GLEANINGS IN COTTON RESEARCH

NOVEMBER 2023

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Preface

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

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

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

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

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

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

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

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

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

Swati Dixit
Incharge Library

Chetali Rodge
Technical Officer (T5)

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Title: Drought Stress and High Temperature Affect the Antioxidant Metabolism of Cotton (*Gossypium hirsutum* L.) Anthers and Reduce Pollen Fertility.

Author: Jipeng Zhang, Mengdie Cheng, Mengdie Cheng, Nan Cao

Imprint: Agronomy 2023, 13(10), 2550; https://doi.org/10.3390/agronomy13102550

Abstract: Both drought and high temperature can influence the antioxidant metabolism of crop reproductive organs in different ways, affecting the fertility of reproductive organs and yield formation. However, the combined effects of drought stress and high temperature on the crop reproductive physiology have not yet been widely considered. In order to broaden our understanding of this mechanism of influence, a pond experiment was conducted using a cotton variety Yuzaomian 9110 divided into four treatment groups: control (CK), drought stress (DS), high temperature (HT), and drought stress coupled with high temperature (DS+HT). Results showed a significant negative correlation between pollen viability and superoxide anion (O_2^-) content, as well as hydrogen peroxide (H_2O_2). Compared with CK, DS did not alter O_2^- content in anthers, but HT treatment resulted in higher anther O_2^-. Compared with single-stress groups, DS+HT further promoted the formation of O_2^- in anthers, leading to more malondialdehyde in anthers. Moreover, a higher H_2O_2 content in anthers was found in DS and HT than in CK. DS+HT did not show altered H_2O_2 content relative to HT treatment, although its H_2O_2 was higher than in DS. Further analyses of the antioxidant enzyme system showed that DS had no significant effect on superoxide dismutase gene (*GhCu/ZnSOD*) expression, but HT and DS+HT significantly downregulated its expression. The expression of *GhCu/ZnSOD* was lower under DS+HT than HT, which might be why O_2^- content was not altered under DS treatment compared with CK and was higher in DS+HT than HT. DS and HT significantly downregulated the expression of the peroxidase gene (*GhPOD*) and catalase gene (*GhCAT*), which should be the main reason for the larger accumulation of H_2O_2 under drought stress and high-temperature conditions. Compared with single-stress groups, DS+HT had lower expression of *GhCAT,* resulting in a larger H_2O_2 content. Regarding the ascorbic acid–glutathione (AsA–GSH) cycle, DS and HT significantly downregulated the expression of monodehydroascorbate reductase gene (*GhMDHAR*) to hinder the production of AsA and upregulated the expression of ascorbate oxidase gene (*GhAAO*) to promote the oxidation of AsA, which was theoretically detrimental to AsA accumulation. However, HT downregulated the expression of the ascorbate peroxidase gene (*GhAPX*), hindering the reduction of H_2O_2 by AsA, which was the reason for AsA and H_2O_2 accumulation. Moreover, DS also significantly upregulated the expression of the dehydroascorbate reductase gene (*GhDHAR2*) to enhance the reduction of dehydroascorbate to form AsA,

leading to a higher content of AsA under DS than HT. The combined stress significantly downregulated the expression of *GhAAO* to inhibit the oxidation of AsA but significantly upregulated the expression of *GhMDHAR* and *GhDHAR2*, promoting the AsA production, and downregulated the expression of *GhAPX*, hindering the reduction of H_2O_2 by AsA. All these resulted in increased AsA content under combined stresses. In addition, HT significantly downregulated the glutathione reductase gene (*GhGR*) expression, hindering the reduction of oxidized glutathione (GSSG), which led to the reduction of GSH. However, DS and DS+HT significantly downregulated the glutathione peroxidase gene (*GhGPX*) expression, resulting in the accumulation of GSH. Overall, compared with single-stress treatments, the effects of DS+HT on cotton pollen fertility and peroxide accumulation were more significant. The effects of DS+HT on the antioxidant enzyme system were mainly caused by high temperature, while the mechanism of abnormal accumulation of AsA and GSH caused by DS+HT was different from those of single-stress groups.

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Title: Comparing the influence of natural farming on cotton (Gossypium hirsutum) yield and economics with integrated and organic farming.

Author: Monicaa. M, R. Krishnan, R. Sunitha

Imprint: Journal of Applied and Natural Science, 15(3), 1268 - 1275. https://doi.org/10.31018

Abstract: Cotton, a vital global cash crop, influences the economy and sustainability. Natural farming is a cost-effective, eco-friendly method. This study examines Natural Farming's effects on cotton yield and the economics of cotton compared to Integrated and organic farming. Field experiments were conducted during 2021-22 and 2022-23 at Tamil Nadu Agricultural College, Coimbatore. The experiment consisted of eight treatments, laid out in Randomized Block Design and replicated thrice. The treatments consist of control (T1), various Indian Natural farming practices including Beejamirit as a seed treatment, Ghanajeevamirit as basal, Jeevamirit with irrigation water, crop residue mulch, intercroping with pulses (T2 to T5), Organic farming practices (T6), Integrated crop management (ICM) practices with organic pest control (T7) and ICM with chemical pest (T8). The results indicated a significant increase in yield components: sympodial branches plant-1 (12.85 and 13.40), number of squares (29.28 and 31.28), bolls plant-1 (10.74 and 11.32), and boll weight (4.30 and 4.38 g) under Integrated Crop Management practices in 2021- 22 and 2022-23, respectively. However, organic farming practices, followed by natural farming practices, were at par with integrated crop management. Integrated crop management practices resulted in significantly higher seed cotton yields (2178 and 2232 kg/ha in 2021-22 and 2022-23, respectively) than organic and natural farming practices with a higher cost of cultivation and a gross return. Complete natural farming outperformed organic and integrated farming in cotton, yielding higher net returns and B: C ratios. This approach holds promise for enhancing yield, economic viability and environmental sustainability in cotton cultivation.

3

Title: Analysis of the histidine kinase gene family and the role of *GhHK8* in response to drought tolerance in cotton.

Author: Lanjie Zhao, Yongbo Wang, Ruifeng Cui, Yupeng Cui, Xuke Lu, Xiugui Chen, Junjuan Wang

Imprint: Physiologia Plantarum, 20 September 2023, https://doi.org/10.1111/ppl.14022

Abstract: As an important member of the two-component system (TCS), histidine kinases (HKs) play important roles in various plant developmental processes and signal transduction in response to a wide range of biotic and abiotic stresses. So far, the *HK* gene family has not been investigated in *Gossypium*. In this study, a total of 177 *HK* gene family members were identified in cotton. They were further divided into seven groups, and the protein characteristics, genetic relationship, gene structure, chromosome location, collinearity, and *cis*-elements identification were comprehensively analyzed. Whole genome duplication (WGD) / segmental duplication may be the reason why the number of *HK* genes doubled in tetraploid *Gossypium* species. Expression analysis revealed that most cotton *HK* genes were mainly expressed in the reproductive organs and the fiber at initial stage. Gene expression analysis revealed that *HK* family genes are involved in cotton abiotic stress, especially drought stress and salt stress. In addition, gene interaction networks showed that HKs were involved in the regulation of cotton abiotic stress, especially drought stress. VIGS experiments have shown that *GhHK8* is a negative regulatory factor in response to drought stress. Our systematic analysis provided insights into the characteristics of the *HK* genes in cotton and laid a foundation for further exploring their potential in drought stress resistance in cotton.

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Title: Morphological and physio-biochemical responses under heat stress in cotton: Overview.

Author: Aamir Ali Abro , Muhammad Anwar , Muhammad
Umer Javwad , Mjie Zhang, Fang Liu

Imprint: Biotechnology Reports, Volume 40, December 2023, e00813

Abstract: Cotton is an important cash crop in addition to being a fiber commodity, and it plays an essential part in the economies of numerous nations. High temperature is the most critical element affecting its yield from fertilization to harvest. The optimal temperature for root formation is 30 C -35 °C; however, root development ends around 40 °C. Increased temperature, in particular, influences different biochemical and physiological processes associated with cotton plant, resulting in low seed cotton production. Many studies in various agroecological zones used various agronomic strategies and contemporary breeding techniques to reduce heat stress and improve cotton productivity. To attain desired traits, cotton breeders should investigate all potential possibilities, such as generating superior cultivars by traditional breeding, employing molecular techniques and transgenic methods, such as using genome editing techniques. The main objective of this review is to provide the recent information on the environmental factors, such as temperature, heat and drought, influence the growth and development, morphology and physio-chemical alteration associated with cotton. Furthermore, recent advancement in cotton breeding to combat the serious threat of drought and heat stress.

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Title: Gene expression pattern of K transporter GhHAK5 gene of potassium efficient and in-efficient cotton cultivars based on morphological physiognomies as affected by potassium nutrition and reduced irrigation.

Author: Akhtar Muhammad Naeem, Haq Tanveer ul, Akhtar Muhammad Waseem

Imprint: Journal of Cotton Research volume 6, Article number: 14 (2023)

Abstract: Under K deficiency the uptake and distribution pattern in plant cells is mediated through different transport proteins and channels which were controlled by specific gene family. Therefore, a hydroponic experiment was conducted under control condition for testing the gene expression pattern of the K transporter under adequate and low K supply levels. After that, a 2-year field experiment was conducted to evaluate five selected cotton cultivars (four K-efficient cultivars, viz., CIM-554, CYTO-124, FH-142, IUB-2013, and one K non-efficient, BH-212) screened from the initial hydroponics culture experiment and two levels of potassium (0 K_2O kg ·ha^{-1} and 50 K_2O kg ·ha^{-1}) were tested under reduced irrigation (50% available water content; 50 AWC) and normal irrigation conditions (100% available water content; 100 AWC).

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Title: Biochar amendment combined with partial root-zone drying irrigation alleviates salinity stress and improves root morphology and water use efficiency in cotton plant.

Author:Jingxiang Hou , Heng Wan , Kehao Liang, Bingjing Cui , Yingying Ma, Yiting C hen , Jie Liu

Imprint: Science of the Total Environment, Volume 904, 15 December 2023, 166978

Abstract: An adsorption experiment and a pot experiment were executed in order to explore the mechanisms by which biochar amendment in combination with reduced irrigation affects sodium and potassium uptake, root morphology, water use efficiency, and salinity tolerance of cotton plants. In the adsorption experiment, ten NaCl concentration gradients (0, 50, 100, 150, 200, 250, 300, 350, 400, and 500 mM) were set for testing isotherm adsorption of Na^+ by biochar. It was found that the isotherms of Na^+ adsorption by wheat straw biochar (WSP) and softwood biochar (SWP) were in accordance with the Langmuir isotherm model, and the Na^+ adsorption ability of WSP (55.20 mg g^{-1}) was superior to that of SWP (47.38 mg g^{-1}). The pot experiment consisted three factors, viz., three biochar amendments (no biochar, WSP, and SWP), three irrigation strategies (deficit irrigation, partial root-zone drying irrigation – PRD, full irrigation), and two NaCl concentrations gradients (0 mM and 200 mM). The findings indicated that salinity stress lowered K^+ concentration, root length, root surface area, and root volume (RV), but increased Na^+ concentration, root average diameter, and root tissue density. However, biochar amendment decreased Na^+ concentration, increased K^+ concentration, and improved root morphology. In particular, the combination of WSP and PRD increased K^+/Na^+ ratio, RV, root weight density, root surface area density, water use efficiency, and partial factor productivity under salt stress, which can be a promising strategy to cope with drought and salinity stress in cotton production.

7

Title: Response of Cotton to Varied Levels of Agronomic Management Under High Density Planting System (HDPS) – A Review .

Author: S. Jaffar Basha and E. Aruna

Imprint: International Journal of Economic Plants 2023, 10(3): 200-203

Abstract: Cotton, a crop of choice, occupies the second premier position next to food crops in providing clothing. Though 53 species of Gossypium are available, only four species are cultivable and among the four, the major cultivable area falls under G. hirsutum. Though varieties with medium, superior medium, long and extra-long staple cotton were released earlier, with the advent of machineries, ginning facilities, mills were literally requiring cotton fiber of any length. With the advent of Bt technology and the release of hybrids during 2002, cotton productivity had gained a momentum. However, considering the duration, cost involved in manual harvesting etc., farmers were looking for alternate option especially under rainfed conditions and High-Density Planting System (HDPS) with compact cotton genotypes is the viable alternative to overcome the stagnant productivity despite following all the suitable agronomic measures like adopting BG II hybrids, maintaining optimum plant population density and following timely plant protection measures. HDPS technology increases the number of bolls per unit area to achieve a high yield, reduces the risk of terminal drought and failure due to pests, gives seed sovereignty to farmers, and is specifically suited for rainfed areas with shallow and medium-deep soils. Under HDPS entries could yield better at 60×10 cm2 spacing under medium depth soils with a planting density of 1.66 lakh plants ha-1. Cotton planted under HDPS need 25% additional fertilizers over the recommendation for varieties.

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Title: Growth and yield attributes under different cotton (Gossypium hirsutum) management systems.

Author: DVS Akshay, ND Parlawar, JP Deshmukh and AS Riar

Imprint: The Pharma Innovation Journal 2023; 12(9): 2470-2472

Abstract: A field investigation was conducted to compare cotton (Gossypium hirsutum) growth and yield attributes under organic, bio-dynamic, Bt-conventional, and non-Bt conventional management systems during the kharif season of 2020–21 at the bio Re-FiBL research trails farm, run by the bioRe Association in Kasrawad, Khurgone, Madhya Pradesh. Five distinct crop management techniques were used in the field experiment, each replicated four times, and the study was set up using a randomized block design. The treatments were distributed at random to different plots. The five approaches are: organic cotton management, biodynamic cotton management, conventional non-Bt cotton management, conventional Bt cotton management, and absolute control (without fertilizers). Regarding the emergence (%) and final plant population, it was determined that none of the treatments were statistically significant. The treatment with conventional Bt had the highest plant height and plant dry matter per hectare whereas the control had the lowest. The Conventional Bt treatment had the greatest observed open and closed boll count at the time of first and second picking, whereas the Control treatment had the lowest. Additionally, it was discovered that treatments with conventional Bt and control had the highest and lowest seed cotton yields per plant and per hectare, respectively. From the experiment, it can be inferred that the Conventional management of Bt cotton had considerably higher maximum growth and yield characteristics than the others.

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Title: Farmers Awareness towards different Bt-Cotton Brands in Guntur District of Andhra Pradesh

Author: K. Siva Shankar Reddy, B. Aparna, P. Ganesh Kumar and P. Lavanya Kumari

Imprint: Andhra Pradesh. J Agril. Sci : 9(1): 59-64, 2023

Abstract: The present study entitled "farmers awareness towards different Bt-cotton brands in Guntur district of Andhra Pradesh" was undertaken mainly to study about the aspects of farmer buying behaviour towards Bt cotton seed. India is 3rd largest producer of cotton with area under cotton crop is 134.77 lakh ha, were as Andhra Pradesh account for 6.57 lakh ha, in A.P., Guntur stands first in terms of production with 9.86 lakh bales and second in terms of area under cultivation with 1,82,000 ha. Guntur district was purposively selected for the study and the top two mandals were chosen which has maximum area and production under cultivation of cotton crop and two villages from each was selected with a sample size of 100 farmers. The selected villages were Gudipudi, Dhulipalla, Mandadi and Veldurithi. There is always a positive relationship between education and awareness of a product. Through Chi square analysis, it was observed that there is a strong association between education of farmers and awareness, also revealed that there is no association between age, income, land holding size with brand awareness. Most of the farmers i.e. 60.26 per cent depended up on the fellow farmers and relatives to select the BT cotton brands, most of the farmers buy the seed from dealers with credit option. Seed regulation authorities should increase the vigilance and ensure the quality of the seed thoroughly before seed certification. Private companies should follow the good CRM to create the more awareness among the rural people.

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Title: Response of Deshi cotton variety Phule dhanwantary to high density planting system

Author: AK Kolage, RS Wagh and NK Bhute

Imprint; The Pharma Innovation Journal 2023; 12(8): 2520-2524

Abstract: A field experiment was conducted during Kharif season of 2016-17, 2017-18 and 2018-19 to find out the optimum spacing for growth, yield and to study economics of arborium cotton in clayey textured soil at Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, (Maharashtra). The experiment was laid out in randomized block design with nine treatments viz., 45 x 15 cm2 , 45 x 30 cm2 , 45 x 45 cm2 , 60 x 15 cm2 , 60 x 30 cm2 , 60 x 45 cm2 , 90 x 15 cm2 , 90 x 30 cm2 and 90 x 45 cm2 in three replications. The pooled result of experiment indicated that the spacing 45 cm x 15 cm2 observed significantly maximum plant height (120.74 cm) than other spacing's. However it was at par with spacing 60 x 15 cm2 (117.68 cm) at harvest. The spacing 90 x 15 cm2 recorded significantly higher number of bolls plant-1 (24.37) and average boll weight (4.60 g) than rest of spacing's. Whereas, the spacing 45 x 15 cm2 recorded significantly higher seed cotton yield (18.30 q ha-1) than rest of all other spacing's and also observed 24% higher seed cotton yield than normal spacing of 45 x 30 cm2 . The spacing 45 cm x 15 cm2 recorded highest gross monetary returns (Rs.93557 ha-1), net monetary returns (Rs. 39297 ha-1) and B:C ratio (1.71) than rest of spacing.

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Title: Genomic study of PIFs in cotton and functional analysis of GhPIF4 in promoting cotton flowering.

Author: Jing-Ruo Zhao, Ya-Mei Feng, Ya-Xin Zheng, Dong-Shuai Liu

Imprint: Plant Growth Regulation (2023)

Abstract: Cotton is the most important commercial crop in the production of fiber for the textile industry worldwide, and flowering time is an important agronomic trait for cotton production. Phytochrome interacting factors (PIFs) are central regulators of photomorphogenesis and promising tools to improve crop productivity. Research on the role of PIFs in crop growth and development has been gradually reported in recent years, but there are few reports of PIFs in cotton. In this study, comprehensive and systematic comparative analysis of PIFs in three Gossypium spp. was performed. We identified 11, 11, and 17 PIF candidates from G. arboreum, G. raimondii, and G. hirsutum, respectively. The phylogenetic analysis placed the cotton PIFs into three groups and indicated the losses of PIF orthologs were independent evolutionary events in G. hirsutum. Conserved domain analysis showed that several conserved domains in cotton PIFs evolved after the origin of Gossypium. Analysis of the cis-acting elements and transcriptome was performed and revealed that the cotton PIFs were highly expressed in meristematic tissues and floral organs. Further, RNA in situ hybridization revealed the dominant expression of GhPIFs was in the meristem of cotton shoot tips during the reproductive stage, and functional analysis suggested that GhPIF4 promotes flower bud formation, thus regulating the flowering time of cotton. This study suggests that PIFs play an important role in regulating the cotton flowering, which brings new insights for subsequent studies aiming to reveal the regulatory network of cotton reproductive development.

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Title: The effect of climatic factors on the cotton productivity using machine learning approaches.

Author: Bakhtiyar Babashli

Imprint: 6th Intercontinental Geoinformation Days (IGD) – 13-14 June 2023 – Baku, Azerbaijan

Abstract: Agriculture and the farming are two of the most important sectors of the economy. An accurate and timely assessment of cotton field productivity is useful for management decisions about cotton supply and sales. Cotton production concentration is influenced by a variety of factors. The impact of climatic conditions (rainfall, temperature, wind, etc.) on cotton productivity is studied in order to determine the quantitative relationship between these parameters and productivity. Several machine learning techniques have been researched and used to estimate crop yield. Errors like RMSE, MSE, MAE, and R2 were employed as indicators, and the polynomial regression model was chosen as the best among them.

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Title: Effect of fertigation on physiological parameters of Bt. cotton (Goss*ypium hirsutum* L.).

Author: Bhumika B Tandel, VP Usadadiya, Sejal K Parmar and AR Kaswala

Imprint: The Pharma Innovation Journal 2023; 12(8): 2499-2500

Abstract: The present experiment was undertaken to evaluate the effect of fertigation on growth and yield of Bt. cotton during 2019–20 at the Soil and Water Management Research Farm, Navsari. The experiment was laid out in a randomized block design with four replications and ten treatments. The results revealed that application of 100% NPK through fertigation (T1) recorded significantly higher leaf area index, chlorophyll content (SPAD reading) and CGR, but it remained at par with 100% N & K through fertigation with 100% P applied as basal (T2), 100% N through fertigation with 100% P & K applied as basal (T3), 80% NPK through fertigation (T4), 80% N & K through fertigation with 80% P applied as basal (T5) and 80% N through fertigation with 80% P & K applied as basal (T6). Lower leaf area index, chlorophyll content (SPAD reading) and CGR were recorded under 60% N fertigation with 60% P and K applied as basal (T9). Net assimilation rate did not remarkably vary under different levels of fertigation.

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Title: Effect of Radiation, Different Types Chlorine And Sulfate Salts on The Dynamics of Nitrate Reductase And Carbonic Anhydrase Enzymes Activities Changes during the Ontogeny of Cotton Plants.

Author: H.G. Babayev , Sh.E. Alakbarova , H.A. Abiyev , E.S. Jafarov

Imprint: Journal of Radiation Researches, vol.10, No.1, 2023, Baku

Abstract: In this study, the effect of γ-irradiation, different doses (K, 5, 10, 50, 100, 200 Gy), and concentrations (K, 5, 10, 50, 100, 200, mM) of different types of chlorine (NaCl, FeCl3) and sulfate salts (Na2SO4, ZnSO4) on the dynamics of changes in the activities of nitrate reductase (NR) and carbonic anhydrase (CA) enzymes in the roots and leaves of Ganja-182 variety of Gossypium hirsitum L cotton species at separate stages of ontogenesis was studied. Firstly, after finding the optimal dose and concentration limit at each stage of ontogenesis of the plant, the dynamics of change of enzyme activity at these doses and concentrations were examined every 10, 20, and 30 days during the period of budding and preparation for flowering of the plant, and interesting results were obtained.

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Title: Use of innovative plant nutrition products (fertilizers, biostimulant and microorganisms) to evaluate their effects in cotton (Gossypium hirsutum L.) agronomic characteristics and lint yield grown in Giannitsa area, Greece.

Author: Baxevanidis, Andreas

Imprint: Thesis, Perrotis College, Cardiff Metropolitan University Jan-2023 http://repository.afs.edu.gr/handle/6000/553

Abstract: The production of cotton (Gossypium hirsutum L.) in the world and in particular in Greece is of significant importance, affecting main areas of social and financial entities. The cost of production is usually increasing every year, and during the 2021-2022 growing seasons, the costs of all inputs increased significantly dur top energy and war in Ukraine. That creates the necessity for farmers to adopt more sustainable practices for cotton production and search for new and innovative products with high use efficiency and cost reduction. The cotton price is mainly a stock market issue and small farmers have no means to affect it. The main goal of this study is to evaluate the effects from application of new and innovative plant nutrition products and their effect in crop productivity. A field study was established in a cotton field located in Giannitsa, Greece and several treatments were used to assess their effect on cotton yield and major agronomic characteristics, such as plant height, number, and weight of open and closed bolls. The results revealed that the product used increased the yield and in some cases the increase was statistically significant, while in all cases it outnumbers the control from 14-54%. Therefore, these products could be used by farmers to achieve higher sustainability. The ROI analysis demonstrated an increase ranged from 2.5 to 5.2.

CROP PROTECTION

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Title: Identification and characterization of the Bicupin domain family and functional analysis of *GhBCD11* in response to verticillium wilt in cotton.

Author: Ying Sun , Yi Wang , Yalin Zhang , Nadeem Hasan , Na Yang

Imprint: Plant Science, Volume 337, December 2023, 111875

Abstract: Bicupin domain protein (BCD) family, an important component of Cupin domain superfamily, plays important roles in oxalic acid (OA) degradation and stress responses in high plants. However, no studies have been reported on the Cupin domain family in cotton up till now. In our study, a total 110 proteins including Cupin domain were identified from the upland cotton (*Gossypium hirsutum*). Among them, 17 proteins contained Bicupin domain. Subsequently, we found that *V. dahliae* produces OA leading to cotton leaf wilting. RT-qPCR analysis of *GhBCDs* revealed that OA and *V. dahliae* Vd080 significantly enhanced the expression of *GhBCD11*. The Virus-induced gene silencing and overexpression analysis showed that *GhBCD11* positively regulates plant resistance to *V. dahliae*. Subcellular localization showed GhBCD11 located on the plasma membrane. The analysis of expression pattern showed that *GhBCD11* can be induced via hormone-mediated signal pathway including salicylic acid (SA), ethephon (ET), methyl jasmonate (JA) and abscisic acid (ABA). In addition, we identified an interaction between 60 S ribosomal protein GhRPL12–3 and GhBCD11 by yeast double hybridization. Overall, this is the first study, where we identified Cupin domain family in cotton, clarified the role of *GhBCD11* in cotton for resistance to *V. dahliae* and found an interaction between GhRPL12–3 and GhBCD11.

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Title: Combined application of effective Trichoderma, Pseudomonas and arbuscular mycorrhiza spp. reduced soil-borne diseases and boosted growth in cotton.

Author: Satish Kumar Sain, Hanwant Dewasi & Amarpreet Singh

Imprint: Egyptian Journal of Biological Pest Control, Published: 18 September 2023, volume 33, Article number: 94 (2023)

Abstract: The most common soil-borne diseases in cotton are root rot and wilt, which are caused by *Rhizoctonia solani* (Taub) Butler and *Fusarium oxysporum* f. sp. *vasinfectum*, respectively. These two diseases significantly reduce plant stand and production. Under extreme circumstances, the application of fungicides does not provide satisfactory management of these diseases and also pollutes the environment. The effect of biocontrol agents, their combinations and fungicides on root rot and wilt management and plant growth in *Gossypium hirsutum* and *G. arboreum* cultivars CSH-3129 and CICR-3 were studied during 2017–18 and 2018–19.**Results:** Out of six isolates of *Trichoderma* spp., *T. asperellum* (Th-11) was the most effective for inhibiting the mycelial growth of *R. solani* and *F. oxysporum* f. sp. *vasinfectum* (64.4–100%). The combined seed treatment of *T. asperellum* (Th-11, c.f.u. 2×10^8/g) + *Pseudomonas fluorescens* (c.f.u. 2×10^8/g) + arbuscular mycorrhizal fungi (AMF; 1200 IP/g) resulted in the highest plant vigour index in CSH-3129 (890.9%) and CICR-3 cultivars (393.5%) at 15 days after treatment. Ninety days after sowing, the combined seed treatments of *T. asperellum* (Th-11) + *P. fluorescens* + AMF followed by *T. asperellum* (Th-11) + *P. fluorescens* showed the lowest area under the disease progress curve in CICR-3 and CSH 3129. Two-year pooled results indicated that the combined seed treatment with *T. asperellum* (Th-11) + *P. fluorescens* + AMF reduced the root rot disease by 51 and 57.5% in CICR-3 and CSH-3129 cultivars, respectively, under field conditions.**Conclusion-**The present investigation suggested that combined application of the most effective strains of *T. asperellum* (Th-11) @10 g/kg + *P. fluorescens* @10 g/kg and AMF @20 g/kg can effectively manage root rot and wilt diseases up to 60 days after sowing and enhance plant growth under field conditions. However, the application rates of these biocontrol agents *vis-à-vis* load of pathogen inoculum in the field must be further evaluated for improved and long-term effects.

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Title: Genome-wide identification of GhRLCK-VII subfamily genes in *Gossypium hirsutum* and investigation of their functions in resistance to Verticillium wilt.

Author: Xiuyan Liu, Zhongping Lei, Yuzhen Yang, Zhenkai Wang, Shengying Ha,

Imprint: *BMC Plant Biology* volume 23, Article number: 421 (2023)

Abstract: The receptor-like cytoplasmic kinases subfamily VII (RLCK-VII) is critical in regulating plant growth, development, and pattern-triggered immunity. However, a comprehensive exploration of these genes in the allotetraploid *Gossypium hirsutum* is still lacking. This study aimed to identify RLCK-VII genes in *G. hirsutum* and investigate their evolutionary history, structural features, expression patterns, and role in plant defense. Results: Seventy-two RLCK-VII genes in the *G. hirsutum* genome were unveiled and classified into nine groups following their phylogenetic analysis with *Arabidopsis thaliana*. Group VII-1 was the largest, accounting for 28%, while Groups VII-2 and VII-3 had only one member each. The analysis using MCScanX revealed that these 72 genes formed 166 collinear gene pairs and were resided on 26 chromosomes of *G. hirsutum*, suggesting that they were derived from whole genome segmental duplication events. Their calculated *Ka*/*Ks* values were below one, implying the occurrence of purification selection during the evolution and inhibition of gene function differentiation/loss. All members of the RLCK-VII subfamily possessed two conserved domains, PKinase-Tyr and PKinase, and several conserved PBS1 kinase subdomains, individually included in one of the ten motifs identified using MEME. The RNA-Seq results showed that RLCK-VII genes exhibited different spatiotemporal expression, indicating their involvement in cotton growth, development, and defense responses to *Verticillium dahliae*. The transcription patterns of RLCK-VII genes found by RNA-Seq were further validated using qRT-PCR assays after inoculating "20B12" (cotton cultivar) with "V991" (*V. dahliae*). The virus-induced gene silencing (VIGS) assays uncovered that two RLCK-VII genes *Gohir.A13G227248* and *Gohir.A10G219900*) were essential to *G. hirsutum* resistance to Verticillium wilt.

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Title: A novel and efficient method for identifying cotton leafroll dwarf virus infection in upland cotton (Gossypium hirsutum)

Author: Serina M. DeSalvio, Brianna L. Cheek, Robert N. Vaughn, Olufemi J. Alabi, John E. Holme, Nisha Jain, David M. Stelly

Imprint: Plant Breed. 2023;142:238–246.

Abstract: We report the development of a novel and more efficient, rapid, cost-effective and simple technique than current PCR-based identification methods for screening cotton (Gossypium hirsutum) plants for the presence of cotton leafroll dwarf virus (CLRDV). This protocol takes advantage of the PACE (PCR Allele Competitive Extension) system and uses PCR amplification of cDNA, coupled with sequence-specific fluorescent probes to differentiate between infected and uninfected cotton plants. This procedure has the potential for application in detection of other RNA viruses in a variety of other crops, by using primers specific for the RNA-dependent RNA polymerase (RdRP) gene and a widely conserved housekeeping gene in the host organism; in this case, the G. hirsutum polyubiquitin gene (GhUB).

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Title: Biorational approaches for management of Pectinophora gossypiella (Saunders) (Lepidoptera: Gelechiidae) in Cotton - an overview

Author: Kumar Vijay, Grewal G.K.

Imprint: Journal of Entomological Research, 2023, 47 (3)

Abstract: Pink bollworm (PBW), Pectinophora gossypiella (Saunders) which is widely regarded as a devastating pest of cotton all over the world has developed resistance against various insecticides. Its management is a major challenge for the cotton growers, specially due to break down of resistance in Bt cotton. Various Integrated pest management practices like sowing of cotton during recommended time of sowing be it long duration Gossypium hirsutum varieties or medium or short season varieties. During the season, regular monitoring for rosette flowers and green boll damage due to PBW until the harvest of the crop is beneficial. Certain off-season Cultural practises, like sanitation of ginning factories and field sanitation, allowing cattle, sheep, and goats to graze on immature green and attacked bolls after final picking, prevents pest carryover to the next crop season. The use of bio agents have also resulted in better suppressing of PBW population. Similarly, the use of certain botanicals like ethanolic extracts of the two plants, Calotropis procera and Ocimum sanctum, compatibility of entomopathogenic fungi (EPFs) with Azadirachta indica extract (alone and in combinations), extracts of tobacco, neem and datura, certain growth regulators like diofenolan reduces the adult emergence to a greater extent. Further, integrated management of pink bollworm using a sex pheromone formulation and mating disruption technique was found practical and ideal approach.

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Title: Comparing the efficiency of fungal spores and their metabolites in some entomopathogenic fungi against cotton leaf worm, Spodoptera littoralis

Author: Reda RH Abdullah

Imprint: Journal of Entomology and Zoology Studies 2023; 11(5): 40-44

Abstract: Spodoptera littoralis is the most destructive insect in Egypt and many other countries, where it attacks several economic crops, such as cotton and vegetables. Entomopathogenic fungi are widely used in controlling many pests. Usually, spores of them were used in the controlling process. In this study, intracellular and extracellular metabolites were extracted from broth cultures of four entomopathogenic fungi: Beauveria bassiana, Metarhizium anisopliae, Cladosporium cladosporioides, and Verticillium lecanii. The extracted metabolites and spores of fungal strains were evaluated to compare their efficiency against the 2nd instar larvae of S. littoralis. The results indicated that highly significant differences were found between the efficiency of intracellular and extracellular metabolites and fungal spores against the treated larvae, where the mortality percentage of S. littoralis larvae increased with the extracellular metabolites extract of C. cladosporioides and V. lecanii more than intracellular metabolites and spore suspension, while the intracellular metabolites extract of M. anisopliae was more effective compared with extracellular metabolites and spore suspension, but the spore suspension of B. bassiana caused significant mortality compared with intracellular and extracellular metabolites extracts. As a result, this study reported that it can be useful to use the metabolites of some entomopathogenic fungi in the control of S. littoralis because they may have more activity than fungal spores in some entomopathogenic fungi.

PLANT GENETICS AND BREEDING

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Title: Genetic Variability among Egyptian Extra-long Staple Cotton Genotypes for Some Economic Traits

Author: Emad A. Amer ; Salah S. Hassan

Imprint: Egyptian Journal of Agronomy, DOI: 10.21608/agro.2023.230545.1386

Abstract: This investigation was completed at Sakha Station of Agricultural Research, over 2021 and 2022 seasons to evaluate the variance among some Egyptian cotton genotypes for yielding potential and fiber quality traits. Materials comprised thirteen extra-long staple cotton genotypes (*Gossypium barbadense* L.). Genotypes were arranged in RCBD design replicated quadric. Data were collected for, boll weight, seed cotton yield, lint yield, lint%, earliness index, micronaire reading, fiber strength, fiber length and uniformity index. Genotypes (G) exhibited significant differences for all traits. Years (Y) had insignificant differences on most of traits, GxY interaction was significant for some traits. Giza 87 and Giza 88 had the lower yield while the rest of genotypes insignificantly varied. Giza 87, Giza 93 and Giza 93 x Menufi genotypes had the finest fibers, Giza 87, Giza 92 and Giza 96 had the strongest fibers. Genotypic and phenotypic exhibited broad scope of variability for all traits. Seed and lint cotton yields had moderate PCV values, while the remainder traits showed low values, GCV showed moderate value for lint yield and low values for the remainder traits. Broad-sense heritability recorded low value for boll weight to very high values for most of traits. For GS%, moderate values were recorded for seed cotton yield, lint yield and earliness index while the rest had low values. In this investigation, seed cotton yield, lint yield and earliness index exhibited high heritability together with moderate genetic advance values, subsequently, direct selection for such traits is anticipated to induce considerable improvement in next generation.

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Title: Breeding Cotton for Determinate Growth Habit: Increasing Cotton Fiber Yield by Remobilization of End-Of-Season Perennial Reserves (2023).

Author: Naveed, Salman

Imprint: All Dissertations. 3431.
https://tigerprints.clemson.edu/all_dissertations/3431

Abstract: Cotton (*Gossypium* spp.) is a major export commodity for the U.S. Despite advances in plant breeding and management practices, the cotton yield gains in the U.S. have stagnated. Therefore, to increase cotton fiber yield, we undertook a novel approach by altering the growth habit of cotton from perennial to annual. In this effort, eight genotypes showing strong expression alleles for five floral induction and meristem identity genes were selected from 44 Upland cotton mini-core collection genotypes and genetically crossed in various combinations to stack the strong expression alleles in a genotype. These efforts have allowed us to develop high-yielding, high-fiber quality, and early-maturing cotton lines exhibiting reduced regrowth after defoliant. In addition, we identified 396 expression trait (e-trait) associated polymorphic SNPs through genome-wide association analysis. Among e-trait-associated markers, 159 were mapped to genes, 50 to untranslated regions, and 187 to random genomic regions. Biased distribution of the e-trait-associated markers was observed, where more markers mapped to D subgenome. Many e-trait-associated SNPs coincided to specific genomic regions. This finding has implications as these traits could be bred together. This analysis also allowed us to identify six candidate genes possibly involved in the regulation of flowering time and meristem identity-related traits. The functions of two candidate genes *Gohir.D05G103700* encoding GATA transcription factor (TF) and *Gohir.D12G153600* encoding SPL-TF, were characterized by virus-induced gene silencing. The downregulation of the *Gohir.D05G103700* gene in two plants produced a unique phenotype where the fourth bract of the cotton square was missing, a trait indicative of indeterminate growth.

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Title: Correlation and association studies for yield contributing traits and fibre quality traits in GMS based interspecific cotton hybrids (Gossypium hirsutum L. x Gossypium barbadense L.).

Author: SD Sanmugapriya, N Premalatha, A Subramanian, N Manikanda Boopathi and Dr. K Gurusamy

Imprint: The Pharma Innovation Journal 2023; 12(9): 1402-1406

Abstract: The present study was focused on the relationship between the yield and fibre quality traits to select the best GMS based hybrids. Thirty five GMS based interspecific tetraploid hybrids were raised from 5 lines (GMS14, GMS17, GMS19, GMS21, GMS27) and 7 testers (CCB26, CCB51, DB1901, CCB2, CCB6, CO18, SUVIN) in Line x Tester design and were evaluated for days to first flowering, days to 50% flowering, days to first bursting, plant height, boll weight, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, ginning outturn, seed index, lint index, upper half mean length, uniformity index, bundle strength, elongation percentage and fiber fineness. The study of correlation on seed cotton yield for 18 traits reported that number of sympodia per plant, boll weight, ginning outturn, lint index, seed index, upper half mean length, uniformity index, bundle strength, elongation percentage and fiber fineness showed significant positive association with the seed cotton yield per plant. The path analysis resulted boll weight, ginning outturn, upper half mean length, elongation percentage, fibre fineness were exhibited positive direct effects on the seed cotton yield per plant. Hence, the above mentioned traits could be considered for further breeding programme.

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Title: Elucidating the genetic diversity and population structure of international cotton germplasm using inter-primer binding site (iPBS) retrotransposon marker system.

Author: Binnur Yeşil Bayrıl, Allah Bakhsh, Muhammad Azhar Nadeem & Ufuk Demirel

Imprint: Genetic Resources and Crop Evolution (2023)

Abstract: Cotton (Gossypium hirsutum L.) is an important crop throughout the world and is one of the most important industrial raw materials. It is very important to characterize the available cotton germplasm aiming to identify novel genetic and genomic resources that can be used for future cotton breeding. Keeping this in view, a total of 179 cotton genotypes were characterized with the inter-primer binding site (iPBS) retrotransposon marker system. Seven iPBS-retrotransposon primers yielded a total of 134 scoreable bands and among these, 128 bands were polymorphic. The mean polymorphic bands per primer were 18.28, with values ranging between 16 and 21. The mean polymorphism rate of 7 iPBS retrotransposon primers was calculated as 96.28%. The polymorphism information content value varied between 0.31 and 0.46 with an average of 0.395. Genetic similarity was calculated using the POPGENE software and values ranged between 0.320 and 0.955. Population structure and neighbor-joining analysis divided the evaluated germplasm into two populations. The analysis of molecular variance revealed that maximum variations (96%) are due to differences within the populations. The information presented here has comprehensively demonstrated the potential of iPBS-retrotransposon markers in detecting genetic diversity and phylogenetic association analyses of cotton. This knowledge will be helpful for future cotton breeding.

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Title: Genetics of biochemical attributes regulating morpho-physiology of upland cotton under high temperature conditions.

Author: Sajid Majeed, Muhammad Tanees Chaudhary, Muhammad Salman Mubarik

Imprint: Research Square, Posted Date: September 11th, 2023 DOI: https://doi.org/10.21203/rs.3.rs-3255086/v1

Abstract: Background. In the global textile industry, cotton is a strategic fibre crop. It has a large impact on the industrial and agricultural economies of many countries. Sustainable cotton production is continuously threatened by the unpredictable changes in climate, specifically high temperatures. One of the main goals of contemporary cotton breeding programs is the production of high-yielding, heat-tolerant cotton cultivars with wide adaptation that can be grown throughout warming climate regions. Methods. The current study was designed to explore how heat stress impacts biochemical parameters that control the morpho-physiology of upland cotton. Two heat susceptible (FH-115 and NIAB-Kiran) and two heat tolerant (IUB-13 and GH-Mubarak) accessions were selected to develop filial and backcross generations. Heat tolerant ability of these generations and parental lines was assessed by determining viability of pollen grains, thermostability of cell membrane, levels of antioxidants and reactive oxygen species and yield related traits under both normal and high temperature environments in the field. Genetic control of these traits was assessed through generation mean analysis. Correlation and heterotic studies helped find the relationship among traits and best cross combination, respectively. Results. The data indicated that heat stress negatively impacted every plant attribute analysed. The IUB13 × FH-115 cross performed best under both normal and high temperatures for yield, biochemical, and physiological attributes. Yield of seed cotton exhibited positive associations with antioxidant levels and pollen viability.

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Title: Quantitative trait loci and candidate genes for yield-related traits of upland cotton revealed by genome-wide association analysis under drought conditions.

Author: Fenglei Sun, Yanlong Yang, Penglong Wang, Jun Ma & Xiongming Du

Imprint: BMC Genomics volume 24, Article number: 531 (2023)

Abstract: Due to the influence of extreme weather, the environment in China's main cotton-producing areas is prone to drought stress conditions, which affect the growth and development of cotton and lead to a decrease in cotton yield.Results-In this study, 188 upland cotton germplasm resources were phenotyped for data of 8 traits (including 3 major yield traits) under drought conditions in three environments for two consecutive years. Correlation analysis revealed significant positive correlations between the three yield traits. Genetic analysis showed that the estimated heritability of the seed cotton index (SC) under drought conditions was the highest (80.81%), followed by that of boll weight (BW) (80.64%) and the lint cotton index (LC) (70.49%) With genome-wide association study (GWAS) analysis, a total of 75 quantitative trait loci (QTLs) were identified, including two highly credible new QTL hotspots. Three candidate genes Gh_D09G064400, Gh_D10G261000 and Gh_D10G254000) located in the two new QTL hotspots, QTL51 and QTL55, were highly expressed in the early stage of fiber development and showed significant correlations with SC, LC and BW. The expression of three candidate genes in two extreme materials after drought stress was analyzed by qRT-PCR, and the expression of these two materials in fibers at 15, 20 and 25 DPA. The expression of these three candidate genes was significantly upregulated after drought stress and was significantly higher in drought-tolerant materials than in drought-sensitive materials. In addition, the expression levels of the three candidate genes were higher in the early stage of fiber development (15 DPA), and the expression levels in drought-tolerant germplasm were higher than those in drought-sensitive germplasm. These three candidate genes may play an important role in determining cotton yield under drought conditions.

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Title: Cotton Germplasm Characterization for Drought Tolerance Based on Morpho-Physiological and Fiber Quality Parameters

Author: M. Asif, A.A. Khan, H.M.N. Cheema, S.H. Khan, and Z. Iqbal

Imprint: SABRAO Journal of Breeding and Genetics 55 (4) 1079-1093, 2023 http://doi.org/10.54910/sabrao2023.55.4.6

Abstract: Drought tolerance is a quantitative trait that is exceedingly challenging to breed, especially for allotetraploids like cotton. The scenario of limited water resources necessitates developing droughttolerant cultivars that conserve significant irrigation water throughout the summer. Therefore, the presented study used a design to statistically analyze the morphological, physiological, and fiber quality parameters linked with drought tolerance, which is a comprehensive method for choosing better genotypes from the available cotton germplasm. Measuring these parameters ensued for plants grown under field conditions. The germplasm comprised 150 cotton genotypes studied at two water regimes, i.e., regular and water-stressed conditions for two consecutive seasons of 2015–2016 and 2016–2017. Data recording ran for different morpho-physiological and fiber quality parameters. Significant differences occurred for all the treatments, genotypes, and Genotype × Environment interaction for all the morphological, physiological, and fiber quality parameters under study. Additive Main effects and Multiplicative Interaction (AMMI) analysis and AMMI biplot analysis helped analyze the results, which revealed that the cotton genotypes FH-900, FH-901, FH-312, AS-1, AS-2, AS-3, RH510, RH-627, AR-2, AR-9, BH-118, BH-175, SLH-74, CIM-1100, CIM-598, and MM-58 were drought tolerant and ranked highest concerning stress condition. Moreover, correlation studies distinguished the relationship between relevant traits concerning drought tolerance.

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Title: Assessing diverse cotton germplasm through genetic evaluation and AMMI analysis.

Author: Alok Shrivastava, Dhruv Chitriya, YA Garde, Nitin Varshney, KG Modha, HE Patil and Pravinsinh Parmar

Imprint: International Journal of Statistics and Applied Mathematics 2023; SP-8(3): 814-819

Abstract: The multi-environment trials (MET) were conducted at various locations of AICRP centers of cotton in 2019-20. In cotton (*Gossypium hirsutum* L.), MET was carried out in different five environments with twenty-two different genotypes for selecting the best genotype and environment. In a simple ANOVA analysis, the genotypes were found significantly different from each other in all five environments. Also, there was significant interaction found in G×E interaction for seed cotton yield. In AMMI analysis, principal component 1 (PC1) expressed about 51.5% of the variation and it was found significant, while PC2 was not found significant so only PC1 was taken under study. Among all the tested genotypes, the genotype GTHV-13/39 (G20) was recorded as the highest yielding genotype and the most stable genotype was GN. Cot. 22 (CC) (G21). But the most ideal genotype was GBHV-203 (G18) in seed cotton yield as well as stability performance in all five environments. Within these five environments, Talod (E3) was observed as the highest yielding environment. The Achhalia (E5) was found as the most stable environment among this environment for seed cotton yield. Thus, our studies suggest that AMMI model is also useful for estimating adaptability of traits other than yield utilized for breeding cotton cultivars.

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Title: Evaluating Combining Abilities and Heterotic Effects for Enhanced Cotton Yield.

Author: Rasheed Z, Anwar Mr, Hanif K, Adrees A, Karim Wa, Amjad K, Hassan A, Mazhar Hsud, Tipu Alk, Khan Tm

Imprint" Biological and Clinical Sciences Research Journal eISSN: 2708-2261; p,ISSN: 2958-4728 www.bcsrj.com DOI: https://doi.org/10.54112/bcsrj.v2023i1.384 Biol. Clin. Sci. Res. J., Volume, 2023: 384

Abstract: The present research was conducted to evaluate heterosis in diallel crosses, determining general and specific combining abilities for yield-related traits and identifying top-performing genotypes for future breeding programs. A field experiment was conducted using selected genotypes (CIM-599, CIM-602, Shahkar, and NS-181) to produce F1 hybrids through frequent pollinations in a diallel fashion. Twelve F1 hybrids and their four parental genotypes were cultivated in a randomized complete block design with two replications. Yield-related traits were recorded, including plant height, branches per plant, bolls per plant, lint percentage, boll weight, seed cotton yield, seed index, and lint index. Analysis of variance and combining ability effects analysis were performed to assess the significance of the genotypes and their interactions. Significant variability among parental genotypes was observed for yield-related traits, indicating genetic variation in the breeding material. Combining ability analysis revealed the predominance of non-additive gene action. General combining ability (GCA) effects were significant for most traits, with CIM-599 exhibiting the highest GCA effects. Specific combining ability (SCA) and reciprocal combining ability (RCA) effects were significant for various traits and hybrid combinations, indicating their potential for trait improvement. The hybrid combination CIM-599 x Shahkar exhibited substantial mid-parent heterosis for seed cotton yield, boll weight, and lint percentage. This cross also displayed notable SCA effects, indicating its importance for hybrid breeding. These findings highlight the potential of hybrid breeding for trait enhancement. Future breeding programs could leverage the insights gained here to create improved cotton varieties with enhanced yield.

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Title: Genome-wide association study (GWAS) of fiber yield-related traits uncovers the novel genomic regions and candidate genes in Indian upland cotton (*Gossypium hirsutum* L.)

Author: Babita Joshi, Sanjay Singh, Gopal Tiwari , Harish Kumar

Imprint: Front. Plant Sci.Sec. Plant Breeding, Volume 14 - 2023 | doi: 10.3389/fpls.2023.1252746

Abstract: Upland cotton (Gossypium hirsutum L.), one of the major fiber crops cultivated worldwide and has significant economic importance. India harbours the largest area for cotton cultivation, but its fiber yield is still compromised and ranks 22 nd position in productivity.Genetic improvement of cotton fiber yield traits is one of the major goals in cotton breeding but the understanding of the genetic architecture underlying cotton fiber yield traits still remains limited and unclear. To better decipher the genetic variation associated with fiber yield traits, we conducted a comprehensive genome-wide association mapping study using 117 Indian cotton germplasm for six yield-related traits. To accomplish this, we generated 2,41,086 high-quality single nucleotide polymorphism (SNP) markers using genotyping-bysequencing (GBS) methods. Population structure, PCA, kinship, and phylogenetic analysis divided the germplasm into two sub-populations, showing weak relatedness among the germplasms. Through association analysis, a total of 205 SNPs and 134 QTLs were identified to be significantly associated with six fiber yield traits. Altogether 39 novel QTLs were identified in the current studies, whereas 95 QTLs overlapped with existing public domain data in a comparative analysis. Eight QTLs, qGhSI_LI_A5, qGhLI_SI_A13, qGhLI_SI_D9, qGhBW_SCY_A10, and qGhLP_BN_A8 exhibited pleiotropic association. Gene annotation of these fiber yield QTLs further revealed 2,509 unique genes. These genes were predominantly enriched for different biological processes like plant cell wall synthesis, nutrient metabolism, and vegetative growth development in the gene ontology (GO) enrichment study. Furthermore, gene expression analysis using RNAseq data from 12 diverse cotton tissues identified 40 candidate genes (23 stable and 17 novel genes) to be transcriptionally active, in different stages of fiber, ovule and seed development. These findings have unveiled a rich tapestry of genetic elements, including SNPs, QTLs, and candidate genes and may have a high potential for improving fiber yield in future breeding programs for Indian cotton.

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Title: Dissection of salt tolerance in cotton germplasm by analyzing agro-physiological traits and ERF genes expression.

Author: Muhammad Mubashar Zafar, Waqas Shafqat Chattha, Arfan Ali

Imprint: Research SquarePosted Date: September 15th, 2023 DOI: https://doi.org/10.21203/rs.3.rs-3232079/v1

Abstract: The development of genotypes that can tolerate high levels of salt is crucial for the efficient use of salt affected land and for enhancing crop productivity worldwide. Therefore, incorporating salinity tolerance is a critical trait that crops must possess. Salt resistance is a complex character, controlled by multiple genes both physiologically and genetically. To examine the genetic foundation of salt tolerance, we assessed 16 F1 hybrids and their eight parental lines under normal and salt stress (15 dS m− 1) conditions. Under salt stress conditions significant reduction was observed for plant height (PH), bolls/plant (NBP), boll weight (BW), seed cotton yield (SCY), lint% (LP), fiber length (FL), fiber strength (FS), potassium to sodium ratio (K+/Na+), potassium contents (K+), total soluble proteins (TSP), carotenoids (Car) and chlorophyll contents. Furthermore, the mean values for hydrogen peroxide (H2O2), sodium contents (Na+), catalase (CAT), superoxidase (SOD), peroxidase (POD), and fiber fineness (FF) were increased under salt stress. Moderate to high heritability and genetic advance was observed for NBP, BW, LP, SCY, K+/Na+, SOD, CAT, POD, Car, TSP, FL, and FS. Mean performance, and multivariate analysis of 24 cotton genotypes based on various agro-physiological and biochemical parameters suggested that the genotypes FBS-Falcon, Barani-333, JSQ-White Hold, Ghauri, along with crosses FBS- FALCON × JSQWhite Hold, FBG-222 × FBG-333, FBG-222 × Barani-222, and Barani-333 × FBG-333 achieved the maximum values for K+/Na+, K+, TSP, POD, Chlb, CAT, Car, LP, FS, FL, PH, NBP, BW, and SCY under salt stress and declared as salt resistant genotypes. The above-mentioned genotypes also showed relatively higher expression levels of Ghi-ERF-2D.6 and Ghi-ERF-7A.6 at 15 dSm− 1 and proved the role of these ERF genes in salt tolerance in cotton. The findings suggest that these genotypes have the potential for the development of salt-tolerant cotton varieties with desirable fiber quality traits

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Title: A Simplified Microscopy Technique to Rapidly Characterize Individual Fiber Traits in Cotton.

Author: Quinn LaFave, Shalini P. Etukuri, Chaney L. Courtney
Imprint: Methods Protoc. 2023, 6(5), 92; https://doi.org/10.3390/mps6050092

Abstract: Recent advances in phenotyping techniques have substantially improved the ability to mitigate type-II errors typically associated with high variance in phenotyping data sets. In particular, the implementation of automated techniques such as the High-Volume Instrument (HVI) and the Advanced Fiber Information System (AFIS) have significantly enhanced the reproducibility and standardization of various fiber quality measurements in cotton. However, micronaire is not a direct measure of either maturity or fineness, lending to limitations. AFIS only provides a calculated form of fiber diameter, not a direct measure, justifying the need for a visual-based reference method. Obtaining direct measurements of individual fibers through cross-sectional analysis and electron microscopy is a widely accepted standard but is time-consuming and requires the use of hazardous chemicals and specialized equipment. In this study, we present a simplified fiber histology and image acquisition technique that is both rapid and reproducible. We also introduce an automated image analysis program that utilizes machine learning to differentiate good fibers from bad and to subsequently collect critical phenotypic measurements. These methods have the potential to improve the efficiency of cotton fiber phenotyping, allowing for greater precision in unravelling the genetic architecture of critical traits such as fiber diameter, shape, areas of the secondary cell wall/lumen, and others, ultimately leading to larger genetic gains in fiber quality and improvements in cotton.

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Title: Assessing genetic variation in *Gossypium barbadense* L. germplasm based on fibre characters.

Author: Alagarsamy Manivannan

Imprint: *Journal of Cotton Research* volume 6, Article number: 15 (2023)

Abstract: *Gossypium barbadense* L. has specific fibre in terms of its length, strength, and fineness, and known as extra-long staple (ELS) cotton, Sea–Island cotton, or Egyptian cotton. Narrow genetic base with less genetic variability is observed in *G. barbadense* germplasm. Hence, this study was aimed to evaluate the genetic variability present in 108 germplasm accessions of *G. barbadense* and to identify the superior genotypes based on the fibre traits. Results- We evaluated 108 accessions for five fibre quality traits along with three checks in augmented block design. All fibre traits showed significant differences among genotypes, indicating that there is genetic potential for improvement. Fibre strength and micronaire (MIC) showed high phenotypic and genotypic coefficients of variation. High heritability combined with high genetic advance as percentage of mean (GAM) was recorded for fibre length, strength, and micronaire. Fibre strength and fibre length were significantly correlated with each other, while both showed negative correlation with micronaire. Principal component analysis and Biplot analysis showed that uniformity index discriminated all the genotypes in higher level, while fibre length and strength were medium in discrimination power. Biplot revealed genotypes DB 16, EC959191, GSB 39, ARBB 20, 5746U, EA 203, and EA 201 were genetically diverse. Hierarchal cluster analysis based on unweighted paired group method using arithmetic average (UPGMA) grouped the genotypes into four clusters, with each cluster consisting of 4, 18, 48, and 38 genotypes, respectively. Conclusion- Among the genotypes, 34 for fibre length (> 35 mm), 18 for fibre strength (> 40.4 g·tex^{-1}) and 66 for micronaire (3.7-4.2, A grade) were identified as potential accessions based on their superiority. The superior fibre genotypes identified in this study are potential lines for the ELS cotton breeding program.

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Title: Genetic components determination of yield and fiber quality properties in cotton (Gossypium barbadense L.)

Author: EL-Shazly, M. W. ; A. H. Mabrouk and A. M. Soliman

Imprint: J. of Plant Production, Mansoura Univ., Vol. 14 (9):413 - 419, 2023

Abstract: This study was conducted at Sakha Agricultural Research Station, Cotton Research Institute, Agricultural Research Center, Kafr El-Sheikh Governorate, Egypt, during two growing seasons (2021 and 2022). Six Egyptian cotton varieties were used as lines with five genotypes as testers, using line x tester analysis. Genotypes, parents, crosses and parents vs. crosses mean squares were extremely significant for all the studied characters, except for micronaire reading in the crosses. Giza 94 x 10229 exhibited significant useful heterosis (BP) for all the studied characters. Lines Giza 86 and Giza 76 recorded significantly and positive desirable general combining ability effects (GCA) for most traits while, Giza 96 was significant desirable general combining ability effects for fiber quality characters. In this respect, testers showed that Uzbekistan had significant and positive desirable for most yield characters while, BBB had significant desirable general combining ability effects for most studied characters. Crosses Giza 96 x Australy13, Giza 86 x 10229 and Giza 75 x C.B.58 were significant desirable specific combining ability effects (SCA) for some yield traits. Generally, Giza 86 could be used for improving high yielding cotton varieties in plant breeding programs, while Giza 96 considered as beneficial parent for breeding programs to produce new varieties characterized with best fiber quality.

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Title: Cotton Fiber and Its Sustainable Alternatives.

Author: Vandana Gupta & Saloni Gupta

Imprint: Part of the Sustainable Textiles: Production, Processing, Manufacturing & Chemistry book series (STPPMC)

Abstract: Cotton fiber is known as the white gold of India and every state thrives on it in many ways: farming, textile, craft, or basic utility products. A shift in the popularity of cotton is seen in the twenty-first century which came up with unprecedented opportunity in terms of technology and new material due to the harmful environmental effects of cotton. Search and application of new fibers such as bamboo, linen, banana, jute, ramie, pineapple, hemp, and lotus by the textile and fashion industry has made these fibers as some of the important alternatives for cotton due to their additional advantage not only as a textile material but also due to their sustainable developmental life cycle. This chapter is a compilation of many studies and researches conducted in the field of sustainable alternatives for cotton, and it explores the ability and inability of these fibers to substitute cotton.

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Title: Molecular genetic diversity in relation to the quantitative and qualitative (fiber quality) traits in upland cotton (Gossypium hirsutum L.).

Author: Rani Chapara, K. V. Siva Reddy, M. Sudha Rani, K. Sudhamani

Imprint: Research Square, Posted Date: September 12th, 2023 DOI: https://doi.org/10.21203/rs.3.rs-3327039/v1

Abstract: An attempt has been made to assess molecular genetic diversity at Regional Agricultural Research Station, Lam, Guntur using fifty-four tetraploid cotton (Gossypium hirsutum L.) genotypes with forty-four SSR markers related to various fibre quality traits. A total number of 24 alleles, with an average of 1.75 effective alleles per locus, were generated by these markers. The polymorphism information content (PIC) value ranged from 0.23 to 0.50 with a mean of 0.44 indicating lesser variation for various fibre quality traits within the investigated material. Using principal coordinate analysis (PCOORDA), cotton genotypes were separated by the first three principal coordinates (PC1, PC2, and PC3) accounting for 11.5, 8.6, and 7.2% of the total genetic variance, respectively. The SSR markers revealed a genetic similarity of 63.21 among the varieties studied.

PLANT BIOTECHNOLOGY

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Title: GhmiR858 Inhibits the Accumulation of Proanthocyanidins by Targeting GhTT2L in Cotton (Gossypium hirsutum).

Author: Jun Mei, Qingqing Niu, Kunling Xu, Yuyi Huang, Shimei Bai, Jiayu Zhu

Imprint: J. Agric. Food Chem. 2023, 71, 41, 15341–15351

Abstract: Proanthocyanidins (PAs) are predominantly regulated at the transcriptional level by sophisticated regulatory networks. In cotton, the role of miRNAs as key regulatory factors at the post-transcriptional level is still unclear. Here, we demonstrated that GhmiR858 negatively regulates PA accumulation in cotton leaves and calli by targeting GhTT2L. Excessive expression of GhmiR858 restrained the expression of GhTT2L, resulting in a significant decrease in PA abundance. Conversely, a reduction in GhmiR858 activity upregulated GhTT2L, which increased PA accumulation. Additionally, GhTT2L was found to positively regulate PA accumulation in both cotton and Arabidopsis. Further analyses showed that GhTT2L interacted with transcription factor GhTTG1, which directly binds to the GhANR promoter, to facilitate its transcription. This study provides new information to guide future studies of the PA regulatory mechanisms affected by miRNAs as well as the breeding of novel varieties of colored cotton with rich PAs.

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Title: Characterization and Expression Analysis of GLABRA3 (GL3) Genes in Cotton: Insights into Trichome Development and Hormonal Regulation .

Author: Naisi Wu, Benyi Lu, Yaofen Cao

Imprint: Research Square, https://doi.org/10.21203/rs.3.rs-3339054/v1

Abstract: GLABRA3 (GL3) and ENHANCER OF GLABRA3 (EGL3) genes encode a typical helix-loop-helix (bHLH) transcription factors that mainly regulate trichome branching and root hair development, DNA endoreduplication, trichoblast size, and stomatal formation. The functions of GL3 genes have been poorly characterized in cotton crop. In this study, we performed genome-wide scans for GL3 and EGL3 homologs to better understand their potential roles in trichome and fiber development in cotton crop. Our finding revealed that Gossypium hirsutum, G. barbadense, G. arboreum, and G. raimondii had a total of 6, 6, 3, and 3 GL3s, unevenly distributed on chromosome 4, 4, 2, and 2, respectively. Gh_A08G2088 and Gb_A09G2187, despite having the same bHLH domain as the other GL3 genes, were not analyzed due to their remarkably short sequences and limited number of motifs they possess, potentially indicating a lack of functional activity. The phylogenetic analysis divided remaining 16 GL3s into three subfamilies (Group I-) closely related to A. thaliana. These 16 GL3s have a complete bHLH domain, encoding 590–631 amino acids, with molecular weights (MWs) ranging from 65.92–71.36 kDa. The GL3s within each subfamily shared similar gene structures and motifs, indicating conserved characteristics within their respective groups. Promoter element analysis revealed 27 cis-acting elements in the GL3 promoter region. These elements include those responsive to salicylic acid, abscisic acid (ABA), methyl jasmonate (MeJA), and gibberellin. The expression of GL3 genes was analyzed in 12 tissues of G. barbadense and G.hirsutum using the publicly available RNA-seq data. Gb_D11G0219, Gb_D11G0214, and Gb_D08G2182, were identified as relatively highly expressed across the tissues, and selected for hormone treatment and expression validation in G. barbadense. RT-qPCR results demonstrated that Gb_D11G0219 and Gb_D11G0214 expression levels were significantly altered after MeJA, GA, and ABA, treatment. Subcellular localization prediction revealed that most GL3 proteins were expressed predominantly in the nucleus, with a few localized in the cytoplasm and chloroplasts. Overall, this study lays the foundation for further functional validation of GL3 genes in cotton trichome formation and fiber development by identifying hormonal regulation patterns and probable sites of action. The results provide a basis to elucidate the roles and regulatory mechanisms of GL3 genes in the intricate process of cotton fibre and trichome development.

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Title: GhIMP10D, an inositol monophosphates family gene, enhances ascorbic acid and antioxidant enzyme activities to confer alkaline tolerance in Gossypium hirsutum L.

Author: Yapeng Fan, Fanjia Peng, Ruifeng Cui, Shuai Wang, Yupeng Cui, Xuke Lu

Imprint: BMC Plant Biology volume 23, Article number: 447 (2023)

Abstract: Inositol monophosphates (IMP) are key enzymes in the ascorbic acid (AsA) synthesis pathways, which play vital roles in regulating plant growth and development and stresses tolerance. To date, no comprehensive analysis of the expression profile of IMP genes and their functions under abiotic stress in cotton has been reported. Results- In this study, the genetic characteristics, phylogenetic evolution, *cis*-acting elements and expression patterns of *IMP* gene family in cotton were systematically analyzed. A total of 28, 27, 13 and 13 *IMP* genes were identified in *Gossypium hirsutum* (*G. hirsutum*), *Gossypium barbadense* (*G. barbadense*), *Gossypium arboreum* (*G. arboreum*), and *Gossypium raimondii* (*G. raimondii*), respectively. Phylogenetic analysis showed that *IMP* family genes could cluster into 3 clades. Structure analysis of genes showed that *GhIMP* genes from the same subgroup had similar genetic structure and exon number. And most *GhIMP* family members contained hormone-related elements (abscisic acid response element, MeJA response element, gibberellin response element) and stress-related elements (low temperature response element, defense and stress response element, wound response element). After exogenous application of abscisic acid (ABA), some *GhIMP* genes containing ABA response elements positively responded to alkaline stress, indicating that ABA response elements played an important role in response to alkaline stress. qRT-PCR showed that most of *GhIMP* genes responded positively to alkaline stress, and *GhIMP10D* significantly upregulated under alkaline stress, with the highest up-regulated expression level. Virus-induced gene silencing (VIGS) experiment showed that compared with 156 plants, MDA content of pYL156:*GhIMP10D* plants increased significantly, while POD, SOD, chlorophyII and AsA content decreased significantly. Conclusions- This study provides a thorough overview of the *IMP* gene family and presents a new perspective on the evolution of this gene family. In particular, some *IMP* genes may be involved in alkaline stress tolerance regulation, and *GhIMP10D* showed high expression levels in leaves, stems and roots under alkaline stress, and preliminary functional verification of *GhIMP10D* gene suggested that it may regulate tolerance to alkaline stress by regulating the activity of antioxidant enzymes and the content of AsA. This study contributes to the subsequent broader discussion of the structure and alkaline resistance of *IMP* genes in cotton.

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Title: Diversification of plant SUPPRESSOR OF MAX2 1 (SMAX1)-like genes and genome-wide identification and characterization of cotton SMXL gene family.

Author: Bin Ma, Jianbo Zhu & Xianzhong Huang

Imprint: BMC Plant Biology Published: 11 September 2023, volume 23, Article number: 419 (2023)

Abstract: Strigolactones (SLs) are a recently discovered class of plant hormones. SUPPRESSOR OF MAX2 1 (SMAX1)-like proteins, key component of the SL signaling pathway, have been studied extensively for their roles in regulating plant growth and development, such as plant branching. However, systematic identification and functional characterization of SMXL genes in cotton (Gossypium sp.), an important fiber and oil crop, has rarely been conducted. Results- We identified 210 SMXL genes from 21 plant genomes and examined their evolutionary relationships. The structural characteristics of the SMXL genes and their encoded proteins exhibited both consistency and diversity. All plant SMXL proteins possess a conserved Clp-N domain, P-loop NTPase, and EAR motif. We identified 63 SMXL genes in cotton and classified these into four evolutionary branches. Gene expression analysis revealed tissue-specific expression patterns of GhSMXL genes, with some upregulated in response to GR24 treatment. Protein co-expression network analysis showed that GhSMXL6, GhSMXL7-1, and GhSMXL7-2 mainly interact with proteins functioning in growth and development, while virus-induced gene silencing revealed that GhSMAX1-1 and GhSMAX1-2 suppress the growth and development of axillary buds. Conclusions- SMXL gene family members show evolutionary diversification through the green plant lineage. GhSMXL6/7–1/7–2 genes play critical roles in the SL signaling pathway, while GhSMXL1-1 and GhSMXL1-2 function redundantly in growth of axillary buds. Characterization of the cotton SMXL gene family provides new insights into their roles in responding to SL signals and in plant growth and development. Genes identified in this study could be used as the candidate genes for improvement of plant architecture and crop yield.

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Title: Multiplex Cas9-based excision of CLCuV betasatellite and DNA-A revealed reduction of viral load with asymptomatic cotton plants.

Author: Sana Shakoor, Abdul Qayyum Rao, Sara Ajmal, Aneela Yasmeen, Muhammad Azmat Ullah Khan,

Imprint: *Planta* volume 258, Article number: 79 (2023)

Abstract: The notorious cotton leaf curl virus (CLCuV), which is transmitted by the sap-sucking insect whitefly, continuously damages cotton crops. Although the application of various toxins and RNAi has shown some promise, sustained control has not been achieved. Consequently, CRISPR_Cas9 was applied by designing multiplex targets against DNA-A (AC2 and AC3) and betasatellite (βC1) of CLCuV using CRISPR direct and ligating into the destination vector of the plant using gateway ligation method. The successful ligation of targets into the destination vector was confirmed by the amplification of 1049 bp using a primer created from the promoter and target, while restriction digestion using the *AflII* and *Asc1* enzymes determined how compact the plasmid developed and the nucleotide specificity of the plasmid was achieved through Sanger sequencing. PCR confirmed the successful introduction of plasmid into CKC-1 cotton variety. Through Sanger sequencing and correlation with the mRNA expression of DNA-A and betasatellite in genome-edited cotton plants subjected to agroinfiltration of CLCuV infectious clone, the effectiveness of knockout was established. The genome-edited cotton plants demonstrated edited efficacy of 72% for AC2 and AC3 and 90% for the (βC1) through amplicon sequencing, Molecular dynamics (MD) simulations were used to further validate the results. Higher RMSD values for the edited βC1 and AC3 proteins indicated functional loss caused by denaturation. Thus, CRISPR_Cas9 constructs can be rationally designed using high-throughput MD simulation technique. The confidence in using this technology to control plant virus and its vector was determined by the knockout efficiency and the virus inoculation assay.

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Title: 2-NBDG Uptake in *Gossypium hirsutum* in vitro ovules: exploring tissue-specific accumulation and its impact on hexokinase-mediated glycolysis regulation.

Author: Melina Shamshoum, Ofir Aharon Kuperman

Imprint: Front. Plant Sci., 25 September 2023, Sec. Plant Metabolism and Chemodiversity, Volume 14 - 2023 | https://doi.org/10.3389/fpls.2023.1242150

Abstract: Fluorescent glucose derivatives are valuable tools as glucose analogs in plant research to explore metabolic pathways, study enzyme activity, and investigate cellular processes related to glucose metabolism and sugar transport. They allow visualization and tracking of glucose uptake, its utilization, and distribution within plant cells and tissues. This study investigates the phenotypic and metabolic impact of the exogenously fed glucose derivative, 2-(N-(7-nitrobenz-2-oxa-1,3-diazol-4-yl)amino)-2-deoxyglucose) (2-NBDG) on the fibers of Gossypium hirsutum (Upland cotton) ovule in vitro cultures. The presence of 2-NBDG in the culture medium did not lead to macroscopic morphological alterations in ovule and fiber development or to the acquisition of fluorescence or yellow coloration. Confocal laser scanning microscope imaging and chromatographic analysis of cotton ovules' outer rim cross-sections showed that the 2-NBDG is transported from the extracellular space and accumulated inside some outer integument cells, epidermal cells, and fertilized epidermal cells (fibers), but is not incorporated into the cell walls. Untargeted metabolic profiling of the fibers revealed significant changes in the relative levels of metabolites involved in glycolysis and upregulation of alternative energy-related pathways. To provide biochemical and structural evidence for the observed downregulation of glycolysis pathways in the fibers containing 2-NBDG, kinetics analysis and docking simulations were performed on hexokinase from G. hirsutum (GhHxk). Notably, the catalytic activity of heterologously expressed recombinant active GhHxk exhibited a five-fold decrease in reaction rates compared to D-glucose. Furthermore, GhHxk exhibited a linear kinetic behavior in the presence of 2-NBDG instead of the Michaelis-Menten kinetics found for D-glucose. Docking simulations suggested that 2-NBDG interacts with a distinct binding site of GhHxk9, possibly inducing a conformational change. These results highlight the importance of considering fluorescent glucose derivatives as ready-to-use analogs for tracking glucose-related biological processes. However, a direct comparison between their mode of action and its extrapolation into biochemical considerations should go beyond microscopic inspection and include complementary analytical techniques.

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Title: Uncovering genomic and transcriptional variations facilitates utilization of wild resources in cotton disease resistance improvement.

Author: Yihao Zhang, Yaning Zhang, Chenxu Gao, Zhibin Zhang, Yuan Yuan, Xiaolin Zeng

Imprint: Theoretical and Applied Genetics volume 136, Article number: 204 (2023)

Abstract: Upland cotton wild/landraces represent a valuable resource for disease resistance alleles. Genetic differentiation between genotypes, as well as variation in Verticillium wilt (VW) resistance, has been poorly characterized for upland cotton accessions on the domestication spectrum (from wild/landraces to elite lines). Results- To illustrate the effects of modern breeding on VW resistance in upland cotton, 37 wild/landraces were resequenced and phenotyped for VW resistance. Genomic patterns of differentiation were identified between wild/landraces and improved upland cotton, and a significant decline in VW resistance was observed in association with improvement. Four genotypes representing different degrees of improvement were used in a full-length transcriptome analysis to study the genetic basis of VW resistance. ROS signaling was highly conserved at the transcriptional level, likely providing the basis for VW resistance in upland cotton. ASN biosynthesis and HSP90-mediated resistance moderated the response to VW in wild/landraces, and loss of induction activity of these genes resulted in VW susceptibility. The observed genomic differentiation contributed to the loss of induction of some important VW resistance genes such as HSP90.4 and PR16. Conclusions- Besides providing new insights into the evolution of upland cotton VW resistance, this study also identifies important resistance pathways and genes for both fundamental research and cotton breeding.

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Title: Comprehensive non-coding RNA analysis reveals specific lncRNA/circRNA–miRNA–mRNA regulatory networks in the cotton response to drought stress.

Author: Baoqi Li, Cheng Feng, Wenhao Zhang, Simin Sun

Imprint: International Journal of Biological Macromolecules

Volume 253, Part 1, 31 December 2023, 126558

Abstract: Root and leaf are essential organs of plants in sensing and responding to drought stress. However, comparative knowledge of non-coding RNAs (ncRNAs) of root and leaf tissues in the regulation of drought response in cotton is limited. Here, we used deep sequencing data of leaf and root tissues of drought-resistant and drought-sensitive cotton varieties for identifying miRNAs, lncRNAs and circRNAs. A total of 1531 differentially expressed (DE) ncRNAs was identified, including 77 DE miRNAs, 1393 DE lncRNAs and 61 DE circRNAs. The tissue-specific and variety-specific competing endogenous RNA (ceRNA) networks of DE lncRNA-miRNA-mRNA response to drought were constructed. Furthermore, the novel drought-responsive lncRNA 1 (*DRL1*), specifically and differentially expressed in root, was verified to positively affect phenotypes of cotton seedlings under drought stress, competitively binding to miR477b with *GhNAC1* and *GhSCL3*. In addition, we also constructed another ceRNA network consisting of 18 DE circRNAs, 26 DE miRNAs and 368 DE mRNAs. Fourteen circRNA were characterized, and a novel molecular regulatory system of circ125- miR7484b/miR7450b was proposed under drought stress. Our findings revealed the specificity of ncRNA expression in tissue- and variety-specific patterns involved in the response to drought stress, and uncovered novel regulatory pathways and potentially effective molecules in genetic improvement for crop drought resistance.

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Title: GhCKX14 responding to drought stress by modulating antioxi-dative enzyme activity in Gossypium hirsutum compared to CKX family genes.

Author: Tengyu Li, Kun Luo, Chenlei Wang, Lanxin Wu, Jingwen Pan, Mingyang Wang, Jinwei Liu,

Imprint: BMC Plant Biology ed: 02 September 2023, **23**, Article number: 409 (2023)

Abstract: Cytokinin oxidase/dehydrogenase (CKX) plays a vital role in response to abiotic stress through modulating the antioxidant enzyme activities. Nevertheless, the biological function of the CKX gene family has yet to be reported in cotton. Result- In this study, a total of 27 GhCKXs were identified by the genome-wide investigation and distributed across 18 chromosomes. Phylogenetic tree analysis revealed that CKX genes were clustered into four clades, and most gene expansions originated from segmental duplications. The CKXs gene structure and motif analysis displayed remarkably well conserved among the four groups. Moreover, the cis-acting elements related to the abiotic stress, hormones, and light response were identified within the promoter regions of GhCKXs. Transcriptome data and RT-qPCR showed that GhCKX genes demonstrated higher expression levels in various tissues and were involved in cotton's abiotic stress and phytohormone response. The protein-protein interaction network indicates that the CKX family probably participated in redox regulation, including oxidoreduction or ATP levels, to mediate plant growth and development. Functionally identified via virus-induced gene silencing (VIGS) found that the GhCKX14 gene improved drought resistance by modulating the antioxidant-related activitie. Conclusions- In this study, the CKX gene family members were analyzed by bioinformatics, and validates the response of GhCKX gene to various phytohormone treatment and abiotic stresses. Our findings established the foundation of GhCKXs in responding to abiotic stress and GhCKX14 in regulating drought resistance in cotton.

SEED SCIENCE AND TECHNOLOGY

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Title: Exogenous strigolactones enhance salinity tolerance in cotton (*Gossypium hirsutum* L.) seedlings.

Author:Yue Song, Donglin Lv , Meng Jiang , Zhiying E, Yifei Han , Yue Sun , Shuijin Zhu , Jinhong Chen , Tianlun Zhao

Imprint: Plant Stress, Volume 10, December 2023, 100235

Abstract: All around the world, salt stress has severely restricted plant development. Cotton is one of the most important cash crops, but the saline soil negatively influences the quality and output of plants. Strigolactones (SLs) is a new type of phytohormone that plays an important role in the development of plants. However, the underlying mechanism of how SLs alleviate the high salinity stress is unclear in cotton. In this research, we observed that exogenous 10 μM GR24 (a synthetic analog of SLs) significantly alleviated the salt stress (200 mM NaCl) in the hydroponically planted seedlings. Under salt stress, the contents of proline, O_2^- malondialdehyde, and hydrogen peroxide were greatly decreased by 48.40%, 45.57%, 31.03%, and 35.52%. Combined with transcriptome analysis and corresponding verification, it was figured out that with the application of exogenous GR24, the genes encoding antioxidant enzymes, chlorophyll *b*iosynthesis, and photosynthesis system were significantly up-regulated, while the activities of antioxidant enzymes, the content of chlorophyll, and the efficiency of photosynthesis were also significantly improved under salt stress in cotton seedlings. Thus, the exogenous application of SLs could enhance the salt tolerance of cotton seedlings, which displayed its great potential for cotton production in salinized land.

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Title: An alternative approach to conducting germination tests on chemically treated and untreated stored cotton seeds.

Author: Nasma Henriqueta Da Sorte Cossa , Everson Reis Carvalho

Imprint: J. Seed Sci. 45 • 2023 • https://doi.org/10.1590/2317-1545v45266896

Abstract: The objective of this study was to assess the impact of incorporating vermiculite into germination tests for both chemically treated and untreated stored cotton seeds. To that end, two independent experiments were conducted using cotton seeds of the cultivar DP1746B2RF under chemical treatment with a mixture of fungicide, insecticides, and nematicide; and both experiments were set up in a completely randomized design with four replications. In Experiment 1, the objective was to determine the ideal water volume for moistening the vermiculite. Four water volumes were used: 1.5, 2.0, 2.5, and 3.0 times the weight of the dry vermiculite. Experiment 2 was conducted in a 2 × 2 × 2 triple factorial arrangement consisting of two substrates (germitest paper and germitest paper + vermiculite), two treatments (chemically treated seeds and untreated seeds), and two storage periods (0 and 150 days). First germination count and germination were evaluated in the two experiments. From the results found in Experiment 1, the water volume corresponding to 3.0 times the weight of the vermiculite provided the best conditions for germination. In Experiment 2, the most appropriate substrate for conducting the germination test of untreated and chemically treated cotton seeds is vermiculite, which led to rapid germination and uniform seedling development.

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Title: Seed hydropriming to alleviate drought stress in germination of two cotton (*Gossypium hirsutum* L.) varieties.

Author: Atalaèsso BOKOBANA, Nambou GNOFAM, Zovodu Kokou KOFFI

Imprint: Research Square, Posted Date: September 14th, 2023 DOI: https://doi.org/10.21203/rs.3.rs-3328668/v1

Abstract: Drought is a serious threat to the farming community, biasing the crop productivity in arid and semi-arid regions of the world. This study aims to evaluate effect of hydropriming on seed germination of two varieties of cotton, STAM 129A and STAM 190, under drought stress. The seed imbibition kinetics allowed to fix various hydropriming delays (3, 6, 9, 12, 15 and 18 hours). The germination test was conducted in four completely randomized repetitions of 25 seeds for each of the four induced osmotic water stress modalities (0 bar, -3bar, -6 bar, -9 bar), which required the use of

PEG-6000 for adjustment. Calculus of germination percentage (GP), mean germination time (MGT), germination index (GI) and the relative PEG injury rate (RPIR) made it possible to evaluate the germinative behavior of the seeds following the different treatments. Results Drought stress-induced damage to seed germination was significantly reduced by priming seeds for 12 hours for both cotton varieties. Under drought stress (average of values measured at -3 bar, -6 bar and − 9 bar), 12H-hydropriming increased the GP by 206.25% for STAM 190 and 179.26% for STAM 190. Germination, previously nil at -6 bar and − 9 bar for unprimed seeds, becomes possible with priming and better with 12H-hydropriming. Increases of 250.76% and 289.55% of GI for respectively STAM 129A and STAM 190 are noted under drought stress. In general, primed seeds germinated one day earlier than unprimed seeds under normal hydrous conditions. Under drought conditions, however, MGT did not vary significantly from the control, approximately 4.56–4.77 days. Longer priming (18H-hydropriming) had a repressive effect on seed germination with total PEG damage, the few seeds that germinated doing so earlier than all the other treatments, at around 3.83–4.02 days under normal hydrous conditions, and 4.33–4.46 days under drought conditions. RPIR was reduced 35.89% (for STAM 129A) and 27.10% (for STAM 190) with 12H-hydropriming.

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Title: Analysis of Gossypol Content on Roots, Seeds, and Leaves of Cotton Plant (*Gossypium hirsutum* L.) cv. Kanesia 12

Author: Nuraida D, Pujiastutik H,

Imprint: Equijost. Online First: 17 Aug, 2023. https://www.equijost.com/?mno=54325 [Access: August 18, 2023].

Abstract: Plants have long been known to produce secondary metabolites that are useful for medicines, insecticides, etc. Gossypol is one of the secondary metabolites produced by cotton plants (Gossypium hirsutum L.). Gossypol plays a role in self-protection for plants, but it also has the potential a medicine. Gossypol is the main pigment found in lisigen glands scattered in some organs and tissues of cotton plants. The content of gossypol in each part of the cotton plant is different. This study aimed to analyze the content of gossypol compounds in three plant parts of Gossypium hirsutum L cv. Kannesia 12, including seeds, roots, and leaves. Gossypol was extracted using petroleum ether. The levels of gossypol were determined using the High-Performance Liquid Chromatography (HPLC) assay. The results showed all parts of Gossypim hirustum L. cv. Kanesia 12 contained gossypol at different levels. The highest gossypol content was found in the seeds (25.75 µg/g), followed by the roots with 8.00 µg/g, and the least gossypol content in leaves was 1.05 µg/g.

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Title: Genetic progress in seed and fiber quality traits of cotton in Argentina.

Author: Gonzalo J. Scarpin , Pablo N. Dileo , H. Martin Winkler

Imprint: Field Crops Research, Volume 302, 15 October 2023, 109106

Abstract: The Argentinian national cotton (*Gossypium hirsutum* L.) breeding program has demonstrated a 3.24 kg ha^{-1} y^{-1} genetic progress in lint yield from 1965 to date. Although previous studies have examined different trends in cotton lint yield, lint quality parameters, and other agronomic traits of cultivars over time, there have been no investigations in Argentina analyzing the genetic progress in the different components of technological fiber quality, cottonseed oil and protein composition. Objectives: (i) to estimate the genetic progress of the lint and seed quality parameters among cultivars released in Argentina since 1965, (ii) to evaluate the variation of genetic progress for the lint and seed quality parameters under different environmental conditions, and (iii) to determine the correlations between lint quality and lint yield traits. Method: This study was conducted over a two-year period, involving 20 cotton cultivars grown in four different environments (achieved through varying sowing dates) in Reconquista, Santa Fe, Argentina. Several fiber variables were evaluated, including upper half mean length (UHML), strength (Str), uniformity index (UI), micronaire (Mic), short fiber index (SFI), and spinning consistency index (SCI), as well as seed measurements, such as cottonseed oil content (Oil), protein content (Prot), and cottonseed oil fatty acid composition.

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Title: Effect of Different Levels of Organic Matter and Genotypes on Seed Yield and Fiber Quality in Cotton (Gossypium hirsutum L).

Author: Saeed Ahmad , Muhammad Iqbal, Muhammad Akram , Muhammad Rafiq Shahid , Muhammad Shahid , Taj Muhammad , Muhammad Ihsan Ullah , Zunera Saeed and Mazhar Ali

Imprint: Sarhad Journal of Agriculture, 39(3): 665- 671. DOI | https://dx.doi.org/10.17582/journal.sja/2023/39.3.665.67

Abstract : The addition of organic matter improves yield, fiber quality and seed germination of cotton. The present studies were conducted at Cotton Research Station Vehari, Punjab, Pakistan during 2016 to find out the impact of organic matter on growth and yield of cotton. Farm yard manure and green manuring of berseem was done for consecutive four years to improve soil organic matter from initial organic matter of 0.7% and improved to 1.0 % after two years and after repeated use, it improved to 1.5 % during fourth year.