GLEANINGS IN COTTON RESEARCH

JANUARY 2025

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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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1

Title: Optimizing plant density and canopy structure to improve light use efficiency and cotton productivity: Two years of field evidence from two locations.

Author: Menghua Zhai, Xuewen Wei, Zhanlei Pan

Imprint: Industrial Crops and Products, Volume 222, Part 4, 15 December 2024, 119946

Abstract: Optimizing the efficiency and effectiveness of light utilization is crucial for increasing cotton (*Gossypium hirsutum L.*) yields. However, how to increase light use efficiency and yield by improving canopy structure has not been fully verified and quantified through field trials, especially at different test sites. To explore this issue in greater depth, split-plot field experiments were conducted from 2019 to 2021 in Dongping and Jinxiang counties, Shandong, China. The effects of different planting densities and cotton varieties on the leaf area index (LAI), PAR interception rate (In), photosynthetically active radiation-use efficiency (PARUE), plant nutrient uptake, and seed cotton yield in a cropping system in which cotton was planted directly after garlic (*Allium sativum L.*) harvest were studied. The results revealed that increasing the planting density from the lowest value of 6.8×10^4 plant·ha^{-1} to 11.3×10^4 plant·ha^{-1} resulted in increases of 4.4–14.7 % in the cotton LAI, 2.5–12.4 % in the net photosynthetic rate (Pn), 5.0–6.8 % in the PAR interception rate, 16.0–53.2 % in the PARUE, and 5.2–13.4 % in the seed cotton yield. Notably, compared with those of Demian 15, the Lumian 532 variety presented greater LAI, Pn, PAR interception rate, PARUE, nutrient uptake, and seed cotton yield at D11.25 in the 2020 experiment in Jinxiang County. Specifically, on D11.25, Lumian 532 had the highest seed cotton yield, reaching 3939.0 kg·ha^{-1}. The LAI had a direct positive effect on nutrient uptake in cotton, with a value of 0.8. In addition, according to the Mantel test ($p < 0.05$), the primary driving factor influencing seed cotton yield was the Pn. This factor was significantly and positively correlated with the PAR interception rate and seed cotton yield ($p < 0.01$). Additionally, the PARUE was most significantly influenced by planting density (R=0.82, $p < 0.01$), with an increase of 2.0×10^{-4} g·MJ^{-1} for each additional planting density. In conclusion, increasing the planting density of direct seeded short season cotton plants after garlic harvesting can increase cotton light interception and utilization efficiency and improve plant nutrient uptake. This increase can result in increased seed cotton yield. Ultimately, the Lumian 532 variety performed optimally at D11.25. These results are essential for improving and managing cropping systems involving the planting of cotton in the Yellow River Basin of China and similar regions.

2

Title: Influence Of Socio-Economic Factors on Sustainable Production of Cotton In Kisumu County.

Author: Kenya Omollo Rose Agina Atieno

Imprint: A thesis submitted to the board of postgraduate studies in partial fulfillment of the requirements of the degree of Doctor of Philosophy in development studies, department of sociology and development studies, KISII university 2024

Abstract: Sustaining cotton production is a challenge facing Kisumu County and the Kenyan government. Cotton is an important crop whose production affects the livelihoods and development of the county. Several interventions have been done in the sector since independence to sustain cotton production in areas with competitive advantages, like Kisumu County, for the related industries to operate at total capacity, with little success. This led to the closure of the industries, negatively affecting livelihoods and development. The sustainable production of locally produced cotton is yet to be realized. This informed the study. The main objective of this study was to investigate the influence of social and economic factors and to evaluate the interventions in place for sustainable cotton production and development in Kisumu County. Specific objectives were to assess the influence of social factors, Gender, Cultural beliefs, Religion, economic factors, Marketing, and Distance from buying centers, and the interventions affecting sustainable cotton production in Kisumu County. The dependent variable was sustainable cotton production, while social and economic factors and the interventions in place formed the independent variables. The study was guided by systems theory by Ludwig Von Bertalanffy,1901-1927. A mixed research design combining inferential and descriptive data was employed and analyzed quantitatively and qualitatively. Data collection included field surveys, interviews with stakeholders, focus group discussions, and the utilization of existing datasets. The target population was 660 cotton farmers, obtained through purposive sampling. The representative sample was 240 cotton farmers, calculated using Israel's (1992) formula. Other respondents linked to cotton production were 53 through stratified random sampling, giving 293 respondents. The study administered 293 questionnaires and received 267, while 26 were not returned. Semi structured interview schedules with questionnaires were used to collect quantitative data, which was analyzed using descriptive and inferential statistics. In contrast, Focus Group Discussions, Key Informant Interviews, and observation were used to collect qualitative data, which was analyzed by categorizing relevant responses to answer research questions. Research instruments were validated before fieldwork, and reliability was determined through the test-retest technique. Findings revealed that many social and economic factors influence sustainable cotton production and development in Kisumu County. Knowledge from research findings will contribute to overcoming constraints to

sustainable cotton production, assist policy and decision-makers in government and non-governmental institutions, and improve the existing cotton literature in Kisumu County. The study concluded that there is a need for the government, private sector, and stakeholders to increase extension services to farmers, lobby for policies that would address social and economic factors surrounding cotton production, reduce or stop the importation of related competing products and improve cotton prices in the local market. The study recommends that adequate extension services be provided to farmers and relevant policies be adopted to assist all the stakeholders in the cotton value chain to sustain cotton production.

3

Title: Biochemical and morpho-physiological insights revealed low moisture stress adaptation mechanisms in cotton (Gossypium hirsutum L.)

Author: Ayesha Safdar, Amjad Hameed & Hafiz Mumtaz Hassan

Imprint: Scientific Reports volume 14, Article number: 25942 (2024)

Abstract: Cotton (Gossypium hirsutum L.) is a multipurpose crop. Abiotic stresses, especially extreme heat and drought, limit crop growth and thus reduce cotton yield by about 50%. In this study, 30 cotton genotypes were tested against low moisture stress in a pot experiment in triplicates along with control under wire house conditions. At the 3–4 leaf stage, different morpho-physiological and biochemical parameters were measured in order to select the low moisture stress-tolerant genotypes. For the selection of the best performing genotypes, Multi-Trait Genotype-Ideotype Distance Index (MGIDI) was used for the ranking of genotypes on the basis of multiple indices. For biochemical traits, 09 (TPC, TF, TSP, MDA, SOD, POD, CAT, APX, and Proline) out of 24 showed significant genotypic effects and were used for MGIDI. Eight genotypes (N-812 N-1296 N-696 N-377 N-121–896 N-T86, and N-3496) were observed to be best performing than others at 25% selection pressure (SI = 25%). For morpho-physiological traits, 14 out of 15 showed significant genotypic effects and used for MGIDI. Ten genotypes (N-1237 N-812 N-1296 N-696 N-9078 N-377 N-512 N-121 N-375, and N-896) were observed to be best performing at 35% selection pressure (SI = 35%). Six genotypes, i.e. N-812–1296 N-696 N-377 N-121, and N-896 were found common in both MGIDI analysis. In conclusion, three genotypes, i.e. N-696, N-896, and N-T86 proved to be most resilient to low moisture stress. Develop protocols, identified genotypes and markers that can be used for development of climate-smart cotton genotypes.

4

Title; Effect of Drought Stress and Response in Cotton.

Author: Muhammad Kashif Shahzad Sarwar, Muhammad Usman, Faizan Asif , Rabia Kalsoom , Sanam Tabbusam and Muhammad Zeeshan

Imprint: TRENDS IN ANIMAL AND PLANT SCIENCES https://doi.org/10.62324/TAPS/2024.048

Abstract: Gossypium hirsutum is one of the most vital economical crops. With climatic changes and global warming, its production is seriously affected and decreased. Among these climatic stresses, drought is the leading abiotic stress that lessens its yields. It affects negatively (directly or indirectly) on several processes including morphological, physiological, anatomical and biochemical processes in cotton plants that leads to down regulation of cotton plant's growth. Under drought stress, cotton plants reduce water loss through rolling of leaf margins, which decreases the surface area exposed to radiation. This response greatly inhibits the rate of photosynthesis, mostly because of reduced stomata conductance. The diminished photosynthetic activity results in a decline in dry matter, suggesting that flowers are somewhat protected from water scarcity compared to neighboring leaves. Various stress-responsive genes also participate in this process and aid the cotton plant in its ability to endure unfavorable conditions. In addition, drought stress decreases the expression of GhSUT-1, a sucrose transporter that is essential for exporting photosynthetic carbon assimilates. Drought stress affects important enzymes involved in starch production, including AGPase, GBSSase, and SSSase. During drought conditions, the activity of GBSSase, which is responsible for the synthesis of amylose, increases. However, the activity of AGPase, which is involved in the development of both amylose and amylopectin, is greatly reduced, thereby impeding the production of both starch components. In addition, a reduction in SSSase activity leads to a decrease in the generation of starch and a decrease in the amount of energy produced by the oxidation of glucose in cellular respiration.

5

Title: Assessment of Yield and Economics under High Density Planting System in Cotton in Kachchh District of Gujarat, India.

Author: Traloki Singh a, S.P. Singh b* , K.B. Anand c , Tralok Nath Rai a , Anjali Sahu a and V. P. Gupta

Imprint: International Journal of Plant & Soil Science Volume 36, Issue 10, Page 441-447, 2024

Abstract: Cotton (Gossypium hirsutum L.) possesses a position of major fiber and cash crop, which plays vital role to sustain national economy. It provides the basic raw material (cotton fiber) to cotton textile industry. Gujarat contributes substantially to the national cotton area (24%) and productions (37%). A field experiment was carried out during the kharif seasons from 2017-18 to 2019-20 atfarmers' fields through ICAR-CAZRI Krishi Vigyan Kendra Kachchh-II to evaluate the impact of frontline demonstrations (FLDs) on cotton productivity and profitability. During the experiment period, a total of 30 FLDs on high density planting system (HDPS) in cotton with the high-yielding variety GTHH-49 were demonstrated in a 12-hectare area across 6 villages in the Bhuj, and Nakhatrana talukas of Kachchh district. The improved variety GTHH-49 with a full package of practices was demonstrated in the plots, while existing technology was treated as the local check. Based on three years of data, the improved practice (IP) resulted in an average seed yield of 2868 kg ha-1 , which was an increase of 13.35% compared to the local check yield of 2530 kg ha-1 . The demonstrated technology showed an average extension gap, technology gap, and technology index of 338.33 kg ha-1 , 631.67 kg ha-1 , and 18.05%, respectively. The economic analysis of the demonstrations revealed the viability of the improved technology, with a net return of 101670.3 Rs. ha-1 and a benefit-cost ratio (BCR) of 3.24, compared to 84964.67 Rs. ha-1 and a BCR of 3.02 for local check. A wide range of extension and technology gaps had a detrimental influence on crop output and net returns in general. The results revealed that the adoption of the high-yielding variety with a full package of practices significantly increased cotton productivity and reduced both extension and technology gaps.

6

Title: Soil bacterial and fungal microbiomes under cotton production are more sensitive to tillage and cover crops than irrigation level in a semi-arid sandy soil.

Author: Billi Jean Petermann, Veronica Acosta-Martinez, Haydee E. Laza , Katie Lewis, Joshua Steffan , Lindsey C. Slaughter

Imprint: Applied Soil Ecology, Volume 204, December 2024, 105711

Abstract: Land managers in semi-arid regions experience challenging climatic conditions, such as variable rainfall, extreme temperature, and prolonged droughts that are expected to intensify over the next few decades. Conservation practices implemented to reduce erosion and restore degraded soils can alter soil properties that affect the composition and function of the soil microbiome. We compared microbiome responses to long-term (> 7 years) tillage and cropping management changes in bulk (0–10 cm, 10–20 cm) and root-associated soils under differing irrigation levels (High, Low) in sandy loam semi-arid soil. Cropping systems included a traditional system (Continuous tillage with continuous monocrop, CCCT) compared to two no-tillage

systems that included a rye cover crop (NTCR) or a cotton/wheat rotation (NTCW). We found that microbiome structure was influenced more by management practices than irrigation across taxonomic levels. Drought-tolerant taxa also dominated bacterial communities, with no significant differences between high and low irrigation. Overall, the results from this sandy-textured soil show that tillage and vegetation management were stronger drivers of bacterial and fungal microbiome composition than irrigation level, demonstrating the efficacy of conservation management practices in semi-arid soils even under water-limited conditions.

7

Title: Drought stimulates root exudation of organic nitrogen in cotton (Gossypium hirsutem).

Author: Harrison R. Coker1Heng-An Lin1Caleb E. B. Shackelford1Malak M. Tfaily2A. Peyton Smith1Julie A. Howe

Imprint: Front. Plant Sci., 19 November 2024, Sec. Plant Abiotic Stress, Volume 15 - 2024 | https://doi.org/10.3389/fpls.2024.1431004

Abstract: Root exudation of N is a plant input to the soil environment and may be differentially regulated by the plant during drought. Organic N released by root systems has important implications in rhizosphere biogeochemical cycling considering the intimate coupling of C and N dynamics by microbial communities. Besides amino acids, diverse molecules exuded by root systems constitute a significant fraction of root exudate organic N but have yet to receive a metabolomic and quantitative investigation during drought. To observe root exudation of N during drought, mature cotton plants received progressive drought and recovery treatments in an aeroponic system throughout their reproductive stage and were compared to control plants receiving full irrigation. Root exudates were nondestructively sampled from the same plants at 9 timepoints over 18 days. Total organic C and N were quantified by combustion, inorganic N with spectrophotometric methods, free amino acids by high performance liquid chromatography (HPLC), and untargeted metabolomics by Fourier-transform ion cyclotron resonance-mass spectrometry (FT-ICR-MS). Results indicate that organic N molecules in root exudates were by far the greatest component of root exudate total N, which accounted for 20-30% of root exudate mass. Drought increased root exudation of organic N (62%), organic C (6%), and free amino acid-N (562%), yet free amino acids were <5% of the N balance. Drought stress significantly increased root exudation of serine, aspartic acid, asparagine, glutamic acid, tryptophan, glutamine, phenylalanine, and lysine compared to the control. There was a total of 3,985 molecules detected across root exudate samples, of which 41% contained N in their molecular formula. There were additionally 349 N-containing molecules unique to drought treatment and 172 unique

to control. Drought increased the relative abundance and redistributed the molecular weights of low molecular weight N-containing molecules. Time-series analysis revealed root exudation of organic N was stimulated by drought and was sensitive to the degree of drought stress.

8

Title: The Photoperiodic Floral Transition in Cotton (Gossypium hirsutum)

Author: Muhammad Usman, Muhammad Zeeshan , Eman Mehrab and Samyka Marium and Muhammad Kashif Shahzad Sarwar

Imprint: TRENDS IN ANIMAL AND PLANT SCIENCES https://doi.org/10.62324/TAPS/2024.054

Abstract: The wild races of Gossypium hirsutum is a tetraploid perennial plant and follows short day photoperiodism for flowerings. But upland cotton, which is cultivated in most parts of world, insensitive to photoperiodism. The flowering or reproductive stage in Gossypium hirsutum's life cycle is important for cotton fiber formation. However, upland cotton is insensitive to the process of photoperiodism but its critical to understand the floral transition process, structure of cotton flower at microscopic level and effect of environmental factors on its flowerings so that it may help scientists in several other processes like speed breeding or to develop good varieties of cotton because fruiting is next stage of flowerings in cotton plant. Many circadian clock genes in cotton plant express according to sunlight duration, temperature, age, and hormonal changes. Cotton flowers at a certain age. Several genes, such as circadian clock genes in cotton leaves, control flowering circumstances such sunshine length, temperature, and more. Phloem transports reproductive signals from cotton leaves to shoot apex. Floral identity genes activate floral identity organ genes that generate cotton flower parts. The photoperiodism in Arabidopsis thialiana, which is considered as model plant also help to understand the photoperiodism in cotton at microscopic and genetic level.

9

Title: The Role of K-Humate and Iron Oxide Nanoparticles for Nutrient Accumulation Under Salinity Stress Condition in Cotton (Gossypium hirsutum L.)

Author: Hatice Kübra GÖREN, Uğur TAN, Seçil KÜÇÜK KAYA

Imprint: MAS Journal of Applied Sciences, 9(Özel Sayı), 879–891. https://doi.org/10.5281/zenodo.13928462

Abstract: Salinity stress poses a significant challenge to cotton (*Gossypium hirsitum* L.) production, particularly during early growth stages. The present study investigates the effects of iron oxide nanoparticles (Fe (II, III) oxide NPs), K-humate, and their combination on nutrient accumulation in cotton plants under saline conditions. Cotton seedlings were subjected to both saline and non-saline environments, with treatments applied to assess their impact on nutrient uptake in the stem and root sections. Principal Component Analysis (PCA) was employed to evaluate nutrient variability across different treatments. Results showed that Fe (II, III) oxide NPs and K-humate enhanced nutrient balance under saline conditions by promoting nutrient uptake and mitigating salinity-induced nutrient imbalances, particularly for potassium (K), sodium (Na), phosphorus (P), and iron (Fe). The combined treatment of iron oxide nanoparticles (Fe (II, III) oxide NPs) and K-humate demonstrated a synergistic effect, improving nutrient interactions and it may contribute to plant resilience. These findings suggest that the use of nanomaterials, particularly in combination with organic compounds like K-humate, holds potential for enhancing cotton tolerance to salinity stress due to alleviating nutrient imbalances caused by salinity stress.

10

Title: Comparative Analysis of Foliar Sprays And Irrigation Regimes on Growth, Physiological Attributes And Yield of Bt Cotton (*Gossypium Hirsutum* L.)

Author: Rajendra R. Lipane1, Amol P. Solanke, Arti M. Ambhore , Bhushan J. Gawhale, Avinash G. Borade and D.V. Durge

Imprint: Plant Archives Vol. 24, No. 2, 2024 pp. 1420-1426

Abstract: The investigation, conducted during the June–Feb 2012 at the Department of Agricultural Botany, Dr. PDKV Akola, Maharashtra, India utilized a randomized block design with three replications to study "the comparative analysis of foliar spraying and irrigation regimes on growth, physiological attributes and yield of Bt Cotton (Gossypium hirsutum L.)." The study examined the effects of foliar fertilizers i.e., T1 - NPK Spray (10:5:5 kg ha1), T2 -AA (500 ppm l-1), T3 -PMA (10 ppm l-1), T4 -Cycocel (500 ppm l-1), T5 -Kinetin (10 ppm l-1), T6 - AA + PMA (500 ppm l-1), T7 -MgSO4 spray (0.5%), T8 -MgSO4 spray (1%), T9 -Micro-nutrients (1ml l-1), T10-DAP (2%), T11- GA3 (50 ppm l-1), T12-KNO3 (1%), T13-Control (No spray). T14-Irrigation at critical stages (flowering and boll development) and T15- Urea (2%) on various parameters of cotton production, including plant height, leaf area plant-1, leaf area index, chlorophyll content index, total dry matter production, red leaf incidence, yield and yield contributing character. Results from the study indicated that applying foliar sprays containing MgSO4 spray at 1% notably increased plant height, leaf area, total dry matter and chlorophyll content index. Additionally, it reduced red leaf incidence and increased cotton yield and yield attributes compared to control plants as well as

treatment involves DAP, Urea and Cycocel showing better results in yield contributing characters like number of bolls plant-1, boll weight and seed cotton production. The findings of the study suggest that foliar application of MgSO4 at 1% can effectively enhance the growth, physiological attributes and yield of Bt cotton.

11

Title: Herbicide residue detection in cotton as influenced by time, drift rate, and sampling method.

Author: Hannah E. Wright-Smith, A. Stanley Culpepper , Carrie R. Crabtree , Timothy L. Grey , Taylor M. Randell-Singleton and Jenna C. Vance

Imprint: Weed Sci. doi: 10.1017/wsc.2024.56

Abstract: Herbicide drift to sensitive crops can result in significant injury, yield loss, and even crop destruction. When pesticide drift is reported to the Georgia Department of Agriculture (GDA), tissue samples are collected and analyzed for residues. Seven field studies were conducted in 2020 and 2021 in cooperation with the GDA to evaluate the effect of (1) time interval between simulated drift event and sampling, (2) low-dose herbicide rates, and (3) the sample collection methods on detecting herbicide residues in cotton (Gossypium hirsutum L.) foliage. Simulated drift rates of 2,4-D, dicamba, and imazapyr were applied to non-tolerant cotton in the 8- to 9- leaf stage with plant samples collected at 7 or 21 d after treatment (DAT). During collection, plant sampling consisted of removing entire plants or removing new growth occurring after the 7-leaf stage. Visual cotton injury from 2,4-D reached 43% to 75% at 0.001 and 0.004 kg ae ha−1 , respectively; for dicamba, it was 9% to 41% at 0.003 or 0.014 kg ae ha−1 , respectively; and for imazapyr, it was 1% to 74% with 0.004 and 0.03 kg ae ha−1 rates, respectively. Yield loss was observed with both rates of 2,4-D (11% to 51%) and with the high rate of imazapyr (52%); dicamba did not influence yield. Herbicide residues were detected in 88%, 88%, and 69% of samples collected from plants treated with 2,4-D, dicamba, and imazapyr, respectively, at 7 DAT compared with 25%, 16%, and 22% when samples were collected at 21 DAT, highlighting the importance of sampling quickly after a drift event. Although the interval between drift event and sampling, drift rate, and sampling method can all influence residue detection for 2,4-D, dicamba, and imazapyr, the factor with the greatest influence is the amount of time between drift and sample collection.

12

Title: "Studies on Major Foliar Diseases of Cotton (*Gossypium* spp.)"

Author: Raut Shubham Ashok (Reg. No. 2022/236)

Imprint: A Thesis submitted to the MAHATMA PHULE KRISHI VIDYAPEETH RAHURI-413 722, DIST-AHMEDNAGAR MAHARASHTRA, INDIA. In partial fulfilment of the requirements for the degree MASTER OF SCIENCE (AGRICULTURE) in PLANT PATHOLOGY

Abstract: India is one of the major cotton growing countries contributing 37% of world's cotton production. Among the states of India, Maharashtra is leading in cotton acreage with 39.41 lakh ha followed by Gujarat, Telangana, Rajasthan and Haryana (Anonymous, 2021). In Maharashtra, Vidharbh, Marathwada and Khandesh are the largest cotton producing regions. Among the many reasons of low productivity and production, diseases caused by pathogens contribute substantially to low yields of cotton. There are numerous diseases that can affect the crop, each with a different severity. Foliar diseases are of major significance as they directly affect the foliage, ultimately reduces the yield. Present investigation was carried out during 2023-24 on major foliar diseases of cotton with the objectives to isolate and identify the pathogens responsible for foliar diseases in cotton and to evaluate efficacy of fungicides against the major fungal foliar pathogens. The diseased cotton leaves were collected from four districts under Western Maharashtra region. During survey the highest average per cent disease intensity was recorded for Alternaria leaf spot (43.94 per cent) followed by anthracnose, Helminthosporium leaf spot and Curvularia leaf spot showing 27.64, 19.90 and 17.08 per cent respectively. Four different fungal pathogens were isolated from the diseased leaves. The isolated pathogens were identified as Alternaria macrospora, Colletotrichum dematium, Curvularia lunata and Helminthosporium gossypii on the basis of their morphological and cultural characteristics. Pathogenicity was proved with spore suspension inoculation method by satisfying Koch's postulates. The In vitro study on the efficacy of seven fungicides with their recommended concentration and half of recommended concentration was conducted in order to identify the most efficient fungicide capable of inhibiting the mycelial growth of above four major fungal foliar pathogens. Among the various fungicides tested, propiconazole 25% EC @0.1 and @0.05% showed 100% inhibitory effect with least mycelial colony diameter (0.0 mm) for Alternaria .XVI macrospora. Similarly, azoxystrobin 18.2% w/w + difenoconazole 11.4% w/w SC @0.1% was the next effective fungicide for Alternaria macrospora.

Among the tested fungicides, propiconazole 25% EC (0.1% and 0.05%), metiram 55% + pyraclostrobin 5% WG (0.2% and 0.1%), and azoxystrobin 18.2% w/w + difenoconazole 11.4% w/w SC (0.1% and 0.05%) showed 100% inhibitory effect with least mycelial colony diameter (0.0 mm) for Colletotrichum dematium. Propiconazole 25% EC at both (0.1% and 0.05%) and azoxystrobin 18.2% w/w + difenoconazole 11.4% w/w SC @0.1% showed 100% inhibitory effect with least mycelial colony diameter (0.0 mm) for Curvularia lunata, similarly the least mycelial colony diameter (7.60 mm) of Curvularia lunata was recorded in the treatment of azoxystrobin 18.2% w/w + difenoconazole 11.4% w/w SC @0.05% with 91.56 per cent inhibition over untreated control. whereas both propiconazole 25% EC and azoxystrobin 18.2% w/w + difenoconazole 11.4% w/w SC at (0.1% and 0.05%) showed 100% inhibitory effect on Helminthosporium gossypii. Least inhibition of mycelial growth was observed with Kresoxim methyl 44.3% SC @0.05% for pathogens, viz. Alternaria macrospora, Colletotrichum dematium, Helminthosporium gossypii and carbendazim 50% WP @0.05% gave least inhibition of Curvularia lunata. Thus, the results indicated that among the all fungicides tested In vitro against four foliar fungal pathogens, propiconazole 25% EC @0.1% and 0.05% showed 100% efficacy in inhibiting the mycelial growth of all these pathogens. Whereas least efficacy was exhibited by kresoxim methyl 44.3% SC @0.05% against Alternaria macrospora, Colletotrichum dematium, Helminthosporium gossypii and carbendazim 50% WP @0.05% against Curvularia lunata.

13

Title: Effect of manual topping on insect pest incidence and cotton yield.

Author: Daouda S. Maiga, Moribo Coulibaly, Amadou Traoré

Imprint: Crop Protection, Volume 188, February 2025, 107016

Abstract: Bollworms and sap-sucking insect pests are a significant constraint to cotton production in Africa. Manual topping of cotton plants, which consists of cutting off the top of the plant, i.e. the terminal bud of the main stem, is a promising alternative to chemical control by removing resources for certain pests or inducing plant defences. In this study, we evaluated the level of protection by topping against bollworms and sap-sucking insect pests and the effect of topping on seed cotton yield. Six experiments combining insecticide protection (sprayed vs. unsprayed plots) and topping (topped vs. non-topped plots) were conducted in Mali and Senegal. Topping by itself conferred weak protection against bollworms with an 11% reduction in the proportion of damaged shed squares and bolls, compared to insecticide protection (−55%). Topping had a low to moderate effectiveness in reducing the incidence of sap-sucking pests (−20 to −48%), but equivalent to insecticide treatments. Although topping significantly reduced the proportion of damaged bolls (−31%) at harvest in the absence of insecticide protection, this did not substantially affect seed cotton yield (+4%), unlike insecticide protection (+52%). However, this technique could be advantageously combined with

threshold-based interventions integrating biopesticides to reduce the environmental impact of crop protection in cotton.

14

Title: Recognition of a Fungal Effector Potentiates Pathogen-Associated Molecular Pattern-Triggered Immunity in Cotton.

Author: Lifan Sun, Xiangguo Li, Jiajie Zhong, Yu Wang, Baiyang Li, Ziqin Ye, and Jie Zhang*

Imprint: Adv. Sci. 2024, 2407787 2407787 (1 of 15) DOI: 10.1002/advs.202407787

Abstract: Plants are equipped with multi-layered immune systems that recognize pathogen-derived elicitors to activate immunity. Verticillium dahliae is a soil-borne fungus that infects a broad range of plants and causes devastating wilt disease. The mechanisms underlying immune recognition between plants and V. dahliae remain elusive. Here, a V. dahliae secretory protein, elicitor of plant defense gene (VdEPD1), acts as an elicitor that triggers defense responses in both Nicotiana benthamiana and cotton plants is identified. Targeted gene deletion of VdEPD1 enhances V. dahliae virulence in plants. Expression of VdEPD1 triggers the accumulation of reactive oxygen species (ROS) and the activation of cell death in cotton plants. Gossypium barbadense EPD1-interacting receptor-like cytoplasmic kinase (GbEIR5A) and GbEIR5D interact with VdEPD1. Silencing of GbEIR5A/D significantly impairs VdEPD1-triggered cell death in cotton plants, indicating the contribution of GbEIR5A/D to VdEPD1-activated effector-triggered immunity (ETI). VdEPD1 stimulates the expression of GbEIR5A and GbEIR5D in cotton plants. Interestingly, cotton plants with silenced GbEIR5A/D genes exhibit compromised pathogen-associated molecular patterns (PAMPs)-triggered ROS accumulation, whereas overexpression of GbEIR5A or GbEIR5D enhances PAMP-induced ROS. These findings indicate that recognition of VdEPD1 potentiates GbEIRs to enhance cotton PAMP-triggered immunity (PTI), uncovering a cooperative interplay of PTI and ETI in cotton.

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Title: Natural SNP Variation in GbOSM1 Promotor Enhances Verticillium Wilt Resistance in Cotton.

Author: Guilin Wang, Dayong Zhang, Haitang Wang , Jinmin Kong, Zhiguo Chen
Imprint: Adv Sci (Weinh), . 2024 Oct 16:e2406522. doi: 10.1002/advs.202406522. Online ahead of print.

Abstract: Osmotin is classified as the pathogenesis-related protein 5 group. However, its molecular mechanism involved in plant disease resistance remains largely unknown. Here, a Verticillium wilt (VW) resistance-related osmotin gene is identified in Gossypium barbadense (Gb), GbOSM1. GbOSM1 is preferentially expressed in the roots of disease-resistant G. barbadense acc. Hai7124 and highly induced by Verticillium dahliae (Vd). Silencing GbOSM1 reduces the VW resistance of Hai7124, while overexpression of GbOSM1 in disease-susceptible G. hirsutum improves tolerance. GbOSM1 predominantly localizes in tonoplasts, while it relocates to the apoplast upon exposure to osmotic stress or Vd infection. GbOSM1 confers VW resistance by hydrolyzing cell wall polysaccharides of Vd and activating plant immune pathways. Natural variation contributes to a differential CCAAT/CCGAT elements in the OSM1 promoter in cotton accessions. All G. hirsutum (Gh) exhibit the CCAAT haplotype, while there are two haplotypes of CCAAT/CCGAT in G. barbadense, with higher expression and stronger VW resistance in CCGAT haplotype. A NFYA5 transcription factor binds to the CCAAT element of GhOSM1 promoter and inhibits its transcription. Silencing GhNFYA5 results in higher GhOSM1 expression and enhances VW resistance. These results broaden the insights into the functional mechanisms of osmotin and provide an effective strategy to breed VW-resistant cotton.

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Title: Plant-to-plant defense induction in cotton is mediated by delayed release of volatiles upon herbivory.

Author: Luca Grandi, Wenfeng Ye , Mary V. Clancy , Armelle Vallat , Gaetan Glauser , Luis Abdala-Roberts , Thierry Brevault, Betty Benrey , Ted C. J. Turling and Carlos Bustos-Segura

Imprint: New Phytologist (2024) 244: 2505–2517: doi: 10.1111/nph.20202

Abstract: Caterpillar feeding immediately triggers the release of volatile compounds stored in the leaves of cotton plants. Additionally, after 1 d of herbivory, the leaves release other newly synthesised volatiles. We investigated whether these volatiles affect chemical defences in neighbouring plants and whether such temporal shifts in emissions matter for signalling between plants. Undamaged receiver plants were exposed to volatiles from plants infested with Spodoptera caterpillars. For receiver plants, we measured changes in defence-related traits such as volatile emissions, secondary metabolites, phytohormones, gene expression, and caterpillar feeding preference. Then, we compared the effects of volatiles emitted before and after 24 h of damage on neighbouring plant defences. Genes that were upregulated in receiver plants following exposure to volatiles from damaged plants were the same as those activated directly by herbivory on a plant. Only volatiles emitted after 24 h of damage, including newly produced volatiles, were found to increase phytohormone levels,

upregulate defence genes, and enhance resistance to caterpillars. These results indicate that the defence induction by volatiles is a specific response to de novo synthesised volatiles, suggesting that these compounds are honest signals of herbivore attack. These findings point to an adaptive origin of airborne signalling between plants.

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Title: Effi cacy of Alternative Insecticides against Dusky Cotton Bug (*Oxycarenus laetus*) to Improve Yield Losses in Cotton Crops through Residue based Bioassay .

Author: Muhammad Salman Hameed, Muhammad Arshad, Khurshied Ahmed Khan and Nida Urooj

Imprint: IgMin Res. October 09, 2024; 2(10): 794-800. IgMin ID: igmin249; DOI: 10.61927/igmin249; Available at: igmin.link/p249

Abstract: The study evaluates the efβicacy of leufenuron, emamectin benzoate, and thiamethoxam against the Dusky Cotton Bug (Oxycarenus laetus Kirby) using residue-based bioassay methods. Key βindings indicate that emamectin benzoate showed the highest efβicacy with the lowest LC50 value, making it the most potent insecticide among those tested. Leufenuron and thiamethoxam followed, displaying moderate effectiveness. The results highlight the comparative advantages of emamectin benzoate in controlling Dusky Cotton Bug populations, suggesting its potential role in integrated pest management strategies. This study underscores the need for environmentally friendly alternatives to traditional insecticides in mitigating yield losses in cotton production.

PLANT BREEDING AND GENETICS

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Title: Introduction of East African Diploid Cotton Genetic Variation into Upland Cotton

Author: Nafissatou Lalaissa Nacoulima, Fatimata Hassedine Diouf, Olivier Nâ€™guessan Konan, Ludivine Lassois

Imprint: Journal of Agricultural Science, Canadian Center of Science and Education, vol. 16(9), pages 1-19, September.2024

Abstract: The African wild diploid cotton species, Gossypium longicalyx Hutch. & Lee. (2n = 2x = 26, F1F1) presents many valuable traits that can be introduced into Gossypium hirsutum to enhance its narrow genetic basis. To assess the possibility of using monosomic alien addition line (MAAL) of G. longicalyx in G. hirsutum in an interspecific breeding program, the progeny of ten MAALs was characterized. Chromosome counting allowed to identify the addition of single alien chromosome in 9 of the 10 lines studied. The analysis of the chromosome configurations at metaphase showed the presence of multivalent associations involving the supernumerary chromosome of G. longicalyx, indicating the occurrence of recombination between the G. longicalyx and G. hirsutum chromosomes. The use of microsatellite markers provided evidence of multiple introgressions of G. longicalyx DNA in the recipient species. It appeared from the SSR analysis that only four different supernumerary alien chromosomes were present in the studied MAALs. These results confirm the low genetic distance existing between the chromosomes of G. longicalyx and those of Ah sub-genome. They highlight the opportunities and constraints associated with the use of G. longicalyx in a breeding program of upland cotton.

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Title: MYB30-INTERACTING E3 LIGASE 1 regulates LONELY GUY 5-mediated cytokinin metabolism to promote drought tolerance in cotton.

Author: Chuan Chen, Dayong Zhang, Xin Niu, Xuanxiang Jin, Huijuan Xu, Weixi Li, Wangzhen Guo

Imprint: *Plant Physiology*, kiae580, https://doi.org/10.1093/plphys/kiae580

Abstract: Ubiquitination plays important roles in modulating the abiotic stress tolerance of plants. Drought seriously restricts agricultural production, but how ubiquitination participates in regulating drought tolerance remains largely unknown. Here, we identified a drought-inducible gene, *MYB30-INTERACTING E3 LIGASE 1* (*GhMIEL1*), which encodes a RING E3 ubiquitin ligase in cotton (*Gossypium hirsutum*). *GhMIEL1* was strongly induced by polyethylene glycol (PEG-6000) and the phytohormone abscisic acid. Overexpression and knockdown of *GhMIEL1* in cotton substantially enhanced and reduced drought tolerance, respectively. GhMIEL1 interacted with the MYB transcription factor GhMYB66 and could ubiquitinate and degrade it in vitro. GhMYB66 directly bound to the *LONELY GUY 5* (*GhLOG5*) promoter, a gene encoding cytokinin riboside 5′-monophosphate phosphoribohydrolase, to repress its transcription. Overexpression of *GhMIEL1* and silencing of *GhMYB66* altered the homeostasis of cytokinin of plant roots, increased total root length and number of root tips, and enhanced plant drought tolerance. Conversely, silencing *GhLOG5* decreased total root

length and number of root tips and reduced plant drought tolerance. Our studies reveal that the GhMIEL1-GhMYB66-GhLOG5 module positively regulates drought tolerance in cotton, which deepens our understanding of plant ubiquitination-mediated drought tolerance and provides insights for improving drought tolerance.

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Title: Integrating Environmental Covariates into Adaptability and Stability Analyses: A Structural Equation Modeling Approach for Cotton Breeding.

Author: Matheus Massariol Suela, Moysés Nascimento, Ana Carolina Campana Nascimento

Imprint*: Agriculture* 2024, *14*(11), 1914; https://doi.org/10.3390/agriculture14111914

Abstract: Breeding programs rely on genotype-by-environment interaction (GEI) to recommend cultivars for specific locations. GEI describes how different genotypes perform under varying environmental conditions. Several methods were proposed to assess adaptability and stability across environments. These methods utilize various statistical approaches like parametric and non-parametric regression, multivariate analysis techniques, and even Bayesian frameworks and artificial intelligence. The accessibility of environmental data through platforms like NASA POWER allows breeders to integrate this information into a breeding process. It has been done by using multi-omics integration models that combine data across various biological levels to create accurate predictive models. In the context of phenotypic adaptability and stability analysis, structural equation modeling (SEM) offers an interesting approach to integrating environmental covariates. This work aimed to propose a novel approach that integrates weather information into adaptability and stability analysis, combining SEM with the established Eberhart and Russell model. Additionally, a user-friendly applet, denoted ECERSEM-AdaptStab, was made available to perform the analysis. This approach utilized data from 12 cotton cultivar trials conducted across two growing seasons at 19 sites. This approach successfully integrated environmental covariates into a phenotypic adaptability and stability analysis of cotton cultivars. Specifically, the genotypes TMG 41 WS, IMA CV 690, DP 555 BGRR, BRS 286 and BRS 369 RF were recommended for favorable environments, while the genotypes TMG 43 WS, IMA 5675 B2RF, IMA 08 WS, NUOPAL, DELTA OPAL, BRS 335, and BRS 368 RF are more suitable for unfavorable environments.

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Title: Convergence and divergence of diploid and tetraploid cotton genomes.

Author: Jianying Li, Zhenping Liu, Chunyuan You, Zhengyang Qi, Jiaqi You, Corrinne E. rover, Yuexuan Long, Xianhui Huang, Sifan Lu, Yuejin Wang, Sainan Zhang,

Imprint: *Nature Genetics* volume 56, pages2562–2573 (2024

Abstract: Polyploidy is an important driving force in speciation and evolution; however, the genomic basis for parallel selection of a particular trait between polyploids and ancestral diploids remains unexplored. Here we construct graph-based pan-genomes for diploid (A_2) and allotetraploid (AD_1) cotton species, enabled by an assembly of 50 genomes of genetically diverse accessions. We delineate a mosaic genome map of tetraploid cultivars that illustrates genomic contributions from semi-wild forms into modern cultivars. Pan-genome comparisons identify syntenic and hyper-divergent regions of continued variation between diploid and tetraploid cottons and suggest an ongoing process of sequence evolution potentially linked to the contrasting genome size change in two subgenomes. We highlight 43% of genetic regulatory relationships for gene expression in diploid encompassing sequence divergence after polyploidy and specifically characterize six underexplored convergent genetic loci contributing to parallel selection of fiber quality. This study offers a framework for pan-genomic dissection of genetic regulatory components underlying parallel selection of desirable traits in organisms.

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Title: Overexpression of *Gossypium arboreum* 3-ketoacyl-CoA synthase 6 (*GaKCS6*) gene enhanced leaf epicuticle wax in *Gossypium hirsutum* L. and improved tolerance against whitefly.

Author:
MuhammadUmair Majid, Rabiah Ashraf, Basit Jabbar, Usman Arif, Fatima Batool, Sam eera Hassan

Imprint: Biocatalysis and Agricultural Biotechnology, Volume 62, December 2024, 103418

Abstract: Cotton Leaf Curl Virus (CLCuV) is a significant threat to cotton production, as it causes Cotton Leaf Curl Disease (CLCuD). Whitefly serves as a vector for the transmission of this virus. It can be controlled by developing barriers against whitefly infestation. The leaf epicuticle wax acts as a protective barrier against whitefly attacks. Research into wax biosynthesis and the fatty acid elongation pathway has highlighted the role of the 3-ketoacyl-CoA synthase (*KCS*) gene family in producing very-long-chain

fatty acids (VLCFAs) in plants. The 3-ketoacyl-CoA synthase 6 (*GaKCS6*) gene, isolated from the CLCuV-resistant FDH-170 variety of *Gossypium arboreum*, was cloned under the control of the *Ca*MV35S constitutive promoter and transformed into the CLCuV-susceptible *Gossypium hirsutum* variety CKC-3 resulting in significantly higher leaf epicuticle wax deposition. Overexpression of *GaKCS6* in the transgenic cotton plants was confirmed through quantitative real-time PCR. The transgenic plants not only exhibited average growth but also showed improvements in agronomic traits. Scanning Electron Microscope (SEM) analysis further validated the enhanced leaf epicuticle wax deposition in transgenic plants compared to non-transgenic (control). A free-choice bioassay against whiteflies demonstrated that the transgenic plants remained free of viral infection, as confirmed by real-time PCR. These findings indicate that increased leaf epicuticle wax deposition in transgenic cotton effectively prevents whitefly attacks and the transmission of CLCuV. It suggests that the *GaKCS6* gene plays a crucial role in producing leaf epicuticle wax through the VLCFAs biosynthesis pathway.

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Title: Genome-wide identification and characterization of FORMIN genes in cotton: Implications for abiotic stress tolerance**.**

Author:Rasmieh Hamid , Feba Jacob , Zahra Ghorbanzadeh ,
Mohsen Mardi , Shohreh Ariaeenejad

Imprint: Plant Gene, Volume 40, December 2024, 100474

Abstract: Formins are highly conserved proteins with multiple domains that play an important role in the interaction with microfilaments and microtubules and thus regulate actin organisation and cytoskeletal dynamics. Despite their importance in plant development and response to stress, the study of FORMIN (FH) genes in cotton, an important fibre crop, remains limited. The genetic diversity of these genes is critical for improving the adaptability of cotton to environmental stress, which is a major challenge for cotton breeding programmes aimed at improving abiotic stress tolerance. Results**:**Through comprehensive bioinformatics approaches, we identified 46, 50 and 27 putative *FH* genes in *Gossypium hirsutum*, *G. barbadense* and their diploid ancestors *G. arboreum* and G. *raimondii*, respectively. A phylogenetic analysis classified these genes into five subfamilies and revealed evolutionary relationships to *Arabidopsis thaliana*. Syntenic and collinear analyses showed that genomic duplications in cotton have driven the expansion of the FH gene family. Structural analysis showed significant variations in sequence length and conserved motifs. Promoter analysis revealed several cis-acting elements associated with growth, stress response and hormonal signalling. Protein-protein interaction predictions suggest involvement in hormone signalling, cytoskeletal regulation and cell wall dynamics. Differential expression of *G. hirsutum* FH (GhFH)

genes in different cotton tissues under drought and osmotic stress was confirmed by qRT-PCR.

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Title: Genome-wide identification of *isopentenyl transferase* genes in cotton and their roles in regulating vegetative branching after topping.

Author: Lin Sun, Yanjun Zhang , Wenting Hou, Rui Li

Imprint: Industrial Crops and Products, Volume 223, January 2025, 119853

Abstract: The promotion of vegetative branching in plants after topping has been observed without a clear understanding of the underlying mechanism. This study aimed to investigate the role of isopentenyl transferase (*IPT*) and cytokinins in the regulation of vegetative branching in cotton (*Gossypium hirsutum* L.), hypothesizing that they play key roles in this process. Plant topping was implemented at peak flowering stage in field-grown cotton, and seedcotton yield, yield components, vegetative branching, fruiting, and cytokinin levels were examined over two consecutive years. The results showed that plant topping significantly enhanced the growth and development of vegetative branches, as evidenced by increased biomass, leaf area, and fruiting of vegetative branches, along with an accumulation of cytokinin accumulation at the tips of vegetative branches. This led to a 10.3 % rise in boll density and an 11.4 % increase in seedcotton yield compared with the non-topped control. The analysis of RNA-seq and qRT-PCR data revealed significant differences in the expression patterns of *IPT* genes, suggesting their importance in regulating the growth and development of vegetative branches. Furthermore, examining the *IPT* gene families in diploid and tetraploid cotton species identified a total of 8, 8, 16, and 16 *IPT* genes, categorized into 6 groups. Prediction of cis-acting elements of *GhIPT* gene family promoters and analysis of their expression profiles demonstrated the involvement of *GhIPT* genes in multiple plant growth pathways with specific spatio-temporal expression. The findings underline that plant topping enhances cytokinins accumulation at vegetative branch tips by up-regulating *IPT* genes, leading to increased vegetative branching, fruiting, and ultimately, seedcotton yield. This study provides valuable insights into enhancing cotton yield formation through the regulation of growth and development of vegetative branches by *GhIPTs* and offers a crucial reference for further investigations into the functions of *IPT* genes.

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Title: Genetic Dissection of Flowering and Plant Architectural Traits to Develop Early Maturing Compact Upland Cotton Genotypes for High-Density Planting.

Author: D. S. Raj Supritha, Rajesh S. Patil, Sai Valli Harshini Kasturi & Bhuvaneshwara R. Patil

Imprint: Tropical Plant Biology , Volume 18, article number 1, (2025)

Abstract: Earliness in cotton is a highly valued trait that allows the crop to dodge late-season stress and facilitates efficient harvesting, ultimately benefiting farmers with optimal yield. Understanding the genetics of these complex traits is a prelude to designing extra-early maturing cotton genotypes. Two crosses with six generations (ESS-20 × FLT-25 and S-32 × FLT-25: P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2) and one cross with five generations (NNDC-30 × NNDC-47: P_1, P_2, F_1, F_2, and $F_{2:3}$) were field-evaluated for ten earliness and plant architecture traits in cotton. ANOVA presented significant generational differences for most traits. The inadequacy of the Additive-Dominance (A-D) model in explaining trait inheritance using scaling and joint-scaling tests highlighted the presence of epistatic gene actions. Further, the analysis of gene action unveiled the predominance of dominance effect [h] and dominance × dominance [l] epistatic effect, influencing the expression of most traits. Contrasting signs of [h] and [l] effects for these traits suggested the occurrence of duplicate epistasis across crosses. Therefore, population improvement strategies and heterosis breeding could be effective in designing extra-early maturing genotypes. All traits exhibited quantitative inheritance, with partial and overdominance favoring early maturity. Notably, days to flowering and boll opening, exhibited negative heterosis, suggesting the efficient development of short-duration cotton hybrids. Besides, the study also predicted less than one gene block for the majority of traits, suggesting a significant role of complex non-allelic interaction in trait expression. These findings offer valuable insights for strategizing efficient breeding methods to develop early maturing cotton genotypes.

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Title: Population-wide DNA methylation polymorphisms at single-nucleotide resolution in 207 cotton accessions reveal epigenomic contributions to complex traits.

Author: Ting Zhao, Xueying Guan, Yan Hu, Ziqian Zhang, Han Yang, Xiaowen Shi, Jin Han

Imprint: *Cell Res* (2024). https://doi.org/10.1038/s41422-024-01027-x

Abstract: DNA methylation plays multiple regulatory roles in crop development. However, the relationships of methylation polymorphisms with genetic polymorphisms, gene expression, and phenotypic variation in natural crop populations remain largely unknown. Here, we surveyed high-quality methylomes, transcriptomes, and genomes obtained from the 20-days-post-anthesis (DPA) cotton fibers of 207 accessions and extended the classical framework of population genetics to epigenetics. Over 287 million single methylation polymorphisms (SMPs) were identified, 100 times more than the number of single nucleotide polymorphisms (SNPs). These SMPs were significantly enriched in intragenic regions while depleted in transposable elements. Association analysis further identified a total of 5,426,782 *cis*-methylation quantitative trait loci (*cis*-meQTLs), 5078 *cis*-expression quantitative trait methylation (*cis*-eQTMs), and 9157 expression quantitative trait loci (eQTLs). Notably, 36.39% of *cis*-eQTM genes were not associated with genetic variation, indicating that a large number of SMPs associated with gene expression variation are independent of SNPs. In addition, out of the 1715 epigenetic loci associated with yield and fiber quality traits, only 36 (2.10%) were shared with genome-wide association study (GWAS) loci. The construction of multi-omics regulatory networks revealed 43 *cis*-eQTM genes potentially involved in fiber development, which cannot be identified by GWAS alone. Among these genes, the role of one encoding CBL-interacting protein kinase 10 in fiber length regulation was successfully validated through gene editing. Taken together, our findings prove that DNA methylation data can serve as an additional resource for breeding purposes and can offer opportunities to enhance and expedite the crop improvement process.

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Title: Comparative Transcriptome Analysis of *Gossypium hirsutum* Mutant (*xin w 139*) and Wild-Type (Xin W 139) Plants During Seed Embryo Development.

Author: Jieyin Zhao, Chunping Li, Yanlong Yang, Jun Ma, Chengxia Lai

Imprint: *Genes* 2024, *15*(11), 1408; https://doi.org/10.3390/genes15111408

Abstract: Background: Cotton seeds are the main byproduct of cotton crops. The phenomenon of plants failing to develop mature and full seeds is called seed embryo abortion, which leads to a decrease in seed yield and potentially causes economic losses. Methods: We report a phenotypic evaluation of seed embryos from *G. hirsutum* mutant (*xin w 139*) and wild-type (Xin W 139) lines and a comparative RNA-seq study at four developmental stages. Results: The field results from two years showed that the sterility rate and malformation rate of *xin w 139* were significantly lower than those of Xin W 139, and the RNA-seq data revealed that the differences in the development of the seed embryos of the two lines mainly occurred after 20 days post anthesis (DPA). Differential analysis revealed a total of 29,151 differentially expressed genes (DEGs), including 2696 transcription factors (TFs), between the two lines, in which the fatty acid and glucose metabolism-related pathways were significantly enriched. These DEGs were divided into 8 clusters, with the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways of each cluster being annotated. Furthermore, a gene regulatory network was built using weighted correlation network analysis (WGCNA), revealing 9 key genes that play crucial roles in shaping the developmental disparities of seed embryos between the two lines, among which 3 are TFs. Conclusions: These findings offer a foundational framework for comprehending the molecular mechanisms underlying cottonseed embryo development, as well as presenting novel genetic reservoirs for further investigations into cottonseed embryo development.

SEED SCIENCE AND TECHNOLOGY

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Title: Unveiling the Microbial Dynamics: Exploring Seed Cotton Microflora Diversity and Its Ramifications on Seed Health.

Author: Kumar Avinash Biswal, Nirakar Ranasingh, Rajeeb Lochan Moharana and Siddhartha Das

Imprint: Curr Agri Res 2024; 12(3).

Abstract: In 2022-24 periods, an investigation was carried out to reveal diverse microflora in cotton seeds at Department of Plant Pathology and the Department of

Seed Science and Technology within the College of Agriculture, Bhawanipatna, OUAT (https://aiccip.cicr.org.in/CZ-OD-Bpatna.html). The study involved seven germplasms, namely V1- Br. 06 a (N) 410, V2- Br. 06 a (N) 409, V3- 4a (Z) 2034, V4- 4a (Z) 2035, V5- CZ 6 a (Z) 2051, V6- Br. 06 a (N) 411, V7- 4a (Z) 2032, obtained from AICRP on Cotton, RRTTS, Bhawanipatna (https://aiccip.cicr.org.in/CZ-OD-Bpatna.html). The seeds were examined using the blotter paper and Potato Dextrose Agar (PDA) method, and the experiment included three replications to assess the associated microbes and seed health status. The blotter paper method revealed the presence of six fungi, *Aspergillus niger* and *Fusarium oxysporum*, were identified in cotton seeds, along with the bacterium *Xanthomonas* spp (8.3%). *Curvularia lunata* was the predominant fungus at (9.8%), followed by *Fusarium oxysporum* (8.7%) and *Alternaria alternata* (8.5%). *Aspergillus niger, Aspergillus flavus, and Macrophomina phaseolina* were also present, each at varying percentages. Where as in PDA method, three fungi—*Macrophomina phaseolina, Fusarium oxysporum*, and *Alternaria alternata*—were identified. *Fusarium oxysporum* dominated at 23.5%, followed by *Alternaria alternata* (22.47%) and *Macrophomina phaseolina* (17.3%), along with *Xanthomonas spp*. at 20.2%. Blotter paper method showed 24.91% seed microflora infection, higher than PDA's 12.07%. CZ 6a (Z) 2051. 75% cotton had the highest infection (30.25%), while BR-06a (N)410 had the lowest (8.35%).

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Title: Regulation of glycerolipid metabolism in germinating cotton (Gossypium hirsutum L.) seeds in response to cold stress.

Author: Bandana Osti

Imprint: A Thesis in Plant and Soil Science Submitted to the Graduate Faculty of Texas Tech University in Partial Fulfillment of the Requirements for the Degree of MASTER OF SCIENCE August 2024

Abstract: Cotton, originating from tropical and subtropical regions, possesses inherent sensitivity to cold stress. This sensitivity to cold stress significantly limits cotton's planting window, especially in temperate regions where the growing season is short. The detrimental effects of low temperature stress are particularly observed during seed germination, leading to germination failure and inadequate seedling establishment. The sustainable and long-term solution to this problem would be the development of cold tolerance in cotton genotypes. To understand the mechanism of cold germination in cotton, we investigated the physio-biochemical and genetic effects of cold stress on cotton seed germination. Cotton recombinant inbred lines (RILs) with different fatty acid profiles (FAM1, FAM2, FAM3, FAM4) and obsolete cotton cultivars (SA2580 and SC9023) were used for this study. The susceptibility of these genotype to cold stress during the second phase of germination was determined by comparing the germination

rate of seeds at an optimum temperature of 30°C and low temperature of 12°C, following imbibition at normal temperature (30°C) for the first 4 hours. When seeds were exposed to cold stress during the second phase of water uptake, germination percentage decreased in all genotypes. FAM1 and FAM2 exhibited better germination ability when subjected to cold stress, maintaining germination percentage above 45%. These RILs have high levels of polyunsaturated fatty acids (PUFAs) in their composition, which may have contributed to their cold germination ability. To study the genetic factor regulating cotton seed germination, we examined the expression of lipase associated genes in dry seeds and after 3, 4, 5, 6 and 8 hours of water uptake at 30°C. For cold stress, we imbibed the seeds for 4 hours at 30°C, then subjected them to 12°C for the following 4 hours. Lipase activation occurred earlier in FAM1. This likely facilitated prompt energy release that aided in earlier seed germination. However, lipase expression decreased under cold stress, which resulted in low free fatty acid (FFA) content. FFAs are susceptible to oxidative damage, so we quantified lipid peroxide and malondialdehyde (MDA) content in the experimental materials. FAM1 and FAM2 exhibited relatively high lipid peroxide and MDA contents under cold stress compared to the other genotypes. Texas Tech University, Bandana Osti, August 2024 vi To investigate the cold induced changes in seed glycerolipid composition, liquid chromatography with tandem mass spectrometry (LC-MS/MS) was performed to profile the seed lipidome of all six cotton genotypes under the following treatments: (1) dry seeds, (2) phase I and phase II of water uptake at normal temperature (30°C), and (3) phase II of water uptake under cold stress (12°C). A total of 3359 lipid molecular species belonging to six different lipid classes were identified in the dry seeds of the six genotypes. The glycerolipids, specifically the triacylglycerols (TAGs) and diacylglycerols (DAGS) were present in significantly high amounts, hence the study focused on the regulation of this lipid class during the second phase of water uptake. Under cold stress, FAM1, FAM2, and SA2580 showed an increase in TAG levels indicating TAG synthesis. DAG content increased under cold stress only in FAM1 and FAM2. Conversely, monoacylglycerol (MAG), as well as the glycerolipids, monogalactosyldiacylglycerol (MGDG) and digalactosyldiacylglycerol (DGDG) decreased in FAM1 under cold stress. The increase in DAG combined with the decrease in MAG, MGDG and DGDG suggest the utilization of the latter lipid classes for DAG synthesis under cold stress. The newly synthesized DAGs are then utilized to produce TAGs. This increase in TAG level ensures the availability of adequate energy reserves to support seed germination under adverse conditions. As cold tolerance is associated with higher levels of unsaturated fatty acids, we also examined the unsaturation to saturation (US/S) ratio in the experimental materials. All cotton genotypes showed an increase in the total US/S ratio under cold stress. Increased unsaturation prevents the cold-induced crystallization of fatty acids and facilitates the normal breakdown of storage reserve. Given that the RILs FAM1 and FAM2 exhibited high total unsaturated fatty acid content compared to the conventional cultivars, this characteristic may have contributed to their better cold germination ability. Based on the results of the study,

FAM1 and FAM1 can be used as donors to breed for cotton cultivars with cold tolerance during the germination stage.

FIBER AND FIBER TECHNOLOGY

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Title: Membrane Interactions of GET1 and GET2 Facilitate Fiber Cell Initiation through the Guided Entry of the TA Protein Pathway in Cotton.

Author: Yang Liu, Zhenzhen Wei, Yanfei Pei, Lu Yang, Xianyan Zou Yayue Pei, Tianen Zhang

Imprint: *Journal of Agricultural and Food Chemistry*, Vol 72/Issue 44

Abstract: The guided entry of TA proteins (GET) pathway, which is responsible for the post-translational targeting and insertion of the tail-anchored (TA) protein into the endoplasmic reticulum (ER), plays an important role in physiological processes such as protein sorting, vesicle trafficking, cell apoptosis, and enzymatic reactions in which the GET1/2 complex is indispensable. However, a comprehensive study of the *GET1* and *GET2* genes and the GET pathway in cotton has not yet been carried out. Here, 12 *GET1* and 21 *GET2* genes were identified in nine representative plant species, and the phylogenetic relationships, gene structures, protein motifs, cis-regulatory elements (CREs), and temporal and spatial expression profiles were analyzed thoroughly. Our study indicated that GhGET1s and GhGET2s might be localized on ER membranes. According to expression profiling and CREs analysis, GhGET2-A02 was identified as a promising candidate for fiber cell development, interacting with two GhGET1s in the membrane, with a binding bias toward GhGET1-A06. Silencing of *GhGET1-A06* or *GhGET2-A02* reduced fiber initiation and elongation. In summary, our research provides important evidence for understanding the gene families and functions of GET1 and GET2 in cotton and provides clues for molecular breeding of high-quality cotton fiber varieties.

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Title: Diallel analysis for combining ability for yield and fiber quality traits in upland cotton (G. hirsutum L.).

Author: Asfand Yar Rahim

Imprint: 2024: 7th International Anatolian Agriculture, Food, Environment and Biology Congress, Kastamonu/Türkiye

Abstract: Cotton *(Gossypium hirsutum* L.) is an important fiber crop, grown in tropical and sub-tropical regions of the world. During 2022-23, cotton contributed approximately 0.3% to GDP and 1.4% to the value addition in agriculture of Pakistan. Seed cotton yield in Pakistan is lower as compared to other countries, emerging challenges of climate change, declining land and water resources require exploration of new breeding approaches like heterosis breeding for sustainable cotton production. For this purpose, research was conducted in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. Three parent genotypes, *i.e.* CIM-663, FH-305 and BS-49 during winter season in glasshouse collected from seedbank of department and crosses made with full diallel mating design. Evaluation of six F_1 genotypes and three parent varieties were proceeded in field by following randomized complete design with two replications during Kharif season 2023. The data for various quantitative traits like plant height, sympodial branches, boll weight, number of bolls per plant, number of nodes per plant, first fruiting node, seeds per boll, seed index, seed cotton yield, lint mass per plant, ginning out turn, fiber length, fiber strength, and fiber fineness were recorded. Recorded data subjected to analysis of variance and analyzed by using Griffing's approach for estimation of GCA and SCA. Among the parents FH-305 and BS-49 exhibited superior GCA for most of the traits. Among the crosses FH-305 × BS-49 showed high specific combining ability. Furthermore, SCA variance found to be better than GCA variance and RCA variance for most of the genotypes. In this study, most of the traits found under the control of dominance gene action. These best performing parents can be further utilized in future breeding programs for varietal improvement purpose.