GLEANINGS IN COTTON RESEARCH

DECEMBER 2023

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Preface

Information plays a vital role in just about everything we do in modern society. Today, the Internet is one of the most effective and efficient ways to collect information. The internet gives us the opportunity to connect with all kinds of different people and read news and information from all over the world.

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. Abstract follows the citation.

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

The guidance provided by Dr H B Santosh, Senior Scientist in this venture is highly appreciated.

We duly thank The Director, Dr Y G Prasad for providing the inspiration and support for this publication.

Suggestions are welcome for further improvement on cicrlib@yahoo.co.in.

Swati Dixit
Incharge Library

Chetali Rodge
Technical Officer (T5)

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AGRONOMY, SOIL SCIENCE AND PLANT PHYSIOLOGY

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Title: HDPS Cotton - Challenges and Opportunities in India

Author: R Gouthami, A. V. Ramanjaneyulu , U. Nagabhushanam , B. Ramprasad , J. Kamalakar and M. Yakadri

Imprint: Chronicle of Bioresource Management 2023, 7(4):061-065

Abstract: This article provides a concise overview of the high density planting system employed in cotton farming. The adoption of high density planting system in cotton cultivation has led to increased yields vis-a-vis traditional planting methods. While the benefits of embracing high density planting system are evident, there are several challenges that farmers encounter throughout the cultivation process, spanning from sowing to harvesting. However, through the selection of appropriate cotton cultivars, the implementation of tailored cultivation techniques and the incorporation of mechanization in high density planting system of cotton farming, these challenges can be effectively addressed.

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Title: Hybrid Bt cotton is failing in India: cautions for Africa

Author: Andrew Paul Gutierrez, Peter E. Kenmore & Luigi Ponti

Imprint: Environmental Sciences Europe, volume 35, Article number: 93 (2023)

Abstract: This paper reviews the ongoing failure of hybrid transgenic Bt (Bacillus thuringiensis) cotton unique to India. The underlying cause for this failure is the high cost of hybrid seed that imposes a suboptimal long-season low plant density system that limits yield potential and has associated elevated levels of late-season pests. Indian hybrid Bt cotton production is further complicated by the development of resistance to Bt toxins in the key pest, the native pink bollworm (Pectinophora gossypiella Saunders, PBW), resulting in increased insecticide use that induces ecological disruption and outbreaks of highly destructive secondary pests. Rainfed cotton production uncertainty is further exacerbated by the variable monsoon rains. While hybrid cotton produces fertile seed, the resulting plant phenotypes are highly variable preventing farmers from replanting saved seed, forcing them to buy seed yearly (i.e., market capture), and effectively protecting industry Intellectual Property Rights (IPRs). The lessons gained from the ongoing market failure of hybrid Bt cotton in India are of utmost importance to its proposed introduction to Africa where, similar to India, cotton is grown mainly in poor rainfed smallholder family farms, and hence similar private–corporate conflicts of interest will occur. Holistic field agroecological studies and weather-driven mechanistic analyses are suggested to help foresee ecological and economic challenges in cotton production in Africa.High-density short-season (HD-SS) non-hybrid non-genetically modified irrigated and rainfed cottons are viable alternatives for India that can potentially produce double the yields of the current low-density hybrid system.

3

Title: Farmers' Production Practices, Incidence and Management of Pests and Diseases, Extension Services, and Factors Limiting Cotton Production and Quality in South Africa.

Author: Malinga, L.N. and Laing, M.D.

Imprint: S. Afr. J. Agric. Ext. Vol. 51 No. 3, 2023: 79-99 10.17159/2413-3221/2023/v51n3a14462

Abstract: Cotton is one of the essential cash crops; however, several factors, such as low yields and pest and disease infestations, affect the production. In South Africa, cotton production has increased among small-scale farmers since the late 1990s. Although the crop is not new to South African farmers, no recent information reflects the current status of cotton production practices. A study evaluated farmers' production practices, the incidence and management of pests and diseases, extension services, and factors limiting cotton production and quality in South Africa. One hundred and forty farmers, mainly smallholder farmers, were interviewed during the 2017/18 growing season. Most farmers planted genetically modified (GM) cotton on less than 5 ha of cotton, with 96% planting under dryland. Most farmers neither practised conservation agriculture (95%) nor conducted soil analyses (87%). A mean cottonseed yield of 700 kg ha-1 was reported on dryland cotton, and 5 000 kg ha-1 was obtained from irrigated cotton. Most of the farmers (99%) harvested their cotton by handpicking. Farmers' pest knowledge was higher than their knowledge of different diseases. Most participants were unaware of nematodes (88%) or disease-resistant cultivars (74%), while 91% were aware of insect-resistant cultivars. Extension officers only mentored and supported many respondents (82%). Most farmers (93%) relied on pesticides to control cotton pests, and the rest (7%) used biological control. Climatic conditions (98%), labour costs (88%), and insect infestations (42%) were identified as the main constraints in cotton production. Although this study had a limited number of surveyed farmers, it gives some insight into their knowledge and challenges.

4

Title: Effect of Nitrogen Levels and Mepiquat Chloride on Yield and Economics of HDPS Cotton.

Author: K. Srikala, T. Prabhakar Reddy, K. Pavan Chandra Reddy and S. G. Mahadevappa

Imprint: International Journal of Environment and Climate Change Volume 13, Issue 11, Page 1960-1967, 2023

Abstract: A field experiment was conducted during Kharif, 2022 at Krishi Vigyan Kendra, Palem, to evaluate the effect of nitrogen levels and mepiquat chloride on the yield and economics of HDPS cotton. The experiment was laid out in a randomized block design with three replications. The results of this experiment revealed that application of T9: 125% RDN applied in splits at 15, 30, 45, 60, 75 DAS along with 2 sprays of 5% mepiquat chloride at 45 and 60 DAS recorded significantly higher number of bolls plant-1 (11.7), boll weight (4.49 g) and seed cotton yield (2484 kg ha-1). In terms of economic analysis, this treatment also exhibited the highest gross returns (₹ 1,78,872 ha-1), net returns (₹ 1,03,878 ha-1) and BC ratio (2.39). Conversely, the application of T1: 75% RDN in recommended splits of 20, 40, 60, 80 DAS recorded the lowest number of bolls plant-1 (8.0), boll weight (2.53 g) and seed cotton yield (1402 kg ha-1), as well as lower gross returns (₹ 1,02,766 ha1), net returns (₹ 33,802 ha-1) and BC ratio (1.50). Based on these findings, it is recommended to adopt the practice of applying T9: 125% RDN (150 kg N ha-1) in splits at 15, 30, 45, 60, 75 DAS along with 2 sprays of 5% mepiquat chloride at 45 and 60 DAS to achieve maximum yield and economic returns of HDPS cotton.

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Title: Effect of plant growth regulator compounding on growth and endogenous hormones in cotton[J].
Author: WANG Wenhao, WANG Dan, SONG Xianpeng, MA Yajie, MA Xiaoyan, WU Changcai, YANG Jun, MA Yan.
Imprint: Chinese Journal of Pesticide Science, 2023, 25(5): 1093-1103. doi: 10.16801/j.issn.1008-7303.2023.0065

Abstract: In order to investigate the effects of different combinations of plant growth regulators on the growth and development of cotton, Zhongmiansuo 117 was used as the test variety, and mepiquat was used to combine with low, medium, and high concentrations of diethyl aminoethyl hexanoate, 24- epibrassinolide and prohexadione calcium in a randomized block group trial, and three sprays were carried out from the early to the full bloom stage of cotton to analyze the effects of the spraying on cotton agronomic traits, dry matter accumulation, yield, and quality and other indexes. The results showed that: mepiquat 98% SP 45 g/hm^2 + diethyl aminoethyl hexanoate 5% SL 120 mL/hm^2 and mepiquat 98% SP 45 g/hm^2 + prohexadione calcium 10% SC 450 mL/hm^2 showed a good effect on stemming control, increased the number of fruiting shoots and the diameter of the main stems, and promoted the bolling of cotton plants. The combination of mepiquat 98% SP 45 g/hm^2 + diethyl aminoethyl hexanoate 5% SL 120 mL/hm^2 significantly increased the seed cotton yield, the number of bolls per hectare and the weight of single bolls, and also improved the degree of neatness to a certain extent; the endogenous GA_3 increased, and the IAA and ABA decreased, which helped to increase the quality of the yield in the actual production. The combination of mepiquat 98% SP 45 g/hm^2 + prohexadione calcium 10% SC 450 mL/hm^2 significantly increased the amount of aboveground dry matter accumulation and dry matter distribution ratio of reproductive organs. It also regulated the increase of endogenous ABA and effectively promoted nutrient transfer to reproductive organs. The study showed that the combination of mepiquat 98% SP 45 g/hm^2 + diethyl aminoethyl hexanoate 5% SL 120 mL/hm^2 and mepiquat 98% SP 45 g/hm^2 + prohexadione calcium 10% SC 450 mL/hm^2 could realize the trait control and yield increase through the endogenous hormone regulation, which is of practical application in production.

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Title: Optimizing Cotton-Wheat System Productivity through Resource Conserving Techniques.

Author: Muhammad Waqas Imam Malik, Khalid Usman, Amir Hamza, & Muhammad Saad

Imprint: Communications in Soil Science and Plant Analysis , Latest Articles https://doi.org/10.1080/00103624.2023.2274037

Abstract: Cotton-wheat cropping system contributes significantly to Pakistan's food security and economy. However, the system productivity is low because of soil degrading tillage, irrational use of irrigation, and potassium which delay cotton maturity and affect succeeding wheat crop. Conservation tillage (MT) with appropriate irrigation and potassium may improve the system's productivity and stability. Experiments were conducted at Gomal University, Pakistan. Treatments included tillage (conventional (CT) and conservation tillage (MT)) and three irrigation intervals viz. 5, 4, and 3 weeks for cotton in first year, while in second year tillage was same and best irrigation interval observed in first year was kept constant. In second year besides tillage, potassium (0, 50, 100, 150, 200, and 250 kg K ha^{-1}) was included in cotton. For succeeding wheat, treatments were tillage (MT & CT) and six irrigations applied at crown root initiation, tillering, jointing, booting, 50% spike emergence, milk and dough stage. Results revealed that MT was better than CT regarding yield and net economic return. Five-week irrigation interval increased yield, improved fiber quality, and caused earlier cotton maturity. 150 kg K ha^{-1} produced higher net return and benefit–cost ratio (BCR) for cotton under MT than CT. Wheat grown with MT produced higher yield, net return, and BCR when irrigated 4 times at jointing, booting, 50% spike emergence, milk and dough stage. MT accumulated more soil organic matter and total soil N than CT. The results suggest that MT with appropriate irrigation and potassium can improve cotton-wheat system productivity and economics besides conservation of resources.

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Title: Effects of row spacing and potassium foliar applications on yield of cotton.

Author: Dorothy Menefee

Imprint: Agrosyst Geosci Environ. 2023; 6:e20432

Abstract: Cotton (Gossypium hirsutum L.) is an important crop in drought-prone central Texas. Foliar potassium (K) application and skip-row planting have the potential to improve productivity of rainfed cotton in this region. The objective of this study was to quantify the effects of skip-row planting and foliar K on cotton lint yield, biomass, nutrient uptake, and lint quality in rainfed cotton from 2017 to 2020. Foliar K was applied at 0, 20, and 40 kg ha−1. Row arrangement treatments consisted of two planting geometries: 2 × 1 skip row and standard full row. Cotton yield was not affected by foliar K in all years or by row spacing in 2017, 2019, or 2020. In 2018 alone, there was greater lint yield from skip row (530 kg ha−1) compared to full row (423 kg ha−1). The skip-row treatment resulted in significantly lower vegetative biomass and vegetative K uptake, but improved fiber quality. While foliar K application did not impact lint yield, total biomass and vegetative nitrogen and phosphorus uptake were increased with foliar K. There were year-to-year differences in seed and vegetative biomass, nutrient uptake, and lint quality, likely driven by differences in rainfall, with 2018 being unusually dry. Weather variation had more impact on cotton productivity than either treatment. However, given that the skip-row treatment increased quality and yield in the driest year while not affecting yield in wetter years makes it a viable option for cotton producers looking to reduce costs and increase profits in drought-prone regions.

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Title: Assessment and projections of climate change impacts on cotton water requirement: a case study.

Author: Mohsen Hamidianpour, Faeze Shoja and Abbas Khashei-Siuki

Imprint: International Journal of Global WarmingVol. 31, No. 2 Published Online: October 6, 2023pp 242-261https://doi.org/10.1504/IJGW.2023.133986

Abstract: This study investigates the effects of climate change on the reference crop evapotranspiration (ET0), crop coefficient (KC), phenology, and crop water requirement (CWR) of cotton in the future. As a result, the LARS-WG model and 5 GCMs, including EC-EARTH, GFDL-CM3, HadGEM2-ES, MIROC5, and MPI-ESM, were used to simulate the climate parameters under the RCP scenarios. The findings show an increasing trend in the minimum and maximum temperatures as well as solar radiation, with increases of 2.84°C, 5.75°C, and 0.38 $MJm^{-2}day^{-1}$ toward the end of the century, respectively. Precipitation has an increasing trend in winter and a decreasing trend in spring. ET0 would rise by 1.32 mm/day. Moreover, the length of the growth period of cotton was reduced from 155 days at the base period to 87 days in the far future. As a result, compared to current conditions, cotton's water requirements will rise by 23% and 26% in the near and far future, respectively.

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Title: Costs, Returns, Resource Use Efficiency of American Cotton Production in Irrigated North Western Plain Zone of Rajasthan, India.

Author: Pradeep Kumar and R. S. Shekhawat

Imprint: Asian Journal of Agricultural Extension, Economics & Sociology Volume 41, Issue 10, Page 759-766, 2023

Abstract: The study was carried out at Irrigated North Western Plain Zone 1b of Rajasthan in agricultural year 2012-13. This zone covers about 80 percent of the total area of cotton in the state. The study focused on the cost and return, efficiency of resource use and problems faced by the farmers in American cotton production under different farm sizes. Two villages namely 4C and Mirjawala were selected from Sriganganagar tehsil of the zone. Thirty farmers were selected at random in proportion to the total number of farmers in each size group from the list of from American cotton farmers group. The total variable cost of per hectare American cotton was Rs 28985. The yield per ha was 18.70 quintals. The return over variable cost per hectare American cotton was Rs 61436. The Cobb Douglas production function, revealed that the in American cotton farmers were underutilized fertilizer. Non-availability of labour during peak season was reported as highly acute constraint for cotton farmers. The damage caused by insect pests was reported as main problem for American cotton sample farmers.

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Title: Assessing Drought Tolerance in a Large Number of Upland Cotton Plants (*Gossypium hirsutum* L.) under Different Irrigation Regimes at the Seedling Stage.

Author: Sadettin Çelik

Imprint: Life 2023, 13(10), 2067; https://doi.org/10.3390/life13102067

Abstract: The cotton plant is important since it provides raw materials for various industry branches. Even though cotton is generally drought-tolerant, it is affected negatively by long-term drought stress. The trial was conducted according to the applied experimental design as a completely randomized design (CRD) with three replications to determine a panel of 93 cotton genotypes' genotypic responses against drought under controlled conditions in 2022. All genotypes were watered with 80 mL^{-1} of water (100% irrigation, field capacity) until three true leaves appeared, and then water stress was applied at a limited irrigation of 75% (60 mL^{-1}), 50% (40 mL^{-1}), and 25% (20 mL^{-1}) of the field capacity. After the trial terminated at 52 days, the cv. G56, G44, G5, and G86 in RL; G1, G56, G44, G86, G51, and G88 in RFW; advanced line G5, followed by the cv. G56, advanced line G44, G75, and the cv. G90 in RDW; G44, followed by G86, the cv. G56, and elite lines G13 and G5 in NLRs were observed as drought-tolerant genotypes, respectively, while G35, G15, G26, G67, and G56 in SL; G15, G52, G60, G31, and G68 in SFW; G35, G52, G57, G41, and G60 in SDW show the highest drought tolerance means, respectively. In conclusion, the commercial varieties with high means in roots, namely G86, G56, G88, and G90, and the genotypes G67, G20, G60, and G57 showing tolerance in shoots, are suggested to be potential parent plants for developing cotton varieties resistant to drought. Using the cultivars found tolerant in the current study as parents in a drought-tolerant variety development marker-assisted selection (MAS) plant breeding program will increase the chance of success in reaching the target after genetic diversity analyses are performed. On the other hand, it is highly recommended to continue the plant breeding program with the G44, G30, G19, G1, G5, G75, G35, G15, G52, G29, and G76 genotypes, which show high tolerance in both root and shoot systems.

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Title: Resilience of cotton cultivars to chilling stress during germination.

Author: Surabhi Gupta, Lekshmy V. Sankarapillai, K. Raja Reddy, Salliana R. Stetina & Raju Bheemanahalli

Imprint: Plant Physiology Reports (2023)

Abstract: Cotton, an important commercial crop, is frequently subjected to various stresses that limit its productivity and growth. Chilling stress is one such stress that can severely impact cotton germination and establishment. Several factors, including stress level, duration of exposure, and cultivar type determine the effect of chilling stress on germination. The present study investigated how chilling stress affected germination and seedling vigor in 25 cotton cultivars. The result of the study showed a significant decline (19%) in germination percentage and time taken for germination under chilling (18 °C) compared to the control temperature (28 °C). On average, the time taken for 50% germination under chilling stress was increased by 51.5 h compared to the control. There was no significant correlation between seed size and germination ability traits. Moreover, cultivars with reduced radicle length and dry weight with a low vigor index were highly vulnerable to chilling stress. Phenotypic variations in the stress tolerance index indicated that cultivars with faster germination rates and higher seedling vigor (PHY400 and STNV4990) displayed greater resilience to chilling. Overall, this study identified variability in chilling tolerance traits and cultivars, which could be exploited in breeding to select suitable cultivars for chillin stress tolerance.

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Title: Manure application enhanced cotton yield by facilitating microbially mediated P bioavailability

Author: Shaomin Zhang, Weige Huo, Baidengsha Maimaitiaili, Yi Peng, Gu Feng

Imprint: Field Crops Research, Volume 304, 1 December 2023, 109153

Abstract: Low soil phosphorus (P) availability affects cotton (*Gossypium hirsutum* L.) yield in arid regions with saline soils, such as Central Asia, due to P sorption by soil particles and precipitation by Ca^{2+}. P-based organic amendment is one potential solution to improve soil P bioavailability by influencing soil microbial processes, although the mechanisms behind this process are unclear.Objective or research question: The aim of this study was to evaluate the influence of soil P availability on cotton production by microbially mediated P mobilization processes under P-based organic amendment conditions in saline soil.Methods: We analyzed the microbially mediated P mobilization and lint yield of a six-year field experiment with P-based organic amendment for manure or straw in Xinjiang, China, the largest oasis-type agricultural region with saline soil in Central Asia. There were seven treatments as follows: CK, without P application; the P1, 32.7 kg ha^{-1} mineral P application; St, straw return (containing 36.0 kg P ha^{-1}); the P2, 65.5 kg ha^{-1} mineral P application; M, manure (containing 65.5 kg P ha^{-1}); the P3, 131 kg ha^{-1} mineral P application, and DM, manure (containing 131 kg P ha^{-1}). Results: The M and DM treatments enhanced the microbial biomass phosphorus (MBP) pool by 71%− 270% and increased the *phoD* gene-harboring bacterial α diversity and abundance of *phoD* genes. The relative abundances of *Pseudomonas*, *Amycolatopsis*, and *Streptomyces* increased by 0.8–4.4 fold. As a

result, alkaline phosphatase activity and subsequently P bioavailability increased. Compared with a similar mineral P application rate, the M treatment enhanced shoot P content by 7%, but there was an absence of differences in the St or DM treatment, and the lint yield in the M and DM treatments was increased by 10% and 16%, respectively.Conclusions: Manure application in saline soil can enhance soil P bioavailability by enlarging the MBP pool and improving alkaline phosphatase activity by enriching the *phoD* gene-harboring bacteria *Streptomyces* and *Amycolatopsis* and therefore improving P uptake and lint yield.Implications or significance:Organic amendments such as manure may be an effective P management practice for improving cotton P uptake and lint yield in mulched fertigation cotton systems in saline soil.

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Title: Sowing Time and Spacing Influenced Yield, Quality and Economics of Bt Cotton (Gossypium hirsutum L.).

Author: P. M. Patel, K. K. Patel and C. K. Patel

Imprint: International Journal of Environment and Climate Change Volume 13, Issue 11, Page 148-155, 2023

Abstract: A field study was conducted in the 2019 kharif season at the Agronomy Instructional Farm, SDAU, SKNagar, and Gujarat, India. To investigate that the sowing time and spacing influenced yield, quality and economics of Bt cotton (Gossypium hirsutum L.) in loamy sand soil. Twelve treatment combinations were examined, involving three sowing times (T1: 3rd week of May, T2: 1st week of June, T3: 3rd week of June) and four plant spacings (S1: 90 cm × 60 cm, S2: 90 cm × 45 cm, S3: 60 cm × 60 cm, S4: 60 cm × 45 cm). Four replications of a split plot design were used for the experiment. The third week of May was consistently the best time to sow cotton, according to the results, producing the maximum yields of seed cotton and stalk cotton. The quantity of monopodial branches/plant, harvest index and plant population as well as quality parameters such as oil content and ginning percentage were not significantly impacted by sowing time. The 3rd week of May sowing also yielded the highest benefit cost ratio and net realization. In terms of plant spacing, the spacing of 60 cm × 45 cm promoted highest plant population, taller plants and increased yield attributes like the bolls/plant, boll weight and seed cotton yield/plant. The highest seed cotton yield and stalk yield were achieved with this spacing. Harvest index and quality parameters were unaffected by plant spacing. The narrow spacing of 60 cm × 45 cm also resulted in the highest benefit cost ratio and net realization. The interaction effect between sowing time and plant spacing did not significantly influence growth, yield, yield attributes and quality parameters of Bt cotton.

CROP PROTECTION

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Title: Elicitor-Driven Defense Mechanisms: Shielding Cotton Plants against the Onslaught of Cotton Leaf Curl Multan Virus (CLCuMuV) Disease.

Author: Muhammad Fahad Khan

Imprint: Metabolites 2023, 13(11), 1148; https://doi.org/10.3390/metabo13111148

Abstract: Salicylic acid (SA), benzothiadiazole (BTH), and methyl jasmonate (MeJA) are potential elicitors found in plants, playing a crucial role against various biotic and abiotic stresses. The systemic acquired resistance (SAR) mechanism was evaluated in cotton plants for the suppression of Cotton leaf curl Multan Virus (CLCuMuV) by the exogenous application of different elicitors. Seven different treatments of SA, MeJA, and BTH were applied exogenously at different concentrations and combinations. In response to elicitors treatment, enzymatic activities such as SOD, POD, CAT, PPO, PAL, β–1,3 glucanse, and chitinase as biochemical markers for resistance were determined from virus-inoculated and uninoculated cotton plants of susceptible and tolerant varieties, respectively. CLCuMuV was inoculated on cotton plants by whitefly (Bemesia tabaci biotype Asia II-1) and detected by PCR using specific primers for the coat protein region and the Cotton leaf curl betasatellite (CLCuMuBV)-associated component of CLCuMuV. The development of disease symptoms was observed and recorded on treated and control plants. The results revealed that BTH applied at a concentration of 1.1 mM appeared to be the most effective treatment for suppressing CLCuMuV disease in both varieties. The enzymatic activities in both varieties were not significantly different, and the disease was almost equally suppressed in BTH-treated cotton plants following virus inoculation. The beta satellite and coat protein regions of CLCuMuV were not detected by PCR in the cotton plants treated with BTH at either concentration. Among all elicitors, 1.1 mM BTH was proven to be the best option for inducing resistance after the onset of CLCuMuV infection and hence it could be part of the integrated disease management program against Cotton leaf curl virus.

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Title: Aphid and caterpillar feeding drive similar patterns of induced defences and resistance to subsequent herbivory in wild cotton.

Author: Teresa Quijano-Medina, Jonathan Interian-Aguiñaga, Uriel Solís-Rodríguez, Marine Mamin, Mary Clancy

Imprint: Planta volume 258, Article number: 113 (2023)

Abstract: Plant-induced responses to attack often mediate interactions between different species of insect herbivores. These effects are predicted to be contingent on the herbivore's feeding guild, whereby prior feeding by insects should negatively impact subsequent feeding by insects of the same guild (induced resistance) but may positively influence insects of a different guild (induced susceptibility) due to interfering crosstalk between plant biochemical pathways specific to each feeding guild. We compared the effects of prior feeding by leaf-chewing caterpillars (Spodoptera frugiperda) vs. sap-sucking aphids (Aphis gossypii) on induced defences in wild cotton (Gossypium hirsutum) and the consequences of these attacks on subsequently feeding caterpillars (S. frugiperda). To this end, we conducted a greenhouse experiment where cotton plants were either left undamaged or first exposed to caterpillar or aphid feeding, and we subsequently placed caterpillars on the plants to assess their performance. We also collected leaves to assess the induction of chemical defences in response to herbivory. We found that prior feeding by both aphids and caterpillars resulted in reductions in consumed leaf area, caterpillar mass gain, and caterpillar survival compared with control plants. Concomitantly, prior aphid and caterpillar herbivory caused similar increases in phenolic compounds (flavonoids and hydroxycinnamic acids) and defensive terpenoids (hemigossypolone) compared with control plants. Overall, these findings indicate that these insects confer a similar mode and level of induced resistance in wild cotton plants, calling for further work addressing the biochemical mechanisms underpinning these effects.

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Title: Relationship between Damage by Cotton Bollworm Helicoverpa armigera (Hübner) and Different Plant Characteristics of Bt and Non-Bt Cotton Varieties in Pakistan.

Author: Muhammad Fahad , Muhammad Asam Riaz , Muhammad Zeeshan Majeed, Saba Tabasum , Saeed Rauf , Saba Tahseen , Abdul Munim Farooq and Idrees Ahmad Nasir

Imprint: Pakistan J. Zool., pp 1-11, 2023. DOI: https://dx.doi.org/10.17582/journal.pjz/20230603100625

Abstract: Helicoverpa armigera (Hübner) is one of the notorious lepidopterous pests of cotton (Gossypium hirsutum L.). Transgenic cotton varieties expressing Bacillus thuringiensis (Bt) induced insecticidal toxin (Cry1Ac) have been a key tool combating infestations of H. armigera and other cotton bollworms. However, the development of resistance in H. armigera to Bt transgenic cotton varieties is of major concern. This study assessed the H. armigera resistance to Cry1Ac expressing cotton varieties and association of plant biochemical, physico-morphic and physiological traits with boll damage by H. armigera. ELISA results revealed significantly high toxin (Cry1Ac) contents in Bt varieties particularly in PB-38, CRS-456 and PB-896 at 30-day post-germination. Moreover, toxin level in leaves decreased after 30 days of germination in most varieties except CRS-456 and PB-896. Bt varieties PB-896, CRS-456, PB-38 and VH-57 had the highest yield with low to moderate bollworm damage and exhibited a high and stable leaf Cry1Ac toxin level. The net photosynthesis rate, stomatal conductance, CO2 emission and absorption were positively, while Bt toxin level, gossypol glands density and yield were negatively and significantly correlated with the boll damage by H. armigera. All Bt cotton varieties exhibited a differential level of Cry1Ac toxin and none of them was found bollworm free, suggesting that H. armigera is able to infest most of the Bt cotton varieties though the level of infestation varied from variety to variety. Overall study findings recommend the cultivation of three Bt (VH-57, CRS-456 and PB-38) and one non-Bt (L.A Fragobract) cotton varieties by indigenous cotton growers to diminish bollworm infestations.

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Title: Impact of Biochar on Fusarium Wilt of Cotton and the Dynamics of Soil Microbial Community.

Author: Mamoona Asif, Muhammad Saleem Haider and Adnan Akhter

Imprint: Sustainability 2023, 15, 12936. https://doi.org/10.3390/ su151712936

Abstract: The effects of biochar on leaf and soil-borne diseases of plants can be seen in addition to its ability to sequester carbon, improve soil quality, and enhance plant performance. However, the mechanisms by which soil-borne pathogens are suppressed and plant performance is enhanced are not well understood. The present work aims to comprehensively establish the links between biochar-induced changes in the richness of the rhizosphere microbial population, in association with the reduction of soil-borne Fusarium wilt disease (Fusarium oxysporum f. sp. vasinfectum), in cotton (Gossypium hirsutum), with improved plant performance. Biochar made from organic waste significantly decreased the colonization and survival of Fusarium in soil, raised the culture-able counts of numerous microbes with biocontrol potential (microorganisms that boost plant growth and development), and inhibited Fusarium wilt of cotton. The biochar amendment significantly enhanced the cotton plant development and physiological parameters such as chlorophyll content, etc. Overall, 9% organic waste biochar had shown a significant impact on cotton growth as compared to other treatments with or without biochar. Compared to the soil-only control, the disease index was considerably reduced in all biochar-amended treatments. In terms of the plant's resistance to Fusarium wilt, biochar-induced increases in the level of overall chlorophyll content and biochemicals such as phenolics, flavonoids, etc. Additionally, cotton plants grown with a 9% biochar composition had considerably greater NPK levels than other treatments with or without biochar. The biochar addition resulted in increased counts of Pseudomonas spp., Actinomycetes spp., and Trichoderma spp., while Acidobacteriales, Rhodospirillales, and Frankiales were less when compared with an un-amended (without biochar) soil control. Thus, the composition of rhizosphere bacteria in the treatments with and without modified biochar was found to differ significantly.

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Title: Neonicotinoid resistance in populations of the cotton aphid, Aphis gossypii Glo gossypii Glover (Hemipter er (Hemiptera: Aphididae) in Cott a: Aphididae) in Cotton Plantation Ar on Plantation Areas of Turkey .

Author: Cahit Kaya Naciye Sena Çağatay John T. Margaritopoulos John Vontas Remzi Atliha

Imprint: Turkish Journal of Agriculture and Forestry: Vol. 47: No. 5, Article 3. https://doi.org/10.55730/1300-011X.3114

Abstract: The cotton aphid, Aphis gossypii Glover (Hemiptera: Aphididae) is a polyphagous pest that could cause economic crop losses in various crops. Cotton production areas are under insecticide application pressure, and the possibility of insecticide resistance development is higher than in other crops. Chemical insecticides, especially neonicotinoids, are the most common instruments of Integrated Pest Management (IPM) strategies against A. gossypii. In this study, the resistance status of A. gossypii populations from the largest cotton plantation areas of Türkiye was analyzed. Nine field-collected aphid populations and a susceptible strain were examined in leaf-dip bioassays with three neonicotinoid insecticides. The resistance ratios of bioassays ranged from 22.6 to 82.6 for acetamiprid, 23.5 to 67.3 for imidacloprid, and 1.1 to 20.8 for thiamethoxam. Comparative sequence analysis between susceptible and resistant strains was analyzed to identify known mutations to confer resistance to neonicotinoids. The mean enzyme activity in some populations was significantly higher than in the susceptible strain. The enzyme activity ratios ranged from 1.9 to 3.9 for CarE and 1.5 to 3.1 for GST. The bioassay data revealed moderate to high resistance levels in acetamiprid and imidacloprid and low to medium levels in thiamethoxam. A partial sequence of the β1 subunit of the nAChR in specimens of the populations examined did not reveal any of the V62I, L80S, and R81T and point mutations. The lack of any correlation between the carboxylesterase or glutathione-S-transferase activity and the LC50 values of three insecticides suggested that these two detoxification enzymes were not involved in the resistance levels observed. However, the resistance levels observed in the present study could be attributed to metabolic resistance mechanisms. Another important point is the cross-resistance observed between the neonicotinoids in the present study. Their extensive use, especially in cotton, might select aphid genotypes resistant to more than one neonicotinoid.

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Title: GhTLP1, a thaumatin-like protein 1, improves Verticillium wilt resistance in cotton via JA, ABA and MAPK signaling pathway-plant pathways.

Author:Heng Zhou , Yijing Xie , Yan Jiang, Hasan Nadeem

Imprint: International Journal of Biological Macromolecules,
Volume 253, Part 7, 31 December 2023, 127388

Abstract: Verticillium wilt of cotton is a very serious soil-borne disease and there is no effective control method. The mechanism of *Gossypium hirsutum* thaumatin-like protein 1(*GhTLP1*) in upland cotton regulating Verticillium wilt resistance has been an uncovered research approach. GhTLP1 is mainly localized in the cell wall. Overexpression of GhTLP1 significantly enhanced *Arabidopsis* plants resistance to *Verticillium dahliae*, while its homologous mutant *tlp1* in *Arabidopsis* was more susceptible to the pathogen, and the heterologous complement line (EC) recovered resistance to *V. dahliae*. *GhTLP1* responds to jasmonate acid (JA) and abscisic acid (ABA) hormones and regulates mitogen-activated protein kinase (MAPK) signaling pathway-plant pathway to enhance *Arabidopsis* plants resistance to *V. dahliae*. Silencing *GhTLP1* resulted decrease in cotton plants resistance to *V. dahliae*. Moreover, the mutation of GhTLP1 at site Tyr97 and Tyr199 with the phosphorylation also decreased plant resistance to *V. dahliae*. Therefore, GhTLP1 phosphorylation was observed important in cotton plants against *V. dahliae*. Further analysis demonstrated that GhTLP1 interacted with *gossypium hirsutum* laccase 14 (GhLAC14) to enhance plants resistance to *V. dahliae*. Silencing *GhLAC14* resulted decrease in cotton plants resistance to *V. dahliae*. Here, we propose that *GhTLP1* is a potential molecular target for improving resistance to Verticillium wilt in cotton.

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Title: Investigating Action Thresholds And Alternative Management Approaches To Control Cotton Bollworm [Helicoverpa Zea (Boddie)] Infestations.

Author: WILFRID CALVIN

Imprint: Submitted to the Graduate and Professional School of Texas A&M University in partial fulfillment of the requirements for the degree of DOCTOR OF PHILOSOPHY

Abstract: Experiments were conducted to devise economic thresholds for foliar insecticide applications targeting bollworms in cotton. Bt cotton technologies including TwinLink™ (TL), TwinLink Plus™ (TLP), Bollgard II® (BG2), Bollgard 3® (BG3), WideStrike® (WS), WideStrike 3 ® (WS3), and a non-Bt (NBT) were evaluated. A 6% fruiting forms injury threshold was selected and compared to preventive treatments utilizing chlorantraniliprole. The 6% fruiting forms injury threshold resulted in a 25 and 75% reduction in insecticide applications relative to preventive sprays for WS and BG2, respectively. Current H. zea threshold recommendations for Texas, Mississippi, and South Carolina were assessed. Three Bt cotton technologies (non-Bt, Bollgard II®, Bollgard® 3) and five thresholds (20% oviposition, 6% fruiting forms injury, >3% large larvae, preventive sprays, non-treated) were utilized. Within NBT, all treatment thresholds provided greater control of H. zea, higher yield, and profitability relative to non-treated NBT. BG2 sprayed based on 20% oviposition or preventively resulted in greater control of H. zea, and all treatments resulted in a yield or profitability equivalent to that of the non-treated BG2. Spraying BG3 based on any of the thresholds was not beneficial. In 2020-2021, sorghum was evaluated as a trap crop of H. zea and a nursery crop for natural enemies of H. zea and HearNPV dissemination into cotton. Treatments including cotton-only, non-treated cotton-sorghum, and HearNPV-treated cotton-sorghum were used. Intercropping cotton with grain sorghum did not result in a consistent increase in H. zea control and beneficial arthropods relative to the cottononly treatment. HearNPV was detected in samples collected from all treatments indicating that the virus is naturally occurring in the locations where the study was conducted. Hence, there was no clear evidence that grain sorghum could serve as a source of HearNPV for nearby cotton. iii Laboratory strains of H. zea including Benzon susceptible, CRY-RR, CRY-RS, VIP-RR-70, VIP-RR-15, and TRE-RR, and 8 field-collected populations were evaluated (2021-2022) for their susceptibility to HearNPV utilizing diet-overlay bioassays. The Benzon strain was consistently more susceptible to HearNPV than any of the field populations evaluated, and the Cry-RR in 2021. However, the TRE-RR, VIP-RR-70, and VIP-RR-15 strains were as susceptible as the Benzon strain.

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Title: Identification of Molecular Diversity in Gossypium hirsutum L. against Whitefly Resistance Using SSR Markers.

Author: Syed Bilal Hussain, Muhammad Tayyab, Muhammad Adnan Shah Bukhari and Muhammad Zubair

Imprint: Asian Journal of Biotechnology and Genetic Engineering Volume 6, Issue 2, Page 164-170, 2023

Abstract: Whitefly is a major factor in reducing cotton yield worldwide more specifically in Asian Countries So to deal with this whitefly there is a need to separate genetically diverse varieties that can combat it due to its unique genetic source. In this study, genetic diversity analysis of cotton cultivars was done against whitefly resistance using simple sequence repeat (SSR) markers. For this, 75 cultivars of cotton were used to analyze genetic diversity by using 25 SSR markers out of which 9 markers were polymorphic. These markers amplified a total of 46 alleles with an average of 5.11 alleles per marker. These varieties showed a high value of gene diversity that ranged from 0.624 to 0.877 with a mean value of 0.735. Polymorphism information content (PIC) for selected genotypes ranged from 0.562 to 0.867 with a mean value of 0.704. Based on these 9 polymorphic markers 75 selected genotypes were divided into 3 major groups in a phylogenetic tree. The elected cultivars of cotton were highly polymorphic and could be used for further breeding to improve cotton accessions.

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Title: Selection of entomopathogenic fungi to control stink bugs and cotton boll weevil.

Author: Larissa Moreira de Sousa, Eliane Dias Quintela, Heloiza Alves Boaventura, José Francisco Arruda e Silva, Bruna Mendes Diniz Tripode, José Ednilson Miranda

Imprint: Pesq. Agropec. Trop., Goiânia, v. 53, e76316, 2023

Abstract: Entomopathogenic fungi stand out in the biological control of several agriculturally important insects. Six isolates of Metarhizium anisopliae, Cordyceps javanica, Beauveria sp. and B. bassiana were screened to control Anthonomus grandis, Euschistus heros, Oebalus poecilus, O. ypsilongriseus and Thyanta perditor, important insect pests of soybean, cotton and rice. The bioassays were conducted in a completely randomized design, with four replications (10 insects/replication). Significant differences for virulence were observed between the tested fungal species and isolates. For A. grandis, the most virulent isolate was M. anisopliae BRM 2335, followed by Beauveria BRM 14527 and BRM 67744 [82.5 to 97.5 % of mortality; average lethal time (LT50) of 5.9 to 7.8 days]. M. anisopliae BRM 2335 was also highly virulent to the four stink bug species (75 to 97.5 % of mortality; LT50 of 5.2 to 9.7 days). For the stink bugs, Beauveria sp. BRM 67744 was infectious to O. poecilus (75 % of mortality), but failed to control E. heros (16.9 % of mortality). C. javanica BRM 27666 and BRM 14526 showed average virulence to the stink bugs and A. grandis (17.5 to 57.3 % of mortality; LT50 of 6.0 to 9.7 days). M. anisopliae was consistently more virulent to the stink bugs than the other fungi. Therefore, M. anisopliae BRM 2335 was selected for further studies under screenhouse and field conditions to control A. grandis and other stink bug species, especially E. heros.

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Title: Evaluation of Genetic Diversity among CLCuD-Resistant Upland Cotton Varieties Using SSR Markers.

Author: Syed Bilal Hussain, Muhammad Adnan Shah Bukhari, Muhammad Tayyab and Muhammad Zubair

Imprint: Asian Journal of Biotechnology and Genetic Engineering Volume 6, Issue 2, Page 155-163, 2023

Abstract: Cotton leaf curl disease (CLCuD) is a dangerous viral disease that affects the productivity of cotton crops. Since early detection, this disease has spread worldwide and has caused serious damage to the production of cotton around the world particularly in Pakistan. In this study, we evaluated the genetic diversity of CLCuD-resistant upland cotton germplasm by using microsatellite markers. For this purpose, 25 pairs of microsatellite primers were screened and 9 were found to be polymorphic. These 9 primers were used for assessing the genetic diversity of 75 upland cotton varieties. Using these markers, a total of 46 loci were amplified with an average of 5.11 loci per primer. BNL0409 and BNL2835 produced the highest number of bands, 8 bands by each primer. Mean gene diversity was 0.651 with 0.91 (BNL2835) being the highest and 0.38 (JESPR0013) being the lowest. Polymorphism information content (PIC) and major allele frequency ranged between 0.91 to 0.36 (for BNL2835 and BNL0341) and 0.77 to 0.32 (for JESPR0013 and BNL0409) respectively. Mean PIC and major allele frequency were 0.62 and 0.49 respectively. BNL2835 showed the highest allele number of 23 and the mean allele number was 11. Principal component analysis (PCA) was performed and the PCA graph was plotted. These results showed that the 75 varieties studied, using 9 microsatellite markers have an average level of genetic diversity. The findings of this study could be utilized for genetic analysis and the outcomes might be useful for cotton breeding programs.

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Title: Prediction of cotton leaf curl virus disease at different potassium doses based on abiotic environmental factors and sowing dates.

Author: Muhammad Umar Shahbaz, Muhammad Ehetisham ul Haq, Muhammad Kamran, Waseem Abbas, Asia Batool

Imprint: Archives of Phytopathology and Plant Protection, Volume 56, 2023 - Issue 15

Abstract: Cotton is a major cash crop that is widely cultivated in tropical and subtropical regions around the globe. Cotton leaf curl virus disease is a major threat to

lower the cotton yield in Pakistan. The present study aimed to predict the disease severity at different potassium (K) dosses based on abiotic environmental factors with respect to two sowing times. Three potassium (K) doses (90, 60, and 30 kg acre−1) were applied to observe the impact on disease severity. In control, no extra K was applied. Two sowings were done at 15 days intervals. Data was recorded using at seven days intervals after the appearance of the disease. A significant difference in disease severity was observed in K applied cotton plants and between the two sowing times. Maximum disease severity was noticed in control plants and was found maximum where 90 kg acre−1 K was applied. Maximum air temperature, minimum air temperature, rainfall, and windspeed exhibited a negative relationship with disease severity. A positive relationship was seen between disease severity and relative humidity irrespective to sowing times. In 1st sowing, maximum air temperature (35–38 °C), minimum air temperature (23–24 °C), relative humidity (65–75%), rainfall (1–2 mm), and windspeed (1.5–2.5 km/h) significantly contributed in disease progression. In second sowing, maximum air temperature (34–36 °C), minimum air temperature (19–21 °C), relative humidity (75–78%), rainfall (0.5–1.5 mm), and windspeed (1.5–2.5 km/h) favoured the disease development.

PLANT GENETICS AND BREEDING

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Title: Inheritance of morphological indicators of Cotton Bolls in geographically distant F1 hybrids

Author: Izzatulla Kahharov, Mamura Mutalova, Mokhidilkhon Kodirova, Abdulahad Azimov, Shaxnoza Yusupova

Imprint: Journal of Wildlife and Biodiversity, 7(Supplementary issue), 173-183. DOI: https://doi.org/10.5281/zenodo.10023408

Abstract: This article presents an analysis of Cotton Bolls' size and shape indicators in geographically distant hybrids F1. It has been established that in hybrid plants obtained by crossing small-boll and large-boll forms, the dominance of the large-boll parent is observed. In the form of a boll in F1 hybrid plants in, all types of inheritance are observed. Significant changes in the shape of the boll are observed in hybrid combinations, where geographically distant samples served as initial forms. It has been

established that in F1 plants the inheritance of morphological traits depends on the genetic structure and on the geographical distance of the crossed forms.

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Title: Genome-wide association study for boll weight in Gossypium hirsutum races
Author: Yuanyuan Wang, Xinlei Guo, Yanchao Xu, Runrun Sun, Xiaoyan Cai

Imprint: Functional & Integrative Genomics volume 23, Article number: 331 (2023)

Abstract: High yield has always been an essential target in almost all of the cotton breeding programs. Boll weight (BW) is a key component of cotton yield. Numerous linkage mapping and genome-wide association studies (GWAS) have been performed to understand the genetic mechanism of BW, but information on the markers/genes controlling BW remains limited. In this study, we conducted a GWAS for BW using 51,268 high-quality single-nucleotide polymorphisms (SNPs) and 189 Gossypium hirsutum accessions across five different environments. A total of 55 SNPs significantly associated with BW were detected, of which 29 and 26 were distributed in the A and D subgenomes, respectively. Five SNPs were simultaneously detected in two environments. For TM5655, TM8662, TM36371, and TM50258, the BW grouped by alleles of each SNP was significantly different. The ± 550 kb regions around these four key SNPs contained 262 genes. Of them, Gh_A02G1473, Gh_A10G1765, and Gh_A02G1442 were expressed highly at 0 to 1 days post-anthesis (dpa), − 3 to 0 dpa, and − 3 to 0 dpa in ovule of TM-1, respectively. They were presumed as the candidate genes for fiber cell differentiation, initiation, or elongation based on gene annotation of their homologs. Overall, these results supplemented valuable information for dissecting the genetic architecture of BW and might help to improve cotton yield through molecular marker-assisted selection breeding and molecular design breeding.

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Title: Exploitation of various physio-morphological and biochemical traits for the identification of drought tolerant genotypes in cotton.

Author: Tahreem Arif, Muhammad Tanees Chaudhary, Sajid Majeed, Iqrar Ahmad Rana, Zulfiqar Ali

Imprint: BMC Plant Biology, Published: 23 October 2023, volume 23, Article number: 508 (2023)

Abstract: Drought is one of the limiting factors for quality and quantity of cotton lint in tropical and sub-tropical regions. Therefore, development of drought tolerant cotton genotypes has become indispensable. The identification of drought tolerant genotypes is pre-requisite to develop high yielding cultivars suitable for drought affected areas. Methods: Forty upland cotton accessions were selected on the basis of their adaptability and yield. The collected germplasm accessions were evaluated at seedling stage on the basis of morphological, physiological and biochemical parameters. The experiment was conducted under controlled conditions in greenhouse where these genotypes were sown under different levels of drought stress by following factorial under completely randomized design. The data were collected at seedling stages for root and shoot lengths, relative leaf water content, excised leaf water losses, peroxidase content and hydrogen peroxide concentrations in leaf tissues. Results: The biometrical analysis revealed that germplasm is significantly varied for recorded parameters, likewise interaction of genotypes and water stress was also significantly varied. The cotton germplasm was categorized in eight clusters based on response to water stress. The genotype Cyto-124 exhibited lowest H2O2 content under drought conditions, minimum excised leaf water loss under stress environment was exhibited by genotypes Ali Akber-802 and CEMB-33. Overall, on the basis of morphological and biochemical traits, SL-516 and Cyto-305 were found to be drought tolerant. Genotypes 1852 − 511, Stoneville 15–17 and Delta Pine-55 showed low values for root length, peroxidase activity and higher value for H2O2 contents. On the basis of these finding, these genotypes were declared as drought susceptible. Conclusion: The categorization of cotton germplasm indicating the differential response of various parameters under the control and drought stress conditions. The recorded parameters particularly relative leaf water contents and biochemical assays could be utilized to screen large number of germplasm of cotton for water deficit conditions. Besides, the drought tolerant genotypes identified in this research can be utilized in cotton breeding programs for the development of improved cultivars.

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Title: Inheritance And Combining Ability for Fiber Length in F1 Diallelcotton Crosses (Gossypium hirsutum L.).

Author: Valentina DIMITROVA, Minka KOLEVA

Imprint: Scientific Papers. Series A. Agronomy, Vol. LXVI, No. 1, 2023

Abstract: The aim of this study was by means of diallel analysis of fiber length of F1 cotton hybrids to establish some genetic parameters and inheritance indexes necessary for specifying the breeding strategy by this character and breeding value of parental forms. The hybrid populations of two diallel combinations, each involving 6 parental components, were studied. A half diallel crossing scheme was used including the parents and one set of F1 hybrids from direct crosses. Each diallel combination was tested in replicated trials in two consecutive years. It was found that additive and non-additive gene effects participated in the genetic control of fiber length. The main component of genetic variance was of nonadditive type (dominance and epistasis). The varieties Darmi, Mytra and Dorina, from the 1st diallel combination, and Natalia, from the 2nd diallel combination, were identified as good general combiners for this trait.

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Title: Regulatory controls of duplicated gene expression during fiber development in allotetraploid cotton.

Author: Jiaqi You, Zhenping Liu, Zhengyang Qi, Yizan Ma

Imprint: Nature Genetics, Published: 16 October 2023

Abstract: Polyploidy complicates transcriptional regulation and increases phenotypic diversity in organisms. The dynamics of genetic regulation of gene expression between coresident subgenomes in polyploids remains to be understood. Here we document the genetic regulation of fiber development in allotetraploid cotton Gossypium hirsutum by sequencing 376 genomes and 2,215 time-series transcriptomes. We characterize 1,258 genes comprising 36 genetic modules that control staged fiber development and uncover genetic components governing their partitioned expression relative to subgenomic duplicated genes (homoeologs). Only about 30% of fiber quality-related homoeologs show phenotypically favorable allele aggregation in cultivars, highlighting the potential for subgenome additivity in fiber improvement. We envision a genome-enabled breeding strategy, with particular attention to 48 favorable alleles related to fiber phenotypes that have been subjected to purifying selection during domestication. Our work delineates the dynamics of gene regulation during fiber development and highlights the potential of subgenomic coordination underpinning phenotypes in polyploid plants.

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Title: COTTON VARIETY 11PADT76

Document Type and Number: United States Patent Application 20230309498

Kind Code:A1

Abstract: The disclosure relates to a cotton variety, designated 1 1PADT76, the plants and seeds of the cotton variety 11PADT76, methods for producing a cotton plant, either varietal or hybrid, produced by crossing the cotton variety 11PADT76 with itself or with another cotton plant, hybrid cotton seeds and plants produced by crossing the variety 11PADT76 with another cotton variety or plan, methods for producing a cotton plant containing in its genetic material one or more transgenes, and the transgenic cotton plants produced by that method. This disclosure also relates to cotton varieties derived from cotton variety 11PADT76, to methods for producing other cotton varieties derived from cotton variety 11PADT76, and to the varieties derived by the use of those methods.

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Title: Genome-wide analysis of the LAZ1 gene family in Gossypium hirsutum

Author: Tingting Deng, Zongjin Pan, Wei Wang, Yingying Tang, Wenxiang Feng

Imprint: Molecular Biology Reports volume 50, pages9273–9282 (2023)

Abstract: As the world's leading fiber crop and a major oil-producing crop, cotton fiber yield and fiber quality are affected by environmental stresses, especially heat, drought and salinity. The LAZ1 (Lazarus 1) family genes are responsive to abscisic acid, drought, and salt treatments. Currently, mining and functional analyses of LAZ1 family genes in cotton have not been reported. Methods and results: In this study, 20 GhLAZ1 genes, designated GhLAZ1-1 - GhLAZ1-20, were identified in the genome of Gossypium hirsutum through the construction of an HMM model, and their molecular properties, chromosomal localization, phylogeny, gene structure, evolutionary selection pressure, promoter cis elements and gene expression under salt stress were analyzed. With the exception of GhLAZ1-17 and GhLAZ1-20, the remaining 18 GhLAZ1 genes were unevenly localized on 13 chromosomes in G. hirsutum; evolutionary analysis showed that these genes could be divided into three subfamilies; and evolutionary selection pressure analysis demonstrated that the GhLAZ1 genes were all under purifying selection. Many elements related to light responses, hormone responses, and abiotic stresses were predicted on the GhLAZ1 family gene promoters, and real-time quantitative PCR results showed that GhLAZ1-2, GhLAZ1-8, and GhLAZ1-18 were upregulated significantly in salt-treated cotton leaves.

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Title: Widespread incomplete lineage sorting and introgression shaped adaptive radiation in the Gossypium genus.

Author: Yanchao Xu, Yangyang Wei, Zhongli Zhou, Xiaoyan Cai1,, Scott A. Boden, Muhammad Jawad Umer, Luqman B. Safdar, Yuling Liu, Dingsha Jin, Yuqing Hou, Yuhong Wang, Sarah Brooke Wall, Kunbo Wang, Shuxun Yu, Baohong Zhang, Renhai Peng and Fang Liu

Imprint: Plant Communications (2023), https://doi.org/10.1016/j.xplc.2023.100728

Abstract: Cotton (Gossypium) stands as a crucial economic crop, serving as the primary source of natural fiber for the textile sector. However, the evolutionary mechanisms driving speciation within the Gossypium genus remain unresolved. In this investigation, we leveraged 25 Gossypium genomes and introduced four novel assemblies—G. harknessii, G. gossypioides, G. trilobum, and G. klotzschianum (Gklo)—to delve into the speciation history of this genus. Notably, we encountered intricate phylogenies potentially stemming from introgression. These complexities are further compounded by incomplete lineage sorting (ILS), a factor likely to have been instrumental in shaping the swift diversification of cotton. Our focus subsequently shifted to the rapid radiation episode during a concise period in Gossypium evolution. For a recently diverged lineage comprising G. davidsonii, Gklo, and G. raimondii, we constructed a finely detailed ILS map. Intriguingly, this analysis revealed the non-random distribution of ILS regions across the reference Gklo genome. Moreover, we identified signs of robust natural selection influencing specific ILS regions. Noteworthy variations pertaining to speciation emerged between the closely related sister species Gklo and G. davidsonii. Approximately 15.74% of speciation structural variation genes and 12.04% of speciation-associated genes were estimated to intersect with ILS signatures. These findings enrich our understanding of the role of ILS in adaptive radiation, shedding fresh light on the intricate speciation history of the Gossypium genus.

FIBER AND FIBER TECHNOLOGY

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Title: Over-expression of GhACTIN1 under the control of GhSCFP promoter improves cotton fiber and yield.

Author: Adnan Iqbal, Sibgha Aslam, Sidra Akhtar, Qurban Ali

Imprint: Scientific Reports volume 13, Article number: 18377 (2023)

Abstract: Actin dynamics is pivotal in controlling cotton fiber elongation and the onset of secondary wall biosynthesis. We report that overexpression of GhACTIN1 under fiber fiber-specific promoter, GhSCFP, improves cotton fiber length, strength, and micronaire value. However, the effect of transgene has a more positive effect on fiber strength and micronaire value than fiber length. F-actin quantification and cellulose contents measurement in transgenic developing cotton fiber during the elongation phase showed an increase of up to 8.7% and 4.7% respectively. Additionally, physiological factors such as water use efficiency showed no significant change in transgenic cotton lines, while stomatal conductance and photosynthetic rate were significantly increased. Moreover, agronomical data determined that lint percentage (GOT) and seed cotton yield also increased up to 4.6% and 29.5% respectively, in transgenic cotton lines compared to the control lines. Our data demonstrate that the GhACTIN1 gene is a strong candidate gene for cotton fiber and yield improvement.

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Title: Impact of intra-boll yield components on lint production per boll and fiber quality in advanced cotton breeding lines.

Author: Gurpreet Virk, John L. Snider, Peng Chee, Simerjeet Virk, Donald Jones

Imprint: Crop Science, 29 October 2023, https://doi.org/10.1002/csc2.21140

Abstract: Cotton (*Gossypium hirsutum* L.) lint yield and fiber quality are associated with various yield components. Research efforts addressing intra-boll yield component contributors to lint production boll^{-1} are limited. Thus, a study was conducted in Tifton, Georgia with the objectives to quantify the contributions of intra-boll yield components to lint production boll^{-1} and to identify yield components most strongly associated with lint production boll^{-1} in advanced breeding lines of upland cotton. Data collected included intra-boll yield components and fiber quality parameters. A strong association was observed between lint production boll^{-1} and seedcotton weight boll^{-1} ($r = 0.896$) compared to lint production boll^{-1} and lint percent (LP, $r = 0.574$). For breeding lines with maximum lint weight boll^{-1}, the contribution of seedcotton weight and LP ranged from 0.17 to 0.36 g boll^{-1} and 0.22 to 0.24 g boll^{-1}, respectively, suggesting a relatively greater influence of seedcotton weight boll^{-1} on lint weight boll^{-1}. Lint production boll^{-1} can be expressed as the product of seeds per boll, seed surface area, fiber density (FD), and individual fiber weight (IFW). IFW was the greatest contributor to lint production boll^{-1} for seven breeding lines and FD for nine breeding lines. A strong positive association was observed between lint production boll^{-1} and IFW ($r = 0.656$, $p < 0.001$); however, no significant association between lint weight boll^{-1} and FD suggesting a relatively greater influence of IFW on lint weight boll^{-1}. Our work provides future direction aimed at improving lint yields through the selection of various yield components.

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Title: Attenuated Total Reflection Fourier Transform Infrared Spectroscopy with Soft Independent Modeling of Class Analogy–Principal Component Analysis for Classifying Cotton Fiber Maturity Phenotypes of Cotton Population Composed of Various Genotypes

Author: Yongliang Liu

Imprint: Applied Spectroscopy, https://doi.org/10.1177/00037028231211942

Abstract: Maturity is a major fiber trait that affects the processing and performance of cotton fiber. Rapid and accurate identification of fiber maturity phenotypes and genotypes is of importance to breeders. Previous studies showed that either conventional fiber measurements or attenuated total reflection Fourier transform infrared spectroscopy (ATR FT-IR) analysis discriminated the immature fiber (*im*) phenotype from the wild type (WT) mature fiber phenotype in a segregating F_2 population from a cross between two upland cotton lines differing in fiber maturity. However, both conventional fiber property measurement methods and FT-IR analyses with current algorithms could not detect the subtle differences among the WT fibers composed of two different genotypes, WT homozygosity (WT-homo) and WT heterozygosity (WT-hetero). This research explored the FT-IR method, in combination with soft independent modeling of class analogy of principal component analysis (SIMCA–PCA), for the discrimination of WT fiber phenotypes consisting of two different genotypes (WT-homo and WT-hetero). The new approach enabled the detection of IR spectral intensity differences between WT-homo and WT-hetero fibers. Successful classification originated from a distinctive spectral difference in the low-wavenumber region ($<700\ \text{cm}^{-1}$) between WT-hetero fibers and WT-homo fibers. This observation emphasized that ATR FT-IR with a SIMCA–PCA approach would be a sensitive tool for classifying the WT fibers demonstrating minor phenotypic differences. The improved sensitivity of the infrared method may provide a way of dissecting genotype–phenotype interactions of cotton fibers rapidly and efficiently.

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Title: Application of Various Genomic Selection Models in Cotton Fiber Quality.

Author: Dongdong Zhai

Imprint: Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 10 November 2023 doi: 10.20944/preprints202311.0677.v1

Abstract: Cotton is the most important natural fiber cash crop, which has high commodity economic benefits and provides an important material foundation for China's construction. With the improvement of textile technology and living standard, higher requirements are put forward for raw cotton quality. Traditional cotton breeding methods need typing and selection. With the development of biotechnology and the research of genomics, genomic selection has been widely used in cotton breeding. Genomic selection is a new breeding method, which can be selected and bred by constructing a prediction model and using high-density molecular markers covering the whole genome. In this study, the application of various genomic selection models in cotton fiber quality was explored, which provided more reliable information for genetic breeding improvement in the future, thus helping to improve the efficiency of actual cotton breeding.

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Title: The synergistic effects of soil-applied boron and foliar-applied silicon on cotton fiber quality and yield.

Author: Priscilla Maria da Silva Liber Lopes, Cid Naudi Silva Campos, Paulo Eduardo Teodoro, Milton Garcia Costa, Jonas Pereira de Souza Júnior

Imprint: *BMC Plant Biology* volume 23, Article number: 520 (2023)

Abstract: Studies of boron (B) and silicon (Si) synergy in cotton crops have shown promising results; however, the focus was on the foliar application of B and Si. Nonetheless, B is an element with little mobility in the plant and its best form of application is in the soil. Thus, the objective of this study was to evaluate the synergistic effect of soil applied B and foliar applied sSi on fiber quality and crop yield of cotton. For this purpose, a field experiment was carried out using cotton cultivar FM 985 GLTP. The soil's B in the experimental site is classified as low for cotton cultivation. The experiment was conducted in a randomized complete-block design, in a 3 × 2 factorial scheme, with three doses of B: 0.0 kg ha^{-1} (deficiency), 2.0 kg ha^{-1} (recommended dose), and 4.0 kg ha^{-1} (high dose) in the absence and presence (920 g L^{-1}) of Si, with four replications. One week after the 4th application of Si, B and Si leaf content was

determined. At boll opening, crop yield was estimated, and fiber quality analysis was realized. Boron deficiency reduced cotton yield, in 11 and 9%, compared to the application of 2 and 4 kg ha^{-1} of B, respectively. The presence of Si, however, increased plant yield in 5% in the treatments with 0 and 2 kg ha^{-1} of B, respectively. Cotton fiber length and elongation were not influenced by the B doses and Si presence. Fiber breaking strength was increased in 5% by the presence of Si and was not influenced by B deficiency. Micronaire was 8% smaller in the treatment with 0 kg ha^{-1} of B and 6% smaller in the absence of Si. Short fiber index was 4% greater in the plants of the treatment with 0 kg ha^{-1} of B. The results of this study reports that the complementation with Si via foliar application increases fiber quality by enhance breaking strength and micronaire. In conclusion, the interaction between soil-applied B and foliar-applied Si is beneficial for cotton cultivation, resulting in high cotton yield with better fiber quality.

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Title: Are yarn quality prediction tools useful in the breeding of high yielding and better fibre quality cotton (Gossypium hirsutum L.)?

Author: Liu Shiming, Gordon Stuart & Stiller Warwick

Imprint: Journal of Cotton Research, Published: 23 October 2023, volume 6, Article number: 18 (2023)

Abstract: The approach of directly testing yarn quality to define fibre quality breeding objectives and progress the selection is attractive but difficult when considering the need for time and labour. The question remains whether yarn prediction tools from textile research can serve as an alternative. In this study, using a dataset from three seasons of field testing recombinant inbred line population, Cottonspec, a software developed by the Commonwealth Scientific and Industrial Research Organisation (CSIRO) for predicting ring spun yarn quality from fibre properties measured by High Volume Instrument (HVI), was used to select improved fibre quality and lint yield in the population. The population was derived from an advanced generation inter-crossing of four CSIRO conventional commercial varieties. The Cottonspec program was able to provide an integrated index of the fibre qualities affecting yarn properties. That was compared with selection based on HVI-measured fibre properties, and two composite fibre quality variables, namely, fibre quality index (FQI), and premium and discount (PD) points. The latter represents the net points of fibre length, strength, and micronaire based on the Premiums and Discounts Schedule used in the market while modified by the inclusion of elongation.

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Title: Genetic diversity and population structure analyses and genome-wide association studies of photoperiod sensitivity in cotton (Gossypium hirsutum L.)

Author: S. Anjan Gowda, Fred M. Bourland, Baljinder Kaur, Don C. Jones &
Vasu Kuraparthy

Imprint: Theoretical and Applied Genetics volume 136, Article number: 230 (2023)

Abstract: Six hundred fifty-seven accessions that included elite cotton germplasm (DIV panel), lines of a public cotton breeding program (FB panel), and tropical landrace accessions (TLA panel) of Gossypium hirsutum L. were genotyped with cottonSNP63K array and phenotyped for photoperiod sensitivity under long day-length conditions. The genetic diversity analysis using 26,952 polymorphic SNPs indicated a progressively narrowed diversity from the landraces (0.230) to the DIV panel accessions (0.195) and FB panel (0.116). Structure analysis in the US germplasm identified seven subpopulations representing all four major regions of the US cotton belt. Three subpopulations were identified within the landrace accessions. The highest fixation index (F_{ST}) of 0.65 was found between landrace accessions of Guatemala and the Plains-type cultivars from Southwest cotton region while the lowest F_{ST} values were between the germplasms of Mid-South and Southeastern regions. Genome wide association studies (GWAS) of photoperiod response using 600 phenotyped accessions identified 14 marker trait associations spread across eight Upland cotton chromosomes. Six of these marker trait associations, on four chromosomes (A10, D04, D05, and D06), showed significant epistatic interactions. Targeted genomic analysis identified regions with 19 candidate genes including Transcription factor Vascular Plant One-Zinc Finger 1 (VOZ1) and Protein Photoperiod-Independent Early Flowering 1 (PIE1) genes. Genetic diversity and genome wide analyses of photoperiod sensitivity in diverse cotton germplasms will enable the use of genomic tools to systematically utilize the tropical germplasm and its beneficial alleles for broadening the genetic base in Upland cotton.

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Title: An insight into the gene-networks playing a crucial role in the cotton plant architecture regulation.

Author: Salman Naveed, Michael Jones, Todd Campbell & Sachin Rustgi

Imprint: The Nucleus (2023)

Abstract: Cotton is a global source of natural fiber and edible oil. Plant architecture and flowering time are key factors in determining the cotton yield and efficiency of mechanical harvesting. The molecular functions of plant architecture and flowering time-related genes are well-studied in Arabidopsis (a long-day plant), tomato (a day-neutral plant), and rice (a short-day plant). It has improved our general understanding of flowering mechanisms in plants. The upland (*Gossypium hirsutum* L.) and Sea Island (*Gossypium barbadense* L.) cotton are intrinsically perennial and exhibit indeterminate growth habit and a complex branching pattern. In this paper, we review the progress on gene identification for plant architecture (including branching patterns, branch angle, fruit branch length, and plant height) and floral induction in cotton. However, attention is given to the genes involved in plant hormone perception and signal transduction, especially the phosphatidyl ethanolamine-binding protein gene family in cotton, i.e., the FT/SFT and SP genes or the florigen and anti-florigen system. Furthermore, we identify areas that need further research. These findings lay the groundwork for engineering cotton cultivars with desirable plant architecture, flowering time, growth habit, and improved yield with suitability for mechanized cotton production.

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Title: Characteristic of *GEX1* genes reveals the essential roles for reproduction in cotton.

Author:Tengyu Li , Shouhong Zhu , Yan Li , Jinbo Yao , Chenlei Wang, Shengtao Fang , Jingwen Pan

Imprint: International Journal of Biological Macromolecules, Volume 253, Part 8, 31 December 2023, 127645

Abstract: GEX1 (gamete expressed 1) proteins are critical membrane proteins conserved among flowering plants that are involved in the nuclear fusion and embryonic development. Herein, we identified the 32 GEX1 proteins from representative land plants. In cotton, *GEX1* genes expressed in various tissues across all stages of the life cycle, especially in pollen. Subcellular localization indicated the position of GhGEX1 protein was localized in the endoplasmic reticulum. Experimental research has demonstrated that *GhGEX1* has the potential to improve the partial abortion phenotype in *Arabidopsis*. CRISPR/Cas9-mediated knockout of *GhGEX1* exhibited the seed abortion. Paraffin section of the ovule revealed that the polar nuclear fusion of *ghgex1* plants remains at a standstill when the wild type has developed into a normal embryo. Comparative transcriptome analysis showed that the DEGs of reproductive-related processes and membrane-related processes were repressed in the pollen of knockout lines. The predicted protein interactions showed that *GhGEX1* probably functioned through interactions with proteins related to reproduction and membrane. From all these investigations, it was possible to conclude that the GEX1 proteins are evolutionarily conserved in flowering plants and elucidated the pivotal roles during fertilization and early embryonic development in cotton.

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Title: Substitution of *Gossypium tomentosum* Chromosome Segments into Upland Cotton *(G. hirsutum*) & Development of Segment-Targeted SNP Assays.

Author: Garcia Ramos, Oriana
Imprint: Master's thesis, Texas A&M University. Available electronically from https: / /hdl .handle .net /1969 .1 /200154.

Abstract: Genetic diversity is essential to the genetic improvement of every crop. Goals of this project have been [1] to genetically diversify upland cotton (Gossypium hirsutum L.) by creating numerous chromosome segment substitution lines (CSSLs), each containing a small amount of G. tomentosum (Nuttall ex Seemann) germplasm, and [2] to empower wide-cross cotton breeding by improving the genome coverage provided by simplex SNP assays. Putative BC5Sn CSSLs were selected using existing simplex SNP assays. Subsequent whole-genome analysis using the CottonSNP63K array identified the locations, sizes and zygosity of all donor segment(s). BC5Sn CSSLs collectively included 43% of the donor genome in homozygous form, and 15% in heterozygous form. Other BC3F1 plants contained another 36% coverage of the donor genome in heterozygous form, i.e., develop BC5Sn CSSLs that expand coverage. Targeted development of 85 PACE assays reduced gaps between SNP assays, thereby improving genome coverage and amenability to marker-assisted selection (MAS).

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Title: Dynamic roles of small RNAs and DNA methylation associated with heterosis in allotetraploid cotton (Gossypium hirsutum L).
Author: Rasmieh Hamid, Feba Jacob, Zahra Ghorbanzadeh, Leila Jafari & Omran Alishah
Imprint: BMC Plant Biology, 23, Article number: 488 (2023)

Abstract: Heterosis is a complex phenomenon wherein the hybrids outperform their parents. Understanding the underlying molecular mechanism by which hybridization leads to higher yields in allopolyploid cotton is critical for effective breeding programs. Here, we integrated DNA methylation, transcriptomes, and small RNA profiles to comprehend the genetic and molecular basis of heterosis in allopolyploid cotton at three developmental stages. Results: Transcriptome analysis revealed that numerous DEGs responsive to phytohormones (auxin and salicylic acid) were drastically altered in F1 hybrid compared to the parental lines. DEGs involved in energy metabolism and plant growth were upregulated, whereas DEGs related to basal defense were downregulated. Differences in homoeologous gene expression in F1 hybrid were greatly reduced after hybridization, suggesting that higher levels of parental expression have a vital role in heterosis. Small RNAome and methylome studies showed that the degree of DNA methylation in hybrid is higher when compared to the parents. A substantial number of allele-specific expression genes were found to be strongly regulated by CG allele-specific methylation levels. The hybrid exhibited higher 24-nt-small RNA (siRNA) expression levels than the parents. The regions in the genome with increased levels of 24-nt-siRNA were chiefly related to genes and their flanking regulatory regions, demonstrating a possible effect of these molecules on gene expression. The transposable elements correlated with siRNA clusters in the F1 hybrid had higher methylation levels but lower expression levels, which suggest that these non-additively expressed siRNA clusters, reduced the activity of transposable elements through DNA methylation in the hybrid.

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Title: The 10-m cotton maps in Xinjiang, China during 2018–2021.
Author: Xiaoyan Kang, Changping Huang, Jing M. Chen, Xin Lv, Jin Wang, Tao Zhong,

Imprint: Scientific Data volume 10, Article number: 688 (2023)

Abstract: Cotton maps (10 m) of Xinjiang (XJ_COTTON10), which is the largest cotton production region of China, were produced from 2018 to 2021 through supervised classification. A two-step mapping strategy, i.e., cropland mapping followed by cotton extraction, was employed to improve the accuracy and efficiency of cotton mapping for a large region of about 1.66 million km2 with high heterogeneity. Additionally, the time-series satellite data related to spectral, textural, structural, and phenological features were combined and used in a supervised random forest classifier. The cotton/non-cotton classification model achieved overall accuracies of about 95% and 90% on the test samples of the same and adjacent years, respectively. The proposed two-step cotton mapping strategy proved promising and effective in producing multi-year and consistent cotton maps. XJ_COTTON10 agreed well with the statistical areas of cotton at the county level (R2 = 0.84–0.94). This is the first cotton mapping for the entire Xinjiang at 10-meter resolution, which can provide a basis for high-precision cotton monitoring and policymaking in China.

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Title: Cloning and Expression Analysis of GhPS2 Gene in *Gossypium hirsutum* L.

Author: MENG Chaomin, QING Guixia , GENG Feifei , LI Xuelin

Imprint: Acta Botanica Sinica Volume 43, Issue 11, 2023 >1820-1826. DOI:10.7606/j.issn.1000-4025.2023.11.1820

Abstract: HAD-like hydrolase plays an important role in regulating plant growth and development and responding to phosphorus deficiency stress. Based on the genome-wide expression profile of cotton seedlings under low phosphorus stress in the early stage of our research group, related genes were excavated and their preliminary expression analysis was conducted. Genomic DNA and cDNA sequence of the gene were cloned and analyzed by bioinformatics method. Fluorescence quantitative PCR (qRT-PCR) were used to detect the changes of gene expression in root, stem, leaf and flower tissues.The relative expression patterns of GhPS2 under low phosphorus stress(0,4,12,24 and 72h) were analyzed by qRT-PCR technology.The results showed that: (1)GhPS2 gene of G. hirsutum L. was successfully cloned, and the full length of the open reading frame of the gene was 813bp, encoding 270 amino acids and containing 3 introns. Analysis revealed that this gene sequence belonged to the HAD family, with a conserved structure named PUT-Phosphatase. (2) Sequence alignment and evolution analysis showed that the similarity of GhPS2 to other cotton varieties PS2 and durian PS2 was 93% and 83.15%, respectively. （3）The results of qRT-PCR showed that GhPS2 gene was predominantly expressed in roots, followed by stems and flowers, with the lowest expression in leaves. The relative expression of GhPS2 gene was the highest in the roots treated with low phosphorus for 4 h, and it was 16.66 times that of suitable phosphorus treatment at 72 h under low phosphorus stress.This study demonstrated that GhPS2 gene belongs to low phosphorus stress response gene and may be involved in Gossypium hirsutum L. response low phosphorus stress.

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Title: Long noncoding RNA TRABA suppresses β-glucosidase-encoding BGLU24 to promote salt tolerance in cotton.

Author: Changjiang Cui, Hui Wan, Zhu Li, Nijiang Ai, Baoliang Zhou

Imprint: Plant Physiology, kiad530, https://doi.org/10.1093/plphys/kiad530

Abstract: Salt stress severely damages the growth and yield of crops. Recently, long noncoding RNAs (lncRNAs) were demonstrated to regulate various biological processes and responses to environmental stresses. However, the regulatory mechanisms of lncRNAs in cotton (*Gossypium hirsutum*) response to salt stress are still poorly understood. Here, we observed that a lncRNA, trans acting of BGLU24 by lncRNA (TRABA), was highly expressed while GhBGLU24-A was weakly expressed in a salt-tolerant cotton accession (DM37) compared to a salt-sensitive accession (TM-1). Using TRABA as an effector and proGhBGLU24-A-driven GUS as a reporter, we showed that TRABA suppressed GhBGLU24-A promoter activity in double transgenic Arabidopsis (Arabidopsis thaliana), which explained why GhBGLU24-A was weakly expressed in the salt-tolerant accession compared to the salt-sensitive accession. GhBGLU24-A encodes an endoplasmic reticulum (ER)–localized β-glucosidase that responds to salt stress. Further investigation revealed that GhBGLU24-

A interacted with RING-type E3 ubiquitin ligase (GhRUBL). Virus-induced gene silencing (VIGS) and transgenic Arabidopsis studies revealed that both GhBGLU24-A and GhRUBL diminish plant tolerance to salt stress and ER stress. Based on its substantial effect on ER-related degradation (ERAD)–associated gene expression, GhBGLU24-A mediates ER stress likely through the ERAD pathway. These findings provide insights into the regulatory role of the lncRNA TRABA in modulating salt and ER stresses in cotton and have potential implications for developing more resilient crops.

SEED SCIENCE AND TECHNOLOGY

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Title: Growth, leaf anatomy, and photosynthesis of cotton (Gossypium hirsutum L.) seedlings in response to four light-emitting diodes and high pressure sodium lamp.

Author: Yichi Zhang, Baopeng Liao

Imprint: Research Square, https://doi.org/10.21203/rs.3.rs-3451836/v1

Abstract: Light is a critical factor of plant growth and development, particularly in controlled environments. Lightemitting diodes (LEDs) have become a reliable alternative to conventional high pressure sodium (HSP) lamps because they are more efficient and versatile light sources. In contrast to well-known specialized LED light spectrums for vegetables, the appropriate LED lights for crops such as cotton remain unknown. In this growth chamber study, we selected and compared four LED lights with varying percentages (26.44-68.68%) of red light (R, 600-700 nm), combined with other lights, for their effects on growth, leaf anatomy and photosynthesis of cotton seedlings, using HSP as a control. The total photosynthetic photon flux density (PPFD) was 215±2 μ mol/m2 ·s for all LEDs and HSP. The results showed significant differences in all tested parameters among lights, and the percentage of far red (FR, 701-780 nm) within the range of 3.03-11.86% was positively correlated with plant growth (characterized by leaf number and area, plant height and diameter, and total biomass), palisade layer thickness, photosynthesis rate (Pn) and stomatal conductance (Gs). The ratio of R/FR (4.445-11.497) negatively influenced the growth of cotton seedlings, and blue light (B) suppressed stem elongation but increased palisade cell length, chlorophyll content and Pn. The LED 2 was superior to other LED lights and HSP. It had the highest ratio of FR within the total PPFD (11.86%) and the lowest ratio of R/FR (4.445); LED 2 may therefore be used to replace HPS under controlled environments for the study of cotton at the seedling stage.

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Title: Purification and Characterization of Alkaline Protease Isolated from Cotton (Gossypium hirsutum) Seeds.

Author: Asghar Ali Shaikh, Muhammad Umar Dahot , Abdul Sajid , Syed Habib, Ahmed Naqvi

Imprint: J. Appl. Res Plant Sci. Vol. 5(1), 34-45, 2024, https://doi.org/10.38211/joarps.2024.05.201

Abstract: Proteases are widely utilized both in physiological and commercial fields such as medicine, food, detergent, and leather. Plant-originated proteases play a significant role in several biomedical fields due to their easy accessibility and activity. Pakistan is an agro-based country and can be an ideal place for the isolation of industrially important proteases from plant sources such as cotton, which is the main crop and frequently available and low cost. Purification of protease was carried out by fractionation with two-fold acetone, ethanol, methanol and various concentrations (40-80%) of ammonium sulphate. The precipitates formed were collected after centrifugation and dialyzed for 24 hours against universal buffer pH 7.0 and was centrifuged in a cooled refrigerated. The dialyzed sample was loaded on Sephadex G–100 gel column. The fractions of the samples were collected and their absorbance of protein was monitored at 280 nm. The homogeneity of the purified enzyme was checked by SDS gel electrophoresis The purified protease enzyme has optimum activity at 30°C and pH 8.0 when casein was used as substrate. The Km and Vmax values of purified cotton seed's alkaline protease activity was recorded as 0.03M and 17 µmol/minute respectively. Protease activity was increased by the addition of cysteine but inhibited by Iodoacetic acid and β-Mercaptoethanol and decreased with some metal ions. These characteristics of the purified enzyme allowed classifying it as a cysteine protease. In conclusion, this study suggests that the alkaline protease enzyme is the best choice for commercial use.

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Title: Regulatory effects of silicon nanoparticles on the growth and photosynthesis of cotton seedlings under salt and low-temperature dual stress.

Author: Yueping Liang, Hao Liu, Yuanyuan Fu, Penghui Li, Shuang Li & Yang Gao

Imprint: BMC Plant Biology volume 23, Article number: 504 (2023)

Abstract: Silicon nanoparticles (SiO_2-NPs) play a crucial role in plants mitigating abiotic stress. However, the regulatory mechanism of SiO_2-NPs in response to multiple stress remains unclear. The objectives of this study were to reveal the regulatory mechanism of SiO_2-NPs on the growth and photosynthesis in cotton seedlings under salt and low-temperature dual stress. It will provide a theoretical basis for perfecting the mechanism of crop resistance and developing the technology of cotton seedling preservation and stable yield in arid and high salt areas.

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Title: Overexpression of GhSWEET42, a SWEET-like gene from cotton, enhances the oil content and seed size.

Author: Deying Wang, Mengxue Du, Jingyu Li, Shuwen Yin, Yongwang Sun & Shangjing Guo

Imprint: Biotechnology & Biotechnological Equipment, 37:1, 2266529, DOI: 10.1080/13102818.2023.2266529

Abstract: SWEET (‘sugars will eventually be exported transporters’) family genes reportedly play a critical role in sugar translocation and oil biosynthesis in various plant species. However, their functions in cotton are unknown. The present study demonstrated that while GhSWEET42 was widely expressed in different cotton tissues, it had the highest expression level in the developing ovules. Hence, it performs a vital role in seed development. We constructed GhSWEET42 transgenic Arabidopsis lines to verify the biological function of this gene and found that the oil content and weight of the seeds produced by the overexpression lines were 18–23% and 19–20% higher, respectively than those of the wild-type. Gas chromatography–mass spectrometry (GC–MS) analysis revealed that it was mainly a relative increase in unsaturated fatty acids (FAs) that contributed to the relative increase in oil content in the transgenic seeds. Moreover, the latter exhibited comparative upregulation of certain genes associated with FA and triacylglycerol biosynthesis as well as cell expansion. GhSWEET42 might work synergistically with the aforementioned genes. This finding indicates that GhSWEET42 may be essential in oil biosynthesis and seed development in cotton. The results of the present work may facilitate further explorations into the molecular mechanism of cottonseed oil biosynthesis as well as the cultivation of novel oil-rich cotton varieties.

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Title: Breeding of high seed oil oleate levels into Upland cotton from wild *Gossypium barbadense* L. germplasm.
Author: Michael K. Dowd, Jay Shockey, Jack C. McCarty Jr., Johnie N. Jenkins
Imprint: Crop Science, 09 October 2023, https://doi.org/10.1002/csc2.21119

Abstract: A high seed oil oleate trait identified in wild *Gossypium barbadense* L. cotton accession GB713 (PI 608139) was bred into Upland cotton (*Gossypium hirsutum* L.) cultivar Sure-Grow 747 (SG747, PVP 9800118). Starting from the F_2 generation of an initial cross between GB713 and SG747, plants were selected by measuring the seed oil fatty acid distributions by gas chromatography. Selected F_3 plants were crossed to M Rk-Rn 6, a line previously created from GB713 and SG747 for improved nematode resistance. High-oleate plants were selected in the F_2 population. Selected plants were then crossed to HOa1 (a ~35% oleate line derived from M Rk-Rn 1, a sibling line to M Rk-Rn 6), and high-oleate plants were again selected in the F_2 population. F_3 plants were re-selected for the high-oleate trait, and four selected F_4 lines were evaluated in 2022 field plots. The four lines had oleate levels between 52% and 57%, approximately triple that found in normal cottonseed oil (15%–19%) and higher than in either the high-oleate wild GB713 parent (~40%) or in the previously released HOa cotton plant lines (33%–35%). The increased oleate levels occurred with an approximately equal reduction in linoleic acid. Other seed and fiber properties were largely like those of SG747, although some residual GB713 character existed within the lines. The resulting oil composition should be ideal for use in deep fat frying, with the high level of oleic acid improving the oil's oxidative stability but with sufficient linoleic acid to maintain frying flavor.