



# GLEANINGS IN COTTON RESEARCH

## JUNE 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](mailto:cicrlib@yahoo.co.in).*

*Swati Dixit  
Incharge Library*

*Chetali Rodge  
Technical Officer (T5)*

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1

**Title:** Application of artificial intelligence technologies to select the optimal cotton crop root scheme.

**Author:** D. T. Muhamediyeva, M. Rahmonova, M. E. Shaazizova

**Imprint:** Proceedings Volume 12637, International Conference on Digital Transformation: Informatics, Economics, and Education (DTIEE2023); 1263712 (2023) <https://doi.org/10.1117/12.2680673> Event: International Conference on Digital Transformation: Informatics, Economics, and Education (DTIEE2023), 2023, Fergana, Uzbekistan

**Abstract:** The optimal organization of the territory of crop rotation fields and arrays allows you to choose the optimal scheme of cotton crop rotation. An analysis of the current level of development of crop rotations in the object under study showed that the agrotechnical foundations of cotton crop rotations have been studied quite fully, and specific recommendations have been developed for individual soil conditions of the region. At the same time, the organizational and economic substantiation of crop rotations has been little studied, taking into account the production and economic conditions of individual farms. This is especially true for the choice of crop rotation system, crop rotation and assessment of the yield of crop rotation fields, as well as linking the placement plan and crop rotation. Implementation allows you to determine in which field a particular crop should be sown. To solve this problem, a genetic algorithm is used. A computational experiment was carried out.

2

**Title:** An Analysis of Cost And Production Function Of Energy Utilisation Of Cotton Cultivation In Thoothukudi District.

**Author:** S. Valarmathi , S. Henry Pandian

**Imprint:** IJFANS International Journal of Food and Nutritional Sciences DOI: 10.48047/ijfans/v11/i11/194

**Abstract:** In this study cost and returns structure of irrigated and un-irrigated farmers, producing cotton are framed. For this purpose the collected data have been analysed for cost and returns structure including various cost components cost function, production

function, input output structure. The Regression model was estimated by the method of least squares for irrigated, un-irrigated and overall farmers cultivating cotton cost separately. There is a positive relationship between the total cost of cotton cultivation and various factor costs. The multiple regression model was estimated by the method of least square. It is found that the independent variables in the regression model are jointly responsible for 93.70 per cent (R<sup>2</sup>) variations in the total cost of cotton cultivation irrigated farmers in the study area. The independent variable human labour is positively related to the total cost of irrigated cotton cultivation in the study area. It means that an additional unit made in this variable may lead to the increase of 1.213 per cent with the total cost in cotton cultivation. It is inferred from the analysis that the variable total cost of irrigated cotton cultivation has a greater influence on the human labour in irrigated area cultivation. The F value (705.510) shows that the model fitted is statistically significant at 5 per cent level. In the case of un-irrigated farmers R<sup>2</sup> value indicated that about 94.10 per cent of variations in the total cost. It was also found that the human labour and fertilizer had a greater influence on the determination of cost of cotton cultivation. The impact of the variable, yield per acre was found to be higher in the case of un-irrigated farmer. Thus it may be concluded from the analysis of cultivation of cotton, cultivation of land and yield of cotton was found to be significant variables in the case of irrigated and un-irrigated farmers and total cost found to be significant in overall farmers. Total cost is considered as an important variable for overall farmers.

### 3

Title: Management of Nitrogen Stress in Cotton (*Gossypium Hirsutum* L.) using GreenSeeker Technology

Author: Medine KARATAS and Emine KARADEMIR

Imprint: Journal of Applied Life Sciences and Environment 2022, 55 (4), 441-456.  
<https://doi.org/10.46909/alse-554075>

ABSTRACT: This study was performed with GreenSeeker technology in order to determine the possibility of nitrogen stress management in cotton and to determine the differences between the normalized difference vegetative index (NDVI) and nitrogen doses determined with GreenSeeker, to determine the nitrogen deficiency and stress conditions by making use of the value of the NDVI in cotton production and to intervene when necessary and direct the producers in this regard. In the study six nitrogen doses (Control, 60, 120, 180, 240 and 300 kg ha<sup>-1</sup>) were used. The results showed significant differences between N applications for leaf chlorophyll content (SPAD), NDVI-2 (in the boll formation period), number of bolls (NB), seed cotton (SCY) and fiber yield (FY). On the other hand, there were non-significant differences in terms of (LA) area, NDVI-1 (in the beginning of the flowering), plant height (PH), node

number of first fruiting branches (NNFFB), number of monopodial branches (NMB) and number of sympodial branches (NSB), number of nodes (NN) height to node ratio (HNR), seed cotton boll weight (SCBW) and ginning percentage (GP). The highest SCY and FY obtained were from doses of 180 and 120 kg ha<sup>-1</sup> N, the highest leaf chlorophyll content and number of bolls obtained were from doses of 120 kg ha<sup>-1</sup> N. The highest values of NDVI-2 obtained were from doses of 120, 240 and 300 kg ha<sup>-1</sup> N, respectively. There were nonsignificant differences between N doses for values of the NDVI-1 of flowering, but significant differences observed for values of NDVI-2 of boll formation periods. The findings obtained from this research indicated that leaf chlorophyll and NDVI of the boll formation period can be used for determining differences due to varying N doses in cotton production.

## 4

**Title:** Assessment of Salt Stress Resistance of Cotton Varieties Based On Different Parameters

**Author:** Shader Alizade , Ruhangiz Mammadova

**Imprint:** Advances in Biology & Earth Sciences Vol.8, No.1, 2023, pp.58-66

**Abstract:** Salinity is one of the serious threats to cotton growth and productivity. The presence of a wide genetic variability of genotypes in germplasm may be an advantage in the creation of salt-resistant varieties in future breeding programs. In this study were analyzed the resistance to salt (NaCl) stress of 48 genotypes belonging to the species *G. hirsutum* L. and *G. barbedense* L., as well as chromosome substitution lines. The effect of different concentrations of NaCl on different parameters of 48 cotton genotypes were evaluated and cluster analysis was performed. The correlation between the concentration of salt and the value of different parameters were studied and the lowest germination rate for all genotypes was observed at 200 mM NaCl. There were found a negative correlation between salt concentration and FGP, CVG, GRI, GI and a positive correlation with MGT. According to results of analysis genotypes Navai-9, Karabakh-11, Agdash-3, Flash, AP-317, Kyrgyzstan-174, Karabakh-12, Tashkent-2 and chromosome substitution lines CSB-11, CSB-14, CSB-05, CSB-17 had the highest germination index and showed high resistance to salt stress.

## 5

**Title:** Potassium Application Alleviated Negative Effects of Soil Waterlogging Stress on Photosynthesis and Dry Biomass in Cotton.

**Author:** Li Huang, Jinxiang Li, Pan Yang, Xianghua Zeng, Yinyi Chen and Haimiao Wan

**Imprint:** Agronomy 2023, 13(4), 1157; <https://doi.org/10.3390/agronomy13041157>

**Abstract:** Soil waterlogging is one of the most serious abiotic stresses on plant growth and crop productivity. In this study, two potassium application levels (0 and 150 kg K<sub>2</sub>O hm<sup>-2</sup>) with three types of soil waterlogging treatments (0 d, 3 d and 6 d) were established during cotton flowering and boll-forming stages. The results showed that soil waterlogging markedly reduced RWC (relative water content), gas exchange parameters and cotton biomass. However, potassium application considerably improved the aforementioned parameters. Specifically, 3 d soil waterlogging with potassium increased Pn (net photosynthetic rate), Gs (stomatal conductance), Ci (intercellular CO<sub>2</sub> concentration) and Tr (transpiration rate) by 4.55%, 27.27%, 5.74% and 3.82%, respectively, compared with 3 d soil waterlogging under no potassium, while the abscission rate reduced by 2.96%. Additionally, the number of bolls and fruit nodes under 6 d soil waterlogging with potassium increased by 16.17% and 4.38%, compared with 6 d soil waterlogging under no potassium. Therefore, it was concluded that regardless of 3 d or 6 d soil waterlogging, potassium application alleviated the negative effects of waterlogging by regulating the plant water status, photosynthetic capacity and plant growth in cotton. These results are expected to provide theoretical references and practical applications for cotton production to mitigate the damage of soil waterlogging.

## 6

**Title:** Stability analysis of Indian cotton exports using Markov Chain analysis

**Author:** Vinay Kumar, SK Goyal, Nirmal Kumar, Amita Girdhar and Manoj Kumar

**Imprint:** The Pharma Innovation Journal 2023; 12(4): 852-854

**Abstract:** The study was conducted on the cotton exports of India using Markov Chain analysis technique. The cotton export data from 2011-12 to 2020-21 was used for the research study. Top major cotton importing countries like- China, Bangladesh, Indonesia, Thailand, Turkey and Korea were selected and total of the cotton imports of rest of the countries was labelled as "Others". The trade directions of Indian cotton exports were analysed using the Markov Chain analysis approach. Transitional probability matrix was formed to know the share of export to each country. The results



revealed China as the most stable market as it retained majority of its cotton imports from India followed by Bangladesh.

## 7

**Title:** Economic Analysis and Resource Use Efficiency of Cotton Production in Haryana

**Author:** Vinay Kumar , S. K. Goyal , Suman Ghalawat, Joginder Singh Malik , Ekta and Arjoo

**Imprint:** Indian Journal of Extension Education Vol. 59, No. 2 (April–June), 2023, (51-54)

**Abstract:** The study was conducted on the economic analysis of cotton crop and its returns in two districts viz. Sirsa and Hisar of Haryana selected purposely having the highest area. The collected data was used to calculate the cost and returns and resource use efficiency of cotton crop in Haryana. The cost benefit ratio for the study area came out as 1:1.22, 1:1.04 and 1:1.13 Sirsa, Hisar and overall, respectively. The findings concluded that resource use efficiency of the cotton farms is showing decreasing returns to scale in both Sirsa (0.419) and Hisar (0.413) districts, which means that there is no scope for improvement in the yield of cotton and there is over-utilization of the resources for the cotton cultivation in Haryana.

## 8

**Title:** Salicylic Acid Application Improves Photosynthetic Performance and Biochemical Responses to Mitigate Saline Stress in Cotton

**Author:** Sanjida Sultana Keya, Mohammad Golam Mostofa, Md. Mezanur Rahman, Ashim Kumar Das, Sharmin Sultana, Protik Kumar Ghosh, Touhidur Rahman Anik, S. M. Ahsan, Md. Abiar ahman, Nusrat Jahan & Lam-Son Phan Tran

**Imprint:** Journal of Plant Growth Regulation (2023)

**Abstract:** Cotton (*Gossypium* spp.) is a crucial industrial crop, particularly grown for fiber; however, its growth, development, and yield are substantially restricted by high salt stress. Salicylic acid (SA) is a crucial phytohormone, exhibiting a multifarious array of roles in the enhancement of plant growth, progression, and resilience to stress. In the current investigation, we provided persuasive evidence on the potential roles of exogenous SA in promoting salinity tolerance in cotton plants by investigating various morphological, biochemical, and physiological features. Our results showed that pre-application of SA to the root zones of cotton plants led to a substantial enhancement of plant biomass, individual leaf area, net photosynthetic rate, stomatal conductance, transpiration rate, water-use-efficiency, and chlorophyll, carotenoid and relative water

contents in leaves, resulting in better growth performance of cotton under salt stress. SA pretreatment further diminished the salinity-induced accumulation of hydrogen peroxide, and the elevated levels of electrolyte leakage and malondialdehyde in the leaves of cotton plants. The SA-pretreated cotton plants experienced reduced oxidative burden because of improved antioxidant defense systems, as manifested by the enhanced activities of catalase, ascorbate peroxidase, peroxidase, and the levels of total flavonoids. Furthermore, the pretreatment with SA resulted in a remarkable elevation in the levels of total free amino acids and total soluble sugars in salt-stressed plants, indicating that SA utilized these compounds for optimal osmotic regulation in the plant tissues amidst adverse saline conditions. Importantly, the pretreatment with SA resulted in a substantial inhibition of  $\text{Na}^+$  uptake and a remarkable increase in the uptake of  $\text{K}^+$ ,  $\text{Mg}^{2+}$ , and  $\text{Ca}^{2+}$  in both roots and leaves of cotton plants. Together, our findings suggest that SA pretreatment could be an effective strategy to increase the resiliency of cotton plants toward salinity, thereby enabling better performance of cotton plants in saline prone areas.

## 9

**Title:** Growth rates of Bt cotton (*Gossypium hirsutum* L.) hybrid NHH-44 as influenced by tillage and integrated nutrient management practices under rainfed conditions.

**Author:** YB Madagoudra, WN Narkhede, Thombre SV and Mane SG

**Imprint:** The Pharma Innovation Journal 2023; 12(3): 5741-5746

**Abstract:** A field experiment was conducted to evaluate the effect of tillage and integrated nutrient management practices on Bt cotton (*Gossypium hirsutum* L.) at AICRP on Dryland Agriculture farm, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani during kharif 2020-21. Fifteen treatment combinations consisting of three tillage practices (conventional tillage, reduced tillage and zero tillage) and five integrated nutrient management practices (100% RDF (120:60:60 kg NPK ha<sup>-1</sup>), 100% RDF + cotton residue @ 3 t ha<sup>-1</sup> + DM @ 12 kg ha<sup>-1</sup>, 75% RDF + FYM 6 t ha<sup>-1</sup> + cotton residue @ 3 t ha<sup>-1</sup> + DM @ 12 kg ha<sup>-1</sup>, 50% RDF + FYM 12 t ha<sup>-1</sup> + cotton residue @ 3 t ha<sup>-1</sup> + DM @ 12 kg ha<sup>-1</sup> and Control) were evaluated in split plot design with three replications. The mean maximum AGR for plant height and dry matter were recorded under conventional tillage. Among different growth intervals 61-90 DAS recorded maximum AGR for plant height (1.397 cm day<sup>-1</sup> plant<sup>-1</sup>), while mean maximum AGR for dry matter (3.393 g day<sup>-1</sup> plant<sup>-1</sup>) were recorded between 91-120 DAS under conventional tillage. Among integrated nutrient management practices, 100% RDF + cotton residue @ 3 t ha<sup>-1</sup> + DM @ 12 kg ha<sup>-1</sup> recorded mean maximum AGR for plant height (1.455 cm day<sup>-1</sup> plant<sup>-1</sup>) 61-90 DAS interval, while mean maximum AGR for dry matter (3.359 g day<sup>-1</sup> plant<sup>-1</sup>) were recorded between 91-120 DAS. The mean CGR, RGR, NAR and LAI were also maximum under conventional tillage and 100% RDF + cotton residue @ 3 t ha<sup>-1</sup> + DM @ 12 kg ha<sup>-1</sup>.

**Title:** GhMYB44 enhances stomatal closure to confer drought stress tolerance in cotton and Arabidopsis

**Author:** Bailin Duan, Xiaofang Xie,

**Imprint:** Plant Physiology and Biochemistry, Volume 198, May 2023, 107692

**Abstract:** MYB genes play crucial roles in plant response to abiotic stress. However, the function of MYB genes in cotton during abiotic stress is less well elucidated. Here, we found an R2R3-type MYB gene, *GhMYB44*, was induced by simulated drought (PEG6000) and ABA in three cotton varieties. After drought stress, the *GhMYB44*-silenced plants showed substantial changes at the physiological level, including significantly increased malondialdehyde content and decreased SOD activity. Silencing the *GhMYB44* gene increased stomatal aperture and water loss rate, reduced plant drought tolerance. Transgenic *Arabidopsis thaliana* over-expressed *GhMYB44* (*GhMYB44*-OE) enhanced resistance to mannitol-simulated osmotic stress. The stomatal aperture of the *GhMYB44*-OE *Arabidopsis* was significantly smaller than those of the wild type (WT), and the *GhMYB44*-OE *Arabidopsis* increased tolerance to drought stress. Transgenic *Arabidopsis* had higher germination rate under ABA treatment compared to WT, and the transcript levels of *AtABI1*, *AtPP2CA* and *AtHAB1* were suppressed in *GhMYB44*-OE plants, indicating a potential role of *GhMYB44* in the ABA signal pathway. These results showed that *GhMYB44* acts as a positive regulator in plant response to drought stress, potentially useful for engineering drought-tolerant cotton.

### 11

**Title:** Study on the Incidence of Sucking Pests and Pink Bollworm in Cotton

**Author:** N. Rajasekhar a, P. Venkata Subbaiah a , P. N. Siva Prasad a , M. Raja Narasimha a and I. Venkata Reddy

**Imprint:** Journal of Experimental Agriculture International Volume 45, Issue 7, Page 18-25, 2023; A

**Abstract:** Sucking pests and pink bollworm are serious pest of cotton one after the other in India by causing serious yield loss. The present investigation was carried out in three major cotton growing mandals of NTR district to understand the level of pest incidence in Bt cotton during Kharif, 2022- 23 on regular interval. Among the sucking pests only thrips population recorded 32.26 no/3 leaves and crossed the ETL at 45 DAS. Remaining sucking pests such as Leafhopper, whitefly and aphid did not cross ETL during crop growth period and highest incidence of 5.92, 4.04 and 27.14 no/3 leaves was recorded respectively at 45, 60 and 120 DAS. Whereas pink bollworm recorded 23.10% rosette flowers, 44.04% boll damage in Bheemavaram village of Vastavai mandal and 40.83% locule damage in Konakanchi village of Penuganchiprolu mandal.

### 12

**Title:** Comparative genomics identifies conserved and variable TAL effectors in African strains of the cotton pathogen *Xanthomonas citri* pv. *malvacearum*

**Author:** Alvaro L. Perez-Quintero, Luis M. Rodriguez-R, Sara Cuesta-Morrondo, Eliška Hakalová, Daniela Betancurt-Anzola

**Imprint:** Published Online:20 Apr 2023<https://doi.org/10.1094/PHYTO-12-22-0477-SC>

**Abstract:** Strains of *Xanthomonas citri* pv. *malvacearum* cause bacterial blight of cotton, a potentially serious threat to cotton production worldwide, including in sub-Saharan countries. Development of disease symptoms, such as water soaking, has been linked to the activity of a class of type 3 effectors, called TAL (transcription activator-like) effectors, which induce susceptibility genes in the host's cells. To gain further insight into the global diversity of the pathogen, to elucidate their repertoires of TAL effector genes and to better understand the evolution of these genes in the cotton-pathogenic xanthomonads, we sequenced the genomes of three African strains of *X. citri* pv.

malvacearum using nanopore technology. We show that the cotton-pathogenic pathovar of *X. citri* is a monophyletic lineage containing at least three distinct genetic subclades, which appear to be mirrored by their repertoires of TAL effectors. We observed an atypical level of TAL effector gene pseudogenization, which might be related to resistance genes that are deployed to control the disease. Our work thus contributes to a better understanding of the conservation and importance of TAL effectors in the interaction with the host plant, which can inform strategies for improving resistance against bacterial blight in cotton.

### 13

**Title:** The outbreak of cotton whitefly *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae) and its management in North India

**Author:** Tenguri Prabhulinga, Gawande Shailesh P., Kumar Rishi

**Imprint:** Journal of Entomological Research, Year : 2023, Volume : 47, Issue : 1  
[10.5958/0974-4576.2023.00004.X](https://doi.org/10.5958/0974-4576.2023.00004.X)

### 14

**Title:** Gene *B<sub>5</sub>* in Cotton Confers High and Broad Resistance to Bacterial Blight and Conditions High Amounts of Sesquiterpenoid Phytoalexins

**Author:** Margaret Essenberg, Kenneth L. McNally, Melanie B. Bayles, Margaret L. Pierce, Judy A. Hall, Christine R. Kuss

**Imprint:** Published Online:14 Apr 2023<https://doi.org/10.1094/PHYTO-08-22-0310-FI>

**Abstract:** Bacterial blight resistance gene *B<sub>5</sub>* has received little attention since it was first described in 1950. A near-isogenic line (NIL) of *Gossypium hirsutum* cotton, *AcB<sub>5</sub>*, was generated in an otherwise bacterial-blight-susceptible ‘Acala 44’ background. The introgressed locus *B<sub>5</sub>* in *AcB<sub>5</sub>* conferred strong and broad-spectrum resistance to bacterial blight. Segregation patterns of test crosses under Oklahoma field conditions indicated that *AcB<sub>5</sub>* is likely homozygous for resistance at two loci with partial dominance gene action. In controlled-environment conditions, two of the four copies of *B<sub>5</sub>* were required for effective resistance. Contrary to expectations of gene-for-gene theory, *AcB<sub>5</sub>* conferred high resistance toward isogenic strains of *Xanthomonas citri* subsp. *malvacearum* carrying cloned avirulence genes *avrB4*, *avrb7*, *avrBIn*, *avrB101*, and *avrB102*, respectively, and weaker resistance toward the strain carrying cloned *avrb6*. The hypothesis that each *B* gene, in the absence of a polygenic complex, triggers sesquiterpenoid phytoalexin production was tested by measurement of cadalene and lacinilene phytoalexins during resistant responses in five NILs carrying different *B* genes, four other lines carrying multiple resistance genes, as well as

susceptible Ac44E. Phytoalexin production was an obvious, but variable, response in all nine resistant lines. AcB<sub>5</sub> accumulated an order of magnitude more of all four phytoalexins than any of the other resistant NILs. Its total levels were comparable to those detected in OK1.2, a highly resistant line that possesses several *B* genes in a polygenic background.

## 15

**Title:** Cotton peroxisome-localized lysophospholipase counteracts the toxic effects of *Verticillium dahliae* NLP1 and confers wilt resistance

**Author:** Guilin Wang, Xinyu Wang, Jian Song, Haitang Wang, Chaofeng Ruan, Wenshu Zhang, Zhan Guo, Weixi Li, Wangzhen Guo

**Imprint:** Plant Journal First published: 07 April 2023, <https://doi.org/10.1111/tpj.16236>

**Abstract:** Plasma membrane represents a critical battleground between plants and attacking microbes. Necrosis-and-ethylene-inducing peptide 1 (Nep1)-like proteins (NLPs), cytolytic toxins produced by some bacterial, fungal and oomycete species, are able to target on lipid membranes by binding eudicot plant-specific sphingolipids (glycosylinositol phosphorylceramide) and form transient small pores, causing membrane leakage and subsequent cell death. NLP-producing phytopathogens are a big threat to agriculture worldwide. However, whether there are R proteins/enzymes that counteract the toxicity of NLPs in plants remains largely unknown. Here we show that cotton produces a peroxisome-localized enzyme lysophospholipase, GhLPL2. Upon *Verticillium dahliae* attack, GhLPL2 accumulates on the membrane and binds to *V. dahliae* secreted NLP, VdNLP1, to block its contribution to virulence. A higher level of lysophospholipase in cells is required to neutralize VdNLP1 toxicity and induce immunity-related genes expression, meanwhile maintaining normal growth of cotton plants, revealing the role of GhLPL2 protein in balancing resistance to *V. dahliae* and growth. Intriguingly, *GhLPL2* silencing cotton plants also display high resistance to *V. dahliae*, but show severe dwarfing phenotype and developmental defects, suggesting *GhLPL2* is an essential gene in cotton. *GhLPL2* silencing results in lysophosphatidylinositol over-accumulation and decreased glycometabolism, leading to a lack of carbon sources required for plants and pathogens to survive. Furthermore, lysophospholipases from several other crops also interact with VdNLP1, implying that blocking NLP virulence by lysophospholipase may be a common strategy in plants. Our work demonstrates that overexpressing lysophospholipase encoding genes have great potential for breeding crops with high resistance against NLP-producing microbial pathogens.

## 16

**Title:** Self-assembled thiophanate-methyl/star polycation complex prevents plant cell-wall penetration and fungal carbon utilization during cotton infection by *Verticillium dahliae*

**Author:** Xiaofeng Su , Shuo Yan , Weisong Zhao , Haiyang Liu , Qinrong Jiang , Ying Wei , Huiming Guo , Meizhen Yin, Jie Shen , Hongmei Cheng

**Imprint:** International Journal of Biological Macromolecules, Volume 239, 1 June 2023, 124354

**Abstract:** No effective fungicides are available for the management of *Verticillium dahliae*, which causes vascular wilt disease. In this study, a star polycation (SPc)-based nanodelivery system was used for the first time to develop a thiophanate-methyl (TM) nanoagent for the management of *V. dahliae*. SPc spontaneously assembled with TM through hydrogen bonding and Van der Waals forces to decrease the particle size of TM from 834 to 86 nm. Compared to TM alone, the SPc-loaded TM further reduced the colony diameter of *V. dahliae* to 1.12 and 0.64 cm, and the spore number to  $1.13 \times 10^8$  and  $0.72 \times 10^8$  cfu/mL at the concentrations of 3.77 and 4.71 mg/L, respectively. The TM nanoagents disturbed the expression of various crucial genes in *V. dahliae*, and contributed to preventing plant cell-wall degradation and carbon utilization by *V. dahliae*, which mainly impaired the infective interaction between pathogens and plants. TM nanoagents remarkably decreased the plant disease index and the fungal biomass in the root compared to TM alone, and its control efficacy was the best (61.20 %) among the various formulations tested in the field. Furthermore, SPc showed negligible acute toxicity toward cotton seeds. To the best of our knowledge, this study is the first to design a self-assembled nanofungicide that efficiently inhibits *V. dahliae* growth and protects cotton from the destructive *Verticillium* wilt.

## 17

**Title:** Evaluation of Different Doses of Diafenthiuron 47.8 Sc against Sucking Pests of Cotton

**Author:** R. K. Kalyan, Deepika Kalyan

**Imprint:** Environment and Ecology 41 (1B) : 371 – 376, January-March 2023

**Abstract:** The present experiments were conducted to evaluate the bio efficacy of different doses of Diafenthiuron 47.8 SC as foliar application against sucking pests of cotton crop along with standard checks i.e. Diafenthiuron 50% WP @ 600g, Imidacloprid 17.8 % SL @ 125 ml, Acetamiprid 20 % SP@ 100 g ha<sup>-1</sup> at Agricultural Research Station-

Borwat Farm, Banswara (Rajasthan) during kharif 2017 and 2018. Among the different treatments, the maximum per cent reduction of 86.05 and 82.33 and 86.83 and 81.06 was recorded in Diafenthiuron 47.8 SC @ 300 g a.i. ha<sup>-1</sup> at 10 days after second spray against whiteflies and jassids during 2017 and 2018, respectively and it was statistically at par with its lower dose i.e. Diafenthiuron 47.8 SC @ 250 g a.i. ha<sup>-1</sup>. Diafenthiuron 50 WP @ 300g a.i. ha<sup>-1</sup> was found to be the next best treatment. There were no symptoms of phytotoxicity observed on spraying the crop with higher dose of the chemical.

## 18

**Title:** Genomic Analyses of Bacterial Blight Resistance, Fiber Quality Traits and Introgression of Thrips Resistance in Upland Cotton

**Author:** Navin Shrestha

**Imprint:** A dissertation submitted to the Graduate Faculty of North Carolina State University in partial fulfillment of the requirements for the degree of Doctor of Philosophy

**Abstract:** Cotton (*Gossypium* spp.) is a globally important economic crop and a major source of natural fiber, oil, and protein. Upland cotton is prized for its lint but its production is impacted by the complicated relationship between fiber quality and yield. It is also threatened by various biotic factors such as cotton bacterial blight (CBB) caused by *Xanthomonas citri* subspecies *malvacearum* (Xcm) and insect pests like thrips (*Frankliniella* spp.). To study the genetic basis of fiber quality, yield and plant height traits, as well as resistance to Xcm and thrips, a series of genetic analyses were performed. To analyze the quantitative trait loci (QTL) responsible for fiber quality, yield and plant height traits, an F5:6 and F6:7 recombinant inbred line (RIL) population of 110 individuals, obtained through intraspecific *G. hirsutum* crosses (NC05AZ06 x NC11-2100) was phenotyped for fiber quality, yield and plant height traits, and genotyped with Cotton 63K single nucleotide polymorphism (CottonSNP63K) array. We developed high-density linkage maps and identified 30 QTL on 15 different chromosomes, 14 of which were major QTL and three were major stable QTL. Candidate gene analysis of the major stable QTL of micronaire and fiber elongation and the plant height with the highest phenotypic variance explained (20.02% PVE) revealed five putative genes linked to fiber quality and yield traits and one to plant height trait.



**Title:** Cotton leafroll dwarf disease: An enigmatic viral disease in cotton.

**Author:** Surendra R. Edula, Sudeep Bag, Hayley Milner, Manish Kumar, Nelson D. Suassuna, Peng W. Chee, Robert C. Kemerait, Lavesta C. Hand, John L. Snider, Rajagovindrababu Srinivasan, Phillip M. Roberts

**Imprint:** Mol Plant Pathol. 2023;24:513–526. DOI: 10.1111/mpp.13335

**Abstract:** Cotton (*Gossypium hirsutum*) is a major cash crop in many parts of the world, including the United States. In 2021, 4.1 million hectares of cotton were harvested in the United States, valued at approximately \$7.4 billion (USDA, 2021). Cotton blue disease (CBD) is a viral disease capable of causing significant losses in the cotton industry. CBD was first described in the Central African Republic in 1949 and has since then been reported from several regions in Africa, Asia, and the Americas (Cauquil, 1977). However, the nature of the causal agent of CBD was not known until 2005, when the entire capsid gene and a partial RNA-dependent RNA polymerase gene revealed its association with a virus belonging to the genus Polerovirus, family Luteoviridae, and named it cotton leafroll dwarf virus (CLRVD) (Corrêa et al., 2005). Distéfano et al. (2010) sequenced the complete genome of a CLRVD isolate from Argentina. Recently, ICTV reclassified CLRVD as a member of the family Solemoviridae (Sõmera et al., 2021). In 2006, a less aggressive resistance-breaking genotype of CLRVD was observed in Brazil on cotton varieties known to be resistant against CBD. This new disease was referred to as “atypical” CBD (Agrofoglio et al., 2017; da Silva et al., 2015). In the United States, CLRVD was first reported in Alabama from cotton in 2019. Plants infected with CLRVD showed symptoms including intense dark green to bluish foliage, reddening of stems and petioles, curling and drooping of leaves, internodal shortening, and moderate to severe stunting. The genome sequences from Alabama and Georgia isolates were characterized. The isolates present in the United States differ from those causing CBD in South America and other regions. The disease caused by CLRVD in the United States is hence referred to as cotton leafroll dwarf disease (CLRDD; Brown et al., 2019). It has been observed that cotton plants infected in younger stages could suffer complete yield loss, whereas the losses decrease when plants are infected at the mature stages of plant development (Parkash et al., 2021). Although the incidence of the virus in some commercial cotton fields in Georgia and Alabama is 80%–100%, no significant yield losses have been reported (Mahas et al.,

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**Title:** Crossability Relationship between Wild Cotton *G. anomalum* and *G. aridum* with Upland Cotton (*G. hirsutum*)

**Author:** Debadatta Panda , M. Kumar , L. Mahalingam , M. Ravendran , S. Manickam , K. Senguttuvan

**Imprint:** Agricultural Science Digest. doi: 10.18805/ag.D-5736.

**Abstract:** Utilizing two wild cotton species, *Gossypium anomalum* [Wawra and Peyritsch ( $2n=2x=26$ ) B1 ] and *Gossypium aridum* [Skovsted ( $2n=2x=26$ ) D4 ], extensive wide hybridization event carried out with upland cotton to assess the feasibility and ease of delivering genetic variation responsible for resistance to various stresses. Methods: The crossing was carried out using the wild species and the cultivate varieties of upland cotton in 2021-2022 at TNAU, Coimbatore. Total of 12 crosses were attempted and the various aspect regarding the feasibility success of different crosses was studied. Result: In contrast to their reciprocals, viable offspring were generated in the direct crosses with tetraploid parents employed as seed parents with both wild species. A huge bulk of bolls dropped during the first seven days of pollination and no matured boll set was observed in reciprocals. Most *G. anomalum* hybrids produce F1 offspring with thick and long leaf hairs which help the plant attain resistance against sucking pests. Through successive backcrosses or chromosome duplication, such genetic material potentially can be utilized furthermore in plant breeding to provide new beneficial resistance traits apart from other significant and relevant features.

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**Title:** Exploring the genetic diversity and population structure of upland cotton germplasm by iPBS-retrotransposons markers .

**Author:** Nurettin Baran, Flavien Shimira, Muhammad Azhar nadeem, Muhammad Tanveer altaf, Mehtap andirman, Faheem Shehzad Baloch, Mefhar Gültekin Temi

**Imprint:** Molecular Biology Reports <https://doi.org/10.1007/s11033-023-08399-0>

**Abstract:** Upland cotton is one of the utmost significant strategic fiber crops, and play a vital role in the global textile industry. Methods and results A total of 128 genotypes comprised *Gossypium hirsutum* L, *Gossypium barbadense* L., and pure lines were used to examine genetic diversity using iPBS-retrotransposon markers system. Eleven highly polymorphic primers yielded 287 bands and 99.65% polymorphism was recorded. The mean polymorphism information content was estimated at 0.297 and the average diversity indices for the effective number of alleles, Shannon's information index, and overall gene diversity were 1.481, 0.443, and 0.265, respectively. The analysis of molecular variance (AMOVA) revealed that 69% of the genetic variation was within the population. A model-based STRUCTURE algorithm divided the entire germplasm into four populations and one un-classified population, the genotypes G42 (originating in Egypt) and G128 (originating in the United States), showed the highest genetic distance (0.996) so these genotypes could be suggested for breeding programs as parental lines. Conclusions This is the first investigation using an iPBS-retrotransposon marker system to examine the genetic diversity and population structure of upland cotton germplasm. The rich diversity found in upland cotton germplasm could be exploited as a genetic resource when developing breeding programs and could also help with efforts to breed cotton around the world. These findings also show the applicability and effectiveness of iPBS-retrotransposons for the molecular characterization of cotton germplasm.

## 22

**Title:** Cloning and functional analysis of GhDFR1, a key gene of flavonoid synthesis pathway in naturally colored cotton.

**Author:** Hongli Zheng, Junye Jiao, Qingqing Niu, Ning Zhu, Yinshuai Huang, Liping Ke, Shouwu Tang, Haifeng Liu & Yuqiang Sun

**Imprint:** Molecular Biology Reports (2023)

**Abstract:** The naturally colored brown cotton fiber is the most widely used environmentally friendly textile material, which primarily contains proanthocyanidins and their derivatives. Many structural genes in the flavonoid synthesis pathway are known to improve the genetic resources of naturally colored cotton. Among them, DFR is a crucial late enzyme to synthesis both anthocyanins and proanthocyanidins in the plant flavonoid pathway.

## 23

**Title:** A novel parent selection strategy for the development of salt-tolerant cotton cultivars

**Imprint:** Published online by Cambridge University Press: 11 April 2023

**Author:** Muhammad Tahir, Muhammad Awais Farooq, Muhammad Tanees Chaudry, Umar Akram, Muhammad Sohaib Shafique and Amir Shakee

**Abstract:** Salinity poses a major obstacle in increasing the yield of cotton. To explore genetic material that can yield better under salt stress conditions, eight parents including 5 females and 3 testers were crossed in line × tester mating design. After successful completion of crossing, parents and their 15 crosses were evaluated for seed cotton yield, within boll yield components, fibre quality, ionic and biochemical traits under control and NaCl salt stressed conditions (10 and 20 dSm<sup>-1</sup>). Under salt stress conditions seed cotton yield, fibre length and fibre strength decreased in all genotypes whereas, lint percentage and fibre fineness increased. Among parents RH-647 and among crosses FH-214 × FH-2015 performed better for seed cotton yield while for fibre quality traits under salt stress conditions among parents KEHKSHAN, and among crosses FH-214 × KEHKSHAN performed better. Results suggested that plant height, boll weight, lint percentage, fibre length and fibre strength are reliable traits for the selection of salt tolerant genotypes in the future cotton breeding programs.

## 24

**Title:** Identification of candidate genes for aphid resistance in upland cotton by QTL mapping and expression analysis

**Author:** Qiushuang An , Zhenyuan Pan , Nurimanguli Aini , Peng Han , Yuanlong Wu , Chunyuan You , Xinhui Nie

**Imprint:** The Crop Journal, Available online 12 April 2023

**Abstract:** Lignin is one of the main components of cell walls and is essential for resistance to insect pests in plants. Cotton plants are damaged by aphid (*Aphis gossypii*) worldwide but resistant breeding is undeveloped due to scarce knowledge on resistance genes and the mechanism. This study reported a lignin biosynthesis-related gene identified in the F<sub>2</sub> population derived from the cross between cotton cultivars Xinluzao 61 (resistant to aphid) and Xinluzao 50 (susceptible to aphid). A quantitative trait locus was mapped on chromosome D04 with a logarithm of odds (LOD) score of 5.99 and phenotypic effect of 27%. RNA-seq analysis of candidate intervals showed that the expression level of *GH\_D04G1418* was higher in the resistant cultivar than in the susceptible cultivar. This locus is close to *AtLAC4* in the phylogenetic tree and contains

a conserved laccase domain. Hence, it was designated *GhLAC4-3*. Silencing of *GhLAC4-3* in Xinluzao 61 via virus-induced gene silencing (VIGS) resulted in decreased lignin content and increased susceptibility to aphids. These results suggest that *GhLAC4-3* might enhance aphid resistance by regulating lignin biosynthesis in cotton.

## 25

**Title:** Exploring the genetic diversity and population structure of upland cotton germplasm by iPBS-retrotransposons markers

**Author:** Nurettin Baran, Flavien Shimira, Muhammad Azhar nadeem, Muhammad Tanveer altaf, Mehtap andirman, Faheem Shehzad Baloch & Mefhar Gültekin Temiz

**Imprint:** *Molecular Biology Reports* (2023)

**Abstract:** A total of 128 genotypes comprised *Gossypium hirsutum* L., *Gossypium barbadense* L., and pure lines were used to examine genetic diversity using iPBS-retrotransposon markers system. Eleven highly polymorphic primers yielded 287 bands and 99.65% polymorphism was recorded. The mean polymorphism information content was estimated at 0.297 and the average diversity indices for the effective number of alleles, Shannon's information index, and overall gene diversity were 1.481, 0.443, and 0.265, respectively. The analysis of molecular variance (AMOVA) revealed that 69% of the genetic variation was within the population. A model-based STRUCTURE algorithm divided the entire germplasm into four populations and one un-classified population, the genotypes G42 (originating in Egypt) and G128 (originating in the United States), showed the highest genetic distance (0.996) so these genotypes could be suggested for breeding programs as parental lines.

## 26

**Title:** Identification and analysis of isoflavone reductase gene family in *Gossypium hirsutum* L.

**Author:** Yanting Gui, Guozhan Fu, Xuelin Li & Yinghao Dai

**Imprint:** *Scientific Reports* volume 13,

**Abstract:** Isoflavone reductase (IFR) is a key enzyme controlling isoflavone synthesis and widely involved in response to various stresses. In this study, the IFR genes in four *Gossypium* species and other 7 species were identified and analyzed in the whole genome, and the physicochemical properties, gene structures, cis-acting elements, chromosomal locations, collinearity relationships and expression patterns of IFR genes

were systematically analyzed. 28, 28, 14 and 15 IFR genes were identified in *Gossypium hirsutum*, *Gossypium barbadense*, *Gossypium arboreum* and *Gossypium raimondii*, respectively, which were divided into five clades according to the evolutionary tree and gene structure. Collinear analysis showed that segmental duplication and whole genome duplication were the main driving forces in the process of evolution, and most genes underwent pure selection. Gene structure analysis showed that IFR gene family was relatively conserved. Cis-element analysis of promoter showed that most GhIFR genes contain cis-elements related to abiotic stresses and plant hormones. Analysis of GhIFR gene expression under different stresses showed that GhIFR genes were involved in the response to drought, salt, heat and cold stresses through corresponding network mechanisms, especially GhIFR9A. Phenotypic analysis after silencing GhIFR9A gene by VIGS was shown that GhIFR9A gene was involved in the response to salt stress. This study laid a foundation for the subsequent functional study of cotton IFR genes.

## 27

**Title:** Identification of MYB gene family and functional analysis of GhMYB4 in cotton (*Gossypium* spp.)

**Author:** Yuanli Dai, Shang Liu, Dongyun Zuo, Qiaolian Wang, Limin Lv, Youping Zhang, Hailiang Cheng, John Z. Yu & Guoli Song

**Imprint:** *Molecular Genetics and Genomics* volume 298, pages755–766 (2023)

**Abstract:** Myeloblastosis (*MYB*) transcription factors (TFs) form a large gene family involved in a variety of biological processes in plants. Little is known about their roles in the development of cotton pigment glands. In this study, 646 *MYB* members were identified in *Gossypium hirsutum* genome and phylogenetic classification was analyzed. Evolution analysis revealed asymmetric evolution of *GhMYBs* during polyploidization and sequence divergence of *MYBs* in *G. hirsutum* was preferentially happened in D sub-genome. WGCNA (weighted gene co-expression network analysis) showed that four modules had potential relationship with gland development or gossypol biosynthesis in cotton. Eight differentially expressed *GhMYB* genes were identified by screening transcriptome data of three pairs of glanded and glandless cotton lines. Of these, four were selected as candidate genes for cotton pigment gland formation or gossypol biosynthesis by qRT-PCR assay. Silencing of *GH\_A11G1361* (*GhMYB4*) downregulated expression of multiple genes in gossypol biosynthesis pathway, indicating it could be involved in gossypol biosynthesis. The potential protein interaction network suggests that several *MYBs* may have indirect interaction with *GhMYC2*-like, a key regulator of pigment gland formation. Our study was the systematic analysis of *MYB* genes in cotton pigment gland development, providing candidate genes for further study on the

roles of cotton *MYB* genes in pigment gland formation, gossypol biosynthesis and future crop plant improvement.

## 28

**Title:** Identification of fertility restoration candidate genes from a restorer line R186 for *Gossypium harknessii* cytoplasmic male sterile cotton.

**Author;** Cheng Cheng, Hushuai Nie, Huijing Li, Daniel Adjibolosoo, Bin Li, Kaiyun Jiang, Yanan Cui, Meng Zhu, Baixue Zhou, Anhui Guo & Jinping Hua

**Imprint:** BMC Plant Biology volume 23, Article number: 175 (2023)

**Abstract:** The utilization of heterosis based on three-line system is an effective strategy in crop breeding. However, cloning and mechanism elucidation of restorer genes for cytoplasmic male sterility (CMS) in upland cotton have yet been realized.

## 29

**Title:** Genome-wide identification of the geranylgeranyl pyrophosphate synthase (GGPS) gene family involved in chlorophyll synthesis in cotton

**Author;** Wenxiang Feng, Teame Gereziher Mehari, Hui Fang, Meijun Ji, Zijian Qu, Mengxue Jia, Dongmei Wang, Allah Ditta, Muhammad K. R. Khan, Yunying Cao, Jianyong Wu & Baohua Wang

**Imprint:** BMC Genomics volume 24, Article number: 176 (2023)

**Abstract:** Geranylgeranyl pyrophosphate synthase (GGPS) is a structural enzyme of the terpene biosynthesis pathway that is involved in regulating plant photosynthesis, growth and development, but this gene family has not been systematically studied in cotton.

**Title:** Functional characterization of TBL genes revealed the role of GhTBL7 and GhTBL58 in cotton fiber elongation

**Author:** Nosheen Kabir , Xuwen Wang , Lili Lu , Ghulam Qanmber, Le Liu , Aijun Si , Li an Zhang

**Imprint:** International Journal of Biological Macromolecules  
Volume 241, 30 June 2023, 124571

**Abstract:** TBL (Trichome Birefringence Like) gene family members are involved in trichome initiation and xylan acetylation in several plant species. In our research, we identified 102 TBLs from *G. hirsutum*. The phylogenetic tree classified TBL genes into five groups. Collinearity analysis of TBL genes indicated 136 paralogous gene pairs in *G. hirsutum*. Gene duplication indicated that WGD or segmental duplication contributed to the GhTBL gene family expansion. Promoter cis-elements of GhTBLs were related to growth and development, seed-specific regulation, light, and stress responses. GhTBL genes (GhTBL7, GhTBL15, GhTBL21, GhTBL25, GhTBL45, GhTBL54, GhTBL67, GhTBL72, and GhTBL77) exhibited upregulated response under exposure to cold, heat, NaCl, and PEG. GhTBL genes exhibited high expression during fiber development stages. Two GhTBL genes (GhTBL7 and GhTBL58) showed differential expression at 10 DPA fiber, as 10 DPA is a fast fiber elongation stage and fiber elongation is a very important stage of cotton fiber development. Subcellular localization of GhTBL7 and GhTBL58 revealed that these genes reside inside the cell membrane. Promoter GUS activity of GhTBL7 and GhTBL58 exhibited deep staining in roots. To further validate the role of these genes in cotton fiber elongation, we silenced these genes and observed a significant reduction in the fiber length at 10 DPA. In conclusion, the functional study of cell membrane-associated genes (GhTBL7 and GhTBL58) showed deep staining in root tissues and potential function during cotton fiber elongation at 10 DPA fiber.



**Title:** Long-term assessments of cotton fiber quality in response to plant population density: Reconciling fiber quality and its temporal stability

**Author:** Shijie Zhang , Yingchun Han , Guoping Wang , Lu Feng , Yaping Lei , Zhanbiao Wang , Shiwu Xiong , Beifang Yang

**Imprint:** Industrial Crops and Products, Volume 198, August 2023, 116741

**Abstract:** Regulation of plant population density is crucial for optimizing cotton fiber quality. However, the relationship between plant density and fiber quality stability under contrasting climatic conditions remains unclear, and the compromise between fiber quality and temporal stability is unknown. In this study, based on a long-term field experiment with various plant densities (1.5–10.5 plants m<sup>-2</sup>) conducted from 2008 to 2021, cotton fiber quality variability, including fiber length, fiber strength, elongation, uniformity index, and micronaire, and their temporal stability, were evaluated. We determined the optimal plant density for cotton cultivation and elucidated the contributions of plant density and climatic conditions to the variability of cotton fiber quality and its temporal stability in China's Yellow River Valley. The results revealed that cotton maintained its upper-intermediate quality throughout the study period, with fiber length, strength, elongation, uniformity index, and micronaire values ranging between 28.04 and 30.03 mm, 26.15–30.05 cN tex<sup>-1</sup>, 5.90–6.83%, 83.85–85.44%, and 4.24–5.14, respectively. An increase in plant density improved fiber quality but impaired temporal stability ( $P < 0.01$ ), and slight increases in stability at lower plant densities resulted in substantially decreased probabilities of years with major declines in fiber quality class. Plant density and climatic conditions regulated the quality traits (23.5% and 69.3% of the explained variance, respectively), including fiber length, fiber strength, and micronaire, while climate was the most important factor (75.9% of the explained variance) in determining their temporal stability. Photosynthetically active radiation and maximum and mean temperature exhibited significant positive effects on fiber quality, whereas mean diurnal temperature range had the opposite effect. A plant density of 3.3–5.1 plants m<sup>-2</sup> ensures the highest temporal stability of cotton fiber quality without declines in the fiber quality class. This study first provides insights into balancing cotton fiber quality and temporal stability through agronomic interventions, with implications for the quantitative prediction of future crop quality changes owing to climatic variation.

**Title:** Coordination of floral and fiber development in cotton (*Gossypium*) by hormone- and flavonoid-signalling associated regulatory miRNAs.

**Author:** Sakshi Arora, Amarjeet Kumar Singh & Bhupendra Chaudhary

**Imprint:** Plant Molecular Biology volume 112, pages1–18 (2023)

**Abstract:** Various plant development activities and stress responses are tightly regulated by various microRNAs (miRNA) and their target genes, or transcription factors in a spatiotemporal manner. Here, to exemplify how flowering-associated regulatory miRNAs synchronize their expression dynamics during floral and fiber development in cotton, constitutive expression diminution transgenic lines of auxin-signaling regulatory Gh-miR167 (35S-MIM167) were developed through target mimicry approach. ‘Moderate’ (58% to 80%)- and ‘high’ (> 80%)-Gh-miR167 diminution mimic lines showed dosage-dependent developmental deformities in anther development, pollen maturation, and fruit (= boll) formation. Cross pollination of ‘moderate’ 35S-MIM167 mimic lines with wild type (WT) plant partially restored boll formation and emergence of fiber initials on the ovule surface. Gh-miR167 diminution favored organ-specific transcription biases in miR159, miR166 as well as miR160, miR164, and miR172 along with their target genes during anther and petal development, respectively. Similarly, accumulative effect of percent Gh-miR167 diminution, cross regulation of its target ARF6/8 genes, and temporal mis-expression of hormone signaling- and flavonoid biosynthesis-associated regulatory miRNAs at early fiber initiation stage caused irregular fiber formation. Spatial and temporal transcription proportions of regulatory miRNAs were also found crucial for the execution of hormone- and flavonoid-dependent progression of floral and fiber development. These observations discover how assorted regulatory genetic circuits get organized in response to Gh-miR167 diminution and converge upon ensuing episodes of floral and fiber development in cotton.

**Title:** Lint percentage and boll weight QTLs in three excellent upland cotton (*Gossypium hirsutum*): ZR014121, CCRI60, and EZ60

**Author:** Hao Niu, Meng Kuang, Longyu Huang, Haihong Shang, Youlu Yuan & Qun Ge

**Imprint:** BMC Plant Biology volume 23, Article number: 179 (2023)

**Abstract:** Upland cotton (*Gossypium hirsutum* L.) is the most economically important species in the cotton genus (*Gossypium* spp.). Enhancing the cotton yield is a major goal in cotton breeding programs. Lint percentage (LP) and boll weight (BW) are the two most important components of cotton lint yield. The identification of stable and effective quantitative trait loci (QTLs) will aid the molecular breeding of cotton cultivars with high yield.

## PLANT BIOTECHNOLOGY

### 34

**Title:** Genome-Wide Analysis of the Rad21/REC8 Gene Family in Cotton (*Gossypium* spp.)

**Author:** Yali Wang , Lili Zhou, Huiming Guo and Hongmei Cheng

**Imprint:** Genes 2023, 14, 993. <https://doi.org/10.3390/genes14050993>

**Abstract:** Cohesin is a ring-shaped protein complex and plays a critical role in sister chromosome cohesion, which is a key event during mitosis and meiosis. Meiotic recombination protein REC8 is one of the subunits of the cohesion complex. Although REC8 genes have been characterized in some plant species, little is known about them in *Gossypium*. In this study, 89 REC8 genes were identified and analyzed in 16 plant species (including 4 *Gossypium* species); 12 REC8 genes were identified in *Gossypium. hirsutum*, 11 in *Gossypium. barbadense*, 7 in *Gossypium. raimondii*, and 5 in *Gossypium. arboreum*. In a phylogenetic analysis, the 89 REC8 genes clustered into 6 subfamilies (I-VI). The chromosome location, exon-intron structure, and motifs of the REC8 genes in the *Gossypium* species were also analyzed. Expression patterns of GhREC8 genes in various tissues and under abiotic stress treatments were analyzed based on public RNA-seq data, which indicated that GhREC8 genes might have different functions in growth and development. Additionally, qRT-PCR analysis showed that MeJA, GA, SA, and ABA treatments could induce the expression of GhREC8 genes. In general, the genes of the REC8 gene family of cotton were systematically analyzed, and their potential function in cotton mitosis, meiosis, and in response to abiotic stress and hormones were preliminary predicted, which provided an important basis for further research on cotton development and resistance to abiotic stress.

**Title:** Large-scale long terminal repeat insertions produced a significant set of novel transcripts in cotton

**Author:** Yan Yang, Xingpeng Wen, Zhiguo Wu, Kun Wang & Yuxian Zhu

**Imprint:** Science China Life Sciences (2023)

**Abstract:** Genomic analysis has revealed that the 1,637-Mb *Gossypium arboreum* genome contains approximately 81% transposable elements (TEs), while only 57% of the 735-Mb *G. raimondii* genome is occupied by TEs. In this study, we investigated whether there were unknown transcripts associated with TE or TE fragments and, if so, how these new transcripts were evolved and regulated. As sequence depths increased from 4 to 100 G, a total of 10,284 novel intergenic transcripts (intergenic genes) were discovered. On average, approximately 84% of these intergenic transcripts possibly overlapped with the long terminal repeat (LTR) insertions in the otherwise untranscribed intergenic regions and were expressed at relatively low levels. Most of these intergenic transcripts possessed no transcription activation markers, while the majority of the regular genic genes possessed at least one such marker. Genes without transcription activation markers formed their +1 and -1 nucleosomes more closely (only  $117 \pm 1.4$  bp apart), while twice as big spaces (approximately  $403.5 \pm 46.0$  bp apart) were detected for genes with the activation markers. The analysis of 183 previously assembled genomes across three different kingdoms demonstrated systematically that intergenic transcript numbers in a given genome correlated positively with its LTR content. Evolutionary analysis revealed that genic genes originated during one of the whole-genome duplication events around 137.7 million years ago (MYA) for all eudicot genomes or 13.7 MYA for the *Gossypium* family, respectively, while the intergenic transcripts evolved around 1.6 MYA, resultant of the last LTR insertion. The characterization of these low-transcribed intergenic transcripts can facilitate our understanding of the potential biological roles played by LTRs during speciation and diversifications.

**Title:** Genome-wide identification and functional analysis of *ICE* genes reveal that *Gossypium thurberi* "*GthICE2*" is responsible for cold and drought stress tolerance

**Author:** Han , Muhammad Jawad  
Umer , Mengying Yang , Yuqing Hou , Teame Gereziher Mehari

**Imprint:** Plant Physiology and Biochemistry, Volume 199, June 2023, 107708

**Abstract:** Cold stress has been found to have a negative impact on cotton growth and annual production. To address this issue, the utilization of cold-tolerant gene resources from wild species of *Gossypium* is crucial for genetic improvements in cultivated cotton. *ICE* (inducer of *CBF* expression) are the key regulators of cold tolerance in plants, however, there is relatively little information on *ICE* genes in cotton. Herein, we performed comprehensive bioinformatics analyses of the *ICE gene family* in eight cotton species. Phylogenetic analysis showed that 52 *ICE* genes were clustered into four subgroups. *Cis*-regulatory elements analysis suggests that the expression of *ICE* genes might be regulated by light, plant hormones, and various environment stresses. Higher expression of *GthICE2* was observed in leaves as compared to roots and stems, in response to cold, drought, and exogenous hormone *ABA*. Furthermore, overexpression of *GthICE2* in *A. thaliana* led to higher germination and survival rates, longer root length, lower ion leakage, and induction under cold and drought stress. Histochemical staining showed that oxidative damage in transgenic lines was much lower compared to wild-type plants. Lower MDA contents and higher SOD and POD activities were observed in overexpressed plants. Y1H and LUC assays revealed that *GthICE2* might activate the expression of *GthCBF4*, a cold-responsive gene, by connecting with the *MYC cis*-element present in the promoter of *GthCBF4*. *GthICE2* confers cold and drought stress tolerance in cotton. Our findings add significantly to the existing knowledge regarding cold stress tolerance and helps to elucidate cold response mechanisms in cotton.

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**Title:** Functional Characterization of Candidate Genes, Gohir.D05G103700 and Gohir.D12G153600, Identified Through the Expression QTL Analysis using Virus Induced Gene Silencing in Upland Cotton (*Gossypium hirsutum* L.)

**Author:** Salman Naveed<sup>1</sup> and Sachin Rustg

**Imprint:** Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 7 April 2023 doi:10.20944/preprints202304.0115.v1

**Abstract:** Cotton (*Gossypium* spp.) is a major source of natural fiber and an important cash crop. The cotton growth habit and architecture determine its productivity and influence management strategies for commercial production. The GATA transcription factors (TFs) control various developmental processes in plants, such as flower, bract and embryo development, and petal differentiation. As stable transformation is still a bottleneck in many plant species, TRV-VIGS was used to manipulate gene expression in different plants, including *Gossypium hirsutum* L. In this study, we undertook the TRV-based VIGS to functionally characterize two candidate genes, Gohir.D05G103700 and Gohir.D12G153600, identified through the expression QTL analysis for five floral induction and meristem identity genes using the upland cotton mini-core collection.

Virus-induced silencing of the Gohir.D05G103700 gene resulted in up to a 1.4-fold reduction in the transcript level in two inoculated plants, G3 and G4, and Gohir.D12G153600 gene resulted in up to a 2.3-fold reduction in transcript level in a single inoculated plant P05 relative to the mock-treated plant. The TRV2-Gohir.D05G103700 inoculated plants precisely G3 and G4 also exhibited loss of the supernumerary (fourth) floral bract in the squares, whereas the TRV2-Gohir.D12G153600 inoculated plants did not show any observable phenotypic change relative to the mock-treated plants. Altogether, this study suggested that TRV-VIGS can be used to characterize genes in cotton relatively rapidly and the cotton Gohir.D05G103700 gene is a positive regulator of the indeterminate growth habit in cotton, which could be manipulated to obtain a cotton plant with architecture best suited for the cultivation area.

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**Title:** Yellow Petal locus GaYP promotes flavonol biosynthesis and yellow coloration in petals of Asiatic cotton (*Gossypium arboreum*)

**Author:** Yaohua Li, Lingfang Ran, Tong Mo, Nian Liu, Jianyan Zeng, Aimin Liang, Chuannan Wang, Qingwei Suo, Zhong Chen, Yi Wang, Nianjuan Fang, Shijia Xu & Yuehua Xiao

**Imprint:** Theoretical and Applied Genetics volume 136, Article number: 98 (2023)

**Abstract:** Petal color is pivotal to ornamental value and reproduction of plants. Yellow coloration in plant petals is mainly attributed to colorants including carotenoids, aurones and some flavonols. To date, the genetic regulatory mechanism of flavonol biosynthesis in petals is still to be elucidated. Here, we employed Asiatic cottons with or without deep yellow coloration in petals to address this question. Multi-omic and biochemical analysis revealed significantly up-regulated transcription of flavonol structural genes and increased levels of flavonols, especially gossypetin and 6-hydroxykaempferol, in yellow petals of Asiatic cotton. Furthermore, the Yellow Petal gene (GaYP) was mapped on chromosome 11 by using a recombinant inbred line population. It was found that GaYP encoded a transcriptional factor belonging to Sg6 R2R3-MYB proteins. GaYP could bind to the promoter of flavonol synthase gene (GaFLS) and activate the transcription of downstream genes. Knocking out of GaYP or GaFLS homologs in upland cotton largely eliminated flavonol accumulation and pale yellow coloration in petals. Our results indicated that flavonol synthesis, up-regulated by the R2R3-MYB transcription activator GaYP, was the causative factor for yellow coloration of Asiatic cotton petals. In addition, knocking out of GaYP homologs also led to decrease in anthocyanin accumulation and petal size in upland cotton, suggesting that GaYP and its homologs might modulate developmental or physiological processes beyond flavonol biosynthesis.

## 39

**Title:** Delinting and neutralizers residue effect on stored cotton seeds physiological quality determined by phenotyping image analysis

**Author:** Juliana Maria Espíndola Lima

**Imprint:** J. Seed Sci. 45 • 2023 • <https://doi.org/10.1590/2317-1545v45267297>

**Abstract:** The cottonseed delinting removes lint from the seed coat to improve plantability and maintain the seed's physiological quality, therefore, this work aimed to determine the effect of delinting and neutralizers' residual on the physiological quality of stored cottonseed by using image analysis phenotyping. The experiment was a randomized factorial design of 3 x 4 x 2 and two periods of storage evaluation (0 and 180 days). The cotton seeds were delinted at three different times (2, 4, and 10 minutes), neutralized using four distinct neutralizers (Quicklime, Hydrated lime, Filler lime, and NaOH), and there were seeds with and without neutralizer residue. The evaluations carried out were: water content, seed residual lint imaging, germination, seedling emergence, and seedling length imaging. The neutralizers Quicklime, Hydrated lime, and Filler lime do not need removal from the cotton seed coat. In storage, only the neutralizer NaOH has a high latent effect in lowering cottonseed quality, and the other neutralizers have lower physiological quality when the residue is removed. The image analysis phenotyping is efficient in identifying seedlings' vigor.

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**Title:** Abiotic Factors and Biotic Interactions Associated with Disease Development in Cotton Seedlings Caused by *Rhizoctonia solani* and *Fusarium oxysporum* F. Sp. *Vasinfectum* Race 4

**Author:** Maddox, Ann Marie

**Imprint:** California State University, Fresno ProQuest Dissertations Publishing, 2023. 30419209.

**Title:** : A DNA extraction method for nondestructive testing and evaluation of cotton seeds (*Gossypium* L.)

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**Imprint:** Research Square, DOI: <https://doi.org/10.21203/rs.3.rs-2787434/v1>

**Abstract:** Kernels of cotton provide lint and linter for textiles, oil and protein for food and feed. Cotton seed is formed following fertilization between an ovule and a pollen grain. The seed coat is maternal in origin, whereas the embryo and attached cotyledonary leaves are hybrids of parental lines. The extraction of genomic DNA from an ungerminated whole, a portion or mixed seeds are prerequisite in genetic and genomic studies of cotton. As far as our knowledge, there is only one method of nondescriptive DNA extraction from ungerminated cotton seeds without affecting the seed germination capability, but it has technical difficulties and requires special equipment. Furthermore, the amount of DNA extracted using the published method is low and, therefore, it is only suitable for routine marker assisted selection studies. In this study, a modified CTAB DNA isolation protocol referred to as the CTAB-LiCl DNA extraction method was developed for single whole cotton seed, a portion of cotton seed and bulked cotton seeds. The CTABLiCl DNA extraction method was evaluated in ninety-six individuals of six different cotton cultivars along with two genetic standards of cotton, TM-1 (*G. hirsutum* L.), Pima 3-79 (*G. barbadense* L.), and several other plant species of different plant genera. Results revealed that this method produced high quality and amounts of DNA as confirmed by spectrophotometry, agarose gel, restriction enzyme digestion, polymerase chain reaction, and library production for next generation sequencing studies of whole genome bisulfite sequencing. It does not require the use of liquid nitrogen, RNase, proteinase K, or betamercaptoethanol and can be completed in approximately 2 h. Small tissues of the chalaza ends of ungerminated cotton seeds could be used to obtain high quality and quantity of DNA ranging from 14 µg to 28 µg without affecting the seeds' germination ability, allowing marker-assisted selection before planting and flowering.