GLEANINGS IN COTTON RESEARCH

APRIL 2024

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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   *Chetali Rodge*
Incharge Library   *Technical Officer (T5)*

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Title: Naturally colored cotton for wearable applications.

Author: Marina Naoumkina, Doug J. Hinchliffe and Gregory N. Thyssen

Imprint: Front. Plant Sci. 15:1350405. doi: 10.3389/fpls.2024.1350405

Abstract: Naturally colored cotton (NCC) offers an environmentally friendly fiber for textile applications. Processing white cotton fiber into textiles requires extensive energy, water, and chemicals, whereas processing of NCC skips the most polluting activity, scouring-bleaching and dyeing; therefore, NCC provides an avenue to minimize the harmful impacts of textile production. NCC varieties are suitable for organic agriculture since they are naturally insect and disease resistant, salt and drought-tolerant. Various fiber shades, ranging from light green to tan and brown, are available in the cultivated NCC (Gossypium hirsutum L.) species. The pigments responsible for the color of brown cotton fiber are proanthocyanidins or their derivatives synthesized by the flavonoid pathway. Due to pigments, the NCC has excellent ultraviolet protection properties. Some brown cotton varieties exhibited superior thermal resistance of fiber that can be used to make fabrics with enhanced flame retardancy. Here, we review molecular mechanisms involved in the pigment production of brown cotton and challenges in breeding NCC varieties with a wide range of colors but without penalty in fiber quality. Also, we discuss opportunities for NCC with flame-retarding properties in textile applications.

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Title: Improving cotton yield and fiber quality in different tropical soils with boron fertilization.

Author: Luis Fernando dos Santos Cordeiro, João Vitor Cordeiro Malenowtch, Carlos Felipe dos Santos Cordeiro

Imprint: Agronomy Journal. 2024; 1–11.

Abstract: Cotton (*Gossypium hirsutum* L.) is responsive to boron (B) fertilization when there is low soil availability, but the best source and rate to be used and whether this response is dependent on soil texture are still unknown. This study aimed to adjust boron fertilization for cotton as a function of the production environment and B source used. Two field experiments were conducted in the 2020/2021 season in Chapadão do Sul, MS (clayey soil—adequate B content) and Dracena, SP (sandy soil—low B content),

Brazil. Treatments consisted of B sources (ulexite [low solubility], borax pentahydrate [BP] [intermediate solubility], and boric acid [BA] [high solubility]), and B rates (0, 1, 2, 4, and 6 kg ha−1) applied to the soil at 25 days after plant emergence. In sandy soil with low B content, application of 2 (high and medium solubility sources) and 4 kg B ha−1 (low solubility source) improved fiber yield between 10% (210 kg ha−1 fiber) and 28% (555 kg ha−1), respectively, as well as micronaire index, strength, elongation, uniformity, and short fibers. Application of B greater than 4 kg ha−1 via soluble sources reduced (between 9% (175 kg ha−1)—BP and 14% (257 kg ha−1)—BA) fiber yield only in sandy soil. When B content in the soil is adequate, B fertilization did not improve yield, but increased fiber strength (4%—1.1 g tex−1) and reduced the short fiber index (16%) by applying 1 kg B ha−1, regardless of the source used. The highest fiber yields were obtained with leaf B contents between 12 and 17 mg kg−1 (sandy soil) and 25 and 27 mg kg−1 (clayey soil). We recommend applying 2 kg B ha−1 (solubility sources) and 4 kg B ha−1 (low solubility source) in sandy soils with low B content to improve yield and fiber quality, and 1 kg B ha−1 in clayey soil with adequate B content to improve fiber quality and replace B amounts removed through harvesting.

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Title: Optimizing crop water productivity and delineating root architecture and water balance in cotton–wheat cropping system through sub-surface drip irrigation and foliar fertilization strategy in an alluvial soil.

Author:Tarandeep Kaur , Pawan Sharma , A.S. Brar , B.B. Vashisht , Anil K. Choudhary

Abstract: Water-intensive agricultural practices in tandem with conventional irrigation methods such as flood irrigation, has caused severe water scarcity in south-Asian Indo-Gangetic Plains (IGPs). The adoption of micro-irrigation systems (sprinker, surface drip and sub-surface drip) instead of flooding offers a great promise in water saving and enhanced fertilizer-use efficiency, and thus, improved productivity. The change in irrigation and fertilization methodology may affect the behavior of plant root growth, root architecture and, crop and water productivity. Hence, current study aimed at evaluating the influence of sub-surface drip-irrigation and fertigation strategy on crop and water productivity besides delineating root architecture and soil water balance in cotton–wheat cropping system (CWCS). Results showed that sub-surface drip irrigation (SSDI) enhanced the root system by stimulating the development of new secondary roots which actively participated in physiological responses. Root length at boll opening stage of cotton increased significantly under SSDI at 60% ET_c (60% of evapo-transpiration) over other treatments. Root mass density in wheat was also significantly higher under SSDI particularly at 15–30 cm depth over surface drip and flood irrigation during 2020–21. SSDI at 100% ET_c (100% of evapo-transpiration) produced statistically

similar seed cotton yield, wheat grain yield and the system productivity (wheat equivalent yield) to 80% ET_c. SSDI at 80% ET_c (80% of evapo-transpiration), resulted in water-saving of ~43.2% over flood irrigation in CWCS. Further, fertigation through SSDI resulted in ~20% reduction in fertilizer needs, while achieving the yield equivalent to that of conventional fertilization. Irrigation water productivity and bio-physical water productivity of this system were ~46.1 and 5.7% higher under 80% ET_c along with F_{80} (80% recommended dose of nitrogen, RDN) and M_{foliar} (foliar application of KNO_3 & $MgSO_4$ at flower initiation and boll development stages of cotton) over flood irrigation. Overall, SSDI at 80% of evapo-transpiration along with 80% RDN and foliar application of KNO_3 & $MgSO_4$ may prove highly beneficial to enhance the crop and water productivity in CWCS, besides saving irrigation water-use by ~43.2% over flood irrigation in water-scarce agro-ecologies of south-Asia.

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Title: Evapotranspiration, fiber yield and quality, and water productivity of cotton (*Gossypium hirsutum* L.) under different irrigation technologies in a semiarid climate.

Author: Komlan Koudahe, Jonathan Aguilar, Koffi Djaman & Aleksey Y. Sheshukov

Abstract: Cotton is a relatively new crop in southern Kansas and its effective irrigation scheduling requires information on crop water requirement and water productivity in a given climatic condition. This study aimed to: (1) assess cotton crop actual evapotranspiration, irrigation water requirement, (2) evaluate lint yield and quality, and (3) determine the water productivity related to total water (irrigation and rainfall), irrigation, and evapotranspiration under different irrigation technologies and rainfed conditions in semi-arid climate of western Kansas. Field experiments were conducted in 2020, 2021, and 2022 at the Southwest Research and Extension Center (SWREC) in Garden City, KS, to evaluate cotton production under four irrigation technologies which were low elevation spray application (LESA), low energy precision application (LEPA), mobile drip irrigation 1 (MDI1 with 3.79 L/h), mobile drip irrigation 2 (MDI2 with 7.57 L/h) and a rainfed treatment under a randomized complete block design with the variety PHY 205 W3FE. Crop management was similar across all treatments for three growing seasons. The results showed that the seasonal actual evapotranspiration (ETa) varied among the irrigation technologies, the rainfed treatment, and years. On average, LESA recorded the highest ETa value of 463.9 mm and LEPA had the lowest ETa value of 457.2 mm. The lint yield and lint quality (micronaire, length, strength, uniformity, color grade) varied significantly among the irrigation technologies and the rainfed setting. The highest lint yield of 1061.94 kg ha−1 was obtained under LEPA, while the rainfed registered the lowest lint yield of 224.13 kg ha−1. The irrigated cotton

had a high value for lint quality parameters with the LEPA having the best lint quality. Furthermore, on average, LEPA recorded the highest evapotranspiration-water, total-water, and irrigation-water use efficiencies, and the values were 0.23, 0.33, and 0.39 kg m−3, respectively. The cotton ETa and water productivity are valuable parameters for effective irrigation scheduling for cotton production under similar climate and soil conditions.

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Title: Application of drone to aid in the evaluation of trials in cotton cultivation (*Gossypium hirsutum* L.) Malvaceae F.

Author: Alexandre Barichello, Matheus Oliveira Rocha, Hugo Manoel de Souza, Igor Vinícius dos Santos Araújo & Daniel Noe Coaguila Nuñez

Abstract: The use of drones to evaluate crops has become increasingly common. Among these uses, the drone helps in the cultivation of cottona crop that is highly prone to intense attacks by pests and diseases. This study aimed to evaluate the use of drones in evaluating trials in cotton cultivation in the Southwest of Goiás, Brazil.A Phantom 4 Pro drone was used to carry out the mapping and WebODM was used to carry out photogrammetry and obtain the ExG vegetation index. ExG proved to be efficient in detecting differences between blocks.The useof drones provided a series of benefits in the assessment process in cotton cultivation. The ability to fly over the area quickly and accurately allowed detailed,and punctual images to be obtainedwhich was essential for monitoring plant health and identifying problem areassuch as pest or disease infestations.

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Title: Exploring the impact of heat stress on inheritance patterns of key agronomic traits in upland cotton (Gossypium Hirsutum L.) through generation mean analysis .

Author: Javed Iqbal , Khadim Hussain , Hafiz Muhammad Ijaz , Muhammad Aleem Sarwar , Muhammad Ashfaq , Muhammad Tariq , Muhammad Zafar

Abstract: The goal of this study is to study the influence of heat stress on the hereditary patterns of different agronomic traits in upland cotton (Gossypium hirsutum L.) by utilizing generation mean analysis. A total of six parental varieties were cultivated in a controlled greenhouse environment, consisting of three heat-tolerant cultivars (CIM-600, Cyto-178, and FH-142) and three heat-susceptible cultivars (Aleppo-1, Marvi and

AMSI-38). Following the development of six primary generations resulting from three crosses (CIM600 × Allepo-1, Cyto-178 × AMSI-38 and FH-142 × Marvi), the seeds were subsequently planted at the farm of the Central Cotton Research Institute, Multan. The dominant component significantly influenced plant height more than the additive component in all crosses under normal conditions. The inheritance of traits in both situations was influenced by epistatic components (i, j, and l), except cross 1 under heat stress. It is worth noting that negative values for component [i] suggest the absence of any fixable additive genetic effect in some crosses. The presence of negative component values [j] in some crosses has led to the proposal of a digenic interaction. Diverse prior investigations have documented both similarities and differences in their respective conclusions.

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Title: Effect of nutrient management practices on yield and economics of organic cotton (*Gossypium hirsutum* L.)

Author: RS Tinku, Satyanarayana Rao, BG Koppalkar, MY Ajayakumar and Mahadeva Swamy

Abstract: A field experiment was conducted in organic block of Main Agricultural Research Station, UAS, Raichur, during kharif 2018 to study the effect of nutrient management practices in organic cotton production under irrigated condition. The experiment was laid out in randomized complete block design with eleven treatments and three replications. The treatments consisted application of 50% RDN through compost (25%) + vermicompost (25%) and compost (25%) + poultry manure (25%) as basal dose along with vermicompost (50%) and poultry manure equivalent to 50% RDN as top dress in equal splits at 30 and 60 DAS alone and in combination with foliar spray of 3% panchagavya alternated with 10% vermiwash at 45, 60, 75 and 90 DAS and compost (100% RDN) as basal dose alone and in combination with vermicompost and poultry manure on equivalent basis (50:50). The results indicated that application of compost + vermicompost equivalent to 50% RDN as basal dose + vermicompost (50% RDN) as top dress + panchagavya spray alternated with vermiwash recorded significantly higher seed cotton yield (1323 kg ha1) and was on par with compost + poultry manure equivalent to 50% RDN as basal dose + vermicompost (50% RDN) as top dress + panchagavya spray alternated with vermiwash (1252 kg ha-1), compost + vermicompost equivalent to 50% RDN as basal dose + poultry manure (50% RDN) as top dress + panchagavya spray alternated with vermiwash (1249 kg ha-1), compost + vermicompost equivalent to 50% RDN as basal dose + vermicompost (50% RDN) as top dress (1248 kg ha-1) and compost + poultry manure equivalent to 50% RDN as basal dose + poultry manure (50% RDN) as top dress + panchagavya spray alternated with

vermiwash (1203 kg ha-1) over compost alone (1044 kg ha-1). Similar trend as that of seed cotton yield in respect of net returns and BC ratio was also seen.

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Title: Boll distribution of cotton effected by varying potassium rates within different irrigation levels.

Author: Amee R. Bumguardner, Katie L. Lewis, Seth A. Byrd, Glen L. Ritchie, Gaylon D. Morgan

Abstract: Cotton (*Gossypium hirsutum* L.) requires potassium (K) in large amounts for crop growth and development and is more sensitive to low K availability in soils than other agronomic crops. Low K concentrations within the plant may decrease the rate of photosynthesis, which will impact plant growth and development. Cotton yield potential has increased due to genetic improvements, which may have increased the quantity and rate at which cotton takes up K. This research aimed to determine the effect of K fertilizer rates within irrigation level on boll distribution and yield contribution from specific node zones. This study was conducted at New Deal, TX in 2016 and 2017. Muriate of potash (KCl) was applied using knife injection at rates of 0, 45, 90, 135, and 180 kg K h−1 with 80% and 30% evapotranspiration (ET) irrigation levels. Differences were not noted for estimated box mapping yield between K rates in 2016 (p = 0.3996). When 180 kg K ha−1 was applied, total bolls and estimated box mapping yield within 30% ET increased in the early and middle node zones and total nodes over all other K application rates in 2017. It was observed with box mapping that the early and middle node zones were able to utilize applied K more effectively due to the increase in bolls and yield compared to the late and vegetative node zones. Our results suggest that K is an important nutrient in cotton production due to the impacts it has on the early and middle node zones.

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Title: Cotton cultivar response to potassium fertilizer under irrigated and dryland conditions.

Author: Savana Davis, Praveen Gajula, Darrin Dodds, Jason Krutz1 Jeff Gore, Jac Varco, Tyson Raper Jagmandeep Dhillon

Abstract: Cotton (*Gossypium hirsutum* L.) cultivars vary in their response to environmental factors. Recently, interest in cotton cultivars' response to varying potassium (K) fertilizer application rates and irrigation has increased. As such, the effect of cotton varieties (early and mid-maturing), K fertilizer application rates, and irrigation on cotton growth, development, and yield were investigated in Starkville, MS, on two soil mapping units (SMUs): a Leeper silty clay loam (LSCL) and a Marietta fine sandy loam (MFSL). Cotton plant height was positively correlated with SMU, especially LSCL, reaching 60–110 cm on average, in both irrigated and rainfed conditions. Cotton lint yield, fiber quality, and leaf K concentration responded to K and irrigation, and these responses were SMU specific. Particularly, in LSCL, the early-maturing cultivar, DP 1518 B2XF, responded to K application rate in a positive linear manner in terms of lint yield under both irrigated and rainfed conditions, whereas mid-maturing DP 1646 B2XF did not. Moreover, lint yield in irrigated MFSL soil increased with K application rate, whereas no responses were observed in rainfed conditions. These data suggest that irrigation, SMU, and cultivar combination could have an impact on K response of cotton and should be considered when making fertility recommendations or decisions.

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Title: Optimizing Cotton Production: Impact of Varied Plant Densities on Yield and Fiber Quality

Author: Hatice Kübra Gören1, Uğur Tan

Abstract: This study investigates the impact of varying planting densities on cotton plants' morphological traits and yield. As planting density increases, there is a reduction in monopodial and sympodial branches, resulting in a more compact plant structure. The study highlights the highest yield achieved with specific planting densities, endorsing the viability of both holl and row planting methods. It suggests adopting narrow or ultra-narrow row systems to enhance yield and economize input costs. The study was conducted in 2017 at the experimental field of Aydın Adnan Menderes University in the Faculty of Agriculture's Department of Field Crops. The material used in this study was the widely cultivated cotton variety "Gloria" in the Aegean region. The investigation was conducted using a randomized block design with 4 replications. In evaluating cotton yield and related parameters, it was observed that D1 and D2 (14.285 plants/da) achieved the highest yield concerning plant density, emphasizing the viability of both holl and row planting methods. The study concluded that augmenting the number of plants within a specific area of production significantly contributes to higher seed cotton yields. To enhance yield and economize cotton input

costs, the adoption of a narrow or ultra-narrow row production system is suggested as an alternative strategy to conventional method.

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Title: Enhancing cotton sustainability: Multi-factorial intercropping, irrigation, and weed effects on productivity, quality and physiology

Author: Basim Mohammed Abdulkareem , Ali Mokhtassi-Bidgoli , Mahdi Ayyari , Eshagh Keshtkar , Hamed Eyni-Nargeseh

Abstract: Drought stress and weed infestation are significant factors that significantly decrease cotton yield. Increasing the variety of plants within a cotton field ecosystem can strengthen its stability and protect it from susceptibility to both biotic and abiotic pressures. In this two-year experiment (2021 and 2022), the effects of intercropping systems (four growth conditions including mono- and inter-cropped cotton varieties Golestan and Hekmat with Nepeta crispa and dragon's head (Lallemantia iberica)), irrigation (three intervals of 3, 6, and 9 days), and weed competition (weed-free and weedy plots) on the agronomic performance, physiological characteristics, and seed quality of cotton in a semi-arid region of Iran were studied. In 2021, the volume of irrigation water applied was 9873, 6100, and 4650 m^3 ha^{-1} for irrigation intervals of 3, 6, and 9 days, respectively. In 2022, the volumes were 9071, 5605, and 4272 m^3 ha^{-1} for the corresponding irrigation intervals. Over two years, Xanthium strumarium, Amaranthus retroflexus, and Portulaca oleracea were the dominant weed species. Weeds had the most significant impact on total dry weight; weed control increased plant vigor and growth, ranging from 1.4 to 2.3 times, while weed impact on cottonseed yield ranged from 18% to 96% reduction. Increasing irrigation intervals resulted in reductions in various parameters, with decreases of 39%–80% in total dry weight, 34%–57% in cottonseed yield, and 48%–72% in lint yield. The harvest indices for seed cotton, cottonseed, and lint ranged from 35.3% to 56.5%, 18.3%–35.0%, and 15.4%–20.5%, respectively. Weeds were responsible for a 17% decrease in the 1000-seed weight. As the irrigation intervals increased from 3 days to 6 days and 9 days, the number of bolls per plant decreased by 19%–85%. Extending the irrigation interval from 3 days to 6 days and 9 days resulted in a substantial decrease in the photosynthetic rate, ranging from 42% to 92%. Mono-cropped Golestan performed well under unstressed conditions such as 3-day interval irrigation and weed-free conditions. On the other hand, intercropped Hekmat demonstrated better resilience to both moisture and weed stresses. The LER (Land equivalent ratio) indices of both intercropping systems were generally favorable, indicating higher productivity compared to sole cropping. The intercropping systems consistently showed the highest LER indices under weedy conditions, highlighting the significance of intercropping as a valuable method in integrated weed management.

Title: Future cultivation of cotton for industrial use: landscape cytogenetics and species distribution modeling

Author: Masoud Sheidai, Zahra Noormohammadi & Omran Alishah

Abstract: Two cultivated tetraploid cotton species, Gossypium hirsutum L. (AD1) and G. barbadense L. (AD2), are economically important plant species. The cytogenetic characteristics can be influenced by environmental and demographic factors. Analysis combining landscape genetics and species distribution modeling can determine the role of global and climatic variables in the genetic makeup of plant species and potentially suitable growing regions. The present study was conducted to gain insight into the spatial cytogenetic structure of cotton cultivars and to identify cytogenetic clines in a global context. For the landscape cytogenetic study, cytogenetic data from 109 genotypes including 61 cotton cultivars of tetraploid of Gossypium barbedense L., and G. hirsutum L were used. We conducted species distribution models (SDM) research of these species in response to current climate change and 2050 climate change. redundancy analysis (RDA) and random forest (RF) of cytogenetic data with geographic variables were performed. This study showed that the cytogenetic characteristics of the cultivars in different countries differ significantly in their meiotic chromosome pairing and chiasma frequency ($P < 0.05$). SDMs also showed that climatic variables related to temperature and precipitation are some of the key variables that can determine the cytogenetic structure and geographic distribution of cultivars around the world and that the suitable area for cultivation will be reduced in response to climate change. In conclusion, longitude, latitude, temperature, and precipitation are some of the key variables that can determine the cytogenetic structure and geographic distribution of cotton cultivars around the world.

Title: Water and nitrogen use efficiencies in cotton production: A meta-analysis

Author:Zhiyu Wang , Kun Zhang , Guangcheng Shao , Jia Lu , Yang Gao , Enze Song

Abstract: Cotton production is influenced by water and nitrogen (N). However, the magnitude and direction of seed cotton yield, water use efficiency (WUE) and N use efficiency (NUE) responses to water and N inputs varied among the available studies due to different experimental and environmental factors (such as cotton varieties, climate types and irrigation systems). Objective- To quantify the relationships between water and N inputs and seed cotton yield, WUE and NUE and estimate the potential for

water and N optimization, 61 studies conducted in 9 countries were collected to establish a meta database. Methods- The relationships between water and N inputs and the interesting response variables were studied using a linear mixed-effects model in a partially restricted dataset. And the potential for water and N optimization was discussed using a meta-analysis in three classified datasets. Results and conclusions- Total water and N inputs had significant positive effects on seed cotton yield. WUE was negatively related to water input and positively related to N input, while NUE was positively related to water input and unrelated to N input. Negative interaction between water and N inputs existed in WUE and NUE, and the interaction was relatively large in NUE compared to in WUE. Reducing over-optimal water input to optimal may increase seed cotton yield by 12.3%, WUE by 25.0% and NUE by 2.2%. Similarly, reducing over-optimal N input to optimal may increase seed cotton yield and WUE by about 16.0% and NUE by 44.6%. There was great potential for optimizing water and N inputs in arid and hot desert climate (BWh) comparing with in arid and cold desert climate (BWk) and arid and cold steppe climate (BSk), and the seed cotton yield, WUE and NUE can be increased by up to around 35.0%, 16.6% and 34.5%, respectively. Surface irrigation had greater potential to optimize water and N inputs than drip irrigation, and the seed cotton yield and WUE can be increased by up to 50.7% and 43.0%, respectively.Significance- The findings provided suggestions for improving irrigation and fertilization in cotton production.

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Title: Boll/leaf ratio improves the source–sink relationship and lint yield during the **boll** setting stage of cotton.

Author: Yuting Liu, Yuyang Dai, Zhenyu Liu, Siqi Sun, Shujuan Wu, Jianing Du, Yuan Chen, Xiang Zhang, Dehua Chen, Yuan Chen

Abstract: Coordination of the cotton source–sink relationship is important. Although some indicators have been used to reflect the source-sink relationship in cotton, few indicators can directly demonstrate the source–sink relationship from the perspective of the cotton population. Objective- This study aimed to determine one or several indicators that can be used to directly reflect the source–sink relationship of the cotton population. Methods- Three field experiments were conducted with a conventional cotton cultivar ('Sikang1') in 2018 and 2019. Experiment I consisted of six planting densities: 3.0×10^4, 3.3×10^4, 3.6×10^4, 3.9×10^4, 4.2×10^4, 4.5×10^4 plants·ha^{-1}. Experiment Ⅱ was composed of two types of studies. One was made up of one control and two square removed treatments, including 10 and 20% of squares removed from the whole plant, with no square removed as the control. The other study consisted of

one control and two leaf-cutting treatments, in which 25 and 50% of the leaf area were cut off from the whole plant. Results- Lint yield was enhanced by 11.2–66.1% in 2018, and the boll number per leaf increased from 0.225 to 0.282 boll·leaf^{-1}. The boll number per square meter of leaf area increased from 22.7 to 27.2 bolls·m^{-2} leaf, and the boll dry weight per square meter of leaf area increased from 119.3 to 149.7 g·m^{-2} leaf in 2018. The results for 2019 were similar to those for 2018. There was significant linear positive correlations between lint yield and the above three measurements of the boll/leaf ratio. Moreover, these three measurements of the boll/leaf ratio were significantly and linearly positively correlated with each other, indicating that the three boll/leaf ratio measurements were similar and represented the coordination of the source–sink relationship of cotton population. The increased proportion of square removal led to a decrease in the boll number per leaf area. The canopy apparent photosynthesis rate, sucrose phosphate synthase and soluble acid invertase activities of subtending leaves decreased, but the sucrose and glucose contents increased and decreased, respectively. The proportion of ^{14}C assimilates exported from the subtending leaf to the opposite boll also decreased, and the dry weight of the reproductive organs decreased. When the leaf area index was adjusted to the optimum level by leaf cutting at the maximum leaf area index above the optimum range, the boll number per square meter of leaf area increased from 10.9 to 26.2 and 21.9 bolls·m^{-2} leaf, and the boll dry weight per square meter leaf area increased from 55.6 to 155.1 and 141.9 g·m^{-2}. The lint yield was also increased by 24.9% in 2018

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Title: Residual Benefits of Poultry Litter Applied by Subsurface Band vs. Surface Broadcast to Cotton.

Author: Haile Tewolde ,Thomas R. Way ,Normie Buehring and Johnie N. Jenkins

Abstract: Poultry litter (PL) is known to have residual effects on crop productivity long after applications cease. Whether this advantage is greater if applied by subsurface vs. surface broadcast is unknown. The objective of this study was to determine whether the residual benefit of PL to corn and cotton production is greater if applied in subsurface bands vs. surface broadcast and identify PL components contributing to this effect. The residual effect of PL applied by the two methods or synthetic nitrogen (sN) at seven plant available N rates (0–292 kg ha^{-1} yr^{-1}) in 2014–2015 was tested on corn and cotton in 2016–2019. Corn was grown without applying PL or sN in 2016, and cotton was grown in 2017–2019 after applying 90 kg ha^{-1} yr^{-1} sN to all plots. Corn produced 40% greater grain and cotton produced 29% more lint yield due to residuals from PL than sN. Residuals from PL distinctly increased cotton leaf K over sN regardless of the method of application. Corn and cotton yield benefits from PL residual were greater if applied by subsurface banding vs. surface broadcast. This difference diminished with

time. The overall results show PL components persist in the soil for up to 4 years and affect corn and cotton production, but this persistence is greater if the PL is applied by subsurface banding. This study identified K as the key PL nutrient that persisted in the soil and benefited cotton yield 4 years after the last application.

CROP PROTECTION

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Title: An ensemble deep learning model for automatic classification of cotton leaves diseases.

 Author: Hirenkumar Kukadiya , Nidhi Arora , Divyakant Meva , Shilpa Srivastava

Abstract: Cotton plant (Gossypium herbaceum), is one of the significant fiber crop grown worldwide. However, the crop is quite prone to leaves diseases, for which deep learning (DL) techniques can be utilized for early disease prediction and prevent stakeholders from losing the harvest. The objective of this paper is to develop a novel ensemble based deep convolutional neural network (DCNN) model developed on two base pretrained models named: VGG16 and InceptionV3 for early detection of cotton leaves diseases. The proposed ensemble model trained on cotton leaves dataset reports higher training and testing prediction accuracies as compared to the base pretrained models. Given that, deep learning architectures have hyper-parameters, this paper presents exhaustive experimental evaluations on ensemble model to tune hyper-parameters named learning rate, optimizer and no of epochs. The suggested hyper-parameter settings can be directly utilized while employing the ensemble model for cotton plant leaves disease detection and prediction. With suggested hyper-parameters settings of learning rate 0.0001, 20 epochs and stochastic gradient descent (SGD) optimizer, ensemble model reported training and testing accuracies of 98% and 95% respectively, which was higher than the training and testing accuracies of VGG16 and InceptionV3 pretrained DCNN models.

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Title: Mechanism of oxalate decarboxylase Oxd_S12 from Bacillus velezensis BvZ45-1 in defense against cotton verticillium wilt .

Author: Ying Sun, Na Yang, Sirui Li, Fei Chen, Yijing Xie, Canming Tang

Abstract: Verticillium wilt, a soilborne vascular disease caused by Verticillium dahliae, strongly affects cotton yield and quality. In this study, an isolated rhizosphere bacterium, designated Bacillus velezensis BvZ45-1, exhibited greater than 46% biocontrol efficacy against cotton verticillium wilt under greenhouse and field conditions. Moreover, through crude protein extraction and mass spectrometry analysis, we found many antifungal compounds present in the crude protein extract of BvZ45-1. The purified oxalate decarboxylase Odx_S12 from BvZ45-1 inhibited the growth of V. dahliae Vd080 by reducing the spore yield, causing mycelia to rupture, and causing spore morphology changes, cell membrane rupture and cell death. Subsequently, overexpression of Odx_S12 in Arabidopsis significantly improved plant resistance to V. dahliae. Through studies of the resistance mechanism of Odx_S12, V. dahliae was shown to produce oxalic acid (OA), which has a toxic effect on Arabidopsis leaves. Odx_S12 overexpression reduced Arabidopsis OA content, enhanced tolerance to OA, and improved resistance to verticillium wilt. Transcriptome analysis and quantitative real-time PCR (qRT-PCR) analysis revealed that Odx_S12 promoted the outbreak of reactive oxygen species (ROS) and a salicylic acid (SA) and abscisic acid (ABA) mediated defense response in Arabidopsis. In summary, this study not only identified B. velezensis BvZ45-1 as an efficient biological control agent, but also identified the resistance gene Odx_S12 as a candidate for cotton breeding against verticillium wilt.

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Title: Screening of different cotton hybrids containing Bt genes against Pectinophora gossypiella (Saunders).

Author: Shrilakshmi RG and Udikeri S S

Abstract: Field experiment was conducted at Agricultural Research Station, Dharwad farm, Dharwad during 2018-19 and 2019-20 to evaluate performance of eighteen different cotton genotypes representing four different Bt events. Damage due to pink boll worm (PBW) was least in interspecific (H×H) hybrids compared to interspecific hybrids (H×B) hybrids. Cotton Hybrid Everest recorded least square damage, flower damage, green boll and locule damage followed By Jadoo in both the seasons. Highest number of GOB/plant 26.68/pl and 25.89/pl observed in interspecific (H×H) hybrid Everest during 2018-19 and 2019-20, respectively, followed by Jadoo (25.61/pl in 2018-19 and 24.45/pl in 2019-20). Further, Everest recorded highest kapas yield of 15.88 q/ha

and 14.52 q/ha followed Jadoo which recorded 14.90 and 13.68 q/ha of kapas yield during 2018-19 and 2019-20, respectively.

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Title: Genome-Wide and Expression Pattern Analysis of the HIT4 Gene Family Uncovers the Involvement of GHHIT4_4 in Response to Verticillium Wilt in Gossypium hirsutum.

Author: Guoli Zhang ,Yang Jiao ,Zengqiang Zhao

Abstract: Chromatin remodelers are essential for regulating plant growth, development, and responses to environmental stresses. HIT4 (HEAT-INTOLERANT 4) is a novel stress-induced chromatin remodeling factor that has been less studied in abiotic stress and stress resistance, particularly in cotton. In this study, we conducted a comprehensive analysis of the members of the HIT4 gene family in Gossypium hirsutum using bioinformatics methods, including phylogenetic relationships, gene organization, transcription profiles, phylogenetic connections, selection pressure, and stress response. A total of 18 HIT4 genes were identified in four cotton species, with six HIT4 gene members in upland cotton. Based on the evolutionary relationships shown in the phylogenetic tree, the 18 HIT4 protein sequences were classified into four distinct subgroups. Furthermore, we conducted chromosome mapping to determine the genomic locations of these genes and visually represented the structural characteristics of HIT4 in G. hirsutum. In addition, we predicted the regulatory elements in HIT4 in G. hirsutum and conducted an analysis of repetitive sequences and gene collinearity among HIT4 in four cotton species. Moreover, we calculated the Ka/Ks ratio for homologous genes to assess the selection pressure acting on HIT4. Using RNA-seq, we explored the expression patterns of HIT4 genes in G. hirsutum and Gossypium barbadense. Through weighted gene co-expression network analysis (WGCNA), we found that GHHIT4_4 belonged to the MEblue module, which was mainly enriched in pathways such as DNA replication, phagosome, pentose and glucuronate interconversions, steroid biosynthesis, and starch and sucrose metabolism. This module may regulate the mechanism of upland cotton resistance to Verticillium wilt through DNA replication, phagosome, and various metabolic pathways. In addition, we performed heterologous overexpression of GH_D11G0591 (GHHIT4_4) in tobacco, and the results showed a significant reduction in disease index compared to the wild type, with higher expression levels of disease resistance genes in the transgenic tobacco. After conducting a VIGS (virus-induced gene silencing) experiment in cotton, the results indicated that silencing GHHIT4_4 had a significant impact, the resistance to Verticillium wilt weakened, and the internode length of the plants significantly decreased by 30.7% while the number of true leaves increased by 41.5%. qRT-PCR

analysis indicated that GHHIT4_4 mainly enhanced cotton resistance to Verticillium wilt by indirectly regulating the PAL, 4CL, and CHI genes. The subcellular localization results revealed that GHHIT4_4 was predominantly distributed in the mitochondria and nucleus. This study offers preliminary evidence for the involvement of the GHHIT4_4 in cotton resistance to Verticillium wilt and lays the foundation for further research on the disease resistance mechanism of this gene in cotton.

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Title: Influence of abiotic factor on incidence of Pink bollworm, Pectinophora gossypiella (SAUNDERS) on Bt cotton.

Author: KM Vora, Dr. YH Ghelani, NM Kachhadiya, BV Patoliya and Dr. MK Ghelani

Abstract: The present research on "Influence of abiotic factor on incidence of pink bollworm, Pectinophora gossypiella (Saunders) infesting Bt cotton" was carried out at Village: Daliya, Ta. Gondal, Dist. Rajkot during Kharif, 2020-21. The results of experiment were revealed that percent rosette flower were continuously increased and get its first peak (12.80 percent/plant) during 40th SMW and second peak (11.20 percent/plant) was observed on 45th SMW, then declined up to the harvest of the crop. The maximum temperature and bright sunshine hours were significantly positively correlated with rosette flower. Larval population was increased and get its first peak (7.00 larvae/20 bolls) during 43rd SMW. The second peak (7.00 larvae/20 bolls) was observed on 46th SMW (23rd WAS) and then declined up to the harvest of the crop. The bright sunshine hours was found highly significant and correlated positively with larval population. The morning and evening relative humidity were found highly significant with negative correlation, while the minimum temperature and wind velocity were found significant with negative correlation with larval population. Percent green boll damage were continuously increased and get its first peak (24.80 percent/plant) during 44th SMW. The second peak (16.80 percent/plant) was observed on 48th SMW and then declined continuously up to the harvest of the crop. The male moth caught from 26th SMW (1.50 moths/trap/week) to 2nd SMW (1.00 moths/trap/week) and ranged from 1.50 to 13.50 per trap/week during the entire crop period.

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Title: A genome-wide association study for resistance to Fusarium wilt (Fusarium oxysporum f. sp. vasinfectum) race 4 in diploid cotton (Gossypium arboreum) and resistance transfer to tetraploid Gossypium hirsutum.

Author: Abdelraheem Abdelraheem, Yi Zhu, Linghe Zeng, Salliana Stetina & Jinfa Zhang

Abstract: Fusarium wilt, caused by the soilborne fungus Fusarium oxysporum f. sp. vasinfectum (FOV), is a devastating disease affecting cotton (Gossypium spp.) worldwide. Understanding the genetic basis of resistance in diploid cotton and successfully transferring the resistance to tetraploid Upland cotton (G. hirsutum) are crucial for developing resistant cotton cultivars. Although numerous studies have been conducted to investigate the genetic basis of Fusarium wilt in tetraploid cotton, little research has been conducted on diploid species. In this study, an association mapping panel consisting of 246 accessions of G. arboreum, was used to identify chromosomal regions for FOV race 4 (FOV4) resistance based on foliar disease severity ratings in four greenhouse tests. Through a genome-wide association study (GWAS) based on 7,009 single nucleotide polymorphic (SNP) markers, 24 FOV4 resistance QTLs, including three major QTLs on chromosomes A04, A06, and A11, were detected. A validation panel consisting of 97 diploid cotton accessions was employed, confirming the presence of several QTLs. Evaluation of an introgressed BC2F7 population derived from G. hirsutum/G. aridum/G. arboreum showed significant differences in disease incidence and mortality rate, as compared to susceptible and resistant controls, suggesting that the resistance in G. arboreum and/or G. aridum was transferred into Upland cotton for the first time. The identification of novel major resistance QTLs, along with the transfer of resistance from the diploid species, expands our understanding of the genomic regions involved in conferring resistance to FOV4 and contributes to the development of resilient Upland cotton cultivars.

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Title: Development of Cotton Plants with Reduced Susceptibility to Meloidogyne Incognita through RNA Interference Approach.

Author: Sara Vitorino da Rocha Lemes, Raíre dos Santos Cavalcante, Maria Eugênia Lisei de Sá, Carolina Vianna Morgante, Maria Fatima Grossi de Sá

Abstract: Plant parasite such as the root-knot nematodes (RKN) of the genus Meloidogyne spp. cause significant damage to important crop plants in most parts of the world. During a compatible interaction, RKNs induce a hyper activation of root cell cycle to form feeding sites, causing root swellings, named galls, which impairs water and nutrient uptake and reduces yield. The restricted availability of chemical nematicides due to its toxicity and the reduced number of tolerant cultivars have

limited RKN control and management. In this work, we used a biotechnological approach based on RNA interference (RNAi) to silence an essential gene of Meloidogyne incognita to develop a RKN-tolerant cotton plant. It was previously demonstrated that the knockdown of the pre-mRNA splicing factor (SF) gene was lethal to the nematode Caenorhabditis elegans. In addition, the expression of dsRNA (double strand RNA) targeting the SF gene in plant hosts reduced susceptibility to Heterodera glycines or M. incognita in tobacco and soybean plants. Herein, we obtained genetically modified (GM) cotton plants expressing a dsRNA hairpin targeting the SF gene of M. incognita. Three independent transformation events were selected for generation advancement and challenged against M. incognita. Fifteenday-old T2 generation plants grown in 20x25 nursery bags were inoculated with 2,000 second stage juveniles (J2). The experiment was arranged in a completely randomized design with 15 replications under greenhouse conditions. Ninety days after inoculation, plants were evaluated for the number of eggs per gram of roots (NE), nematode reproduction factor (RF) and galls incidence through rating scale. We observed a decrease of 40% in the NE and a reduction of 60% in the RF in GM-genotypes compared to non-transformed plants. Our results reinforce that the production of dsRNA in hosts is an effective strategy to control endoparasitic nematodes. In addition, this method has the potential as a powerful tool to characterize the functions of parasite genes.

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Title: Differential biochemical and physiological responses to cotton leaf curl virus infection in contrasting cotton genotypes.

Author: Taranjeet Kaur, Shiwani Mandhania, Vikram Singh, Rashi Datten, Prakash Banakar, Karmal Malik, K. Sankaranarayanan, Minakshi Jattan, Sandeep Kumar, Anil Kumar Saini & Anil Jakhar

Abstract: Cotton production is tremendously impacted by the cotton leaf curl virus (CLCuV) in the Indian subcontinent. Viral infection modifies physiological and biochemical processes in plants, which leads to the appearance of symptoms. Hence, the current study was to discern the quantifiable changes in physiological and biochemical parameters in leaves of cotton plants graft inoculated with CLCuV on different days after infestation (DAI). The results revealed that in the CLCuV-infected plants, the relative water content (RWC) and total soluble protein were decreased. Some enzymes involved in the activities like anti-oxidative and defence mechanisms such as polyphenol oxidase (PPO), catalase (CAT), phenylalanine ammonia-lyase (PAL), and peroxidase (POX) were increased as the infestation period progressed with a concomitant increase in gossypol and total phenolic level. Contents of total soluble sugar, chlorophyll (Chl) along with hydrogen peroxide (H_2O_2) were increased initially and decreased afterwards in all genotypes. Correlation analysis elucidates that RWC is

negatively associated with electrolyte leakage (EL) and malondialdehyde (MDA) content. In contrast, Chl content showed a positive correlation with total soluble proteins, secondary metabolites like phenol and gossypol, anti-oxidative and defence enzymes. Three principal components (PCs) were produced by the principal component analysis (PCA) contributing 87.33% of the total variability in various physiological and biochemical traits of different genotypes. Phenolics profiling reveals that concentrations of rutin hydrate in the infected sample increased by 49.6% compared to the control one. Overall, the findings imply that CLCuV infection causes substantial changes in enzyme levels that result in the development of unrectifiable symptoms in susceptible genotypes.

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Title: Survival and alterations in reproductive organs of the cotton boll weevil, Anthonomus grandis grandis, fed alternative food.

Author: Matheus da Costa Moura, Bruna Mendes Diniz Tripode, Pedro Vale de Azevedo Brito, José Francisco Arruda e Silva, João Luis da Silva Filho

Abstract: The cotton boll weevil, Anthonomus grandis grandis Boheman (Coleoptera: Curculionidae), is one of the most important insect pests of cotton, causing significant yield losses. This insect completes its life cycle only on the flower structures of some Malvaceae species, with cotton being its preferred host. However, during the cotton off-season, the boll weevil enters a reproductive dormancy state, in tropical regions, with important alterations in their reproduction organs. During this period, a remaining insect population survives feeding on a variety of other food sources, but the insects do not reproduce. We hypothesized that these alterations in the insect's reproductive organs are associated with the nutritional levels provided by alternative food sources during the cotton off-season. To test our hypothesis, we first investigated food sources that sustain insect survival for long periods, such as weed species and fruits of cultivated crops. Then, we evaluated how various food sources affect the reproductive organs and reproductive capacity of the boll weevil. Among the alternative food sources tested, insect longevity was highest on banana (Musa paradisiaca L.), mango (Mangifera indica L.), papaya (Carica papaya L.), milkweed (Euphorbia heterophylla L.), and lilac tasselflower (Emilia sonchifolia L.). However, only banana and mango resulted in greater longevity than cotton squares. Banana was the preferred food and resulted in the highest levels of nutrients in the insects. Additionally, insects previously fed on banana made more oviposition punctures on cotton squares than those fed only on cotton squares, which resulted in a significantly higher number of emerged adults. Histological analysis of the insects' reproductive organs showed that feeding on papaya resulted in morphological changes and testicle degradation. In

conclusion, we present evidence that boll weevils fed on alternative food sources (other than cotton squares or similar-quality food) display a nutritional imbalance, associated with substantial alterations in the reproductive tissues of this insect, which may trigger the reproductive dormancy state.

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Title: Transcriptome Analysis of Resistant Cotton Germplasm Responding to Reniform Nematodes

Author: Chunda Feng ,Salliana R. Stetina andJohn E. Erpelding

Abstract: Reniform nematode (Rotylenchulus reniformis) is an important microparasite for Upland cotton (Gossypium hirsutum L.) production. Growing resistant cultivars is the most economical management method, but only a few G. barbadense genotypes and some diploid Gossypium species confer high levels of resistance. This study conducted a transcriptome analysis of resistant genotypes to identify genes involved in host plant defense. Seedlings of G. arboreum accessions PI 529728 (A2-100) and PI 615699 (A2-190), and G. barbadense genotypes PI 608139 (GB 713) and PI 163608 (TX 110), were inoculated with the reniform nematode population MSRR04 and root samples were collected on the fifth (D5) and ninth (D9) day after inoculation. Differentially expressed genes (DEGs) were identified by comparing root transcriptomes from inoculated plants with those from non-inoculated plants. Accessions A2-100 and A2-190 showed 52 and 29 DEGs on D5, respectively, with 14 DEGs in common, and 18 DEGs for A2-100 and 11 DEGs for A2-190 on chromosome 5. On D9, four DEGs were found in A2-100 and two DEGs in A2-190. For GB 713, 52 and 43 DEGs were found, and for TX 110, 29 and 117 DEGs were observed on D5 and D9, respectively. Six DEGs were common at the two sampling times for these genotypes. Some DEGs were identified as Meloidogyne-induced cotton (MIC) 3 and 4, resistance gene analogs, or receptor-like proteins. Other DEGs have potential roles in plant defense, such as peroxidases, programmed cell death, pathogenesis related proteins, and systemic acquired resistance. Further research on these DEGs will aid in understanding the mechanisms of resistance to explore new applications for the development of resistant cultivars

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Title: Opportunistic pathogenicity observed for the endophytic fungus Diaporthe ueckerae on Gossypium hirsutum plants

Author: Matheus Mendonça de Souza Marques,   Isabella de Oliveira Silva,   Layara Alexandre Bessa &   Luciana Cristina Vitorino

Abstract: Cotton crops are routinely threatened by emerging fungal diseases. Fungal endophytes also can be considered latent phytopathogens. In this study we tested the hypothesis that an endophytic strain of Diaporthe, isolated from chlorotic leaves of cotton (Gossypium hirsutum), could trigger physiological effects of biotic stress in this oilseed plant. We also assessed the histopathological aspects of the mycelial interaction of the endophyte with the adaxial surface of G. hirsutum leaves. Thus, we studied the synthesis of photosynthetic pigments, pattern of gas exchange, and photochemistry of cotton plants subjected to inoculation with Diaporthe ueckerae via root and leaf at three different phenological stages (vegetative, reproductive, and maturation). Additionally, we histopathologically analyzed infected leaves using electron microscopy to study the process of leaf colonization by this endophytic fungus. We evidenced that D. ueckerae inoculation negatively affected the synthesis of photosynthetic pigments in plants at vegetative and reproductive stages. Moreover, inoculation also negatively affected the photosynthetic rate and carboxylation efficiency of these plants. We also found that the presence of the endophyte increased transpiration and decreased water use efficiency in the plants. Furthermore, foliar inoculation negatively affected stomatal conductance, whereas inoculation via leaf or root reduced the photochemical performance of cotton. We also observed that D. ueckerae colonizes the leaf tissues of G. hirsutum via glandular trichomes and forces penetration into the epidermis using appressoria, and the plant responds by closing the stomata. The observed physiological alterations are indicative of biotic stress, confirming the hypothesis that D. ueckerae may be an opportunistic phytopathogen for cotton plants.

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Title: Integrated Management of the Cotton Charcoal Rot Disease Using Biological Agents and Chemical Pesticides.

Author: Ofir Degani , Assaf Chen , Elhanan Dimant , Asaf Gordani , Tamir Malul and Onn Rabinovitz

Abstract: Charcoal rot disease (CRD), caused by the phytopathogenic fungus Macrophomina phaseolina,is a significant threat to cotton production in Israel and worldwide. The pathogen secretes toxins and degrading enzymes that disrupt the water and nutrient uptake, leading to death at the late stages of growth. While many control strategies were tested over the years to reduce CRD impact, reaching that goal remains a significant challenge. The current study aimed to establish, improve, and deepen our understanding of a new approach combining biological agents and chemical pesticides. Such intervention relies on reducing fungicides while providing stability and a head start to eco-friendly bio-protective Trichoderma species. The research design included

sprouts in a growth room and commercial field plants receiving the same treatments. Under a controlled environment, comparing the bio-based coating treatments with their corresponding chemical coating partners resulted in similar outcomes in most measures. At 52 days, these practices gained up to 38% and 45% higher root and shoot weight and up to 78% decreased pathogen root infection (tracked by Real-Time PCR), compared to non-infected control plants. Yet, in the shoot weight assessment (day 29 post-sowing),the treatment with only biological seed coating outperformed (p < 0.05) all other biological-based treatments and all Azoxystrobin-based irrigation treatments. In contrast, adverse effects are observed in the chemical seed coating group, particularly in above ground plant parts, which are attributable to the addition of Azoxystrobin irrigation. In the field, the biological treatments had the same impact as the chemical intervention, increasing the cotton plants' yield (up to 17%), improving the health (up to 27%) and reducing M. phaseolina DNA in the roots (up to 37%). When considering all treatments within each approach, a significant benefit to plant health was observed with the biochemo integrated management compared to using only chemical interventions. Specific integrated treatments have shown potential in reducing CRD symptoms, such as applying bio-coating and sprinkling Azoxystrobin during sowing. Aerial remote sensing based on high-resolution visible channel (RGB), green–red vegetation index (GRVI), and thermal imaging supported the above findings and proved its value for studying CRD control management. This research validates the combined biological and chemical intervention potential to shield cotton crops from CRD.

PLANT GENETICS AND BREEDING

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Title: Selena – a new cotton variety.

Authors: Dimitrova, Valentina; Nedyalkova, Spasimira

Imprint: Bulgarian Journal of Crop Science / Rastenievdni Nauki, 2024, Vol 61, Issue 1, p31

Abstract: The aim of this research was to study the productive potential and evaluate the fiber properties of the new Selena cotton variety. The variety was studied in competition variety trials conducted in 2017-2022 in the experimental field of the Field Crops Institute in the town of Chirpan. In the IASAS system the variety was tested in 2021-2022. It was approved as a new cotton variety in 2023. Selena variety was created by remote hybridization from the crossing of the allotetraploid Gossypium thurberi Tod. × Gossypium raimondii Ulbr. With Dorina variety and subsequent backcrossing

with Darmi variety. Selena variety is an early and productive new cotton variety with improved fiber quality. The vegetation period was 106-111 days. In seed cotton yield of 1663 kg/ha, on average for 6 years, it surpassed the standard cultivar Chirpan-539 by 12.3%. According to the IASAS data, in seed cotton yield of 2163 kg/ha it exceeded the two standard cultivars, Chirpan-539 - by 2.2%, Avangard-264 - by 1.3%, the average standard (average of the two standards) - by 1.8%. In lint yield of 95.5 kg/ha Selena variety was equal to Avangard-264, surpassed Chirpan-539 by 2.9% and respectively the average standard - by 1.4%. Selena variety had a number of valuable technological fiber qualities and in some indicators surpassed both standard cultivars. Compared to the two standard cultivars it had better Spinning Consistency Index (SCI), greater Upper Half Mean Length and fiber strength, lower micronaire, better spectroscopy with RD difference reflection than Chirpan-539, less yellowness than Avangard-264 and better fiber whiteness. Selena variety combines better productivity with better technological fiber qualities than the standard cultivars, which defines it as a new achievement in the selection of cotton in our country.

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Title: Study of DNA Synthesis Activity in High Yielding Cotton Hybrids and Their Parental Forms.

Author: Mammadova Afet Dadash, Mammadova Naila Khurshud

Abstract: The purpose of this work was a comparative study of the DNA content in heterotic cotton hybrids and their parental forms. As a result of the research, it was found that the hybrids exceeded the original forms in terms of the content of DNA per leaf cell. So, for example, in the M-4 x AK-4-42 hybrid, the amount of DNA per somatic cell was 13.4 pg, in the maternal form it was 6.2 pg, in the paternal form - 12.0 pg. In the M-4 × C-460 hybrid, the content of DNA per leaf cell was 11.1 pg, in the parents, it was 6.2 pg and 5.0 pg, respectively An increase in the absolute content of DNA in hybrids is observed due to the activation of all DNA fractions. For example, the hybrid M-4 x C-460 exceeds the maternal form in terms of the content of labile DNA by 2.2 pg, stable DNA by 2.3 pg, and residual DNA by 0.4 pg. The increase in DNA fractions in the hybrid in comparison with the paternal form was 2.7 pg, 2.8, 0.6 pg, respectively.At the same time, in heterotic hybrids of cotton, a decrease in the number of cells per unit area is noted, which indicates an increase in the size of the cells of the hybrid. In the M-4 x AK-4-42 hybrid, the number of cells per unit leaf area was 19 x 106 versus 24 x 106 and 21 x 106 in the original forms. At the same time, the mass of cells also increases in hybrids: the mass of one cell of the hybrid M-4 x AK 4-42 is 14.1 x 10-9 g, in parental forms - 10.7 x 10-9 and 12.8 x 10-9 g, respectively. The study of the nature of DNA

synthesis in cytoplasmic organelles revealed the activation of chloroplast DNA synthesis in hybrids compared to parents. The highest content of chloroplast DNA in comparison with parents was noted in the M-4 x 152F hybrid. The increase in the content of chloroplast DNA in comparison with the original forms in this hybrid was 76.9%.

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Title: Auxin resistant 2 and short hypocotyl 2 regulate cotton fiber initiation and elongation .

Author: Fei Jin, Liping Zhu, Liyong Hou, Hongbin Li, Ling Li, Guanghui Xiao

Abstract: Auxin, a pivotal regulator of diverse plant growth processes, remains central to development. The auxin-responsive genes auxin/indole-3-acetic acids (AUX/IAAs) are indispensable for auxin signal transduction, which is achieved through intricate interactions with auxin response factors (ARFs). Despite this, the potential of AUX/IAAs to govern the development of the most fundamental biological unit, the single cell, remains unclear. In this study, we harnessed cotton (Gossypium hirsutum) fiber, a classic model for plant single-cell investigation, to determine the complexities of AUX/IAAs. Our research identified 2 pivotal AUX/IAAs, auxin resistant 2 (GhAXR2) and short hypocotyl 2 (GhSHY2), which exhibit opposite control over fiber development. Notably, suppressing GhAXR2 reduced fiber elongation, while silencing GhSHY2 fostered enhanced fiber elongation. Investigating the mechanistic intricacies, we identified specific interactions between GhAXR2 and GhSHY2 with distinct ARFs. GhAXR2's interaction with GhARF6-1 and GhARF23-2 promoted fiber cell development through direct binding to the AuxRE cis-element in the constitutive triple response 1 promoter, resulting in transcriptional inhibition. In contrast, the interaction of GhSHY2 with GhARF7-1 and GhARF19-1 exerted a negative regulatory effect, inhibiting fiber cell growth by activating the transcription of xyloglucan endotransglucosylase/hydrolase 9 and cinnamate-4-hydroxylase. Thus, our study reveals the intricate regulatory networks surrounding GhAXR2 and GhSHY2, elucidating the complex interplay of multiple ARFs in AUX/IAA-mediated fiber cell growth. This work enhances our understanding of single-cell development and has potential implications for advancing plant growth strategies and agricultural enhancements.

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Title: Unravelling the Complex Interactions among Yield Attributes in Upland Cotton (Gossypium hirsutum L.) through Principal Component Analysis.

Author: Bana Venkata Ravi Prakash Reddy, Kalapati Mohan Vishnuvardhan, U. Nikhil Sagar, D. Lakshmi Kalyani, M. Siva Ramakrishna, K. Amarnath and N.C. Venkateswarlu

Abstract: Present investigation was carried out with 34 upland cotton genotypes to assess the genetic divergence for seven yields and yield attributes through principal component analysis to identify the factors contributing to yield variability. The PCA showed that the first two principal components explained 59.89% of the total variation. PC1 components showed positive relationship with ginning percentage whereas PC2 showed positive relationship with plant height, bolls per plant and seed cotton yield. Hence, these characters will be given priority in future for upland cotton breeding programme. Cluster analysis using Ward's method was performed with seven quantitative traits displayed that four clusters were formed in which largest contribution was shared by cluster I with a maximum of 15 genotypes followed by cluster II consists of 10 genotypes. Based on PCA scores and cluster mean values, the genotypes NH 702, NDLH 2051-3, NH 703, AKH 2013-2 and CPD 1951 were considered to be desirable for utilization in upland cotton improvement.

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Title: Environment-specific selection of high-quality cotton cultivars from on-station and on-farm trials

Author: Heer, Alexander; Joshi, Tanay; Messmer, Monika and Riar, Amritbir

Abstract: Selecting qualitatively high cotton cultivars is a critical aspect of cotton breeding programs. However, choosing cultivars is not straightforward. Genotype × environment (G×E) interactions have to be considered when choosing varieties for cultivation. This holds especially true in organic farming where natural stress resistance is crucial in the absence of genetic modifications. For on-station trials, GGE biplots have become a popular tool for selecting cultivars. We applied the method to data from our on-station trials conducted at five sites in India and for 29 cotton cultivars. The sites included different farming conditions and the cultivars were a mix of hybrids and non-hybrids from the Gossypium hirsutum and Gossypium arboreum species. Using the PPBstats package in R, we identified suitable varieties for each site. Cultivar performance varied greatly between sites. Varieties bred at a site performed particularly well, showing the importance of environment-specific breeding. On-farm trials are a

participatory breeding approach that enables farmers to participate directly in the decision-making. However, estimating G×E effects is difficult due to the trial design. To analyse our on-farm trials conducted on 102 farms in India, testing 32 G. hirsutum and G. arboreum varieties, we applied a hierarchical Bayesian G×E model. The analysis was done using the PPBstats package in R. Farm clusters in which the tested cultivars performed similarly were identified. Well-performing varieties for each cluster were found through mean comparisons within each farm. Furthermore, a GGE biplot analysis was performed by pooling farms along agroclimatic zones to identify suitable cultivars on an agroclimatic level. The preliminary results from the GGE biplots have lower precision for the individual farmers that participated in the trials than the hierarchical Bayesian method but can be used for giving recommendations to policymakers and stakeholders for selecting cultivars based on agroclimatic zones. Thus, the combination of the two approaches can be used for decision making on G×E cultivar selection through on-farm trials while providing participating farmers with tailored recommendations for their own cultivation.

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Title: Diversity evaluation of machine-picked agronomic traits in Gossypium barbadense L. germplasm resources

Author: HUANG Xinglei), WANG Weiran, WANG Meng, ZHU Jiahui, LIN Feng, QIN Guol, YANG Jing

Abstract: The agronomic characters of sea island cotton germplasm resources were analyzed in order to provide candidate materials for its parent selection and variety cultivation in the future.【Methods】125 sea island cotton germplasm resources with zero fruit branches were selected to analyze the coefficient of variation,genetic diversity,correlation,principal component and agronomic characters. 【 Results 】 Indicating that the 125 sea island cotton germplasm resources in this study had great differences and were rich in germplasm diversity.The coefficient of variation of 12 characters was between 3.54% and 23.85%,and the genetic diversity index between 1.96 and 2.10.The results of correlation analysis showed that there was an extremely significant positive correlation between plant height and initial fruit branch height,initial fruit branch node position and boll weight,extremely significant positive correlation between initial fruit branch height and initial fruit branch node position and boll weight,and extremely significant positive correlation between middle fruit branch length and middle fruit branch length. The length of the lower fruit branch and the angle between the lower fruit branch were significantly positively correlated,so it is

necessary to consider each other and analyze comprehensively when cultivating cotton varieties picked by machine. By principal component analysis,the cumulative contribution rate of 12 agronomic characters divided into 6 principal components reached 78.59%,which were plant height factor,fruit branch factor,stem diameter factor,lint percentage factor,boll number factor and boll weight factor. The germplasm resources of sea island cotton were divided into five groups by cluster analysis. The fifth group showed good mechanical picking characters,and the representative varieties were Xinhai 43,Xinhai 55,Shihezi V7-4,K426,Xin78,16DJC01,Xinku K2442 and Xinku 198-1.【Conclusion】The 125 resources are rich in diversity,and the clustering analysis of the fifth group shoes that it has good machine-harvestability,and 21 breeding materials with good machine-harvestability were obtained,which could be used as the basic machine-picked materials.

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Title: Cotton Genetics and Breeding.

Author: Anbesaw Gate, Alemu Abate & Bizuayehu Kerisew Semahagn

Imprint: Cotton Sector Development in Ethiopia , ChapterPart of the book series: Textile Science and Clothing Technology, Springer Publishing

Abstract: Cotton (Gossypium spp.) is a soft, fluffy staple fibre that develops in a boll, or protective casing, around the seeds of cotton plants of the genus Gossypium in the mallow family Malvaceae. Arboreums are thought to be indigenous to India. G. herbaceum may have been introduced into western India from Arabia, Persia and Baluchistan, as well as race acerifolium. Cotton is the most widely used fibre in the production of clothing and other textiles. Around 25 million tonnes of cotton are currently produced worldwide. China and India produce the most cotton, followed by Brazil and the United States of America. Cotton is Ethiopia's most important cash crop, and it is vital to the country's agricultural, industrial and economic development. It provides basic raw materials (cotton fibre) to the textile industry for use in the domestic or export markets. Currently, 96% of cotton varieties grown in the country are upland, with DP 90 covering 80% of the acreage, Stam 59A (15%), Acala SJ2 (0.5%), and land races and local varieties accounting for the remaining 4%. Cotton cultivation has long been practiced in Ethiopia. Cotton is grown primarily in the Awash Valley, Gambela, Humera and Metema. Cotton has grown in many parts of the country. There are large potential areas in each region: Tigray has 269,130 ha; Amhara has 678,710 ha; South nations, nationalities and people region (SNNPR) has 600,900 ha; Oromia has 407,420 ha; Gambella has 316,450 ha; Benshangul has 303,170 ha; Afar has 200,000 ha and Somali has 225,000 ha. Germplasm enhancement, a lack of cotton seed production, and abiotic and biotic stresses are major production and cotton breeding constraints. Breeders are currently experimenting with these factors. Cotton breeding in Ethiopia has achieved

varietal development. Among those released varieties, the major ones include disease resistance, high yield, pest resistance, high fibre quality, comfort to mechanical harvesting by increasing cotton height, early maturity and adaptability to harsh environments. In light of the challenges, we recommended the following feature directions for cotton breeders in Ethiopia. Work on extra-long cotton varieties, varieties suitable for mechanical harvesting, varieties for high fibre quality, varieties for biotic and abiotic resistance and upgrading breeding activities to modern biotechnological tools

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Title: Genotypic variation in functional contributors to yield for a diverse collection of field-grown cotton.

Author: Navneet Kaur, John L. Snider, Andrew H. Paterson, Gurpreet Virk, Ved Parkash, Phillip Roberts, Changying Li

Abstract: Yield improvement in cotton could be accelerated through selection for functional yield drivers such as interception of cumulative photosynthetically active radiation ($\sum$IPAR), radiation use efficiency (RUE), and harvest index (HI). However, information on the extent to which these traits vary in cotton in the southeastern United States is limited. It was hypothesized that functional yield drivers would vary significantly within a diverse cotton collection. This study was conducted in Tifton and Athens, GA, and included a total of 4 site-years. Lint yield, total biomass production, $\sum$IPAR, RUE, and HI were all affected by genotype. Biomass was more strongly correlated with RUE than $\sum$IPAR. Even among the highest yielding genotypes, values for functional yield drivers (biomass and harvest index) differed significantly, indicating that high yields could be achieved by differentially manipulating these underlying traits. However, when considered for all genotypes, only HI exhibited a significant positive correlation with yield. Boll production and intra-boll yield components were also affected by genotype. When considered across upland genotypes, lint per boll, lint per seed, and lint percent were strongly associated with HI and lint yield, whereas boll mass and seed number per boll were not. We conclude that the genotypes evaluated in the current study achieve high lint production per boll and lint yields by manipulating different yield drivers. However, lint yield was primarily maximized through an increase in HI due to increases in boll production and within-boll distribution of biomass to fiber, not due to increases in total biomass production or boll size.

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Title: Integrated analysis of the transcriptome and metabolome reveals the molecular mechanism regulating cotton boll abscission under low light intensity.

Author: Ning Zhao, Zhao Geng, Guiyuan Zhao, Jianguang Liu, Zetong An, Hanshuang Zhang, Pengfei Ai & Yongqiang Wang

Abstract: Cotton boll shedding is one of the main factors adversely affecting the cotton yield. During the cotton plant growth period, low light conditions can cause cotton bolls to fall off prematurely. In this study, we clarified the regulatory effects of low light intensity on cotton boll abscission by comprehensively analyzing the transcriptome and metabolome. Results- When the fruiting branch leaves were shaded after pollination, all of the cotton bolls fell off within 5 days. Additionally, H_2O_2 accumulated during the formation of the abscission zone. Moreover, 10,172 differentially expressed genes (DEGs) and 81 differentially accumulated metabolites (DAMs) were identified. A KEGG pathway enrichment analysis revealed that the identified DEGs and DAMs were associated with plant hormone signal transduction and flavonoid biosynthesis pathways. The results of the transcriptome analysis suggested that the expression of ethylene (ETH) and abscisic acid (ABA) signaling-related genes was induced, which was in contrast to the decrease in the expression of most of the IAA signaling-related genes. A combined transcriptomics and metabolomics analysis revealed that flavonoids may help regulate plant organ abscission. A weighted gene co-expression network analysis detected two gene modules significantly related to abscission. The genes in these modules were mainly related to exosome, flavonoid biosynthesis, ubiquitin-mediated proteolysis, plant hormone signal transduction, photosynthesis, and cytoskeleton proteins. Furthermore, TIP1;1, UGT71C4, KMD3, TRFL6, REV, and FRA1 were identified as the hub genes in these two modules. Conclusions- In this study, we elucidated the mechanisms underlying cotton boll abscission induced by shading on the basis of comprehensive transcriptomics and metabolomics analyses of the boll abscission process. The study findings have clarified the molecular basis of cotton boll abscission under low light intensity, and suggested that H_2O_2, phytohormone, and flavonoid have the potential to affect the shedding process of cotton bolls under low light stress.

Title: Genome-Wide Analysis of VILLIN Gene Family Associated with Stress Responses in Cotton (*Gossypium* spp.)

Author: Akash Deep andDhananjay K. Pandey

Abstract: The VILLIN (VLN) protein plays a crucial role in regulating the actin cytoskeleton, which is involved in numerous developmental processes, and is crucial for plant responses to both biotic and abiotic factors. Although various plants have been studied to understand the VLN gene family and its potential functions, there has been limited exploration of VLN genes in Gossypium and fiber crops. In the present study, we characterized 94 VLNs from Gossypium species and 101 VLNs from related higher plants such as Oryza sativa and Zea mays and some fungal, algal, and animal species. By combining these VLN sequences with other Gossypium spp., we classified the VLN gene family into three distinct groups, based on their phylogenetic relationships. A more in-depth examination of Gossypium hirsutum VLNs revealed that 14 GhVLNs were distributed across 12 of the 26 chromosomes. These genes exhibit specific structures and protein motifs corresponding to their respective groups. GhVLN promoters are enriched with cis-elements related to abiotic stress responses, hormonal signals, and developmental processes. Notably, a significant number of cis-elements were associated with the light responses. Additionally, our analysis of gene-expression patterns indicated that most GhVLNs were expressed in various tissues, with certain members exhibiting particularly high expression levels in sepals, stems, and tori, as well as in stress responses. The present study potentially provides fundamental insights into the VLN gene family and could serve as a valuable reference for further elucidating the diverse functions of VLN genes in cotton.

Title: Targeted genome editing for cotton improvement: prospects and challenges.

Author: Rakesh Kumar, Joy Das, Raghavendra Keelara Puttaswamy, Manoj Kumar,

Ganesan Balasubramani & Yenumula Gerard Prasad

Imprint: The Nucleus, Published: 21 March 2024

Abstract: Cotton is a highly profitable agricultural crop globally, valued for its valuable natural cellulosic fibres, renewable biofuel potential, and rich edible oil content. Global

cotton production is impeded by multiple biotic and abiotic stresses, compounded with the ever-increasing human population and demands, necessitating enhanced and sustainable yields. Although traditional breeding and transgenic technologies have demonstrated efficiency in enhancing economic agronomic traits, their effectiveness is hindered by reliance on limited genetic variability and a time-consuming process involving multiple backcrosses and stringent trait selections. The relatively large and complex genome (~ 2.5 Gb) with high functional gene redundancy poses significant challenges to genomic manipulations in cotton. The rapid advancement of sequence-specific engineered nucleases, particularly RNA-guided CRISPR-based Cas nucleases, have revolutionised gene manipulation techniques, proving effective in precise targeted mutagenesis and multiplexed genome editing across diverse organisms, including plants. The CRISPR/Cas9 genome editing technology, known for its simplicity, flexibility, consistency, and remarkable efficiency, has the potential to facilitate extensive genetic modifications in cotton traits, heralding a new era of precision cotton breeding. Recent cotton genome sequencing initiatives provide valuable data for identifying new gene targets, paving the way for advancements in crop sustainability. Integrated genome sequencing and gene editing signify a precision era in cotton breeding, facilitating progress in functional genomics and trait improvement. In this review, we summarised the genome editing tools available for targeted genome modification in plants and the current status of targeted genome editing applications in cotton for trait improvement. Additionally, we highlighted the existing cotton genes, which have been functionally validated as both negative and positive regulators of important agronomic traits for their utilization in future cotton genome editing programs. Finally, we discussed the current challenges and future prospects of these genome engineering tools for their comprehensive applications in cotton functional genomics and breeding to enhance productivity and resilience to climate change.

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Title: Cotton Biotechnology.

Author: Dawit Tesfaye Degefu & Zerihun Desalegn Gebregiorgis
Imprint: Cotton Sector Development in Ethiopia , ChapterPart of the book series: Textile Science and Clothing Technology, Springer Publishing
Abstract: The cotton plant, Gossypium hirsutum L., is one of the four cultivated cotton varieties grown in tropical environments primarily for its natural fiber. Cotton is cultivated by many farmers in Ethiopia as a source of income in both rainfed and irrigated areas. It can also create job opportunities for thousands of individuals. In addition to its fiber, the by-products are utilized for various purposes. Despite these advantages, the production of cotton faces challenges from both biotic and abiotic constraints. Among these, insect pests such as Helicoverpa armigera and Pectinophora gossypiella are significant threats to cotton in Ethiopia, and managing these pests

through insecticide spraying is difficult due to their concealed feeding habits. The extensive use of different types of insecticides poses numerous challenges to humans, animals, and the environment. Moreover, these pests have developed resistance to multiple insecticides. Therefore, finding environmentally friendly alternatives for pest control is crucial. However, the limited genetic diversity among cotton germplasms presents a breeding challenge for developing cultivars that can overcome various production constraints. In plant breeding, molecular markers are valuable tools for measuring and identifying economically important traits that are otherwise difficult to assess visually. Molecular markers are essential for plant breeders in the development of cotton cultivars that meet market demands. Additionally, advancements in recombinant DNA technology offer the potential to improve crops with limited genetic diversity, such as cotton. Through genetic engineering, desirable traits such as insect resistance, herbicide tolerance, increased lint strength, length, and fineness can be introduced to cotton, adding value to the crop. This technology can help farmers achieve lower production costs, protect them from hazardous chemical exposure, ensure environmental safety, and maximize potential profits by reducing pest infestation at the early boll formation stage and providing high-quality cotton lint.

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Title: Mapping QTL for fiber- and seed-related traits in *Gossypium tomentosum* CSSLs with G. *hirsutum* background.

Author:Yongshui Hao, Xueying Liu, Qianqian Wang, Shuxin Wang, Qingqing Li, Yaqin Wang, Zhongni Guo, Tiantian Wu, Qing Yang,

Abstract: Introducing the inherent genetic diversity of wild species into cultivars has become one of the hot spots in crop genetic breeding and genetic resources research. Fiber- and seed-related traits, which are critical to the global economy and people's livelihoods, occupy the principal status of cotton breeding. Here, a wild cotton species Gossypium tomentosum, was used to broaden the genetic basis of G. hirsutum and identify QTL for fiber- and seed-related traits. A population of 559 chromosome segment substitution lines (CSSLs) was established with various chromosome segments from G. tomentosum in a G. hirsutum cultivar background. A total of 72, 89, and 76 QTLs were identified for three yield traits, five fiber quality traits, and six cottonseed nutrient quality traits, respectively. Favorable alleles of 104 QTLs were contributed by G. tomentosum. Sixty-four QTL were identified in two or more environments, and candidate genes for three of them were further identified. The results of this study contributed to further study on the genetic basis of the morphogenesis of these economic traits, as well as indicating that the great breeding potentials of G. tomentosum in improving the fiber- and seed-related traits in G. hirsutum.

Title: AmCBF1 activates the expression of GhClpR1 to mediate dark-green leaves in cotton (*Gossypium hirsutum*).

Author: Qianqian Zhang, Peilin Wang, Weilong Li, Man Liu, Lili Zhou, Xiaofeng Su, Hongmei Cheng & Huiming Guo

Abstract: The ATP-dependent caseinolytic protease (Clp protease) family plays a crucial role within chloroplasts, comprising several Clp proteins to maintain chloroplast homeostasis. At present, research on Clp proteins mainly focuses on Arabidopsis, leaving its function in other plants, particularly in crops, less explored. In this study, we overexpressed AmCBF1 from Ammopiptanthus mongolicus (A. mongolicus) in wild type (R15), and found a significant darkening of leaf colour in transgenic plants (L28 and L30). RNA-seq analysis showed an enrichment of pathways associated with photosynthesis. Subsequent screening of differentially expressed genes revealed a significant up-regulation of GhClpR1, a gene linked to chloroplast development, in the transgenic strain. In addition, GhClpR1 was consistently expressed in upland cotton, with the highest expression observed in leaves. Subcellular localization analysis revealed that the protein encoded by GhClpR1 was located in chloroplasts. Yeast one hybrid and dual luciferase experiments showed that the AmCBF1 transcription factor positively regulates the expression of GhClpR1. VIGs-mediated silencing of GhClpR1 led to a significant yellowing phenotype in the leaves. This was accompanied by a reduction in chlorophyll content, and microscopic examination of chloroplast ultrastructure revealed severe developmental impairment. Finally, yeast two-hybrid assays showed that GhClpR1 interacts with the Clp protease complex accessory protein GhClpT2. Our study provides a foundation for studying the function of the Clp protease complex and a new strategy for cultivating high-light-efficiency cotton resources.

Title: GhCOL2 Positively Regulates Flowering by Activating the Transcription of GhHD3A in Upland Cotton (*Gossypium hirsutum* L.)

Author: Xiaoyu Yin, Ye Liu, Hang Zhao, Qi Su, Juan Zong, Xueying Zhu & Ying Bao

Abstract: Plants have evolved sophisticated signaling networks to adjust flowering time, ensuring successful reproduction. Two crucial flowering regulators, FLOWERING LOCUS T (FT) and CONSTANS (CO), play pivotal roles in regulating flowering across various species. Previous studies have indicated that suppressing Gossypium hirsutum CONSTANS-LIKE 2 (GhCOL2), a homolog of Arabidopsis CO, leads to delayed flowering in cultivated cotton. However, the underlying regulatory mechanisms remain unknown. In this study, a yeast one-hybrid and dual-LUC expression assays were used to elucidate the molecular mechanism through which GhCOL2 regulates the transcription of GhHD3A. RT-qPCR was used to examine the expression of GhCOL2 and GhHD3A. Our findings reveal that GhCOL2 directly binds to CCACA cis-elements and atypical CORE (TGTGTATG) cis-elements in the promoter regions of HEADING DATE 3 A (HD3A), thereby activating GhHD3A transcription. Notably, GhCOL2 and GhHD3A exhibited high expression levels in the adult stage and low levels in the juvenile stage. Interestingly, the expression of GhCOL2 and GhHD3A varied significant between the two cotton varieties (Tx2094 and Maxxa). In summary, our study enhances the understanding of the molecular mechanism by which cotton GhCOL2-GhHD3A regulates flowering at the molecular level. Furthermore, it contributes to a broader comprehension of the GhCOL2-GhHD3A model in G. hirsutum.

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Title: Multi-omics analysis of pigmentation related to proanthocyanidin biosynthesis in brown cotton (*Gossypium hirsutum* L.)

Author: Doug J. Hinchliffe, Marina Naoumkina, Gregory N. Thyssen, Sunghyun Nam, SeChin Chang, Jack C. McCarty and Johnie N. Jenkins

Abstract: Naturally-colored brown cotton (NBC) fiber is an environmentally friendly raw source of fiber for textile applications. The fiber of some NBC cultivars exhibits flame-retardant properties, which can be used in textiles that require flame resistance. Proanthocyanidins or their derivatives are responsible for the brown pigment in NBC; however, how flame retardancy is related to pigmentation in NBC is poorly understood. To gain insight into brown pigment biosynthesis, we conducted comparative transcripts and metabolites profiling analysis of developing cotton fibers between the brown (MC-BL) and white (MC-WL) cotton near-isogenic lines (NILs), genetically different only in the Lc1 locus. In this study, mass spectrometry was used to detect metabolites in BL and WL developing fibers at 8, 12, 16, 20, 24, 36, and 40 days post anthesis (DPA) and mature fibers. Transcripts analysis was performed at two critical fiber developmental points, 8 DPA (fiber elongation) and 20 DPA (secondary cell

wall deposition). We found 5836 (ESI MS positive mode) and 4541 (ESI MS negative mode) metabolites significantly different accumulated between BL and WL. Among them, 142 were known non-redundant metabolites, including organic acids, amino acids, and derivatives of the phenylpropanoid pathway. Transcript analysis determined 1691 (8 DPA) and 5073 (20 DPA) differentially expressed genes (DEGs) between BL and WL, with the majority of DEGs downregulated at 20 DPA. Organic acids of the citric acid cycle were induced, while most of the detected amino acids were reduced in the MC-BL line. Both cis- and trans-stereoisomers of flavan-3-ols were detected in developing MC-WL and MC-BL fibers; however, the gallocatechin and catechin accumulated multiple times higher. Gas chromatography-mass spectrometry (GC-MS) analysis of fatty acids determined that palmitic acid long-chain alcohols were the main constituents of waxes of mature fibers. Energy-dispersive X-ray spectrometry (EDS) analysis of mature fibers revealed that potassium accumulated three times greater in MC-BL than in MC-WL mature fibers. This study provides novel insights into the biosynthesis of pigments and its association with flame retardancy in NBC fibers.

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Title: The GaKAN2, a KANADI transcription factor, modulates stem trichomes in Gossypium arboretum.

Author: Xujiao Ren, Luying Yang, Yasir Muhammad, Yuxing Xie, Xinyi Lin, Li Yu, Yuefen Cao, Mingquan Ding, Yurong Jiang & Junkang Rong

Abstract: GaKAN2, a member of the KANADI family, was found to be widely expressed in the cotton tissues and regulates trichome development through complex pathways. Cotton trichomes are believed to be the defense barrier against insect pests. Cotton fiber and trichomes are single-cell epidermal extensions with shared regulatory mechanisms. Despite several studies underlying mechanism of trichome development remains elusive. The KANADI is one of the key transcription factors (TFs) family, regulating Arabidopsis trichomes growth. However, the function of KANADI genes in cotton remains unknown. In the current study genome-wide scanning, transcriptomic analysis, gene silencing, subcellular localization, and yeast two-hybrid techniques were employed to decipher the function of KANADI TFs family genes in cotton crop. A total of 7 GaKAN genes were found in the Gossypium arboreum. Transcriptomic data revealed that these genes were significantly expressed in stem and root. Moreover, GaKAN2 was widely expressed in other tissues also. Subsequently, we selected GaKAN2 to validate the function of KANADI genes. Silencing of GaKAN2 resulted in a 24.99% decrease in single-cell trichomes and an 11.33% reduction in internodal distance, indicating its potential role in regulating trichomes and plant growth. RNA-Seq analysis elucidated that GaSuS and GaERS were the

downstream genes of GaKAN2. The transcriptional activation and similarity in silencing phenotype between GaKAN2 and GaERS suggested that GaKAN2 regulates trichomes development through GaERS. Moreover, KEGG analysis revealed that a significant number of genes were enriched in the biosynthesis of secondary metabolites and plant hormone signal transduction pathways, thereby suggesting that GaKAN2 regulates the stem trichomes and plant growth. The GFP subcellular localization and yeast transcriptional activation analysis elucidated that GaKAN2 was located in the nucleus and capable of regulating the transcription of downstream genes. This study elucidated the function and characteristics of the KANADI gene family in cotton, providing a fundamental basis for further research on GaKAN2 gene in cotton plant trichomes and plant developmental processes.

SEED SCIENCE AND TECHNOLOGY

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Title: Genetics of oil and yield related traits in cotton.

Author: Dr. Nagappa Govanakoppa and Dr. BM Khadi

Abstract: Genetics of oil content, plant height, lint index, ginning out turn and lint weight showed that these traits were controlled by dominant genes and dominance x dominance interactions. The traits viz., monopodial branches, seed cotton yield, boll weight, sympodial branches per plant and number of bolls per plant were controlled by dominance gene effects and additive ×additive gene interactions. For seed index, additive gene interaction was prominent.

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Title: Melatonin reduces cadmium accumulation through cell wall fraction fixation capacity in cotton seedlings.

Author: Uzair Muhammad , Yi Zhang , Abid Ali , Huazu Li , Yifei Han , Yue Sun , Jielin Wang

Abstract: Melatonin (MT) participates in plants' responses in plants' response to cadmium (Cd) tolerance, although its work model remains elusive. Here, the function

of MT in adjusting Cd accumulation in Gossypium hirsutum (CCRI12) was investigated. In this research we observed that exogenous 50 μM MT significantly reduced the Cd accumulation under 100 μM Cd stress for 7 days of treatment in cotton seedlings. Cd markedly induced the ROS (H_2O_2, O_2-) accumulation and elevated the expression of transporters for Cd uptake and translocation. After application of MT reduced ROS and MDA accumulation in response to high induction of antioxidant defense system; the genes encoding superoxide dismutase (GhSOD), catalase (GhCAT), and peroxidase (GhPOD), ascorbate peroxidase (GhAPX), and glutathione S-transferase (GhGST) were significantly upregulated accompanied by their level of content. Furthermore, MT down-regulated transporters for Cd uptake include Natural Resistance-Associated Macrophage Protein 1 (GhNRAMP3), Zinc/Iron-regulated transporter-like protein (GhZIP1/4/6), Heavy Metal ATPase gene (GhHMA2), and ATP-binding Cassette sub family C (GhABCC3/2). Exogenous application of MT raised the hemicelluloses, cellulose and pectin content accompanied by their expression levels, xyloglucan endotransglucosylase/hydrolase (GhXTH28/6/9/B), cellulose synthase like (GhCSLG1/2) and COBRA-like (GhCOBL4), pectin acetylesterases (GhPAE8/7), pectin methylesterases (GhPME31) which in turn increased the cell wall's binding capacity to Cd.

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Title: Assessment of Cotton Genotypes at the Seedling Stage: A Comparative Study of Morphophysiological and Biochemical Responses to Various Salinity Stress Levels .

Author: Nimra Gul, Asif Saeed, Azeem Iqbal Khan, Faisal Saeed Awan

Abstract: Cotton (Gossypium spp.) is a vital raw product for the global textile industry. Its production is affected by salt stress. This study was designed to investigate the morph-physiological and biochemical responses of cotton genotypes to salt, aiming to identify mechanisms of salt tolerance and susceptibility. Within a glasshouse, diverse genotypes were grown in polythene bags filled with sand, subjected to three salt stress levels i.e., control, moderate stress (12dS/m), and severe stress (17dSm), in a two-factor factorial design under a Completely Randomized Design (CRD). Physiological measurements and biochemical assays under varying salt conditions revealed significant decreases in growth related traits (shoot and root lengths, fresh and dry weights) with increased salt severity. Alongside antioxidant defense mechanisms were upregulated, as evidenced by increased peroxidase (POD), catalase (CAT), superoxide Dismutase (SOD) activities, and proline levels, indicating adaptive responses to oxidative stress. Principal Component Analysis (PCA) showed the results for that the

first two principal components accounted for approximately 76% of the variance, summarizing the major contribution by genotypes' salt responses. Cluster analysis further delineated the genotypes into three clusters, representing distinct salt response strategies. This study revealed the complex dynamics between cotton's genetic makeup, physiological responses, and biochemical processes in facing salt conditions and to ascertain the salt tolerant and susceptible genotypes.

FIBER AND FIBER TECHNOLOGY

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Title: Study of the impact of biotechnology methods on the quality of cottonseeds and cotton fiber .

Author: Abdurakhim Khojiev

Imprint: AIP Conf. Proc. 3045, 040032 (2024), https://doi.org/10.1063/5.0197795

Abstract: The purpose of research is to improve the quality of cotton fiber and seed. Using biotechnological methods, a solution and fertilizer were prepared that restores the natural structure of the soil. When treated with a biosolution, it was observed that the amount of gossypol in the seed was broken down into vitamins, and cottonseed oil turned into a healing agent. The technological properties of raw cotton grown with the support of biosolution and biosolution were studied. According to the properties of biotechnologically grown cotton raw material, staple length, proportion of long fibers in the sample, uniformity index, tensile strength increase, and the amount of short fibers decreases compared to the cotton fiber produced by the traditional method. This leads to an increase in the hardness of yarn and fabric produced from cotton raw materials.

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Title: Aspartyl proteases identified as candidate genes of a fiber length QTL, qFLD05, that regulates fiber length in cotton (Gossypium hirsutum L.)

Author: Sujun Zhang, Haitao Wang, Xinghe Li, Liyuan Tang, Xiao Cai, Cunjing Liu, Xiangyun Zhang & Jianhong Zhang
Imprint: Theoretical and Applied Genetics , Volume 137, article number 59, (2024)

Abstract: Fiber length (FL) is an economically important fiber quality trait. Although several genes controlling cotton fiber development have been identified, our understanding of this process remains limited. In this study, an FL QTL (qFL$_{D05}$) was fine-mapped to a 216.9-kb interval using a secondary F$_{2:3}$ population derived from the upland hybrid cultivar Ji1518. This mapped genomic segment included 15 coding genes, four of which were annotated as aspartyl proteases (GhAP1-GhAP4). GhAPs were identified as candidates for qFL$_{D05}$ as the sequence variations in GhAPs were associated with FL deviations in the mapping population, and functional validation of GhAP3 and GhAP4 indicated a longer FL following decreases in their expression levels through virus-induced gene silencing (VIGS). Subsequently, the potential involvement of GhWRKY40 in the regulatory network was revealed: GhWRKY40 positively regulated GhAP3's expression according to transcriptional profiling, VIGS, yeast one-hybrid assays and dual-luciferase experiments. Furthermore, alterations in the expression of the eight previously reported cotton FL-responsive genes from the above three VIGS lines (GhAP3, GhAP4 and GhWRKY40) implied that MYB5_A12 was involved in the GhWRKY40-GhAP network. In short, we unveiled the unprecedented FL regulation roles of GhAPs in cotton, which was possibly further regulated by GhWRKY40. These findings will reveal the genetic basis of FL development associated with qFL$_{D05}$ and be beneficial for the marker-assisted selection of long-staple cotton.

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Title: Combining ability analysis for fibre quality traits in desi cotton (Gossypium arboreum L.) across the environment.

Author: DN Pachkhande, HV Kalpande, VN Chinchane, KS Baig, JD Deshmukh MP Wankhade and AR Gaikwad

Abstract: Cotton is one of the most important fibre and cash crop of India and plays a dominant role in the industrial and agricultural economy of the country. In present investigation total fourty eight crosses with fourteen parents and three checks viz., PKV Suvarna, PKV DH 1 and NACH 12 were grown in Randomized Block Design with two replications during kharif, 2022 at three locations viz., Cotton Research Station, Mahboob Baugh Farm, Parbhani (L1), Cotton Research Station, Nanded (L2), and Agricultural Research Station, Badnapur (L3). Pooled over the environments, the highest GCA effect for fibre quality traits was showed by line PAIG 411, PA 810 and testers AKA 7, PA 402. Pooled over the environments, among the crosses highest significant SCA for fibre quality traits was recorded in PAIG 411 x AKA 7 exhibiting significant SCA for GOT (2.79), UHML (1.18) and micronaire (-0.47) pooled over the

locations. Next highest significant SCA recorded by PA 810 x PA 402 exhibiting significant SCA for GOT (1.39), UHML (1.64), micronaire (-0.26) and uniformity index (1.84) pooled over the locations. Selection in further generations would be rewarding to get best transgressive segregants for fibre quality

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Title: A dominant negative mutation of GhMYB25-like alters cotton fiber initiation, reducing lint and fuzz .

Author: Guannan Zhao, Yu Le, Mengling Sun, Jiawen Xu, Yuan Qin, She Men, Zhengxiu Ye, Haozhe Tan, Haiyan Hu, Jiaqi You

Abstract: Cotton (*Gossypium hirsutum*) fibers, vital natural textile materials, are single-cell trichomes that differentiate from the ovule epidermis. These fibers are categorized as lint (longer fibers useful for spinning) or fuzz (shorter, less useful fibers). Currently, developing cotton varieties with high lint yield but without fuzz remains challenging due to our limited knowledge of the molecular mechanisms underlying fiber initiation. This study presents the identification and characterization of a naturally occurring dominant negative mutation GhMYB25-like_At^{hapT}, which results in a reduced lint and fuzzless phenotype. The GhMYB25-like_At^{hapT} protein exerts its dominant negative effect by suppressing the activity of GhMYB25-like during lint and fuzz initiation. Intriguingly, the negative effect of GhMYB25-like_At^{hapT} could be alleviated by high expression levels of GhMYB25-like. We also uncovered the role of GhMYB25-like in regulating the expression of key genes such as GhPDF2 (PROTODERMAL FACTOR 2), CYCD3; 1 (CYCLIN D3; 1) and PLD (Phospholipase D), establishing its significance as a pivotal transcription factor in fiber initiation. We identified other genes within this regulatory network, expanding our understanding of the determinants of fiber cell fate. These findings offer valuable insights for cotton breeding and contribute to our fundamental understanding of fiber development.

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Title: Combined genome and transcriptome analysis of elite fiber quality in Gossypium barbadense.

Author: Xiaohui Song, Guozhong Zhu, Xiujuan Su, Yujia Yu, Yujia Duan, Haitang Wang

Abstract: Gossypium barbadense, which is one of several species of cotton, is well known for its superior fiber quality. However, the genetic basis of its high-quality fiber remains largely unexplored. Here, we resequenced 269 G. barbadense accessions. Phylogenetic structure analysis showed that the set of accessions was clustered into 3 groups: G1 and G2 mainly included modern cultivars from Xinjiang, China, and G3 was related to widely introduced accessions in different regions worldwide. A genome-wide association study of 5 fiber quality traits across multiple field environments identified a total of 512 qtls (main-effect QTLs) and 94 qtlEs (QTL-by-environment interactions) related to fiber quality, of which 292 qtls and 57 qtlEs colocated with previous studies. We extracted the genes located in these loci and performed expression comparison, local association analysis, and introgression segment identification. The results showed that high expression of hormone-related genes during fiber development, introgressions from *Gossypium hirsutum*, and the recombination of domesticated elite allelic variation were 3 major contributors to improve the fiber quality of G. barbadense. In total, 839 candidate genes with encoding region variations associated with elite fiber quality were mined. We confirmed that haplotype GB_D03G0092H traced to G. hirsutum introgression, with a 1-bp deletion leading to a frameshift mutation compared with GB_D03G0092B, significantly improved fiber quality. GB_D03G0092H is localized in the plasma membrane, while GB_D03G0092B is in both the nucleus and plasma membrane. Overexpression of GB_D03G0092H in Arabidopsis (Arabidopsis thaliana) significantly improved the elongation of longitudinal cells. Our study systematically reveals the genetic basis of the superior fiber quality of G. barbadense and provides elite segments and gene resources for breeding high-quality cotton cultivars.