GLEANINGS IN COTTON RESEARCH

DECEMBER 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
Incharge Library

Chetali Rodge
Technical Officer (T5)

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AGRONOMY, SOIL SCIENCE AND PLANT PHYSIOLOGY

1

Title: Use of Herbicides Coated onto Fertilizer and Applied Over-the-Top of Cotton.

Author: Summer Linn

Imprint: A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science in Crop, Soil, and Environmental Science. August 2024 University of Arkansas

Abstract: Cotton (*Gossypium hirsutum* L.) production faces numerous challenges, many related to weed management. A herbicide application method that focuses on combing resources that producers already have access to, such as herbicide-coated fertilizers, could be a practical approach for addressing late-season control of Palmer amaranth (Amaranthus palmeri S. Wats) and other problematic weed species. Two main factors would potentially impact the efficiency of utilizing this method: cotton tolerance to the application and weed control provided by the herbicide coated fertilizers. Some considerations could affect the efficacy of these applications, such as when the treatments are applied and when they are activated by rainfall or irrigation. Therefore, experiments were conducted to 1) understand cotton tolerance to herbicides coated onto fertilizer, 2) evaluate the residual control of Palmer amaranth with herbicide-coated fertilizers, and 3) determine the influence of irrigation and application timing on weed control and cotton tolerance. In general, herbicide-coated fertilizer applications did not cause adverse effects on the crop, and there was no reduction in seed cotton yield was evident for any treatment. These coated fertilizer applications did not affect cotton groundcover compared to the nontreated check. All herbicide-coated fertilizer treatments provided at least 73% Palmer amaranth control at 28 d after treatment (DAT). While some herbicide treatments did experience a decrease in control across evaluation dates, from 14 to 28 DAT, certain treatments provided weed control that was similar at both evaluation dates, such as fluridone, fluridone plus fluometuron, pyroxasulfone, pyroxasulfone plus fluridone, and Smetolachlor. Palmer amaranth present in plots did not interfere with cotton growth and development, and no reduction in seedcotton yield occurred. Irrigation/activation timing of the herbicide-coated fertilizers can greatly impact the efficacy of the application. Control of both Palmer amaranth and barnyardgrass [Echinochloa crus-galli (L.) P. Beauv.] was decreased when irrigation was applied 10 d after application (DAA). Applying irrigation 0 or 3 DAA greatly increases herbicide activity, resulting in greater Palmer amaranth and barnyardgrass control. Florpyrauxifen-benzyl, while not labeled in cotton, did not cause more than 20% injury regardless of application timing when

applied coated onto fertilizer. Many herbicides applied in this manner provide added residual Palmer amaranth control without causing adverse effects to cotton. Based on the results of these experiments, many herbicides have the potential to be integrated into cotton production systems in season coated onto fertilizers.

2

Title: Physio-morphological and molecular characterization of ethyl methanesulfonate-derived mutant population of Gossypium herbaceum L. cv. (Wagad) for drought tolerance.

Author: Sushma, Umesh Kumar, Vipin Kumar Tiwari, Priyamvada Mishra, Vaishali, Hemant Kumar Yadav, Samir V. Sawant & Pramod Arvind Shirke

Imprint: 3 Biotech, Volume 14, article number 237, (2024)

Abstract: This study investigates the response of ethyl methane sulfonate-derived twenty mutant lines of Gossypium herbaceum, along with the parent type Wagad cultivar, to drought stress. Physiological parameters, such as relative water content (RWC), net photosynthesis (A), stomatal conductance (gs), transpiration rate (E), and water use efficiency (WUE), were examined. The mutant line mut_3219 exhibited superior drought tolerance, maintaining high RWC and water retention capacity, with minimal reductions in A, gs, and E, leading to higher WUE than parent type and other mutant lines. Chlorophyll pigments declined in all the mutants under drought. However, mut_3219 retained higher levels than mut_4785. Anthocyanin accumulation indicated a protective response. Chlorophyll fluorescence showed mut_3219 is less sensitive to drought-induced PSII damage than mut_4785, with better membrane stability and higher proline accumulation, among all other mutant lines and parent type. The morphological parameters were less affected in mut_3219 compared to mut_4785 and parent type. Molecular analyses under control and drought conditions revealed significant variations in the expression of seven drought-related genes (GhbHLH, GhMYB5, GhWRKY33, GhRAF4, GhRAF19, GhNAC2, and GhCAMTA). The relative expression of GhbHLH, GhNAC2, GhRAF4, GhRAF19, and GhCAMTA increased under drought conditions, with notable changes in mut_3219 compared to parent type and all other mutant lines, indicating its enhanced drought tolerance. These findings provide valuable insights into the molecular and physiological mechanisms underlying drought tolerance in cotton.

3

Title: Remote detection of water stress in cotton using a center pivot irrigation system-mounted sensor package.

Author: Bala R. Sapkota, Curtis B. Adams, Qiong Su & Srinivasulu Ale

Imprint: *Scientific Reports* volume 14, Article number: 23436 (2024)

Abstract: Much research has been invested in infrared temperature (IRT)-based methods for cotton (*Gossypium hirsutism* L.) water stress detection using in-field sensors, but adoption of these is low, perhaps due to logistical challenges. Alternatively, the Water Deficit Index (WDI) was developed for crop water stress assessment using remote sensors not embedded in the canopy. The objective of this research was to evaluate the performance of a sensor package—including modern IRT and normalized difference vegetation index (NDVI) sensors facing downward at 45°, and a mini weather station—attached unintrusively to a center pivot irrigation system for detecting cotton water stress using WDI. Sensor packages were evaluated in a two-year field study that included four irrigation treatments (0, 30, 60, and 90% ET replacement) and in two production cotton fields. Overall, the tested system was effective at distinguishing crop water stress among irrigation rates. Comparison of the results to a ground-based station and simulations indicated that WDI overestimated water stress at the highest irrigation rate, but performed well otherwise. Accuracy of the system could be improved by measuring canopy coverage (*Fc*) from the same vantage point as the IRT and NDVI sensors (from the pivot, downward at a 45° angle).

4

Title: Biochar improves water and nitrogen use efficiency of cotton under mulched drip irrigation in arid regions.

Author :Yue Han, Jinzhu Zhang , Pengpeng Chen

Imprint: Industrial Crops and Products, Volume 222, Part 3, 15 December 2024, 119830
Abstract: Soil degradation and water scarcity constitute critical impediments to crop production in arid regions. The innovation of efficient resource utilization technology is necessary for agricultural development in arid regions. While biochar application's effects on enhancing soil quality and promoting crop growth have been well documented, the mechanism of biochar application under mulching drip irrigation in cotton field to improve soil hydrothermal environment and then to promote cotton production is unclear. To explore the effects of different amounts of biochar application on soil hydrothermal characteristics, cotton yield, and water-nitrogen utilization

efficiency in cotton field under mulched drip irrigation. The experiment encompassed five rates of biochar applications: B1 (20 Mg ha^{-1}), B2 (40 Mg ha^{-1}), B3 (60 Mg ha^{-1}), B4 (80 Mg ha^{-1}) and CK (0 Mg ha^{-1}). Compared to CK, the application of biochar could increase soil water storage, soil accumulated active temperature and soil inorganic nitrogen in the top 40 cm of soil. The crop water productivity, crop N uptake, nitrogen partial factor productivity and cotton yield increased by 2.49 13.39 %, 2.66 15.30 %, 3.43 12.00 % and 3.41 11.98 % in treatments with biochar applications, respectively. Besides, the crop N uptake was closely related to cotton yield, which was stemmed from the improvement of soil water storage and soil active accumulated temperature by biochar application, and therefore an increase of the soil inorganic nitrogen content. According to the dual-objective regression analysis of cotton water productivity and cotton N uptake, the optimal biochar application rate was 42.42 Mg ha^{-1}. The results highlighted that further increasing water and fertilizer use efficiency is feasible under optimized biochar application rate to promote agriculture development in arid regions.

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Title: Optimizing agricultural water resources: a study on cotton cultivation using non-conventional water sources in Khuzestan, Iran.

Author: Ali Mokhtaran, Saloome Sepehri, Ghorban Ghorbanni-Nasrabad & Ghorban Ali Roshani

Imprint: Environment, Development and Sustainability , Published: 08 October 2024

Abstract: In light of the scarcity of freshwater resources, a fundamental approach to addressing the need for agricultural water resources involves the utilization of non-conventional water sources. The problem of producing agricultural drainage water in Iran, particularly in Khuzestan province in the south, is one of the most serious. Therefore, in line with the reuse of agricultural drainage water, a two-year study was conducted by considering different irrigation management methods and taking into consideration different planting dates to determine the qualitative and quantitative characteristics of cotton varieties (*Gossypium hirsutum L.*), and soil properties (2019 − 2020). The experimental design was split-split-plot with three replications. The investigated treatments included three different planting dates including March 1st (PD1), April 1st (PD2), and May 1st (PD3), and three irrigation managements including irrigation with water from Karun River (IM1, as freshwater), irrigation with agricultural drainage water (IM2) and rotational irrigation using freshwater and drainage water (IM3) as well as three cotton varieties. The statistical analysis of the simple effects of planting date on yield revealed that PD1 achieved the highest cotton yield, at 1712 kg/ha. Additionally, there was no significant difference in cotton yield between the various irrigation management practices. Furthermore, an analysis of the interaction effect between planting date and irrigation management indicated that the PD1IM1 treatment produced the highest cotton yield, reaching 1968 kg/ha. As a result of monitoring changes in soil EC_e and ESP during the research period, the topsoil and subsoil layers in both IM1 and IM2 treatments were classified in the non-saline-non-sodic category. In the IM2 treatment, however, the topsoil reached salinity-sodic levels (EC_e=8.5 dS/m and ESP = 15.62%). In conclusion, rotational irrigation management is a suitable option for the long-term reuse of agricultural drainage water for cotton cultivation, as it maintains an optimal salt balance in the soil and prevents harmful elements from accumulating in the rootzone.

6

Title: Optimizing type, date, and dose of compost fertilization of organic cotton under climate change in Mali: A modeling study.

Author: Dembélé G., Loison R., Traoré A., Dembélé S.G., Sissoko F.. 2024. *PloS One*, 19 (8) : 18 p..
Imprint: DOI: 10.1371/journal.pone.0308736
Abstract: Adapting organic farming to climate change is a major issue. Cotton yields in Mali are declining due to deteriorating climatic conditions, soil fertility, and poor management. This study aimed to improve organic cotton yield in Mali in the future climate with the optimal choice of compost type, date, and dose of application. Experimental data collected in 2021 from the Sotuba research station in Mali was used for calibration and evaluation of the crop model DSSAT CSM-CROPGRO-Cotton model using phenology, leaf area index, and seed cotton yield. Climate data from the RCP4.5 and RCP8.5 scenarios of the GFDL-ESM2M model were used for future weather datasets for 2020-2039, 2040-2059, and 2060-2079. The model was able to simulate anthesis and maturity with excellent results, with nRMSE < 4%, and seed cotton yields moderately well, an nRMSE of 26% during calibration and 20.3% in evaluation. The scenario RCP8.5 from 2060 to 2079 gave the best seed cotton yields. Seed cotton yields with RCP4.5 and RCP8.5 were all better with the mid-May application period of small ruminant silo compost at 7.5 t/ha. In such conditions, more than 75% of the cases would produce more than 2000 kg/ha of seed cotton.

7

Title: Agronomic Strategies for Sustainable Cotton Production: A Systematic Literature Review.

Author: Giuseppe Salvatore Vitale, Aurelio Scavo, Silvia Zingale, Teresa Tuttolomondo, Carmelo Santonoceto, Gaetano Pandino
Imprint: *Agriculture* 2024, *14*(9), 1597; https://doi.org/10.3390/agriculture14091597

Abstract: Cotton, with a cultivated area of 31.92×10^6 ha^{-1} across 80 countries and an estimated annual turnover of USD 5.68 billion, is the world's leading natural textile fiber. However, many cotton-producing countries have neglected to improve production practices, adversely affecting the environment and society. A systematic review of the sustainable cotton cultivation literature was performed for the first time to identify and suggest context-specific agricultural strategies that can be applied within different agroecosystems. The key aspects include (1) inoculation with arbuscular mycorrhizal species such as *Gigaspora margarita*, *Funneliformis mosseae*, and *Acaulospora scrobiculata* to enhance root exploration, biomass, and nutrient uptake; (2) using grass, legume, and brassica cover crops as a valid alternative to monoculture and fallow crop rotations to reduce resource depletion and increase the sustainability of cotton production; (3) adopting drip and mulched drip irrigation systems over traditional furrow and sprinkler systems for water conservation; (4) exploring the feasibility of prematurely terminating irrigation in humid subtropical and Mediterranean climates as an alternative to chemical defoliation without affecting cotton yield. This paper, which describes various farming practices adopted in different climates, provides farmers a guide for eco-friendly cotton agronomic management without sacrificing productivity.

8

Title: Sustainable practices for cotton production in Bangladesh: economic and environmental perspectives.

Author: Shanzida Akter Dristy, Aurup Ratan Dhar & Md. Taj Uddin

Imprint: Discover Agriculture , Volume 2, article number 53, (2024)

Abstract: Cotton is a major cash crop in the agriculture of Bangladesh, primarily fueling its substantial textile industry. Although local production is limited, cotton has the potential to bolster the country's economic growth by supporting local economies and improving agricultural sustainability. An in-depth sustainability assessment of this integral crop is essential to ensure its long-term economic and environmental viability. This study aims to evaluate the sustainability of cotton production in Bangladesh and suggest strategic enhancements and policy measures to improve its environmental, economic, and social aspects. Data were collected from 60 farmers in two villages of

Jashore district using a simple random sampling technique. A combination of descriptive, mathematical and statistical techniques was used to analyze the data. The findings highlighted a profitable benefit–cost ratio of 1.88 for cotton production. Positive impacts on cotton profitability were notably linked to the costs of labor, land preparation, and insecticides and pesticides. Despite this, 60% of farmers faced substantial challenges, including financial barriers, limited access to modern agricultural technologies, and a lack of training in sustainable practices. Economic constraints were a major barrier, although the environmental benefits of sustainable practices were widely acknowledged. To address these issues, the study recommends optimizing inputs like labor, land preparation, and pest management, and advocates for policy actions such as subsidies, tax incentives, and enhanced training programs to support the widespread adoption of sustainable practices across Bangladesh.

9

Title: Effects of planting date and density on cotton cultivars in sub-Saharan Africa rainfed conditions: A case study in Mali.

Author: Elhadji Mamoudou Kassambara, Romain Loison, Sory Sissoko, Abdou Traoré, Alhousseini Bretaudeau

Imprint: Agronomy Journal. 2024;1–12.

Abstract: Mali is among Africa's three biggest cotton (Gossypium hirsutum L.)-producing countries, and cotton growing is the principal driving force behind Mali's agricultural sector. Cotton production is rainfed on small-scale family farms as a commercial crop alongside staple crops grown for subsistence. Cultivar choice, planting date, and planting density are critical elements for seed cotton yield that should be optimized. This study aimed to understand the interactions between planting dates and planting densities for the optimal production of four cotton cultivars in Mali. Two trials were set up in two seasons at the Finkolo and N'Tarla research stations. A split-plot design with four replications was used, with planting dates (early and delayed by 3 weeks) as the main plots and planting density (41,666; 83,333; and 166,666 plants/ha) and cultivar (Malian NTA MS334, Togolese STAM 129A, Australian SIOKRA L23, and Brazilian BRS 293) as the subplots. In 2021, seed cotton yield was 1263 kg/ha for early planting versus 361 kg/ha for late planting. Medium and high planting densities produced the same yield level, higher than the low planting density. Regardless of the planting density, early plantings' average capsular weight and seed index were higher than those of late plantings. The African cultivars (STAM 129A and Malian cultivar NTA MS334) were the most productive. Due to significant interactions on fiber percentage and to optimize cotton yields in Mali, planting should be early, with planting densities higher than 41,666 plants/ha, and either of the African cultivars tested should be used.

10

Title: Multiomics approaches to explore drought tolerance in cotton.

Author: Sharif Iram, Aleem Saba, Junaid Jamshaid Ali, Ali Zulfiqar, Aleem Muqadas, Shahzad Rahil, Farooq Jehanzeb, Khan Muhammad Imran, Arshad Waheed & Ellahi Farrukh

Imprint: Journal of Cotton Research, Volume 7, article number 32, (2024)

Abstract: The situation of global warming imparts negative impacts on crop growth and development. Cotton is the most important fiber crop around the globe. However, frequent drought episodes pose serious threats to cotton production worldwide. Due to the complex genetic structure of drought tolerance, the development of a tolerant cultivar is cumbersome via conventional breeding. Multiple omics techniques have appeared as successful tool for cotton improvement in drought tolerance. Advanced omics-based biotechniques have paved the way for generation of omics data like transcriptomics, genomics, metabolomics and proteomics, which greatly expand the knowledge of cotton response to drought stress. Omics methodologies and have provided ways for the identification of quantitative trait loci (QTLs), gene regulatory networks, and other regulatory pathways against drought stress in cotton. These resources could speed up the discovery and incorporation of drought tolerant traits in the elite genotypes. The genome wide association study (GWAS), gene-editing system CRISPER/Cas9, gene silencing through RNAi are efficient tools to explore the molecular mechanism of drought tolerance and facilitate the identification of mechanisms and candidate genes for the improvement of drought tolerance in cotton.

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Title: GhPME36 aggravates susceptibility to Liriomyza sativae by affecting cell wall biosynthesis in cotton leaves.

Author: Zheng Yang, Menglei Wang, Senmiao Fan, Zhen Zhang, Doudou Zhang, Jie He, Tongyi Li, Renhui Wei, Panpan Wang,

Imprint: BMC Biology , Volume 22, article number 197, (2024)

Abstract: Cotton is an important economic crop and a host of Liriomyza sativae. Pectin methylesterase (PME)-mediated pectin metabolism plays an indispensable role in multiple biological processes in planta. However, the pleiotropic functions of PME often lead to unpredictable effects on crop resistance to pests. Additionally, whether and how PME affects susceptibility to Liriomyza sativae remain unclear. Results- Here, we isolated GhPME36, which is located in the cell wall, from upland cotton (Gossypium hirsutum L.). Interestingly, the overexpression of GhPME36 in cotton caused severe susceptibility to Liriomyza sativae but increased leaf biomass in Arabidopsis.

Cytological observations revealed that the cell wall was thinner with more demethylesterified pectins in GhPME36-OE cotton leaves than in WT leaves, whereas the soluble sugar content of GhPME36-OE cotton leaf cell walls was accordingly higher; both factors attracted Liriomyza sativae to feed on GhPME36-OE cotton leaves. Metabolomic analysis demonstrated that glucose was significantly differentially accumulated. Transcriptomic analysis further revealed DEGs enriched in glucose metabolic pathways when GhPME36 was overexpressed, suggesting that GhPME36 aggravates susceptibility to Liriomyza sativae by affecting both the structure and components of cell wall biosynthesis. Moreover, GhPME36 interacts with another pectin-modifying enzyme, GhC/VIF1, to maintain the dynamic stability of pectin methyl esterification. Conclusions- Taken together, our results reveal the cytological and molecular mechanisms by which GhPME36 aggravates susceptibility to Liriomyza sativae. This study broadens the knowledge of PME function and provides new insights into plant resistance to pests and the safety of genetically modified plants.

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Title: Morphophysiological and biochemical responses of cotton (*Gossypium barbadense* L.) to nano zinc (ZnO-NPs) and *Azospirillum* sp. under water deficit stress conditions.

Author: Hossam S. El-Beltagi, Essam Abdelaziz El-Waraky, Hayfa Habes Almutairi

Imprint: Journal of Plant Nutrition, https://doi.org/10.1080/01904167.2024.2402882

Abstract: Water deficit stress (WDS) is one of the most significant abiotic limiting factors in cultivated crops, including cotton (*Gossypium barbadense* L.). With global climate change and the destruction of ecological balance, the frequency and severity of drought events are increasing in many regions around the world. Therefore, the aim of the present work was to investigate the potential of using nano zinc particles (ZnO-NPs), plant growth-promoting rhizobacteria (*Azospirillum* sp.), and their combination to mitigate the negative impacts of WDS on cotton var. Giza 96. Extended irrigation intervals of 30 and 45 days led to considerable decreases in plant height, chlorophyll content, relative water content (RWC), yield, and cotton fiber quality compared to the optimal irrigation interval (every 15 days). When applied individually or in combination, ZnO-NPs and *Azospirillum* sp. can ameliorate the negative effects of WDS on cotton growth and productivity. Overall, the use of *Azospirillum* sp. and ZnO-NPs, either individually or in combination, has demonstrated their potential to enhance cotton growth and yield parameters (plant height, dry weight, leaf area, chlorophyll pigment, seed index, seed yield, and lint%) under prolonged irrigation intervals during 2021 and 2022 seasons. Antioxidant enzymes activity comprising catalase (CAT), peroxidase (POD), and polyphenol oxidase (PPO) and proline content were increased under drought stress. Cotton fiber quality parameters including length, strength, and micronaire were insignificantly affected under low irrigation rate. The combination of

ZnO-NPs and *Azospirillum* sp. provided the most effective mitigation of WDS during both experimental seasons, outperforming the effects of individual applications.

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Title: Evaluation of physiological responses and yield stability during long-term water deficiency memory of cotton (*Gossypium hirsutum* L.).

Author: Omolbanin Checkani, Elham Faghani, Mohammad Reza dadashi, Hossein Ajam Nourouzi, Borhan Sohrabi

Imprint: J.of Applied Plant Biology, Vol. 2 No. 1 (2024): Vo2,No1,2024

Abstract: Drought stress, as one of the major abiotic stresses, has been expanded by global warming, with negative effects on cotton seed potential, cotton fiber, plant growth and yield. Therefore, many plant species have activated a drought stress memory on the physiological and biochemical level to increase drought stress threshold by balancing carbohydrate and starch and reducing water loss. The experiment in this study was carried out to improve our understanding of water-shortage memory in cotton. Golestan cotton genotype was planted in the double and triple water-stress exposures using split-plot factorial design. There were four levels of water requirements (rain-fed, 33%, 66%, and 100% FC). Bioinformatics results showed that catalase enzyme (CAT) with regulatory elements and Abscisic acid regulatory element (ABRE) play a role in abiotic stresses. On the other hand, STI, YSI, glucose content of the leaves and early-maturity of the seeds in S_{33} and starch content of S_{23} were the highest among the corresponding indices resulted from other seed treatments. Among fiber quality traits, fiber length and fiber strength of seeds planted in the triple water-stress exposure were greater than those in the double water-stress exposure. In addition, PCA data represented that total yield, STI and YSI were observed in the largest group. Finally, seed reproduction in triple water-stress exposure with 33%FC (S_{33}) had more STI and YSI than that in double water-stress exposure. In conclusion, stress memory and preserving some physiological mechanisms are more effective against 33% FC under triple water deficiency exposure.

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Title: Interactive Effect of Zinc and Phosphorus Application on Growth and Yield of Bt. Cotton.

Author: Usman, M., Hammad, H. M., Shahzad, M. S., Abid, A. D., Anwar, A., Shaheen, M. ... Al-Dosary, M. A. (2024)

Imprint: Polish Journal of Environmental Studies. https://doi.org/10.15244/pjoes/192973

Abstract: Cotton is the main cash and fiber crop worldwide, including Pakistan. Sustainable cotton production is threatened by excessive and injudicious use of inorganic fertilizers, especially phosphorus (P) and zinc (Zn). Due to their antagonistic interaction, P and Zn levels must be optimized. This study examined P-Zn interactions in the cotton crop under arid circumstances. A split-plot design was used to provide five doses of P (P1=0, P2=30, P3=60, P4=90, and P5=120 kg ha-1) and three doses of Zn (Zn1=6, Zn2=12, and Zn3=18 kg ha-1). Cotton crop data included soil P and Zn availability, plant growth, morphology, and yield. This demonstrated that increasing Zn and P dosages steadily boosted the growth, physiology, and yield traits of the cotton crop. Compared to other combinations, 12 kg Zn ha-1 and 90 kg P ha-1 improved the studied growth, physiological, and yield parameters of the cotton crop. This combination had the maximum chlorophyll contents (62.2 SPAD value), net leaf photosynthetic rate (13.6 μmol CO2 m−2 s−1), stomatal conductance (0.47 mmol m-2 s-1), sub-sub conductance (292.3 μmol H2O m−2 s−1), leaf transpiration rate (9.6 mmol m-2 s-1), and water usage efficiency (2.42 kg ha-1 mm-1). Similarly, the highest plant height, peak leaf area index, sympodial branches, total bolls, and mean boll weight were obtained with the application of 12 kg Zn ha-1 and 90 kg P ha-1. The maximum soil available P (16.0±0.240 mg kg-1) and Zn (9.00±0.335 mg kg-1) was recorded in the P4Zn2 treatment. Thus, the present study found that increasing Zn and P dosages increased cotton crop growth, morphology, physiology, yield traits, and availability of P and Zn in the soil. The growth, morphological, physiological, and yield parameters of the cotton crop and soil available P and Zn were recorded the highest with 12 kg Zn ha-1 and 90 kg P ha-1. Therefore, the highest seed cotton yield (1.278-ton ha-1) and biological yield (10.492 ton ha-1) were with the application of 12 kg Zn ha-1 and 90 kg P ha-1. The findings of this research work suggest that the combined application of 12 kg Zn ha-1 and 90 kg P ha-1 is the best fertilizer management approach to increase cotton seed yield under the conditions of an arid climate.

CROP PROTECTION

15

Title: Number of Generations Expected to Appear in 2050 to 2100 for the Spiny Bollworm, Earias insulana (Boisd.) Based on Variations in Temperature.

Author: El-Sayed, A. A ; M. M. Nada and A. E. A. Amer

Imprint: J. of Plant Protection and Pathology, Mansoura Univ., Vol. 15 (9):283 - 291, 2024

Abstract: The study set out to ascertain how the number of generations of Earias insulana (Boisd.) moths would be affected by rising temperatures in 2050, 2075, and 2100. The Sharkyia Governorate was the site of a four-year comparative field research conducted between 2019 and 2022 in order to achieve this goal. There were nine field generations recorded. The generations and peak-to-peak, general average durations were 39.0±17 and 36±11 days, respectively, with a coefficient variance CV of 43.0 and 30.4 days. The overall average for thermal heat units was 507± 6 and 520± 19 units, while the CV values were 1.2 and 3.6 days. The estimated average duration of a generation for the years 2050–2100 was 32–34 days, with 11–13-day standard deviation. Compared to the field study, the CV values were 34.9–37.2 days lower. Due to a shorter generation growth period in the anticipated years than in the field research, the generations will occur earlier. The thermal constant remained nearly constant throughout generations and from peak to peak, even though the year's thermal units increased from 4595 units in the average of four years of field study to 5207, 5418, and 5595 units in the anticipated years 2050, 2075, and 2100, respectively. Nine generations of E. insulana moths were recorded in 2019–2022, rising to ten in 2050, remaining at ten in 2075, and reaching eleven in 2100. The number of days required to complete the generation growth is clearly correlated with temperature; the generation period decreases with increasing temperature.

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Title: Histone deacetylase GhHDA5 negatively regulates Verticillium wilt resistance in cotton.

Author: Chunyan Wei, Chaofan Wang, Xin Zhang, Weiyi Huang, Minghui Xing

Imprint: Plant Physiology, kiae490, https://doi.org/10.1093/plphys/kiae490

Abstract: Verticillium wilt (VW) caused by Verticillium dahliae (V. dahliae) is one of the most destructive diseases in cotton (Gossypium spp.). Histone acetylation plays critical roles in plant development and adaptive responses to biotic and abiotic stresses. However, the relevance of histone acetylation in cotton VW resistance remains largely unclear. Here, we identified histone deacetylase 5 (GhHDA5) from upland cotton (Gossypium hirsutum L.), as a negative regulator of VW resistance. GhHDA5 expression was responsive to V. dahliae infection. Silencing GhHDA5 in upland cotton led to improved resistance to V. dahliae, while heterologous expression of GhHDA5 in Arabidopsis (Arabidopsis thaliana) compromised V. dahliae tolerance. GhHDA5 repressed the expression of several lignin biosynthesis-related genes, such as 4-coumarate:CoA ligase gene Gh4CL3 and ferulate 5-hydroxylase gene GhF5H, through reducing the acetylation level of histone H3 lysine 9 and 14 (H3K9K14ac) at their promoter regions, thereby resulting in an increased deposition of lignin, especially S monomers, in the GhHDA5-silenced cotton plants. The silencing of GhF5H impaired cotton VW tolerance. Additionally, the silencing of GhHDA5 also promoted the production of reactive oxygen species (ROS), elevated the expression of several pathogenesis-related genes (PRs), and altered the content and signaling of the phytohormones salicylic acid (SA), jasmonic acid (JA), and strigolactones (SLs) after V. dahliae infection. Taken together, our findings suggest that GhHDA5 negatively regulates cotton VW resistance through modulating disease-induced lignification and the ROS- and phytohormone-mediated defense response.

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Title: Efficacy of different insecticides against major sucking insect-pests infesting Bt cotton.

Author: Rank VH, Dulera JG and Bagul GD

Imprint: International Journal of Advanced Biochemistry Research 2024; 8(9): 170-175

Abstract : A field experiment was conducted during kharif, 2023-2024 to evaluate the bio-efficacy of major sucking insect-pests infesting Bt cotton at regional research station, Anand agricultural university, Anand, Gujarat. Among evaluated different insecticides dinotefuran 20% SG, clothianidin 50% WDG and tolfenpyrad 15% EC were most effective in reducing leafhopper and aphid population while, acetamiprid 20% SP, spiromesifen 240 SC and afidopyropen 50 gL-1 DC were most effective for whiteflies, whereas clothianidin 50% WDG, fipronil 5% SC and tolfenpyrad 15% EC significantly reduced thrips population. The highest cotton yield was recorded from the treatment dinotefuran followed by clothianidin and tolfenpyrad. Looking to the ICBR dinotefuran provided the highest return (1:11.34), followed by acetamiprid (1:10.29) and acephate (1:8.23).

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Title: Spatiotemporal Distribution of Sucking and Bollworm Insect Pests on Transgenic and Conventional Cotton Cultivars at Sahati Region of Central Sindh.

Author: Wali Muhammad Mangrio, Hakim Ali Sahito , Abdul Hafeez Mastoi , Sanaullah Sattar , Fahmeeda Imdad Sahit and Shahid Ali Jakhrani

Imprint: Pakistan Journal of Agricultural Research, 37(3): 282-289. DOI | https://dx.doi.org/10.17582/journal.pjar/2024/37.3.282.289

Abstract: Gossypium hirsutum L. is referred as the "king of fiber", "white gold" cash crop with prominent economic value. This study aims to seek out and examine the potential resistance against infestation of sucking and bollworm insect pests on promising transgenic and non-transgenic cotton genotypes in farmer's field condition, Naushahro Feroze. The seeds of three popularly grown genetically hybrid cotton varieties namely; KMG-1, KMG-2, KMG-3, and non-Bt NIAB-78 were sown on 8th May 2023. After 6th week of cotton sowing, the data of pest infestation were gathered through randomized complete block design on a weekly interval basis on recommended cotton cultivars. The maximum infestation of the thrips population per leaf was recorded on KMG-3, 1.66, followed by KMG-2, 1.35, KMG-1, 1.12, and 1.01 on NIAB-78. The population of spotted bollworms at 1.63, 0.96, 0.89, and 0.84 were counted. Jassid infestation was recorded at 1.24, 1.02, 0.96, 0.93, and whitefly population fluctuations at 1.18, 0.95, 0.83, and 0.79. Overall maximum pest infestation of thrips was recorded at 1.29 compared to spotted bollworms at 1.08, jassid 1.04, and whitefly 0.94, respectively. Present studies are planned to carry out and collect data for the information of the farming community and to fill the scientific information gap on these cotton genotypes in Sindh, Pakistan. Cotton growers immediately take some control measures before to avoid pest infestation. This study also have significant implications for pest management against destructive insect pest species of the cotton crop in future endeavors.

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Title: *Rhioctonia solani* and *Fusarium oxysporum f. sp. vasinfectum*: Plant Host and Interaction of Soil Moisture and Soil Textures that Influence Disease Development for Two Important Fungal Pathogens of Cotton.

Author: Garcia, Jorge

Imprint: California State University, Fresno ProQuest Dissertations & Theses, 2024. 31560715.

Abstract: Rhizoctonia solani and Fusarium f. sp. vasinfectum (FOV) cause seedling damping-off and Fusarium wilt in cotton (Gossypium). The objectives of this study were to: (1) screen historical and current cotton germplasm for resistance/susceptibility to R. solani; (2) identify FOV isolates collected from CA cotton fields in 2021 and to evaluate the pathogenicity of FOV and FOV Race 4 (FOV4) genotypes in Pima and Upland cotton; (3) evaluate the effects of soil texture and soil moisture levels in cotton inoculated with FOV4 and R. solani and their impact on disease development. The results of the R. solani screening found no significant differences among 96 cotton genotypes (P=0.05), which were all similarly susceptible to R. solani based on data for fresh root weight and germination percent. For the 2021 survey, FOV isolates were mostly identified as FOV4, however isolates of FOV3 were found to be more diverse than FOV3 isolates previously reported. Additionally, an unclassified FOV was identified that did not group with any of the known FOV races or Australian biotypes of FOV. For the pathogenicity assay, a rootdip inoculation demonstrated that all FOV isolates tested were able to induce symptoms in cotton. However, the aggressiveness of the isolates varied, where FOV4 isolates T20 and CSU-TX1 were the most aggressive, while FOV3 B23 and the unclassified FOV isolate U35 were the least aggressive. To evaluate the effect of soil texture and soil moisture, three levels of soil moisture (WP + 7%, WP + 14% and WP + 21 %) were set for each soil texture (clay, silty clay loam, and sandy loam soils) and cotton growth and disease development were evaluated for cotton inoculated with R. solani or FOV4 and anon-inoculated control. Overall, soil texture emerged as the most critical determinant impacting plant growth and disease development with better growth and less disease development in the silty clay loam soil. Soil moisture levels also significantly impacted plant growth, with the best growth observed in WP + 14%. The impact of soil moisture on disease development was less apparent or consistent in cotton inoculated with R. solani or FOV4.

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Title: A comprehensive cotton leaf disease dataset for enhanced detection and classification

Author: Prayma Bishshash, Asraful Sharker Nirob, Habibur Shikder, Afjal Hossan Sarower, Touhid Bhuiyan, Sheak Rashed Haider Noori

Imprint: Data in Brief, Volume 57, December 2024, 110913

Abstract: The creation and use of a comprehensive cotton leaf disease dataset offer significant benefits in agricultural research, precision farming, and disease management. This dataset enables the development of accurate machine learning models for early disease detection, reducing manual inspections and facilitating timely interventions. It serves as a benchmark for testing algorithms and training deep learning models, aiding in automated monitoring and decision support tools in precision agriculture. This leads to targeted interventions, reduced chemical use, and

improved crop management. Global collaboration is fostered, contributing to the development of disease-resistant cotton varieties and effective management strategies, ultimately reducing economic losses and promoting sustainable farming. Field surveys conducted from October 2023 to January 2024 ensured meticulous image capture under diverse conditions. The images are categorized into eight classes, representing specific disease manifestations, pests, or environmental stress in cotton plants. The dataset comprises 2137 original images and 7000 augmented images, enhancing deep learning model training. The Inception V3 model demonstrated high performance, with an overall accuracy of 96.03 %. This underscores the dataset's potential in advancing automated disease detection in cotton agriculture.

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Title: Detection of Verticillium infection in cotton leaves using ATR-FTIR spectroscopy coupled with machine learning algorithms.

Author:Xianchang Li a, Lipeng Zhang b, Shiding Zhang c, Haihong Shang b, Yizhong X u d, Yongping Luo

Imprint: Spectrochimica Acta Part A: Molecular and Biomolecular Spectroscopy

Volume 325, 15 January 2025, 125127

Abstract: Verticillium wilt (VW) is a soil-borne vascular disease that affects upland cotton and is caused by Verticillium dahliae Kleb. A rapid and user-friendly early diagnostic technique is essential for the preventing and controlling VW disease. In this study, Fourier transform infrared (FTIR) spectroscopy with attenuated total reflectance (ATR) technology was used to detect VW infection in cotton leaves. About 1800 FTIR spectra were obtained from 348 cotton leaves. The cotton leaves were collected from three categories: VW group, infected group and control group (non-infected). The vibrational peak of chitins at 1558 cm−1 was identified through mean and differential analysis of FTIR spectra as a criterion to differentiate the VW or infected group from the control group. Classification models were constructed using various machine learning algorithms. The support vector machines (SVM) model exhibited the highest predictive accuracy (>96 %) in each group and a total accuracy (>97 %) for the three groups. These results provide a new approach for detecting Verticillium infection in cotton leaves and shows a promising potential for the future applications of the method in plant science.

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Title: Field Evaluation of Plant Oil Formulations as Potential Control Measures Against the Cotton Mealybug (Phenacoccus Solenopsis Tinsley).

Author: Aneeta Lashari, Bhai Khan Solangi, Abdul Waheed Solangi, Kaneez Fatima, Sajjad Hussain Rind

Imprint: Plant Protection, Vol 8, No 3 (2024)

Abstract: The cotton crop is heavily infested by various insect pests, including Phenacoccus solenopsis. Antagonistic plants offer an alternative source of insect biocontrol agents because they contain various bioactive materials, many of which are selective or have no adverse effects on non-target organisms or the environment, unlike synthetic insecticides. Therefore, three locally available plant oils were tested to evaluate their efficacy in reducing P. solenopsis in cotton fields. Statistical analysis showed a highly significant difference (DF = 3, 23; F = 194.42; P = 0.0000) for the reduction of the P. solenopsis population. After the first spray, the highest overall mean reduction of P. solenopsis (61.26±10.69%) was recorded in the cotton plot sprayed with neem oil, followed by castor oil (50.11±10.94%) and mustard oil (38.30±8.39%). After the second spray, the highest overall mean reduction of P. solenopsis (70.01±9.26%) was again observed with neem oil, followed by castor oil (50.51±8.90%) and mustard oil (40.06±8.74%). Furthermore, results concluded that neem oil achieved the highest reduction of P. solenopsis population (84.45%) on the third day, with an overall reduction of 65.64±9.94%. The second-highest reduction (68.96%) with an overall reduction of 50.31±9.9% was recorded in the plot sprayed with castor oil, followed by mustard oil, which reduced the population by 54.05% with an overall reduction of 39.18±8.55%. The results also indicate that the efficacy of neem oil remained effective until the third day after spraying, while on the seventh day, the P. solenopsis population began to increase gradually.

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Title: Impact of insecticides applied in cotton fields on some piercing-sucking insects, pink bollworm, associated predators and Bemisia tabaci parasitoids.

Author: Amany A Khalifa, Hend S El-Tahawe and Ahmad I Saad Allah

Imprint: Acta Entomology and Zoology 2024; 5(2): 58-63

Abstract: Cotton, Gossypium barbadense L. is the most important and widely cultivated fiber crop in Egypt and all over the world. Unfortunately, this crop is subject to infestations of too many insect pests which result in considerable yield losses, particularly piercing-sucking insect pests and pink bollworm, Pectinophora gossypiella. This work was carried out at the experimental farm of Cotton Research Institute, located at Sakha Agricultural Research Station, during 2022 and 2023 seasons to assess the effect of periodical insecticide applications on infestations of aphids, leafhoppers, whitefly, pink bollworm, associated insect predators, as well as Bemisia tabaci parasitoids. Aphid population decreased by 83.12 - 84.82% due to insecticide treatments, leafhoppers and whitefly decreased by 50.44- 63.99% and 78.91% - 93.79%, respectively. The insect predatory populations were also negatively affected by the periodical applications of insecticides, with 49.12- 83.04%, 65.29 -71.16% and 23.12- 40.21% for Orius spp, coccinellids and Chrysoperla carnea. The seasonal bollworm infestations averaged 42.29% and 24.00% in the first season and 52.57 and 24.57% in the second season in untreated and treated cotton plots, respectively. The seasonal averages of parasitsm of Bemisia tabaci nymphs by Eretmocerus mondus and Encarsia lutea were 22.28 and 7.50% in the first season and 24.00 and 6.34% in the second season in the untreated and treated cotton fields, respectively. Data of the current research reveal the high hazards of periodical applications of insecticides against natural enemies prevailing in cotton fields. So, these synthetic insecticides should carefully be applied within the integrated pest management.

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Title: Molecular characterization of *Fusarium* isolates from Upland cotton roots in Uzbekistan and whole-genome comparison with isolates from the USA.

Author: Timothy O. Jobe, Ibrokhim Y. Abdurakhmonov, Mauricio Ulloa, Mohamed Fokar, Zabardast T. Buriev, Shukhrat E. Shermatov

Imprint: Phytopathology, Published Online:10 Oct 2024 https://doi.org/10.1094/PHYTO-04-24-0152-R

Abstract: Fusarium oxysporum f. sp. vasinfectum (FOV) is a significant cotton (Gossypium spp.) pathogen causing vascular wilt, browning of the vascular tissues, and plant death in the most severe cases. This global disease is responsible for sizeable crop losses annually and is found in many cotton producing regions, including the Republic of Uzbekistan and the USA. Specifically, FOV race 4 (FOV4) has been disrupting production for years. This study aimed to genetically characterize FOV4 isolates causing disease in the main cotton producing region of Uzbekistan and compare with FOV4 isolates from the USA. A field study conducted in the Bukhara region of the Republic of Uzbekistan in the spring of 2022 identified both FOV4 and new Fusarium isolates from Upland cotton exhibiting typical Fusarium wilt symptoms. Molecular markers were initially used to identify isolates of interest, and a phylogenetic analysis was performed using partial EF1-α sequences, followed by a comparative genomic analysis. We also report for the first time the isolation of F. solani and F.

commune causing Fusarium wilt in Uzbekistan. Furthermore, we show that the FOV4 population within our sampling region of Uzbekistan may be dominated by a single biotype with an effector profile similar to that of FOV race 7 (FOV7). One of these effector proteins is also present in the F. commune isolate showing virulence to cotton. Whole genome comparisons between FOV races can identify unique genetic markers for FOV4 and aid in the development of tools for breeding FOV resistant cotton varieties.

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Title: Genomic insights into Verticillium: a review of progress in the genomics era.

Author: M. Sayari, A. Dolatabadian, M. El-Shetehy and F. Daayf

Imprint: Front. Microbiol. 15:1463779. doi: 10.3389/fmicb.2024.1463779

Abstract: Genomics has emerged as a great tool in enhancing our understanding of the biology of Verticillium species and their interactions with the host plants. Through different genomic approaches, researchers have gained insights into genes, pathways and virulence factors that play crucial roles in both Verticillium pathogenesis and the defense responses of their host organisms. This review emphasizes the significance of genomics in uncovering the mechanisms that underlie pathogenicity, virulence, and host resistance in Verticillium fungi. Our goal is to summarize recent discoveries in Verticillium research highlighting progress made in comprehending the biology and interactions of Verticillium fungi. The integration of genomics into Verticillium studies has the potential to open avenues for developing strategies to control diseases and produce crop varieties resistant to verticillium, thereby offering sustainable solutions for enhancing agricultural productivity.

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Title: Introgression and Mapping of Cotton Leaf Curl Disease (CLCuD) Resistance from Wild Gossypium armourianum Kearney into Upland Cotton (*G. hirsutum* L.).

Author: Dharminder Pathak, Pankaj Rathore, Harpreet Kaur, Bhupinder Singh, Harish Kumar, Akhtar Ali, Sunayana Punia, Parvinder Singh Sekhon, and Kuldeep Singh

Imprint: Plant Disease, Published Online:16 Oct 2024https://doi.org/10.1094/PDIS-08-24-1645-SC

Abstract: Cotton leaf curl disease (CLCuD), caused by the whitefly transmitted gemini virus complex (Cotton leaf curl virus - CLCuV and their satellite molecules), is a serious threat to successful upland cotton production in northwest India, Pakistan, and China. The disease causes significant losses in fibre yield and the quality of cotton. Owing to the regular emergence of resistance breaking strains of CLCuV, all the previously available CLCuD resistant germplasms of upland cotton have become compromised and none of the extant upland cotton cultivars is resistant to this disease. Therefore, alternate sources of CLCuD resistance need to be explored, as genetic resistance is the only pragmatic and tenable management strategy to combat this malady. Here, we report for the first time the introgression and mapping of CLCuD resistance from a related non-progenitor wild diploid D-genome cotton species, G. armourianum into upland cotton. A backcross population (G. hirsutum/G. armourianum/G. hirsutum) was developed for this purpose. A single major QTL was found to be associated with resistance to CLCuD and was located on chromosome D01 through the genotyping-by-sequencing technique.

PLANT BREEDING AND GENETICS

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Title: Genome-wide analysis of cotton SCAMP genes and functional characterization of GhSCAMP2 and GhSCAMP4 in salt tolerance.

Author: Zhaojie He, Xiaohu Ma, Qian-Hao Zhu, Shuaishuai Cheng, Feng Liu, Tao Zhang, Caixia Zhang, Jianbin Li, Xianpeng Xiong & Jie Sun

Imprint: BMC Plant Biology, Volume 24, article number 870, (2024)

Abstract: Secretory carrier membrane proteins (SCAMPs) form a family of integral membrane proteins and play a crucial role in mediating exocytosis in both animals and plants. While SCAMP genes have been studied in several plant species, their functions in cotton, particularly in response to abiotic stress, have not yet been reported. Results- In this study, a total of 53 SCAMP genes were identified in G. arboreum, G. raimondii, G. hirsutum, and G. barbadense. These genes were classified into five groups based on a phylogenetic analysis with SCAMPs from Arabidopsis thaliana. The main factor driving the expansion of the SCAMP gene family in G. hirsutum is tandem and segmental duplication events. Using MEME, in addition to the conserved SCAMP domain, we identified 3–13 other domains in each GhSCAMP. The cis-element analysis suggested that GhSCAMPs were widely involved in cotton growth and development, and responses to abiotic stresses. RNA sequencing (RNA-Seq) and reverse transcription-quantitative polymerase chain reaction (RT-qPCR) results showed that most GhSCAMPs were expressed highly in many tissues and had differential expression responses to drought, cold, and heat stresses. Knock-down of GhSCAMP2 and GhSCAMP4 by virus-induced gene silencing (VIGS) lead to a salt-sensitive phenotype and had a lower content of CAT, POD, and SOD. Conclusions- This study identified SCAMP genes in four cotton species, enhancing our understanding of the potential biological functions of SCAMPs. Additionally, we demonstrated that GhSCAMP2 and GhSCAMP4 positively regulate cotton tolerance to salt stress.

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Title: Correlation and Path Coefficient Analysis for Some Quantitative Traits of Cotton (Gossypium hirsutum L.) Genotypes under Irrigated Conditions.

Author: Merdasa Balcha, Samuel Damtew, Donis Gurmessa, Arkebe G/Egziabher

Imprint: Ethiop. J. Agric. Sci. 34(2) 81-89 (2024)

Abstract: Comprehensive understanding about the crop nature, performance level and association of numerous agronomic attributes with yield is necessary for plant researchers to tackle the cotton yield limiting constraints. However, there is a lack of sufficient information on cotton yield, yield related and fiber quality traits correlation and path coefficient analysis in Ethiopia. Knowledge of correlation between different traits and the further partitioning of correlation coefficients into direct and indirect effects is a prerequisite for any underutilized crop improvements of sustainable genetic enhancement. The experiment was conducted on twelve genotypes with three checks in order to assess the association, direct and indirect effects of different characters on lint yield. The experiment was planted at Werer Agricultural Research Center and Nasa/Birale Farm under irrigated condition in a Randomized Complete Block Design with three replications during the 2016 to 2018 cropping seasons. Data were collected on yield, yield related and fiber quality traits. Correlation studies revealed that lint yield was significantly and positively correlated with the number of bolls per plant, seed cotton yield, ginning outturn and micronaire, whereas it was significantly and negatively correlated with fiber length at both phenotypic and genotypic levels. Path coefficient analysis, both at phenotypic and genotypic levels, revealed that seed cotton had the greatest direct effect on lint yield followed by ginning outturn and number of bolls per plant. Both correlation and path analysis indicated that seed cotton yield, ginning outturn and the number of bolls per plant were the major direct contributors to lint yield. Hence, the present study suggests that more seed cotton yield, ginning outturn and number of bolls per plant are major yield factors in selecting high lint yielding cotton genotypes.

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Title: The genetic basis of leaf hair development in upland cotton (Gossypium hirsutum).

Author: Xiaoyang Wang , Panhong Dai , Hongge Li , Jingjing Wang , Xu Gao

Imprint: Plant J,. 2024 Oct;120(2):729-747. doi: 10.1111/tpj.17017. Epub 2024 Sep 11.

Abstract: Trichomes, which originate from the epidermal cell of aerial organs, provide plants with defense and secretion functions. Although numerous genes have been implicated in trichome development, the molecular mechanisms underlying trichome cell formation in plants remain incompletely understood. Here, we using genome-wide association study (GWAS) across 1037 diverse accessions in upland cotton (Gossypium hirsutum) to identify three loci associated with leaf pubescence (hair) amount, located on chromosome A06 (LPA1), A08 (LPA2) and A11 (LPA3), respectively. GhHD1, a previously characterized candidate gene, was identified on LPA1 and encodes an HD-Zip transcription factor. For LPA2 and LPA3, we identified two candidate genes, GhGIR1 and GhGIR2, both encoding proteins with WD40 and RING domains that act as inhibitors of leaf hair formation. Expression analysis revealed that GhHD1 was predominantly expressed in hairy accessions, whereas GhGIR1 and GhGIR2 were expressed in hairless accessions. Silencing GhHD1 or overexpressing GhGIR1 in hairy accessions induced in a hairless phenotype, whereas silencing GhGIR2 in hairless accessions resulted in a hairy phenotype. We also demonstrated that GhHD1 interact with both GhGIR1 and GhGIR2, and GhGIR1 can interact with GhGIR2. Further investigation indicated that GhHD1 functions as a transcriptional activator, binding to the promoters of the GhGIR1 and GhGIR2 to active their expression, whereas GhGIR1 and GhGIR2 can suppress the transcriptional activation of GhHD1. Our findings shed light on the intricate regulatory network involving GhHD1, GhGIR1 and GhGIR2 in the initiation and development of plant epidermal hairs in cotton.

PLANT BIOTECHNOLOGY

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Title: Evolutionary comparison of lncRNAs in four cotton species and functional identification of *LncR4682-PAS2-KCS19* module in fiber elongation.

Author: Hushuai Nie, Nan Zhao, Bin Li, Kaiyun Jiang, Huijing Li, Jingrou Zhang, Anhui Guo, Jinping Hua

Imprint: Plant Journal, First published: 07 October 2024, https://doi.org/10.1111/tpj.17058

Abstract: Long non-coding RNAs (lncRNAs) play an important role in various biological processes in plants. However, there have been few reports on the evolutionary signatures of lncRNAs in closely related cotton species. The lncRNA transcription patterns in two tetraploid cotton species and their putative diploid ancestors were compared in this paper. By performing deep RNA sequencing, we identified 280 429 lncRNAs from 21 tissues in four cotton species. lncRNA transcription evolves more rapidly than mRNAs, and exhibits more severe turnover phenomenon in diploid species compared to that in tetraploid species. Evolutionarily conserved lncRNAs exhibit higher expression levels, and lower tissue specificity compared with species-specific lncRNAs. Remarkably, tissue expression of homologous lncRNAs in *Gossypium hirsutum* and *G. barbadense* exhibited similar patterns, suggesting that these lncRNAs may be functionally conserved and selectively maintained during domestication. An orthologous lncRNA, *lncR4682*, was identified and validated in fibers of *G. hirsutum* and *G. barbadense* with the highest conservatism and expression abundance. Through virus-induced gene silencing in upland cotton, we found that *lncR4682* and its target genes *GHPAS2* and *GHKCS19* positively regulated fiber elongation. In summary, the present study provides a systematic analysis of lncRNAs in four closely related cotton species, extending the understanding of transcriptional conservation of lncRNAs across cotton species. In addition, *LncR4682-PAS2-KCS19* contributes to cotton fiber elongation by participating in the biosynthesis of very long-chain fatty acids.

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Title: Application of an endogenous pGhαGloA promoter in CRISPR/Cas12a system for efficient genome editing to creat glandless cotton germplasm.

Author: Chenyu Li1, Zumuremu Tuerxun1, Yang Yang , Xiaorong Li , Fengjiao Hui , Juan Li , Zhigang Liu , GuoChen , Darun Cai , Hui Zhang , Xunji Chen , Shuangxia Jin

Imprint: Journal of Integrative Agriculture, Received 24 April, 2024 Accepted 10 July, 2024

Abstract: The efficient genome editing tool (the CRISPR/Cas12a system) has been used in research on plant functionional genomics and improvement of agronomic traits. In this study, CRISPR/Cas12a system wasoptimized by using the endogenous pGhαGloA promoter in cotton. Using this system, crRNAs was driven bythe Pol II pGhaGloA promoter to construct the pGhRBE3-pGhαGloA-GhPGF vector and carry out genetictransformation. The vector could work efficiently in all positive transgenic plants and the editing efficiency at the crRNA1 target site was up to 93.37%, and the editing efficiency of the crRNA2 target was up to 88.24%, which is significantly higher in editing efficiency of the pGhRBE3 system with Pol III promoter-Ubi 6.7promoter, this result indicates that the Pol II promoter is more suitable for expressing multiple sgRNA or crRNA than thepol III promoter in cotton. The vector mainly generated the editing type of fragment deletion and the deletionsize was in the range of 3-12 bp with the editing sites spanning at the 14th to 29th bases downstream of the protospacer adjacent motif (PAM). All the targeted mutation loci were stably inherited from T0 to T2 generationand three transgene-free lines with target site mutations of GhPGF gene were obtained and these glandless andgossypol-free/(low contents) cotton germplasm will play key role for healthy cottonseeds oil/cake production. Therefore, the CRISPR/Cas12a system driven by the pGhαGloA promoter can efficiently edit target genes incotton, which provides a powerful tool for cotton functionional genomics and genetic improvement.

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Title: Graph-based analysis of DNA sequence comparison in closed cotton species: A generalized method to unveil genetic connections.

Author: Riaz Hussain Khan, Nadeem Salamat, A. Q. Baig,Zaffar Ahmed Shaikh,Amr Yousef
Imprint: Plos One, Published: September 17, 2024, https://doi.org/10.1371/journal.pone.0306608

Abstract: Graph theory provides a systematic method for modeling and analysing complicated biological data as an effective bioinformatics tool. Based on current trends, the number of DNA sequences in the DNA database is growing quickly. To determine the origin of a species and identify homologous sequences, it is crucial to detect similarities in DNA sequences. Alignment-free techniques are required for accurate measures of sequence similarity, which has been one of the main issues facing computational biologists. The current study provides a mathematical technique for comparing DNA sequences that are constructed in graph theory. The sequences of each DNA were divided into pairs of nucleotides, from which weighted loop digraphs and corresponding weighted vectors were computed. To check the sequence similarity, distance measures like Cosine, Correlation, and Jaccard were employed. To verify the method, DNA segments from the genomes of ten species of cotton were tested. Furthermore, to evaluate the efficacy of the proposed methodology, a K-means clustering method was performed. This study proposes a proof-of-model that utilises a distance matrix approach that promises impressive outcomes with future optimisations to be made to the suggested solution to get the hundred percent accurate result. In the realm of bioinformatics, this paper highlights the use of graph theory as an effective tool for biological data study and sequence comparison. It’s expected that further optimization in the proposed solution can bring remarkable results, as this paper presents a proof-of-concept implementation for a given set of data using the proposed distance matrix technique.

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Title: Natural variations in the Cis-elements of GhRPRS1 contributing to petal colour diversity in cotton.

Author: Wei Hu1, Yanli Chen, Zhenzhen Xu, Linqiang Liu, Da Yan, Miaoyang Liu

Imprint: Plant Biotechnology Journal (2024), pp. 1–16 doi: 10.1111/pbi.14468

Abstract: The cotton genus comprises both diploid and allotetraploid species, and the diversity in petal colour within this genus offers valuable targets for studying orthologous gene function differentiation and evolution. However, the genetic basis for this diversity in petal colour remains largely unknown. The red petal colour primarily comes from C, G, K, and D genome species, and it is likely that the common ancestor of cotton had red petals. Here, by employing a clone mapping strategy, we mapped the red petal trait to a specific region on chromosome A07 in upland cotton. Genomic comparisons and phylogenetic analyses revealed that the red petal phenotype introgressed from G. bickii. Transcriptome analysis indicated that GhRPRS1, which encodes a glutathione S-transferase, was the causative gene for the red petal colour. Knocking out GhRPRS1 resulted in white petals and the absence of red spots, while overexpression of both genotypes of GhRPRS1 led to red petals. Further analysis suggested that GhRPRS1 played a role in transporting pelargonidin-3-O-glucoside and cyanidin-3-O-glucoside. Promoter activity analysis indicated that variations in the promoter, but not in the gene body of GhRPRS1, have led to different petal colours within the genus. Our findings provide new insights into orthologous gene evolution as well as new strategies for modifying promoters in cotton breeding.

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Title: Biosynthesis and Signaling of Strigolactones Act Synergistically with That of ABA and JA to Enhance *Verticillium dahliae* Resistance in Cotton (*Gossypium hirsutum* L.).

Author: Yifei Han, Yue Sun, Haoqi Wang, Huazu Li, Meng Jiang, Xueying Liu, Yuefen Cao, Wanru Wang, Hong Yin

Imprint: Plant, Cell and Environment, 17 September 2024, https://doi.org/10.1111/pce.15148

Abstract: Verticillium wilt (VW) caused by the soil-borne fungal pathogen *Verticillium dahliae* reduces cotton productivity and quality. Numerous studies have explored the genetic and molecular mechanisms regulating VW resistance in cotton, but the role and mechanism of strigolactone (SL) is still elusive. We investigated the function of SL in cotton's immune response to *V. dahliae* infection by exogenously applying SL analog, blocking or enhancing biosynthesis of endogenous SLs in combination with comparative transcriptome analysis and by exploring cross-talk between SL and other phytohormones. Silencing *GhDWARF27* and applying the SL analog GR24 or overexpressing *GhDWARF27* decreased and enhanced *V. dahliae* resistance, respectively. Transcriptome analysis revealed SL-mediated activation of abscisic acid (ABA) and jasmonic acid (JA) biosynthesis and signaling pathways. Enhanced ABA biosynthesis and signaling led to increased activity of antioxidant enzymes and reduced buildup of excess reactive oxygen species. Enhanced JA biosynthesis and signaling facilitated transcription of JA–dependent disease resistance genes. One of the components of the SL signal transduction pathway, GhD53, was found to interact with GhNCED5 and GhLOX2, the key enzymes of ABA and JA biosynthesis, respectively. We revealed the molecular mechanism underlying SL–enabled *V. dahliae* resistance and provided potential solutions for improving VW resistance in cotton.

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Title: TRANSPARENT TESTA 16 collaborates with the MYB-bHLH-WD40 transcriptional complex to produce brown fiber cotton.

Author: Yuanxue Li, Tian Yao, Chao Fu, Nian Wang, Zhiyong Xu, Ningyu Yang, Xianlong Zhang, Tianwang Wen, Zhongxu Lin

Imprint: Plant Physiology, 2024, 00, 1–16 https://doi.org/10.1093/plphys/kiae530

Abstract: Naturally colored cotton (NCC; Gossypium spp.) does not require additional chemical dyeing and is an environmentally friendly textile material with great research potential and applications. Our previous study using linkage and association mapping identified TRANSPARENT TESTA 2 (Gh_TT2) as acting on the proanthocyanin synthesis pathway. However, limited information is available about the genetic regulatory network of NCC. Here, we verified the effectiveness of Gh_TT2 and the roles of Gh_TT2 and red foliated mutant gene (Re) in pigment formation and deposition of brown fiber cotton (BFC). Variations in Gh_TT2 derived from interspecific hybridization between Gossypium barbadense acc. Pima 90-53 and Gossypium hirsutum acc. Handan208 resulted in gene expression differences, thereby causing phenotypic variation. Additionally, the MYB-bHLH-WD complex was found to be negatively modulated by TRANSPARENT TESTA 16/ARABIDOPSIS BSISTER (TT16/ABS). RNA-seq suggested that differential expression of homologous genes of key enzymes in the proanthocyanin synthesis pathway strongly contributes to the color rendering of natural dark brown and light brown cotton. Our study proposes a regulatory model in BFC, which will provide theoretical guidance for the genetic improvement of NCC.

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Title: Simultaneous improvement of fiber yield and quality in upland cotton (Gossypium hirsutum L.) by integration of auxin transport and synthesis.

Author: Qingqing Chu, Xingxian Fu, Juan Zhao, Yuxin Li, Lina Liu, Liuqin Zhang, Yujie Zhang

Imprint: Molecular Breeding, Volume 44, article number 64, (2024)

Abstract: Cotton is a widely planted commercial crop in the world. Enhancing fiber yield and quality is a long-term goal for cotton breeders. Our previous work has demonstrated that fine promotion of auxin biosynthesis in ovule epidermis, by overexpressing *FBP7pro::iaaM*, has a significant improvement on lint yield and fiber fineness. Lately, transgenic cottons overexpressing *GhROP6* variants modify mature fiber length by controlling GhPIN3a-mediated polar auxin transport in ovules. Here, this study showed that all these *GhROP6*-related cottons displayed unsatisfactory agronomic performance in field conditions. Yet extra auxin supply could promote their fiber development, suggesting inadequate auxin supply in the ovules. Thus, these cottons were integrated with enhanced auxin synthesis by crossing with *FBP7pro::iaaM* cotton. All the transgene-stacked cottons exhibited synergetic effects on cotton yield (seedcotton yield, lint yield, and lint percentage) and quality (length, strength, and micronaire). Notably, comparing to the *FBP7pro::iaaM* background, the transgene-stacked cotton co-expressing *FBP7pro::iaaM* and *CA-ghrop6* (constitutively active *GhROP6*) exhibited a 12.6% increase in seedcotton yield and a 19.0% increase in lint yield over a three-year field trial, and simultaneously resulted in further improvement on fiber length, strength, and micronaire. Collectively, our data provide a potential strategy for genetic improvement on cotton fiber yield and quality.

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Title: Analysis of CYP701A1 genes in *Gossypium* species and functional characterization through gene silencing.

Author: Zhao Liang, Di Jiachun , Guo Qi , Xu Zhenzhen

Imprint: Crop Design, Available online 16 September 2024, 100081

Abstract: Gibberellins (GA) are known to play crucial roles in various aspects of plant growth and development. The cytochrome P450 enzyme family is recognized for its significance in plant metabolic processes. Specifically, CYP701s, a subgroup of CYP71, encode *ent*-kaurene oxidase in the gibberellin synthesis pathway. In this study, we analyzed genomic data from 30 *Gossypium* species, including nine allotetraploid genomes (AD1-AD7, with two each for AD1 and AD2), 21 diploid genomes (A-G, K, with two A-genomes and 12 D-genomes), and *Gossypioides kirkii* genome as an outgroup for evolutionary analysis, totaling 31 genomes. Subsequently, 40 CYP701A1 genes were identified from various genomes and conducted a comprehensive analysis of their structure and evolution. Virus-induced gene silencing (VIGS) technology was utilized to knock out the *GhCYP701A1* gene in *Gossypium hirsutum* ac TM-1. Subsequent analysis revealed changes in hormone content, with decreased gibberellin levels and notable increases in auxin, cytokinin, and jasmonic acid contents. Conversely, salicylic acid content decreased, while the precursor for ethylene synthesis, 1-aminocyclopropane-1-carboxylic acid (ACC), remained relatively stable. Transcriptome analysis of the gene silencing plants identified 15,962 differentially expressed genes, including 8,376 upregulated and 7,586 downregulated genes. Enrichment analysis through KEGG pathway analysis highlighted 'Plant hormone signal transduction' as a prominent pathway with 234 differentially expressed genes. The study provided insights into the function and regulatory network of the gene.

SEED SCIENCE AND TECHNOLOGY

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Title: Pressures on seeding lines influencing cotton emergence and initial growth.

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Imprint: Revista de Ciências Agroveterinárias 23 (2): 2024

Abstract: The force applied to the seeding unit can influence the emergence of cotton seedlings, which may result in a decrease in the development and productive potential of the plant. Thus, the work aimed to evaluate the effect of different pressures exerted on cotton sowing lines on the emergence and initial growth of plants. A randomized block design was used with eight treatments and three replications, totaling 24 plots. The treatments consisted of pressures, manual 16, 45, and 120 kg, light automatic, standard and heavy, personalized automatic 36 and 59 kg. Seedling emergence was evaluated at 5; 6; 7th and 8th days after sowing, the total number of plants that emerged on the 8th day, the number of exposed seeds, plant height 20 and 25 days after sowing, and main root length 15 days after sowing. In the fastest emergence, 5 days after sowing, the 16 and 45 kg manual pressure system obtained a greater number of emerged plants, surpassing the equipment's standard automatic system by 44.6%, however, the use of 16 kg also resulted in a greater number of exposed seeds. The use of an automatic pressure system during sowing was not favorable to the emergence of cotton seedlings, with manual systems being more appropriate. There was no difference in plant height 25 days after sowing and root length 15 days after sowing, about the different pressure systems used.

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Title: Use of Beauveria bassiana and Bacillus amyloliquefaciens Strains as Gossypium hirsutum Seed Coatings: Evaluation of the Bioinsecticidal and Biostimulant Effects in Semi-Field Conditions.

Author: Vasileios Papantzikos, Spiridon Mantzoukas, Alexandra Koutsompina, Evangelia M. Karali, Panagiotis A. Eliopoulos, Dimitrios Servis, Stergios Bitivanos, and George Patakioutas

Imprint: Agronomy 2024, 14(10), 2335; https://doi.org/10.3390/agronomy14102335

Abstract: There are many challenges in cotton cultivation, which are mainly linked to management practices and market demands. The textile commerce requirements are increasing but the effects of climate change on cotton cultivation are becoming an issue, as its commercial development depends significantly on the availability of favorable climatic parameters and the absence of insect pests. In this research, it was studied whether the use of two commercial strains as cotton seed coatings could effectively contribute to the previous obstacles. The experiment was carried out in semi-field conditions at the University of Ioannina. It used a completely randomized design and lasted for 150 days. The following treatments were tested: (a) coated seeds with a commercial strain of Beauveria bassiana (Velifer®); (b) coated seeds with a combination of Velifer® and a commercial strain of Beauveria bassiana (Selifer®); and (c) uncoated cotton seeds (control). The biostimulant effect of the two seed coatings was assessed against the growth characteristics of cotton, and the total chlorophyll and proline content. The bioinsecticidal effect was evaluated by measuring the population of Aphis gossypii on the cotton leaves. The proline effect increased by 15% in the treated plants, whereas the total chlorophyll was higher in the use of both Velifer® and Velifer®–Selifer® treatments by 32% and 19%, respectively. Aphid populations also decreased in the treated plants compared to the control plants (29.9% in Velifer® and 22.4% in Velifer®–Selifer®). Based on an assessment of the above parameters, it follows that the two seed coatings can significantly enhance the growth performance of cotton and reduce the abundance of A. gossypii.

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Title: Exogenous application of silica nanoparticles mitigates combined salt and low-temperature stress in cotton seedlings by improving the K^+/Na^+ ratio and antioxidant defense.

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

Imprint: Plant Stress, Volume 14, December 2024, 100597

Abstract: Silica nanoparticles (SiO_2-NPs) have been demonstrated to alleviate the adverse impacts of salt or low temperature on crop growth, especially for individual stress. The aim of this study was to elucidate the regulatory effect of SiO_2-NPs on plant performance under combined salt and low-temperature stress. Therefore, a phytotron experiment was performed to explore the effects of SiO_2-NPs application (0, 50, 100, 200 mg L^{-1}) on the plant growth, ionic content, antioxidant activities, photosynthetic parameters, and osmoregulator concentrations of cotton seedlings subjected to the combined stress of salinity (50, 100, and 150 mmol L^{-1} NaCl) and low temperature (day and night temperatures of 15 and 10 °C). The results indicated that the combinatorial stress strongly decreased the plant height and leaf area of cotton seedlings, and obviously suppressed the aboveground biomass by 10.26 %, 11.42 %, and 15.70 % with the increase in salinity. While SiO_2-NPs application significantly increased the plant growth, photosynthetic rate, transpiration rate, stomatal conductance, superoxide dismutase, catalase and glutathione reductase activities, leaf water potential, K^+, and proline contents, and reduced the Na^+ content and Na^+/K^+ ratio of cotton seedlings under the combinatorial stress. However, the effects of SiO_2-NPs on reduced glutathione, total soluble sugar and protein content, and peroxidase activity did not exhibit a clear pattern. The aboveground biomass of cotton seedlings subjected to the combinatorial stress was closely correlated with the Na^+/K^+ ratio, Na^+ content, K^+ content, proline content, SOD activity, and CAT activity, indicating that SiO_2-NPs could alleviate the suppression of combinatorial stress on cotton seedling growth by decreasing the Na^+/K^+ ratio and increasing the antioxidant capacity.

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Title: Cottonseed meal soil application, nutrient uptake, biochemical attributes of cotton (Gossypium hirsutum L.) and activities of soil enzymes in saline soil.

Author: Emrah Ramazanoglu, Suat Cun, Cevher İlhan Cevheri, Vedat Beyyavas, Erdal Sakin

Imprint: Journal of Elementology, 29(3), 647-664, https://doi.org/10.5601/jelem.2024.29.2.3332

Abstract: High salinity levels exert detrimental effects on plant growth and development by disturbing photosynthesis, water relations, and nutrient absorption. Different soil amendments are used to alleviate the adverse effects of soil salinity on plant growth and development. This study investigated the impact of cottonseed meal (CSM) application as soil amendment on soil enzymes, macro- and micro-nutrients, and phenol and sugar content in cotton plants grown on normal and saline soil. Three different CSM levels, i.e. 0 (CK), 40 and 80 Mg ha-1 were included in the study. Soil amendment with CSM significantly increased soil enzyme activities, organic carbon, and available nutrients, and improved soil structure. Soil amendment with 40 Mg ha-1 CSM improved dehydrogenase and urease enzyme activities by 15.38 and 40.51%, whereas amendment with 80 Mg ha-1 improved the activities of these enzymes by 15.29 and 21.47%, respectively. However, the activity of catalase enzyme was decreased by 32.18 and 48.28% under 40 and 80 Mg ha-1 CSM amendment, respectively. Soil amendment with 40 Mg ha-1 CSM to increased N, K, Ca, and Mg content by 65.90, 52.29, 5.71, 15.79%, and decreased Na content by 28.85%, whereas 80 Mg ha-1 increased these nutrients by 87.12, 53.63, 10.60, 40.63% and decreased Na content by 4.19%. Similarly, application of 40 Mg ha-1 CSM significantly increased B and Mn content in plants by 7.12, 8.6% on saline soil and by 1.13, and 10.09% on normal soil. Likewise, while 80 Mg ha-1 CSM application increased the B and Mn content by 1.84, and 9.46% on saline soil and 4.0, and 8.94% on normal soil. The application of 80 Mg ha-1 CSM improved total sugar content by 45.5% in saline soil and 3.97% in normal soil. The total phenol content of the plants was improved by 17.25% in saline soil and 2.9% in normal soil. It is concluded that CSM can be used alone or in combination with other organic amendments, such as compost and poultry manure, to alleviate the adverse effects of soil salinity on soil enzymes and nutrient uptake by plants.

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Title: Glycine betaine application improved seed cotton yield and economic returns under deficit irrigation.

Author:Emrah Ramazanoglu , Nimet Kılınçoğlu , Vedat Beyyavas , Cevher
İlhan Cevheri , Erdal Sakin

Imprint: Journal of King Saud University - Science, Volume 36, Issue 10, November 2024, 103445

Abstract: Deficit irrigation exerts devastating effects on the productivity and economic returns of cotton crop, as well as carbon dioxide (CO_2) emission from soil. Osmolytes play a significant role in facilitating the adaptation of cotton plants to abiotic stresses and improve productivity. Methods- This study investigated the effects of different osmolytes (glycine betaine, ascorbic acid, salicylic acid 100 mg L^{-1} each) and deficit irrigation (50 %-I_{50}, 75 %-I_{75}, and 100 %-I_{100}) on seed cotton yield, greenhouse gas emission (CO_2-C), emission factor (EFs) and economic returns of cotton in Southern Anatolia, Türkiye. Results- Deficit irrigation and osmolyte treatment, both separately and in combination, had a substantial impact on seed cotton yield, CO_2-C emission and EFs. The lowest (3800 kg ha^{-1}) and the highest (4746 kg ha^{-1}) seed cotton yield was noted under I_{50}, and I_{100} treatments, respectively. Similarly, no osmolyte application and application of glycine betaine resulted in the lowest (4097 kg ha^{-1}) and the highest (4545 kg ha^{-1}) seed cotton yield, respectively. The interactive effect indicated that application of glycine betaine and salicylic acid produced better yield than control treatment under all irrigation treatments. The lowest (1.55) and the highest (1.94 mg) CO_2-C emission (mg CO_2-C $m^{-2} h^{-1}$) was recorded for I_{50}, and I_{100} treatments respectively. Likewise, the lowest (1.52) and the highest (2.19) daily carbon emission were recorded for salicylic acid and glycine betaine application, respectively. The lowest and the highest EFs values were observed for glycine betaine and ascorbic acid application, respectively. Application of glycine betaine resulted in the highest economic returns under all irrigation treatments which was comparable to salicylic acid, whereas the lower economic returns were recorded for control treatment. Conclusion- It is concluded that application of glycine betaine can be used to improve seed cotton yield and economic returns under deficit irrigation. Similarly, glycine betaine proved helpful in reducing CO_2-C emission under deficit irrigation compared to normal irrigation.

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Title: Impact of dielectric barrier discharge plasma and plasma-activated water on cotton seed germination and seedling growth.

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Imprint: Heliyon, Volume 10, Issue 19e38160October 15, 2024

Abstract: Unfavorable environmental conditions during planting can reduce seed germination and hinder seedling growth. To address this issue, manufacturers are exploring innovative and cost-effective methods, such as cold plasma discharge. This simple, low-cost, and efficient physical technique induces significant biological responses in seeds and plants without the use of traditional, environmentally hazardous chemicals. This study investigated the impact of dielectric barrier discharge (DBD) plasma and plasma-activated water (PAW), produced by gliding arc plasma, on the germination and seedling growth of My344 cotton seeds. The seeds were pre-treated with 80 W of DBD plasma for 0, 1, 2, and 3 min, and subsequently soaked for 90 min in PAW with varying pH levels of 5.82, 3.88, 3.63, and 3.38. The results showed that plasma treatment positively influenced seed germination and seedling growth. The highest germination percentage (98.89 %) was observed with 1 min of DBD treatment, followed by PAW priming at pH levels of 3.63 and 3.38. Additionally, a 3-min DBD treatment followed by soaking in PAW with a pH of 3.63 led to significant increases in stem length (76.76 %), root length (48.77 %), and wet weight (76.44 %). Furthermore, it was observed that the electrical conductivity of the seeds in all groups decreased significantly with increased PAW acidity. The physical and chemical effects of cold DBD plasma on the seed surface, as well as changes in hydrophilicity, were further examined using scanning electron microscopy (SEM), Fourier-transform infrared spectroscopy (FTIR), and water contact angle imaging.

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Title: Selection of productive early maturing cotton genotypes with improved fibre quality parameters.

Author: Sabir Makhmadjanov, Laura Tokhetova, Nurman Daurenbek

Imprint: Scientific Horizons, 27(8), 69-79. doi: 10.48077/scihor8.2024.69.

Abstract: The results showed that Tashkent-6 and Maktaral-5027 had the best parameters: yield 3.8 t/ha and 3.5 t/ha, flowering time 55 days and maturity 120 days, plant height 120 cm and 115 cm, number of bolls 45 and 42. The fibre quality of these genotypes was also high: length 32 mm and 31 mm, tensile strength 30 g/tex and 29 g/tex, fineness 2.5 dtex and 2.6 dtex. Namangan-1 and Bukhara-8 genotypes showed moderate results: yield 3.2 t/ha and 3.0 t/ha, flowering time 60 days and ripening time 130 days, plant height 110 cm and 105 cm, number of bolls 40 and 38, fibre length 30 mm and 29 mm, tensile strength 28 g/tex and 27 g/tex, fineness 2.8 dtex and 2.9 dtex. Statistical analysis confirmed the significance of differences between genotypes. The results of the study confirmed high productivity and fibre quality of genotypes Tashkent-6 and Maktaral-5027, which makes them promising for commercial cultivation in Kazakhstan, while genotypes Namangan-1 and Bukhara-8 also have potential for certain agronomic conditions.

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Title: Regulatory networks of coresident subgenomes during rapid fiber cell elongation in upland cotton.

Author: Lan Yang, Wenqiang Qin, Xi Wei, Rui Liu, Jiaxiang Yang, Zhi Wang, Qingdi Yan, Yihao Zhang, Wei Hu, Xiao Han, Chenxu Gao, Jingjing Zhan, Baibai Gao, Xiaoyang Ge, Fuguang Li and Zhaoen Yang

Imprint: Plant Communications (2024), https://doi.org/10.1016/j.xplc.2024.101130

Abstract: Cotton, an intriguing plant species shaped by polyploidization, evolution, and domestication, holds particular interest due to the complex mechanisms governing fiber traits across its two subgenomes. However, the regulatory elements or transcriptional networks between subgenomes during fiber elongation remain to be fully clarified. Here, we analyzed 1462 cotton fiber samples to reconstruct the gene-expression regulatory networks that influence fiber cell elongation. Inter-subgenome expression quantitative trait loci (eQTLs) largely dictate gene transcription, with a notable tendency for the D subgenome to regulate A-subgenome eGenes. This regulation reveals synchronized homoeologous gene expression driven by co-localized eQTLs and divergent patterns that diminish genetic correlations, thus leading to preferential expression in the A and D subgenomes. Hotspot456 emerged as a key regulator of fiber initiation and elongation, and artificial selection of trans-eQTLs in hotspot456 that positively regulate KCS1 has facilitated cell elongation. Experiments designed to clarify the roles of trans-eQTLs in improved fiber breeding confirmed the inhibition of GhTOL9 by a specific trans-eQTL via GhWRKY28, which negatively affects fiber elongation. We propose a model in which the GhWRKY28–GhTOL9 module regulates this process through the ESCRT (endosomal sorting complex required for transport) pathway. This research significantly advances our understanding of cotton's evolutionary and domestication processes and the intricate regulatory mechanisms that underlie significant plant traits.