GLEANINGS IN COTTON RESEARCH

AUGUST 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)

INDEX

AGRONOMY, SOIL SCIENCE AND PLANT PHYSIOLOGY

1

Title: Stochastic Modeling for *Gossypium Arboreum* Production in India

Author: T. Jai Sankar and P. Pushpa

Imprint: International Conference on "Computational Statistics & Mathematical Applications" (ICCSMA 2K22) Organized by Department of Statistics Apollo Arts and Science College Chennai (Tamilnadu) India

ABSTRACT: This paper describes an empirical study of stochastic modeling for time series data of Gossypium arboreum (Cotton) productions in India. The Box Jenkins ARIMA methodology has been applied for forecasting. The diagnostic checking has shown that ARIMA (2, 1, and 2) is appropriate. The selected model has to be considered for the forecasts from 2019 to 2023. These forecasts would be useful for the policy makers to take necessary action for the future requirements of suitable measures in this regard. Based on the chosen model, it could be predicted that *G. arboreum* production would increase to 31.63 million tons in 2023 from 28.71 million tons in 2018.

2

Title: Smart Agricultural Genetic Divergence Pattern Estimation of Morphological Traits in Cotton.

Author: Muhammad Arslan, Fatima Javeria, Dua Noor, Ameer Hussain Chang, Zulqarnain Channa, Faisal Nabi

Imprint: VFAST Transactions on Software Engineering http://vfast.org/journals/index.php/VTSE@ 2023, ISSN (e): 2309-3978, ISSN (p): 2411-6246 131 Volume 11, Number 2, April-June 2023 pp: 131-139

Abstract: Cotton (*Gossypium hirsutum* L.), an important agricultural fiber crop belonging to the Malvaceae family, exhibits wide genetic diversity that requires thorough investigation for the development of climate-smart cotton. This study aimed to assess the genetic variation of cotton varieties in relation to yield-related characteristics. A total of fifty genotypes were sown at the Cotton Research Institute (CRI) in Multan using a randomized complete block design (RCBD) with two replications. The row-to-row and plant-to-plant distances were maintained at 75 cm and 23 cm, respectively.

Data were collected for various morphological traits, including plant height (PH), monopodial branches per plant (MO), sympodial branches per plant (SY), number of nodes (NO), boll length (BL), boll width (W), boll weight (BW), total boll weight per plant (TB), and seed cotton yield (SCY). Maximum values were recorded for PH (109.40 cm), MO (8.0500 branches/plant), SY (25.100 branches/plant), NO (41.550 nodes), BL (41.750 mm), W (41.300 mm), BW (3.9500 mg), TB (33.750 g), and SCY (95.400 g). ANOVA results indicated significant differences among all the genotypes. Positive and significant correlations were observed between PH, SCY, and BL, demonstrating the successful utilization of selection criteria based on these traits to improve cotton yields. Cladogenesis studies revealed that class I, II, and III were represented by FH-183, VH-281, and AGC-2, respectively, exhibiting superior genetic potential in terms of morphological traits. Principal component analysis (PCA) demonstrated that 81.88% of the total variance was primarily attributed to traits such as SY, TB, PH, SCY, and BW, with the first five components having eigenvalues greater than 1. These findings provide breeders with valuable insights into selecting desirable characteristics for cotton varieties.

3

Title: Using Some Fertilization Treatments to Reduce the Negative Impact of Calcareous Soils on Productivity of Egyptian Cotton

Author: El-Sayed, Shaimaa, O. and Kattosh, A. A.

Imprint: Menoufia J. Plant Prod., Volume 8 Issue 6 (2023): 105 – 124

Abstract: A field experiment was carried out through the two growing seasons of 2021 and 2022 to find out the impact of the addition of humic acid and sulphur at soil and foliar spraying with chelated Zn and/or chelated B in addition to their interactions on cotton cultivar Super Giza 94 (Gossypium barbadense L.) grown under calcareous soil located at El-Nubaria Station Farm, Agricultural Research Center, Egypt. The layout of the experiment was a split plot design with three replications. The obtained results revealed that humic acid as well as a mixture of chelated Zn and chelated B increased numbers of monopodia and sympodia/plant, plant height at harvest, total fruiting points number/plant and total bolls number set/plant, bolls setting%, seed cotton yield /feddan, yield components and fiber length in both seasons. Bolls shedding% was decreased in this respect. Humic acid alone significantly improved fiber fineness and decreased the 1st sympodium node. Similarly, a mixture of chelated Zn and chelated B significantly increased fiber strength. Using humic acid interacting with a mixture of chelated Zn and chelated B significantly increased numbers of monopodia and total bolls set/plant, yield of seed cotton/feddan, yield components, fiber fineness and strength in the two seasons of study. In addition, it increased bolls setting% and number of sympodia/plant only in the 1st season. However, bolls shedding% was

decreased. Addition of humic acid to the soil interacting with chelated Zn foliar spraying recorded taller plants. It could be concluded that using humic acid interacting with a mixture of chelated Zn and chelated B alleviated and counteracted harmful effects of calcareous soil in El-Nubaria region on cotton productivity of cultivar Super Giza 94.

4

Title: Identification, characterization and expression profiling of salt-stress responsive proteinase inhibitor in *Gossypium arboreum* L.

Author: Muhammad Naveed Shahid , Sarfraz Kiani , Bushra Rashid, Tayyab Husnain

Imprint: South African Journal of Botany, Volume 160, September 2023, Pages 194-200

Abstract: Cotton production in the world is constrained due to various abiotic stresses. Among these, salt-stress plays a key role in declining the cotton yield. The study of genetic makeup in cotton plants for salt-stress responsive factors may open a way to understand the molecular mechanism of the plant against salt-stress. The differentially expressed gene, proteinase inhibitor (gpi) was isolated at the transcript level from salt-tolerant Gossypium arboreum (local cultivar FDH-171) by differential display technique, which was made full-length using gene RACER kit and was characterized through expression profiling under salt, cold and drought stresses, and predicted 3-D structure of gpi protein. The size of full-length gpi was found 496 bps with one intronic region from 74 to 156 bases in sequence. The gpi showed maximum homology with pi of Macleaya cordata 73%, Lactuca sativa 72%, Daucus carota 71%, Corchorus olitorius 70%, Corchorus capsularis 70%, Artemisia annua 70%, Trema orientale 67%, and Ricinus communis 65%. The protein homology search in protein database revealed that gpi has 63% homology with Linum usitatissimum trypsin inhibitor (LUTI). When *gpi* was subjected to predictive secondary structure, sheets, beta turns, coils and helixes were evident but with the most solvent buried area rather than exposed area according to solvent accessibility standards. The expression analysis of gpi in different tissues of salt-stressed G. arboreum plant indicated that gpi has 31-fold higher expression in salt-stressed root tissue, 13-fold in leaf tissue and no expression in stem tissue compared to control; while gpi indicated 13-fold expression under salt, 7-fold in cold and 4-fold in drought stress compared to control. Subsequent analysis showed that *gpi* gene expression was up-regulated and its transcription might enhance salt tolerance in plants. Therefore, *gpi* gene would be helpful to develop salt-stress tolerant cotton plants.

5

Title: Effect of Planting Spaces And Topping Time on Productivity of Cotton Variety Super Giza 97.

Author: El-Sayed, Shaimaa O. and El-Hendawy, Azza A

Imprint: Menoufia J. Plant Prod., Volume 8 Issue 6 (2023): 125 – 149

Abstract: A field experiment was carried out in 2021 season and repeated in 2022 season at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, Egypt to assess the effect of using hill spacing and topping time in addition to their interactions on productivity and quality of cotton cultivar Super Giza 97 (Gossypium barbadense L.). The experimental design was a split-plot with 3 replicates. The main plots were devoted to hill spacing (25, 30 and 35 cm), whereas plant topping time (no topping, manual topping at the formation of 12, 14 and 16 fruiting branches/plant) was allocated in the sub-plots. Data indicated that the widder hill spacing (35 cm) significantly increased total bolls number set/plant and bolls setting%, yield of seed cotton per feddan and its contributory characters as well as fiber length. However, plant height, bolls shedding% and the number of actual plants per feddan at harvest in both seasons were decreased. No topping treatment gave a significant excess in the final plant height and sympodia number/plant in the two seasons of study. Topping when 16 fruiting branches were formed on the plant gave a significant decrease in bolls shedding% and significant increase in numbers of total fruiting points and total bolls set/plant and bolls setting%, yield of seed cotton per feddan and its contributory characters in the two seasons in addition to length in the first season. Sowing cotton at 35 cm between plants interacted with topping cotton plants just after the formation of 16 fruiting branches gave the best results. It could be advised to apply this interaction treatment under Sakha region, to increase cotton productivity of cotton cultivar Super Giza 97.

6

Title: Appraisal on Morphometry, Gas Exchange Characteristics, and Ions Uptake Under Cadmium Stress In Early- And Late-Sown of Cotton.

Author: Sufyan, M., Daraz, U., Iqbal, R., Roy, R.,

Imprint: Applied Ecology and Environmental Research 21(4):2953-2968

Abstract: Cadmium (Cd) is a water-soluble metal pollutant that is not required for plants, but its mobility in the soil-plant continuum has lately attracted substantial interest due to its harmful effects on plants. It may cause serious morphological and physiological abnormalities in addition to inhibiting cotton growth. Thereby, the present study was conducted to explore the effect of different concentrations of Cd on the growth, morphological, biochemical, and physiological processes of cotton (Gossypium hirsutum L.) varieties. Understanding the morphological, biochemical, and physiological responses to Cd stress is necessary for a holistic approach to plant resistance mechanisms to Cd stress. A net house experiment was conducted to investigate the growth and adaptation mechanism of G. hirsutum varieties (V1: KLMNH-142 and V2: KL-FH-886) with different sowing times (i.e., early and late) under Cd stress (250 µM, 500 µM, 750 µM, and 1000 µM). The results showed that Cd predominately accumulated in the root at a higher dose, which consequently led to a reduction in the root biomass. During the late sowing time, transpiration rate (1.01 ± 0.04) and stomatal gas exchange rate (0.01 ± 0.003) were recorded to be significantly decreased by the application of Cd at 1000 µM to variety V2 (KL-MNH886) as compared to the early sowing interval and respective control (1.63 ± 0.06). Calcium contents (1.4 ± 0.5) in the root were decreased in the early sowing period in V1 as compared to the late sowing period. Besides, the application of Cd (1000 µM) has significantly decreased root soluble sugar (0.13 ± 0.001) in V1 under the late sowing period compared with the early sowing period and respective control. Cd not only led to the decrease in root anthocyanin but also changed the chlorophyll content. Our study proved that G. hirsutum has good tolerance to Cd stress during early time intervals as compared to the late time interval and is the best species for soil and ecological environment restoration.

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Title: Cover plants in second crop: nutrients in straw and cotton yield in succession

Author: Alexandre Cunha de Barcellos Ferreira, Ana Luiza Dias Coelho Borin, Fernando Mendes Lamas

Imprint: Pesqui. Agropecu. Trop. 53 • 2023 • https://doi.org/10.1590/1983-40632023v5375032

Abstract: The cultivation of cover plants is a strategy for improving the agricultural production environment and providing straw for soil cover in the no-tillage system, in addition to cycling and providing nutrients to succeeding crops. This study aimed to assess the dry matter yield and nutrients accumulation by cover plants grown alone or intercropped in the second crop after soybean and their effects on cotton grown in succession. The treatments were: *Urochloa ruziziensis; Pennisetum glaucum* (millet); *Zea mays* (corn); *Crotalaria spectabilis; Crotalaria ochroleuca; Cajanus cajan* (pigeon pea); corn + *U. ruziziensis; C. spectabilis* + *U. ruziziensis; C. ochroleuca* + *U. ruziziensis*; pigeon pea + *U. ruziziensis*; corn + *C. spectabilis*; corn + *C. ochroleuca*; and corn + pigeon pea. The experimental design consisted of randomized blocks, with four replications, and the experiment was carried out in two crop seasons. In the cotton pre-seeding, the maximum amount of corn straw dry matter was 2,699 kg ha^{-1}, with low macronutrient contents. The pigeon pea intercropped with *U. ruziziensis* produced between 8,400 and 12,941 kg ha^{-1} of dry matter, with a maximum content of 223 and 323 kg ha^{-1} of nitrogen and potassium, respectively. The *U. ruziziensis*, grown alone or intercropped, provided between 140 and 323 kg ha^{-1} of potassium in the straw. A high yield is obtained by cotton grown in the no-tillage system in succession to *C. spectabilis*.

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Title: Feasibility of Multispectral Observations for Detecting Nitrogen Stress and Yield Potential in Cotton (Gossypium hirsutum L.) through Remote Sensing

Author: A. A. Dongarwar , M. R. Deshmukh, Usha Dongarwar , Hema Pardhi and S. R. Kashiwar

Imprint: International Journal of Plant & Soil Science Volume 35, Issue 16, Page 261-265, 2023

Abstract: The present investigation was conducted during kharif 2019-20 at Department of Agronomy farm, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The experiment was laid out in randomized block design with seven treatments and three replications. Treatments consisted of different nutrient management practices including FYM and nitrogen doses viz., Absolute Control (N1), FYM @ 5 t ha-1 (N2), N2 + 30 kg N ha-1 (N3), N2 + 60 kg N ha-1 (N4), N2 + 90 kg N ha-1 (N5), N2 +120 kg N (N6) and N2 + 150 kg N ha-1 (N7). Cotton crop was sown on 29th June 2019 and was harvested in four pickings. Among various spectral bands, significantly higher positive and negative correlation coefficient values (at 0.05 % level of significance) for plant chlorophyll content were noted with the simple ratio of NIR/G (r 2 =0.829) and G/NIR(r 2 =-0.826), respectively, being most efficient in detecting the nitrogen stress in cotton crop. Yield potential of cotton was established (at 0.05 % level of significance) with negative and positive (both) correlation coefficient of simple ratio of R/NIR (r 2 =-0.815 and r2 =-0.869) and NIR/R (r 2 =0.811and r 2 =0.865) respectively at 180 DAS.

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Title: Profile of cotton flavonoids: Their composition and important roles in development and adaptation to adverse environments.

Author: Lu Long, Xiao-Tong Zhao, Ya-Mei Feng, Zhi-Hao Fan, Jing-Ruo Zhao, Jian-Feng Wu

Imprint: Plant Physiology and Biochemistry, Volume 201, August 2023, 107866

Abstract: Cotton is a commercial crop that is cultivated in more than 50 countries. The production of cotton has severely diminished in recent years owing to adverse environments. Thus, it is a high priority of the cotton industry to produce resistant cultivars to prevent diminished cotton yields and quality. Flavonoids comprise one of the most important groups of phenolic metabolites in plants. However, the advantage and biological roles of flavonoids in cotton have yet not been studied in depth. In this study, we performed a widely targeted metabolic study and identified 190 flavonoids in cotton leaves that span seven different classes with flavones and flavonols as the dominant groups. Furthermore, flavanone-3-hydroxylase was cloned and silenced to knock down flavonoid production. The results show that the inhibition of flavonoid biosynthesis affects the growth and development of cotton and causes semi-dwarfing in cotton seedlings. We also revealed that the flavonoids contribute to cotton defense against ultraviolet radiation and *Verticillium dahliae*. Moreover, we discuss the promising role of flavonoids in cotton development and defense against biotic and abiotic stresses. This study provides valuable information to study the variety and biological functions of flavonoids in cotton and will help to profile the advantages of flavonoids in cotton breeding.

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Title: Collective effects of irrigation and nutrients on agronomic performance of upland cotton (*Gossypium hirsutum* L.)

Author: Muhammad Akbar Zardari, Aijaz Ahmed Soomro, Muhammad Hamayoon Khan, Robina Karim, Azra Nadeem, Nasir Shahzad Memon

Imprint: Pure and Applied Biology Vol 12 No 2, 2023http://dx.doi.org/10.19045/bspab.2023.120139

Abstract: Cotton is regarded as backbone of Pakistan economy; as textile industry entirely dependent on cotton for raw material; while cotton seed is principal source of edible oil production contributing around 80% to the domestically produced total edible oil. In enhancing crop yields and fiber quality, optimum use of NPK fertilizers and irrigation frequency is critical; while interactive effect of these two major factors on cotton is not fully understood. Therefore, this research was conducted to examine the interactive effect of NPK fertilizers and irrigation frequency on cotton growth, development and yield. The NPK treatments included: 124-62-62 kg ha^{-1} (10% beyond recommendation); 112-56-56 kg ha^{-1} (recommended) and 100-50-50 kg ha^{-1} (10% less than recommendation); while tested irrigation frequencies included: 7 irrigations (30, 45, 60, 75, 90, 105, 120 DAS); 6 irrigations (30, 50, 70, 90, 110, 130 DAS [existing recommendation] and 5 irrigations (30, 55, 80, 105, 130 DAS). The interaction study showed that growth and yield contributing traits were optimally influenced in positive

direction under the interactive effect of 124-62-62 kg ha^{-1} NPK × 5 irrigations. The seed cotton yield ha^{-1} was slightly higher (3482 kg) in crop fertilized with 124-62-62 kg ha^{-1} NPK × 7 irrigations as compared to seed cotton yield of 3456.50 and 3448 kg ha^{-1} realized in the interactive effect of NPK at 124-62-62 kg ha^{-1} × 6 irrigations and NPK at 124-62-62 kg ha^{-1} × 5 irrigations; while the least seed cotton yield (2691 kg ha^{-1}) was obtained in treatment interaction of 100-50-50 kg ha^{-1} × 7 irrigations. However, 7, 6 and 5 irrigations regardless of rate of NPK application showed similarity ($P>0.05$) in agronomic performance of cotton; while NPK level of 124-62-62 kg ha^{-1} (10% higher than existing recommendation) showed economically viable results. Hence, the treatment based on interaction of NPK @124-62-62 kg ha^{-1} × 5 irrigations (at 30, 55, 80, 105, 130 DAS) could be practically suggestible for cotton growers, particularly while growing newly evolved variety Sindh-1.

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Title: Synergistic effect of key inputs (irrigation and nutrients) on physiological behaviors and yield of upland cotton (Gossypium hirsutum L.)

Author: Muhammad Akbar Zardari, Aijaz Ahmed Soomro, Nasir Shahzad Memon, Azra Nadeem, Robina Karim

Imprint: Pure and Applied Biology Vol 12 No 2: June-2023http://dx.doi.org/10.19045/bspab.2023.120139

Abstract: In order to determine the synergistic effects of key inputs (Irrigation and nutrients) on physiological behaviors and seed cotton yield of cotton, the experiments were conducted for consecutive two years (2017 and 2018). The data for both the years was pooled and effects were determined from the average data. The existing recommended dose of fertilizers (RDF) 112-56-56 kg ha^{-1} (T_2) was kept as control to investigate the crop response to 10% increase over RDF (T_1=124-62-62 kg ha^{-1}) and 10% decrease over RDF (T_3=100-50-50 kg ha^{-1}). These NPK rates were applied in integration with varied irrigation frequency such as: 7 irrigations (30, 45, 60, 75, 90, 105, 120 DAS); 6 irrigations (30, 50, 70, 90, 110, 130 DAS [existing recommendation] and 5 irrigations (30, 55, 80, 105, 130 DAS). The results showed that seed cotton yield $plant^{-1}$ and its allied traits were significantly ($P<0.05$) affected by the interactive effect of NPK levels and irrigation frequency. The interaction of 124-62-62 kg ha^{-1} NPK × 7 irrigations resulted in slightly higher seed cotton yield $plant^{-1}$ (141.46 g); closely followed by yield of 139.80 g and 139.44 g $plant^{-1}$ achieved in the interactive effect of NPK at 124-62-62 kg ha^{-1} × 6 irrigations and 124-62-62 × 5 irrigations, respectively. Although, treatment interaction 124-62-62 kg ha^{-1} NPK × 7 irrigations had slight edge for seed cotton yield $plant^{-1}$ over rest of the treatment interactions; but statistically the difference amongst 7, 6 or 5 irrigations under 124-62-62 kg ha^{-1} NPK were insignificant ($P>0.05$); suggesting that irrigating crop 7 or 6 times was uneconomical regardless of NPK application. Hence, interaction of NPK @124-62-62 kg ha^{-1} × 5 irrigations would be optimum combination to achieve economical seed cotton, seed and lint yields. However, all the physiological traits showed markedly greater values under the interaction of 124-62-62 kg ha^{-1} NPK × 7 irrigation suggestive of excessive plant growth, swelling foliage, but all these had adverse effect on seed-cotton, seed and lint yield.

CROP PROTECTION

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Title: Cotton Stalk Management and Cover Crop Use on CLRDV Incidence and Soil Properties

Author: Samuel Frazier

Imprint: A thesis submitted to the Graduate Faculty of Auburn University in partial fulfillment of the requirements for the Degree of Master of Science Auburn, Alabama August 5, 2023

Abstract: Cotton leaf roll dwarf virus (CLRDV) was reported in cotton (*Gossypium hirsutum* L.) in Alabama in 2017. CLRDV can now be found as far west as Texas, and as north as Virginia. Due to such wide distribution and potential yield loss, CLRDV has been explored across various disciplines. However, there have been few investigations involving agronomic management. This study recorded CLRDV presence in cotton following various cotton stalk destruction methods with and without a cover crop, as well as the effect on soil properties in 2021-2022. Stalk destruction methods were (1) Destroy, which included two diskings, followed by chisel plowing and a repeat disking for final leveling, (2) mowing (Mow), and (3) mowing followed by pulling (Mow/Pull) with a stalk puller. A mixture of cereal rye (*Secale cereale* L.) and crimson clover (*Trifolium incarnatum* L.) was used for the cover crop treatment. Two cotton varieties were included, DP 2055 B3XF and PHY 400 W3FE. Trial locations were in the Alabama Agricultural Experiment Station System at the E. V. Smith Research Center (EVS), Shorter, AL; Wiregrass Research and Extension Center (WREC), Headland, AL; and Gulf Coast Research and Extension Center (GCREC), Fairhope, AL. Data collection included soil moisture and soil strength values, cover crop biomass, various cotton growth measurements, prebloom aphid presence, CLRDV infection, and cotton lint yield. Soil moisture results show that all values are relatively consistent across stalk management treatments. At all locations in both years, soil moisture values in the 0-6 in depth tended to be higher in cover crop treatments at all locations as expected. Some discrepancies were seen between the two sampling depths but overall no dramatic differences were observed. Area under the curve for cone index (AUCC.I.) was used to represent soil strength across all depths and row positions. In 5 of 6 site years, Destroy treatments resulted in the lowest cone index values. In 2022, elevated soil strength values at WREC were seen across all stalk destruction methods, regardless of cover crop. While there were differences among treatments, cotton stands were adequate at all locations. Greater cover crop biomass was obtained across all locations in 1 2022 (7720 lb/A) as compared to 2021 (5878 lb/A). In regards to locations, cover crop biomass was least at EVS (4102 lb/A) as compared to GCREC (8074 lb/A) and WREC (8216 lb/A). Overall, presence or absence of a cover crop failed to consistently reduce CLRDV incidence or affect yield or fiber quality. Stalk management treatment had no effect on yield in 5 of 6 site years. Fiber quality results showed minimal differences among treatments. CLRDV was confirmed at all locations in both years through PCR testing. August sample results from GCREC in 2021 indicated extremely low virus incidence, and thus, re-sampling for CLRDV and PCR testing was initiated after harvest at all locations in November. From the August to November sampling dates, incidence of CLRDV increased 2 to almost 12-fold, with an average of 309% increase over the 6 site locations. Even though significant main effects and few interactions were observed within the recorded data, results suggest that imposed treatments lacked a consistent effect on CLRDV incidence, cotton yield, or fiber quality. However, it was especially noteworthy that CLRDV sampling dates (August and November), revealed dramatic differences in detectable virus incidence, and the high level of virus present in November indicated prevalence of the virus across the region. More research is needed in order to determine ways to mitigate CLRDV incidence in cotton.

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Title: Comparative Study oF Different ML Algorithms for Cotton Disease Prediction.

Author: Sanika Patankar, Sakshi Hiremath, Sahil Jadhav, Sakshi Deshpande, Prathmesh Deshpande, Gajanan Jadhav

Imprint: International Journal of Current Science Volume 12, Issue 4 December 2022

Abstract: One of the main industries in many nations, including India, is agriculture. Given that the majority of the Indian financial system depends on agricultural production, the issue of production requires close attention. In the Agricultural Industry, the taxonomy and identification of crop infection received significant technological and financial attention. The relevant approach is to create an algorithm that can identify illnesses of cotton leaves. Hence, this work presents a comparison between various ML algorithms to prediction cotton disease. The algorithms included the proposed paper are compared on the basis confusion matrix with parameters such as precession, recall, F1-score, accuracy. According to results VGG 16 is most accurate amongst the algorithms but requires more time.

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Title: Isolation and Characterization of Fusarium Oxysporum F.Sp. Vasinfectum Causative Agent of Cotton Wilt Disease in Punjab, Pakistan.

Author: Rizwan Asif, Saima Muzammil, Riffat Yasmin, Hammad Ahmad, Ana Ambreen

Imprint: Pak. J. Phytopathol., Vol. 35 (01) 2023. 103-110

DOI: 10.33866/phytopathol.035.01.0855

Abstract: Fusarium cotton wilt (FW) is one of the most economically devastating cotton diseases worldwide and the threatening agent of this disease is Fusarium oxysporum f.sp. vasinfectum (FOV). This study aimed to add more information towards the isolation and identification of F. oxysporum f. sp. vasinfectum (FOV), which could probably be responsible for the wilting of their corresponding host, Gossypium hirsutum. Roots samples were collected from plants showing typical symptoms of wilting from three different regions (Kasur, Faisalabad, Multan) of province Punjab, Pakistan. For further analysis, samples were immediately transported to the microbiology laboratory of Government College University Faisalabad, Pakistan (GCUF). After surface sterilization of root, each cut piece (5 mm) of the root was inoculated on Potato Dextrose Agar (PDA) media and incubated at 25°C±2 °C for 7 days. The different obtained co1lonies were identified using the standard microbiological techniques such as macro-morphological, microscopic, and Polymerase Chain Reaction (PCR). The pathogenicity test was also performed in the greenhouse for confirmation of Koch's postulate. This test showed that plants infected with FOV start wilting and yellowing of leaves which confirmed that FOV was linked with cotton wilt and responsible for significant economic loss. Good agricultural practices and proper management of FOV will permit the production of healthy seedlings and subsequently aid in the improvement in cotton yield.

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Title: Enhanced phenylpropanoid metabolism underlies resistance to Fusarium oxysporum vasinfectum f. sp. race 4 infection in the cotton cultivar Pima-S6 (*Gossypium barbadense* L.)

Author: Jonathan Ojeda-Rivera, Mauricio Ulloa, Hector Rogelio Najera-Gonzalez

Imprint: Research Square https://doi.org/10.21203/rs.3.rs-3089030/v1

Abstract: *Fusarium oxysporum* f. sp. vasinfectum (FOV) race 4 (FOV4) is a highly pathogenic soil-borne fungus responsible for Fusarium wilt in cotton (*Gossypium* spp.) and represents a continuing threat to cotton production in the southwest states of the U.S., including California, New Mexico, and Texas. Even though the Pima (G. barbadense L.) cotton gene pool shows more susceptibility to this pathogen than Upland (*G. hirsutum* L.) cotton, fortunately, some Pima cultivars present resistance to FOV4 infection, like Pima-S6. To gain insights into the mechanism underlying FOV4 resistance, we performed comparative transcriptional and metabolomic profiling of FOV4-resistant Pima-S6 and FOV4-susceptible Pima S-7 and Pima 3–79 cotton.

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Title: In vitro evaluation of different bioagents against Corynespora cassiicola causing target leaf spot disease of cotton under South Gujarat of India.

Author: Nirva Patel, Prashant B Sandipan, Nishi Saini, PS Patel and RK Patel

Imprint: The Pharma Innovation Journal 2023; 12(7): 218-221

Abstract: Cotton (*Gossypium hirsutum* L.) is one of the most important fiber crops playing a key role in the economic and social scenario of the globe. India is one of the major cotton growing countries in the world. India ranks first in area and second in the total production of cotton in the world. Cotton is grown worldwide for its natural fiber and oil. Cotton is primarily a raw material for a thriving textile industry and is also one of the most ancient and essential commercial crops, second only to food grains. In the present experiment, five different bioagents were screened in vitro for the growth inhibition of C. cassiicola by dual culture method, which inhibited the growth of pathogen by 65.55 to 80.97 percent. Among the Trichoderma isolates, T. viride followed by T. harzianum showed the most promising results compared to other isolates. The highest growth inhibition of C. cassiicola was recorded by T. viride (80.97%) followed by T. harzianum (76.25%). The least growth inhibition was recorded in T. fasciculatum (65.55%). B. subtilis (67.92%) and P. fluorescens (68.88%) were proved less effective as compared to fungal bioagents.

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Title: Studies on Morphophysiological and Biochemical Parameters for Sucking Pest Tolerance in Organic Cotton

Author: Shradha S. Aherkar, Surendra B. Deshmukh, Nitin. M. Konde
Imprint*: Agriculture* 2023, *13*(7), 1402; https://doi.org/10.3390/agriculture13071402

Abstract: The demand for organic cotton is primarily driven by manufacturers and brands with a corporate focus on environmental and social responsibility. These entities strive to be responsible stewards by seeking organic cotton, which not only offers environmental benefits but also provides softer, more durable, and longer-lasting clothing. Unlike conventional cotton, organic cotton is processed without the use of harsh chemicals, making it more comfortable for individuals with sensitive skin. A study was conducted at the Center of Organic Agriculture Research and Training Center, Department of Agronomy, Dr. PDKV, Akola, Maharashtra, India to evaluate 22 cotton genotypes, including control samples, using a randomized block design with three replications during the kharif (June–October) season in the years 2019–2020 and 2020–2021, under complete organic conditions. During the initial year of the study (2019–2020), visual observations were made to assess the incidence of sucking pests on the cotton genotypes' leaves, including the top, middle, and bottom portions. The observations indicated promising results, leading to a more detailed study in the subsequent year (2020–2021). This extended study identified several tolerant genotypes to sucking pests, such as AV-G11, PA-255, GA-8004, AV-C14, and AV-G13 from the *arboreum* species, as well as AKH-09-5, a *hirsutum* cultivar. Among the recorded data, it was found that the lowest mean aphid population occurred at 90 days after sowing (DAS), with only 1.53 aphids per leaf. Similarly, the lowest mean populations of Cicadellidae, thrips, and whitefly were recorded at 0.75, 0.97, and 0.63 per leaf, respectively, all at 30 DAS. Microscopic analysis of trichome density and gossypol glands revealed a negative and significant correlation with *Aphis gossypi* (aphids), *Cicadellidae* sp. (*Cicadellidae*), and *Thrips tabaci* (thrips). However, a positive and significant correlation was found with *Bemesia tabaci* (whitefly). Furthermore, the estimation of total soluble sugar using the Anthrone method, total nitrogen, and crude protein showed positive and significant correlations with aphids, *Cicadellidae*, and thrips, but negative, significant correlations with whitefly. The findings indicate that higher trichome density provides greater resistance to sucking pest infestation. It was concluded that *G. arboreum* genotypes exhibit greater tolerance to sucking pests compared to *G. hirsutum* varieties. This implies that *G. arboreum* varieties may require less intensive pest management, aligning with organic farming principles. The discovery of these genotypes opens up possibilities for utilizing them as sustainable and pest-resistant options in cotton cultivation, promoting environmentally friendly and organic farming practices in cotton fiber production.

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Title: Categories of resistance in cotton genotypes, Gossypium spp. against cotton-melon aphid, *Aphis gossypii* (Hemiptera: Aphididae)

Author: Pirithiraj Uthirapathy, Murugan Marimuthu, Balasubramani Venkatasamy, Senguttuvan Kannan, N Manikanda Boopathi, Hari Ramakrishnan Selladurai, Premalatha Nallathambi

Imprint: Journal of Economic Entomology, toad136, https://doi.org/10.1093/jee/toad136

Abstract: Cotton-melon aphid, Aphis gossypii Glover (Hemiptera: Aphididae), is emerging as a potential threat to cotton cultivation worldwide. The resistance categories in Gossypium arboreum to A. gossypii still need to be explored. We screened 87 G. arboreum and 20 Gossypium hirsutum genotypes against aphids under natural field conditions. Twenty-six selected genotypes from these 2 species were tested under glasshouse conditions for resistance categories (antixenosis, antibiosis, and tolerance). Resistance categories were assessed by no-choice antibiosis assay, free-choice aphid settling assay, cumulative aphid days using population buildup tests, chlorophyl loss index, and damage ratings. No-choice antibiosis experiment revealed that the G. arboreum genotypes GAM156, PA785, CNA1008, DSV1202, FDX235, AKA2009-6, DAS1032, DHH05-1, GAM532, and GAM216 had a significant adverse effect on aphid development time, longevity, and fecundity. Gossypium arboreum genotypes CISA111 and AKA2008-7 expressed a low level of antixenosis but possessed antibiosis and tolerance. Aphid resistance persisted uniformly at different plant developmental stages studied. The chlorophyl loss percentage and damage rating scores were lower in G. arboreum than in G. hirsutum genotypes, indicating the existence of tolerance in G. arboreum to aphids. Logical relations analysis of resistance contributing factors depicted the presence of antixenosis, antibiosis, and tolerance in the G. arboreum genotypes PA785, CNA1008, DSV1202, and FDX235, indicating their utility for evaluating the mechanisms of resistance and aphid resistance introgression breeding into G. hirsutum to develop commercially cultivated cotton lines.

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Title: Effect of Salt (NACL) Against Wilt Disease of Cotton Caused By Verticillium Dahliae Kleb. Under In Vitro Conditions

Author: Ş. E. Arıcı, O. Erdoğan and Z. N. Tuncel

Imprint: J. Anim. Plant Sci., 33 (5) 2023

Abstract: Verticillium wilt disease causes economic yield losses in cotton growing areas in the world. In addition, an increase in salinity is observed in the soils of our country due to improper agricultural practices. This present study was carried out to find out the efficiency of NaCl with Verticillium dahliae Kleb. for two cotton cultivars following Completely Randomized Design (CRD). In this study, cotton cultivars (Gossypium hirsutum L.) of Nazilli 84 and Gloria were cultured in MS medium (40 ml per all magenta) containing 3 mycelial disc of Verticillium dahliae (0.5 mm) and different NaCL concentrations (0, 25, 50, 100, 150 mM) under in vitro conditions. The lowest disease severity value was found in the cv. Nazilli 84 in 150 mM NaCl + Verticillium dahliae application (48%), and in 100 mm NaCl + Verticillium dahliae application (50%) in cv. Gloria. In control plants, the disease severity was found to be 83% for cv. Nazilli 84 and 62% for cv. Gloria. Different results regarding plant height and leaf count were obtained with NaCl + Verticillium dahliae in cvs. Nazilli 84 and Gloria. Only with salt application, while the tallest plant height was determined to be 3.92 cm for cv. Nazilli 84 at 100 mM NaCl application, cv. Gloria was adversely affected by this application and plant height was measured at 1.83 cm determined. In conclusion, NaCl causes inhibition of V dahliae in both the cultivars of cotton at particular concentration. The analysis of variance for all the parameters (Plant height and number of leaves) were found to be significant at P≤ 0.05. These results show that salinity-tolerant cotton plants can increase their tolerance to V. dahliae infection. V dahliae disease can be suppressed by applying the NaCl concentration in the soil at appropriate doses depending on the cotton cultivars.

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Title: Statistical Analysis for Estimating Resistance of Cotton Lines and Cultivars to Wilt Pathogen Disease

Author: N.N. Khusenov, J.K. Norbekov, U.A. Boykobilov, A.Kh. Makamov, E.E. Khurshut, F.N. Kushanov, Z.T. Buriev

Imprint: Uzbek Biological Journal 2022, No. 4

Abstract: Verticillium wilt disease is the main factor that reduced the economic benefit in the production of cotton cultivation. This research paper is carried out research results that is obtained between 2017-2019. In the study, among cotton cultivars, the resistant cultivars Ravnaq-1, Las_Brenas_347, Mabane_B_1, Tupe_4_AVB5, PD_747, and Hopijones_79_4480 have demonstrated significantly tolerance to Verticillium wilt. For Identifying quantitative trait locus (QTLs) controlling fiber quality and yield-related traits were used for marker-assisted selection (MAS), and (QTLs) controlling fiber quality and yield parameters were introgressed into cultivars and lines, in result of that were obtained 17 combinations. The developed combinations provide a practical basis

for improving Verticillium wilt diseases resistance, cotton yield and fiber quality for molecular marker-assisted selection.

PLANT GENETICS AND BREEDING

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Title: COTTON VARIETY 20R741B3XF
Document Type and Number: United States Patent Application 20230200342
Kind Code: A1
Inventors: Fraser, Dawn E. (Fuquay Varina, NC, US) Jones, Darren G. (Lubbock, TX, US) May, Lloyd O. (Tifton, GA, US)

Abstract: The invention relates to the novel cotton variety designated 20R741B3XF. Provided by the invention are the seeds, plants, plant parts and derivatives of the cotton variety 20R741B3XF. Also provided by the invention are methods of using cotton variety 20R741B3XF and products derived therefrom. Still further provided by the invention are methods for producing cotton plants by crossing the cotton variety 20R741B3XF with itself or another cotton variety and plants and seeds produced by such methods.

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Title: COTTON VARIETY 20R816B3TXF
Document Type and Number: United States Patent Application 20230200343
Kind Code:A1
Inventors: Fraser, Dawn E. (Fuquay Varina, NC, US)Jones, Darren G. (Lubbock, TX, US)May, Lloyd O. (Tifton, GA, US}

Abstract: The invention relates to the novel cotton variety designated 20R816B3TXF. Provided by the invention are the seeds, plants, plant parts and derivatives of the cotton variety 20R816B3TXF. Also provided by the invention are methods of using cotton variety 20R816B3TXF and products derived therefrom. Still further provided by the invention are methods for producing cotton plants by crossing the cotton variety 20R816B3TXF with itself or another cotton variety and plants and seeds produced by such methods.

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Title: COTTON VARIETY 19R325B3TXF
Document Type and Number: United States Patent Application 20230200341
Kind Code: A1
Inventors: Fraser, Dawn E. (Fuquay Varina, NC, US) Jones, Darren G. (Lubbock, TX, US) May, Lloyd O. (Tifton, GA, US)

Abstract: The invention relates to the novel cotton variety designated 19R325B3TXF. Provided by the invention are the seeds, plants, plant parts and derivatives of the cotton variety 19R325B3TXF. Also provided by the invention are methods of using cotton variety 19R325B3TXF and products derived therefrom. Still further provided by the invention are methods for producing cotton plants by crossing the cotton variety 19R325B3TXF with itself or another cotton variety and plants and seeds produced by such methods.

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Title: Genetic diversity analysis in cotton using morphological traits (Gossypium hirsutum L.)
Author: Salve Surekha Bhanudas, Minnu Sasi and Manisha Phaugat
Imprint: The Pharma Innovation Journal 2023; 12(7): 1089-1096

Abstract : A study "Genetic diversity analysis in cotton using morphological traits (G. hirsutum L.)" was undertaken to estimate the degree of divergence among the 50 genotypes of upland cotton using multivariate Mahalanobis D2 statistics on the field of SDMVM's college of agriculture, Paithan road, Aurangabad (MH). The analysis of variance revealed significant differences among 50 genotypes for all fourteen characters. This is also confirmed by Wilk's criterion. The canonical analysis revealed that about 85.96 per cent of the total variation was accounted by the first six canonical roots. In vector I, number of monopodia per plant was important sources of variation. Whereas 2.5 per cent span length was important sources of variation in vector II. In vector III, number of bolls per plant, in vector IV seed index, in vector V, fibre strength and in vector VI, number of bolls per plant played important role in variation. Plant height, seed index and number of bolls per plant were contributing towards genetic divergence. By using Tocher's method, all 50 genotypes were grouped into seven clusters. Cluster I had highest number of genotypes (19) followed by cluster III (14), cluster IV (8), cluster II (6) and cluster V, VI and VII represented by single genotypes. The maximum genetic distance was recorded between cluster V and cluster VII (D=9.66). By considering the mean statistical distance as a guideline to select the divergent genotypes, 18 cluster combinations were identified. The divergent parents selected from these combinations may yield better segregants in hybridization programme. However, when divergent parents are crossed, heterosis is not always found to occur. Therefore, while selecting the divergent parents from a particular cluster, the information on mean and standard deviation of the genetic variance among the divergent parents should be taken into consideration as practically suggested by Arunachalam and Bandyopadhyay (1984). Hence, on the basis of mean and standard deviation of parental divergence, 41 cross combinations out of 192 parental combinations have been finally suggested which are expected to yield desirable genetic gain in breeding programmes.

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Title: Genomic level of Gossypium sp., screening - an eagle's view - a Comprehensive Review

Author: Sumayya Rehaman

Imprint: International Journal of Cotton Research and Technology 2023
https://www.sciplatform.com › index.php › ijcrt

Abstract: Cotton, a prime crop to give tuff competition to the synthetic textile industry specified for the cotton cultivation and major contribution for the fossil fuel and involves itself for bioenergy production was an amazing ancient discovery atleast 7000 years ago has resulted in the genomic level variation research in this century as its evolutionary history. This review article highlights *Gossipium sp.*, evolutionary hitherto from olden days to the varieties level (State and Area wise cultivation) and also helps to differentiate a reader a comprehensive outlook Cotton as Genetically Modified Organism (Cotton Hybrids) , its screening through specific GMO Event and effective screening technology.

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Title: Inheritance of Morpho-Economic Traits And Combining Ability Analysis in Intraspecific Hybrids of *Gossypium Barbadense* L.

Author: N.E. Chorshanbiev, S.M. Nabiev , A.A. Azimov , J.Sh. Shavkiev , E.A. Pardaev , And A.O. Quziboev

Imprint: SABRAO Journal of Breeding and Genetics 55 (3) 640-652, 2023
http://doi.org/10.54910/sabrao2023.55.3.4

Abstract: In intraspecific F1 diallel hybrids of *Gossypium barbadense* L., the inheritance study of traits plant height, boll weight, plant productivity, and 1000-seed weight, with combining ability analysis took place in 2020–2022 at the Institute of Genetics and Plant Experimental Biology, Academy of Sciences, Uzbekistan. These polygenic traits'

inheritance showed different ways in the fine-fiber cotton F1 hybrids. The plant height trait's inheritance with overdominance and intermediate level of the high/low-performance cultivars. The boll weight trait was mainly in negative overdominance with incomplete dominance of the low-performance cultivar. The inheritance of seed cotton yield had the positive overdominance main control, while the 1000-seed weight had negative and positive overdominance. According to combining ability analysis, the highest positive general combining ability effects resulted in fine-fiber cotton cultivars Surkhan-14 (ĝi = 8.71) and Bo'ston (ĝi =1.86) for plant height, Guzor (ĝi = 0.12) for boll weight, in genotypes Marvarid (ĝi = 2.44) and Surkhan-14 (ĝi = 2.95) for plant productivity, and in cultivars Marvarid (ĝi = 2.3) and Guzor (ĝi = 2.8) for 1000-seed weight. The F1 hybrids Guzor × Surkhan-14, Marvarid × Bo'ston, and Bo'ston × Surkhan-14 showed the highest positive and desirable specific combining ability effects for 1000-seed weight and seed cotton yield. Results concluded that fine-fiber cotton cultivars Marvarid, Surkhan-14, and Guzor can benefit as initial breeding material in selecting high-yielding cotton cultivars.

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Title: Assessment of heterotic potential and association analysis in direct and reciprocal hybrids for seed cotton yield and fiber quality traits involving lintless – fuzzless genotypes in upland cotton (Gossypium hirsutum. L)

Author: L. Ananda Lekshmi , M. Kumar2, S. Rajeswari , M. Raveendran , D. Uma and S. Manickam

Imprint: Electronic Journal of Plant Breeding https://doi.org/10.37992/2023.1402.052 Vol 14(2): 410 – 418

Abstract: The present investigation focused on studying heterosis for yield and fibre quality traits among nine parents and their 36 hybrids developed through hybridization between six elite varieties as females and three fuzzless genotypes as pollen parent, along with their reciprocal crosses. Analysis of variance indicated the presence of substantial variability among the experimental materials for yield and fibre quality traits. The study indicated that the direct cross-hybrids generated using elite cultivars as female parents performed better than the reciprocal hybrids. The hybrids CO17 / AKH98-81, CO17 / TCH1646, CO14 / TCH1646 and MCU 5 / AKH 98-81 had recorded significant positive heterosis for a majority of traits including seed cotton yield and fibre quality. An association analysis revealed that seed cotton yield exhibited a positive and highly significant correlation with number of sympodia, number of bolls, boll weight, lint index, ginning out turn and all fibre quality traits. The analysis of the direct effect of various traits on seed cotton yield revealed that the traits like number of bolls, boll weight, number of seeds per boll, ginning out turn, fibre length, fibre strength,

uniformity index, micronaire value and elongation percentage had expressed very high positive direct effects.

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Title: Assembly and phylogenomic analysis of cotton mitochondrial genomes provide insights into the history of cotton evolution

Author :Yanlei Feng , Yukang Wang , Hejun Lu , Jun Li

Imprint: The Crop Journal, Available online 29 June 2023 https://doi.org/10.1016/j.cj.2023.05.004
Abstract: Cotton is a major crop that provides the most important renewable textile fibers in the world. Studies of the taxonomy and evolution of cotton species have received wide attentions, not only due to cotton's economic value but also due to the fact that *Gossypium* is an ideal model system to study the origin, evolution, and cultivation of polyploid species. Previous studies suggested the involvement of mitochondrial genome editing sites and copy number as well as mitochondrial functions in cotton fiber elongation. Whereas, with only a few mitogenomes assembled in the cotton genus *Gossypium*, our knowledge about their roles in cotton evolution and speciation is still scarce. To close this gap, here we assembled 20 mitogenomes from 15 cotton species spanning all the cotton clades (A–G, K, and AD genomes) and 5 cotton relatives using short and long sequencing reads. Systematic analyses uncovered a high level of mitochondrial gene sequence conservation, abundant sequence repeats and many insertions of foreign sequences, as well as extensive structural variations in cotton mitogenomes. The sequence repeats and foreign sequences caused significant mitogenome size inflation in *Gossypium* and its close relative *Kokia* in general, while there is no significant difference between the lint and fuzz cotton mitogenomes in terms of gene content, RNA editing, and gene expression level. Interestingly, we further revealed the specific presence and expression of two novel mitochondrial open reading frames (ORFs) in lint-fiber cotton species. Finally, these structural features and novel ORFs help us gain valuable insights into the history of cotton evolution and polyploidization and the origin of species producing long lint fibers from a mitogenomic perspective.

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Title: Genomic and epigenomic insights into the mechanism of cold response in upland cotton.

Author: Junduo Wang, Yajun Liang, Zhaolong Gong, Juyun Zheng

Imprint: Research Square, DOI: https://doi.org/10.21203/rs.3.rs-3022509/v1

Abstract: Functional genome research, including gene transcriptional and posttranslational modifications of histones, can benefit greatly from a high-quality genome assembly. Histone modification plays a significant role in modulating the responses to abiotic stress in plants. However, there are limited reports on the involvement of dynamic changes in histone modification in cold stress response in cotton. In this study, the genome of an elite accession, YM11, with considerable cold stress resistance was de novo assembled, which yielded a genome of 2343.06 Mb with a contig N50 of 88.96 Mb, and a total of 73,821 protein-coding gene models were annotated. Comparisons among YM11 and five Gossypium allopolyploid cotton assemblies highlighted a large amount of structural variations and presence/absence variations. We analyzed transcriptome and metabolome changes in YM11 seedlings subjected to cold stress. Using the CUT&Tag method, genome-wide H3K3me3 and H3K9ac modification patterns and effect of histone changes on gene expression were profiled during cold stress. Significant and consistently changing histone modifications and the gene expressions were screened, of which transcription factors (TFs) were highlighted. Our results suggest a positive correlation between the changes in H3K4me3, H3K9ac modifications and cold stress-responsive gene activation. This genome assembly and comprehensive analysis of genome-wide histone modifications and gene expression provide insights into the genomic variation and epigenetic responses to cold stress in upland cotton.

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Title: Combining abillity and Heterosis for yield traits in cotton (Gossypium hirsutum .)

Author: R.Muthu, G.Kandasamy, T.S.Raveendran, R.Ravikesavan

Imprint: Madras Agricultural Journal Vol: 92, Issue:jan-mar

DOI:https://doi.org/10.29321/MAJ.10.A00005

Abstract: The ratio between gca and sca variances estimated from 9 lines, 6 testers and their 54 hybrids obtained by line x tester mating design indicated the predominance of non-additive gene action for all the yield traits viz, days to first flowering, plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, seed cotton yield per plant and number of locules per boll. Identification of superior heterotic hybrids is mostly done based on the high per se performance, high sca effect associated with heterotic effect (standard heterosis). The following hybrids viz., TCH 1452 x Halden, MCU 12 x MCU 5, KC 2 x MCU 5, KC 2 x EC 35556, MCU 12 x Hancock and TCH 1452 x Uganda -8-9 were considered as superior and worth studying further.

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Title: Cloning and expression analysis of phosphorus efficient gene *GhMYB*4 in *Gossypium hirsutum* L.

Author: GENG Feifei, MENG Chaomin, QING Guixia, ZHOU Jiamin, ZHANG Fuhou, LIU Fengju

Imprint: Xinjiang Agricultural Sciences ›› 2023, Vol. 60 ›› Issue (6): 1406-1412.DOI: 10.6048/j.issn.1001-4330.2023.06.013

Abstract: To excavate related genes based on the genome-wide expression profile of cotton seedlings under low phosphorus stress in the early stage and conducted analysis of their preliminary expression. This study results will provide a scientific reference for further research into the biological functions of *GhMYB*4 gene and the cultivation of new cotton germplasm with the efficient utilization of phosphorus. Genomic DNA and cDNA sequence of the gene were cloned and analyzed by bioinformatics method. Semi-quantitative RT-PCR and fluorescence quantitative PCR (QRT-PCR) were used to detect the changes of gene expression in root, stem, leaf and flower tissues. The *GhMYB*4 gene was cloned, whose open reading frame length was 774 bp. Altogether 257 amino acids were encoded and analysis revealed that this gene sequence belonged to the MYB family. The results of semi-quantitative RT-PCR and QRT-PCR showed that *GhMYB*4 gene was mainly expressed in root, medium expression in stems and leaf, and trace expression in flower. The *GhMYB*4 gene is preliminarily obtained. The gene has the highest expression level in cotton roots, relatively less expressed in flowers, moderately expressed in stems and leaves.

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Title: Identification of salt stress tolerant candidate genes in the BC2F2 population at the seedling stages of *G. hirsutum* and G. darwinii using NGS-based bulked segregant analysis.

Author: Muhammad Shehzad, Allah Ditta, Xiaoyan Cai

Imprint: Front. Plant Sci., 03 July 2023, Sec. Plant Breeding, Volume 14 - 2023 | https://doi.org/10.3389/fpls.2023.1125805

Abstract: Salinity is a major threat to the yield and productivity of cotton seedlings. In the present study, we developed a BC_2F_2 population of cotton plants from *Gossypium darwinii* (5–7) and *Gossypium hirsutum* (CCRI 12–4) salt-susceptible parents to identify salt-resistant candidate genes. The Illumina HiSeq™ strategy was used with bulked segregant analysis. Salt-resistant and salt-susceptible DNA bulks were pooled by using

30 plants from a BC_2F_2 population. Next-generation sequencing (NGS) technology was used for the sequencing of parents and both bulks. Four significant genomic regions were identified: the first genomic region was located on chromosome 18 (1.86 Mb), the second and third genomic regions were on chromosome 25 (1.06 Mb and 1.94 Mb, respectively), and the fourth was on chromosome 8 (1.41 Mb). The reads of bulk1 and bulk2 were aligned to the *G. darwinii* and *G. hirsutum* genomes, respectively, leading to the identification of 20,664,007 single-nucleotide polymorphisms (SNPs) and insertions/deletions (indels). After the screening, 6,573 polymorphic markers were obtained after filtration of the candidate regions. The SNP indices in resistant and susceptible bulks and Δ(SNP-index) values of resistant and susceptible bulks were measured. Based on the higher Δ(SNP-index) value, six effective polymorphic SNPs were selected in a different chromosome. Six effective SNPs were linked to five candidate genes in four genomic regions. Further validation of these five candidate genes was carried out using reverse transcription-quantitative polymerase chain reaction (RT-qPCR), resulting in an expression profile that showed two highly upregulated genes in the salt-tolerant species *G. darwinii*, i.e., *Gohir.D05G367800* and *Gohir.D12G239100*; however, the opposite was shown in *G. hirsutum*, for which all genes, except one, showed partial expression. The results indicated that *Gohir.D05G367800* and *Gohir.D12G239100* may be salt-tolerant genes. We are confident that this study could be helpful for the cloning, transformation, and development of salt-resistant cotton varieties.

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Title: Evaluation of genetic variability parameters for yield, yield attributes and fibre quality traits in the F2 population of Gossypium hirsutum L.

Author: Keerthivarman Krishnan, Subhashini Selvaraj, Banoth Madhu

Imprint: Environment Conservation Journal. https://doi.org/10.36953/ECJ.16812531

Abstract: The F_2 populations of the crossings CO 14 × NDLH 1938 and CO17 × NDLH 1755 were used to investigate variability and heritability studies in order to better understand the gene action involved in each characteristic studied. Morphological data *viz.,* days to first flowering, plant height (cm), number of sympodials, number of bolls per plant, boll weight (g), ginning outturn (%), upper half mean length (mm), elongation percentage (%) and micronaire value (µg/inch) were all recorded in each plant of both the populations. Studies of heritability and genetic advance as a percent of mean help us determine if a gene is additive or epistatic in nature, and so undergo appropriate breeding programmes for population enhancement. The value of PCV (Phenotypic Coefficient of variation) was always greater than GCV (Genotypic coefficient of variation) indicating the environment also plays a major role in contributing to the variations. The seed cotton yield per plant alone was shown to exhibit additive gene action with high heritability and strong genetic advance as percent of mean, suggesting that it might be used in direct selection since it is the most important attribute for population development.

FIBER AND FIBER TECHNOLOGY

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Title: Genetic diversity among coloured cotton genotypes in relation to their fibre colour and ploidy level based on SSR markers.

Author: Revanasiddayya & Jayaprakash Mohan Nidagundi & Bashasab Fakrudin & Prakash Kuchanur & Lingappa Neelagiri Yogeesh & Shivanand Hanchinal & Talagunda Chandrashekar Suma & Gururaj Sunkad & Bharamappanavar

Imprint: Czech Journal of Genetics and Plant Breeding, Handle: *RePEc:caa:jnlcjg:v:preprint:id:12-2023-cjgpb,* DOI: 10.17221/12/2023-CJGPB

Abstract: Genetic diversity is referred to as any variation at the phenotypic, DNA or genomic level of an individual, population or species. The appraisal of diversity is important to understand its pattern and evolutionary relationships between germplasms or genotypes, which will aid in sampling the genetic resources in a more systematic manner for conservation and crop improvement. The present study employed 50 simple sequence repeat (SSR) markers linked to the yield and fibre quality/colour traits for estimating the genetic diversity in 33 cotton genotypes of diploid and tetraploid species differing in fibre colour. The diversity analysis was performed in GenAlEx (Ver. 6.41) and Powermarker (Ver. 3.25) while DARwin (Ver. 6.0.21) software was used to establish the phylogenetic relationships following neighbour-joining (NJ) and unweighted pair group method with arithmetic (UPGMA) mean method. Markers generated 186 polymorphic loci as genotypic data with an average of 3.72 alleles and an average polymorphic information content (PIC) value of 0.59 per SSR locus. The NJ and UPGMA grouped 33 genotypes into three major clusters I, II and III consisting of 21 tetraploid Gossypium hirsutum, 10 G. arboreum coloured and 2 white cotton genotypes, respectively. In the PCA, the first two components (PC1 and PC2) explained 74.69% of the variation and the biplot plotted the 33 genotypes in three groups. The study established the diverse nature of 33 cotton genotypes based on their fibre colour and ploidy level. With confirmation of the prevalent genetic diversity, we suggest that hybridisation can be planned among diverse genotypes to unleash greater variation in the fibre colour or to derive superior cross combinations.

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Title: Study on interplay of yield-related characteristics and fibre quality traits in arboreum cotton (Gossypium arboreum L.)

Author: B. Sukrutha1, S. Rajeswari, N. Premalatha , NM. Boopathi, K. Thirukumaran and A. Manivannan

Imprint: Electronic Journal of Plant Breeding https://doi.org/10.37992/2023.1402.052 Vol 14(2)633-645

Abstract: The purpose of the study was to examine the genetic variability, heritability and genetic advance as a per cent of mean among the six parents selected through principal component analysis and 30 hybrids of desi cotton. The experiment was laid out in during kharif,2022, at the Department of Cotton, TNAU. Five fibre quality traits and 13 yield contributing traits were analysed as a part of genetic variability investigations. With the exception of the uniformity index, ANOVA demonstrated significance for all of the characteristics examined, suggesting that parents and hybrids have adequate amount of variation. An increased environmental influence on these traits is indicated by the fact that the phenotypic coefficient of variation was marginally greater than the genotypic coefficient of variance. Positive and significant correlation with seed cotton yield per plant was observed for plant height, number of sympodia per plant, number of bolls per plant, boll weight and number of seeds per boll which suggested that increase or improvement in these characters lead to improvement in seed cotton yield/ plant. The traits namely, fibre strength, lint index and number of bolls exerted a high direct effect on seed cotton yield while, boll weight and plant height exerted a moderate positive direct effect on seed cotton yield. The hybrids K12 × RG763 and CNA1007 × RG763 can be used for the better attainment of yield as they have highest boll weight along with seed cotton yield per plant and ginning outturn.

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Title: Strigolactones modulate cotton fiber elongation and secondary cell wall thickening

Author: WEN Yun-ze, HE Peng, BAI Xiao-han, ZHANG Hui-zhi, ZHANG Yun-feng, YU Jia-ning

Imprint: Journal of Integrative Agriculture Received 27 February, 2023 Accepted 14 June, 2023

ABSTRACT: Cotton is one of the most important economic crops in the world and is a major source of fiber in the textile industry. Strigolactones (SLs) are a class of carotenoid-derived plant hormones involved in many processes of plant growth and development; however, SL functions in fiber development remain largely unknown. Here, we found that the endogenous SLs were significantly higher in fibers 20 days post-anthesis (DPA). Exogenous SLs significantly increased fiber length and cell wall thickness. Furthermore, we cloned three key SLS biosynthetic genes, namely GhD27, GhMAX3, and GhMAX4, which were highly expressed in fibers, and subcellular localization analyses revealed that GhD27, GhMAX3, and GhMAX4 were localized in the chloroplast. The exogenous expression of GhD27, GhMAX3, and GhMAX4 complemented the physiological phenotypes of d27, max3, and max4 mutations in Arabidopsis, respectively. Knockdown of GhD27, GhMAX3, and GhMAX4 in cotton resulted in an increased number of axillary buds and leaves, decreased fiber length, and significantly reduced fiber thickness. These findings revealed that SLs participate in plant growth, fiber elongation, and secondary cell wall formation in cotton. These results provide new and effective genetic resources for improving cotton fiber yield and plant architecture.

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Title: Impact of various boron doses applied at different growth stages on fiber quality traits of cotton (Gossypium hirsutum L.)

Author: Hasan Haliloglu, Cemile Ceylan

Imprint: Journal of Elementology, 28(2), 375-392, available: http://dx.doi.org/10.5601/jelem.2023.28.2.2372

Abstract: Cotton (Gossypium hirsutum L.) requires boron (B), which plays a crucial role in the development of fruiting branches and bolls, in the pollination, boll retention and fiber quality of this plant. However, B is mostly unavailable during flower development and pollination stages; therefore, it must be supplied in order to harvest higher yield and high-quality fiber. This study investigated the impact of different B doses (applied at various growth stages) on some of the fiber quality traits of cotton crop. Four B doses (i.e., 0, 1000, 2000 and 3000 ml ha-1) were applied at three growth stages (i.e., square initiation, flower initiation and peak flowering). The cotton genotype 'Stoneville-468', widely cultivated in the study region, was submitted to this experiment. Data relating to fiber uniformity, fiber strength, fiber fineness, fiber maturity, uniformity index, short fiber index, fiber elongation, reflectance, and yellowness were recorded. The results revealed that the application of 2000 ml ha-1 B at the square initiation stage resulted in the highest fiber length and uniformity. Similarly, higher B application during peak flowering resulted in the finest fiber. The increase in B application doses decreased fiber strength, negatively affected short fiber index, and had a non-significant effect on fiber maturity. The application of 1000 ml ha-1 B at flowering initiation resulted in the highest uniformity index. Similarly, the application of 2000 ml ha-1 B at flowering initiation resulted in the highest reflectance value. Likewise, the B application resulted in the lower yellowness values compared to the control treatment of the study. It is concluded that B should be applied to cotton grown on B-deficit soils. However, fiber quality traits are differently affected by B doses and application timing. Therefore, B application dose and timing should be decided according to the desired fiber traits.

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Title: Characterization of chromatin accessibility and gene expression reveal the key genes involved in cotton fiber elongation

Author: Guoquan Chen , Zhao Liu, Shengdong Li, Le Liu , Lili Lu, Zhi Wang

Imprint: Physiologia Plantarum 2023 Jul 5.doi: 10.1111/ppl.13972.

Abstract: Cotton (Gossypium hirsutum L.) is an important economic crop, and cotton fiber is one of the longest plant cells, which provides an ideal model for the study of cell elongation and secondary cell wall synthesis. Cotton fiber length is regulated by a variety of transcription factors (TF) and their target genes; however, the mechanism of fiber elongation mediated by transcriptional regulatory networks is still unclear to a large extent. Here, we used a comparative assay for transposase-accessible chromatin with high-throughput sequencing (ATAC-seq) assay and RNA-seq analysis to identify fiber elongation transcription factors and genes using the short-fiber mutant ligon linless-2 (Li_2) and wild type (WT). A total of 499 differential target genes were identified and GO analysis shows that differential genes are mainly involved in plant secondary wall synthesis and microtubule-binding processes. Analysis of the genomic regions preferentially accessible (Peak) has identified a number of overrepresented TF-binding motifs, highlighting sets of TFs that are important for cotton fiber development. Using ATAC-seq and RNA-seq data, we have constructed a functional regulatory network of each TF regulatory target gene and also the network pattern of TF regulating differential target genes. Further, to obtain the genes related to fiber length, the differential target genes were combined with FLGWAS data to identify the genes highly related to fiber length. Our work provides new insights into cotton fiber elongation.

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Title: Analysis of transgenic cotton plants containing Universal Stress Protein (GaUSP-1, GaUSP-2) and Zinc Finger Transcriptional Factor (GaZnF) genes under drought stress.
Author: Muhammad Hamza Basit, Zoha Masood, Kausar Basit, Samia Afzal

Imprint: Critical Reviews™ in Eukaryotic Gene Expression
DOI: 10.1615/CritRevEukaryotGeneExpr.2023048905

Abstract: Water is the most limiting factor for plant growth and crop productivity. Drought stress adversely affects crop yield throughout the world. Up to 50 per cent of crop yield in Pakistan is severely affected by the shortage of water. Cotton is an important cash crop for Pakistan known as "white gold". It accounts for 8.2 per cent of the value added in agriculture and about 3.2 per cent of GDP. Besides, being the world's fourth-largest cotton producer, our yield per acre ranks 13th in the world. If we look at the Pakistan scenario, water deficiency is one of the major yield-limiting factors. Limitations related to conventional breeding and the advancements in plant genomics and biotechnology applications have opened new horizons to plant improvements. Therefore, in the current study, we carry out a comparative analysis to evaluate the morphological, physiological biochemical and molecular parameters in transgenic plants containing GaUSP-1, GaUSP-2 and GaZinc Finger genes under different drought stress conditions. Data showed that transgenic plants showed more tolerance as compared to non-transgenic plants. Transgenic and non-transgenic assist us in our better understanding of the drought-responsive mechanism and its effect on different plant growth traits, so, in this way, we would be able to explore drought tolerance mechanism and this will open the doors for the identification of drought-related genes.

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Title: Transcriptome Analysis of Interaction between *Gossypium barbadense* and *Fusarium oxysporum* f. sp. *Vasinfectum*

Author: YANG Yang), ZHU Jin-cheng, LOU Hui, HAN Ze-gang), ZHANG Wei

Imprint: Biotechnology Bulletin 2023, Vol. 39 Issue (6): 259-273.doi: 10.13560/j.cnki.biotech.bull.1985.2022-1316

Abstract: Cotton Fusarium wilt is a common disease in cotton production, especially very seriously in island cotton（*Gossypium barbadense*）, affecting its yield and quality, which pose a great threat to the development of island cotton industry. To understand the molecular mechanism of the interaction between cotton and *Fusarium oxysporum*, RNA-seq sequencing technology was applied to analyze the gene expression characteristics of the interaction between *Fusarium oxysporum* and cotton using the resistant and susceptible cotton root tissues and pathogenic bodies infected by *Fusarium oxysporum* for 48 h as materials. The results showed that 15 218 and 9 358 differentially expressed genes were detected in resistant and susceptible cotton varieties respectively, 3 708 and 3 656 differentially expressed genes were identified in *Fusarium oxysporum* after infecting the resistant and susceptible cotton varieties. Through GO enrichment analysis, we found that the main processes in cotton after interaction were oxidative stress, auxin-activated signaling pathway, response to stimulus, response to injury and transcription factor activity. KEGG pathways were significantly enriched in endocytosis, plant hormone signal transduction, amino acid biosynthesis, carbon metabolism, plant-pathogen interactions, phenylpropane biosynthesis and other metabolic pathways. Disease-resistant cultivars were significantly up-regulated in responses to stimulation and injury. In the *Fusarium oxysporum* after interaction, GO enrichment analysis found that differentially expressed genes were mostly involved in membrane components, catalytic activity regulation, ATP binding etc. KEGG was significantly enriched in peroxisome, mitogen-activated protein kinase signaling pathways, valine, leucine and L-Isoleucine degradation, glycine, serine and threonine metabolism, carbon metabolism, amino acid biosynthesis, starch and sucrose metabolism and other metabolic pathways. This study provids an abundant gene resources for studying the responses of cotton to Fusarium wilt and the pathogenicity of *F. oxysporum*, and laid a foundation for an in-depth analysis of the mechanism of interaction between *Fusarium oxysporum* and cotton.

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Title: Salicylic acid-functionalized chitosan nanoparticles restore impaired sucrose metabolism in the developing anther of cotton (Gossypium hirsutum L.) under heat stress.

Author: Khyati Savani, Harsukh Gajera , Darshna Hirpara, Disha Savaliya, U. Kandoliya

Imprint: Functional Plant Biology FP22309 Accepted 15 July 2023 CSIRO 2023

Abstract: Nanotechnology provides tremendous potential in agriculture mitigating climate change impact and improving abiotic stress management strategy. The chitosan nanoparticles (NCS) were synthesized using the ion gelation method and characterized for size (75.5nm in PSA), shape (spherical under SEM), and stability (132.2mv as ZETA).

Further, salicylic acid was incorporated into NCS to craft salicylic acid functionalized chitosan nanoparticles (SA-NCS) and illustrated for size (517nm), shape (spherical), and stability (197.1mv). The influence of the exogenous application of SA-NCS (0.08%) was studied at the reproductive stage of cotton (three genotypes: heat tolerant Solar-651 BGII; moderately tolerant Solar-701 BGII; susceptible Solar-805 BGII) exposed to different temperature regimes (H1: optimal-32/20 ± 2℃; H2: sub-optimal-38/24± 2℃; H3: supra-optimal-45/30± 2℃). Heat stress significantly reduces carbon-fixing RUBISCO, enzymes related to sucrose metabolism and pollen tube length. Considering three genotypes and reproductive stages (sepal and anther tissues), activities of RUBISCO (sepals), invertase (sepals), SPS (anthers), sucrose content (sepals), and pollen tube length were elevated under high-temperature regimes, signifying better source to sink transposition of sucrose influenced by SA-NCS. The study provides new insights into SA-NCS to improve source-sink imbalance and restore sucrose metabolism for better growth of reproductive structure under heat stress in cotton.

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Title: A Truncated ETHYLENE INSENSITIVE3/EIN3-Like protein, GhLYI, Regulates Senescence in Cotton.

Author: Yayao Zhang, Yihao Zang, Jinwen Chen, Shouli Feng, Zhiyuan Zhang, Yan Hu, Tianzhen Zhang

Imprint: Plant Physiology, kiad395, https://doi.org/10.1093/plphys/kiad395

Abstract: Numerous endogenous and environmental signals regulate the intricate and highly orchestrated process of plant senescence. Ethylene (ET), which accumulates as senescence progresses, is a major promoter of leaf senescence.The master transcription activator ETHYLENE INSENSITIVE3 (EIN3) activates the expression of a wide range of downstream genes during leaf senescence. Here, we found that a unique EIN3-LIKE 1 (EIL1) gene, Cotton LINT YIELD INCREASING (GhLYI), encodes a truncated EIN3 protein in upland cotton (Gossypium hirsutum L.) that functions as an ET signal response factor and a positive regulator of senescence. Ectopic expression or overexpression of GhLYI accelerated leaf senescence in both Arabidopsis (Arabidopsis thaliana) and cotton. Cleavage under targets and tagmentation (CUT&Tag) analyses revealed SENESCENCE-ASSOCIATED GENE 20 (SAG20) was a target of GhLYI. Electrophoretic mobility shift assay (EMSA), yeast one-hybrid (Y1H), and dual-luciferase transient expression assay confirmed that GhLYI directly bound the promoter of SAG20 to activate its expression. Transcriptome analysis revealed that transcript levels of a series of senescence related genes, SAG12, NAC LIKE, ACTIVATED by APETALA 3/PISTILLATA (NAP/ANAC029), and WRKY53, are substantially induced in GhLYI overexpression plants compared with wild-type plants. VIGS(Virus-induced gene silencing) preliminarily confirmed that knockdown of GhSAG20 delayed leaf senescence. Collectively, our findings provide a regulatory module involving GhLYI-GhSAG20 in controlling senescence in cotton.

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Title: Genome-wide association study reveals novel SNPs and genes in Gossypium hirsutum underlying Aphis gossypii resistance

Author: Jun Yang, Huimin Zhang, Haonan Chen, Zhengwen Sun, Huifeng Ke, Guoning Wang, Chengsheng Meng,Liqiang Wu, Yan Zhang, Xingfen Wang & Zhiying Ma

Imprint: Theoretical and Applied Genetics volume 136, Article number: 171 (2023)

Abstract: Aphis gossypii is an economically important sap-feeding pest and is widely distributed in the world's cotton-producing regions. Identification of cotton genotypes and developing cultivars with improved A. gossypii resistance (AGR) is essential and desirable for sustainable agriculture. In the present study, A. gossypii was offered no choice but to propagate on 200 Gossypium hirsutum accessions. A relative aphid reproduction index (RARI) was used to evaluate the AGR, which showed large variability in cotton accessions and was classified into 6 grades. A significantly positive correlation was found between AGR and Verticillium wilt resistance. A total of 176 SNPs significantly associated with the RARI were identified using GWAS. Of these, 21 SNPs could be repeatedly detected in three replicates. Cleaved amplified polymorphic sequence, a restriction digestion-based genotyping assay, was developed using SNP1 with the highest observed $-\log_{10}$(P-value). Four genes within the 650 kb region of SNP1 were further identified, including GhRem (remorin-like), GhLAF1 (long after far-red light 1), GhCFIm25 (pre-mRNA cleavage factor Im 25 kDa subunit) and GhPMEI (plant invertase/pectin methylesterase inhibitor superfamily protein). The aphid infection could induce their expression and showed a significant difference between resistant and susceptible cotton varieties. Silencing of GhRem, GhLAF1 or GhCFIm25 could significantly increase aphid reproduction on cotton seedlings. Silencing of GhRem significantly reduced callose deposition, which is reasonably believed to be the cause for the higher AGR. Our results provide insights into understanding the genetic regulation of AGR in cotton and suggest candidate germplasms, SNPs and genes for developing cultivars with improved AGR.

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Title: GoSTR, a negative modulator of stem trichome formation in cotton.

Author: Biyu Xu, Jun Zhang, Yue Shi , Fan Dai , Tao Jiang

Imprint: Plant J, . 2023 Jul 5., doi: 10.1111/tpj.16379.

Abstract: Trichomes, the outward projection of plant epidermal tissue, provide an effective defense against stress and insect pests. Although numerous genes have been identified to be involved in trichome development, the molecular mechanism for trichome cell fate determination is not well enunciated. Here, we reported GoSTR functions as a master repressor for stem trichome formation, which was isolated by map-based cloning based on a large F_2 segregating population derived from a cross between TM-1 (pubescent stem) and J220 (smooth stem). Sequence alignment revealed a critical G-to-T point mutation in GoSTR's coding region that converted codon 2 from GCA (Alanine) to TCA (Serine). This mutation occurred between the majority of Gossypium hirsutum with pubescent stem (GG-haplotype) and G. barbadense with glabrous stem (TT-haplotype). Silencing of GoSTR in J220 and Hai7124 via virus-induced gene silencing resulted in the pubescent stems but no visible change in leaf trichomes, suggesting stem trichomes and leaf trichomes are genetically distinct. Yeast two-hybrid assay and luciferase complementation imaging assay showed GoSTR interacts with GoHD1 and GoHOX3, two key regulators of trichome development. Comparative transcriptomic analysis further indicated that many transcription factors such as GhMYB109, GhTTG1, and GhMYC1/GhDEL65 which function as positive regulators of trichomes were significantly upregulated in the stem from the GoSTR-silencing plant. Taken together, these results indicate that GoSTR functions as an essential negative modulator of stem trichomes and its transcripts will greatly repress trichome cell differentiation and growth. Plant epidermal hair initiation and differentiation research.

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Title: Identification of Shaker Potassium Channel Family Members in Gossypium hirsutum L. and Characterization of GhKAT1aD.

Author; Qianqian Wang, Shuying Li, Fangjun Li, Xiaoli Tian

Imprint: Life 2023, 13(7), 1461; https://doi.org/10.3390/life13071461

Abstract: K^+ channels of the Shaker family have been shown to play crucial roles in K^+ uptake and transport. Cotton (Gossypium hirsutum) is an important cash crop. In this study, the 24 Shaker family genes were identified in cotton. Phylogenetic analysis

suggests that they were assigned to five clusters. Additionally, their chromosomal location, conserved motifs and gene structure were analyzed. The promoter of cotton Shaker K^+ channel genes comprises drought-, low-temperature-, phytohormone-response elements, etc. As indicated by qRT-PCR (quantitative real-time PCR), cotton Shaker K^+ channel genes responded to low K^+ and NaCl, and especially dehydration stress, at the transcript level. Moreover, one of the Shaker K^+ channel genes, GhKAT1aD, was characterized. This gene is localized in the plasma membrane and is predicted to contain six transmembrane segments. It restored the growth of the yeast mutant strain defective in K^+ uptake, and silencing GhKAT1a via VIGS (virus-induced gene silencing) resulted in more severe symptoms of K^+ deficiency in cotton leaves as well as a lower net K^+ uptake rate. The results of this study showed the overall picture of the cotton Shaker K^+ channel family regarding bioinformatics as well as the function of one of its members, which provide clues for future investigations of cotton K^+ transport and molecular insights for breeding K^+-efficient cotton varieties.

SEED SCIENCE AND TECHNOLOGY

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Title: Increasing root-lower improves drought tolerance in cotton cultivars at the seedling stage.

Author: GUO Cong-cong, SUN Hong-chun, BAO Xiao-yuan, ZHU Ling-xiao

Imprint: Journal of Integrative Agriculture Received 17 April, 2023 Accepted 12 June, 2023

Abstract: Drought is an important abiotic stress factor in cotton production. The root system architecture (RSA) of cotton shows high plasticity in alleviating drought-related stress under drought stress (DS); however, this alleviation is cultivar dependent. Therefore, this study aimed to estimate the genetic variability of RSA in cotton under DS. Using the paper-based growth system, we assessed the RSA variability in 80 cotton cultivars at the seedling stage, with 0 and 10% polyethylene glycol 6000 (PEG6000) as the control and the DS treatment, respectively. Analysis of 23 above-ground and root traits in the 80 cotton cultivars revealed different responses to DS. On the 10th day after DS treatment, the variation degree of RSA traits under DS (5-55%) was greater than that of the control (5-49%). The 80 cultivars were divided into drought-tolerant cultivars (group 1), intermediate drought-tolerant cultivars (group 2), and drought-sensitive cultivars (group 3) based on the comprehensive evaluation value of drought resistance.

Under DS, the root length-lower, root area-lower, root volume-lower, and root length density-lower were significantly reduced by 63, 71, 76, and 4% in the drought-sensitive cultivars compared to the control. Notably, the drought-tolerant cultivars maintained their root length-lower, root area-lower, root volume-lower, and root length density–lower. Compared to the control, the root diameter (0-2 mm)-lower increased by 21% in group 1 but decreased by 3 and 64% in groups 2 and 3, respectively, under DS. Additionally, the drought-tolerant cultivars displayed a plastic response under DS, characterized by an increase in the root-lower. Drought resistance was positively correlated with the root area-lower and root length density-lower. Overall, the RSA of the different cotton cultivars greatly varied under DS. Therefore, important root traits, such as the root-lower, provide great insights for exploring whether drought resistant cotton cultivars can effectively withstand adverse environments.