesize them *de novo*. *CrSMT*, a sterol methyltransferase gene, can alter sterol profiles. We introduced *CrSMT* into cotton (*Gossypium hirsutum*) to modify sterol content. This has enabled the investigation of the potential of *CrSMT* in pest management. RESULTS- *CrSMT*-transgenic lines were generated *via Agrobacterium*-mediated transformation, and CrSMT was successfully expressed in the transgenic lines L17 and L25. The proportional expression of the three main phytosterols was altered in transgenic cotton. RNA sequencing results showed that numerous pathways associated with insect resistance were enriched in the L17 and L25 transgenic lines, and these pathways contribute to the ability of plants to produce large quantities of volatile secondary metabolites, helping them build defense responses against herbivorous insects. *Spodoptera litura* preferred

R15 (wild-type) to L17 and L25 leaves in selective and non-selective feeding assays. Feeding experiments revealed that growth and development were delayed in *S. litura* fed transgenic cotton. Similar results were obtained for *Apolygus lucorum* and *Helicoverpa armigera*. Larval growth and development were delayed, and the length significantly decreased. In addition, the mortality rate of *A. lucorum* increased. CONCLUSION- The results of functional and molecular mechanism analyses of *CrSMT* overexpression in cotton indicate that *CrSMT* transgenesis is a promising broad-spectrum and eco-friendly insect-resistance strategy that can alter the sterol content of plant tissues without adverse effects on plants. © 2025 Society of Chemical Industry.

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Title: Synergizing Genetic Resistance and Antibiotics to Combat Xanthomonas Blight in Upland Cotton.

Author: Usman Arshad, Muhammad Usman, Salma Malik, Ayesha Khalid, Zia Ullah Ashraf, Saima Yousaf, Muhammad Ehetisham-ul-Haq, Huma Abbas, Muhammad Huzaifa Tanveer, Amjad Abbas

Abstract: Cotton (Gossypium hirsutum) is an important crop in Pakistan that is used to get fiber and many other industrial products that are helpful in making the country's economy better. Cotton is attacked by the Xanthomonas axonopodis pv. malvacearum (Xam) causes the bacterial blight disease, which is a major worldwide cause in every country. Five different isolates of Xam were used after biochemical characterization and 48 cotton genotypes were screened in the field against Xam and evaluated on the basis of morphological and physiological traits. Out of 48 cotton genotypes, none showed an immune response, only 3 genotypes showed a resistant response, 13 genotypes showed a tolerant response, 24 were susceptible to Xam and 7 genotypes were highly susceptible. Two different antibiotics, Tetracycline and Ampicillin were also tested in vitro on 5 isolates as well as In planta against one susceptible genotype at six different concentrations for their efficacy. In vitro test was checked through a spectrophotometer. Tetracycline was found to be most effective even at low concentrations. The susceptible genotype (CIM-591) showed a tolerant response on the application of tetracycline at low concentrations in the field but showed resistance at high concentrations.

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Title: First Report of Fusarium oxysporum f. sp. vasinfectum VCG 0114 (Race 4) Inciting Wilt in Tetraploid Cotton from India.

Author: Anil Kumar Saini, Shubham Saini, Satish Kumar Sain, Anil Kumar, Jagdeep Singh, Karmal Singh, Anil Jakhar, Shiwani Mandhania, Somveer Nimbal, Sandeep Kumar, Minakshi Jattan, Shubham Lamba, and Deepak Kumar

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Title: Salicylic acid-induced defense responses against a newly identified cotton pathogen, *Pantoea vagans.*

Author: Muneeb Anwer, Muhammad Waqas Azam, Muhammad Taimoor Shakeel, Anam Moosa , Hongwei Zha

Abstract: Bacterial blight of cotton is a severe disease that significantly impacts cotton production worldwide. In 2022, cotton (*Gossypium* spp. plants exhibiting angular leaf spots, necrotic lesions, and blackened stems were observed in fields across Bahawalpur, Punjab, Pakistan. Pathogen isolation from symptomatic plants yielded *Pantoea vagans* (strains CPVB#1, CPVB#2, and CPVB#3), identified through morphological, biochemical, and molecular analyses. Molecular identification using 16S rRNA sequencing (GenBank Accession Nos. OQ925871, OQ925897, OQ925910) revealed high sequence similarity (99.8 %, 98.59 %, and 97.78 %) to *Pantoea vagans* reference strain *MN661279*. Further confirmation was achieved via multilocus sequence analysis (MLA) of *fusA* (OR184128–OR184130) and *leuS* (OR184131, OR188816, OR188817) genes, confirming the close genetic relationship. Our research revealed that, for the first time in Pakistan, *Pantoea vagans* is causing bacterial blight in cotton, according to our knowledge. To control bacterial blight in cotton, the efficacy of salicylic acid (SA) as a sustainable control method was also evaluated under greenhouse conditions. SA treatments at 0.5 mM, 1.0 mM, and 1.5 mM reduced disease severity significantly, with 1.5 mM SA achieving the greatest suppression (82.3 %). In addition to lowering disease severity, SA treatments increased total phenolic content and enhanced the activity of enzymes that are related to defense mechanisms, including CAT, POD, SOD, PAL and PPO with maximum enzyme activity observed four Days post-treatment. These results demonstrate the potential of SA as an eco-friendly and effective management strategy for bacterial blight in cotton. Further research is warranted to investigate the epidemiology of *Pantoea vagans* and develop integrated approaches to mitigate its impact on cotton production.

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Title: Response of cotton cultivars with varying maturity traits to cotton fleahopper (Hemiptera: Miridae) feeding.

Author: Malek A Alwedyan , Anjel M Helms , Michael J Brewer

Abstract: Cotton fleahopper, Pseudatomoscelis seriatus Reuter (Hemiptera: Miridae), is an early season pest of upland cotton, Gossypium hirsutum L. Feeding damage from this pest causes square abscission. The response of commercial cotton cultivars with varying maturity traits to cotton fleahopper feeding was assessed. The hypothesis was that feeding affects early and late-maturing cultivars differently in maturity delays and yield. Field experiments with natural and artificial infestations were conducted in Corpus Christi, TX. For the natural infestation experiment, 4 cultivars (DP 2020 B3XF, DP 2012 B3XF, PHY 332 W3FE, and PHY 545 W3FE) were assigned to main plots, with subplots either sprayed or not sprayed with thiamethoxam insecticide to control cotton fleahopper early in the season. The artificial infestation experiment used 2 cultivars (DP 2020 B3XF and PHY 545 W3FE) as main plots, with subplots infested to or not infested with cotton fleahopper using single square caging. In the no-spray subplots of the natural infestation experiment, cotton fleahopper feeding increased square abscission, leading to yield loss and delayed boll maturity, especially in cultivars classified as late-maturing. Early maturing cultivars consistently showed faster boll opening regardless of cotton fleahopper. Artificial infestation experiments further confirmed increased square abscission, reduced boll numbers, and lower lint weights when infested with cotton fleahopper. Early maturing cultivars are more resilient and may be particularly useful in areas with high cotton fleahopper pressure, especially when scheduling an early harvest is desirable.

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Title: Blooming resilience: transcriptomic insights into cotton flower responses to boll weevil infestation.

Author: Nardeli, S. M., de Freitas, A. L. A., Arge, L. W. P., Macedo, L. L. P., Ribeiro-Alves, M., Corrêa, R. L., Alves-Ferreira, M.

Abstract: Cotton plants undergo a drastic transcriptional reprogramming after cotton boll weevil infestation, modulating several defense pathways to cope with the damage. The global demand for cotton fiber continues to rise, but pests and pathogens significantly hinder cotton production, causing substantial losses. Among these, the cotton boll weevil (Anthonomus grandis) is one of the most destructive pests. To investigate the molecular responses of cotton (Gossypium hirsutum) to boll weevil infestation, we evaluated the global gene expression of floral buds using mRNA-seq. Additionally, we analyzed the expression of non-coding RNAs, including microRNAs (miRNAs) and long intergenic non-coding RNAs (lincRNAs). Infestation by cotton boll weevil larvae triggered a rapid and drastic transcriptional reprogramming, with 1,656 and 1.698 genes modulated after two and twelve hours, respectively. Gene ontology enrichment analysis revealed significant regulation of defense-related and developmental processes, including photosynthesis, primary metabolism, and cell organization. Transcription factor families such as ERF, WRKY, GRAS, and NAC were strongly affected, highlighting their roles in coordinating defense responses. The

jasmonate pathway showed intensive modulation, alongside secondary metabolite pathways like terpenoids and phenylpropanoids, which contribute to plant defense mechanisms. Non-coding RNAs also played a critical role in the response. We identified 921 unique known and novel miRNAs, with 36 modulated by the infestation, and predicted 98,850 putative lincRNAs, several of which were differentially expressed. Understanding the genetic and molecular mechanisms underlying cotton's defense against boll weevil, particularly during early infestation stages, is vital for developing biotechnological strategies to reduce pest damage. Our findings provide critical insights to enhance cotton resilience against herbivores.

PLANT BREEDING AND GENETICS

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Title: Genome-Wide Profiling of WRKY, HSC, and ProDh Gene Families and VIGS-Mediated Functional Analysis of Negative Regulators of Cotton's Stress Response to Drought, Heat, and Whiteflies.

Author: Mariam Akhtar, Rubab Zahra Naqvi, Muhammad Jawad Akbar Awan, Ifrah Imran,

Abstract: Biotic and abiotic stress are fundamental contributors to restricting cotton yield and performance. Comprehension of molecular mechanisms behind these responses is necessary for elevating stress resistance. Genome wide profiling classified 100 WRKY, 63 HSC, and 10 ProDh family proteins identified in *Gossypium hirsutum* based on conserved domains and motif, and phylogenetic analysis. In the present study *HSC70-1*, *WRKY27*, and *ProDh* were characterized as negative stress regulators of heat, drought, and whiteflies and their functional analyses were performed to validate the roles of these genes in modulating the intensity of stress response and defense mechanism via Virus-Induced Gene Silencing (VIGS) using foliar sprays – a novel approach for transient gene silencing in cotton. Downregulation of *HSC70-1* resulted in strong resilience to drought and heat stress. *WRKY27* was the strong negative modulator of whiteflies and heat, and *ProDh* silenced plants showed susceptibility to all stresses. The relative expression of some other genes, *BBX18*, *GASA5*, *MAP3K65*, and *CKX1*, involved in these stress related pathways was also quantified. *BBX18* and *GASA5* were found downregulated in all silenced plants whereas *MAP3K65* showed upregulation in *HSC70-1* silenced plants while *CKX1* was upregulated in *WRKY27* silenced plants. Overall, this study aims to provide the functional importance of down-regulators to make heat, drought, and whitefly tolerant plants.

Title: Studies on Combining Ability and Heterosis through Diallel Analysis in Cotton (Gossypium hirsutum L.).

Author: Karthickeyan S, P. Thangavel, N. Senthilkumar, C. Kathirvelu , Vignesh T

Abstract: The study aimed to investigate the genetic mechanisms influencing yield and fibre quality traits in cotton (Gossypium hirsutum L.) using a diallel mating system, and to identify superior hybrids with potential for cotton breeding programmes. Study Design: The study was based on a full diallel mating design involving seven parental genotypes and their hybrids. Place and Duration of Study: The field experiment was conducted at the Department of Genetics and Plant Breeding, Annamalai University, Tamil Nadu, India, over two consecutive growing seasons from 2021 to 2023. Methodology: A total of 42 hybrids were developed through a diallel mating system using seven genetically diverse cotton genotypes, along with a standard check variety, Suraksha. The genotypes were evaluated in a randomized complete block design (RCBD) with three replications. Data were recorded on key yield attributes and fibre quality parameters. General Combining Ability (GCA), Specific Combining Ability (SCA), and heterosis analysis were conducted to identify superior parental combinations. Results: Significant genetic variability was observed among parents and hybrids for all studied traits. The hybrids Subiksha × Anjali, Anjali × Suraksha, Suraksha × Sunantha, and LRA 5166 × Sunantha exhibited high SCA effects and better heterotic performance for yield and fibre quality traits. These combinations also showed promising potential in terms of boll number, boll weight, lint index, fibre length, strength, and micronaire values. The analysis indicated both additive and non-additive gene actions influencing the traits. Conclusion: The identified hybrids showed superior performance and possess desirable genetic potential for yield and fibre quality improvement. These results provide valuable insights for future cotton breeding programmes aiming to develop high-yielding, quality fibre cultivars.

Title: Transcriptome dynamics along with expression analysis of key genes involved in fiber development between Gossypium barbadense and Gossypium darwinii.

Author: Allah Ditta, Xiaoyan Cai, Muhammad Shehzad, Sajid Fiaz, Yanchao Xu, Yuqing Hou, Zunaira Anwar, Aqsa Ijaz, Najla B. S. Al-Saud, Fang Liu,

Abstract: The transcriptome profiling for underpinning the role of key genes controlling formation of fiber in cultivated *Gossypium barbadense* compared to wild allotetraploid cotton *Gossypium darwinii* which remained less investigated. Owing to excellent fiber quality of both *Gossypium barbadense* and *Gossypium darwinii* and information obtained via Simple Sequence Repeat (SSR) markers, two lines: Xh-18 and *darwinii* 5–7 were selected for transcriptome sequencing during developmental stages i.e., fiber initiation, elongation, and secondary cell wall (SCW) biosynthesis followed by 0 day after anthesis (DPA), 5DPA, 10DPA, 15DPA and 25DPA, respectively. Twelve libraries of RNA-seq were generated and sequenced individually generating approximately 818 million clean reads of *Gossypium darwinii*. However, for *Gossypium barbadense* more than 844 million clean reads were recorded. The Pearson Correlation Coefficient (PCC) analysis results indicated that gene expressions for both *Gossypium barbadense* and *Gossypium darwinii* indicated more than 90% of the commonalities at the same stage of fiber growth. However, genes found among *Gossypium darwinii* at 5, 6 and 7 DPA and XH-18 at 10 and 25 DPA were found disimilar. The expression quantity of RNA sequencing data, 31 genes were found common throughout all stages of DPAs in *Gossypium darwinii* 5–7 whereas, 377 genes were common in *Gossypium barbadense* XH-18 at 0, 5, 10, 15, 20, and 25 DPA stages of fiber development. Three genes *XLOC_080616* (*LTPG2_ARATH/ NLTL2_ARATH*; GPI-anchored 2 non-specific lipid transfer protein, like *At2 g13820*), *XLOC_065471* (*LPAT2_ARATH/LPAT2_BRAOL 1-acyl-sn-glycerol-3-phosphate acyltransferase2*), and *XLOC_077416* (uncharacterized protein) shown up-regulated expression during 15 and 20 DPA for both *Gossypium barbadense* and *Gossypium darwinii*. It will also explore the possible role of *Gossypium barbadense* DNA segment associated with development of fiber quality. Furthermore, this research will decipher the underlying process of fiber development and the possible role of genes for fiber formation in both Sea Island and wild cotton species.

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Title: Quantitative Genetic Analysis of Cotton Traits: GCA, Gene Action and Proportion of Variance via Line × Tester Design.

Author: Aneeq ur REHMAN, Azeem Iqbal Khan, Iqrar Ahmad Rana, Muhammad Tehseen Azhar

Abstract: Cotton plant faces various biotic and abiotic stresses from its environment and among these stresses, high temperature is a limiting factor to cotton productivity. The temperature has increased gradually worldwide due to climate change. Therefore,

there is a dire need to identify genotypes against high temperature stress. For this purpose, an experiment was designed to identify high temperature resilient genotypes. The hybrids were made on already identified parents under line × tester pattern and then F_0 seeds were sown in two planting dates, early sowing for high temperature stress and late sowing for control. Hybrid population was assessed on the basis of general combining ability. The physiological parameters namely pollen germination, pollen viability, CMT, biochemical assays namely proline, POD were estimated according to recommended protocol at the onset of flowering in both conditions. Additionally, various yield parameters were also observed at harvesting. The data collected were analyzed by using various biometrical approaches to determine the presence of genetic diversity and response of genotypes under both treatments.

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Title: Three Decades of Cotton Improvement: Research and Progresses in Ethiopia.

Author: Merdasa Balcha, Donis Gurmessa, Samuel Damtew and Arkebe Gebregziabher

Abstract: Scientific research on cotton in Ethiopia started in 1964, following various earlier attempts. The major objectives of the cotton research have been to develop and promote high-yielding cotton cultivars with superior fiber quality, along with improved production management packages. Thus, the purpose of this paper is to present the cotton breeding progresses made over the past three decades. Introduction of germplasm and hybridization of selected parental lines have been considered as the priority approaches to enhance cotton production in the country. The introduced germplasm has been utilized directly in variety trials, and as parental lines for hybridization. Subsequently, crossing and evaluation of segregating populations (F2-F6) are being done every year. The germplasm enhancement, subsequent variety evaluation and verification programs over the last six decades resulted in releases of 44 improved new cotton varieties in which 32 cotton varieties were released or registered in the last three decades. In research station trials, the productivity of these varieties in irrigated areas has increased from 2.43-ton ha-1 (Ionia) to 5.4 ton ha-1 (Arkebe) in seed cotton yield. Another important trait, namely, ginning outturn ranged from 29.0% (VBCH 1527) to 46.5% (Arkebe). Besides conventional research achievement, two single gene (Bt) varieties and one triple genes (Bt-Gt) of cotton variety (ACH3) registered during 2018 and 2025 cropping season, respectively, following standard institutional procedures and the biosafety law of the country under close supervision of the Ethiopian Environmental Protection Authority.

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Title: Transgressive segregation in cotton (Gossypium hirsutum L.) affects the combining ability and heterotic patterns.

Author: Fatma Polat, Volkan Mehmet Çınar & Aydın Ünay

Abstract: The inheritance of the studied traits in cotton breeding studies directs the selection method, and it is crucial to identify suitable parents and promising hybrids to be transferred to the next generations. Ten F_2 hybrid populations generated by line × tester mating design were compared with their parents and F_1 hybrids for seed cotton yield per plant, ginning out-turn, fiber length, fiber fineness, and fiber strength. The general/specific combining ability variance ratio in F_1 and results of a minimum norm quadratic unbiased estimation indicated that the dominant gene effect for seed cotton yield, additive gene effect for ginning out-turn and fiber fineness, both dominant and additive gene effects for fiber length and fiber strength were greater. Significant correlation coefficients between F_1 and F_2 hybrid performance and general combining ability effects for ginning our-turn and fiber length confirmed additive gene effects in the control of these traits. Although F_2 populations were higher than their parents and lower than F_1 populations regarding seed cotton yield and fiber strength, F_2 populations had the finest fibers. As a result of the combined evaluation of average performance, general combining ability effects, and predicted additive effects for parents, Fiona and Gloria for ginning out-turn, İpek-607 for fiber length, Özbek-100 for fiber fineness, and Flash for fiber strength were the best combiners. Claudia × Özbek-100 was determined as the most promising F_1 hybrid combination for both hybrid variety breeding and transfer to the next generations in terms of all traits. Gloria × Flash, Claudia × Özbek-100, and Gloria × Özbek-100 hybrid combinations within the F_2 populations should be transferred to the next generations by applying the bulk method.

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Title: Comprehensive hybrid evaluation: integrating diallel analysis and biplot techniques for genetic insights on intra-hirsutum cotton hybrids.

Author: Puja Mandal & Rajesh S. Patil

Abstract: Hybrids are the most prospective plant types in cotton. To this end, heterosis breeding programs have developed hybrids and exploited high heterotic effects, which provide superior genetic combinations and segregating populations on generation advancement. The objectives of this study were to identify the parents with high GCA and hybrids with high SCA, interpret combining ability from biplots and seek notable conclusive results from heterosis, per se performance and a combination of biplot and numerical diallel approaches. The experiment aimed to evaluate ten parents and ninety F_1 hybrids obtained by diallel crossing for seed cotton yield (SCY) and yield-attributing traits. Analysis of variance, diallel analysis, correlation and multiple-regression analyses were performed, which pointed out the major yield contributing and predictor traits,

number of bolls per plant (NBP) and boll weight per plant (BW). Most of the traits exhibited lower GCA/SCA ratios, thereby indicating the preponderance of non-additive gene action. A significantly positive correlation was found between SCY and NBP in both parental and hybrid populations with r = 0.79 and r = 0.70, respectively. Stepwise multiple regression further aided in eliminating variables and generating a regression equation (R^2 = 0.654) with only the variables that are most potent for predicting the dependent variable, SCY. Biplot analyses were conducted for these trait variables (NBP and BW) along with SCY. From the integrated biplot and numerical diallel analyses, the genotypes ESS-12, GBHV-200, ESS-5 and CPD-1652 were found to exhibit high GCA for SCY, NBP and BW. The hybrids GBHV-200 × CPD-1652 and RAH-1075 × ESS-12 could be identified as the best hybrids as a result of the combined study. The study provides a more comprehensive analysis of a large dataset generated from diallel analyses. Also, when biplots are combined with the numerical approach, it provides more robust results and aids in the selection of hybrids and parents with better performance and combining abilities.

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Title: Centromere-size reduction and chromatin state dynamics following intergenomic hybridization in cotton.

Author: Jinlei Han, Guanjing Hu, Yan Dai, Xin Zhang, Jingjing Initialing Zhuiqin Xu,Qi Chen, Xiaobing Kou,

Abstract: Centromeres are pivotal for accurate chromosome segregation, yet their regulation and evolutionary dynamics remain poorly understood. Here, we investigate centromeres of the diploid species *Gossypium anomalum* (Ga, B-genome) that were transferred into tetraploid cotton *G. hirsutum* (Gh, AD-genome) as either an additional or integrated chromosome, as well as in synthetic allohexaploid (AABBDD) lines. We demonstrate consistent size reduction for all Ga centromeres in the Gh background. Histone modification profiling across 10 marks revealed heightened levels of both active and repressive chromatin marks within the Ga centromeres when transferred into the Gh background, particularly for H3K36me2. The centromeric histone modification perturbation extended into pericentromeric regions, with variable CENH3-binding domains consistently exhibiting a more pronounced increase in histone modification levels compared to stable centromere regions, highlighting the role of histone modification elevation in centromere dynamics. In addition, we observed enhanced chromatin accessibility and the presence of non-B-form DNA motifs, such as A-phased DNA repeats within stable centromere domains that are correlated with centromere stability. Hi-C analysis reveals a reorganized 3D chromatin architecture within the introgression line centromeres, including the formation of new topologically associating domains linked to H3K36me2 dynamics, emphasizing the importance of H3K36me2 in centromere organization. Together, these findings elucidate epigenetic mechanisms

underlying centromere composition following intergenomic hybridization and allopolyploid formation, offering insights into centromere evolution in plants and its myriad epigenetic and potentially functional dimensions.

PLANT BIOTECHNOLOGY

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Title: Recent Advances in Cotton Transformation and Genome Editing Techniques: The Prospects and Challenges.

Author: Oluwaseun Olayemi Aluko, Vincent Ninkuu, Zhixin Liu, Aizhi Qin, Hao Liu, Jincheng Yang, Mengke Hu, Xiongfeng Ma, Xuwu Sun

Abstract: Genetic transformation in cotton facilitates the integration of stress-resilient traits, contributing to improved abiotic and biotic stress tolerance. Consequently, sustained efforts to optimise transformation and regeneration protocols are critical for advancing cotton genetic improvement and boosting yield potential. This review discusses the recent advances in cotton plant transformation, in cognisance of the prospects and challenges characterising each technique and the variations in the transformation efficiency (TE) of specific explants. Furthermore, the mechanisms by which morphogenesis-related genes and other molecular cascades have been used to

improve the TE and regeneration of recalcitrant plant species are also addressed. Factors that affect the cotton transformation efficiency were also discussed. These updates could help cotton breeders design more effective strategies for transforming and regenerating recalcitrant plants.

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Title: Blooming resilience: transcriptomic insights into cotton flower responses to boll weevil infestation.

Author: Sarah Muniz Nardeli, Ana Luiza Atella de Freitas, Luis Willian Pacheco Arge, Leonardo Lima Pepino Macedo, Marcelo Ribeiro-Alves, Régis Lopes Corrêa, Maria Fatima Grossi-de-Sa & Marcio Alves-Ferreira

Abstract: The global demand for cotton fiber continues to rise, but pests and pathogens significantly hinder cotton production, causing substantial losses. Among these, the cotton boll weevil (*Anthonomus grandis*) is one of the most destructive pests. To investigate the molecular responses of cotton (*Gossypium hirsutum*) to boll weevil infestation, we evaluated the global gene expression of floral buds using mRNA-seq. Additionally, we analyzed the expression of non-coding RNAs, including microRNAs (miRNAs) and long intergenic non-coding RNAs (lincRNAs). Infestation by cotton boll weevil larvae triggered a rapid and drastic transcriptional reprogramming, with 1,656 and 1.698 genes modulated after two and twelve hours, respectively. Gene ontology enrichment analysis revealed significant regulation of defense-related and developmental processes, including photosynthesis, primary metabolism, and cell organization. Transcription factor families such as ERF, WRKY, GRAS, and NAC were strongly affected, highlighting their roles in coordinating defense responses. The jasmonate pathway showed intensive modulation, alongside secondary metabolite pathways like terpenoids and phenylpropanoids, which contribute to plant defense mechanisms. Non-coding RNAs also played a critical role in the response. We identified 921 unique known and novel miRNAs, with 36 modulated by the infestation, and predicted 98,850 putative lincRNAs, several of which were differentially expressed. Understanding the genetic and molecular mechanisms underlying cotton's defense against boll weevil, particularly during early infestation stages, is vital for developing biotechnological strategies to reduce pest damage. Our findings provide critical insights to enhance cotton resilience against herbivores.

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Title: Global landscape of protein phosphorylation during plant regeneration initiation in cotton (*Gossypium hirsutum* L.).

Author: Huihui Guo, Xiushan Qi, Li Zhang, Haixia Guo, Fan Gao, Xindi Tian, Jianfei Wu, Tongtong Li, Tongdi Yan, Xiwang Cui, Jiawei Xu & Fanchang Zeng

Abstract: Phosphorylation is one of the most common post-translational modifications and is central to many cellular signaling events; however, little is currently known about the phosphorylation landscape during somatic embryogenesis (SE) for plant regeneration.Results- Here, we systematically analyzed the phosphoproteomic profile of three typical developmentally staged cultures of SE, non-embryogenic calli (NEC), primary embryogenic calli (PEC), and globular embryos (GE), in cotton (*Gossypium hirsutum* L.), the pioneer crop for genetic biotechnology applications. Our data revealed a total of 6301 quantifiable phosphorylation sites in 2627 quantifiable phosphoproteins from 5548 modified peptides, of which 1105 phosphoproteins (2147 sites) were differentially phosphorylated. Functional enrichment analyses revealed that differentially regulated phosphoproteins (DRPPs) were significantly enriched in DNA mismatch repair and peroxisome during callus embryogenic differentiation (PEC vs. NEC) and somatic embryo initiation (GE vs. PEC), respectively. Notably, six dynamic trajectory patterns of DRPP enrichment were observed. In addition, preferentially activated DRPPs with specific phosphorylation patterns were identified at different developmental stages. These DRPPs were mainly involved in hormone-responsive and photosystem events during initiation of plant regeneration. Conclusions- Overall, this study identified a series of potential phosphoproteins responsible for SE trans-differentiation and plant regeneration, providing a valuable resource and molecular basis for understanding the regulatory pathways underlying cell totipotency at the post-translational modification level.

SEED SCIENCE AND TECHNOLOGY

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Title: Phosphatidic acid accumulation in response to extended cold water imbibition disrupts membrane structure that inhibits germination of cotton (*Gossypium hirsutum* L.) seeds.

Author :Lakhvir Kaur Dhaliwal, Bandana Osti, Rosalyn B. Angeles-Shim

Abstract: This work aimed to understand glycerophospholipid regulation in cotton seeds that imbibed under cold stress and determine how such regulation affects overall germination performance. Lipidomics analysis showed that imbibition under cold stress

drastically increase phosphatidic acid (PA) levels, while significantly reducing the content of other membrane lipids including phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, phosphatidylinositol and phosphatidylserine in seeds. The observed PA accumulation was associated with the upregulation of genes encoding phospholipases that catalyze PA synthesis through the hydrolysis of other membrane lipids. Alongside modifications in glycerophospholipid contents, the cold-imbibed seeds leaked excessively and germinated poorly, suggesting deleterious effects of cold-induced PA accumulation. Exogenous PA treatment of cotton seeds demonstrated a time- and concentration-dependent inhibition of germination, whereas suppression of phospholipase D activity under cold stress attenuated electrolyte leakage and improved seed germination. Together, these support our hypothesis on the harmful effects of excessive PA on seed germination. PA is conical and has a structural propensity to induce negative curvatures on membranes. Under cold stress, negative curvatures exacerbate cellular leakage which is injurious to germinating seeds. Microscopic analysis of PA-treated plant tissue indicates disruption in membrane structure that increased with increasing concentrations of PA. Based on our findings, we propose that under cold stress, germinating seeds rapidly synthesize PA via the phospholipase pathway to signal distress. With prolonged cold-water imbibition, however, induction of negative curvature due to PA accumulation combined with the breakdown of other membrane lipids disrupts membrane integrity, exacerbating cytoplasmic leakage and causing poor germination in seeds.

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Title: Multivariate Analysis of Elite Bt Cotton Genotypes for Seed Cotton Yield and Fiber Quality Traits Under Semi-Arid Conditions.

Author: Muhammad Younas, Muhammad Zafar, Babar Hussain Babar, Muhammad Jamil, Muhammad Kashif Munir, Muhammad Mahmod Iqbal, Ali Aziz Awan

Abstract: Cotton production in semi-arid regions like Pakistan is constrained by water scarcity and heat stress, resulting in yields significantly lower than global leaders like China. This study evaluated ten elite Bt cotton genotypes (BH-318, BH-348, BH-224, BH-563, BH-405, BH-410, BH-606, BH-248, BH-184, CIM-600) for yield, fiber quality, and associated traits under semi-arid conditions at the Cotton Research Station, Bahawalpur, using a Randomized Complete Block Design with three replications. ANOVA confirmed significant genotypic variation ($p \leq 0.01$) for plant height, nodes, sympodial branches, photosynthetic rate, fiber strength, and yield, with BH-348 and BH-224 achieving the maximum yields (2169.1 kg/ha in Cluster 1). Correlation analysis revealed positive associations between yield and nodes ($r = 0.741^{**}$), plant height ($r = 0.548$), and sympodial branches ($r = 0.416$), while PCA showed PC1 (29.4%) and PC2 (22.6%) explaining 52% of the variation, driven by yield and fiber quality traits, respectively. Cluster analysis grouped genotypes into two clusters, with Cluster-1 (BH-318, BH-348, BH-224, BH-606, BH-410, BH-248) excelling in yield and Cluster-2 (BH-

563, BH-405, BH-184, CIM-600) in fiber quality (fiber length: 28.9 mm, fiber strength: 35.4 g/tex). The findings from the present multivariate analyses highlight BH-348 and BH-224 as ideal for yield-focused breeding and BH-563 for quality improvement, offering strategies to enhance cotton productivity and quality in semi-arid environments.

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Title: Effect of different bacterial treatment strategies on the damping-off disease control in cotton seedlings.

Author:Karima Ali Sayed; Ashraf M Essa; Amany Reyad

Abstract: Bacillus halotolerans, that was isolated from Gossypium barbadense and molecularly identified using 16S rRNA gene sequencing analysis, was tested for its antifungal potential in cotton seedlings infected with the phytopathogenic fungus Rhizoctonia solani. The antifungal activity of the rhizobacterial strain was studied under greenhouse conditions. In soil contaminated with R. solani, the bacterial strain was applied in three replicates as a seed presoaking, seed coating, or soil drench. Evaluating their efficacy based on plant growth and disease suppression. According to our findings, seed coating and the soil drench treatments were more effective than the seed presoaking. Significant improvements in seed emergence, 26, 34, and 40 % increase for seed presoaking, soil drench, and seed coating. Comparing the treated plants to the uninoculated ones, the fresh and dry weights of the soil drench group increased significantly by 21.6 and 23.4%, respectively. While 45.1 and 33.7% for seed presoaking group. Also 51.3 and 47.87% for seed coating group. Furthermore, it appeared that the treated seedlings' levels of the enzymatic and non-enzymatic antioxidants, glutathione reductase, superoxide dismutase, ascorbate peroxidase, catalase, glutathione, and ascorbic acid were positively inducted specifically for seed presoaking group. The total protein and carbohydrate contents of the different treatments varied greatly with the highest levels in the soil drench group. While the highest levels of total phosphorus and chlorophyll_a were observed in the seed coating group. GC-MS analysis showed that the bacterial supernatant included a number of antifungal bioactive compounds, including di-ethyl phthalate and 2,4-di-tertbutyl phenol.

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Title: Method of using/applying a keratin hydrolysis peptide solution to promote growth and development of cotton seedling.

Inventor: Jenn Wen Huang, Yi-Chiao CHAN, Yu-Lun LIU, Nai-Hua YE

Current Assignee: CH BIOTECH R&D Co Ltd201, United States, Patent application publication US Patent App. 18/409,792, 2025

Abstract: Present invention teaches the method of using a keratin hydrolysis peptide ("KHP") solution to promote the development and growth of cotton seedlings. By selectively choosing specific weights of feathers and water, and treating the mixture to a high-temperature high-pressure hydrolysis process, the resulting solution is confirmed to contain at least 253 peptides and, at seedling stage and early growth stage, applied to the soil around the cotton plants, and sprayed to the young plants. Optionally, the KHP solution can be diluted by water, as disclosed in the specification, before administering as taught herein.

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Title: Chemical Characterization and Comparative Analysis of Alkyd resins from Gossypium Hirsutum Seed Oil Using Maleic and Phthalic Anhydrides.

Author: Ibrahim, Sulyman O.; Kenneth, Stephen; Abdulkadir, Fatimah R.; Hamid, Abdulmumeen A.; Ibukun, Olamilekan J.; Zubair, Marili F.; and Atolani, Olubunmi

Abstract: Oilseeds are a significant source of raw materials for industry. Because of the overuse of edible fixed oil of plant origin in cosmetics, paints, and other manufacturing industries, the price of edible oils has increased, creating a considerable imbalance between the domestic and industrial markets. Local production of industrial intermediates such as alkyd resins is necessary to lessen import dependency. Alcoholysis methods were used to prepare alkyd resin from under-utilized seed oil of Gossypium hirsutum using maleic and phthalic anhydride. The prepared alkyd resins were characterized, and their physiochemical and chemical stability were compared to industrial grade commercial alkyd resin. Alkyd resin prepared from seed oil and maleic anhydride (COTMA) has the highest yield of 70.44%, compared to the one made from phthalic anhydride (COTPA) at 58.88%. The two alkyds show better total solids between 82.68–85.75% compared to 51.56% for commercial alkyd resin indicating possibilities of getting paint from the prepared alkyd. The alkyd formed also shows comparable drying time (60–75 mins) relative to the commercial counterpart (70 mins). Fourier-transform infrared (FT-IR), UV-Visible and 1H Nuclear Magnetic Resonance (1H NMR) spectroscopy were used to characterize the modified products (confirming a successful reaction). The study shows G. hirsutum seed oil can replace dietary vegetable oils currently used in the vegetable oil-dependent industries.

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Title: Diversity in the Rubisco temperature response kinetics and photosynthesis among four linted cotton species.

Author: Demi Sargent , Spencer M Whitney , Katrina Broughton , Susan Y Jaconis , David T Tissue , Michael Bange , Warren C Conaty , Robert E Sharwood

Abstract: There is increasing urgency for more productive and resource-use-efficient crops to cope with changing climates. One possibility to improve crop productivity is to enhance photosynthesis. Here, we studied four linted cotton species (Gossypium hirsutum, G. barbadense, G. arboreum, and G. herbaceum) for diversity in the temperature response of Rubisco catalysis and impact on carbon assimilation. Compared with the model C_3 plant tobacco, each cotton Rubisco had a slower carboxylation rate (kcatc) and higher CO_2 affinity (lower $KC_{21\%O_2}$) in response to temperature, with the specificity for CO_2 over O_2 (Sc/o) of G. hirsutum Rubisco being thermally advantaged above 20 °C relative to tobacco. Consistent with high homology between the cotton species Rubisco large subunits, there was little difference in the response of kcatc or $KC_{21\%O_2}$ to temperature. However, at temperatures above 15 °C, the carboxylation efficiency (kcatc/$KC_{21\%O_2}$) of G. herbaceum Rubisco significantly exceeded that of G. hirsutum Rubisco by 23–29%, with the G. herbaceum enzyme predicted to support 20% higher rates of photosynthesis than tobacco Rubisco at 35 °C. Leaf-level photosynthetic measurements at 28 °C, however, showed no significant variation in the net photosynthetic CO_2 assimilation rates, stomatal conductance, transpiration rate, intrinsic water-use efficiency, or photosynthetic electron transport rates between each cotton species. Using the 'OptiFitACi' A/Ci model parameterized with cotton Rubisco and mesophyll conductance (gm) values, the maximum Rubisco carboxylase activity (Vcmax) was 20% lower in G. herbaceum leaves compared with G. hirsutum. However, the greater Rubisco kinetics of G. herbaceum did not confer higher leaf photosynthesis.

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Title: Enhancements in Cotton Fiber Length Phenotyping and Optimization of Weighted Gene Co-expression Network Analysis through Fiber Elongation Rate Metrics.

Author:Leidi Liu, Cheng Li , Feng Hu , Jingzhe Zhao , Roshan Zameer , Jingyao Li , Chengde Yu, Huazhong Shi

Abstract: Cotton fiber length is a crucial attribute that significantly affects yarn production and fabric quality, making it a primary focus in cotton breeding efforts. Both current and previous studies have indicated a lack of correlation between fiber length and gene expression dynamics, underscoring the importance of phenotyping fiber elongation. traditional methods for measuring fiber length, however, tend to be impractical and labor-intensive, particularly for developing fibers that are fragile and prone to twisting.

In this study, we present an innovative phenotyping method to measure the elongation of developing cotton fibers. Our key findings reveal a strong linear relationship between the total volume of fiber bundles and fiber length. This relationship allows for the straightforward estimation of the linear correlation coefficient from the final fiber length and the final volume of the fiber bundle within a boll. Upon measuring both the fiber bundle volume and fiber length, we discovered that their growth dynamics were well-represented by a logistic curve. Additionally, the expression dynamics of several newly identified genes demonstrated a significant positive correlation with the rate of fiber elongation.

This research marks an important advancement in quantifying gene expression dynamics and fiber elongation. We believe that measuring the elongation of developing fibers will greatly accelerate the development of high-quality cotton varieties and enhance our understanding of plant developmental biology.

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Title: Genetic Analysis in Upland Cotton for Fiber Quality Parameters.

Author: Bilal Ayub, Muhammad Mubashir Asim, Swaiba Rani, Naghina Kanwal and Awais Tariq

Abstract: Cotton is a major industrial fiber crop that is extensively grown worldwide and has a big impact on the political and socioeconomic problems that many nations face. That's why there is a dire need to develop cotton varieties with high fiber quality. The study will determine the combining ability effects of parental lines and crosses in upland cotton (Gossypium hirsutum L.) using line × tester mating design. The four lines Kehkashan, Tarzen, BS80, CRS-2, and four testers MNH-998, NS-131, AGC-2, and KZ-191 were crossed in line tester fashion to study the genetic analysis of different fiber quality traits in cotton. Four lines were crossed with four testers at the time of flowering in line × tester design in the glass house. Eight parents and 16 crosses (F1) were grown

in the field with three replications using a randomized complete block design. A significant GCA result was observed for Kehkashan and BS-80, showing that both lines combine well for fiber strength. Among testers, KZ-191 showed a highly significant GCA effect for fiber fineness, while MNH-998 showed highly significant GCA effects for fiber strength and fiber elongation. Tester NS-131 emerged as a good general combiner for fiber maturity and fiber elongation. The results showed that germplasm has the potential for the development of cotton varieties, and may be used in cotton breeding programs