

# **WORLD COTTON RESEARCH CONFERENCE-8**

# 3-7 October 2024

International Hotel Tashkent, 107A, Amir Temur Street, Tashkent, Uzbekistan











INTERNATIONAL COTTON ADVISORY COMMITTEE

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# **BOOK OF ABSTRACTS**

# **WORLD COTTON RESEARCH CONFERENCE-8**

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International Hotel Tashkent, 107A, Amir Temur Street, Tashkent, Uzbekistan

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# ORAL PRESENTATIONS CROP PRODUCTION



# Agronomic Interventions for Sustainable Weed Management in Cotton

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Aditi Agrawal

**Background:** Cotton (*Gossypium hirsutum* L.) is a major global crop, with India being the second-largest cotton producer. The advent of Bt cotton has revolutionized cotton cultivation, but weeds remain a persistent challenge to productivity. This paper re-investigates the impact of weeds on cotton yield and explores various agronomic interventions for effective weed management.

**Results:** Weeds significantly reduce cotton yield by competing for essential resources like water, nutrients, sunlight, and space. They also act as hosts for pests and diseases, further diminishing crop health and fiber quality. The critical period for weed competition in cotton is the initial 11-12 weeks from 1-2 weeks after the emergence of crop, during which unmanaged weed infestations can lead to substantial yield losses (10-90%). Various weed management strategies are discussed, including preventive measures (e.g., clean cultivation, weed-free seeds), cultural practices (e.g., crop rotation, intercropping), mechanical methods (e.g., hoeing, inter-row cultivation), and chemical interventions (e.g., herbi-

cides). Each method has its advantages and limitations, necessitating an integrated approach for sustainable weed management.



**Conclusion:** The study concludes that an integrated weed management (IWM) approach, combining multiple strategies tailored to specific agro-ecological conditions, is crucial for effective weed control in cotton. Future research should focus on weed modelling to predict weed emergence patterns and develop precise weed control thresholds. Additionally, exploring methods to enhance crop competitiveness through cultivar selection, row spacing optimization, and irrigation/fertilization management can further improve weed management outcomes in cotton production.

Keywords: Cotton, weed management, Integrated weed management, Herbicides, Cultural practices, Crop yield

# Cotton Intelligent Revolution: How Artificial Intelligence is Transforming Cotton in Egypt

#### **Amal Saber Owis**

Cotton Research Institute, Egypt



**Amal Saber Owis** 

Cotton, a natural fiber that has clothed civilizations for millennia, is now experiencing a new wave of innovation through the integration of Artificial Intelligence (AI).

AI is fundamentally changing how cotton is produced, from planting to harvest, with the potential to improve yields, optimize resource use, and promote sustainable practices.

This paper explores the multifaceted applications of AI in cotton production, highlighting its impact on various aspects of the agricultural process.

AI driven chemical modification: Chemical modification plays a crucial role in enhancing cotton's properties for various applications. AI is transforming this process by offering greater precision and control:

**Smart Dosing Systems:** AI algorithms can analyze data of fabric properties, fiber characteristics, and environmental conditions to determine the optimal amount and type of chemicals needed for treatment. This not only reduces chemical waste but also ensures consistent and efficient finishing processes.

**Predictive Modeling for Dyeing Processes:** AI models can predict how different dyes will interact with specific cotton fibers under varying conditions. This allows manufacturers to optimize dyeing processes, resulting in vibrant, even colors and improved colorfastness of the final textile product.

**Developing Novel Bio-based Treatments:** AI can be used to screen vast libraries of natural compounds and predict their potential effectiveness as substitutes for conventional, often harsh, chemical treatments. This paves the way for developing sustainable and eco-friendly approaches to cotton modification.



#### Integrated Nutrient Management Improves The Productivity of Cotton-Wheat Cropping System in North India

Amarpreet Singh<sup>1\*</sup>, Kanjana Duraisamy.<sup>2</sup>, Sankaranarayanan K.<sup>2</sup>, Kumar Rishi<sup>1</sup>, Sain Satish Kumar<sup>1</sup>, Paul Debashis<sup>1</sup>, Chandra Subhash<sup>1</sup> and Verma Surender Kumar<sup>1</sup>

<sup>1</sup>Regional Station Sirsa; <sup>2</sup>Regional Station Coimbatore, Central Institute for Cotton Research, Nagpur, India.



Amarpreet Singh

**Background:** Sustaining the productivity of irrigated cotton-wheat system in the alluvial soils of Punjab, Haryana and Rajasthan, an important cropping system in the country, is pivotal to national food security and economic wellbeing. The existing system of fertilizer management is based on the nutrient requirement of individual crop, ignoring the carryover effect of the manure or fertilizer applied to the preceding crop. A judicious combination of manures and fertilizers depending upon the type of crops grown will improve the cropping system productivity.

**Results:** The field experiments were conducted with cotton-wheat cropping systems in split plot design, keeping five cropping systems in main plots ( $M_1$  to  $M_5$ ) and five sources of nutrients in sub-plots ( $S_1$  to  $S_5$ ) (applied to cotton crop only) and were replicated thrice. Among the cropping systems, seed cotton yield was in the order; *Bt* cotton hybrid – cultivated fallow > *Bt* cotton hybrid – wheat > non-*Bt* cotton hybrid–wheat > *Bt* cotton variety – wheat > non Bt cotton variety – wheat.

Highest seed cotton equivalent yield of wheat was obtained with non-*Bt* cotton hybrid – wheat cropping. However, no significant differences were observed in wheat grain yield with respect to cropping systems. Among the nutrient regimes, recommended dose of NPK + secondary nutrients ( $MgSO_4$ ) + micronutrients ( $ZnSO_4$  + Boron) and FYM @ 5 t/ha once in two years out yielded other nutrient regimes with respect to seed cotton, wheat grain yield, seed cotton equivalent yield of wheat and system productivity. Among the cropping systems, systems productivity was in the order; *Bt* cotton hybrid – wheat > non-*Bt* cotton hybrid – wheat > *Bt* cotton variety – wheat > non Bt cotton variety – wheat > *Bt* cotton hybrid – fallow.

**Conclusion:** The results showed that the application of recommended dose of NPK + secondary nutrients (MgSO<sub>4</sub>) + micronutrients (ZnSO<sub>4</sub> + Boron) and FYM @ 5 t/ha once in two years increased the seed cotton yield, wheat grain yield, thus achieving higher system productivity of cotton-wheat cropping system.

Key words: Cotton-wheat cropping system, integrated nutrient management, seed cotton yield, wheat grain yield.

### The transformative impact of regenerative agriculture on sustainable cotton cultivation: a case study



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**Background:** The textile industry contributes significantly to global warming. Sustainable cotton cultivation is crucial for its environmental impact and market demands. Pakistani cotton farmers face challenges like soil degradation, water scarcity, and climate variability, jeopardizing crop viability. Regenerative agriculture offers a solution with its focus on sustainable practices.

**Results:** Artistic Milliners Pvt. Limited (AM) implemented a pilot project (AM-Regen) to introduce regenerative practices to farmers, emphasizing soil health, biodiversity, and ecosystem resilience. Data collected for one year showed significant improvements for AM-Regen farmers compared to control

groups. Reductions were reported in tillage practices (13.39%), pesticide use (15.10%), fertilizer application (32.14%), and irrigation volume (16.67%). Notably, seed cotton yield increased by 17.75%, and tree density rose, indicating positive biodiversity impacts. AM-Regen farmers achieved a remarkable reduction in greenhouse gas emissions (172,189kg  $CO_2e$ ).

**Conclusion:** These results demonstrate the effectiveness of regenerative agriculture in enhancing agricultural productivity, reducing the environmental footprint of cotton cultivation, and contributing to environmental stewardship. AM's commitment to sustainable practices paves the way for a more resilient agricultural future that meets the demand for eco-friendly and socially responsible products.

Keywords: Regenerative agriculture, sustainable cotton cultivation, climate change mitigation, AM-Regen, Pakistan

# Technology Demonstration of High-Density Planting of *Bt* cotton on Shallow Soils under Rainfed Situation in Vidarbha region of Maharashtra, India

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**Background:** High density cotton planting is emerging as a scalable yield enhancement technology for improving rainfed cotton yields on marginal soils. Large scale demonstrations on farmers' fields under diverse environments would improve the pace of adoption of this technology. Hence, for the first time a mega demonstration of high-density planting system (HDPS) in Bt cotton hybrids specially developed for the new agronomy was carried out in farmer's field of Maharashtra, India.





Results: Three newly developed Bt cotton hybrids viz.; Rasi THCT-5380, Ankur Kirti 3060 and Mahyco-7399 were planted each on 1.2 ha in a sequence at four locations in farmers' field at villages Lakhori, Metpanjara (Nagpur dist.), Talegaon (Wardha dist.) and Kanshivani (Akola dist.) at 90 cm x 15 cm. The villages selected had shallow to medium deep black soils but differed in annual rainfall. The average rainfall of Akola is 747mm, Wardha is 983 mm and Nagpur is 1083 mm. Around 90% of the annual rainfall is received during the crop season from June to December. All the hybrids produced better growth in HDPS plots in respect of height, branches, squares, and green bolls as compared to the non-HDPS plots. The best growth was observed in Rasi THCT-5380 as it remained compact suiting to the close planting. However, all the hybrids outyielded and gave 31 to 44 % higher yield in HDPS plots than the respective non-HDPS fields where planting was done at conventional spacing of 90 cm x 60 cm or 120 cm x 75 cm. The seed cotton yield of Rasi THCT hybrid (2100 kg ha-1) was slightly superior to other two hybrids viz. Ankur Kirti (1848 kg ha-1) and Mahyco-7399 (1942 kg ha-1). The location influence was visible as the yields obtained at Talegaon and Kanshivani were of high order in all the hybrids than plots of Nagpur district. Analysis of weather data revealed that Nagpur district villages received nearly double the rainfall during crop season as compared with Akola and Wardha villages.

Table. Seed cotton yield (Kg/ha) of Bt hybrids at four locations in HDPS demos. Figures in parenthesis are for yield of respective control plots

Hybrid	Lakhori	% increase over non- HDPS	Metpanjara	% increase over non- HDPS	Talegaon	% increase over non- HDPS	Kanshivani	% increase over non- HDPS	Mean	% increase
Ankur Kirti-3066	1216 (850)	43	1250 (1000)	25	1500 (800)	88	3426 (1800)	90	1848 (1113)	40
Rasi THCT- 5380	1544 (900)	72	1869 (1560)	20	2280 (1200)	90	2710 (1050)	72	2100 (1178)	44
Mahyco MRC-7399	1438 (1040)	38	1800 (1050)	71	2383 (2000)	19	2148 (1300)	65	1942 (1348)	31

**Conclusion:** Adoption of HDPS technology using *Bt* cotton hybrids produced 31 to 44% higher seed cotton yields as compared to conventional cotton production system. Among the hybrids tested, Rasi THCT hybrid, with a mean seed cotton yield of 2100 kg/ha was the best performing hybrid.

Keywords: HDPS, Bt Cotton technology, Rainfed Cotton

# From Conventional to Regenerative Farming – A Step Towards Sustainability

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Conventional agriculture accounts for nearly 24% of greenhouse gas emissions and threatens over 80% of species at risk of extinction. The heavy use of agrochemical inputs, intense tillage, and lack of biodiversity, typical of conventional farming, drives these environmental crises. Regenerative agriculture has a long-rooted history in indigenous practices. However, its ability to go beyond the harm-reduction approach of sustainable farming and improve farmer resilience has put it at the forefront of the climate agenda. The fundamental principles of regenerative agriculture are to keep the soil covered, minimize soil disturbance, preserve living roots in the soil year-round, increase species diversity, integrate livestock, and limit or eliminate the use of synthetic pesticides and fertilizers with overall objectives of rejuvenating the soil, enhance biodiversity and provide environmental, economic, and social benefits to the wider community. Despite the claimed benefits of regenerative agriculture, a vast majority of growers are reluctant to adopt these practices due to a lack of availability of well-structured programme and empirical evidence on the claimed benefits and profitability.

Cotton Connect REEL Regenerative Agriculture programme is a well-structured private impact verification code that reflects an advanced 3-year training programme for REEL cotton farmers focusing on regenerative farming practices and their effects on functional biodiversity, improved livelihoods, income diversification and climate adaptation. The programme builds upon the REEL baseline code, a state of the art 3-year entrance programme for sustainable farming practices that already contains a large number of regenerative practices. Both programmes, therefore, stand in very close relation to each other to facilitate wider adoption of regenerative practices. It is the only programme that relates regenerative interventions to dedicated impact targets and actively monitors and evaluates goals, including 3<sup>rd</sup> party verification.



The benefits of regenerative agriculture practices can vary among different agroecosystems and may not necessarily be applicable across multiple agroecological regions. It is important to implement rigorous, long-term farming system trials to compare conventional and regenerative agriculture practices in order to build knowledge on the benefits and mechanisms associated with these practices on regional scales. This will provide farmers and other stakeholders with an evidence base to make informed decisions about adopting these practices to realize their social and economic benefits and to achieve resilience against climate change. For consumers, it gives satisfaction to use the products made from the raw materials made using the regenerative farming. Regenerative Agriculture holds possible answer to issues related to climate change.

Keywords: Soil health; regenerative agriculture; soil organic matter; biodiversity and microbial function.

# Drip Irrigation of Cotton in Saline Soils of Karakalpakstan

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**Background:** The Republic of Karakalpakstan is situated at the confluence of the Amu Darya and the Syr Darya rivers, which collectively represent the country's principal source of water. Consequently, the issue of irrigation of agricultural crops, in particular cotton, is of paramount importance. The quantity and quality of the harvest of cotton is directly related to the quantity and quality of irrigation. However, due to the scarcity of water resources, irrigation water must be used as efficiently as possible. Therefore, the implementation of drip irrigation for cotton cultivation represents one of the most effective measures for the conservation of water resources. Nevertheless, farmers are reluctant to adopt this irrigation technology due to concerns about soil salinisation, given that furrow irrigation simultaneously results in the partial washing of salts into the lower soil horizons.

**Results:** A series of field experiments were conducted in the Khodjeyli district of Karakalpakstan, where the soils are meadow-alluvial moderately saline. The groundwater depth is 1.5-2.0 meters. The predominant type of salinisation observed in the study area is chloride-sulfate and sulfate. The results of the agrochemical analysis of the soil of the experimental plot for humus, total nitrogen, phosphorus and potassium indicate that the soil is poor in these nutrients. The planned leaching of salts was conducted annually on the experimental plot.

At the end of the growing season, under drip irrigation, the total salt content in the variant with the residual effect of 4.5 t/ ha of bentonite clays in the plow layer was 0.498%, while with the annual application of 1.5 and 3.0 t/ha, this indicator was 0.326% and 0.441%, respectively, and in the control variant without the introduction of bentonite clays, the sum of salts was 0.352% in the arable soil layer. Whereas against the background of furrow irrigation in the aftereffect of 4.5 t/ha of bentonite clay, the sum of salts was 0.439% with a predominance of calcium cations (0.059%) and sulfate anions (0.246%), and with the annual application of bentonite clays at a rate of 1.5 and 3.0 t/ha, the sum of salts in the arable horizon of the soil was 0.489 and 0.384%, respectively, also with a predominance of calcium cations (0.088 and 0.073%) and sulfate anions (0.294 and 0.226%). In the control variant without the use of bentonite clays, the sum of salts was 0.585% with a predominance of calcium cations (0.066%) and sulfate anions (0.384%). As a result, with the annual application of bentonite clay at a rate of 3.0 t/ha against the background of mineral fertilizers NPK = 150-105-75 kg/ha using drip irrigation, the increase in the yield of raw cotton due to the use of bentonite clays amounted to an average of 10.7 c/ha, and relative to the irrigation method it was 14.1 c/ha.



**Conclusion**. In the context of moderately saline meadow-alluvial soils in Karakalpakstan, it is recommended that drip irrigation of cotton be accompanied by the application of bentonite clays in addition to mineral fertilizers. This approach is expected to result in an improvement in the ameliorative state of the soils and an increase in the yield of raw cotton.

Key words: salinization, drip irrigation, bentonite clay, the amount of salts, the yield of raw cotton.

#### What kind of cotton ideotype is adapted to agroecological cropping systems and climate change in Benin

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**Background:** Faced with the degradation of soil fertility and climate change in Benin, agroecological cropping systems are being recognized as an alternative for ensuring the sustainability of cotton production.

The objectives of this study were (i) to evaluate the relative contribution of plant traits driving the G by E by M interactions for cotton yield as measured during field experiments and to explain the results using CSM-CROPGRO-cotton model from Decision Support System for Agrotechnology Transfer (DSSAT), (ii) to identify morpho-physiological traits for yield enhancement in agroecological cropping systems and (iii) to identify the optimum combinations of different cultivar parameters used in the CSM under current and future weather conditions.

The experimental study, conducted from 2020 to 2023, in two sites (Savalou and Soaodou) compared four cropping systems with cowpea/maize//cotton rotation, namely Plough based Tillage (PT), PT with Incorporation of biomass (PTI), Conservation Agriculture with Strip Tillage (CA\_ST) and CA with No Tillage (CA\_NT). Six different cultivars from the world's major cotton-growing regions were compared as subplots in every cropping system.







Simulated changes in seed cotton yield for ideotypes and the control at Savalou by 2050 under RCP assumptions 2.6, 4.5, and 8.5.

Simulated changes in seed cotton yield for ideotypes and the control at Soaodou by 2050 under RCP assumptions 2.6, 4.5, and 8.5.

**Results:** The cultivars Tamcot\_camde in north Benin, and Okp768 in central zone resulted in higher yields in the agroecological cropping systems. High seed mass, large and thick leaves combined with a higher rate of photosynthesis and late leaf expansion are the traits of cultivars best suited to agroecological cropping systems. Cultivars and news ideotypes combining these traits benefit from the enhanced nitrogen availability and soil moisture status of CA systems, contributing to nitrogen use efficiency and water use efficiency. Under the baseline (2003-2023) and for the future under different climatic scenario by 2050 the new ideotypes improve the seed cotton yield of the control cultivars currently grown in Benin, 189% for Ang956 and ranging 3.2 to 10% for Okp768.

**Conclusion:** A good seedling and vegetative vigour that cultivars can have through morpho-physiological traits is necessary to ensure a good seed cotton yield in agroecological cropping systems. These results provide useful traits and scientific evidence for breeders and cropping systems research programs focused of the adaptation of cotton to climate change.

Keywords: Tillage, agroecological practices, water status, Gossypium hirsutum, cover crop, nitrogen, CSM-CROPGRO-cotton.

# **Resource-Saving Technologies for Growing Crops**

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**Background:** The soils of Uzbekistan with a low humus content, with poor structure, saline as a result of winter-spring precipitation and irrigation form a dense crust. Repeated treatments with powerful tractors and mechanisms during crop cultivation leads to compaction of the arable and sub-arable soil layer, deteriorating its structure and ecological environment, which ultimately reduces yields.

#### **Results:**

1) Studies conducted in conditions of typical sierozem and takyr soils have shown the negative effect of repeated passage of wheeled tractors during soil preparation, since during this period, as a result of winter and spring rains, moisture accumulates in the soil in large quantities, which in the process of spring soil preparation leads to compaction, and this in turn is negative due to the uniform sowing, as a result, cotton seedlings germinate at different times. It has been established, in the spring period, the expediency of using tracked tractors in preparing the soil for sowing in.

2) One of the ways to reduce soil compaction is seeding along the ridges, autumn fakes of the ridges reduce the number of tractor passes in the spring 3-4 times, the volume mass on the ridges was 1.25 - 1.35 g/cm3, porosity improved by 4-5%, due to moisture retention and an increase in soil temperature by 4-7 °C, compared with sowing on a smooth field, it is possible to sow early, another advantage is that the rains passing during this period do not negatively affect seedlings, also eliminates the appearance of a crust, which causes great damage when sowing on a smooth field, requiring additional costs.

3) Application of the technology of mulching with vegetable, compost, organic fertilizers, both on smooth crops and on ridges, increasing the temperature in the soil surface, retaining naturally accumulated soil moisture, improving the structure, water permeability increases 1.5-2 times, soil compaction decreases, ensures early 5-7 days of cotton seedlings. The use of soil mulching technology makes it possible to sow cotton in the second half of March and early April. During this period, the soil temperature is higher by 3-5 °C, which will allow you to quickly get seedlings and eventually an early harvest with high quality fiber, with an additional cotton yield of 0.6-0.8 t ha<sup>-1</sup> and 1.0-1.5 t ha<sup>-1</sup> wheat grain yield and more.



**Conclusion:** In order to obtain a high and high-quality harvest from agricultural crops that meet international standards, it is necessary to create an environmentally safe and at the same time cost-effective tillage technology taking into account the conditions of each type of soil.

Keywords: soil, technology, agrophysical properties, high yield.

# Cotton Production Challenges in Pakistan Under Climate Change Scenario; A Review

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**Ghulam Sarwar** 

Cotton is the second-largest crop grown in Pakistan. More than 40% of industries are engaged directly or indirectly with the cotton production. Over the past decades, its production has suffered multiple shocks due to conventional agricultural management practices and climate change (high temperature and erratic rainfall). Temperature plays a vital role in the growth of cotton, with a critical threshold of 32°C beyond which yield is adversely affected. Unpredicted and heavy rainfalls result in severe losses to cotton crop.

The global temperature is expected to increase by 1.5°C by 2050; an uneven rise in both max- day and night temperatures. High day temperature ( $\geq$ 35°C) effect reproductive development; reduce seed number and fruit retention, and increase flower abscission. Whereas, high night temperature (>28°C) increases respiration restricting carbohydrate mobilization to the sink, ultimately reducing fiber per seed. As a result of heat stress at 42°C, photosynthesis is reduced by 30%, electron transport

by 12%, and membrane integrity by 23%. Both high day and night temperature stresses restrict photo-assimilate supply to developing fruits resulting in a lower accumulation of total soluble carbohydrate in reproductive tissues and young bolls leading to improper fertilization and boll abortion. Only 1°C increase results in 10% decrease in lint yield due to 6% reduction in boll mass, associated with 7% less seeds/boll, whereas, 04°C increase in average growing season temperatures result in 9% reduction cotton yields. High temp >35°C can have significant negative impact on fiber quality traits (length, strength, uniformity, elongation, maturity, micronaire, and lint percent).

Erratic rainfall patterns damages cotton crop in many regions of the country due to lack of hypoxia tolerance in current cotton varieties. Water-logging due to excessive rains affect crop physiology, growth, and yield. Poor drainage of rainwater nega-

tively impacts leaf area index, photosynthesis, fruiting nodes, flowering, fiber quality and seed index.





**Conclusion:** To accomplish goals in a shorter period of time, contemporary plant breeding techniques, particularly modern breeding techniques /technologies can be used to develop climate resilient cotton varieties. Exploring heat and hypoxia tolerance in local germplasm will be helpful to cope with the changing climatic conditions. In addition, this document will serve as a basis and reference for the restoration of the cotton crop in Pakistan.

Keywords: Cotton, Climate change, Heat stress, Hypoxia, Climate resilient breeding.

# The Influence of Salt Stress on Morpho-Biological Traits Of Cotton

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**Background:** Currently, approximately 830 million hectares of agricultural land are used for human consumption, and 6 % of it being highly saline. It is estimated that if salinity levels continue to rise, 50 % of existing cropland may be under salinity stress by 2050. Cotton, an important natural fiber crop that has been grown worldwide for many years, is facing serious problems due to increasing soil salinity. Yearly escalation of soil salinity negatively impacts cotton growth. In general, cotton exhibits moderate resistance to salt stress, with tolerance levels reported up to 7.7 dS/m-1 (decisiemens per meter). Abiotic stress-resistant cotton lines and modern molecular breeding methods are important for developing high-quality and high-yield new cotton varieties in abiotic stress conditions.

**Results:** Recombinant Inbred Line (RIL) population obtained based on Namangan-77 and An-Boyovut 2 were phenotypically evaluated under 0 dS/m-1, 10 dS/m-1 and 20 dS/m-1 salt stress conditions. Various morpho-biological traits were evaluated, including germination rate (ranged between 30 to 90%), total plant length (ranged between 19 to 36.4 cm), shoot length ( ranged between 10.3 to 25.1cm), root length (ranged between 7.2 to 15.03 cm), fresh plant weight (ranged between 0.55 to 2.59 g), fresh shoot weight (ranged between 0.41 to 2.13 g), fresh root weight (ranged between 0.14 to 0.81 g), dry shoot weight (ranged between 0.08 to 0.45 g), dry root weight (ranged between 0.02 to 0.1 g), chlorophyll content, and number of true leaves (ranged between 3 to 6 in lab condition). Additionally cultivated in saline field conditions, key cotton traits like plant height (ranged between 3 to 6 in lab condition). Additionally cultivated in saline field conditions, key cotton traits like plant height (ranged between 3 to 21), boll weight (ranged between 3.3 to 6.6 g), fiber staple length (ranged between 29.9 to 38.1 mm), lint percentage (ranged between 27.3 to 37.9%), and 1000-seed weight (ranged between 85.3 to 143.3 g) were measured.

The analysis revealed that more than 10 RILs performed more than all collected phenotypic traits under saline stress conditions. Furthermore, a correlation analysis of the collected traits was conducted. Correlation analysis of morphological traits

#### Correlation coefficient, scatter plot, and distribution of morphological and agronomic traits in RIL population

Pearson correlation was conducted among the important morphological and agronomic traits of the RILs planted in Tashkent, Syrdarya, and Navoiy regions.

GR-Germination rate, PH-Plant height, SBN-Sympodial branch number, BNPP-Boll number per plant, BW-Boll weight, FSL-Fiber staple length, LP-Lint percentage, SW-1000 Seed weight.





revealed highly significant correlations among the 10 cotton traits grown in laboratory conditions. TPL showed a significant and strong correlation with FPW ( $r = 0.80^{***}$ ), and significantly positive correlations were identified between DShW ( $r = 0.70^{***}$ ) and LN ( $r = 0.65^{***}$ ). Also, TRL exhibited a significant positive correlation with FRW ( $r=60^{***}$ ) and DRW ( $r=70^{***}$ ) under 20 dS/m-1 salt stress conditions. Correlation analysis was also carried out on cotton (seven yield-related traits) cultivated in the natural saline environment. The correlation analysis showed that there were significant positive correlations of PH with SBNPP ( $r = 0.45^{**}$ ), BNPP ( $r = 0.48^{**}$ ), and BW ( $r = 0.25^{*}$ ), while 1000 SW was negatively associated with LP ( $r = -0.77^{***}$ ). Statistical analyses were conducted using Stata 17 and OriginPro-2022.

**Conclusion:** These selected lines will be valuable genetic materials for developing salt-stress-resistant cotton varieties.

Keywords: Cotton (Gossypium hirsutum L.), Salt stress, Plant biomass, RILs, Correlation

# Preliminary Investigation into the Effect of Priming Defoliation on Cotton Yield and Fibre Quality

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Van Der Sluijs

Defoliation is the application of chemicals to encourage or force cotton leaves to drop from the plant in preparation for mechanical harvesting. This application is often a combination of defoliants, boll openers and crop oil. Cotton crops are generally considered ready for defoliation at either 60% open bolls, or as more commonly used, due to its easier calculation, four nodes above cracked boll (4 NACB). The question usually asked is how defoliation can be sped up, without sacrificing quality and yield, thus allowing spindle harvesters into the field earlier before the autumn break occurs which could result in a delay in harvesting and possibly result in quality and yield penalties as has been the case this year. One method of accomplishing this is by the theory of priming defoliation, which is the application at 6 to 8 NACB of low rates of Thidazuron followed by normal defoliation applications. A number of commercial and small-scale trials have been conducted over the past five years in Australia and this presentation will provide further information on the results.



# Characterisation of Cotton-Based Cropping Systems in Côte D'ivoire: Which Cropping Practices Should be Improved to Increase Production by Ivorian Cotton Growers?

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**Background:** Characterisation of cotton-based cropping systems is essential for understanding and improving cotton production in Côte d'Ivoire. The aim of this study was to determine the effects of cropping practices on seed cotton yields. A survey of a network of 600 growers in all the cotton-growing areas was carried out to gather information on the type of soil preparation (manual, harnessed and motorised), the sowing decade, the previous crop, the cotton variety, the sowing density, the date of fertiliser application (NPK and urea), the number of weeding operations, the number of insecticide treatments and, finally, the seed cotton yield.

**Results:** The results showed that during the last cotton season (2023-2024), the sowing time, crop precedents and number of insecticide treatments had a highly significant effect on yield. Sowing in the first, second or third dekad of June (1 to 10 June, 11 to 20 June and 21 to 30 June respectively) was ideal. In addition, the best seed cotton yields were obtained by growers who applied NPKSB base fertiliser and cover fertiliser (urea) within the sowing period at 10 days before sowing (0-10 days before sowing) and 45-60 days after sowing, respectively. In addition, better yields of close to 2 tonnes per hectare (1725 kg/ha) were observed among growers who applied eleven insecticide treatments (that was six more than that recommended by the research and development services).

**Conclusion:** Further analysis will be carried out, taking into account parameters such as plot size, fertiliser doses (NPK and urea), climatic parameters (rainfall and temperature), agro-ecological zones and the physico-chemical parameters of the growers' soils. With this in mind, the Ivorian cotton companies will be able to provide farmers with a decision-making tool to help them monitor cultivation operations and improve farm performance.

Keywords: Cotton, sowing decade, basal fertilizer, cover fertilizer, plant protection, yield.

# Supporting Cotton Productivity in Côte d'Ivoire Through Agronomic Interventions

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**Background:** Modern agronomic concepts such as high-density planting systems are emerging in cotton-based cropping systems. Agronomic practices specific to new cotton varieties made in specific niches, management of the vegetation cover using growth regulators (retardants and defoliants) for better quality and above all the improvement of crop health through integrated nutrient management with an emphasis on the foliar feeding pattern, can significantly increase cotton productivity and improve the socio-economic status of cotton farmers. It is in this context that studies on cotton sowing densities, the supplementation of mineral fertilization with trace elements and the management of the resumption of vegetation of cotton plants at the end of the cycle have been carried out in a farming environment and in research stations.



Results: The results of the survey in the farmer's environment, of the trials conducted in stations and on observation posts showed a positive correlation between sowing densities and seed cotton yield. About 22% of the variations in seed cotton yield are related to sowing density. The best seed cotton yields are obtained with the high sowing densities in the north and the low densities in the south of the Ivorian cotton basin. Studies on the supplementation of basal fertilizer with trace elements have shown that the combined application of 200 kg/ ha of NPK + 50 kg/ha of urea + 2 kg/ha of ZnS04 increases the seed cotton yield and provides a monetary gain of 36,622 CFA francs/ha. The study on the management of vegetation resumption at the end of the cycle showed that the application of 4 l/ha of Ethephon and 62.5 ml/ha of Diuron at 100 days after emergence improves defoliation and capsule opening for better management of vegetation recovery at the end of the season.

**Conclusion:** Studies have shown that seeding density is a factor in seed cotton yield. Seed cotton yields were improved by supplementing with mineral fertiliser with zinc and adding desiccants and defoliants at the end of the cycle.

Keywords: Cotton, seeding density, trace elements, desiccants, defoliants, vegetation recovery.

### Future Challenges for Cotton Consumption and Fiber Market Competition

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The Uzbek cotton industry has undergone significant transformation, shifting towards sustainability and traceability in response to both international market demands and the need for enhanced human rights protections. In 2018, President Mirziyoyev invited efforts to modernize the country's agricultural practices, resulting in a partnership aimed at mechanizing cotton harvesting. The Silverleafe Cotton Cluster in Jizzakh has since become the most mechanized cotton cluster in Central Asia, achieving full mechanization by the 2024 harvest season. Despite these advancements, the Uzbek cotton industry faced challenges in regaining trust from international buyers due to concerns over human rights, particularly forced and child labor. To address these concerns, Silverleafe Cotton Tracing was launched to provide digitally verified, machine-harvested cotton, free from labor abuses. By ensuring complete traceability and compliance with human rights standards, Silverleafe Cotton Tracing offers a solution to global supply chains now held accountable for human rights practices. This initiative represents a key step in promoting conflict-free, sustainable cotton sourcing to meet the increasing demand for ethically produced materials.

# **Production of Furfural From Cottonseed Hulls:** A Sustainable Approach for Cotton By-product Utilization

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Background: The utilization of lignocellulosic biomass for producing value-added chemicals like furfural is gaining significant attention in the bio-refinery industry. Cottonseed hulls, an abundant byproduct of the cotton industry, represent a promising feedstock for furfural production due to relatively high hemicellulose content (11.6-24.5%). Furfural, a platform chemical with wide industrial applications, is typically produced via the acid-catalyzed dehydration of pentose sugars derived from hemicellulose. This study focuses on optimizing the production process using the Box-Behnken design (BBD), a response surface methodology (RSM), to maximize furfural yield from cottonseed hulls.

**Results:** Using the BBD, the effects of three critical variables pre-treatment condition (A): ratio of Manoj Kumar varying ratio (5:11 to 15:1) of 1% H<sub>2</sub>SO<sub>4</sub> to the cottonseed hulls (1% H<sub>2</sub>SO<sub>4</sub>: CSH), acid hydrolysis condition (B): ratio of varying concentration (2.5-7.5%) of H<sub>2</sub>SO<sub>4</sub> to CSH (% H<sub>2</sub>SO<sub>4</sub>: CSH); reaction time (C): 30-90 min—on furfural yield were systematically investigated. Experiments were conducted based on the design matrix, and the data obtained were fitted to a second-order polynomial model. Response surface plots were generated to visualize the variables' interaction effects and identify the optimal conditions. The optimized conditions, determined through the desirability function approach, resulted in a maximum furfural yield of 14.34%. Statistical analysis using ANOVA confirmed the significance of the model (p < 0.05) and revealed that all three variables (either individual or interactions) had significant effects on furfural vield.

# Unan add. rfural alcohol (130 Acid sprinkli FTIR transmittance spectra of standard furfural (red) and furfural 1 Ton capacity plan 5 crore inv Lacre land produced from cottonseed hulls (blue)

#### Figures: Industrial process for furfural production

**Conclusions:** The study successfully demonstrates BBD's application in optimizing furfural production from cottonseed hulls. The optimized process conditions—pretreatment condition of 11.731 (1% H2SO4: CSH), acid hydrolysis condition of 6.74% (%H2SO4: CSH), and a reaction time of 81.2 min with desirability 1 resulted in a furfural yield of 14.34%, demonstrating the efficiency of the proposed method. This research enhances the potential of cottonseed hulls as a sustainable and economically viable feedstock for the bio-refinery industry. By optimizing the production process, this study contributes to advancing biomass conversion technologies and promotes the utilization of agricultural byproducts for the sustainable production of high-value chemicals.

Keywords: Cottonseed hulls, furfural, lignocellulosic biomass, Box-Behnken design, Response Surface Methodology, optimization, bio-refinery.

# Cotton Irrigation Scheduling Improvements Using Wetting Front Detectors in Uzbekistan.

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**Background:** The challenges of global population growth and the required growth of requirements for food and natural resource use, including water and land, are not new phenomena. The doubling population of Central Asia since 1980 increased demand for food, which escalated water demand. All water resources in both of the main river basins in Uzbekistan, the Amudarya and Syrdarya, are fully allocated between water users. Limited water resources are one of the crucial issues in Uzbekistan and worldwide. Only 9.6% of total runoff of transboundary rivers in the Aral Sea basin is formed within Uzbekistan. In other words, Uzbekistan is quite dependent upon other riparian countries from the point of view of available water resources. Irrigation is an essential component of crop production in many areas of the world, including most of Uzbekistan. Water scarcity issues have prompted an interest in improved irrigation scheduling methods and enhanced crop water productivity (CWP) of cotton varieties. Considering the aforementioned, we developed objectives for conducting and demonstrating best water management practices through field trials directed to improving efficient use of water in comparison with conventional on-farm irrigation practices in Uzbekistan. The specific objectives of the field trials were:

- 1. To test crop-growth-stage specific Fc-based irrigation scheduling regimes applied to two cotton varieties for optimization of yield and irrigation crop water productivity (ICWP);
- 2. To study the potential of improving irrigation efficiency (IE) by using wetting front detectors and the effects on yield and ICWP.

Results: Previous research established growth-stage-specific irrigation scheduling for upland cotton (Gossypium hirsutum L.) in Uzbekistan. We report further investigation of irrigation scheduling for different cotton varieties and its effect on seed-lint yield and irrigation crop water productivity with and without the use of a wetting front detector (WFD) to trigger irrigation cessation. Field trials were conducted in silt loam soil near Tashkent, Uzbekistan, in 2016, 2017, and 2018. The growth stages of germination to flowering, flowering to boll formation, and maturation were considered for the development of irrigation scheduling regimes with respect to field capacity water content (Fc). The best growth, development and seed-lint yield for the Sultan cotton variety were achieved with irrigations scheduled at soil water content levels of 70, 75, and 65% of Fc during the aforementioned three growth stages, respectively, and were achieved for variety UzPITI-103 with irrigations scheduled at 70, 70, and 60% of Fc during the aforementioned plant growth stages, respectively. There were appreciable varietal differences in water requirement with the early maturing Sultan variety having a more significant water requirement. In contrast, irrigation scheduling with larger Fc values did not result in increasing the yield for the UzPITI-103 cotton variety. In comparison with irrigation without WFD, the use of the WFD decreased irrigation duration by 2.0 to 3.5 hours, net irrigation amount by 7 to 90 m<sup>3</sup> ha<sup>-1</sup>, irrigation runoff by 69 to 134 m<sup>3</sup> ha<sup>-1</sup>, and deep percolation below the root zone by 10 to 17 m<sup>3</sup> ha<sup>-1</sup>, while increasing irrigation crop water productivity by 0.08 to 0.10 kg m<sup>-3</sup> and seed-lint yield by 0.04 to 0.10 Mg ha<sup>-1</sup>. Irrigation scheduling regimes based on percentages of Fc and irrigation with WFD should be considered applicable practices for upland cotton varieties on silt loam soils of the central zone of Uzbekistan and for similar soil-climatic conditions of Central Asian countries.

**Conclusion:** The study investigated the effects of two irrigation scheduling regimes based on percentages of field capacity and the effects of two irrigation methods, with and without wetting front detectors (WFDs) on yield and water use of two cotton cultivars over three seasons on old irrigated silty loam soil of eastern Uzbekistan. The study results revealed that the 70-75-65% of Fc irrigation scheduling regime improved irrigation crop water productivity (ICWP) for the Sultan cotton variety compared with the 70-70-60% of Fc irrigation scheduling regime. In contrast, the 70-70-60% of Fc irrigation scheduling regime resulted in improved ICWP for the UzPITI-103 cotton variety compared with a regime of 70-75-65% of Fc. The 70-70-60% of Fc irrigation scheduling regime resulted in saving 10.7 % of irrigation water compared with the 70-75-65% of Fc regime for the UzPITI-103 cotton variety.

The study results also showed that losses of runoff water and deep percolation below the rooting zone can be reduced by using wetting front detectors (WFDs) with a data logging network that allows the irrigator to achieve wetting of the entire rooting zone while decreasing irrigation duration, runoff and deep percolation of irrigation water, thus increasing irrigation efficiency. Compared with irrigation without WFDs, using WFDs increased irrigation crop water productivity (ICWP) on average by 11.9 and 12.3%, for irrigation scheduling done using the 70-75-65% of Fc regime and 70-70-60% of Fc regime, respectively.

Keywords: cotton; irrigation scheduling; crop water productivity (CWP); wetting front detector.

# Comparative Assessment of Okra and Non-Okra Leaf Cotton (*Gossypium hirsutum* L.) Genotypes for Drought Tolerance

#### Muhammad Iqbal, Certus Seed PVT Ltd Pakistan



**Muhammad Iqbal** 

**Challenges in Pakistan:** Pakistan's cotton production faces several challenges, including the adverse effects of climate change, such as erratic rainfall patterns, high and low temperatures, and water shortages or drought conditions. Cotton crops are also threatened by pests like whiteflies and pink bollworms (PBW), as well as the Cotton Leaf Curl Virus (CLCuV), which reduce crop productivity and quality. Additionally, the gap in GMO technology, high production costs, competition with easier-to-grow crops, and labor-intensive picking practices further contribute to low productivity and profitability in the cotton sector.

**Materials and Methods:** This study focused on evaluating four cotton genotypes: IUB 13 and MM 58 (normal leaf types) and IUB-14052 and IUB-14053 (okra leaf types, derived from IUB 13 and MM 58, respectively). A factorial CRD design was applied, using polyvinyl chloride (PVC) pipes (20 cm diameter, 105 cm column length) with a spacing of 60 cm between plants and 90 cm between rows.

Drought stress was induced 30 days after germination by withholding irrigation. Soil moisture levels were monitored using a Pro Check soil moisture sensor connected to a GS3 sensor (Decagon Inc., Pullman, WA, USA). Various plant traits were measured, including root parameters, leaf area, chlorophyll content, stomatal conductance, transpiration rate, plant height, boll characteristics, and fiber quality using instruments such as the CL-202 leaf area meter and HVI-900-SA fiber testing system.

**Results:** Under drought conditions, the okra leaf genotypes exhibited better drought tolerance than normal leaf genotypes. Parameters such as primary root length, lateral root numbers, root fresh weight, and root dry weight were significantly higher in the okra leaf genotypes. Additionally, stomatal conductance and transpiration rates were reduced in the okra leaf types, indicating enhanced water conservation under moisture stress.



**Conclusions:** The study concludes that okra leaf cotton genotypes demonstrated higher drought tolerance, with improved root growth and water conservation mechanisms. Selection of these genotypes with more lateral roots and deeper primary roots is recommended for enhancing cotton production in regions facing water scarcity and climate change. These findings can inform breeding strategies to improve cotton sustainability under changing environmental conditions.

### Assessment of Physiological and Biochemical Assays in Gossypium hirsutum Under Salt Stress Conditions

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Tehseen Azhar

**Background:** There are several abiotic stresses limiting the productivity of cotton crop. Among those stresses, salinity is an abiotic stress that significantly reduce the crop productivity. The primary purpose of this research was to explore the breeding potential of cotton for salinity tolerance.

**Results:** For this purpose, 100 cotton genotypes were grown in control, 10 dSm-1, 15 dSm-1 and 20 dSm-1 salt stress conditions. Significant level of variation was found in genotypes for chlorophyll contents, root and shoot length, fresh shoot and root weight, dry root and shoot weight, Na+, K+ and K+/ Na+, proline, H2O2, POD and CAT. The genotypes, NIAB-545, CIM-595, Coker-307, FH-113, FH-942, DNH-40 were found to be salt tolerant and Cyto-178, VH-363, FH-326 as salt sensitive genotypes. So, these accessions were hybridized in Line × Tester mating design to find out the genetic components for yield contributing traits in control, 10 dSm-1, 15 dSm-1 and 20 dSm-1 salt stress. Analysis of variance indicated that there were significant differences among genotypes for certain traits. The salt stress

caused the reduction in all traits except Na+, GOT, H2O2 and proline. Non-additive gene action was found for yield, fiber, ionic and biochemical traits except Na+ ions. Proportional contribution to total variance for all the traits was found to be maximum in lines, whereas in was less for testers. Amongst the lines, FH-942 was found to be the best general combiner for plant height, number of bolls and seed cotton yield under control, 10 dSm-1 and 15 dSm-1 and 20 dSm-1, whereas NIAB-545 proved as best general combiner for fiber fineness, fiber length, fiber strength, GOT and catalase under control, 10 dSm-1 and 15 dSm-1 and 20 dSm-1 salt stress and FH-942 had greater GCA effects for K+, proline and CAT under control and various levels of salt stress. Amongst the testers, FH-326 was best general combiner for most of traits, while Cyto-178 had positive and significant GCA effects for fiber fineness, fiber length, fiber strength, POD and catalase under control and salt stress.



Figure-1. The response of NIAB-545 (G88) under various levels of salinity

Figure-2. Salinity affected areas of Pakistan



**Conclusion:** FH-942  $\times$  FH-326 had positive and significant specific combining ability effects for most of the traits and also exhibited significant mid- and better parent heterosis for most of studied traits. The selected hybrid can be utilized in breeding programs against salt stress.

Keywords: Biochemical traits; germplasm; upland cotton; salinity stress

# Improving Soil Health and Mitigating Climate Change With Trichoderma Culture in Cotton

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Muhammad Umar Iqbal

*Trichoderma*, a soil-dwelling fungus, establishes a symbiotic association with various plants, including cotton. A *Trichoderma* strain indigenous to the area was obtained and cultivated to assess its efficacy in treating cotton crops and promoting water stewardship. Various experts have already found and documented that the utilization of *Trichoderma* spp. culture not only decreases the reliance on mineral fertilizer in agriculture but also enhances soil health by augmenting the biological activity of soil. Furthermore, *Trichoderma* spp. function as bio-control agents and enhance plant growth. It is necessary to disseminate the significance of *Trichoderma* for enhancing soil health. A research study was devised using a randomized complete block design (RCBD) in the city of Vehari. Each treatment and control had a plot size of 1 Kanal, which is equivalent to 1/8th of an acre. The treatments consisted of T1, which involved applying *Trichoderma* Culture to the seeds at a rate of one liter per acre, T2, which involved flooding irrigation water with *Trichoderma* Culture at the same rate, T3, which involved applying synthetic Gel with flood irrigation, and T4, which served as the control group with no treatment.



**Results:** The field trial yielded highly favorable results, with T2 and T3 plots requiring 28% less irrigations compared to the control plot. Comparatively, the T2 treatment exhibited a 30% increase in the number of bolls, while the T3 treatment showed a 19% increase in shoot length and a 12% increase in root length compared to the control plot. Similarly, the yield obtained from the control plot was 24% lower than that of T3.

Keywords: Trichoderma, Soil Health, water holding capacity, cotton

#### The Usage of Various Water- and Resource-Saving Technologies in Preparation of Elite Cotton Seeds

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**Background:** Nowadays, our local scientists have created new varieties of cotton that are adaptable to different soil-climate regions and at the same time have high fiber output. However, consistent breeding of quality seeds of their elite and first reproduction generations while preserving the variety characteristics and purity of the varieties, introducing modern resource-saving and water-saving technologies into the seed production system to further increase the weight of the accumulated seeds is based on the negative ecological situation that is observed in our country every year.

Results: Based on the data presented below, we have seen that cotton grown under film has a shorter growing season compared to open grown options. At the same time, we found out how much the role of this technology was felt in the formation of valuable agricultural traits of the seed samples planted under the film. The indicators were different in both planting methods, and the indicators of options under the film and grown by drip irrigation were higher. That is, family 39, in the 1st variant, the weight of one skein of cotton is 6.11 g, the variability between samples is 0.16 g, in the 2nd version, the weight of one skein of cotton is 5.64 g, the variability is 0.24 organized g. Corresponding variations were observed in the rest of the varieties grown in the open air, 20-25% of the 3-8 harvest branch elites, and 35-45% of the 9-12 harvest branches of the varieties irrigated under the film and drip-irrigated under the film were observed. At the same time, it took 114 days until 50% of the bolls opened in the seeds of options 5-6, the weight of 200 bolls of cotton picked for the test was 1210-1194 g, and the weight of one boll of cotton was 6.05-5.97 g, control 1-7-9 days earlier compared to option 2, the weight of the sample was 102.0 g and the weight of one boll of cotton was 0.51-0.60 g higher. In the options grown on the basis of drip irrigation under the film, the day before the opening of 50% of the bolls was delayed by 4-9 days compared to the control option and the option that was irrigated under the film, by the weight of 200 bolls of cotton picked by 60-110g, by the weight of one boll of 0 cotton .16-0.49 g higher, depending on the growth conditions, we observed that it was premature. After conducting a purity check of the varieties grown in 2021, we planted the elites harvested from 3-12 harvest branches in 2022, and conducted comparative studies on the weight of 200 bolls of cotton and the weight of one boll of cotton on the day before 50% of the bolls opened. According to this, 50% bud opening in 201 family 5-6 variants 3-8(3-12) and 9-12(3-12) harvest branch elites is 115-117 days, with this indicator both harvest branch elites compared to the control It ripened 6-5 days earlier than the 3-4 option, which was irrigated under a film for 9 days. The weight of 200 sacks of cotton collected as a test sample was 1254-1256 g, compared to the control by 50-112 g, and compared to the 3-4 option, it was heavier by 34-94 g. 6.38-6.35 g of one boll of cotton was 0.25-0.56 g higher than the control. Family 106 matured 115-117 days in 115-117 days of 50% bud opening in our 11-12 variant, 8-7 days earlier than the control 7-8 variant, and 3 days earlier than the 9-10 variant. The weight of 200 skeins of cotton is 1178-1154 g, compared to the control by 112-110 g, by 78 g compared to the 9-10 option, the weight of one skein of cotton is 5.89-5.77 g, by 0.39 g compared to the control. was high. Also, 50% bud opening in the 17-18 variant elite of family 205 ripened 116-117 days earlier than the control 13-14 variant, 7-8 days earlier, and 6-5 days earlier than the 15-16 variant. The weight of 200 bolls of cotton is 1206-1188 g, 60-104 g less than the control, 24-52 g less than the version irrigated under the film, the weight of one boll cotton is 6.03-5.94 g, 0.12- It was higher by 0.26 g.



**Conclusion:** It can be said that in all three variants of drip irrigation under the film, compared to the parameters of the control and the variant irrigated under the film, the vegetation period was shortened, the weight of one boll of cotton and the weight of 200 bolls of cotton picked for analysis were found to be heavier. Temperature and soil moisture were sufficient for such a difference between planting methods that the film was not taken until the end of the season. As a result, the root system of the plant developed freely without compaction of the soil, it was found that there was little competition in cotton nutrition due to the fact that there were few weeds.

Keywords: Cotton, elite variety, irrigation technology, climate change, film

# Enhancing Carbon Sequestration, Seed Cotton Yield and Sustainability Through Alley Cropping of *Desmanthus virgatus* With Cotton

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Nalayini

**Background:** Inclusion of legume in the cropping system imparts sustainability and improves soil health and saves huge inorganic nitrogen fertilizer. Field experiment was conducted during 2016-17 to 2019-20 cropping seasons at the Central Institute for Cotton research, regional station, Coimbatore to find out the suitable perennial legume crop to be grown as an alley crop in cotton to improve the soil organic carbon status for sustainability and to reduce the inorganic nitrogen requirement of irrigated cotton – maize cropping system. Three perennial legumes viz, *Desmanthus virgatus* (hedge lucern), *Medicago sativa* (lucern) and *Mimosa invisa* (Thornless mimosa) were compared with sole cotton for their suitability to be grown as alley crop during 2016-17 and 17-18 cropping seasons. The best performing perennial legume, *Desmanthus virgatus* was evaluated under graded levels of 75,100 and 125 % RDN along with sole cotton without alley cropping under these three N levels during 2018-19 and 2019-20 cropping season.

**Results:** *Desmanthus virgatus* has been identified as the most suitable perennial legume to be grown as an alley crop in cotton-maize system. Growing of *Desmanthus virgatus* resulted in 208 kg additional seed cotton yield and 319 kg additional maize grain yield during initial screening of perennial legumes. However, the yield improvement due to alley cropping was significant from third year of experimentation with the additional seed cotton yield of 861 kg/ha at 100 % RDN. While the yield improvement of 228 kg /ha and saving of 50 % inorganic N was achieved at 75 % RDN plus alley cropping of *Desmanthus virgatus* as compared to 125 % RDN under sole cotton. Alley cropping resulted in a higher sustainable yield index (SYI) than sole cotton. The soil organic carbon status of soil improved from 0.52 % to 0.86 % in 42 months indicating the feasibility of introducing *Desmanthus virgatus* as alley cropping with cotton for soil health improvement and enhancing the productivity of cotton- maize system under irrigated agro-ecosystem.



**Conclusion:** *Desmanthus virgatus* is the most suitable perennial legume identified for alley cropping in cotton - maize system. This system enhanced the organic carbon status of the soil enhanced the productivity of cotton - maize system and saved inorganic N fertilizers.

Key words: Alley cropping, Desmanthus virgatus, perennial legume, organic carbon and seed cotton yield

### Homogenization of Cotton Fiber Lots Using A Permanent Bale Identification System & Software Tools

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In the Republic of Uzbekistan, a system of identification and automated accounting of cotton fiber bales in accordance with the Permanent Bale Identification (PBI) standards has been developed and introduced. The implementation of this system allows the formation and shipment of homogeneous lots of cotton fiber based on fiber quality indicators determined for each bale on the SCITC (HVI) instrument systems, which are classified according to grade, class, and type. In contrast to the existing system, the formation of homogeneous lots of cotton fibers of wagons or container norms is carried out at the cotton terminals. As part of the project, a stationary bale identification device (console) and software for the identification, accounting, and separation of cotton fiber bales were developed. The implementation of the system was conducted at five cotton ginneries of the "Buxoro Agroklaster" LLC.

**Keywords:** cotton ginnery, cotton fiber, bales, lots, accounting, permanent bale identification (PBI), quantity, quality, SCITC system (HVI), grade, class, data collection terminal (DCT), program, traceability

### Enhanced Lignin Extraction From Cotton Stalk Using Ultrasound-Assisted Ionic Liquid Method

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Lignocellulosic biomass is the second most abundant natural polymer, comprising approximately 10–25% of lignocellulosic biomass. Lignin is widely known for its potential use in the production of biomaterials. In this study, an agricultural waste



cotton stalk is utilized to extract lignin by a pretreatment of liquid hot water (LHW) followed by ultrasound-assisted ionic liquid (UA-IL) extraction, where LHW is utilized to break down pectin and hemicellulose. Response surface methodology (RSM) was used to optimize the extraction process, including extraction time (60 – 180 min), temperature (40 – 60 min), and sample-to-ionic liquid ratio (1/15 – 1/25). The predicted optimized conditions for UA-IL extraction were 52 min, 126 min, and a ratio of 1/25, which resulted in an 8.75% lignin yield. Further research is needed to enhance the purity of the extracted lignin and investigate its functional properties in various applications. Overall, this study highlights the potential use of cotton stalks, an agricultural byproduct, as a valuable resource for lignin extraction, contributing to the advancement of sustainable bioprocessing technologies.

# Physiological Indicators in Plants of Colored Fiber Cotton (Gossypium hirsutum L.)

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In the context of global climate change and the presence of environmental stress factors (drought and salinity) in Uzbekistan, specialists in the field of cotton growing are tasked with creating cotton varieties that combine high with high-quality yields and resistance to adverse environmental factors. On the other hand, the demand for environmentally friendly products of plant origin is increasing globally.

In this study, cotton samples of *G. hirsutum* L. species having naturally colored fibers were grown in lysimeters with 1) optimal water supply; 2) simulated drought- reduced volume of irrigation water); 3) chloride-sulfate type soil salinization of medium degree.

Analysis of the data showed that under conditions of optimal water supply with pre-irrigation soil moisture maintained at 70-72% of the maximum field moisture of the soil, all cotton samples had a higher total water content in the leaves (LWC) than under conditions of stress factors. In the favorable water regime, the highest indicator of the trait was sample A-2384 (77.1%), and the lowest was sample A-800 (68.9%)., both with brown fiber.

Under water deficit conditions, a decrease in the total water content of varying degrees in the leaves was observed. In the water stressed background, the highest indicators of the trait were in samples A-1025 and 010105 (70.0% each), and the lowest in samples 02408 and 011250 with brown fiber and 011302 with green fiber, having 65%,66.7%, and 66.2% LWC, respectively.

In the saline soil also, the LWC was lower than that in the control. Samples with brown fiber (010105, 04494, and A-2384) distinguished by high indicators of the trait having 73.6%, 73.2%, and 72.4% LWC, respectively while sample A-800 contained 68.0% water in the leaves. Plants grown under saline soil had higher LWC than under soil water deficiency.

The transpiration rate was higher under optimal water supply. Under such condition, maximum expression of the trait was observed in sample 04489 and the minimum expression in sample 010105 representing 387.42 mg and 214.93 mg  $H_20^{-1}g$  of raw leaf hour<sup>-1</sup>. Under soil moisture deficient conditions, leaf transpiration intensity in all samples decreased sharply compared to the control. The decrease in these indicators ranged from 30.4% for sample 011460 with green fiber to 61.6% for the Gulshan variety with white fiber. In moisture deficit soil, sample 011302 had a relatively high indicator (181.09 mg) trait and sample 04494 had the lowest (121.83 mg)

In saline soil also, a decrease in the intensity of transpiration of plants was recorded compared to the control, but to a lesser extent than that in water deficit soil. Sample 04489 recorded the highest transpiration rate (297.88 mg) sample A-800 the lowest (151.83 mg).

All cotton samples, in contrast to the two previous traits, had a lower water-holding capacity (WHC) in leaves under stress conditions. Under simulated drought, relatively high WHC values were observed in samples 04494, A-800 and Gulshan variety amounting to 12.7%; 14.3%, and 14.3%, respectively. However, under soil salinity, high leaf WHC was observed in samples 010108 and A-800 with brown fibers (20.6% and 21.6%, respectively)

All cotton samples studied in the experiment had a lower water-holding capacity of leaves under moisture deficit soil than under saline soil. This indicates that water deficit exerts a stronger external stress on cotton plants than average soil salinity. The results indicate different genotypic responses of cotton samples with colored fiber to different external stress conditions, which must be considered when researching adaptive cotton breeding.

Key words: Colored fibre, cotton, leaf water content, transpiration rate, salinity, water stress

# Sustainable Soil Health: The Surge of the ICAC Open-Earth-Cone-Pit Biochar and Bokashi Composting Methods Among Smallholder Farmers in Africa and India

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Sandhya Kranthi

**Training Initiatives:** Over the past three years, post-COVID, with funding support from ITC and GIZ, the ICAC has been conducting training sessions on regenerative agriculture (Regen-Ag) for scientists, agricultural field staff, and farmers in Africa, India, and Bangladesh. The trainings focused on two main technologies: Bokashi composting (Teruo Higa, 1984) and the ICAC open-earth-cone-pit method (Schmidt and Taylor, 2014; Kranthi and Kranthi, 2023) for producing biochar.

**Biochar and Bokashi:** Complementary Technologies for Soil Health Biochar is a robust method for carbon sequestration, while Bokashi is the fastest method of composting. Freshly produced biochar is alkaline (pH 8.0 to 11.0) depending on the feedstock and production method, whereas freshly produced Bokashi is acidic (pH 3.5 to 4.0). Both are carbon-rich, but biochar's carbon is recalcitrant and remains in the soil for several decades, while Bokashi provides nutrients for soil microorganisms and plants, enhancing soil fertility and health. Biochar improves soil structure, water holding capacity,

cation exchange capacity, and reduces carbon emissions.

**Tailoring Soil Amendments to Local Conditions:** In many cotton-growing regions of Zambia and neighboring countries with acidic soils, biochar alone has been effective in soil remediation, increasing productivity of cotton and other crops. In Kenya, Tanzania, and Uganda, where soils are alkaline, Bokashi alone could serve as an excellent compost to improve soil health. A combination of Bokashi and biochar creates a neutral, carbon-rich material called biochar-compost, which can be tailored for any type of soil.

**Practical Implementation and Farmer Training:** The ICAC open-earth-cone-pit method requires only a shovel, dry stalks, a matchstick, and water or soil to produce several tons of biochar in a day. The Bokashi method requires plastic trash bags or buckets, organic farm waste such as finely crushed weeds or leaves, molasses, effective microorganisms (EM), and water to produce excellent compost quickly. Techniques were developed to calculate the optimal proportions of biochar and Bokashi for a potent carbon-rich soil amendment called biochar-compost (Kranthi and Kranthi, 2024). These methods are adaptable by any smallholder farmer globally. The training also emphasized adapting local practices to the six principles of Regen-Ag: avoiding harmful agrochemicals, no-till, cover crops and crop diversity, mulching and organic amendments, crop rotations for year-round live roots, and integrating animal husbandry. Global meta-analyses of scientific evidence show that practices like biochar application can sequester 4.2 tons of CO2 per hectare annually (Chen et al., 2023), no-till farming can sequester up to 1.76 tons of CO2 per hectare (Tadiello et al., 2022), and cover crops can sequester about 1.17 tons of CO2 per hectare (Poeplau and Don, 2015).

**Overcoming Challenges in Adoption:** Smallholder farmers are generally amenable to adopting practices such as cover cropping, avoiding harmful chemicals, crop rotations, organic mulching, and organic amendments, and integrating animal husbandry. However, they often express reservations about no-till farming due to the need for tillage to control weeds. Incorporating Bokashi compost into the topsoil and mulching with either biochar alone or biochar-compost reduces weed problems, encouraging farmers to adopt minimum tillage or no-till farming.

**Success Stories and Impact:** Agricultural transformation efforts under the 'Regenerative Agriculture for Sustainable High Yields' project, funded by the ITC-EU, have yielded remarkable results. Over 350 model farm demonstrations showcased the four essential steps for enhancing crop yields, resulting in more than double the yields in most locations compared to control fields, with some achieving seed cotton yields of up to 2760 kg per hectare. Addressing acidic Zambian soils, the project introduced biochar from cotton stalks, which proved to be highly effective in soil remediation. Training on the mass

production of biochar using the open-earth cone-pit method was provided to over 2000 farmers, leading to the production of about 500 tons of biochar and significantly improving soil health. Eighteen comprehensive training sessions across Zambia from 2021 to 2024 reached approximately 4000 participants, including 25% women. WhatsApp groups were created for participants to exchange project activities, results, field experiences, and technical knowledge, demonstrating the project's transformative potential in enhancing agricultural productivity and sustainability. In April 2023, ICAC conducted a practical training program on the open-earth-cone-pit biochar production technology for about 50 participants, including ESA, Yamoussoukro, SECO Cote d'Ivoire, and Ivoire Coton staff. Under Mr. Mahesh Ramakrishnan's leadership, SECO produced 630 tons of biochar in 2023 and registered 2648 farmers to produce 4100 tons of biochar in 2024. ICAC, with GIZ funding, conducted training programs in Burkina Faso for 60 participants, including 39 master trainers and 28 INERA scientists. A one-week training session in June 2022 included field visits and practical training on biochar production and composting methods. INERA scientists reported positive results from experimental field trials in 2023, showing yield increases in both conventional and organic cotton.



**Field Training Camps and Collaborative Projects:** Field training camps on regenerative agriculture, biochar production, and Bokashi composting methods were conducted in Bangladesh for about 100 field staff of Cotton Connect, in India for about 80 field staff each of Cotton Connect and Better Cotton Initiative (BCI), and in Tanzania for about 50 participants, including senior staff of AbTF, CMiA, ACF, Parrogate, Alliance ginneries, Biosustain, SECO, Louis Dreyfus, SodeCoton, and others, coordinated by the African Cotton Foundation (ACF) and the Aid by Trade Foundation (AbTF). In collaboration with CIRAD, France, ICAC recently launched a project titled 'Adapting Innovations for Resilience to Climate Change for Smallholder Cotton Farmers in Africa' to be imple-

mented in Cameroon from Dec 2023 to Dec 2026. Funded by GIZ and implemented by the Institute of Agricultural Research for Development (IRAD) and SodeCoton, this project aims to rejuvenate soil health for 4,800 smallholder farmers (over 15% women), increase income through higher yields and climate-resilient technologies, generate additional income for women entrepreneurs, and train 60 extension workers in each of the two countries.

**Conclusion:** The simplicity of the ICAC open-earth cone-pit biochar method and Bokashi production techniques is enabling rapid adoption of these carbon-sequestering technologies among smallholder farmers in Africa and India. The straightforward, low-cost approach of the open-earth cone-pit method, requiring only basic tools and materials, along with the easily implementable Bokashi composting process, makes these technologies accessible to farmers with limited resources. This accessibility has led to widespread adoption, significantly enhancing sustainable soil health. By integrating these practices, farmers are improving soil structure, increasing nutrient availability, and enhancing water retention, all while sequestering carbon and mitigating climate change. The surge in adoption of these methods is a testament to their effectiveness and practicality, driving a transformation in agricultural practices that promises long-term soil fertility and sustainable farming for smallholder communities in these regions.

#### References

- Chen, S., Zhu, L., Sun, L., Huang, Q., Zhang, Y., Li, X., Ye, X., Li, Y. and Wang, L., 2023. A systematic review of the life cycle environmental performance of cotton textile products. Science of The Total Environment, 883, pp. 1636-59. https://doi.org/10.1016/j.scitotenv.2023.163659.
- Kranthi, K.R. and Kranthi, S., 2023. Production of Biochar from Cotton Stalks Using the Cone-Pit Open Earth Kiln Technique. The ICAC Recorder, March 2023, pp. 6-23.
- Kranthi, K.R. and Kranthi, S., 2024. A Practical Guide on Production and Application of Biochar and Bokashi to Rejuvenate Soil Health. International Cotton Advisory Committee, June 2024.
- Poeplau, C. and Don, A., 2015. Carbon sequestration in agricultural soils via cultivation of cover crops A meta-analysis. Agriculture, Ecosystems & Environment, 200, pp. 33-41.
- Schmidt, H.P. and Taylor, P., 2014. Kon-Tiki flame cap pyrolysis for the democratization of biochar production. Ithaka-Journal for Biochar Materials, Ecosystems and Agriculture (IJ-bea), Arbaz, Switzerland, pp. 338-348. Available at: <u>www.ithaka-journal.net/86</u>.
- Tadiello, T., Acutis, M., Perego, A., Schillaci, C. and Valkama, E., 2023. Soil organic carbon under conservation agriculture in Mediterranean and humid subtropical climates: Global meta-analysis. European Journal of Soil Science, 74(1), p. e13338.
- Higa, T. and Parr, J.F., 1994. Beneficial and effective microorganisms for a sustainable agriculture and environment (Vol. 1, pp. 16-16). Atami: International Nature Farming Research Center.

# Trend Analysis of Time Series Precipitation Data & Its Genesis Effect on Cotton in India

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Sankaranarayanan

**Background:** Increasing frequency of extreme weather events such as increasing trend in wet and dry spell periods and occurrence of intense rainfall events in a short span are some of the reasons attributed for low productivity of cotton in India during the recent years. In this study, one location each was selected from the north (Bathinda, Punjab state), central (Nanded, Maharashtra) and southern (Nandyal, Andhra Pradesh) cotton growing zones and analysis of long-term rainfall was performed to understand changes in rainfall pattern on cotton productivity. Daily rainfall intensity, wet spell, dry spell and seasonal rainfall data were analysed for trends employing Modified Mann-Kendall (MMK) and Innovative Trend Analysis Method (ITAM).

**Results:** The analysis of extreme rainfall intensity per day at Bathinda (North Zone), Nanded (Central Zone) and Nandyal (South Zone) indicated significant increasing rate with P values of 0.0015, 0.047

and 0.0001, respectively. Weather aberration of wet spell periods analysis revealed significant increasing trend at Bathinda (P value- <0.001) and Nanded (P value- 0.011). At Nandyal decreasing trend of wet spell periods was noticed (p-value - <0.001). Increasing extreme rainfall events and wet spell periods lead to water logging and subsequently affect cotton crop growth and production. Analysis of dry spell periods revealed a significant declining trend at Bathinda (P value- <0.001), however, a significant increasing trend was observed at Nanded and Nandyal (p-values - 0.046 and - <0.001, respectively). The increasing dry spell periods within the crop duration affected crop growth at Nanded in the central zone and at Nandyal in the South Zone, where more than 60 percent of cotton crop is rainfed.

Crop growth stage-wise analysis of rainfall pattern by performing MMK and ITAM tests revealed that at Bathinda, an increase in rainfall was observed during the early vegetative stage, squaring and flowering stages (p-values of 0.0011 and 0.0015). At Nanded, a significant increase in rainfall pattern was noticed at the boll maturity stage (p value of 0.03). At Nandyal, a significant increase in the early vegetative stage (p=<0.001) and a decreasing trend in rainfall pattern were observed during the squaring and flowering stages (p=<0.001).



**Conclusion:** Trend analysis indicated increasing extreme rainfall intensity in all the three zones, increasing dry spells in the central and southern zones and increasing wet spells in the north and central zones. Increase in the trend in wet spells coinciding with the early growth stage and dry spells at squaring and flowering stages adversely affected crop growth. Hence, adoption of best practices to cope with the increasing trend in extreme weather events is imperative to impart climate resilience in both irrigated north zone and rainfed central and southern cotton growing zones in India.

Keywords: Climate change; rainfall variability, Extreme rainfall intensity, Dry spell, Wet spell, cotton production and productivity

# Development of Regenerative Agroforestry-Based Cotton Production in Italy

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**Introduction:** Cotton is an ancient crop and the most widely used fiber in various parts of the world. Since the Middle Ages, cotton consumption, cultivation, and production have been prevalent throughout the Mediterranean Basin, particularly in Italy. However, cotton production in Italy declined in the latter half of the 20th century due to competition from synthetic fibers and high input costs associated with cotton farming systems. Nevertheless, driven by the fashion industry's keen interest in developing an Italian cotton value chain, the European Forest Institute, in collaboration with the Circular Bioeconomy Alliance and with support from Giorgio Armani SpA, has initiated a five-year cotton regenerative agroforestry project experiment at the CREA-AA Experimental Farm in Rutigliano (BA). This project serves as a showcase for the Mediterranean regions of Italy.

Scarascia-Mugnozza

**Objectives:** The primary goal of this research is to restore and scientifically evaluate regenerative agroforestry-based cotton production systems in Italy. Specific objectives include:

- 1. Testing alternative agroforestry and regenerative farming practices to produce sustainable cotton.
- 2. Applying precision farming techniques to optimize irrigation and soil fertility in cotton crop management.
- 3. Monitoring the provision of agroforestry ecosystem services.

**Methodology:** The initial experiment was conducted with regenerative monocropping of cotton (MC) on a plot of about 0.7 hectares and cotton regenerative agroforestry (CAF) on a 0.3-hectare plot, where cotton was grown intercropped with a seven-year-old late-ripening peach orchard.





Results: Measurements of leaf area index (LAI), plant productivity, physiological parameters, water status, and soil water content were taken throughout the growing season. The results showed no significant difference in the final LAI between the two systems, although the MC cotton exhibited a higher LAI during the mid-growth stages. Cotton plant productivity was comparable between the two systems (AF:  $32.21 \pm 4.28$  g; MC:  $34.12 \pm 3.77$  g per plant), with no significant difference in water productivity (WPi) between treatments (p>0.05). WPi was 0.96 kg m-3 for MC and 1.03 kg m-3 for AF. It is important to note that the reduced seed fiber cotton production in the CAF treatment is attributed to the presence of the densely planted peach orchard, which is adapted to an agroforestry system for cotton. Physiologically, CAF cotton showed improved performance during the late flowering stage, with higher net assimilation rates (AF:  $36.03 \pm$  $0.92 \ \mu mol \ m-2 \ s-1$ ; MC:  $28.59 \pm 1.69 \ \mu mol \ m-2 \ s-1$ ) and electron transport rates (AF:  $255.85 \pm 0.88 \mu mol m - 2 s - 1$ ; MC:  $206.95 \pm 9.87$  $\mu$ mol m-2 s-1). The land equivalent ratio (1.35) indicated higher land-use efficiency in the CAF system. Additionally, CAF cotton demonstrated enhanced soil water retention and water-use efficiency. Other monitored ecosystem services include carbon sequestration in soil and biomass, annual GHG budget (utilizing the eddy covariance approach), and impacts on the landscape of the agroforestry system. These findings suggest that intercropping cotton with peach trees may provide a viable approach to improving land productivity and resource use in Mediterranean agroecosystems.

**Conclusions:** The study will continue to validate the production impacts of the regenerative cotton production system in the study region. Additionally, a certification scheme for regenerative agroforestry will be implemented.

Key words: Cotton, Regenerative agroforestry, Italy, Mediterranean region.
# Cotton Root Configuration Typing & Cotton Root Plasticity Development Under Drought Resistance

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Minsun Si

**Background:** Due to the global climate change and the low utilization rate of agricultural irrigation water, drought stress has become an important factor restricting cotton production. The root system is the main organ to absorb water and nutrients, and the growth state of the root system will directly affect the absorption and utilization of nutrients, the ability to resist abiotic stress and the yield of cotton. Cotton root system is a straight root system, which is composed of deep taproots, widely distributed lateral roots, branch roots and thin heels. Four main phenotypic characters, namely taproot length, root fresh weight, root dry weight and lateral root Angle, were collected from 220 upland cotton natural population cultured by hydroponics.

**Results**: The analysis showed that the four root traits were distributed continuously, conforming to normal distribution, and the variation range was wide. Cotton roots were divided into 3 grades and 9 types by principal component analysis with fresh root weight and taproot length as main indexes.

In the natural population, the number of materials with high fresh root weight and long taproots was more, accounting for 47% of the total number of materials, the number of lateral roots was denser, the root system was more developed, and the absorption and utilization of nutrients were stronger, which was conducive to the later growth of cotton. Ten resource materials with long taproot length and high fresh weight, such as ZY126, ZY318 and ZY406, were selected. The study further conducted genome-wide association analysis of natural populations and correlated them to two loci by fresh root weight and dry root weight. On the other hand, the high-flux root phenotype platform was used to collect the root growth morphology of the natural population materials under normal and drought stress in multiple periods, and 23 digital indexes such as root area and root depth were obtained, and the drought resistance coefficient and drought resistance index of each index were calculated. Through the drought resistance coefficient of root area, root depth, root area below 20cm and other indicators, the root configuration of cotton under drought treatment and normal conditions were compared and analyzed and combined with the evaluation of the above-ground digital index, the ideal drought resistance root configuration of cotton was defined.

Figure: Ideal drought resistant root system of cotton





**Conclusion:** This study comprehensively evaluated the root configuration of cotton under drought treatment and normal conditions through high-throughput collection of root phenotypic traits of natural populations, combined with digitization indexes of the ground part, and identified the ideal root configuration for drought resistance of cotton. It provides resources and theoretical basis for analyzing the mechanism of cotton root plasticity development under drought and the genetic mechanism of cotton response to drought stress through root configuration changes.

# Potential Impacts of Climate Change on Cotton Production in the High Plains & Rolling Plains of Texas

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**Background:** Air temperature and carbon dioxide  $(CO_2)$  concentration are important abiotic factors that control the growth and development of cotton (*Gossypium hirsutum* L.). Global climate models (GCMs) project an increase in air temperature and  $CO_2$  concentration in the future in the Texas High Plains (THP) and Texas Rolling Plains (TRP), which are major cotton growing regions in the United States.

The objective of this study was to evaluate the effects of projected changes in future climate on cotton production at Halfway in the THP and Chillicothe in the TRP using the DSSAT CROPGRO-Cotton model. The latest Coupled Model Intercomparison Project Phase 6 (CMIP6) climate projections of nine GCMs from 1950 to 2100 were obtained for the study sites for four Shared Socioeconomic Pathway (SSP) scenarios: SSP1-2.6, SSP2-4.5, SSP3-7.0, and SSP4-8.5.

Data was categorized into four time periods: Historic (1950-2014), Near-future (2015-2040), Mid-century (2041-2070), and Late-century (2071-2100) to assess the effects of projected climate change on cotton phenology, harvest dates, seed cotton yield, and irrigation water requirement at both sites.

**Results:** Compared to the historical period, growing season length (i.e., time to harvest) is expected to reduce by 17-25 days at Halfway and 6-10 days at Chillicothe in the future.

In contrast, irrigated seed cotton yield is expected to increase in the future within a range of 11-18% at Halfway and 3-13% at Chillicothe, with the highest increase being in the mid-century period at both the sites. However, the expected yield increase in the future could be possible only with the increase in irrigation water requirement, which ranged from 1% to 10% at Halfway and from 13% to 30% at Chillicothe.

Differences among SSPs at Halfway were mainly for changes in season length ranging from 14 to 35 days, and those at Chillicothe were largely for changes in irrigation water requirement ranging from 103 to 184 mm.



**Crop Yield** 

**Irrigation Demand** 

**Heat Stress** 

**Pest Infestation** 

**Conclusion:** Irrigated seed cotton yield and irrigation water requirement are expected to increase while the growing season length is expected to decrease in the future at both sites. However, the magnitude of the change could vary spatially, and hence site-specific adaptation strategies must be considered to achieve higher cotton yields with minimum increase in irrigation water use in the future.

Key words: Air temperature; CO<sub>2</sub> concentration; CMIP6; DSSAT model; irrigation water requirement; seed cotton yield.

# Hyperspectral Reflectance-Based Water Stress Analysis of Irrigated Cotton in Semi-Arid Regions of India.

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**Background:** It has been observed that the water stress of various crops can be identified and quantified by the hyperspectral response of the crop canopy. To investigate the hyperspectral response of cotton under different water stress levels and to explore the potential of using this response for cotton irrigation and water management, an experiment was conducted in clayey soil at the experimental farm of the RKVY-IWARS Project at Mahatma Phule Agricultural University, Rahuri. The cotton was subjected to six water stress regimes, namely 100, 80, 60, 40, 20, and 0% of crop evapotranspiration (ETc) corresponding to I1: No WS, I2: 20% WS, I3: 40% WS, I4: 60% WS, I5: 80% WS, and I6: 100% WS. Irrigations were applied according to the specific water stress levels using a drip irrigation system. The experimental design was a randomized block with four replications and six irrigation regime treatments.

### Sunil Gorantiwar

**Results:** Hyperspectral reflectance was measured weekly for all treatments using a Spectroradiometer (350-2500 nm) at a spectral interval of 1 nm, covering the full electromagnetic spectrum throughout the cotton growth period. Spectral signatures were developed from the measured hyperspectral reflectance data. The indirect water-sensitive spectral vegetation index, NDVI (Normalized Difference Vegetation Index), and the direct water-sensitive spectral index, NDWI (Normalized Difference Water Index), were derived from these signatures. The spectral signatures indicated that hyperspectral reflectance in the visible range (350-700 nm) increased with heightened water stress, while it decreased in the near-infrared range (NIR, 700-1300 nm). Both NDVI and NDWI decreased progressively as water stress increased from 0% to 100% WS. This analysis demonstrated that water stress in cotton could be quantified using spectral reflectances, particularly in the IR and NIR regions.



**Conclusions:** Ground-based hyperspectral reflectance measurements of the crop canopy are crucial for quantifying water stress, making it a valuable tool for irrigation water management in semi-arid conditions. The use of NDVI and NDWI provides a practical approach to monitor and manage water resources effectively in cotton cultivation under varying water stress conditions.

# Using Natural Biomarker to Authenticate the Textile Cotton Materials

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Suzan Sanad

The present investigation describes a process designed to integrate biomarkers into textile substrates (either fibers, yarns, knitted or woven fabrics, or garments). The stage of application and related application conditions are selected to ensure the stability and durability of the biomarker activity for the required shelf life and life span. Textile fibers that can be treated with the method of the invention include all-natural fibers (both plant and animal fibers, including but not limited to cotton, flax, hemp, wool, and silk). Accordingly, two- and three-dimensional textile constructions obtained

from the blow room, carding, combing, spinning, weaving, knitting, nonwoven, and knitting are possible substrates for the invention.

**Figure:** Affixed binding: Direct Binding of DNA to Textile



# Assessment of Best Farm Practices and Extension Innovations to Improve Yield In Cotton - A Pilot Study

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UshaRani Joshua

**Background:** Cotton productivity in India has remained stagnant and low for a long period. Technologies, development programs, supporting policies and meticulous farmers are around to increase crop yield but reach to the stakeholders with appropriate technologies and diffusion tools is the pressing priority. Additionally, efforts to transform the climate sensitive cotton production to a climate resilient production system is an immediate priority to prevent recurrence of disruption in cotton supply and provide available quality cotton for domestic consumption by the cotton-based textile sector.

**Results**: To demonstrate the Best Farm Practices (BFP) through establishment of action learning field sites and field demonstrations, a total of 421 demonstrations were conducted in 632 farmers' fields at 25 districts in 11 cotton growing states of India. In addition to demonstrations by the scientists, the BFP beneficiaries were supported with Best Extension Practices (BEP) viz., pre and post season stakeholders interface meetings, training programs, special programs, Farmers Field Schools, voice

advisories, Information Education and Communication (IEC) products and their dissemination through Information Communication Technology (ICT) tools. The impact of the demonstrations on BFPs supported by good extension practices was measured in terms of increase in yield in comparison to the local farmer's practices. Diffusion of BFP in cotton using BEP in all three agro climatic zones has increased the seed cotton yield from 225 kg to 2100 kg per hectare in a sustainable manner and brought desirable changes in the knowledge augmentation of cotton growers.

**Conclusion:** Targeting these BFPs and BEPs tailored to the agro-ecological conditions, bio-physical endowments and socio-economic profile at district level would pave way for yield realization and knowledge augmentation in Indian cotton production system.

**Keywords:** Cotton, India, Best Farm Practices (BFP), Best Extension Practices (BEP), stakeholders, Participatory Action Research (PAR), Information, Education and Communication (IEC), Information Communication Technology (ICT)

# Planting Date and Plant Density Effects on the Performance of Contemporary Asiatic Diploid (*Gossypium arboreum* L.) Genotypes on Rainfed Vertsol and Inceptisol

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MV Venugopalan

**Background:** The Asiatic diploid cotton, *Gossypium arboreum*, has a rich history rooted in the Indian sub-continent. Despite possessing desirable traits such as resistance to abiotic stresses, tolerance to pests, and disease resistance, *G. arboreum* faced challenges in adoption due to factors like lanky plant architecture, long duration, poor productivity, and fiber quality issues. In recent decades, concerted efforts by cotton breeders have overcome many of these challenges. To enhance their yield, site-specific agronomic interventions, such as selecting suitable soil-site combinations, choosing appropriate cultivars, and optimizing planting times and plant densities are required. This field experiment was conducted during the monsoon seasons of 2017-18 and 2018-19 to evaluate the productivity potential of contemporary *G. arboreum* genotypes under rainfed conditions on two dominant soil types - Vertsol and Vertic Inceptisol at the ICAR-Central institute for Cotton Research, Nagpur, India.

**Results:** The study involved seven *G. arboreum* genotypes (DLSa-17, PA-528, PA-402, PA-812, PA-760, CNA-1041 and Phule Dhanwantary) planted across two plant densities (high density: 111,111 plants/ha and normal density: 55,555 plants/ha) on two sowing dates (Timely: with onset of monsoon and late: 14 days delay). Analysis of pooled data (over years) indicated that planting date and plant density significantly influenced various parameters such as boll density, seed cotton yield, plant height, and days to first flower. Under identical climatic conditions, averaged over sowing dates, planting densities and genotypes, the seed cotton yield of *G. arboreum* cotton was 2516 kg/ha on Vertic Incepisol as against 2151 kg/ha on Vertisol. A delay in sowing by a fortnight significantly reduced the seed cotton yield from 2889 kg/ha to 2142 kg/ha on a Vertic Inceptisol but this reduction was lower, from 2275 kg/ha to 2028 kg/ha on a Vertisol. Averaged over sowing dates and genotypes, planting in a high-density system (111,111 plants/ha) provided a yield advantage of 326 kg/ha on a Veric Inceptisol and 239 kg/ha on the Vertisol over normal spacing (55,555 plants/ha). The interaction between genotype and sowing date was significant on both the soil types. The yield of long linted genotypes (PA 812 and PA 760) were not significantly lower than that of medium long genotypes viz. PA 402 and CNA 1041. Genotype PA812 had the highest fibre length of 29.1 mm whereas Phule Dhanwantari, was short-stapled (15.6 mm) and coarse with high elongation index.



**Conclusion:** Timely sowing with the onset of monsoon and high-density planting systems demonstrated positive effects on boll density and seed cotton yield of contemporary *G. arboreum* genotypes. The magnitude of yield increases due to HDPS higher in the Vertic Inceptisol as compared to the Vertisol. The study revealed significant interactions between planting dates and genotypes, emphasizing the need for tailored agronomic practices based on both environmental conditions and genotype characteristics.

Keywords: Asiatic cotton, crop density, fiber quality, productivity, sowing window

# POSTER PRESENTATIONS CROP PRODUCTION



# Designing a Biodiversity Enhancement Strategy for Better Cotton

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**Introduction:** Agricultural land-use change poses a significant threat to global biodiversity, exacerbated by the need for agricultural expansion. This underscores the urgency for a globally replicable strategy for biodiversity conservation, especially in agriculture. Cotton, a major non-food crop, is central to sustainability efforts, and leading certification Better Cotton have placed biodiversity as a key aspect of their Principles and Criteria which is followed by with over 2.2 million farmers globally. Through this research, Better Cotton are actively working to understand how biodiversity standards can be met at farm level through baselining and the delivery of interventions following a methodology that is scalable and replicable.

**Methodology:** The aim of this work has been to develop the baseline methodology which directly leads to biodiversity enhancement in cotton growing communities, to meet the biodiversity aspect of the Better Cotton Principle and Criteria. To design a methodology, research centered in Shujabad, Multan, Pakistan. Three Better Cotton Learning Groups (LGs) were selected based on habitat diversity and community access. A Biodiversity baseline methodology involving desk research, remote sensing, and field surveys for both primary data collection and community perceptions and values was developed through a codesign and learning cycles. Primary data on species were collected through opportunistic transect and vantage point surveys, and these methods were chosen through field trials to understand the most suitable methodologies for the implementing partners and communities to ensure long term data collection and scalability. Community interactions and focus group discussions provided insights into indigenous knowledge and biodiversity values to provide a ground up understanding of what enhancement was needed. These data streams lead to the creation of the biodiversity profile for the LG and then guides the creation of Community Biodiversity Enhancement Plans (CBEPs).

**Results:** Findings highlighted the need for multifaceted data collection, integrating social dynamics and field data to baseline biodiversity in small holder farming communities for cotton. Focus groups revealed community practices impacting biodiversity, such as excessive pesticide use and extermination of certain species which spoke to further holistic thinking of biodiversity as part of the wider ecosystem services. While detailed assessments were conducted in specific areas in the initial design of the methodology, global scalability requires balancing community data collection with scientific rigor and will include a sampling methodology. CBEPs were designed with interventions that focus on both on-farm and off-farm interventions, whilst considering the governance of such interventions and the cost and implementation challenges with training for local staff proving effective, indicating scalability potential.



**Conclusions:** Agricultural practices impact biodiversity, evident in Better Cotton small holder communities. This research offers a comprehensive, replicable methodology for biodiversity baselining and enhancement planning. It aligns with global sustainability frameworks, providing a model adaptable to various landscapes. Future work should refine this methodology in further learning cycles, testing it across diverse contexts, commodities, and scales. The paper aims to invite others to pilot and adapt this method for broader applicability.

Keywords: Biodiversity, Cotton, Community Engagement, Baseline Methodology, Biodiversity enhancement, Farm Systems, Global Frameworks.

# Biodegradation of Gossypol in Cottonseed Meal Using Gut Bacteria Isolated From Cotton Bollworm, *Helicoverpa armiger*a (Hubner)

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**Background:** Cottonseed meal is a by-product of the cotton crop obtained after the seeds are crushed to extract oil. Cotton seeds are a rich source of high-quality proteins. However, the consumption of cottonseed is hampered due to the presence of gossypol, which is highly toxic to monogastric and ruminant animals and may impede growth and cause abnormalities in the intestine, reproductive, and other internal organs. In this study, we have isolated gossypol-degrading bacteria from the gut of *Helicoverpa armigera* to study its potential impact on the biodegradation of gossypol in cottonseed meal.

**Results:** About 42x10<sup>2</sup> cfu/ml microbial load was isolated from the gut of H. armigera on LB medium. From this, twenty-three isolates could grow on an LB medium containing gossypol. Among the 23 isolates, three utilized gossypol as the sole carbon source. They were identified as *Klebsiella tremonti* (H6), *Kosakonia cowan* (H8), and *Enterobacter bugandensis* (H10) based on 16S rRNA sequencing and phylogenetic analysis. The fermentation conditions for the biodegradation of gossypol in cottonseed meal using the isolated bacterial isolates were optimized. The biodegradation of gossypol in cottonseed meal was maximum when the incubation period was 72 h, with a pH of 10.0, temperature of 40 C, and moisture content of 70%. The amount of gossypol degraded by H6, H8, and H10 isolates at optimized conditions was 65, 68, and 73%, respectively.

**Conclusion:** The results indicate that the isolated bacterial isolates were able to utilize gossypol as sole carbon source and thus can be implicated in the biodegradation of gossypol in cotton seed meal.

# Introduction of organic farming in Uzbekistan

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**Background:** Reforms carried out in agriculture in Uzbekistan are aimed at increasing the production of high-quality seeds, increasing yields, increasing the yield of products, as well as reducing the impact of agro-industrial chemicals on the environment. The development of organic agriculture not only allows the production of high quality food products that are healthy for human health, but also contributes to the preservation of the environment, increasing the sustainability of ecological, social and economic development of the country's regions. Organic farming is becoming increasingly popular around the world, as it provides a number of benefits such as environmental protection, improvement of human health, positive development of the economy of countries.

**Results:** The research was conducted at the Cotton Breeding, Seed Production Agrotechnology Research Institute, on cotton fields belonging to 'POLY TEX SIRDARYO' LLC in Syrdarya region, 'BCT Cluster Agrokompleks' LLC in Bukhara region and 'UCHKURGAN TEXTILE' LLC in Namangan region. Also, for cultivation of organic cotton seeds 'ORGANIC CHLOPOK' LLC was established on a 10-ha plot of land in Boston district of Saikhunabad district, District No. 191, owned by 'POLY TEX SIRDARYO' company. Seeds of cotton varieties (C-8296, C-6580, C-5707, C-6575, Bukhara-102) included in the State Register and recommended for planting in the Republic of Uzbekistan were used for the study. Seed yield, fibre and raw cotton weight of one boll in variety C-8296 were 62.1-63.5%, 33.6-34.6% and 4, 7-4.9 g, in variety C-6580 - 61.9-63.1%, 34.3-35.6% and 4.4-4.6 g, in variety C-5707 - 62.6-64.1%, 33.3-34.7% and 5.0-5.1 g, and in variety Bukhara-102 - 61.5-62.1%, 33.6-34.6% and 6.2- 6.4 g. When cultivating cotton under organic farming conditions it was possible to obtain additional yield compared to the control in variety C-8296 1.0-2.9 c/ha, in variety C-6580 - 2.8-3.7 c/ha, in variety C-5707 - 1.4-3.3 tonnes/ha and in variety Bukhara-102 - 2.1-3.2 c/ha. In production experiments cotton yield was 22.3-24.5 c/ha in Syrdarya region, 36.4-40.3 c/ha in Namangan region, 23.9-25.6 c/ha in Bukhara region with additional yields of 0.7-2.2 c/ha, 1.2-1.9 c/ha and 0.8-1.7 c/ha, respectively.

**Conclusion:** The results demonstrate the feasibility to introduce organic farming in Uzbekistan.

# Effect of Irrigation Scheduling, Fertilizer Rate & Plant Density on the Root System of Cotton Varieties

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**Background:** In the advanced stages of cotton development, including harvesting, the root system plays a crucial role among various important organs. Creating the necessary conditions for obtaining a high-quality cotton harvest is essential. Only a well-formed and developed root system can provide the above-ground parts of the cotton plant with sufficient moisture and nutrients. One of the most important physiological properties of roots is their ability to absorb water and nutrients from the soil. Substances transferred to the plant body through the root react with carbonic acid in the process of photosynthesis, which then spread to all organs of the plant, including the root. Another critical feature of the roots is that they release various acids and absorb insoluble micronutrients. The root consists of the growing meristem and elongation parts, which divide continuously and support the growth of the root; after division stops, elongation begins. This occurs under the influence of morphophysiological changes, and the last tip of the root sheath is called the rhizodermis. The rhizodermis consists of a single layer of cells that form the root hairs, enhancing water absorption.

**Results:** During our scientific research conducted from 2015-2017, we annually dug up the roots of cotton varieties at the end of the growing period, cleaned the soil stuck to the roots, and recorded the image of the root on millimeter paper. We determined that the thickest part of the tap root was at the root neck and measured 1.0-1.7 cm in diameter. We observed that when the taproot penetrates 5-7 cm from the surface of the earth to the lower layers, primary side roots gradually begin to appear. The first lateral root gave rise to the second-order root, and from it, the third-order rhizomes and other root hairs developed. In irrigation schedules of 75-75-65% field capacity (Fc), when fertilizers were applied at the rate of N180, P126, K90 kg/ha, and with a plant density of 80-90 thousand plants/ha, in the "Sultan" cotton variety, it was found that the roots stretched downward up to 1.0 - 1.15 meters. In this irrigation system, the root system extended deeper than in plant densities of 100-110 thousand plants/ha, where it was found that there is less evaporation in the soil. For a plant density of 80-90 thousand plants/ha, it was concluded that the ability to retain moisture in the soil is better compared to a plant density of 100-110 thousand plants/ha. The root system of the S-6541 cotton variety spread laterally to 0.38-0.45 meters at an acceptable depth, different from the "Sultan" cotton variety. From our research, it was found that compared to the Sultan variety, the roots of the S-6524 cotton variety grew sideways under appropriate conditions.

**Conclusions:** As a result of our research, it was found that with the increase of irrigation rates in the studied cotton varieties, instead of growing deep, the root system spread laterally up to 50-55 cm, and down to 0.80-0.90 m. Therefore, watering procedures and nutrition standards have a direct effect on the development of not only the above-ground part but also on the changes in their root system. From the above, it became clear that in irrigation scheduling of 75-75-65% Fc, and when fertilizers were applied at the rate of N220, P154, K110 kg/ha, the roots of the cotton variety "Sultan" were 0.90-1.0 meters deep and 0.35-0.40 meters wide. When the above rates of fertilizers are used, and with irrigation scheduling of 75-75-65% Fc, it was observed that instead of growing deep, the roots of the S-6524 cotton variety spread to the sides up to 0.50-0.60 meters, and up to 0.80-0.85 meters deep. When comparing irrigation scheduling of 75-75-65% Fc with fertilizer norms N180, P126, K90 to those of N220, P154, K110 kg/ha, the roots of cotton are located closer to the surface of the earth due to sufficient moisture and nutrients in the soil.



# Evaluation of Last Effective Bloom Dates of Cotton in North Carolina

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In North Carolina, cotton planting typically begins around April 25<sup>th</sup>, and the first crop insurance deadline is May 25<sup>th</sup>, with gradual deductions in insurance coverage continuing to the end of May, at which point, coverage expires. In North Carolina, adversely cool and/or wet weather often occurs during the typical planting window, which can delay planting into June, beyond the crop insurance deadlines. As such, cotton growers in North Carolina have a more compressed planting season than most other states in the U.S., and the problem is exacerbated by the increase in acreage of modern growers compared to that of 20 years ago. In some years, slow early season growth can result from prolonged cool weather that occurs after planting is completed, which can further delay maturity. Additionally, summer rainfall patterns occasionally reward later planted cotton, as well as tropical events that can occur during early Fall which often penalizes the bottom crop of early planted cotton. It has long been believed that the last effective bloom dates were on, or around, August 15<sup>th</sup> for the northern regions of North Carolina, which have been extended into August 20-25<sup>th</sup> more recently.

Anecdotal observations in recent years also suggest that the probability of a bloom maturing into a harvestable boll is noticeably higher at later dates than previously thought. Additionally, other observations suggest that the probability of blooms maturing into harvestable bolls may be dependent on defoliation timing relative to prevailing heat unit accumulation in the Fall. For these reasons, additional research was conducted, with the primary objective to determine the latest date at which a bloom has a reasonable chance of maturing into a harvestable boll in North Carolina, and to determine how different harvest aid termination dates may affect last effective bloom date.

Research was conducted in six locations during 2021-2022 to observe last effective bloom dates across multiple environments in NC. This research was expanded to four locations (Sandhills, Rocky Mount, Lewiston, and Plymouth NC) in 2023 to evaluate the effect of termination date on last effective bloom date. Cotton was planted around June 20-25<sup>th</sup> during 2021-2022, and July 6<sup>th</sup> in 2023, which is significantly later than normal, in order to delay cutout as late as possible with intentions to ensure the continuity of progressive upward blooming further into the Fall.

Weekly insecticide sprays were conducted during the growing season in order to maximize retention of blooms/bolls, and to minimize losses due to lygus insects. Treatments consisted of six flagging dates and two defoliation/termination dates, and were arranged in a randomized complete block design with four replications. Fifteen white blooms per plot were flagged, beginning around August 25<sup>th</sup> in each year, and were conducted weekly through September 20<sup>th</sup>. Two termination dates were implemented in 2023: October 16<sup>th</sup>, 2023 (Average date at which additional meaningful heat unit accumulation becomes unlikely) and November 1<sup>st</sup>, 2023 (average date of first frost) using standard rates of thidiazuron plus diuron, and ethephon, to defoliate leaves, remove and prevent regrowth, and to accelerate boll opening, all of which is a typical practice of cotton growers in this region. Flagged bolls were counted during the week of 11/6/2023 and categorized as fully open and harvestable, cracked/partially open, cracked when light pressure was applied, or closed/not likely to open. Data were subjected to ANOVA and means were separated according to Fishers Protected LSD at  $p \le 0.05$ . Data were also subjected to regression analysis.

The initial phase of this research, which was conducted during 2021-2022, suggested that last effective bloom dates were around the end of August during years with cooler Fall temperatures, and mid-September for more southern environments, but this was inconsistent among the site years evaluated (data not shown). This inconsistency led to the question of whether or not defoliation timing may influence the probability of blooms maturing into harvestable bolls. As seen in Figure 1., the average heat unit accumulation across locations that occurred between mid-August and September 20th, was nearly identical during 2020-2023.

Differentiation between heat unit accumulation in each of the years evaluated was first slightly noticeable between September 20<sup>th</sup> and October 1<sup>st</sup>, with a clear differentiation occurring between October 1<sup>st</sup> and 15<sup>th</sup>. Little heat unit accumulation occurred beyond October 15<sup>th</sup> in any year, however there was some heat remaining during this time to activate boll opener harvest aids. In all years, first frost occurred between the last week of October and the first week of November. As seen in Figure 2., the Rocky Mount and Plymouth locations ceased blooming beyond September 18<sup>th</sup>, simply due to drought conditions, whereas the Sandhills and Lewiston location were irrigated and continued to set additional blooms until late September. This resulted in lower R2 values since the tail-end of the regression curves could not be developed for these two locations, whereas the irrigated locations continued blooming to develop a more precise regression curve. During 2023, 50% or more white blooms matured into open, harvestable bolls as late as September 16<sup>th</sup> in all locations when cotton was defoliated in the

middle of October. Additionally, if defoliation was delayed until just before first frost, 50% or more white blooms were likely to mature into open, harvestable bolls, or bolls that would open with little pressure applied, as late as September 6<sup>th</sup> in Sandhills, September 11 in Rocky Mount, and as late as September 16<sup>th</sup> in Plymouth and Lewiston. However, when defoliation was initiated in mid-October, which allowed additional time and a few heat units for boll openers to perform, harvestable bolls could be developed in as little as 200-250 heat units. When defoliation was delayed until near first frost, likely harvestable

**Figure 1.** Heat Unit Accumulation Across Trial Locations from mid August until November 1<sup>st</sup> during 2020-2023.



bolls (fully open, or cracked under light pressure) required 250-400 heat units to develop. This data suggest that last effective bloom dates could be extended to mid-September in years with warmer Fall temperatures, and especially if defoliation occurs during mid-October, allowing boll openers to work with additional, modest heat unit accumulation and time before a frost occurs. Delaving defoliation until first frost allows for additional heat unit accumulation to develop bolls prior to defoliation or crop termination, but does not allow enough heat nor time for boll openers to be effective, therefore, results become more erratic. In summary, defoliation during mid-October, with a few heat units remaining before first frost, resulted in last effective blooms dates being extended into early or mid-September. Therefore, last effective bloom dates were found to be noticeably later than previously thought, however defoliation timing clearly influences that probability and consistency of success.

Figure 2. Percent Harvestable or Likely Harvestable Bolls by Bloom Date, and Accompanied Heat Unit Accumulation.



# Multivariate Analysis of Cotton Genotypes Based on Assessment for Drought Tolerance Upland Cotton Cultivars

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Globally, the water and energy demand are increasing and are expected to rise by 6.9 trillion cubic meters by 2030, and the demand will exceed 40% of the available water supplies. Climate change and increasing temperature caused water shortages due to lesser and irregular monsoon, leading to lower crop production. The current research was conducted in a randomized complete block design (RCBD) in three replications with factorial arrangement and two irrigation regimes (non-stress, and water stress at the seedling stage) at the experimental field of the Institute of Genetics and Plants Experimental Biology, District Kibray, Tashkent Region, Uzbekistan. Twenty-two upland cotton cultivars i.e., T-1001, Armugon, Sadaf, T-860, T-1033, T-1037, T-1002, T-1003, T-924, Navbahor-2, Gulshan, Zafar, T-500, Hosilot, T-1048, T-1024, T-1050, Guliston, C-6524, Zamin, T-1023, T-1068 with diverse agronomic characters were selected for the studying their potential yield during 2022 and 2023 growing seasons under two different environments (Optimal and Water deficit condition). Drought indices revealed significant differences among lines, except golden mean (GM). Results in the ranking method, indicate that among drought tolerance indices, mean productivity (MP), geometric mean productivity (GMP), stress tolerance index (STI), mean relative performance (MRP), relative efficiency index (REI), and relative drought index (RDY) were the most suitable indicators because of the highest correlation with seed cotton yield. Cluster analysis and three-dimensional plots showed the cotton inbred lines with the highest tolerance to drought under both irrigation conditions. The first three principal components (PCs) explained 65.61 % of the total variation and PC1 can be nominated as a potentially stable yield. The biplot diagram based on PCs and drought tolerance indices showed that MP, GMP, STI, MRP, REI, and YI were the best indices for screening the tolerant cotton inbred lines such as T-1050.

# Enhancement of Cotton Seed Germination Under Salinity Stress Using Priming

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**Background:** Priming is one of seed improvement techniques that increase germination percentage, germination speed and emergence at environmental stresses such as salinity, temperatures and drought. We investigated the effect of hydro priming –osmo priming on seed germination and growth of cotton (*Gossypium hirsutum* L.) in salinity stress. A factorial experiment based on completely randomized design with four replications, was conducted in laboratory. Thirty treatments of this factorial experiment  $3\times5\times2$  were composed of 3 priming levels, including 2 priming levels (hydro priming, osmo priming by nitrate potassium) and one control level (no priming) and second factor (salinity stress) at 5 levels (0,4,8,12,16 ds/m) according salt table and third factor: seed type at two levels (delinted and non-delinted seed ).

**Results:** Germination percentage, germination rate, root and shoot length, root and shoot dry weight and root to shoot ratio were measured. Results showed that by increasing salinity, examined properties related to germination and early growth showed significant decrease. Priming treatments reduced the effect of salinity. The highest germination percentage, root length, the least time for achieving % 90 germination at hydro prime treatment was higher than other treatments. Also, highest germination percentage and germination speed, root length, the least time for achieving %5, %10, %50, %90, %95 germination were observed at delinted seeds.

**Conclusion:** Results showed that all measured characteristics were affected by salinity and priming levels. Germination rate was affected by seed type and delinted seeds showed higher germination rate compared with fuzzy ones. The effect of salinity was reduced by priming and the best priming solution was  $KNO_3$ .

Key words: Salinity, Priming, cotton, germination, delinted and non-delinted seed

### Agroecological Cotton Production in Argentina as a Socioeconomic and Eco-friendly Alternative

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**Background:** The adoption of agroecological practices in cotton production in Argentina, focusing on intercropping with food crops and the use of biological inputs has a deep social and economy component. Agroecology aims to promote sustainable agriculture by enhancing biodiversity, reducing chemical inputs and improving social equity. The objective of this study was to evaluate different bio-inputs' efficacy, together with monitoring pathogens, insect pests and the biodiversity developed in a intercropped agroecological production system (cotton-corn-peanut).

**Result:** No significant difference in cotton yields compared with conventional production was observed, suggesting that it is possible to produce agroecological cotton on a small scale in Argentina. The study recorded diverse beneficial arthropods and the presence of entomopathogens like Nomuraea sp. infecting pests like Spodoptera frugiperda. Moreover, the integration of peanuts as a trap crop for pests was noted as beneficial in protecting cotton and maize crops.

**Conclusion:** The study underscores agroecology's potential to enhance sustainability in cotton production through diversified farming systems and reduced environmental impact compared to conventional methods.

Keywords: Cotton; Sustainability; Agroecology; Bioinputs; Intercropping

### Climate change and sustainable cotton production: Climate-Smart Agriculture as a multifaceted approach

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Agriculture and ecosystems worldwide are increasingly affected by the escalating severity of climate change. Within this shifting landscape, cotton cultivation confronts multiple agronomical challenges. These challenges are not only a consequence of climate change but also stem from the competition between natural and synthetic fibres. Additionally, sustainability in cotton production remains a pivotal concern, encompassing three fundamental pillars: social, environmental, and economic aspects. Climate-smart agriculture (CSA) is a multifaceted approach carefully crafted by the United Nations Food and Agriculture Organization (FAO) to guide farmers' decision-making processes, foster environmentally sustainable agrifood systems, and implement resilient methods that can withstand the challenges posed by a changing climate.

The objective of the present work is to share and analyse various components of management practices involved in Climate-Smart Regenerative Agriculture for sustainable production of rainfed cotton, in the Republic of Argentina, withstand the challenges posed by a changing climate.

The adoption of CSA is contingent upon numerous factors, including institutional arrangements, landscape governance, resource availability, and the prevailing economic, social, and climatic conditions. Therefore, the pursuit of climate-smart agriculture needs the active participation and collaboration of a diverse array of stakeholders, farmers, researchers, representatives from the public and private sectors such as APPA (Association for Promotion of cotton Production from Santa Fe) and RAMA (Argentinean Network of Woman in Cotton), and civil society. Research, development and extension actions are essential keys for the adoption of agronomical management practices at local and regional levels, as happens with many cotton farmers in Argentina.

Key words: Cotton; Climate Change; Climate-Smart Agronomy; Regenerative Agriculture; Organization; Sustainability.

# Genome Editing in Yeast for the Sustainable Conversion of Cotton Lignocellulosic Biomass Into Xylitol

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India, a leading cotton producer, generates significant amount of lignocellulosic biomass as a byproduct of the cotton industry. This biomass offers a sustainable opportunity for production of high-value products such as xylitol, a C5 sugar alcohol, having diverse applications in food, pharmaceuticals, and dental care. Microbial production of xylitol offers cost-effective and environmentally friendly method from the cotton lignocellulosic biomass. This study investigates the microbial production of xylitol from cottonseed hull biomass using *Saccharomyces cerevisiae*. Preliminary trials were carried out to screen yeast strains for xylose utilization, identifying 6933 GDS as particularly effective. This strain was confirmed as *Saccharomyces cerevisiae* through sequencing of the Internal Transcribed Spacer (ITS) region.

The orcinol assay was standardized to estimate xylose concentration and identify the strain that efficiently utilized xylose for potential xylitol production. The strain demonstrated effective xylose utilization, evidenced by a reduction in xylose content over time. Further, biochemical analysis confirmed the presence of xylitol, demonstrating the strain's capability to convert low-cost biomass into xylitol efficiently.

Experiments are underway for enhancing the accumulation of xylitol in *Saccharomyces cerevisiae* using CRSPR/Cas9 genome editing approach. This research enhances the utilization of cotton lignocellulosic biomass by optimizing microbial pathways for xylitol production, contributing to sustainable bioprocessing technologies and the production of value-added products from agricultural residues.

Keywords: xylitol, xylose, lignocellulosic biomass, *Saccharomyces cerevisiae* 

# Nanotechnology Utilization for Characterization of Nano-Crystalline Cellulose Extracted from Upland and Egyptian Cotton and their Environmental Applications in Technical Textile

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The first step including the Egyptian Extra Long Staple Giza88 (Egyptian ELS) which belongs to *G. barbadense* offer the more level of fiber length, length uniformity, maturity index, strength, micronaire and degree of polymerization in comparison with the Upland Medium Long Staple Burkina Faso cotton BF - FK37 (Upland MLS) which represented as the *G. hirsutum*.

The present study has been undertaken to studied the effect of slack mercerization and bleaching treatments on the mechanical properties of both two genotypes cotton fibers. Furthermore, there was remarkable improvement in fiber elongation after slack mercerization in both of genotypes under studied compared with untreated fibers. Slack mercerization decreases fiber strength and fiber length and increased elongation percent, Micronaire reading and improved fiber color attribute. Bleaching decrease fiber strength and fiber length and increased elongation percent and Micronaire reading.

The thermal stability observed that the Egyptian ELS is significantly higher than Upland MLS. The second step aimed to assess the nanocellulose crystals that were extracted from two genetically different types of cottons, the extraction was performed by 60% w/w of H2SO4 rendered active effect for acid depolymerisation of cellulose at 60 min and 60 min of time with high crystallinity (>70%).

The TEM images indicated that acid hydrolysis is able to depolymerize cellulose micro chain into nanocrystallites CNC loading was applied alone as well as in a combination with binder finish. It was seen that viscose fabric exhibited better wet strength after applying CNC and binder finishes on it. This improved property of viscose is important through the process of manufacturing and uses of viscose woven fabric.

# Will Cotton win Over Weeds During Changing Climate?

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**Background:** The global atmospheric  $CO_2$  is already 419 ppm and it has been projected to cross 550 and 1000 ppm respectively by the middle and end of this century. The impact of climate change on weeds may results in alterations in species life cycles, population dynamics and competition. Contrary to other pests, weeds share a similar trophic level with crop plants for resources causing severe crop losses. Hence, a thorough understanding of weeds and their competitive ability under changing climate is a key determining factor to design a successful weed management. We at Central Institute for Cotton Research, Regional Station, Coimbatore, Tamil Nadu, India conducted Open Top Chambers (OTC) experimentation during 2020-2023 to study the impact of elevated carbon dioxide ( $CO_2$ ) on crop weed interactions in irrigated cotton. Five treatments viz., Integrated Weed Management (IWM) and unweeded check under ambient and e.CO<sub>2</sub> (480 ppm) and weed free open field in randomized block design with four replications were studied in Suraj *Bt* as test cultivar.

**Results:** This study interestingly brought out the visible changes in relative density (RD) of weed species, dry matter accumulation, nutrient uptake and pests incidence due to e.CO<sub>2</sub>. The RD of dominant weed, *Trianthema portulacastrum* at 60DAS has shown a steep reduction from 47.3 % under ambient to 30.8 % in e. CO<sub>2</sub>. Notable reduction in RD of *Cyperus rotundus* and *Bracchiaria ramosa* were recorded consistently for all three years. While, the RD of minor weed, *Digera arvensis* enhanced from 6.43 % under ambient to 28.21 % under e. CO<sub>2</sub> and similar enhancement observed with *Dactyloctenium aegyptium*. The favourable growth condition under e. CO<sub>2</sub> resulted in many fold enhancement in phtosysnthetc rate, crop growth rate, dry matter accumulation and nutrients uptake. The elevated CO<sub>2</sub> recorded significant enhancement in soil enzymes like urease, phosphatase and dehydrogenase. Among pests, Aphids population was significantly enhanced under e. CO<sub>2</sub> while the boll damage by *Spodoptera* reduced and locule damage by pink bollworm enhanced. The SEM image of cotton leaf has shown the partial closure of stomata under eCO<sub>2</sub>. The average seed cotton yield enhancement was 30.5 % over ambient condition.

**Conclusion:** Some minor weeds of today will become major and vice versa during changing climate. Cotton crop will be water efficient and yield enhancement of 30.5 % over ambient indicates better prospects for cotton crop.

Key words: cotton: elevated CO<sub>2</sub>, relative density, photosynthetic rate, dry matter production, seed cotton yield.

# The Expansin-Like a Proteins Dependent on Charge Interactions With Pectin During Cell Wall Loosening

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Wall loosening contributes for the cell wall growth, which requires the involvement of several structural proteins such as expansin and expansin-like. Nevertheless, understanding of its biomechanical properties in cell walls extension remains elusive since the protein is difficult to express. We expressed and purified the recombinant EXLA from the secreted expression system protein. EXLAs analyzed bind preferentially to negatively charged PGA and RG-I. The crystal structure for GhEXLA1 with three binding surfaces is presented. The EXLA-pectin interaction exerts a condensing effect is essential for cell wall expansion.

Thus, EXLAs interact with demethylesterified pectin in a charge-dependent manner through polycationic surface during cell wall loosening in nature.

Keywords: Expansin, EXLA, Plant cell wall, PGA, RG-I, cotton

# Heterosis and its Physiological Aspects in Cotton

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To date, there are few studies on the physiological causes of heterosis in cotton, and most are devoted to the study of enzymes in hybrid seeds, oil content, and nucleic acid content. Fundamental physiological studies, such as the structure and functions of the photosynthetic apparatus of intra- and interspecific hybrids in connection with heterosis, have been scarcely studied. Our studies revealed that in F1 cotton hybrids, the formation of an optimal chloroplast structure is observed, the assimilation surface of cells increases, the chlorophyll content increases, the intensity of phosphorylation, the activity of the Hill reaction, and ATP increases. The heterotic effect is more pronounced in interspecific hybrids. In terms of photosynthetic potential, the hybrids exceed maternal forms by 20%, and paternal forms by 40%. Therefore, it is assumed that interspecific hybrids in terms of the intensity of all photosynthesis reactions suggests the possibility of using these parameters to predict the degree of heterosis in the early stages of growth and development of hybrid plants. A positive correlation was found between the intensity of photosynthesis per plant and the hybrid productivity of intraspecific (r=0.57) and interspecific (r=0.8) hybrids. This dependence indicates that to achieve high productivity, it is rational to perform selection simultaneously to increase the area and photosynthetic activity of leaves.

Chlorophyll content in leaves was higher in varieties of *G. barbadense*, although their photosynthetic activity was weak. No reciprocal differences in this trait were observed among interspecific hybrids. It is likely that chlorophyll is regulated mainly by the nuclear genome, whereas cytoplasmic genes do not affect chlorophyll formation. Hybridization, especially interspecific hybridization, causes a significant increase in the photochemical activity of hybrids in the first generation, which is then inherited and transmitted to subsequent generations from the maternal form. At the same time, the photochemical activity of chloroplasts and the intensity of photosynthesis are not dependent on the chlorophyll content in the leaves of the studied forms of cotton. The photosynthesis and photochemical activities of chloroplasts in varieties of *G.hirsutum* are higher than those of G. barbadense. In reciprocal interspecific hybrids, maternal inheritance of the properties and functional activity of chloroplasts was observed. Reciprocal differences in photosynthesis intensity in interspecific hybrids indicate a larger role of cytoplasmic genes in chloroplast biogenesis and genetic control of photosynthesis. This circumstance must be taken into account when programing selection for heterotic productivity.

**Key words:** Heterosis, hybrid, cotton, interspecific hybridization, intraspecific hybridization, photosynthesis, chloroplasts, inheritance, chlorophyll.

# Effects of Mepiquat Chloride on Yield, Fiber Quality, and Biochemical Constituents of Cotton

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Cotton is a tropical crop where controlling plant height and canopy cover is challenging. The regulation of plant height and canopy cover provides a source-sink relationship that yields high. To determine the effect of mepiquat chloride, an anti-gibberellin growth regulator was used to manage vegetative growth, canopy, increase chlorophyll content, improve yield, fiber quality and biochemical constituents in cotton crops. The results of a field experiment conducted during kharif, 2023 in Bt Cotton (RCH-659) are discussed. The data indicated that application of mepiquat chloride @45ppm at square initiation and 15 days later and 15 days after second spray (need based- $T_7$ ) recorded maximum seed cotton yield (1196.36kg/ha.). This was followed by  $T_6$ -Mepiquat chloride @45ppm at square initiation and 15 days after the first spray +Detopping (1159.62 kg/ha.) The upper-half mean length (mm) was maximum in Detopping (29.90) treatment( $T_2$ ) and minimum in  $T_6$  (27.60). The uniformity index was maximum in the control (83.0) treatment ( $T_1$ ),  $T_2$  and  $T_5$ . The lowest uniformity index was recorded in  $T_6$  and  $T_8$  treatments. Biochemical constituents of RCH-659 were estimated, and the results indicated that the primary (carbohydrates and total soluble proteins) and secondary metabolites (tannins, phenols, flavonoids and gossypol) were significantly reduced in all treatments compared to the control. Mepiquat chloride@45 ppm at square initiation and 15 days after the first spray and 15 days after the first spray (need based) treatment were found to be the best for yield enhancement. However, mepiquat chloride did not affect carbohydrate metabolism or lint yield in late-grown cotton under high density planting.

Key words: Mepiquat chloride, detopping, tannin, protein.

# Improving Cotton Row Tillage Technology for Increasing Cotton Yield

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**Background:** In Uzbekistan's cotton industry, special attention is given to achieving an abundant and high-quality cotton harvest through resource-saving agro-technologies. One such technology involves determining the optimal depth of soil cultivation by improving tillage technology between cotton rows. This trial studied the effects of deep tillage between cotton rows on the agrochemical, agrophysical, and microbiological properties of the soil, as well as on the growth, development, yield of cotton, the incidence of wilt disease, and the quality indicators of the fiber in the irrigated barren soils of the Kashkadarya region.

**Results:** To enhance the water-physical properties of the soil and increase cotton yield, optimal deep tillage depths have been developed for the "Bukhara-8" variety during the cotton development period. Deep tillage between the rows at a depth of 30-32 cm improved soil fertility, increasing the humus content by 0.004%, nitrogen by 0.007%, and phosphorus by 0.006%. At this depth, the bulk density of the soil in the plowed and under-plowed layers decreased by 0.02-0.03 g/cm<sup>3</sup>, porosity increased by 2.0-2.1%, and water permeability increased by 100-120 m<sup>3</sup>/ha. Extending the depth of cultivation between rows from 18-20 cm to 30-32 cm reduced the incidence of cotton wilt from 2.5% to 3.5%. The rapid development of the cotton root system led to increased efficiency in moisture and nutrient use, resulting in an additional yield of 4-5 tons/ha of cotton.

**Conclusion:** In the conditions of the grassy, irrigated barren soils of the Kashkadarya region, it is recommended to perform deep tillage at a depth of 30-32 cm in cotton fields planted with the Bukhara-8 variety, maintaining a row spacing of 90 cm in the winter wheat-cotton rotation system.

Keywords: "Bukhara-8" variety of cotton, deep cultivation, chisel cultivator, productivity.

# **Evaluation of Cellulose and C-SAP (cellulosic Superabsorbent Polymer) in Cotton**

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**Background:** Rainfed cotton growing zone of the northern transition part of the state is characterized by the frequent dry spells especially during the early part of the crop cycle. Under that situation crop which was depending on the rainfall suffers due to moisture stress. Any practices that help to improve the moisture conservation practices or extra moisture holding in the pore space of the soil certainly helps to improve the crop performance. Cotton textile industry which had the lot of textile waste which needs to be recycled to save from the pollution. Under that situation a value-added product cellulosic superabsorbent polymer and cellulose which had the capacity to conserve the soil moisture upon application increased the soil moisture.

Results: A field experiment was conducted at MARS; Dharwad, Karnataka, India during 2023-24 to evaluate the different levels of Cellulose with rates as 0,4,8,12,16,20,24,28 g per plant and their combinations with and without 15 g/plant of C SAP was made at sowing. Soil moisture observations were recorded periodically and the growth and yield parameters at harvesting. Soil moisture observations made at 60 DAS indicated significant difference among the treatments. Increased soil moisture was observed in T10 (C4+ C SAP 15) (36.4%) as compared to any other treatments. However, it was on par with all except T1, T2, & T3 treatments. It shows that there is an increase in the moisture levels in soil due to application of cellulose & C-SAP products. Soil moisture observations made at 75, 90 and 105 DAS indicated no significant difference among the treatments. However, soil moisture levels were numerically increased with increased application of cellulose & C SAP. Especially the observations made at 75 & 105 DAS indicated the marginal increase of soil moisture & in T15 & T16 showing the higher soil moisture. Effect of Cellulose and C SAP on growth and growth components indicated that observations on growth components especially plant height, no of monopodial per plant, No of sympodial per plant were not showing significant effect due to the various treatments. Among the different treatments T11 recorded numerically higher plant height (146.9 cm) as compared to any other treatments. Though it was not significant, higher doses of treatments were produced higher plant height. Similar trend is also observed in No of monopodial per plant wherein showing higher nos with higher doses of cellulose and C-SAP (T15 &T16). Effect of Cellulose and C SAP on yield and yield components indicated that Seed cotton yield was significantly affected by different treatments of cellulose and C SAP. Significantly higher seed cotton yield was recorded with T16 (1871 kg/ha as compared to any other treatments. However, it was on par with T15. Significant increased yield may be associated with increased seed cotton yield per plant (258g) and more no of bolls per plant (48.5). Significantly lowest seed cotton yield was recorded with T1 (control) (1224 kg/ha). Numerical increase of yield recorded as the dosage of cellulose increased from T3 to T8. However, their combinations of cellulose and C-SAP have an advantage of yield at higher levels of cellulose from 24 to 28 g/plant. Similar was also from T10 to T16 treatments.

**Conclusion:** Experimental results shows that application of C SAP @ 15 g/plant along with higher doses of cellulose @24 to 28 g /plant can enhance the seed cotton yield and no of bolls per plant. Increased seed cotton yield may be attributed to the moisture levels. Key words: C-SAP, Soil moisture, cellulose, seed cotton

# Multi-Tier Cropping System to Enhance Resource Utilization, Profitability and Sustainability of *Bt* Cotton (*Gossypium hirsutum*) Production System

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**Background:** Ranifed cotton is characterized by the dependence of the crop on the erratic rainfall and this leads to frequent crop failures. Under such situations the area under cotton is likely to reduce drastically. Net income is an important aspect for the resource poor farmers to adopt a particular cropping system. Cotton is a long duration crop with slow growth during the first 50-60days. Wider row spacing and slow growth facilitates growing short duration inter- crops like vegetables and green gram etc. Encashment of this period without affecting the growth of the main crop cotton is the main idea of the intercropping with vegetables and pulse.

**Results:** Field experiment was conducted at ARS, Dharwad, UAS, Dharwad, India during 2021 and 2022. The experiment consists of 10 treatments (Table 1)with paired row planting of cotton with different intercrops like vegetable beans, coriander and green gram in 1:2 row ratio. Effect of these intercrops on the growth of cotton indicated that among the different growth parameters plant height and no of sympodia per plant were not significantly affected by different intercropping systems. Whereas, no of monopodia per plant were significantly increased with farmers practice ( $T_8$ ) (1.53) when compared with any other treatments. However, it was on par with paired row planting of sole *Bt* cotton (1.37) ( $T_1$ ). It shows that cotton without intercropping helped to increase the monopodia of the crop. Sole cotton recorded significantly higher seed cotton yield (2361 kg/ha) as compared to any other treatments. However, it was on par with  $T_8$ ,  $T_{10}$ ,  $T_4$  and  $T_6$  treatments. Higher boll numbers and seed cotton yield per plant were also observed in these treatments. Marginal decrease in the cotton yields were noticed in all intercropping systems. Effect on equivalent yield (CEY) and economics of multitier cropping with pooled mean of two years data shows that different multitier cropping systems significantly affected CEY and economic returns. Among the different treatments CEY (3214 kg/ha), gross returns (Rs.1,87,903/ha), net returns (Rs.1,45,633/ha) and B:C ratio (3.34) were significantly increased with recommended intercropping of cotton +Green gram ( $T_9$ ) as compared to any other treatments (Table 2). However, it was on par with  $T_5$  and  $T_7$  treatments. Increased CEY and economic returns of these treatments (Table 2). However, it was on par with  $T_5$  and  $T_7$  treatments. Increased CEY and economic returns of these treatments (Table 2). However, it was on par with  $T_5$  and  $T_7$  treatments. Increased CEY and economic returns of these treatments were mainly because of increased seed cotton yield, interc

**Conclusion:** Intercropping of cotton+ one row of green gram  $(T_9)$  can produce higher CEY and net returns. Other best options of cotton intercropping are paired row cotton + 1 row of Green gram + 1 row of Beans  $(T_5)$  or paired row cotton + 1 row of Green gram + 1 row of Coriander  $(T_7)$ , which can produce CEY and net returns higher than sole cotton under assured rainfall conditions.

Treatments	Plant height (CM)	Mono- podia/ plant	Sym- podia/ plant	No. of Bolls/ Sq M	Boll weight (g)	Seed cot- ton Yield (kg/ha)	Gross return (Rs./ha)	Net Return (Rs/ha)	B:C ratio
T1. Paired row Sole <i>Bt</i> cotton (60-120-60x 60cm)		1.37	18.8	66.8	5.41	2,361	152,435	94,593	2.64
T2. Paired row planting of <i>Bt</i> cotton with two rows of inter- crop (A) (Green gram)		0.97	17	58.3	5.39	2,049	177,182	132,412	3.10
T3. Paired row planting of <i>Bt</i> cotton with two rows of intercrop (B) (Beans)		1.17	17.5	62.6	5.16	2,069	167,388	112,747	2.71
T4. Paired row planting of $Bt$ cotton with two rows of intercrop (C) (Coriander)	109.9	1.27	18.6	66.4	5.32	2,229	163,537	119,749	2.87
T5. Paired row planting of <i>Bt</i> cotton with one row (A) (Green gram) +one row (B) (Beans)	110.6	1.03	17.4	63.5	5.49	2,081	183,975	136,445	3.08
T6 Paired row planting of <i>Bt</i> cotton with one row (B) (Beans) +one row (C) (Coriander)	104.7	1.03	17.6	67	5.39	2,218	170,323	119,518	2.80
T7 Paired row planting of <i>Bt</i> cotton with one row (C) (Coriander) +one row (A) (Green gram)	104.5	1	17.2	59.5	5.39	2,159	177,820	137,317	3.09
T8. Farmers practice ( without intercrop with 90x60 cm spacing	110.1	1.53	18.2	72.7	5.28	2,323	150,543	92,251	2.58
T9. Recommended intercropping ( Cotton + Green gram at 90x60 cm)	110.2	0.67	16.9	58.6	5.35	2,119	187,903	145,633	3.34
T10: Recommended intercropping ( Cotton + Beans at 90x60 cm)	112.3	1.13	18.1	70.5	5.4	2,293	185,947	129,302	2.94
C.D.	NS	0.39	NS	5.4	NS	172	10,909	10,175	0.14
SE(m)	2.5	0.13	0.5	1.8	0.07	57	3,644	3,398	0.05
SE(d)	3.5	0.18	0.6	2.6	0.1	81	5,153	4,806	0.07

Table: Growth, Seed cotton yield (kg/ha) and economic analysis as influenced by multi-tier cropping (Pooled analysis of 2021 and 2022)

# Re-evaluation of The Degree Day Base 60°F Concept in US Cotton (*Gossypium hirsutum* L.) Production

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Cotton (*Gossypium hirsutum* L.) management decisions to abet early growth, fruit set, boll maturation, and harvest preparation are often facilitated by prediction of the date when critical developmental stages are reached. In the United States, growing degree days calculated with a base 60° F (DD60s) are commonly used to predict cotton development. Observations suggest development of modern cultivars differs from previously established guidelines. The objectives were to (1) reevaluate DD60s required for an early, mid-maturing and late maturing cultivar to reach key growth stages across the US Cotton Belt; and (2) determine if predictions of growth stages are strengthened by optimizing base temperature or including an upper thresh- old by growth stage. During 2018 and 2019, 22 field trials were established in 10 states. Plant growth stages were monitored weekly and air temperature was computed from interpolated surface observations weighted by a physical, geographic model. Observed DD60s to reach growth stages varied slightly by cultivar and region (<85 DD60s and <130 DD60s, respective-ly). Required DD60s to reach growth stages exceeded most published ranges. Optimization of base temperature and inclusion of an upper threshold by growth stage did not substantially decrease errors in predicting date of growth stage occurrence. The DD55 and DD55 with an upper threshold of 86° F calculations resulted in slightly lower errors in predicting date of growth stage orgen thresholds will drastically increase the predictive ability over the DD60 calculation.

# **Bt**-Cotton Performed Better in Closer Spacing as Compared To HDPS in Medium Deep Soils Under Rainfed Situations in Peninsular India

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**Background:** Cotton is an important commercial crop of many countries including India. Introduction of *Bt* cotton hybrids in India reduced the cotton bollworm damage, increasing the production and productivity of cotton to an extent of about 40 to 60 per cent. The extant Bt cotton hybrids are of medium to long duration with bushy plant type having lower harvest index and productivity (<500 kg lint/ha), whereas in other countries (Australia, Brazil, Turkey, China, USA, Mexico etc.), cotton varieties are of short to medium duration, erect and compact plant type having higher harvest index and productivity (>1500 kg lint/ha). Hence, there is a need to adopt novel production technologies in cotton cultivation to achieve the targeted cotton production and productivity.

**Results:** During Kharif (monsoon season) 2024, 12 field demonstrations at Harobelavadi village in Dharwad taluk and Byalal village in Navalagund taluk of Dharwad district in Northern part of Karnataka, Peninsular India were conducted to study the effect of spacing on different plant varieties and irrigation on the growth and yield of compact-type private sector bred Bt-cotton hybrids. The demonstrations followed three cotton hybrids (RASI SWIFT, RASI NEO and MAX-929), two levels of plant spacing (90 cm x 15 cm for HDPS and 90 cm x 30 cm for closer spacing) with irrigation versus non-irrigation situations. The results revealed that cotton variety RASI SWIFT recorded significantly highest yield and yield attributes, highest number of sympodial branches and number of squares per plant under closer spacing (90 cm x 30 cm) as compared to other varieties. The highest number of bolls per plant and higher boll weight was recorded and maximum seed cotton yield harvested with RASI NEO variety under HDPS (90 cm x 15 cm) than others. Results also revealed that at least one light irrigation during flowering stage gave 30 per cent higher seed cotton yield as compared to non-irrigated field under HDPS system.

**Conclusion:** Among the two spacing's, closer spacing (90 cm x 30 cm) performed better as compared to HDPS (90 cm x 15 cm) on medium deep soils in a year when the rainfall was deficient by 30%. Among the hybrids tested, RASI NEO was more suitable for planting at 90 cm x 15 cm, whereas the hybris RASI SWIFT performed best at 90 x 30 cm spacing.

Keywords: Cotton, Bt-genotypes, HDPS, Closer spacing, Irrigation, Yield attributes, Yield

# ORAL PRESENTATIONS CROP PROTECTION



# Role of Different Pheromone Formulations for Area Wide Management of Pink Bollworm, *Pectinophora gossypiella* (Saunders)

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AG Sreenivas

**Background:** Cotton (*Gossypium hirsutum* L.) is one of the major fibre crops cultivated across India, whose yield is severely hindered due to the infestation of Pink bollworm, *Pectinophora gossypiella* (Saunders). Due to the indiscriminate use of the insecticides and non-compliance of refugia, control failure of the pest is being reported (Resistance against Bt toxins). Hence, the current investigation was planned and executed to evaluate eco-friendly and novel mating disruption tools for the effective management of pest.

**Results:** The mating disruption tools such as Controlled Release Emission Mating Interruption Technology-PBW (CREMIT-PBW) a wax-based formulation and PB-Knot dispensers were found superior over Integrated Pest Management and Conventional farmers' practices. These treatments were implemented in the farmers' field and efficacy was compared in terms of different infestation

parameters viz., per cent green boll damage, locule damage and mean moth catches per trap. Mating disruption tools were found to be effective with less green boll damage of 5.91 and 8.38% and locule damage of 7.47 and 10.32% from CRE-MIT-PBW and PB-Knot plots, respectively. Significant mating disruption was also reported up to an extent of 80.30% from the CREMIT-PBW treated field. Ultimately, higher yields with remunerative benefit cost ratio of 2.49 (CREMIT-PBW) depicted the suitability of the tool in management of pink bollworm.



Figure1. Pink bollworm infestation in different management strategies

**Conclusions:** The incidence of pink bollworm and damage caused by it was reduced significantly due to the adoption of mating disruption tools viz., CREMIT-PBW and PB-Knot over Conventional farmers' practice. Apart from pest control, the abundance of the natural enemies was also higher depicting the safety of the management strategy.

Keywords: Cotton, CREMIT-PBW, Mating Disruption, PB-Knot, Pink bollworm

# Proteomics of Leafhopper (Amrasca biguttula biguttula. Ishida) Resistance in Cotton

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Manivannan

**Background:** Cotton crop faces significant challenges from insect pests, among them cotton leafhopper (*Amrasca biguttula biguttula* (Ishida)) that causes severe damages and is considered a destructive pest. Understanding induced plant defense mechanisms of cotton in response to leafhopper infestations helps in devising the leafhopper control strategies. In this study, a resistant hybrid resulting from a cross between leafhopper resistant (NDLH2010) and susceptible (LRA5166) varieties was subjected to leafhopper infestation. Differentially Expressed Proteins (DEPs) of leafhopper resistance genes were studied using a label-free proteomic approach.

**Results:** Proteome profiling revealed a total of 2,274 proteins and 7,218 unique peptides were identified between leafhopper infested and control plants. Further, 620 DEPs wherein 329 are upregulated whereas 291 are downregulated at  $\log_2$ -fold change of  $\geq 1.5$  or < 0.65 and p-value  $\leq 0.05$ . DEPs were primarily associated with plant stress response, primary metabolism, photosynthesis, antioxidants,

and secondary metabolites. Notably, DEPs such as pathogenesis-related protein, heat shock proteins, acyl-coenzyme A oxidase, polyphenol oxidase, catalase, and superoxide dismutase were significantly upregulated. Quantitative real-time PCR (qRT-PCR) analysis confirmed a positive correlation between protein abundances and transcripts for all genes.

**Conclusions:** This research provides comprehensive insights into cellular and molecular response of cotton hybrid towards leafhopper infestation, thereby aiding the development of leafhopper resistant cotton genotypes.

Keywords: Cotton, hybrid, leafhopper resistance, label-free proteomics, molecular mechanism

# Segregation of Bt Genes in Cotton And Development of Pink Bollworm Resistance

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Balasubramani

**Background:** India is the only country that cultivates Bt-cotton in the form of hybrids concerning the heterotic vigor for different climatic conditions. The hybrids even with both Cry1Ac and Cry2Ab genes were found to be susceptible to pink bollworm (PBW) attack. A study was conducted to analyze the segregating pattern of these genes in the selfed bolls of different generations to correlate with the PBW damage.

**Results:** The proportion of plants containing Cry1Ac gene and Cry2Ab in F1 was  $14.8 \pm 1.303$  (2022) and  $13.8 \pm 2.16$  (2023) and  $12.4 \pm 0.894$  (2022) and  $17.8 \pm 1.64$  (2023). In F2 single boll selfed seeds, the proportion was reduced compared to F1 for Cry1Ac gene whereas, for Cry2Ab, the range was similar as F1. In advanced breeding lines, the proportion of positive plant range was high compared to F1 and F2 for Cry1Ac gene. For both Cry1Ac and Cry2Ab genes, approximately an expected ratio

of 3:1 was observed for two years. The highest incidence of pink bollworm infection was noted in the field conditions of the Bt variety "Rajat-Bt" in 2022 and 2023. The results may vary based on the zygosity of the parents used in the developmental process of hybrids.

**Conclusion:** Research reveals that segregation lowers Bt toxicity and increases PBW on Bt plants' chances of surviving. The parental lines involved in developing hybrids should be homozygous for the insect-resistant transgenes. The other way to overcome the problem is stacking of these Cry genes in a variety rather than a hybrid. As all genes will be homozygous, then the toxicity produced will be higher and uniform throughout the entire population. Along with the Bt variety, the addition of refugia becomes essential to prevent the other major bollworms from developing resistance against the Cry genes.

Keywords: Cry1Ac, Cry2Ab, ELISA, Bt cotton, Segregation, Pectinophora gossypiella

# In Silico Analysis of Nimbolide, a Tetranortriterpenoid (Limonoid) Compound Isolated From the Leaves of *Azadirachta indica* for Nematicidal Activity Against Nematode Pests of Cotton

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Gulsar Banu

**Background:** Plant parasitic nematodes cause a yield loss of up to 10 % annually in Cotton, which is managed mainly through the application of chemical nematicides. The yield loss is increased several folds when they interact with fungus. Owing to increased awareness about the detrimental effect of chemical nematicides on non-target organisms, human beings and the environment besides phytotoxicity, necessitate safer approaches for nematode management in cropping systems. To develop eco-friendly alternatives, a wide spectrum of plant metabolites with nematostatic and nematicidal actions has extensively been reported. Phytochemicals have been extensively reported as potential sources of bioactive ingredients for the development of natural Nematicides. In the present study, in silico analysis of Nimbolide, a tetranortriterpenoid (limonoid) compound isolated from the leaves of *Azadirachta indica* for nematicidal activity was carried out.

**Result:** Molecular modeling and docking studies were performed on nematode protein targets such as Cytochrome c oxidase subunit 1, AChE, Hsp90, ODR1, ODR3, Neuropeptide, GPCR, CLAVATA3/ESR (CLE)-related Protein, Heat shock protein, C type lectin, cathepsin L-like cysteine proteinase,  $\beta$ -1,4 –endoglucanase, calreticulin, Reticulocalbin, venom allergen-like protein and serine carboxypeptidase to understand the mode of action. Structurally validated protein targets of nematodes were docked with biomolecules through Auto Dock Vina module in PyRx 0.8 software to predict the binding energy of ligand and target protein. Docking analysis revealed that Nimbolide had the highest binding affinity for the protein targets followed by nematicide, Fluopyrum and Fluensulfone. Carbofuran recorded the lowest binding affinity towards the target proteins. Nimbolide served as a potential inhibitor of the target sites associated with interrupting the functions of several protein targets of nematodes. Besides, the increased binding affinity of Nimbolide with the protein target sites facilitated exploring it as a novel nematicidal molecule for the management of nematodes in cotton.

**Conclusion:** The insight on biochemical ligand-target protein interactions described in the present work will be helpful in logical selection of biomolecules for the development of practically viable bionematicidal products.

### Challenges Facing U.S. Cotton Production: A Focus on Pathogens and Nematodes

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Cotton production in the U.S. spans from the eastern to the western seaboard representing multiple climates, each favoring different pathogens and nematodes. As environmental conditions have begun to change in U.S. cotton production regions, so too have the pathogen and nematode threats. These include not only re-emerging and endemic threats, but also newly emerging and invasive threats. This talk will focus on Cotton Incorporated's priorities in pathology and nematology for the U.S. cotton production system. To prioritize threats in the U.S., the cotton producing states are divided into production regions, eastern and western, based on environmental conditions and dominant pathogen and nematode threats. Emphasis will be placed on research advances and Cotton Incorporated's engagement with researchers to address threats relevant to the global cotton community.

# Integrated Management of Cotton Mealybug, *Phenacoccus solenopsis* Tinsley (Sternorrhyncha: Pseudococcidae) Under Semi-Field and Field Conditions

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Two trials were carried out under field and semi-field conditions for two consecutive years to evaluate the compatibility of native predators, *Chrysoperla carnea* larvae and adults of *Brumus suturalis* and the exotic predator *Cryptolaemus montrouzieri* with neem oil for the control of *Phenacoccus solenopsis* during 2018-2019 and 2019-2020. The assessments were based on mealybug control (scale 0-9) and percent recovery of predators at the end of the experiment showing conservation and colonization capability of the predator to local conditions. Both native predators, *C. carnea* and *B. suturalis* showed better control of the mealybug under semi-field and field conditions over the control and were also recovered at the end of the trials during both the study years. In contrast to these, exotic predator *C. montrouzieri* though proved to be the most efficient predator of P. solenopsis under semi-field conditions but it failed to establish under field conditions and reducing mealybug populations. No recoveries were made of the predator in either of the treatments under field conditions. Maximum reduction in the population of mealybug was noticed in the insecticide treated plants. The present study showed that application of neem oil followed by release of *C. car*.

**Khalid Abdullah** *nea* larvae and *B. suturalis* adults can be swapped to synthetic insecticides for the safer management of mealybug.

Keywords: P. solenopsis, C. carnea, B. suturalis, C. montrouzieri, neem oil

# Effects of Basal Exposure to Extreme Temperatures on Survival and Reproduction of Whitefly, *Bemisia tabaci* (Gennadius)

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Rishi Kumar

**Background:** Whitefly infestations cause major crop losses worldwide. Notably, whitefly outbreaks occurred in the North zone of India in 2015 and 2022 led to yield reductions of 40 to 50%. The temperatures along with other factors including extended sowing window, bushy and hairy geno-types, insecticide resistance were the possible reasons for these outbreaks. In north India, whitefly populations experience extreme temperatures both during summer and winter, which could impact various fitness traits. This study aimed to explore how basal temperature stress, ranging from low to high, influenced the development, survival, and reproductive behavior of whiteflies in these environments.

**Results:** Whitefly adults were exposed to twenty-eight (28) different low and high temperatures for 1 hour along with a standard control temperature at 26°C and survivors were maintained at 26°C for further studies. Between the two host environments, adults subjected to basal exposure under no-host environment were more affected by both low and high temperatures. In case of high tem-

perature basal exposure under no-host environment, 100% mortality was observed at 45°C but in case of low temperature exposure maximum mortality obtained was 75.55 % at 3°C indicating higher endurance towards low temperature. Fecundity was significantly affected at 43 and 45°C when *B. tabaci* adults were heat-shocked while the effect was significant at all low temperature exposures. The overall conversion of eggs to adults declined when the whitefly adults were subjected to basal exposure to low (41.22-64.12%) and high temperatures (40.24 to 70.12%) deviating from the optimum rearing temperature (26-28°C) having conversion percentage of 80.30. Similarly, pre-exposed populations collected from field conditions were comparatively less affected by basal exposure to low and high temperatures indicating an induced thermo-tolerance.

**Conclusion:** In this study, whiteflies exposed to cold or heat stress in absence of host plant were affected more in comparison to host associated environment. Overall, survival and reproduction declined at both high and low temperature extremes compared to optimum rearing temperatures. This research indicated wide adaptability in whitefly to temperature fluctuations wherein climate change may significantly impact whitefly incidence in northern India.

# Supporting Sustainable Insect Pest Management Practices in U.S. Cotton

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Almost three decades following boll weevil eradication and the introduction of transgenic cotton, insect pests still challenge cotton grown in the United States (U.S.). Cotton producers and importers value research and Extension programs that provide practical solutions to current and future pest management issues. The mission of Cotton Incorporated's Agricultural and Environmental Research division is to help farmers increase yields, manage costs, and reduce their environmental footprint. This presentation briefly summarizes insect control collaborations across the U.S. cotton belt and highlights some of the basic and applied research programs that help to monitor and develop tools to



Sally Taylor

manage these pests.

# Selection of Novel Entomopathogenic Fungi to Manage *Bemisia tabaci* Under Integrated and Organic Cotton Cultivation Systems

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**Background:** Cotton (*Gossypium* spp.) is one of the important commercial crops of the world and plays a noteworthy role in sustaining the livelihood of 6 million farmers and 40-50 million people engaged in cotton industries. Among several insect pests and diseases, whitefly (*Bemisia tabaci*, Genn.) is the most devastating threat to cotton production worldwide due to the direct damage and transmission of cotton leaf curl virus disease. Entomopathogenic fungi (EPF) are considered the safest bioinsecticides causing the natural mortality of whitefly nymphs and adults without deleterious effects on the environment and ecosystem. We evaluated 373 EPF strains of 17 genera isolated from whiteflies and other insect cadavers to find out the most virulent and chemical pesticide-compatible strains. The main aim was to utilize novel virulent EPF for the management of B. tabaci in integrated pest management as well as organic cotton cultivation systems.

#### Satish Sain

Results: The highest bio-efficacy index (mycelial growth, conidia production, nymphal mortality under polyhouse) was recorded with Beauveria bassiana (Bb)-4511 (78.1%), Cordyceps javanica (Cj)-102 ((77.0%) and Metarhizium anisopliae (Ma)-1299 (71%) (CD 4.03 at P<0.05). Among the top ten virulent EPFs evaluated for two consecutive years (2018) and 2019) in field trials, the highest pooled nymphal mortality at 7 days after sprays was recorded with Bb-4511 (86.3%), Cj -0102 (84.7%) and Ma-1299 (79.4%) (CD 5.08 at P<0.05). The lowest LC<sub>50</sub> values  $0.2x10^4$  and  $0.5x10^4$  conidia ml<sup>-1</sup> were observed with Cj-089 and Bb-4511, respectively (SE ±2.12-3.61). These virulent EPFs were also evaluated for their compatibility with 17 insecticides belonging to neonicotinoids, pyrethrins, spinosyns and organophosphates groups and botanicals under in vitro conditions. The toxicity index values ranged from 19.5 to 106.9% irrespective of EPF strains and chemicals. Comparatively, the neonicotinoids and spinosyns were found to be compatible to moderately toxic to most of the EPFs. Organophosphates (ethion) and pyrethrins (bifenthrin) were toxic to very toxic to most of the EPFs. Overall, Cj- 089, Cj-102, Ma-1299, and Bb-4511 were among the most compatible EPFs with full and half doses of the chemical and botanicals tested. The top three novel EPF strains (Cj-102, Bb-4511 and Ma-1299) selected based on the bio efficacy index, chemical insecticides & botanicals compatibility and field trials were further evaluated in IPM and biomodules under field conditions for three consecutive seasons (2020-2023) at five locations. The IPM module consisted of sequential foliar sprays of botanicals, chemicals and EPFs at regular time intervals, while biomodules included botanicals and EPF sprays. The pooled nymphal and adult mortality at five trials locations in IPM module-1, 2 and 3 ranged from 21.5-64.4%, 20.3-61.6% and 22-60.1%; and 33.2-57.4%, 30.2-76.8% and 39.8-70.9%, respectively. The nymphal and adult mortality in biomodule -1, 2, and 3 ranged from 33.8-69.5%, 24.1-64.3% and 21-66.6% and from 51.8-70.2%, 48.9-66.8% and 45.0-72.6%, respectively. The ICBR of 2.2-2.4 and 1.9-2.2 were recorded in IPM and biomodules, respectively. Additionally, these EPFs were also effective in controlling thrips (35-41%) without having negative effects on natural enemies (bioinsecticide formulation recorded a higher population than chemicals and botanicals).

**Conclusion:** The novel bioinsecticide formulations of EPF strains Cj-102, Ma-1299, and Bb-4511 alone or in combination with the insecticides and botanicals are capable to manage whitefly considerably better in integrated and organic cotton cultivation systems for achieving higher yield.

# Untangling the Molecular and Biochemical Basis of Insecticide Resistance in Cotton Thrips From North Indian Cotton Agro-Ecosystem

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**Background:** Thrips, important sucking pests of American cotton, are known to reduce crop productivity through direct feeding and by transmitting viral pathogens. Thrips were once considered a minor pest in cotton, where they cause damage during the crop's early growth stage and could be managed by the use of neonicotinoids as seed dressers or prophylactic spray application. However, their incidence has increased over the past decade and they rank among the top three sucking insect pests, necessitating cotton growers to use insecticides to manage this pest. In spite of increased use of insecticides against this pest their management is posing a challenge, which may be attributed to the development of resistance. The study aimed at resistance monitoring of commonly used insecticides and understanding the molecular and biochemical mechanisms underlying this resistance in *Thrips palmi* populations from north India. This will help to devise the insecticide resistance management plan for the effective management of this pest in cotton in north Indian cotton growing zone.

Satnam Singh

**Results:** The mtCOI sequencing confirmed the presence of *T. palmi* population in the north Indian cotton growing areas. Resistance levels varied among populations, with Jind and Abohar showing high level of resistance to most of the insecticides. Jind population exhibited the highest LC50 for cypermethrin (248.8 ppm) and neonicotinoids (237.5 ppm for imidacloprid). Biochemical assays revealed higher activity of detoxifying enzymes (MFOs, GSTs, esterases) in resistant populations. The study identified 30 CYP450 transcripts in T. palmi within clan 3 showing the highest expression. qRT- PCR confirmed over-expression of six CYP450 genes in resistant populations. RNAi mediated knockdown of CYP6a13, CYP6a14, and CYP6k1 resulted in increased sensitivity to imidacloprid and cypermethrin, confirming the key role of these genes in resistance to targeted insecticides. Sequencing of the para sodium channel gene revealed for the first time a point mutation (M918L) associated with resistance to synthetic pyrethroids in the *T. palmi*.



Figure: Target site alteration in the Na channel of Thrips palmi

I-Amplification para gene (sodium channel) from various *Thrips palmi* populations where, M- Molecular marker (100bp), A-H: Ampliefied sample of different locations; A-B: Jind; C-D: Sirsa; EF: Faridkot; GH- Ellenabad; II-Multiple sequence alignment of amino acid sequences of the para gene of *Thrips palmi* samples from Jind, Sirsa, Faridkot and Ellenabad with reference sequences of *Musa domestica* and *Thrips tabaci* indicating substitution of methionine to leucine amino acid residue at 918 position

**Conclusions:** Overall, these findings highlight the complex molecular and biochemical mechanisms contributing to insecticide resistance in *T. palmi* populations from north India. The less susceptibility to both synthetic pyrethroids and neonicotinoids was associated with high expression of MFOs, GSTs and CYPs. The studies suggest the restricted use of synthetic pyrethroids and neonicotinoids as an Insecticide Resistance Management (IRM) strategy for the thrips in north India.

Keywords: Thrips palmi, Cotton, insecticide resistance, MFOs, GSTs, CYP450s, RNAi

# Understanding the Interaction Between Leaf hopper, *Amrasca biguttula biguttula* Ishida and *Gossypium* species: A chemo-ecological approach

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Shashikant Udikeri

**Background:** The cotton leafhopper, *Amrasca biguttula biguttula* (Ishida) (Homoptera: Cicadellidae), is an alarming pest that causes both quantitative and qualitative losses, It has developed resistance to commonly used insecticides, In this contest it is necessary to develop the non-pesticidal approach/ alternate mode of management for cotton leaf hopper, Another option to control insect-pest is to use natural plant defense pathways, such as the production of volatile semiochemicals. This study was carried out to identify the kairomonal cues that are responsible to elicit biological response in adult female hoppers.

**Results:** A positive behavioural response was observed when females of *A. biguttula biguttula* were exposed to four entries representing the cultivable species of cotton plants headspace volatiles in olfactometer assays. In the dual choice assay, *G. barbadense* healthy plant volatiles were found to be highly attractive to the female hoppers, further the HIPVs of *G. herbacium* was

found to be repellent. The volatile profiles of the selected four healthy plant headspace samples and respective HIPVs were found to differ significantly, Principle component analysis (PCA) showed 2,4,6-triisopropylphenol, 2,5-dimethylacetophenone, 4-ethylacetophenone, methyl salicylate and n-undecane were causing major variation among healthy plant VOCs. Gas Chromatography linked to Electroantennodetector (GC-EAD) with female hoppers for healthy volatiles of *G. barbadense, G. herbaceum* and HIPVs of *G. herbaceum* revealed 28 active fractions, among them 10 were tested through olfactometer assay. n-undecane, methyl salicylate, 4-ethylacetophenone, n-tridecane, n-pentadecane and farnesane were found to be attractive whereas  $\alpha$ -pinene and benzoic acid-ethyl ester were repellents for female *A. biguttula biguttula*.

GC-EAD traces showing the antennal response of adult female to G. herbaceum headspace volatiles



GC-EAD traces showing the antennal response of adult female to G. barbadense headspace volatiles



**Conclusion:** Kairomonal cues have been disclosed for susceptibility of *G. hirsutum* and *G. barbadense* genotypes to leaf hoppers and may key role alternate management options.

# Exploring the Co-existence of two Gelechiid Species, *Pectinophora gossypiella* and *Pexicopia tungabhadrai* on Indian Mallow (*Abutilon indicum* L.)

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**Background:** Surveys were carried out in the north-eastern region of Karnataka, India during the cotton growing season and off-season to study the survival of two gelechiid species, namely *Pectinophora gossypiella* and *Pexicopia tungabhadrai* on plants belonging to the Malvaceae family. The study revealed for the first time that *Abutilon indicum* L is an important alternate host for the cotton pink bollworm in this region. Additionally, the study also identified a new species, *Pexicopia tungabhadrai*, feeding on Abutilon in this area.

**Results:** A study was conducted in the northeastern part of Karnataka, India from 2021 to 2023 to explore the malvaceous plants as alternative hosts of pink bollworm (*Pectinophora gossypiella* Saunders). It was discovered that both *P. gossypiella* and a new species in the genus *Pexicopia*, later named *Pexicopia tungabhadrai* Varnitha, Hanchinal & Shashank, coexist on the Indian Mallow plant (*Abutilon indicum* L.) in this region. The feeding behaviour of both species is similar, as their larvae cause interlocular burrowing and feed on the seeds of abutilon. An alternate host plays an important role in favouring the carry-over of pink bollworm. A series of roving surveys were conducted in the Kalyana-Karnataka region (Karnataka, India) to document the occurrence of *P. gossypiella* and *P. tungabhadrai* on *A. indicum* within this region. The results confirmed the natural occurrence of pink bollworm within the locules of *A. indicum*. During 2021-2022, the highest mean percentage of *P. gossypiella* emerged from abutilon capsules collected from Kalaburgi district (4.89%), followed by Raichur district (0.7%) and Ballari district (0.46%). Conversely, for adult emergence during 2022-23, Manvi taluk recorded the highest mean percentage of adult emergence (41.25%), followed by Raichur taluk (28.33%) and Devadurga taluk (21.87%). Regarding *P. tungabhadrai*, during 2021-22, the highest mean percentage of adult emergence (26.66%) was recorded in Raichur (5.30%). Similarly, for adult emergence in 2022-23, the highest mean percentage of adult emergence (26.66%) was recorded in Raichur taluk, followed by Manvi (20.00%) and Devadurga taluk (18.12%).

Figure: Variations in genitalia and morphological characteristics of adult *P. gossypiella* and *Pexicopia tungabhadrai* 

P. gossypiella	Antennal scape with 5-6 hair scales	Terminal segment of labial palpi shorter than the previous	Male genitalia with tapering uncus; gnathos elongate and tapering;	In female genitalia, corpus bursae with prominent sword shaped signa
Pexicopia sp.	Antennal scape with 3-5 hair scales	Terminal segment of labial palpi equal to the previous	Male genitalia with bilobed uncus; gnathos short and spatulate	In female genitalia, corpus bursae with signa reduced to dentate patches

**Conclusion:** The collected specimens were confirmed through adult external morphology and genitalia characteristics of males and females. The collected specimens were identified as *P. gossypiella* and *P. tungabhadrai*, belonging to the family Gelichiidae, and both coexist on *A. indicum*. The natural occurrence of pink bollworm, *P. gossypiella*, on *A. indicum* as a major alternate host was recorded for the first time in this region.

# POSTER PRESENTATIONS CROP PROTECTION



# Investigating the Natural Mortality of *Aphis gossypii* (Hemiptera: Aphididae) on Cotton Crops in Tropical Regions Using Ecological Life Tables

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Studies on the natural factors contributing to pest regulation are fundamental to developing efficient integrated pest management programs. Chemical control is the main management method used for pests [e.g., Aphis gossypii (Glover)]. The studies of pest management with chemical control provide information that can be incorporated into integrated pest management programs to promote more sustainable pest control approaches. Here, we report the critical stages of A. gossypii and its abiotic and biotic natural mortality factors in cotton crops as a function of plant phenology using a life table. The critical stages of A. gossypii were the first and fourth in stars. Together, the abiotic and biotic factors caused 94.31% of the mortality in the A. gossypii populations in cotton crops with plants in the vegetative, flowering, and fruiting stages. The key mortality factors were rainfall and predation. Syrphidae Allograpta exotica (Wiedemann) (Diptera: Syrphidae) and Chrysopidae Chrysoperla externa (Hagen) (Neuroptera: Chrysopidae) larvae, many Coccinellidae species Cycloneda sanguinea (L.) (Coleoptera: Coccinellidae), Eriopsis connexa (Germar) (Coleoptera: Coccinellidae), Harmonia axyridis (Pallas) (Coleoptera: Coccinellidae), Hippodamia convergens (Guérin-Meneville) (Coleoptera: Coccinellidae), Scymnus rubicundus (Erichson) (Coleoptera: Coccinellidae) and Stethorus punctillum (Weise) (Coleoptera: Coccinellidae), one Anthocoridae species Orius insidiosus (Say) (Hemiptera: Anthocoridae), and individuals from the Araneidae family were responsible for the predation of A. gossypii. The results obtained in this study provide support for the idea that efforts to preserve natural enemies (e.g., predators) and rainfall monitoring should be adapted due to their importance for the regulation of A. gossypii populations in all the phenological stages of cotton in tropical regions.

Key words: cotton aphid, life table, predation, rainfall, natural mortality

# Molecular Characterization of Native Entomopathogenic Nematode - Bacterial Complex (*Steinernema siamkayai - Xenorhabdus stockiae*) and Chemo Profiling of Secondary Metabolites of *X. stockiae* For Management of Insect Pests Of Cotton.

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**Background:** Entomopathogenic nematode-bacterial complex is being widely exploited for the management of insect pests in India. Infective juveniles of Heterorhabditis and Steinernematid nematodes actively seek the host in the soil, penetrating through insect's openings to reach the hemocoel where symbiotic bacteria in the genera *Photorhabdus* or *Xenorhabdus*, respectively, are released. The bacteria replicate and produce virulence factors that rapidly kill the insect host, providing nutrients for the nematode's development and reproduction within the insect cadaver. Studies are carried out to better understand the factors implicated in the nematode- bacteria association.

**Result:** Molecular characterization of a native isolate of an entomopathogenic nematode, *Steinernema siamkayai* isolated from cotton ecosystem and its bacterial symbiont, *X. stockiae* was carried out and submitted to Gen Bank. Pathogenicity of *X. stockiae* to *Helicoverpa armigera, Spodoptera litura, Sylepta derogate, Corcyra cephalonica* and *Galleria mellonella* larvae proved its insecticidal activity. Interaction between *X. stockiae* with entomopathogenic (*Metarhizium anisopliae, Lecanicillium lecanii* and *Fusarium pallidoroseum*) and plant pathogenic fungi (*Pythium* sp., *Fusarium* sp., *Macrophomina* sp., *Colletotrichum* sp., *Rhizoctonia* sp. and *Sclerotium* sp.) revealed that *X. stockiae* inhibited the growth and sporulation of entomopathogenic fungi. *X. stockiae* also demonstrated good potential in controlling the growth of plant pathogenic fungus. Chemo profiling of its secondary metabolite by GC-MS revealed the production of antimicrobial and insecticidal compound and supported the mode of action of bacterial symbiont of entomopathogenic nematode.

**Conclusion:** The results proved the wide spectrum (insecticidal, antifungal) action of *X. stockiae* which can be exploited for biological control of insect and fungus.

Keywords: Entomopathogenic nematodes, Xenorhabdus stockiae, Steinernema siamkayai, metabolites,

# Caulimovirid-like Sequences in Upland Cotton (Gossypium hirsutum L.) and Related Species

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**Background:** High-throughput sequencing data generated during the characterization of the cotton leafroll dwarf virus population in Mississippi (2020–2022) led to the identification of contigs with mutually identical nucleotide content that share similarities with existing plant pararetroviruses (family Caulimoviridae). This discovery prompted further investigations using both wet lab and bioinformatic approaches to determine the exact nature and origins of these sequences.

**Results:** The analyses identified endogenous viral elements (EVEs) related to extant members of the family Caulimoviridae, integrated into the genome of upland cotton (*Gossypium hirsutum*). These elements were provisionally named "endogenous cotton pararetroviral elements" (eCPRVE). The origin of these Caulimoviridae-related sequences was traced to a ~15 kbp-long locus on the A04 chromosome. This locus contains head-to-head (sense-antisense) oriented tandem copies located on both positive- and negative-sense DNA strands. The Caulimoviridae-related sequences comprise near-complete, slightly decayed genome information, including open reading frames (ORFs) coding for major viral proteins such as the movement protein (MP), coat protein (CP), reverse transcriptase (RTase), and transactivator/viroplasm protein (TA). Phylogenetic analyses of these viral proteins suggest that eCPRVE likely originated from a cognate virus belonging to a putative new genus within the family Caulimoviridae.

**Conclusions:** This research provides evidence of endogenous viral elements integrated into the upland cotton genome, offering insights into the relatively recent evolutionary history of the cotton family. The ongoing study aims to further elucidate the evolutionary significance of these Caulimoviridae-related sequences and to explore their potential practical implications for cotton biology and crop improvement.

# Detection of *Fusarium* Contamination in Seed of Some Iranian Cotton Cultivars

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**Background:** Cotton is one of the most important crops in the oil extraction and textile industries. Since cotton seeds form the foundation of crop production, their health is crucial. *Fusarium* is one of the most serious pathogens that endangers seed health. Seed transmission can lead to reduced germination, damping-off, root and crown rot, and ultimately reduced production. In this study, we evaluated the contamination of cotton seeds with *Fusarium* fungus.

**Results:** Samples from different varieties and seed categories were collected from across the country. Various sections of the seeds, including the whole seed, seed coat, kernel (endosperm and embryo), endosperm, and embryo, were cultured on nutrient media such as potato dextrose agar and water agar. The Fusarium isolates were purified using the single spore method and identified based on macroscopic and microscopic characteristics as well as diagnostic keys. The contamination rates in fuzzy and delinted seeds were 98.7% and 1.3%, respectively. The highest percentage of purified Fusarium was obtained from the kernel. The number of purified fungal isolates from the cultivars Varamin, Khordad, Bakhtegan, Kashmar, Armaghan, Khorshid, Golestan, Sahel, Dr. Omumi, and T-14 were 35, 14, 10, 8, 5, 2, 1, 1, 0, and 0, respectively. The *Fusarium* species detected in this research included *F. equiseti* (39 isolates), *F. proliferatum* (23 isolates), *F. compactum* (10 isolates), *F. semitectum* (2 isolates), *F. nygamai* (1 isolate), and *F. solani* (1 isolate). Notably, *F. compactum* and *F. nygamai* are reported for the first time in Iran. The application of Polymerase Chain Reaction (PCR) and specific primers for *F. equiseti* and *F. proliferatum*—the dominant species—resulted in the production of proprietary DNA bands using the DNA of the relevant fungal species as well as the DNA of naturally contaminated seeds.

**Conclusion:** The identification of these two *Fusarium* species based on morphological traits was confirmed through molecular methods. This study demonstrates that the traceability of these *Fusarium* species in contaminated seeds is possible using PCR techniques.

# Influence of Seed Treatment With Insecticide at Different Temperatures on Germination and Development of Upland Cotton Cultivars (*Gossypium hirsutum*)

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**Background:** Cotton Thrips (*Thrips tabaci* Lindeman, 1889) is the most important insect pest at the beginning of the cotton growing season. Nymphs and mature insects of Thrips cause deformation of leaves, reduction of green area, loss of terminal bud, dwarfing and multiple branching of plants, reduced growth and consequently lower yield. One way to prevent pest infestation is to treat the seed with insecticides. In order to evaluate germination and establishment of non-delinted and delinted seeds of two cotton cultivars under the seed treatments with insecticides at different temperatures in laboratory and farm conditions, this research was conducted in two separate sections as a factorial experiment with four factors based on completely randomized design (CRD) with four replications in lab and a factorial experiment with four based on randomized complete block design (RCBD) with four replications on the research farm. The first factor includes two types of seeds (non-delinted and delinted seeds), the second factor are two Iranian cotton cultivar (Varamin and Khorshid) and the third factor is temperature at four levels (18, 20, 22 and 24 oC) and insecticide at three levels (control, Gaucho and Cruiser) are the fourth factor.

**Results:** The results of laboratory section showed the simple effect of cultivar, temperature, insecticide and also the interaction of seed type  $\times$  cultivar, seed type  $\times$  temperature, seed type  $\times$  insecticide type, cultivar and insecticide effect, temperature  $\times$  cultivar effect are significant on seedling length and germination rate at 1% probability level. Also, the results of the farm section showed that the simple effect of seed type, cultivar, planting date and insecticide as well as the interaction of seed type, cultivar, planting date and insecticide on plant height at 1% probability level was significant. The results of the average comparison showed that the highest percentage of germination was related to delinted seeds without treatment (93.98%) and treated seeds with Gaucho (93.43%). Also, the highest height of cotton plant was related to delinted seeds of Varamin cultivar (42.92 cm).

**Conclusion:** To produce seeds with a high germination percentage, Khorshid seeds and application of Gaucho leaded to increase the number of plants in square and Varamin cultivar in the first planting date with application of Gaucho was recommended.

Keywords: Germination, Cotton seed, Gaucho Insecticides, Cruiser Insecticides, cultivar

# Efficient Dose of Thiamethoxam as a Seed Treatment Product to Reduce Early Damage of Cotton Leafhoppers *Amrasca biguttula* (Hemiptera: Cicadellidae) in Côte D'ivoire

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**Background:** Over the past decade, leafhoppers have become major pests of cotton. In June 2022, a new species, *Amrasca biguttula*, appeared in Côte d'Ivoire and has caused losses of more than 50% of cotton production. To manage early infestations of this pest, the study was conducted with a view to determine an effective dose of thiamethoxam as a seed treatment for cotton. The effects of five doses (from 1 to 5 g of thiamethoxam/kg of seed) on leafhopper germination, growth and damage were evaluated.

**Results:** The results showed a better emergence rate and better growth with the 4 and 5 g of thiamethoxam/kg of seed. The use of 3 to 5 g of thiamethoxam/kg of seed significantly reduced damages (p < 0.001), with reduction rates of 60 to 80%.

**Conclusion:** 3 to 5 g of thiamethoxam per kilogram of seed had an influence on the infestation levels of the leafhopper *Amrasca biguttula*. Thus, seed treatment with these doses will help manage early infestations of this leafhopper during the first 30 days after germination before the start of the insecticide treatment program.

Keywords: Cotton, Amrasca biguttula, seed treatment, Côte d'Ivoire.

# A Ghlac1-Centered Transcriptional Regulatory Cascade Mediates Cotton Resistance to *Verticillium dahliae* Through the Lignin Biosynthesis Pathway

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Lignin biosynthesis pathway plays a central role in plant defense response against *V. dahliae*, and identifying the key regulators in the lignin pathway is necessary for cotton disease-resistance breeding. In a previous study, we identified a cotton laccase gene GhLac1 that mediates plant broad-spectrum biotic stress tolerance through manipulating phenylpropanoid metabolism. However, the upstream master regulators and regulatory mechanism of lignin remain largely unclear. Here, we performed Y1H library screening using the GhLac1 promoter and identified three WRKY, three MYB, and one APETALA2/ ETHYLENE RESPONSIVE FACTOR (ERF) TFs, which differentially respond to *V. dahliae* infection in cotton.

Among these seven TFs, GhWRKY30, GhWRKY41, GhMYB42, and GhTINY2 directly bind to the GhLac1 promoter and activate its expression. Furthermore, GhWRKY30 and GhWRKY41 interact with themselves and with each other, as well as in combination synergistically transactivated the GhLac1 promoter.

Transient overexpression of these four TFs in cotton obviously increased the expression of GhLac1 and other members of the laccase family, while knockdown of these TFs impaired the accumulation of lignin and made cotton more susceptible to *V. dahliae*. Taken together, we mapped a transcription regulatory cascade of lignin synthesis, which contributed to cotton defense response through modulating lignin metabolism.

# Evaluation of Sequential Sprays of Novel Molecules for Management of Pink Bollworm, *Pectinophora gossypiella* (Saund.) In *Bt* Cotton

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**Background:** Pink bollworm presents unique challenges in *Bt* cotton systems due to its internal feeding habits within developing cotton seeds poses less vulnerability to insecticides. Cotton growers have experienced severe economic loss from cotton bollworms, especially the pink bollworm, *Pectinophora gossypiella* (Saund.) as incidence in *Bt* cotton has progressively grown, and outbreaks have been detected in key cotton-growing states across the country, so a field experiment was carried out to determine efficiency of insecticides in their sequence programs to evaluate the best solution for pink bollworm during two successive seasons 2022 and 2023 at ARS Dharwad in *Bt* Cotton (Jadhoo BGII).

**Results:** In all the treatments sequence of insecticides with new chemistries were used so as to evaluate which sequence is effective in managing pink bollworm, a total of three sprays were imposed at 50-75, 75-100 and >120 days after sowing (DAS). Average of two years data showed, sequential application of insecticides including Profenofos 50EC @ 2.00 ml/lit at 50-75DAS followed by Profenofos 40% + Cypermethrin 4% @ 2.00 ml/lit at 75-100DAS and followed by Lambdacyhalothrin 5EC @ 0.50ml/lit resulted least mean larval load of 7.44 per 20 bolls with a significant reduction of 61.28% green boll damage and 10.88 locule damage which resulted in maximum seed cotton yield of 22.02 q/ha as compared to untreated block (9.47q/ha). Whereas, 60.64 per cent green boll damage noticed in tested sequence of Profenofos @ 2.00 ml/lit at 50-75DAS followed by Chloropyrifos 50% + Cypermethrin 5% EC @ 2.00 ml/lit at 75- 100DAS followed by Lambdacyhalothrin 5EC @0.50ml/lit found to be the next best treatment with 8.25 larvae per 20 bolls and 11.22 per cent locule damage registering 20.38 q/ha seed cotton yield. However, sequence with combi products resulted in relatively lowest coccinellids compared to sequence including Spinetroam 11.7SC and Spinosad 45SC proving less hazardous.

**Conclusion:** Findings points out to minimize repetition of insecticide application; furthermore, the importance of sequence insecticide programs included new groups of insecticides to directing tactics to fight against resistance development for conventional insecticides. The integration of these novel molecules in sequential pattern proved to be effective in the management of pink bollworm under field conditions.

Key words: *Pectinophora gossypiella*, *Bt* Cotton, Coccinellid, % GBD, % locule Damage Profenofos 40% + Cypermethrin 4%.

# Pink Bollworm, *Pectinophora gossypiella* (Saunders) Infestation Escalates from Incipient to Serious Proportions in North Cotton Zone of India

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**Background:** The increasing infestation of pink bollworm (*Pectinophora gossypiella*) poses a significant threat to sustainable cotton production in the North cotton zone of India. Over the past six years, research has been conducted to investigate the key factors driving the escalating pink bollworm (PBW) infestation. Studies were designed to monitor PBW populations on non-*Bt* and BG-II genotypes under unprotected conditions, assess pheromone trap catches, evaluate infestation patterns on BG-II hybrids, and analyze PBW infestation at farmers' fields, focusing on factors contributing to its establishment.

**Results:** The study revealed that the pink bollworm (*Pectinophora gossypiella*) initially survived near cotton processing mills before establishing regular infestations in the North cotton zone. As a functionally monophagous pest, PBW was found to persist during the off-season in cotton stalk stacks and stored seeds, which served as critical reservoirs. The outbreak in 2023 was exacerbated by a lack of awareness among farmers regarding the pest's survival mechanisms. Monitoring efforts showed that PBW populations were particularly high in areas where off-season sources, such as cotton debris, were not managed properly. Pheromone traps proved effective in detecting and tracking pest activity, while infestation patterns indicated that BG-II hybrids were more vulnerable under unprotected conditions.

**Figure-1:** Larval recovery (%) through destructive sampling in BG-II & N-*Bt* genotype under unprotected Conditions during 2016-2023.



**Figure-3:** Weekly trap catches of PBW A: Round the year B. Trap catches for weekly average 16th -44th SMW during crop season



**Figure-2:** Pink Bollworm Infestation (in terms of green boll damage or rosette flower formation) recorded at farmers field locations surveyed during the season indicating Incipient to Serious proportions (2019-23).



**Figure-4:** Contour plots representing PBW infestations (Green boll damage %) in common zonal trial (BG-II genotypes) based on destructive sampling during 2021-2023.



**Conclusions:** To mitigate PBW infestations and enhance cotton productivity, several key recommendations were made. These include timely sowing to avoid peak pest activity periods, regular monitoring of PBW populations using pheromone traps, and the release of biological control agents like parasitoids. Targeted insecticide applications should also be implemented to manage active infestations effectively. Off-season management practices, including the removal and proper disposal of cotton stalks and residues, are essential to minimize pest carryover. Additionally, ginning and oil extraction mill owners are advised to adopt proper storage practices and install pheromone traps to reduce post-season PBW emergence. Continuous research and extension efforts are critical to addressing this emerging threat and ensuring sustainable cotton production in the region. Continuous research and extension efforts are essential to address this emerging threat and enhance cotton productivity in the region.

# Whitefly, Endosymbionts and Cotton Leaf Curl Virus: Understand Transmission Intricacies

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Bemisia tabaci is an important pest of numerous food and fibre crops across the globe causing direct damage through feeding as well as by transmitting a number of begomoviruses. Among the transmitted viruses Cotton Leaf Curl Virus is one of the most serious threats to cotton in northern India as well as neighboring countries Pakistan and Bangladesh. The vector itself exists as a cryptic species complex comprising of many genetic groups also known as haplotypes, biotypes, strains etc. These cryptic species vary in vector competence, insecticide resistance, host preference and many other physiological parameters. The present studies focused on diversity of endosymbionts in the cryptic Asia II-1 and Asia 1 species followed by the role of these endosymbionts in the virus transmission by the host. The endosymboints diversity was investigated across 30 different locations covering five Indian states Punjab, Haryana, Gujarat, Maharastra and Uttar Pradesh and two pre-dominant cryptic species based on 16S rRNA gene sequences. The primary endosymbiont; Portiera was present in all the B. tabaci as samples and cryptic species. However, insignificant differences were observed in the circulation frequencies of secondary endosymbionts among the *B. tabaci* populations. Arsenophonus (88%), Cardinium (92%), and Rickettsia (96%) were detected in whiteflies from different places. Finally, 86 sequences obtained in this study (Portiera-24, Arsenophonus-21, Cardinium-22, Rickettsia-23) have been submitted to GENBANK. We observed that the Asia-II-1 genetic group of whiteflies predominantly harbored two secondary endosymbionts, Arsenophonus and Cardinium. We established a standardized protocol for eliminating these endosymbionts using various concentrations of antibiotics-kanamycin, tetracycline, ampicillin, chloramphenicol, and rifampicin-administered through a sucrose diet. Complete elimination of Arsenophonus was achieved with tetracycline and rifampicin at a concentration of 90 µg/ml. However, the primary endosymbiont remained unaffected by all tested antibiotics at different concentrations. Furthermore, the elimination of Arsenophonus resulted in a significant reduction in the titer of Cotton Leaf Curl Virus (CLCuV) in viruliferous whiteflies, thereby impeding its transmission compared to control flies with Arsenophonus. The variable expression of the GroEL protein gene in Arsenophonus-positive and Arsenophonus-negative whiteflies confirmed the role of this chaperonin in virus transmission. Cardinium, the other secondary endosymbiont, showed no response to the tested antibiotics, and its role in virus transmission could not be determined in this study. Importantly, the elimination of Arsenophonus did not adversely affect the biology and fitness of B. tabaci. These studies also confirmed no adverse impact of Arsenophonus elimination on biology and fitness of B. tabaci. The higher density of endosymbiont Arsenophonus in females of Asia II-1 may be possibly imparting higher vector competency. The studies give some insights through series of experiments into the complex interactions of cryptic species between the endosymbionts and its vectored CLCuV.

# Revealing and Identification of Cotton Leaf Roll Dwarf Virus in Uzbekistan

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Cotton is a woody perennial plant belonging to the family of marigolds, *G. hirsutum L., G. barbadense L., G. herbaceum L.*, and *G. arboreum* L. large and rich gene pool of species has been established in Uzbekistan. The climatic conditions of Uzbekistan are favorable for cotton cultivation; the resistance of cotton to drought, blight, pests, *Fusarium* and *Verticillium* wilt diseases has been studied and a number of varieties resistant to them have been created by the selection scientists.

In recent years, viruses have been found to be widespread in agricultural crops of our Republic (tomato, wheat, potato, peas, barley, cotton, etc.). Of these, viruses belonging to the Luteovirus family and their vectors are aphids, both of them are widespread in agricultural crops. So, PAV, MAV, RPV and SGV isolates of Barley Yellow Dwarf virus in cereal plants, Cucurbit aphid-borne Yellows Virus, Beet Western Yellows Virus, Soybean Dwarf Virus, and Bean Leaf Roll Virus in peas (Cicer arientinum L.). and Potato Leaf Roll Virus has been identified.

In previous studies, Cotton Mosaic Tobamovirus and Cotton Leaf Curl geminivirus were detected in cotton plants in the Republic of Uzbekistan, isolated, and observed under an electron microscope and their effect on cotton plant productivity was studied. In our country, Cotton Leaf Roll Dwarf Virus (CLRDV) was first detected in leguminous crops in 2012. CLRDV belongs Polerovirus is a genus of viruses in the family Solemoviridae and is spherical virions, 25–30 nm in diameter, single-straned RNA. It is not mechanically transmitted, it is not spread by seed or flower pollen. The vector of CLRDV is the aphids - main *Aphis gossypii*. CLRDV diseases in cotton plants show symptoms, such as yellow and red leaf mosaic, curling, twisting, leaf shrinkage, reduction between joints, and cause 10% to 80% cotton yield loss and great damage to cotton fiber quantity and quality.

# Detection and Management of Seed Borne Diseases of Bt Cotton

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**Background:** One of the reasons for the low productivity of Indian cotton is the biotic and abiotic stresses; various seed and soil borne diseases of this crop mitigates germination of seeds, seedling emergence along with its survival and plant stand in the field, as a result of which decline in cotton production and productivity is seen across the globe. The present investigations were under taken in this regard.

**Results:** Among the four different seed health testing methods employed to assess their efficacy and reliability for the detection of seed borne fungal pathogens in *Bt* cotton seeds (DCH-32), deep freezing blotter method was found effective for the detection of *Alternaria* spp. and *Fusarium* spp. whereas the potato dextrose agar plate method was found to be suitable for detecting *Aspergillus niger* and *Aspergillus flavus*. Out of eleven seed dressing fungicides tested against seed borne fungal infections associated with *B*t cotton by paper towel method, carboxin 37.5% WS + thiram 37.5% WS @ 0.2 % and penflufen 13.28% w/w FS + trifloxystrobin 13.28% w/w FS @ 0.2 % were found effective in reducing per cent seed infection and increasing per cent germination and were on par with each other. Compatibility test was conducted to study the compatibility of in vitro effective seed dressing chemicals with bioagents. Among the three bioagents studied, *Pseudomonas fluorescens* was found compatible with carboxin 37.5% WS + thiram 37.5% WS (@ 0.2%), whereas *Trichoderma harzianum* and *Bacillus subtilis* were found incompatible. In case of penflufen 13.28% w/w FS + trifloxystrobin 13.28% w/w FS (@ 0.2%), whereas *Trichoderma harzianum* and *Bacillus subtilis* were found incompatible. In case of penflufen 13.28% w/w FS + trifloxystrobin 13.28% w/w FS (@ 0.2%), all the three bioagents were found compatible. Under field evaluation, seed treatment with carboxin 37.5% WS + thiram 37.5% WS + *Trichoderma harzianum* recorded least per cent disease index (18.43%) of Alternaria leaf spot @ 75 DAS and mean per cent germination was 91.11, which was found on par with carboxin 37.5% WS + thiram 37.5% WS.

**Conclusion:** Deep freezing blotter method was found effective for the detection of *Alternaria* spp. and *Fusarium* spp. whereas the potato dextrose agar plate method was found to be suitable for detecting *Aspergillus niger* and *Aspergillus flavus*. Under field evaluation, seed treatment with carboxin 37.5% WS + thiram 37.5% WS + *Trichoderma harzianum* recorded least per cent disease index (18.43%) of Alternaria leaf spot @ 75 DAS and mean per cent germination was 91.11, which was found on par with carboxin 37.5% WS + thiram 37.5% WS

Key words: Cotton, Seed borne, Management, Seed certification.

# Mapping out the Causal Agents, Based on Morphological and Molecular Characterization of Boll Rot Complex Pathogens Affecting Cotton in Karnataka

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**Background:** The economic losses in cotton due to boll rot complex has increased in recent years due to climate change in in major cotton growing areas of the India. The disease complex has substantially affected the production chain, either by production losses and/ or fibre quality. There is no comprehensive information and research on boll rot complex which is affecting the final product. The present investigations were under taken in this regard.

**Results:** The intensive roving survey was taken to collect infected boll samples from the farmers' fields of northern parts of Karnataka covering Five major cotton growing districts, 17 talukas and 84 villages. The pathogenicity, morphological and molecular studies confirmed the association of an array of more than half a dozen Fungal pathogens such as *Alternaria macrospora, Fusarium oxysporum* f. sp. *vasinfectum, Exserohilum rostratum, Colletotrichum gossypii, Phoma* sp., *Trichothecium roseum, Aspergillus niger, Nigrospora oryzae* and *Rhizopus stolonifer* and a bacterial pathogen viz., *Xanthomonas citri* subsp. *malvacearum* in causing boll rot complex disease of *Bt*. Cotton. The study identified effectiveness injection infiltration technique as the best method to inoculate the pathogen into the host tissues which can be used as a standard method for inoculation of pathogens of boll rot complex. These pathogens were further identified by ITS1 and ITS4 sequence analysis. The sequence similarity of majority of the associated pathogens was more than 90 per cent except for *Exserohilum rostratum*, which showed 88 per cent sequence similarity with Chinese isolates and Phoma sp., which showed 86 per cent sequence similarity with Korean isolate. *Xanthomonas citri* subsp. *malvacearum*, which showed 81 per cent sequence similarity with Indian isolates.

**Conclusion:** Nine fungal pathogens and one bacterial pathogen were associated in causing boll rot complex of cotton in northern Karnataka. Identification was carried out based on pathogenicity, morphological and molecular methods. Among two methods of artificial inoculation tested, injection infiltration method was found better to inoculate the pathogen.
# ORAL PRESENTATIONS COTTON BREEDING & GENETICS



# A Multi-model Stability Analysis Employing AMMI and BLUP-Based Simultaneous Selection for *Gossypium barbadense* Genotypes

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Baghyalakshmi

**Background:** With increasing temperature and irregular weather patterns annually, the selection of stable, high-performing, regional-specific *G. barbadense* premium cotton cultivars become essential. The development of an Egyptian cotton plant appropriate for a target area becomes crucial because the preference of a variety may vary depending on the climatic zone. Nineteen *G. barbadense* genotypes from the germplasm were evaluated over five consecutive Kharif seasons from 2019 to 2024.

**Results:** The principal component analysis of the first two interactions revealed 96.2% of the variation, with significant genotype-environment interactions. According to AMMI 1 analysis, genotypes G8 and G18 consistently excelled across all environments with high mean yields. The G4, G14, G2, G10, G8, and G18 genotypes exhibited greater yield than average yield and were ranked based on mean performance. Genotypes G4, G14, G6, and G16 were more stable throughout all the

tested years. As there were more interactions, the principal component best linear unbiased prediction (BLUP)-based simultaneous selection was estimated using harmonic mean of genotypic values (HMGV), the relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotypic values (HMRPGV). Of the 19 genotypes, 8 had plant yields above the mean value. The genotypes G9, G3, and G18 had the highest predicted means for single-plant yield. Furthermore, genotypes namely, G18, G13, G2, G5, and G7, such as HMGV, RPGV, and HMRPGV, were identified as being highly stable and high in yield according to their stability parameters. Based on WAASBY, some genotypes (G12, G18, G13, and G7) exhibited high stability and yield performance.

#### **RESULTS FROM AMMI ANALYSIS**

- The majority of the total variation (79.30%) was attributed to the environment, while the genotype and GEI contributed approximately 14.11 and 6.55%, respectively.
- AMMI analysis showed that the first four principal components explained the GEI. The first PC contributed 67% to the total GEI, while other PCs contributed the remaining 33%.
- Environments 1, 3 and 2 had long vectors, whereas 4 and 5 had shorter vectors. Environments E4 and E5, which represent plot yield, had PCA1 scores closer to zero. This suggests the strong performance of all the genotypes in these environments.
- E1 and E2 had vectors parallel to PC1 (67%), indicating a greater contribution to the overall variation. E1 and E4 had relatively high average yields, and E3, E5, and E2 had below-average yields. Genotypes G8 and G18 consistently excelled across all environments, with high mean yields near the origin of the axis.



**Conclusion:** Best linear unbiased prediction (BLUP) outperformed all other AMMI family members in terms of accuracy when more genotypes were tested. The weighted average absolute score of BLUP (WAASB) is an ideal tool for discerning variations and identifying stable genotypes among all methods. The genotypes that performed better in investigated circumstances can be used as best parental lines in breeding programs for changing climate conditions.

Keywords: AMMI, BLUP, cotton, genotype-environment interaction, stability

# Predominant Gene Effects for Fibre Elongation in Levant Cotton (Gossypium herbaceum)

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**Background:** Cotton seed trichomes are single epidermal cells that form lint and fuzz fibres. Cotton fibre development involves four stages: initiation, elongation, secondary cell wall synthesis and maturation. Only 30% of ovule epidermal cells become spinnable fibres during initiation. The initiation and elongation stages significantly impact fibre quality and yield. We studied the inheritance pattern and genetic effects of fibre initiation and elongation in Levant cotton cross, Fuzzy-linted (FL) × Fuzzy-lintless (Fl) through six generations mean analysis for improving yield and fibre quality.

**Results:** Inheritance studies revealed that 15 linted: 1 lintless segregation ratio in 2 population which was also confirmed in backcross populations, indicating the lintlessness trait is controlled by a double recessive gene. Six-parameter generation mean analyses showed duplicate gene action and complementary gene interaction for various yield and fibre related traits, with duplicate gene action observed for fibre length, representing fibre elongation. Scanning electron microscopy of 2 dpa ovules revealed differences in lint formation between parents and the  $F_1$  hybrid. The chalazal and middle parts of the ovules were covered with fibre initials and elongated fibres, while the micropylar part had fewer and smaller fibres. Fuzzy-lintless ( $F_1$ ) parents had fibre initials that did not elongate. whereas,  $F_2$  and backcross (BC1P1 and BC1P2) generations showed varying fibre initial coverage and lint percentages, with the fibreless phenotype absent in BC1P1, indicating duplicate dominant epistasis. Non-segregating generations showed significant differences in fibre numbers corresponding to their lint percentage es, highlighting the importance of increasing elongating fibres per unit area to enhance lint percentage as a key research focus. This was further supported by association studies that revealed a strong positive correlation between the total number of fibre-initiated cells at 2 dpa and other fibre-related traits, such as the number of fibres per seed, the number of fibres per mm<sup>2</sup> of seed surface, lint percentage, and UHML. Thus, increasing the number of elongated fibres can enhance lint percentage.

Scanning Electron Microscopic images of ovule at 2 dpa (bar: 100 µm) showing the development of fibre initials in *G. herbaceum* 



**Conclusion:** The F2 segregants from the Fuzzy-linted (FL) × Fuzzy-lintless ( $F_1$ ) cross showed a 15:1 linted to lintless ratio, indicating two genes with duplicate dominant effects. Duplicated gene action was observed for traits like number of monopodia, bolls per plant, boll weight, seed index, lint index, lint yield, seed cotton yield, and fibre length, while complementary gene interaction was noted for number of sympodia, lint percentage, and uniformity index. The Castle-Wright and Burton formulas suggested two-gene control for UHML. SEM at 2 days post-anthesis (dpa) revealed fibre initials in FL and minimal protrusions in Fl. A strong correlation was found between fibre-initiated cells and traits like fibres per seed, fibres per mm<sup>2</sup>, lint percentage, and fibre length, indicating that increasing fibre initial density can predict and enhance lint yield in cotton breeding.

Keywords: Diploid cotton, fibre elongation, mutant, generation means, epistasis, duplicate gene interaction

# Influence of the Impurity Level of Seed Cotton on The Ginning Yield and the Technological Characteristics of the Fiber in Côte d'Ivoire

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**Background:** Cotton growing in Côte d'Ivoire faces a number of constraints, not least climate change, which is having an increasingly visible impact on production. In addition to the drop in cotton production, one of the problems facing the Ivorian cotton industry is the low fibre yield at ginning factories and the poor quality of the fibre sold on the international market. The causes identified include the poor quality of seed cotton purchased on local markets, particularly the level of impurities.

This study was therefore carried out to determine the influence of the waste contained in the seed cotton ginned in factories on the fibre yield and the technological characteristics of cotton fibre in Côte d'Ivoire.

The work consisted in carrying out ginning trials in ginning factories to assess fibre yield in relation to the level of impurities in the cotton harvested. The fibre samples taken from the bales during the ginning trials were analysed on an HVI 1000/1000 integrated measurement chain. The data collected were used to perform a multivariate analysis (PCA) and simple regressions.

**Results:** The results showed that the waste rate increased from 2.96% to 5.33% from the youngest production generations to the oldest. Principal component analysis revealed correlations between parameters collected n fectories. The level of impurity was negatively correlated with fiber ginning yield, fibre length (y = -0.4408x + 28.991;  $R^2 = 0.3956$ ; p=0.005) and length uniformity (y = -0.5963x + 81.078;  $R^2 = 0.5185$ ; p=0.001). It is positively correlated with short fibre content (y = 1.8376x + 8.8186;  $R^2 = 0.5833$ ; p=0.000) and trash in baled fibres (y = 4.8515x + 25.759;  $R^2 = 0.4054$ ; p=0.004).



**Conclusion:** Impurities in seed cotton contribute to reducing the fibre yield at ginning in factories and to degrading the fibre characteristics by reducing fibre length and uniformity on the one hand, and by increasing short fibre rates on the other. This contributes to reducing the market value of cotton fibre.

Keywords: Seed cotton, quality, fibre yield, technological characteristics, fibre, ginning, Côte d'Ivoire Coast

# Molecular Mapping of Cotton Leaf Curl Disease and Whitefly Resistance in Upland Cotton

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**Background:** Cotton leaf curl disease (CLCuD) and whitefly are the major biotic stresses threatening upland cotton cultivation in North-Western India and Pakistan. The extant upland cotton cultivars grown in NW Indian states are vulnerable to both CLCuD and whitefly. Resistance to these biotic stresses is not available in the upland cotton germplasm. Therefore, efforts are underway to introgress resistance to CLCuD and whitefly from the related progenitor and non-progenitor species to upland cotton.

**Results:** Synthetic Polyploid (A2D1), *Gossypium armourianum* (a wild diploid D-genome cotton species), Mac 7 (an introgression line of cotton with complex pedigree) and G. arboreum are being utilized besides other cotton species as the donors for transferring resistance against CLCuD, whitefly and other biotic and abiotic stresses in upland cotton at the Punjab Agricultural University. Two dominant genes conferring resistance to CLCuD have been identified in Synthetic Polyploid (A2D1) and mapped on chromosomes A01 and D07.

Introgression lines resistant to whitefly have also been identified from the Synthetic Polyploid/Upland cotton/Upland cotton crosses. Similarly, a major CLCuD resistance gene has been mapped in *G. armourianum*. Besides CLCuD resistance, *G. armourianum* has also been found to be resistant to whitefly. Genetic analyses indicate that CLCuD resistance in Mac 7 is multigenic, whereas at least two major genes are involved in whitefly resistance. Mapping of genes associated with this biotic stress resistance in Mac 7 is underway.

**Figures:** Introgression and Mapping of Cotton Leaf Curl Disease (CLCuD) Resistance from Wild *Gossypium armourianum*-Kearney into Upland Cotton (*G. hirsutum* L.). Pathak et al. (2024, Plant Disease., doi.org/10.1094/PDIS-08-24-1645-SC).



**Conclusion:** CLCuD resistance is simply inherited in Synthetic Polyploid and *G. armourianum* and the underlying genes has been mapped. In Mac 7, CLCuD resistance has been found to be multi-genic, whereas atleast two major genes are involved in whitefly resistance.

Keywords: Gossypium, Gemini virus, B. tabaci, alien introgression, wide-hybridization

# Cotton Breeding Strategies in West and Central Africa: Challenges and Perspectives

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Over the past decade, cotton breeding programs in West and Central Africa (WCA) have shown minimal genetic advancement in key traits like seed cotton yield. This stagnation is due to the reliance on similar gene pools since the 1960s and outdated breeding methods that do not utilize modern technological advances or address new challenges. Cotton is economically vital in WCA, with Africa being the fifth largest producer and third largest exporter. Cotton production is concentrated in countries like Benin and Mali, with about 16 million people depending on it for income. Challenges faced by cotton breeding include: i) Technical Issues: Narrow genetic base, ineffective selection methods, and lack of advanced biotechnological tools, ii) socio-economic and environmental factors: need for varieties that adapt to climate change, improve labor efficiency, and reduce environmental and health impacts, iii) current methods and limitations: traditional genealogical selection and limited genetic resources have led to stagnation in performance. New genetic resources and more complex breeding methods are needed.

Amangoua Ferdinand

**Figure:** Schematic representation of an integrated cotton breeding program. Prospects for improving varietal selection programs. Ultimately, an integrated selection scheme combining genomic modelling, genetic progress simulation and new statistical analysis models will be implemented to revitalize genetic progress.



To address these issues, the network of member countries of the Regional Program for Integrated Cotton Production in Africa (PR-PICA) has initiated efforts to i) enhance genetic diversity through international resource exchanges and creation of mega-populations, ii) improve selection schemes by incorporating modern tools and techniques, such as genomic analyses and marker-assisted selection, iii) strengthen the capacity of researchers and technicians through training and resource pooling.

The network aims to revitalize breeding programs by combining resources and adopting innovative practices to meet evolving challenges and boost genetic progress.

Key words: Cotton, varietal selection, genetic variability, biotechnology, genetic gain

# Exploiting Uzbek Germplasm Resources for Improvement of Upland Cotton

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**Background:** Cotton genetic resources are a strategic asset essential for the development of sustainable cultivars and the global textile industry. The Uzbek Cotton Germplasm Resources are recognized as one of the most valuable collections worldwide, comprising wild, semi-wild, and ruderal forms sourced from diverse geographical regions. The Cotton GenBank primarily includes cultivated tetraploid species (2n = 52) and diploid species (2n = 26) from the *Gossypium* genus, encompassing 28 of the at least 50 known species. With 9,023 accessions, including American cotton (*G. hirsutum* L.), Peruvian cotton (*G. barbadense* L.), Afro-Asian cotton (*G. herbaceum* L.), Indo-Sino cotton (*G. arboreum* L.), wild samples, and synthetic hybrids, this GenBank serves as a critical resource for breeding programs and cotton research.

**Results:** Recent studies have highlighted significant findings from the Uzbek Cotton GenBank. DNA marker analyses revealed phylogenetic relationships between *G. mustelinum* Miers ex Watt and *G. arboreum* L., with *G. mustelinum* closely related to the subspecies *G. mustelinum* ssp. nanking. Promising cotton lines with bright fiber, fiber yields of 40.0–42.0%, and cotton weights per boll of 6.1–7.0 grams were identified. Additionally, subspecies and landraces of *G. herbaceum* L. and Australian wild cotton (subsp. *pseudoarboreum f. harga*) were found to be phylogenetically close to *G. nelsonii* and *G. australe* of the "G" genome.

Structural studies of hybrids and wild species revealed high tolerance to biotic and abiotic stresses and low seed coat contamination. Moreover, phylogenetic analysis and genetic selection of *G. mustelinum* × *G. herbaceum* allopolyploid hybrids produced transgressive cotton plants with long fiber lengths. However, mutational changes in F1C subsp. *africanum* × *G. mustelinum* hybrids caused pollen sterility and reduced flower production, contributing to plant sterility.



Figures: Cotton varieties developed using Marker Assisted Selection (MAS) technology

**Conclusions**: The findings from this research enhance our understanding of the molecular diversity and phylogenetic relationships within the *Gossypium* genus. These insights enable the identification of economically valuable traits, such as fiber quality, yield, and stress tolerance, which can be utilized in breeding programs to improve Upland cotton. The study also underscores the importance of preserving and enriching the Cotton GenBank as a resource for future generations, ensuring its role in supporting sustainable cotton production and global textile needs.

Keywords: Genetic resources, GenBank, Gossypium species, Interspecific hybridization, Cotton improvement

# **Evolutionary Divergence of Duplicated Genomes in Allotetraploid Cottons**

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**Background:** Cotton (*Gossypium*) is a vital economic crop and the primary source of natural fiber for the textile industry. Despite its importance, the evolutionary mechanisms driving speciation within the Gossypium genus remain poorly understood. This study leveraged genomic data from 25 Gossypium genomes and incorporated four newly assembled genomes-G. harknessii, G. gossypioides, G. trilobum, and G. klotzschianum (Gklo)-to investigate the speciation history of this genus. Complex phylogenies were observed, potentially influenced by introgression and incomplete lineage sorting (ILS), both of which likely played significant roles in the rapid diversification of Gossypium.

**Results:** The study focused on the rapid radiation episode during a concise period of *Gossypium* evolution. For a recently diverged lineage comprising G. davidsonii, Gklo, and G. raimondii, a detailed ILS map was constructed. This analysis revealed a non-random distribution of ILS regions across the reference Gklo genome, with specific regions showing signs of strong natural selection. Significant variations in speciation mechanisms were identified between closely related sister species Gklo and G. davidsonii. Approximately 15.74% of speciation-related structural variation genes and 12.04% of speciation-associated genes were found to intersect with ILS signatures. These findings indicate that ILS has been a key driver in shaping the speciation process within this genus.

Figure: Population Structure and History of Tetraploid Cotton. Figure: Gene flow among tetraploid cotton populations. Schematic Over the past million years, tetraploid cotton has undergone diagram of the optimal population historical model inferred using population shrinkage, particularly in G. mustelinum, which con-fastsimcoal2. The results show that G. hirsutum was domesticated tinues today. G. hirsutum and G. barbadense were domesticated around 5400 years ago. G. barbadense has a domestication history independently, with G. hirsutum being domesticated earlier. The of about 300 years, aligning with its expansion from the Caribbepopulation history of G. barbadense resembles that of G. darwinii, an Sea to high-latitude regions after improvement. Approximatewith potential gene flow between them. The genetic diversity of G. ly 420,000 years ago, the ancestral species of G. barbadense-like barbadense is lower than that of wild G. hirsutum, likely due to G. and G. hirsutum-like diverged from G. mustelinum, and around barbadense's shorter domestication history.

240,000 years ago, they split into two separate branches.



**Conclusions:** This research highlights the role of incomplete lineage sorting in the adaptive radiation of the *Gossypium* genus. The non-random distribution of ILS regions, coupled with evidence of natural selection, underscores the complexity of Gossypium speciation. The study advances our understanding of the evolutionary history of cotton and provides valuable insights into the genetic mechanisms underpinning its diversification, which could have implications for future cotton breeding and conservation efforts.

Key words: cotton speciation, Gossypium genus, incomplete lineage sorting, ILS, phylogenetic analysis, gene tree

# The Cotton Historical Lines Project: Genome Changes Over Time

#### **Grant Billings**

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How has genetic diversity changed over the past 100 years of breeding, and what implications do these changes have for cotton productivity? To answer this question, we re-sequenced 173 cotton genotypes to 30X coverage. Single nucleotide polymorphisms and small insertions and deletions were identified in this dataset. We determined which genomic loci are most strongly associated with changes in phenotypes.

Overall, our findings contribute to the understanding of genetic diversity and the impacts of breeding on the cultivated cotton gene pool. The data and results presented here will serve as an important foundational resource in planning how to track alleles in breeding programs as breeders begin to implement genomics technologies for decision-making.

**Grant Billings** 

#### Changes during the four Eras of cotton breeding in the United States



#### Changes in Yield components:

Bolls have gotten smaller, with higher lint percentage and lower seed index, but lint yield per acre has increased.



#### Changes in fiber length over time:

Fiber length has steadily increased over time, with the largest changes coming after the adoption of HVI.





Changes in net returns over time, as estimated using the 2023 Cotton Incorporated Loan Calculator





Genetic diversity has decreased over time, going down by 17% over 50 years



# Genetic Diversity and Evolutionary History of Truly Wild Upland Cotton

#### Xuan Liu, \*Guanjing Hu

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**Background:** Understanding the genetic diversity of wild forms of upland cotton (*Gossypium hirsutum*) is vital for gaining insights into domestication processes and leveraging wild germplasm for future crop breeding. While upland cotton is a primary source of natural fibers and has been extensively studied among cultivars, wild populations remain under-researched due to their scarcity and the challenges of distinguishing them from feral derivatives.

**Results:** In this study, representative wild upland cotton samples from Central and South America were selected for ultralong-read sequencing to characterize structural variations (SVs) and construct a pan-genome of wild upland cotton. Analysis of 12 wild samples revealed significant genetic diversity. Phylogenetic analysis based on single nucleotide polymorphism (SNP) and SV data consistently resolved two distinct clades:

- 1. The Yucatan clade encompassing populations from the northern Yucatan Peninsula, recognized as the center of origin and domestication.
- 2. The Eastern clade comprising scattered populations throughout the Caribbean.

Both clades exhibited substantial genetic dissimilarity from modern cultivars, highlighting the untapped natural diversity present in wild upland cotton. Ancestral reconstruction of evolutionary gains and losses of SVs identified 6,377 SVs involving 6,370 genes associated with domestication.

#### Wild forms hold untapped diversity for cotton breeding and crop improvement:

From genetic diversity to phenotypic diversity and from ecological adaptivity and plasticity to climate responsive and resilient traits



#### Wild Cotton

#### Innovative breeding materials

**Conclusions**: This study enhances our understanding of the genetic diversity and evolutionary history of wild upland cotton. The findings underscore the importance of exploring natural genetic diversity to inform future breeding programs. Untapped diversity in wild populations offers immense potential for improving cultivated cotton, particularly in traits associated with resilience, adaptability, and productivity. This research provides a critical resource for integrating wild germplasm into modern cotton breeding strategies.

Keywords: SNP, polymorphism, Genetic diversity, upland cotton Genetic distribution.

# Cotton Pedigree Genome Reveals Restriction of Cultivar-Driven Strategy in Cotton Breeding

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Guoli Song

**Background:** Cotton genomic data have facilitated the identification of many elite genes, offering a wealth of genetic resources for gene-driven breeding. However, cultivar-driven breeding, based on backbone cultivars, remains the most widely applied strategy in cotton improvement. Understanding the genetic limitations of the cultivar-driven approach is critical for transitioning to a gene-driven breeding strategy. CRI12, a widely used backbone cultivar, serves as a model to investigate the genetic basis of this restriction.

**Results:** Using Nanopore long-read sequencing, the pedigree of CRI12 was sequenced to construct a graphical pedigree genome. This high-quality genome incorporated 13,138 structural variations across 20 different pedigree members. The analysis revealed that low hereditary stability of elite genomic segments in backbone cultivars is a key limitation of the cultivar-driven strategy. Through presence- and absence-variation-based genome-wide association studies (GWAS) on three cohorts, 623 functional

segments associated with multiple agronomic traits were identified in CRI12. Furthermore, 25 deleterious genomic segments were found to influence the geographical divergence of cotton pathogen resistance. An elite pathogen-resistant gene, GhKHCP, was characterized, highlighting its role in modern cotton breeding programs. Comparative analysis between the CRI12 pedigree and a large cotton population identified 386 pedigree fingerprint segments, which were instrumental in understanding the genetic patterns of functional segments in the CRI12 pedigree.

The restriction of cultivar-driven breeding strategy. High ratio of favorable CRI12-specific segments, while their low hereditary stability suggests that they may be difficult to utilize adequately in a cultivar-driven strategy.







Cohort under cultivar-driven strategy



**Conclusions:** This study provides critical insights into the genetic patterns and limitations of the cultivar-driven breeding strategy. The graphical genome method revealed that low hereditary stability and deleterious genomic segments pose significant challenges to the effectiveness of this approach. The findings support the theoretical transition from cultivar-driven to gene-driven breeding strategies, offering a roadmap for future cotton breeding efforts. The identification of elite genes, functional segments, and genetic patterns provides valuable resources for the development of more sustainable and efficient cotton breeding programs.

Keywords: Cotton pedigree, Nanopore long read, Graphical genome, Cultivar-driven strategy

# **Utility of Breeding Value-Based Selection in Deriving Desirable Segregants for Multiple** Traits in Cotton (Gossypium hirsutum L.)

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**Background:** Genetic gain in any crop depends on ability of a genotype to transmit desirable combination of genes into their progenies which can be accounted in terms of breeding value. It results from independent gene effects which can be estimated based on general combining ability. Cotton breeders always aim at identifying desirable segregants superior for multiple traits to derive lines with desirable combination of yield and fibre quality traits. This study used parental lines with higher positive GCA effects and breeding values for the traits followed to arrive at single and double cross derivatives in the segregating populations with a blend of productivity and fibre quality features in the selected progenies.

JM Nidagundi

Results: A eleven parental lines with higher positive GCA effects were crossed in half diallel fashion to develop 55 single and double crosses which were evaluated under seven environments over two seasons. Among them, four single cross hybrids, two double cross hybrids, and six F2 populations whose parents exhibited higher breeding values/general combining ability for multiple traits (SCYP, NOBP, BW, GOT, UHML, FS) were chosen for current study. The positive and significantly higher gca effects in these parents is indicative of the presence of additive genetic variance and additive × additive gene interaction. Approximately, an optimal population size of 910-935 and 3040-3055 plants was raised for single and double crosses, respectively. A total 19, 22 and 24 plants transgressive in nature for yield in combination with five other characters viz., NOBP, BW (g), GOT (%), UHML (mm) and FS (g/tex) in single crosses (RAHH-1755, RAHH-455) and double cross (RHDC 1933) of group I, respectively. While in group II, 22, 22 and 24 plants showed

simultaneous transgressive segregation in RAHH-1702, SHH-818 and RHDC-1940, respectively for same set of traits. Percentage of segregants showing transgressive segregation when multiple traits were considered was found to be 3.60 per cent in both the double crosses which was way higher when compared to their respective single crosses, possibly for the reason that double crosses involved a greater number of parents owing to increased recombination.

Figures: Transgressive expression of individual plant selections in single crosses viz., RAHH-1702, RAHH-1755 and double crosses RHDC-1933 and RHDC-1940

**RAHH-1702 RAHH-1755 RHDC-1933 RHDC-1940** 

Conclusion: Breeding value and multiple parent-based crosses have yielded higher proportion of simultaneous transgressive segregants superior for multiple traits. Breeding value based selection can be used as an effective approach to derive desirable transgressive segregants superior for multiple traits.

Keywords: Breeding value, Combining ability, Multiple parents, Transgressive segregants, GCA effects

# CottonGen: A Central Data Repository and Analysis Resource for Cotton Research and Crop Improvement

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CottonGen is the long-established cotton community's genomics, genetics, and breeding database. It provides a comprehensive collection of integrated data, various analysis tools, a Breeding Information Management System, and links to external resources of interest to cotton researchers. CottonGen contains 10 million genes/transcripts, 123 genetic maps; 708,524 markers; 7,589 QTLs; 20,460 germplasm; 93 whole genomes for 33 species of 11 genome groups (AD, A, B, C, D, E, F, G, K, kirkii, Kokia), metabolic pathways for 18 species of the 10 genome groups; 34 million SNP and 16,692 SSR genotype measurements; 579,218 phenotype measurements (includes germplasm evaluations from United States, China, Uzbekistan, and the US Regional Breeders Testing Network), 45,155 images and synteny data for 87 genomes with links to genes, mRNA, orthologs and function. Analysis and visualization tools in CottonGen include the genome browser JBrowse, Synteny Viewer, MapViewer, CottonCyc, BLAST+, BIMS (the Breeding Information Management System for public and private data) and MegaSearch, a powerful search engine, both with recently added new features and functions. All the data are integrated within CottonGen and can easily be queried through various CottonGen search pages.

Keywords: CottonGen, bioinformatics analysis, Database, Cottons, Breeding Information Management System

- **CottonGen** is a long-term central data repository of genomics, genetics, and breeding (GGB) data and analysis resource for the worldwide cotton community
- Built using an open-source, user-friendly, Tripal database infrastructure used by several other databases
- Manages and integrates available GGB data into a single portal with a suite of easy-to-use querying and analysis tools



# A Revised Cotton Breeding Programme in South Africa

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**Background:** Cotton is an important fibre and cash crop globally. Currently, South Africa exports its produce on high price in international market. However, cotton production in South Africa (SA) has experienced a decline over the past seasons. A significant decrease in area of cotton in SA is decreased by 58% from 38,785 ha in 2018/19 to an estimated 16,176 ha in 2023/24. The dramatic decrease in production is predominantly due to lack of access to alternative planting materials. Two *Bt* cultivars (Candia and DP1240) of the available three cultivars grown by commercial farmers in SA, dominating commercial cotton production. This situation highlights the lack of alternative options when compared to other crops such as maize.

Mhelembe KG

**Result:** The Agricultural Research Council (ARC) – Vegetables, Industrial and Medicinal Plants (VIMP) has been mandated by the Department of Agriculture, Land Reform and Rural Development (DALRRD) to review the cotton breeding programme in South Africa. Previous cotton breeding

efforts at the ARC – Industrial Crops have been only on conventional plant material. Preliminary engagement with the industry representatives highlights the need for a revised strategy, to support the farmers' needs to have access to alternative plant materials. Therefore, a new demand-led breeding initiative is being developed, driven by objectives arising from engagements with industry representatives, farmers, seed companies and smallholder farmers. The breeding programme will employ a multifaceted approach focussing on the identification of genes that are important for SA conditions from available germplasms, with emphasis on trait integration, while using biotechnological approaches such as gene editing.



**Conclusion:** There is wealth of experience both locally and internationally to address this challenge. Thus, necessary collaborations from both local and international research institutes and universities are being aligned to develop unique, locally adapted, and technologically advanced cotton cultivars for the South African growers.

Keywords: Breeding, Cotton, Genome editing, GMO, Cultivars

# Genetic Improvement of Iranian Endemic Cotton Varieties (*Gossypium herbaceum*) Through Hybridization with Exotic Germplasm (*G. arboreum*)

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Reza Ramazani

**Background:** *Gossypium herbaceum* is a diploid species within the genus *Gossypium*, characterized by coarse fibers (micronaire >5) and short staple length (18–22 mm). This species, due to its origin, harbors valuable genes for salinity tolerance. In contrast, upland cotton (*G. hirsutum*) cultivars are tetraploid, producing finer fibers (micronaire <5) with longer staple length (28–32 mm). In this breeding program, 10 cultivars of *G. herbaceum* from Varamin and Kashmar were crossed with *G. arboreum* cultivar VTDL, introduced from India for its superior fiber quality. During the second and third years, F1 hybrids were backcrossed with their *G. herbaceum* parents to further enhance fiber traits.

**Results**: The hybrids exhibited significant improvements in fiber quality. The F1 hybrid from Bandar-Abbas  $\times$  *G. arboreum* displayed the longest span length fibers (27.6 mm). In the third year, back-cross populations from Sabzevar  $\times$  VTDL, Shahreza  $\times$  VTDL, and Bandar-Abbas  $\times$  VTDL produced

fibers with span lengths of 23.5 mm, 24.6 mm, and 25.1 mm, respectively, surpassing the maximum fiber span length observed in *G. herbaceum* cultivars (22.6 mm). During the fourth year, backcrosses, F3 generations, and parental seeds were cultivated for further selection and backcrossing. Results demonstrated that fiber length in cultivars such as Qom could be significantly improved through crossing with *G. arboreum*. However, high variability within offspring groups necessitates rigorous selection to stabilize desirable traits and identify elite plants. Evaluation revealed that some progeny outperformed their maternal parents in one or more traits. Notably, while certain hybrids exhibited excellent fiber length, they showed poorer fiber strength compared to their maternal parents.

#### Distinctness Uniformity and Stability (DUS) Test & Value for Cultivation and Use (VCU) Test



G. herbaceum F1 Hybrid G. arboreum parent parent





G. herbaceum F1 Hybrid G. arboreum parent parent

Genotype	Seed cotton yield per plant(gr)	Lint yield (gr)	Lint %	Fiber length	Uniformity %	Micronair index	Strength (g/tex)	Elongatio n %
KD-92-11	3022.5	1024.6	33.9	25.9	83.8	4.8	29	6.5
<b>KD-92-1</b> 7	2891.3	1101.6	38.1	27.7	84.2	4.9	28.2	6.2
KD-92-19	2800.6	988.6	35.3	28.1	85.1	4.5	30.6	7.2
Ghoozeh Ghermez (check1)	1965.9	684.1	34.8	22.7	80.4	5.8	20.4	6.2
Aria (check2)	2315.0	784.8	33.9	22.1	81.6	5.6	19.9	6.3

Table- Quantitative and qualitative traits of varieties achieved from *herbaceum*×*arboreum* crosses.

**Conclusions:** This study concludes that crossing *G. herbaceum* with *G. arboreum*, followed by repeated backcrossing, can break or mitigate unfavorable correlations between fiber traits such as length and strength. These findings emphasize the potential for improving fiber quality traits in *G. herbaceum* through strategic hybridization and selection. Future breeding efforts should focus on fixing favorable traits in progeny to develop elite lines for sustainable cotton production.

Keywords: Hybridization, fibre quality, Exotic cottons, Iranian cottons.

# Changes of Genetic Homogeneousity of Cotton Varieties During Individual Selection in Combination With Self-Pollination

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**Background:** In process of using even well-selected variety, the economic and biological characteristics of this variety gradually decrease and it deteriorates, population homeostasis is disrupted. This is due to mechanical and biological, clogging, splitting, increased disease and insect-pest complex. At the same time, cotton also has a tendency to cross, which means biological mixing is quite possible.



**Results:** We used the technique of artificial self-pollination (inbreeding) of flowers followed by testing of generation, culling of unwanted individuals and selection to stabilize the economically valuable traits and to increase homogeneity. The inbred lines of cotton varieties retained their typical features. However, as compared to cross-pollinated lines, heterogeneity in individual quantitative traits was more. It was revealed that depressive effect of self-pollination affects the rate of setting of fruit and decrease in weight of boll, likewise increase of sterile style is noted due to self-pollination. The co-efficient of variation of yield and fiber length in self-pollinated and cross-pollinated lines is insignificant, which indicates the stability of these traits. Their deterioration under the influence of self-pollination was not observed. Plants in a seed propagation nursery were studied for yield, boll weight, yield and fiber length. Noticeable deviations were observed in individual varieties in terms of boll weight, yield and fiber length. For example, in Sultan variety, the boll weight is higher in the cross-pollinated version - 7.8 g versus 7.2 in self-pollinated one. In contrary, self-pollinated plants of S-6524 have more boll weight.

Varieties	Yield, c/ha		Weight of	bolls, g	Fiber leng	Ginning, %	
	M±m	V %	M±m	V %	M±m	V %	C C
Sultan x	88,0±2,7	35,6	7,0±0,18	6,5	33,1±0,27	2,7	35,4
Sultan xx	88,0±1,8	35,2	6,7±0,11	6,3	33,5±0,29	4,0	35,6
Jarkurgan x	80,0±2,6	36,2	6,7±0,10	4,1	31,4±0,28	2,8	36,2
Jarkurgan xx	78,0±2,3	36,4	6,6±0,10	4,2	31,1±0,35	3,5	35,8
S-6524x	72,0+2,3	38,3	6,3+0,2	6,0	32,2+0,28	2,7	37,8
S-6524 xx	86,0±2,8	38,0	6,5±0,2	3,8	34,5±0,20	1,8	38,0
Namangan 77 x	84,0±3,0	35,2	6,5±0,3	5,8	33,2±0,34	3,6	36,7
Namangan 77 xx	76,0±2,2	35,8	6,4±0,18	7,0	33,4±0,33	1,7	37,1

**Table.** Comparative characteristics of varieties between self-pollination and cross-pollination of cotton by variability of traits. The variability coefficients for fiber yield and length in self-pollinated and cross-pollinated lines do not differ particularly, indicating the relative stability of these traits. No deterioration was observed under the influence of self-pollination.

**Conclusion:** It is found that in self-pollinating crops no depression of degeneration or deterioration occurs under the influence of self-pollination.

Keywords: Cotton plant, individual selection, self-pollination

# Genotype by Environment Interaction, Adaptability and Stability Analysis of Cotton (*Gossypium hirsutum* L. race latifolium H.) in Northern Mozambique

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Manuel Maleia

**Background:** Cotton, often referred to as "white gold," is one of the most important crops worldwide. In Mozambique, cotton is a significant cash and foreign exchange crop, regularly featured among the country's agricultural exports. Cotton cultivation is predominantly carried out by small-scale farmers who face numerous challenges, including low yields (<500 kg/ha). These challenges are attributed to the use of unimproved seed varieties poorly adapted to local conditions and the frequent use of recycled, uncertified seed. To address these issues, research has focused on introducing new varieties and developing locally adapted genotypes. This study aimed to evaluate the adaptability and stability of two cotton varieties and two inbred lines for seed cotton and fiber yield. Field trials were conducted under rainfed conditions across multiple locations in Mozambique, including Namialo, Namapa, Montepuez, Ribáuè, and Cuamba. The trials spanned three consecutive seasons (2021, 2022, 2023)

in most locations, with additional data from Cuamba for 2001 and 2023. Nine cotton varieties/genotypes were evaluated using a randomized complete block design (RCBD) with four replications. Combined and individual ANOVA analyses were performed for seed cotton and fiber yields, and adaptability and stability were assessed using the GGE biplot methodology.

**Results:** Among the evaluated genotypes, PL-164/2 exhibited the highest stability and predictability, followed by Flash and MP2020. The MP2020 genotype demonstrated superior fiber maturity, while PL-164/2 met the standard fiber length requirements. These genotypes consistently outperformed others in both seed cotton and fiber yields across diverse environments, indicating their adaptability and stability under rainfed conditions.

Table.	Comparison	of mean	seedcotton	yield	across a	all the	evaluated	environments.	
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Varieties or					ENVIR	ONMENTS				
Genotypes	Namialo	2021	Namapa	2021	Montep	ez 2021	Ribius 3	021	Cuant	a 2021
FLASH	1313.21 #	E	2623.42 a	ABC	1498.26	b DE	1498.34	a DE	1315.12 1	b E
ALBAR QM 302	1163.97	D	2356.69 a	AB	2893.04	a A	1368.34	a CD	1482.95	6 BCD
FDFSSA	1290.07	DE	2303.74 a	AB	2799.11	* A	1407.86	BCDE	1350.85 1	6 CDE
CIMSAN1	1350.86 a	ι Ε	2731.39 a	ABC	1680.72	b DE	1514.76	a DE	1809.30 :	a DI
CIMSAN2	1454.76 a	1 IF	2540.95 a	ABC	1766.71	b CDEF	1805.96	a BCDEF	1548.25 :	ab DIF
CA 324	1421.15 a	1 E	2199.05 a	BCDE	1535.53	bΣ	1636.43	a DE	1569.90 :	ab E
ALBAR SZ 9314	1252.09 a	a F	2576.43 a	ABC	1394.68	b IF	1578.81	a DEF	1612.05 :	a DIF
MEP2020	1374.94 #	D	2440.39 a	ABC	1330.29	ь р	1740.48	a CD	1425.13	ab D
PL-164/2	1323.33	DE	2367.95 a	ABC	1589.28	b CDE	1519.29	CDE	1565.99	ab CDE
Moun (kg.ha-)	1327.93	1	2160.00	¢	1831.96	FCH	1363.36	HIJ	1319.93	u u
CV(%)	24.47		11.89		29.98		1731		4.79	
Varieties or Genotypes	Namialo	2022	Namapa	2022	Montep	ez 2022	Ribiuè 2	022	Cuant	a 2022
FLASH	2242.60	BCD	1880.00 +	CDE	1591.43	b CDE	2103.62	th CDE	1861.67	CDE
ALBAR OM 102	1810 58	BCD	2273.81	ABC	1923.81	a BCD	2385.08	ab All	1822.79	BCD
ETESSA	1955.70	BCD	2121.01	ABCD	1557 38	b BCDE	2216.77	th CDE	1686.82	BCDE
CIMSANI	2016.89	CDE	2239.76	BCDE	1660.24	h DE	2349.91	ABCD	1838 47	CDE
CIMSAN2	2455.16	ABCD	2297.38	ABCDE	171238	ab CDEF	2904.05	A	1864.47	BCDE
CA 324	1916.35	CDE	1921.19 a	CDE	2050.00	a BCDI	2450.22	ABCDE.	2078.48	BCDE
ALBAR SZ 9314	2059.44	CDEF	2444.05 a	BCD	2201.91	a BCDI	2436.87	ab BCE	1900.47	CDEF
MP2020	2336.24	ABC	2011.43 a	BCD	1641.67	ab CD	1927.81	CDE	180132	CD CD
PL-164/2	2052.22	BCDE	2062.14 a	BCDE	1708.33	ab CDE	2147.19	ab BCDE	2060.80	BCDE
Moun (kg.ha-)	2104.47	DEF	2139.07	DE	1782.46	GHI	2327.94	CD	1879.70	EFG
CV (%)	15.84		14.75		14.77		14.27		28.49	
Varieties or Genotypes	Namialo	2023	Namap	2023	Montep	en 2023	Ribius 2	023	Overall Me	an(kg.ha-i)
FLASH	3261.88 a	A A	1405.\$3 a	DE	3046.26	a AB	2631.74	ab ABC	2019.81 :	2
ALBAR QM 302	3015.91	ib A	1282.35 a	D	3078.66	a A	3123.09	a A .	2143.93	
EDESSA	2669.65	ib A	1131.81 a	E	2709.35	a A	2612.34	ab A	1986.17	
CIMSANI	3114.27 4	ab AB	1388.04 a	E	3224.51	* *	2088.76	D CDE	2072.28	
CIMSAN2	2577.33 a	ab ABC	1289.22 a	F	2978.95	a A	2689.78	ab AB	2134.67 :	1
CA 324	2876.96	ab AB	1329.33 a	E	3171.44	a A	2786.35	ab ABC	2069.46	
ALBAR SZ 9314	3054.03	ib AB	1299.51 a	EF	3353.92	a A	2315.00	ab BCD	2107.80	
MP2020	2925.00 s	ib A	1250.83 a	D	2845.69	a AB	2540.47	ab ABC	1970.98	
PL-164/2	2380.05 b	ABC	1190.45 a	E	3130.56	a A	2868.51	ab AB	1997.58 :	1
Meen (kg.ha*)	2875.45	AB	1285.26 3		3059.92	A	2628.45	BC	2055.85	
CVCO	18.60			15.02			11.50		24.69	

**Table legend:** Means followed by the same lowercase letters in the columns do not differ significantly from each other, according to the Tukey test, at 5% probability. Means followed by the same uppercase letters along the lines do not differ significantly from each other, according to the Tukey test, at 5% probability.



**Conclusions:** The genotypes PL-164/2, Flash, and MP2020 are recommended for registration and release for production in Mozambique due to their superior adaptability, stability, and fiber quality traits. These findings highlight the potential of improved genotypes to enhance cotton production and support smallholder farmers in achieving better yields and economic returns. Further research and dissemination efforts should focus on promoting these varieties and improving seed distribution systems to maximize their impact.

Keywords: Biplot, cottonseed yield, fiber quality, GGE analysis, inbred lines

# Advances and Strategies in Cotton Genetic Optimisation: From Molecular Innovations to the Development of Locally Adapted Materials.

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**Background:** The National Institute of Agricultural Technology (INTA) at Reconquista, Argentina, has developed an integrated research and breeding program aimed at enhancing cotton (*Gossypium hirsutum*) production through genetic improvement, mutagenesis, molecular marker applications, and local adaptation strategies. This program focuses on improving yield, fiber quality, and disease resistance to suit the environmental conditions of northern Santa Fe province. The goal is to optimize cotton performance in the region while maintaining stability in quality traits.

Marcelo Paytas

**Results:** The breeding program demonstrated an annual genetic progress in lint yield (LY) of 3.24 kg/ ha, equating to a 0.47% yearly increase. These improvements were driven by enhancements in seed

cotton yield (SCY), lint percentage (LP), boll number (BN), and lint per seed (LS), with LP and BN identified as significant contributors to LY gains. While fiber and seed quality traits remained stable, oil content increased over time. Mutagenesis techniques, including the use of ethyl methanesulfonate (EMS), sodium azide (SA), and X-ray irradiation, effectively induced genetic variability, producing mutants with traits such as herbicide tolerance and enhanced resilience to salinity and drought. Molecular markers, particularly simple sequence repeats (SSRs), accelerated the identification of genetic linkages for traits like yield, fiber quality, and disease resistance, increasing breeding efficiency.

Heritability studies revealed high genetic control over traits such as LP, fiber length (FL), and micronaire (MIC), while moderate heritability was observed for SCY, LY, boll weight (BW), BN, and fiber strength (FS). Phenotypic and genetic correlations showed strong associations between LY and BN, emphasizing the importance of boll number in improving lint yield. Integrated disease management strategies combining genetic resistance, cultural practices, and chemical treatments were critical in mitigating the impact of cotton diseases.



Figure. Breeding program: traditional with the use of molecular markers

The breeding program, which combines traditional methods with the use of molecular markers, focuses on characterizing SSR (simple sequence repeat) markers associated with yield, fiber quality, and disease resistance in cotton. The process includes the selection of SSRs (a total of 73), DNA isolation, PCR amplification, and gel electrophoresis for marker analysis. Heritability studies are also being conducted. The cotton collection at INTA Reconquista is currently being characterized using known SSR markers associated with diseases such as Cotton Bacterial Blight and Cotton Blue Disease. Thus far, 70% of the collection has been analyzed, identifying genotypes that are either susceptible or resistant to these diseases.

**Conclusions:** The integrated breeding approach at INTA Reconquista has successfully enhanced cotton productivity through genetic and molecular innovations while ensuring local adaptation. The findings highlight the importance of boll number in yield improvement, the potential of mutagenesis for stress resilience, and the utility of molecular markers in accelerating breeding efforts. This framework offers a robust model for balancing yield improvement with fiber quality and disease resistance, serving as a foundation for advancing cotton breeding programs in Argentina and beyond.

# The Past, Present and Future of Colored Cotton and the Studies Carried out (*Gossypium hirsutum*.L) in Turkiye.

#### Nazife ÖZKAN

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Nazife Ozkan

**Background:** Colored cotton, due to its environmental benefits, has attracted significant interest from the private sector. Cotton plays a crucial role in the economy and social standards of living with its versatile applications, employment opportunities, and value addition. In light of global climate change, nations are focusing on environmentally friendly production methods that are cost-effective and sustainable. Colored cotton offers a production model that aligns with these objectives. Additionally, the post-COVID-19 emphasis on natural products has increased interest in environmentally conscious solutions like naturally colored cotton, which eliminates the need for toxic dyes and water-intensive dyeing processes.

**Results:** Turkiye is among the world's leading countries in the textile industry, and expanding the range of cotton textile products with unique features is key to enhancing market share. Naturally colored cotton, with its high yield and fiber quality, offers a promising opportunity. Varieties such as Nazilli Dt15 (2005), Emirel and Akdeniz (2009), and Sarıgelin and Gelincik (2014) have been registered and are now being produced. The Cotton Research Institute in Turkey initiated three breeding projects for colored cotton, including one led by the author. This project, launched in 2023, focuses on developing naturally colored cotton genotypes with high productivity and fiber quality.



Hybridization studies began with selected colored cotton genotypes such as Nazilli Dt15, Gs372 Green, Gs741 Green, and Gs274 Brown, along with testers like Ramses, Ezo, Eliza, Nysa, Novelia, Veritas Lycus, and Veritas Imperium. The line × tester analysis method was employed to create hybrid combinations. In the second year, parental varieties and F1 hybrids will be planted together to select promising populations. These efforts aim to reduce costs in the textile industry by minimizing the use of water, energy, and toxic dyes. Dyeing, the most expensive stage in textile production, is 2.9 times cheaper for naturally colored cotton compared to traditional white cotton dyeing. Furthermore, this approach eliminates toxic dye waste, supporting clean and sustainable production.

**Conclusions:** Colored cotton production aligns with the global focus on protecting nature and fostering sustainable practices. The development of high-quality, naturally colored cotton varieties offers a viable solution for reducing environmental impacts and dyeing costs in the textile industry. Future breeding programs will prioritize enhancing fiber quality and yield while expanding the use of colored cotton to support clean and sustainable textile production. Colored cotton represents a critical step towards a cleaner and more environmentally friendly future in the cotton and textile industries.

# Applications of Hyperspectral Imaging: New Dimensions to Cotton Breeding

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Pawan Kulwal

**Background:** Many agriculturally important traits depend on physiological and biochemical parameters that influence a plant's response to biotic and abiotic stresses. However, these traits are often expensive or time-consuming to measure, and significant gaps exist between plant physiology, genetics, and phenomics research. To address this challenge, high-throughput, non-destructive techniques such as hyperspectral imaging (HSI) are increasingly being utilized. HSI-based canopy reflectance captures spectral signatures from plant canopies at different wavelengths, providing critical insights into specific plant characteristics responsible for phenotyping. These spectral signatures can act as surrogate traits for early stress detection, allowing forecasting and timely implementation of control measures. This study utilized HSI to characterize eight species of cotton, including seven diploid species (*G. arboreum, G. thurberi, G. armourianum, G. davidsonii, G. aridum, G. raimondii,* and *G. somalense*) and one tetraploid species (*G. hirsutum*), as well as different races of *G. arboreum* and

*G. hirsutum* and their tri-species derivatives. The plant material was maintained at Mahatma Phule Agricultural University, Rahuri. Spectral reflectance data were collected using a spectroradiometer (350–2500 nm) at a 1-nm interval across the full electromagnetic spectrum.

**Results:** The spectral analysis revealed that each species exhibited unique spectral signatures, enabling precise differentiation among species and their derivatives. These spectral signatures also hold potential for characterizing desirable traits such as fiber quality, drought tolerance, and disease resistance. Diploid species, which harbor valuable traits for biotic and abiotic stress tolerance, showed distinct spectral patterns, providing critical information for breeding programs. The spectral signatures can be used to identify desirable lines, facilitating targeted breeding strategies for stress adaptation.



**Conclusions:** This study demonstrates the potential of canopy spectral signatures in phenotype sensing and cotton breeding. By integrating hyperspectral data collected at various growth stages under different stress levels, breeders can use artificial intelligence techniques to analyze high-dimensional data effectively. This approach enhances the identification of genotypes well-adapted to biotic and abiotic stresses, improving the efficiency of cotton breeding programs. Hyperspectral imaging thus offers a promising tool for bridging the gap between plant physiology, genetics, and phenomics, supporting the development of resilient cotton varieties.

Keywords: Hyperspectral imaging; spectral signature; biotic and abiotic stresses; Gossypium Species

# Pangenome Analysis Reveals Yield and Fiber-Related Diversity and Interspecific Gene Flow in *Gossypium barbadense* L.

#### **Qingying Meng**

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**Background:** Pangenome analysis has the potential to provide insight into causal genomic variations of agronomic traits in multiple crop species. To date, pangenome analyses in *Gossypium barbadense* have identified few causal genomic variations related to fiber length, fiber strength, and lint percentage using few wild *G. barbadense* genome assemblies.

**Results:** We de novo assembled 12 *G. barbadens*e accessions that range from the wild-to-domesticated cotton and constructed a graph-based pangenome. Whole genome comparative analyses identified 350,995 non-redundant structural variations (SVs) by integrating 16 *G. barbadense* and 12 other tetraploid cotton accessions. We clarified the genetic relationships within *G. barbadense* and identified selection signals using 671 *G. barbadense* genomes for which re-sequencing data were available. Interspecific introgression originated from Caribbean Sea region and subsequently selection drove the genomic differentiation on chromosome A01, which provided insight for understanding improvement in *G. barbadense*. Furthermore, SV-GWAS analysis identified four, three, and seven causal structural variations for fiber length, fiber strength and lint percentage, respectively. Two pleiotropic favorable alleles were combined into Xinhai cotton to significantly improve fiber length and fiber strength, and three favorable alleles were combined into Pima cotton, which significantly improved lint percentage.

**Figure:** Genetic architecture of fiber quality and yield in *G. barbadense.* SV-based GWAS analysis revealed 14 SVs loci, including four fiber length-related loci; three fiber strength-related loci; and seven lint percentage-related loci; Accessions carrying more favorable alleles exhibited increased fiber quality and yield.



**Conclusions:** In this study, we de novo assembled 12 *G. barbadense* genomes and identified four, three, and seven causal structural variations for fiber length, fiber strength, and lint percentage in *G. barbadense*. Identification of these SVs provides insight into and resources for improving cotton fiber quality.

# A Comprehensive Approach for Breeding High Yielding *Bt* Cotton (*Gossypium hirsutum* L.) Varieties and Hybrids Suited for Specific Growing Situations

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**Background:** The present cotton scenario in India is dominated by Bt hybrids with an almost complete role being played by the private industry. But for the Bt varieties to arrive, it took more than two decades majorly due to the *Bt* gene being intellectually protected. The coming of the Cry1Ac gene in India was followed by the commercial release of *Bt*-Cotton hybrids in the year 2002. Since then, there were no varieties with the Bt gene and it was felt that the poor Indian farmer should have an option to save his own seed which is possible only with varieties. An additional requirement in the mostly rainfed areas of the country, was compact varieties amenable to machine harvesting. So, the varying situations of irrigation and rainfed cultivation needed different varieties with regards to plant type. With the intellectual rights on BG-II expiring, it became conducive to breed for genotypes with the Cry1Ac+Cry2Ab gene combination.

**Results:** The public institutions in India began their *Bt* breeding programs around 2014-15 and today we **Rajesh Patil** have Bt varieties released for cultivation. At about the same time, Dharwad Centre began its Bt breeding programme. We had to rapidly adapt to the *Bt* gene and a simultaneous multi-pronged approach seemed to be the best option. The entire process involved limited back-cross and straight pedigree selection towards producing Cry 1Ac (BG-I) varieties. The present exercise began with the objective of developing high yielding Bt (Cry1Ac) varieties of Gossypium hirsutum. Three locally adapted promising genotypes were chosen to be converted in to Bt genotypes by using one good Cry1Ac ICAR donor line. In 2017-18 these 3 genotypes, NNDC-56 (compact type), FLT-44 and FLT-39, were crossed with the *Bt* genotype and the F1 was grown in 2018-19. Here, it was decided to take a simultaneous two-pronged approach to developing superior *Bt* plants, a limited back-cross approach and the regular pedigree method. The two-pronged approach was taken so as not to miss any good segregant arising in the straight progenies vis-à-vis in the more dependable back-cross progenies. Two back crosses were done followed by selection in the next three years and simultaneously the F1 was segregated till F5. Fifteen stabilized Bt genotypes including both types of progenies were evaluated during 2022-23 and 2023-24. Genotype E-21-4 (2611 kg/ha) was the highest yielder followed by CPDBt-1951, E-21-3, H-25-1, I-7-42 and others. The yield improvement over check CICR-23Bt ranged from 43.8% to 110.0% with seven genotypes significantly better consistently over two years. The plant type characterization, Ideotype breeding, classified 12 test genotypes into compact, super compact and tall-compact classes. These genotypes can be used for High Density Planting System (HDPS). The genotype E-21-4 has also topped the Bt trials of the All India Co-ordinated Project on Cotton, proving its worth. The strategy of simultaneous breeding of back-cross and pedigree methods was rewarding as among the top five, three were back-cross and two were straight pedigree progenies. In fact, when the initial crosses were made and individual plant selections within the three back-cross and three straight pedigree populations were made, in F<sub>2</sub> we arrived at a 67% and 33% composition, respectively, thus emphasizing that simultaneous two-pronged approach can give better rewards than only a straight forward back-cross conversion program. Other promising progenies numbering 50 generated from the above six populations were also evaluated and yields of these progenies ranged from 4174 kg/ha in a Tall-Compact type (E-23-1-4) to 3140 kg/ha in a Super-compact type (B-7) for HDPS. In the second approach, Mixed-pollination technique was used to breed the Cry1Ac+Cry2Ab (BG-II) genotypes. Twelve popular BG-II hybrids from the market were used in this exercise. Pollen from a fixed number of flowers from each hybrid was mixed and pollinated on to every hybrid. Each hybrid served as female to the other eleven males and 12 populations were created. Individual plant selections began in each population and it was continued till four generations. Forty-two promising progenies were evaluated in 2023-24 in F<sub>5</sub>. The top five genotypes came from different pedigree. The five best progenies showed seed cotton yield ranging from 3344 kg/ha (BG2Bt-21) to 3010 kg/ha (BG2Bt-36). Additionally, the boll weight in these BG-II progenies was impressive with an average of 4.6 g with a high of 5.43 g. The promising plant types here were again the super-compact category with average yield of 2952 kg/ha and the tall-compact category with 2609 kg/ha. This program too has produced genotypes meant for HDPS. Robust genotypes like BG2*Bt*-45 and BG2*Bt*-40 and those produced in the BG-I background can be adopted under wider spacing with irrigation. As these are Bt varieties, the overall cost of cultivation would go down as the farmer can save his own seed and will also spend less on bollworm control. The third component of the comprehensive strategy was to make hybrids out of these new Bt genotypes. Two methods viz., Path-of-Productivity and Diversity analyses were used to identify the would-be parents from both the groups of BG-I and BG-II genotypes produced in the above exercises. Care was also taken to accommodate plant type, boll weight, fibre properties and seed cotton yield in the selection of parents apart from the two analyses done over two years. Ten BG-II and six BG-I genotypes were used as Lines and four Bt genotypes independent of any of the above pedigrees were used as Testers to produce F1s which are currently under evaluation. These varieties and hybrids were built up from genetic material bred and stabilized under the envisaged comprehensive program of Bt cotton research at the University of Agricultural Sciences, Dharwad.

Conclusion: The comprehensive Bt Cotton breeding program was successful with the isolation of BG-I and BG-II promising genotypes. New Bt hybrids produced from the above genotypes are also being evaluated. Varieties under HDPS together with mechanical harvesting are the future for revitalizing the cotton scenario again in India.

# Metabolic Engineering of Cotton (G. hirsutum) for Artemisinin Synthesis

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with proven efficacy against parasitic and viral diseases, including malaria. However, its limited natural availability necessitates the development of sustainable and scalable production methods. Metabolic engineering of alternative plant hosts, such as cotton (*Gossypium hirsutum*), offers a promising solution. Cotton shares biosynthetic similarities with *A. annua* in the production of artemisinin precursors like dimethylallyl diphosphate (DMAPP) and isopentenyl diphosphate (IPP), making it a viable candidate for artemisinin synthesis.

Background: Artemisinin, a sesquiterpene lactone derived from Artemisia annua, is a crucial compound

**Results:** This study employed metabolic engineering techniques to harness the biosynthetic potential of cotton for artemisinin production. Key enzymes from the artemisinin biosynthetic pathway in A. annua were introduced into cotton via genetic constructs, leveraging parallels in precursor biosynthesis pathways. Transgenic cotton plants were successfully generated through somatic embryogenesis, with preliminary

results confirming the incorporation of target genes.

Further investigations are underway to characterize these transgenic plants through ectopic gene expression analysis and metabolomic profiling. Initial data indicate alterations in metabolic pathways, suggesting progress toward the production of artemisinin or its intermediates. Comparative studies between control and transgenic plants are revealing insights into metabolic flux changes and the potential emergence of novel compounds with therapeutic applications.

**Conclusion:** This research represents a significant advancement in establishing cotton as a sustainable platform for artemisinin production. By integrating enzymes from *A. annua* into the cotton metabolic framework, this work paves the way for scalable production of artemisinin and its derivatives. The findings also contribute to the broader field of metabolic engineering, highlighting the potential of cotton as a host for synthesizing valuable medicinal compounds. Future efforts will focus on optimizing biosynthetic pathways and scaling production to meet global demand for this vital antimalarial compound.



# Use of Biotechnological Methods to Overcome the Incompatibility of Remote Interspecific Hybridization of Cotton

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**Background:** Overcoming the incompatibility between cultivated tetraploid cotton species and wild diploid species with unique economically valuable traits remains a significant challenge in cotton breeding. Wild diploid species harbor traits such as disease resistance, drought tolerance, and other desirable characteristics that can enhance cultivated cotton varieties. This study focused on developing optimal nutrient media for in vitro embryo culture and post-culture embryo rooting, as well as establishing schemes for creating distant interspecific cotton hybrids.

**Methods:** Innovative nutrient media and in vitro embryo culture techniques were utilized to overcome barriers in distant interspecific hybridization. Exogenous phytohormones were applied to stimulate pollen tube growth, guide pollen grain movement, and regulate the zygote and primary endosperm nucleus division, enhancing seed set rates. Abortive embryos of distant hybrids were cultivated on artificial nutrient media, and additional nutritional supplements based on Knop's medium were used to address challenges in soil rooting.

**Results:** The research demonstrated that in vitro embryo culture prevents endosperm tissue death and supports the growth and development of hybrid embryos. Abortive embryos began development at various stages, including the formation of initial stem cells of embryonic organs or rudiments, but often exhibited morphoses. The most significant morphosis was the inhibition of root hair formation, leading to challenges in soil rooting. By applying additional nutrition using Knop's medium, the ability of test tube plant regenerants to root in soil was restored. As a result, fertile hexaploid amphidiploids were successfully synthesized, incorporating wild species such as *G. sturtii, G. harknessii, G. aridum, G. stocksii,* and *G. triphyllous.* These amphidiploids facilitate the introduction of valuable wild-species genes into the cultivated cotton genome, and some lines have been advanced to a linear state for further breeding.

**Table:** Characteristics of cotton lines obtained on the basis of interspecific hybridisation. Note: B-83, B-84, B-30 - lines isolated from the combination F18 BC3 Tashkent- 6 x F1 BC2 C-6524 x F1 BC1 108-F x F1 (108-F x *G.s turtii* Müll. B-85, B-103, B-104, B-30, B-339, B-162, B-189 - lines isolated from the combination F18 BC3 C-6524 x F1 BC2 C-6524 x F1 BC1 108-F x F14 (Deltapine-80 x *G. aridum* Skov.). B-26 - line isolated from the combination F14 BC3 C-6530 x F1BC2 C-6524 x F1 BC1 C-4880 x *G. triphyllum* Horch

Varieties and lines	<b>Yield</b> 100 Kg/ha	<b>Maturit</b> y days	Boll weight (g)	Weight (g) 1000 seeds	Ginning %	Length inch	Micronaire	Strength g/tex
C-6524 – st.	36,1	110,7	5,3	125	35,1	1,12	4,6	30,1
Наманган-77 – st.	37	110,5	5,0	115	36,2	1,08	4,7	27,6
B-30 (F18BC3 xx <i>G. sturtii</i> )	42,3	105,5	5,7	112	37,3	1,19	4,5	32,9
B-83 (F18BC3 xx <i>G. sturtii</i> )	40,5	110,9	5,6	122	37,2	1,23	4,1	29,1
B-84 (F18 BC3 xx <i>G. sturtii</i> )	41,2	108,9	6,2	124	38,7	1,22	4,2	30,4
B-85 (F18 BC3 xx G. aridum)	43,3	104,7	5,2	119	39,6	1,23	4,3	30,4
B-103 (F18 BC3 x x G. aridum)	41,1	112,5	5,9	120	37,5	1,26	4,3	32,4
B-104 (F18 BC3 xx G. aridum)	41,8	114,5	5,6	120	38,4	1,21	4,1	30,9
B-339 (F18 BC3 x x G. aridum)	39,2	113	5,6	120	38,2	1,22	4,4	31,6
B-162 (F18 BC3 x x G. aridum)	43,2	104,6	5,5	126	39,2	1,21	4,6	30,7
B-189 (F18 BC3 x x G. aridum)	40,7	108,1	5,6	121	38,8	1,18	3,8	30,9
B-26 (F13 BC3 x x <i>G. triphyllum</i> )	45,2	104,8	5,8	121	38,1	1,2	4,5	30

**Conclusions:** This study highlights the potential of in vitro embryo culture and the use of optimized nutrient media in overcoming incompatibility barriers between cultivated tetraploid and wild diploid cotton species. The synthesized fertile hexaploid amphidiploids serve as a valuable resource for transferring desirable traits from wild species into cultivated cotton. These findings contribute to expanding genetic diversity in cotton breeding programs and pave the way for the development of resilient and high-performing cotton varieties.

Key words: Biotechnology, cotton plant, remote interspecific hybridization, incompatibility, non-cross ability, in vitro embryo culture, nutrient medium, embryo, endosperm

# Blending Breeding Approaches of Self-Pollinated and Random Mating Crops for Efficient Genetic Improvement in Cotton

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Shreekant Patil

**Background:** The methods used in varietal breeding differ significantly between self-pollinated crops and random-mating crops due to differences in the target genotype or population aimed at in the two systems. A common misconception is that these breeding methods are isolated, restricted by the mating system barrier. However, there is a need to understand the genetic basis of combining and adapting steps across mating systems.

In self-pollinated crops, varietal development follows three distinct phases: creation of variability, selection, and stabilization of transgressive segregants into new varietal lines. In contrast, random-mating crops involve selection followed by random mating in every cycle of population improvement. Random mating among selected plants blends genetic backgrounds, creating a new equilibrium population with improved allelic frequencies for productivity and desired traits. In conventional breeding of self-pollinated crops, blending genetic backgrounds typically occurs only once at the start, during

parental crossing to create variability, often involving just two parents. This limits the diversity and complementation of traits in the base population. Innovative modifications are needed at all stages of varietal development in cotton, particularly in blending steps that span mating system barriers, to enhance breeding outcomes.

**Results:** In cotton, the choice of parents for hybridization has traditionally been limited, often lacking sufficient diversity and complementation for productivity, fiber quality, and stress tolerance traits. Our studies explored the use of multiple parents selected based on their complementation patterns for desirable traits. The variability released in base populations created from crosses involving multiple parents was compared with those derived from conventional two-parent crosses. The results demonstrated that base populations created using a team of complementary parents released a significantly higher proportion of desirable variability. This variability encompassed a broader range of productivity, fiber quality, and stress tolerance traits compared to two-parent-based crosses. Additionally, by raising initial segregating generations in off-season environments, the total time required to exploit this variability was effectively reduced.



**Conclusions:** This study highlights the potential for blending genetic backgrounds across mating system barriers to improve varietal development in cotton. Selecting a team of complementary parents for hybridization significantly enhances the desirable variability in the base population, providing a robust foundation for breeding programs. This approach enables the development of cotton varieties with a broader range of productivity, fiber quality, and stress tolerance traits. Furthermore, by optimizing the timing of initial segregating generations, the duration required for exploiting this variability can be reduced, making the process more efficient. These findings emphasize the need for innovative breeding strategies that transcend traditional approaches and leverage genetic diversity for improved crop development.

**Keywords:** Random mating, Heterotic groups, reciprocal selection for combining ability, mating system, transgressive segregants, minimum population size

# Improving the Methodology for Development of Cottonseeds of Elite Lines

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Shukhrat Kozubaev

**Background:** One of the main breeding goals based on increasing growth of industry is to develop high-yielding cotton varieties that are resistant to abiotic and biotic conditions, as well as to establish a sustainable industry of cottonseed. A sustainable seed infrastructure not only has positive effect on yield, but also significantly improves product quality.

**Results:** Preservation of genetic identity through various methods of reproduction of registered breeding varieties, is one of the main goals of preventing accelerated genetic degradation during seed propagation. The development of an optimal methodology for production of elite (basic) cotton seeds is a prerequisite of seed industry. We have investigated several methods of elite production for selection of suitable methodology that can address the current issue. The comparative tests included: The Menbane method, which involves the mass collection (more than 40 thousand) of individual selections,

with their further combining and sowing to obtain elite seeds; Method of field clearing from atypical plants - 10 thousand plants typical for the variety were sown in a special field and after field clearing were collected, one part was left for the next year of reproduction, the second part was sown to obtain elite seeds; The method of the modal sample system, which involves preparing the most leveled selection material and sowing 10 thousand into-selections into the so-called "initial field", and around it is completely sown with elite material. This method involves sowing 6 thousand reproductive plants and 300-500 individual selections are taken from them and after three consecutive cullings, the remaining plant seeds are mixed and a modal sample is obtained for propagation of elite seeds. The pedigree method, which involves repeated individual selection within a variety and testing with rejection over a number of years, until the most improved line remains out of 1000 selections. However, this method is better applicable in breeding than in seed production; The method of repeated testing of rows of progeny roughly corresponds to the method of individual selection with testing on progeny without intra-varietal crossing, which basically corresponded to the elite production used in our country at present. Having analyzed and combined the results of all of the above methods, we came to the conclusion that under the current environmental, economic and social conditions of seed production in Uzbekistan, it is necessary to apply the system of "seed reservation" proposed and modified by us, on the basis of which it is proposed to reproduce the elite once every 5 years, and take 1/5 of reserve annually for production. In this case, it becomes possible to preserve longer the economically valuable indicators and genetic homogeneity of the varieties originally laid down by the breeder. It is important to note that if, with the existing method, the variability occur after 5 years, then with the reservation method it will be observed after 25 years, since mechanical displacement and biological degradation of the variety are eliminated as much as possible.



**Conclusion:** The above-mentioned field and laboratory experiments turned out to be reliable tools for high-quality propagation of promising cotton varieties. In addition, these studies enable seed specialists to more specifically identify specific methodologies for increasing efficiency in propagation of selected cotton varieties.

Keywords: Cotton, seeds, seed production, variety, elite, productivity, product quality

# Pre-Breeding Using Wild Germplasm of Gossypium Spp.

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Vinita Gotmare

The genus *Gossypium* to which cotton belongs has more than 52 well-established species while only four species are cultivated. In terms of fiber production and quality, the wild species of cotton are relatively inferior compared to the cultivated species. Despite this, the wild *Gossypium* germplasm serves as a rich reservoir of novel alleles that can be utilized to improve trait performance in cultivated cotton. Wild or exotic germplasm constitutes an important resource that can provide novel genetic diversity in cultivated cotton. Wild germplasm accessions of *Gossypium* were imported and introduced from United States Department of Agriculture (USDA), USA to enrich the collection at the active germplasm site i.e., ICAR-Central Institute for Cotton Research, Nagpur, India. A total of 16 accessions of 8 wild species namely *G. areysianum, G. costulatum, G. darwinii, G. gossypioides, G. incanum, G. mustelinum, G. sturtianum,* and *G. tomentosum* have been established. All of these imported wild species were free from listed cotton pests and also weeds as per Plant Quarantine (PQ) Order(2003)

of the ICAR- National Bureau of Plant Genetic Resources, New Delhi, India for exotic seed-borne/ germplasm-borne viruses/ pathogens / pests namely: Fungi- *Colletotricum gossypii* var. *cephalosporioides* (Witches broom), Bacteria - *Xanthomonas campestrispv* malvecearum - African strain (Bacterial Blight) and Insects – *Anthonomus grandis, Anthonomus spp, Amblycerus spp., Megacerus spp.* and *Spermophagus sp*p. Utilisation of naturally occurring genetic variation available abundantly in these wild species for pre-breeding to broaden the genetic base of the existing cultivars has been initiated for improvement of cultivated cotton.

Keywords: Pathogens, wild relatives of Gossypium, pre-breeding, upland cottons

# G. ekmanianum G. mustelinum G. darwinii G. darwinii G. gossypioides

#### Figures: Wild species of cotton

Wild species introduced in India are free from the following listed cotton pests and diseases: Fungi : Colletotrichum gossypii var. cephalosporioides (Witches broom) Bacteria : Xanthomonas campestris pv malvecearum – African strain (Bacterial Blight) Insects : Anthonomus grandis, Anthonomus spp., Amblycerus spp., Megacerus spp. & Spermophagus spp.

# North Carolina Design-Ii Analysis for Estimating Combining Ability Analysis for Earliness, Yield and Fiber Traits of Cotton (*Gossypium hirsutum* L.)

#### Wajid Jatoi

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**Background:** Cotton hybrids are a crucial component of breeding programs aimed at improving yield, fiber quality, and other agronomic traits. This study evaluated the performance of three male and three female cotton parents, along with their nine F1 hybrids, to estimate heterotic effects, general combining ability (GCA), and specific combining ability (SCA) effects for various traits.

The research was conducted during Kharif 2023 at the Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam, using a randomized complete block design (RCBD) with three replications.

Wajid Jatoi

**Results:** The analysis of variance (ANOVA) revealed significant differences among genotypes, parents, females, males, and female  $\times$  male interactions for all traits studied, including days to first squaring,

bolls formed at 90 days after planting (DAP), bolls opened at 120 DAP, sympodial branches, bolls per plant, boll weight, seed yield, internode length, ginning outturn (GOT), and staple length.

#### Parental Performance:

- Male parent Sindh-1 showed earliness in days to first squaring, shorter sympodia, and internode lengths.
- Female parent NIA-Ufaq recorded the highest boll weight and seed cotton yield per plant, while FH-901 had the maximum number of bolls and staple length.
- IR-3701 exhibited higher sympodial branches and GOT among female parents.

#### F1 Hybrid Performance:

- $FH-901 \times NIA$ -Noori recorded the shortest days to first squaring, internode length, and the highest seed cotton yield per plant and staple length.
- FH-901 × NIA-Ufaq showed shorter sympodia, more sympodial branches, higher GOT, and a greater number of bolls per plant.
- $CRIS-134 \times NIA$ -Noori had the maximum number of bolls formed at 90 DAP and larger bolls.

#### Combining Ability:

- Male parent Sindh-1 and female parents IR-3701, FH-901, and NIA-Ufaq were the best general combiners for the traits studied.
- Hybrids such as FH-901 × NIA-Noori, IR-3701 × Sindh-1, FH-901 × NIA-Ufaq, and CRIS-134 × Sindh-1 demonstrated the most desirable heterotic and SCA effects for yield and fiber quality traits.

**Conclusions**: The study identified promising parental lines and hybrids that can be effectively utilized in hybridization and selection programs for earliness, yield, and fiber traits. F1 hybrids such as FH-901  $\times$  NIA-Noori, IR-3701  $\times$  Sindh-1, FH-901  $\times$  NIA-Ufaq, and CRIS-134  $\times$  Sindh-1 emerged as the best specific combiners and are recommended for future breeding programs to enhance cotton productivity and quality.

Keywords: Hybridization, North Carolina mating design, Yield related traits, Upland cotton

# Identification of Salinity- and Drought-Tolerant Germplasm and Innovation of Tolerant Cotton Varieties

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**Background:** Cotton (*Gossypium hirsutum*), known for its strong drought and salt resistance, serves as a valuable resource for exploring genes associated with these traits. Improving drought and salt tolerance in cotton is essential for enhancing its adaptability to stress conditions. This study utilized *G. hirsutum* cultivars ZhongH177 and Zhong9807 to isolate and analyze mitochondrial genes associated with drought and salt resistance.

**Results:** A total of 12 drought- and salinity-resistance genes were isolated from cotton mitochondria, which play a critical role in stress tolerance. Under 0.4% salt stress conditions, three salt-tolerance-related genes—ccmC, rps12, and nad3—were identified and cloned from a salt- and drought-tolerant upland cotton variety. Subcellular localization of these genes was determined using bioinformatics analysis. Over-expression vectors (pBI121-rps12, pBI121-ccmC, and pBI121-nad3) were constructed and transformed into *Arabidopsis thaliana* using the floral-dip method and into cotton via gene gun transgenic technology.



**Conclusions:** The successful cloning and over-expression of ccmC, rps12, and nad3 provide foundational insights into the molecular mechanisms underlying salt tolerance in cotton. These genes can serve as valuable resources for further research into salt-tolerance pathways and for the development of salt-resistant cotton germplasm. This study lays the groundwork for future innovation in enhancing the stress resistance of cotton through molecular breeding techniques.

Key words: cotton, mitochondria, drought- and salt-tolerance, gene cloning, expression analysis

# Comprehensive Insight Into the Divergence and Adaptive Potential of a Forgotten Landrace *Gossypium hirsutum* L. *purpurascens*

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**Background:** Wild progenitors and landraces are invaluable genetic resources for enriching the genetic base of modern cultivars. They can provide desirable variations lost due to directional selection and adaptation during domestication. This study focuses on re-evaluating a landrace of *Gossypium hirsutum*, historically classified as *Gossypium purpurascens*, found in the South China Sea Islands. The aim is to investigate its genomic structure, variation, and breeding potential while providing insights into its biogeographic history and domestication-related genomic changes. A core set of accessions, including *G. purpurascens*, modern cultivars, and obsolete accessions, were analyzed for genetic diversity, phenotypic traits, and responses to abiotic stress.

**Results:** Genotyping and multilocation phenotyping revealed marked genomic differentiation between *G. purpurascens* and other groups of *G. hirsutum*, with population fixation statistics highlighting its divergent genomic behavior. Phylogenetic analysis confirmed the primitive nature of *G. purpurascens*, identifying it as a vital source of functional variation that can enhance the genetic base of upland cotton. The genomic analysis revealed extensive chromosomal rearrangements in *G. purpurascens* compared to the advanced line ZMS637-9, including large-scale inversions such as those on chromosome A05. These inversions restructured topologically associating domain (TAD) boundaries, leading to differential gene expression of loci such as A05.g22621 and A05.g24002, which may influence phenotypic diversity. Genome-wide association studies pinpointed multiple loci within domestication regions linked to traits such as flowering time and fiber quality. Phenotypic evaluations under salt stress conditions revealed that *G. purpurascens* displayed robust tolerance, with significant differences in morphology, biomass, and biochemical traits compared to upland cotton. Comprehensive transcriptomic analysis identified key gene co-expression networks and biologically significant pathways, providing a molecular basis for salt tolerance in *G. purpurascens*.



Figure. Geographical distribution map of 385 upland cotton and 45 *G. purpurascens* 

G. purpurascens

**Conclusions:** This study highlights the potential of *G. purpurascens* as a genetic resource for broadening the genetic diversity of upland cotton and enhancing its breeding potential. The unique genomic rearrangements and differential gene expressions observed in *G. purpurascens* provide valuable insights into its evolutionary trajectory and the selective pressures it experienced. The robust salt tolerance observed in *G. purpurascens* underscores its utility in developing stress-resilient cotton varieties. These findings contribute to a deeper understanding of the genomic and phenotypic diversity within *G. hirsutum* and offer a foundation for future breeding strategies aimed at improving cotton resilience and productivity.

Keywords: Upland cotton, *G. purpurascens*, divergence, selection and adaption

# POSTER PRESENTATIONS COTTON BREEDING & GENETICS



# Effect of Morpho-Yield Traits of Plants When the Seeds of Colored Cotton Genotypes Were Treated With Different Doses of <sup>60</sup>Co-γ-ray Irradiation

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**Background:** Cotton is a highly valued technical and industrial crop cultivated in both developed and developing countries. Colored cotton genotypes have gained increasing attention due to their potential for sustainable textile production, as they eliminate the need for chemical dyeing. This study explores the impact of cobalt-60- $\gamma$ -ray irradiation at varying doses (0, 100, 150, and 200 Gy) on the morpho-yield traits of colored cotton plants to assess their potential for breeding and selection programs.

**Results:** The study revealed significant effects of irradiation on the morpho-yield traits of colored cotton genotypes. Early flowering was observed in plants treated with 100 Gy rays, advancing by 6 to 10 days compared to the control (0 Gy) and higher doses (150 and 200 Gy). Early maturity traits were prominent in plants treated with 100 and 200 Gy. The number of bolls per plant increased in cream-colored cotton genotypes treated with irradiation, with the 200 Gy dose being particularly effective, while a decrease was observed in green-colored genotypes. Seed cotton yield per plant showed notable improvement in the gold-colored genotype treated with 100 Gy and in green-colored genotypes treated with 200 Gy. Fiber length exhibited slight elongation in plants treated with 200 Gy compared to other doses, indicating a dose-dependent response.

**Conclusions:** The study demonstrated that cobalt- $60-\gamma$ -ray irradiation at 100 and 200 Gy positively influenced key morpho-yield traits in colored cotton genotypes. These doses promoted early flowering and maturity, increased boll production in certain genotypes, and improved fiber properties, making them valuable for breeding programs. The findings suggest that irradiated genotypes, particularly at optimal doses of 100 and 200 Gy, have significant potential for the development of enhanced colored cotton varieties.

Keywords: Upland cotton (Gossypium hirsutum L.), colored cotton, genotype, flowering, mature, fiber.

# Use of *G. mustelinum* Miers. Watt. (AD4), *G. darwinii* Watt (AD5) tetraploids in improving Salinity tolerance of Upland Cotton

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Various abiotic factors are limiting the normal growth, development, and productivity of cotton is soil salinity in many parts of the world. Based on previous studies, after 20-25 years, 50% of the total cultivated areas may shift into saline areas. In order to adequately meet the demand for raw cotton in such conditions, scientists need to develop varieties and genotypes that can grow in saline soils and achieve high productivity. In this case, the use of resistance properties of wild representatives of Gossypium L. in enriching the gene pool of cultivated species can lead to effective results. Because in the long evolutionary process due to natural selection, resistance mechanisms have been formed in wild species and forms to various stress factors, including salinity.

Wild species of tetraploids such as *G. mustelinum* Miers. Watt. (AD4), *G. darwinii* Watt (AD5) have been recognized by many researchers as a valuable source of salt stress tolerance. Most of the studies related to the salinity tolerance in cotton genetics and breeding have focused on the heritability and variability of salt stress tolerance traits in crosses of *G. mustelinum*, *G. darwinii* or *G. tomentosum* with the cultivar *G. hirsutum* L. The purpose of this study was to study the effect of salinity on the progeny of wild interspecific hybrids.

Keywords: Wild cotton, tetraploid, salinity, abiotic stresses, growth and development

# New Early Maturing Cotton Variety S-6302

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**Background:** The current problem of cotton growing in Uzbekistan is increasing its profitability, but it cannot be achieved without the accelerated breeding tools and introduction of new accessions in the region. These accessions should have broader genetic base, early maturity, highly productive, and distinguished by high quantity and quality of fiber, resistant to some biotic and abiotic environmental factors, cotton varieties.

**Results:** Variety C-6302 was bred by synthetic selection using American varieties based on hybrid combination of F4 Lambright GL-5 x Hopi oraibi BI. The parent plant of new variety was isolated in 2015, and selection of the parent family No. 541 was carried out during 2016. According to the results of 3 years of testing in field conditions, which were carried out in 2019-2021, the S-6302 variety showed stable increases in raw cotton and fiber yields over the standard S-6524 variety ranging from 1.9 to 5.4 c/ha. The S-6302 variety has a higher quality IV type fiber than the widely sown S-6524 variety, but at the same time requires fewer vegetation irrigations, which are carried out at reduced irrigation rates. With timely implementation of all necessary agrotechnical measures, the S-6302 variety during the growing season tolerates reduced irrigation rates well at the seedling stage. At the same time, it is highly resistant to *V. dahliae* during the formation and ripening of the crop, when on average over 3 years the standard variety S-6524 was affected by an average of 78.5%, while the new variety S-6302 was affected by 10.3%, including the variety S-6302 was strongly affected by 2.6%, and the variety S-6524 by 28.2%.

**Conclusion**: Based on the analysis of the research results, the following conclusion should be drawn: The higher yield of new variety S-6302 provides up to 40-50% additional profit from its cultivation due to a higher yield of quality and quantity of fiber.

# The Role of Polyploidy in Cotton Breeding

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**Background:** This study explores the potential of using chemical methods to induce polyploidy in *Gossypium arboreum* and subsequently hybridizing it with tetraploid *G. mustelinum*. The objective was to broaden the genetic base of *G. hirsutum* by integrating genetic material from both tetraploid and diploid cotton species. This approach aims to overcome the limited genetic diversity in modern *G. hirsutum* cultivars and enhance their adaptability and performance.

**Results:** Autopolyploid plants were successfully generated from accessions of *G. arboreum*, marking a significant step toward achieving compatibility with tetraploid species. In the second year of the study, hybridization efforts shifted to crosses between tetraploid *G. mustelinum* and autopolyploid *G. arboreum*. Meiotic analysis of the hybrids revealed disruptions in chromosome pairing, including an average of 12 univalents, 18 bivalents, and 2 quadrivalents. These anomalies indicated challenges in achieving stable chromosomal alignment during meiosis. Tetrad analysis further demonstrated deviations in allelic segregation, highlighting the genetic complexities and irregularities within the hybrids.

**Conclusions:** The study provides valuable insights into the challenges and potential of using induced polyploidy and hybridization to increase genetic diversity in cotton breeding programs. While meiotic irregularities and segregation deviations in the hybrids underscore the complexities of integrating genetic material across different ploidy levels, these findings offer a foundational understanding of polyploidy's role in cotton improvement. The results support further exploration of this approach to develop novel and diverse genetic resources for *G. hirsutum*.

Keywords: Polyploidy, allopolyploidy, *G. arboreum* L., *G. mustelinum* Miers ex Watt.

# Identification of Genes Responsible for Fiber Color in Upland Cotton (Gossypium hirsutum L.)

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Naturally colored fiber offers significant potential and opportunities for reducing costs associated with chemical dyeing while promoting ecologically friendly products that are safe, antimicrobial, and meet both domestic and international market. Fiber color is a quality trait in Upland cotton, influencing its market value and processing potential. So, understanding the genetic basis of fiber color variation is crucial for breeding programs focusing on developing cotton varieties with desired color attributes. This study employs various methods of molecular genetics, classical genetics, and physiology to identify candidate genes responsible for fiber color in cotton. Colored fiber samples from the cotton collection of G. hirsutum L. were selected for mapping of QTL associated with fiber color and later on, crossed with white fiber varieties. Genomic DNA was extracted from phenotypically contrasting populations. On going research includes molecular mapping of QTL loci in F2 hybrids using DNA marker technologies. This study identifies potential candidate genes and pathways underlying fiber color variation in cotton. The outcome will lead to the ways for future molecular breeding plans to enhance cotton fiber color quality. These findings contribute to meet the market demands and bolstering the textile industry for competitiveness through improved cotton varieties.

Keywords: *Gossypium hirsutum* L., fiber color, interspecific hybridization, QTL mapping

# Utilization of Genetic Diversity of Interspecific Hybridization of Commercial Upland and Gossypium barbadense Cultivars

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**Background:** The inter-specific hybridizations were used in order to enhancing the fiber quality of current commercial cotton cultivars (upland) as well as improving yield and earliness of *G. barbadense* cottons. The cultivars of two species (*G. barbadense*: cultivars Dr. omomi, Termes14; *G. hirsutum*: cultivars Varamin, Sahel, Bakhtegan, Saiokra, Mehr and Khordad ) were hybridized at the farm station. All hybrids were selfed and crossed with both parents during second to forth year and seeds were picked separately. Morphological characters like leaf, boll, and flower shape of  $F_1$  hybrids were intermediate and height showed outstanding heterosis.

**Results:** Hybrids showed high fiber quality and average fiber length was 35.7 mm while it was 34.2 mm in *G. barbadense*. In the third-year high variability in term of morphological characters such as leaf shape, flowering patterns and various degrees of sterilities were appear among back-crossed offspring. In addition to back-crossing, selection was also performed on all segregating populations of offspring during fourth year. In total 182 plant were selected based on agro-morphology performance. At Kashmar station, all the F1 hybrids as well as their parents were compared statistically using RCBD with 3 replications. Analysis of variance showed significant differences among genotypes in term of boll weight, cotton seed yield, earliness, number of sympodia and number of bolls per plant. In the fourth year 32 plants were selected according to plant shape, productivity and some agronomic characters. During next three years all hybrids were back-crossed to parents and selfed as well. Selection was directed toward both parents on the base of yield, earliness, boll number, boll weight, boll opening, ginning turn out% and fiber quality characters.

**Conclusion:** Now we have a number of labeled hybrid cultivar to grow in various regions of Iran.

Keywords: Cotton, G. hirsutum, G. barbadense, tetraploid, fiber quality, hybrid seed

# Exploiting Broad Based Heterotic Groups of Cotton to Increase the Performance of Cotton Hybrids Under Organic Conditions

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**Background:** Performance of hybrids (heterosis) depends on genetic diversity and extent of dominance existing at various yield influencing loci. The basic formula of heterosis (HF1 =  $\Sigma$ dy2) explains how It means heterosis can be enhanced either by increasing genetic distance or dominance. For enhancing genetic distances, it is necessary to identify the groups of genotypes which are genetically diverse from each other. There are few attempts made in various crops to form heterotic groups and further exploit them by following population improvement schemes. The process of development of such groups of diverse genotypes is itself called as development of heterotic groups and need for developing heterotic groups and exploiting them for improving hybrids performance is slowly being realized in different crops. We are working on different heterotic groups of cotton made based on general complementation pattern of parents contributing to heterosis. It was found that parents representing various plant types i.e., robust and compact when crossed reveal complementation of desirable features of two groups in hybrid. It was also observed that complementation for physiological processes involved in the development of biomass and its partition can give rise to potential hybrids. Initially pairs of two parents from each group were used for creation of variability and later exploiting them through procedure of reciprocal recurrent selection.

**Results:** In this study, four parent based heterotic boxes were developed using double cross (four parent based) F1s (SG 102  $\times$  SG 109)  $\times$  (SG 16  $\times$  SG 358) on Stay Green group side and using DC F1s (RGR 2572  $\times$  RGR 30)  $\times$  (RGR 46  $\times$  RCR 4) on High RGR group side i.e., Broad based heterotic populations representing high RGR and SG groups were developed as base populations with sufficient diversity inherently available between them. These opposite populations were assessed for ability to combine with opposite groups four original parents as testers. Assessment of combining ability was initiated as early as double cross F2 stage (4 parent based). Consistency of combining ability of these lines was confirmed once again in double cross F3 and double cross F4 generations. In this study, 10 elite combiner lines of a group were subjected to random mating to obtain random mated populations (RMP) in the two opposite groups. After this step of creating variability based on elite combiners a continuous selfing in this population lead to new F3 lines on the opposite sides. Based on test cross performance involving two parents of opposite groups potentiality 10 elite lines from opposite groups were identified. The elite combiners were identified on two sides in RMP. Now these lines in F4 were crosses between them(10X10) apart from repeating their crosses with opposite parents (10X2 for a group). Both between group crosses and test crosses were evaluated simultaneously under organic conditions during 2023-24 at bio Re research farm in Kasrawad Madhya Pradesh. The between group crosses involving these elite combiners were in general found to be most potential than crosses of lines with opposite parents.

**Conclusion:** The second cycle of recombination created enhancement in genetic distance between the opposite groups and it led to pooling of favorable alleles distributed among the elite combiners used for recombination. The extent of transgressive segregation for combining ability of these elite lines was determined with these F1 performances with that of benchmark crosses (these are crosses between the original parents of opposite groups). The performance of the group of crosses involving RMP lines with the parents of opposite groups is giving a measure of first level of improvement in reciprocal selection based on opposite populations. As compared to this the performance of group of crosses involving elite combiner of opposite groups is expected to give a measure of next level of measuring improvement achievable when cycle of combining ability ends. Between groups elite combiner crosses give overall performance improvement that is possible in hybrid performance through a cycle of reciprocal recurrent selection for combining ability in self-pollinated crop like cotton. These results and inferences were bearing on hybrid breeding procedure to be followed in cross populated crops as well as self-pollinated crops; these studies explore the possibility of exploiting groups for improving hybrid performance under organic conditions.

Keywords: Heterosis, heterotic group, reciprocal selection for combining ability, transgressive segregation

# Preservation of Genetic Diversity in Genus *Gossypium* in Côte d'Ivoire: Survey and Collection of Traditional Cotton Forms

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**Background:** Local genetic resources are vital for breeding programs as they offer a diverse pool of traits essential for crop improvement and resilience. This study aimed to collect, enhance, and conserve the genetic diversity of traditional cotton plants in Côte d'Ivoire. Such efforts are crucial in addressing challenges like climate change and the narrowing genetic base of cultivated cotton varieties.

**Results:** Surveys were conducted across 120 localities in central, south-western, and eastern Côte d'Ivoire, resulting in the collection of 357 seed cotton samples. These were preserved ex situ at the Bouake Research Station. The duration of in situ conservation by local populations ranged from 1 to 14 years, with plants typically found in forests, along trails, or near homes. Beyond agricultural value, traditional uses of cotton included medicinal applications of leaves and young bolls for treating eye and stomach ailments, and the use of fiber for crafting traditional garments. The collected samples revealed a wide range of ecotypes from both diploid species (*Gossypium arboreum* and *G. herbaceum*) and tetraploid species (*G. hirsutum* and *G. barbadense*). The plants exhibited significant diversity in traits such as height (1–3 meters), growth form (bushy or shrubby), and morphological features like leaf shape, capsule shape, down color, flower color, and fiber color.

**Conclusions:** The genetic diversity observed in traditional cotton forms, including their unique traits and adaptations, holds significant potential for breeding programs. These resources are particularly valuable in the face of climate change and the genetic narrowing of commercial cotton varieties. The conservation of traditional cotton forms, both in situ and ex situ, provides a crucial reservoir of genetic material that could support the development of more resilient and diverse cotton varieties.

Keywords: Diploid, tetraploid cottons, collections, medical value, traditional garments

### Inheritance of Morpho-Economic Traits in Fine-Fiber Cotton Varieties

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**Background:** Understanding the inheritance of productivity traits and seed characteristics is critical for improving cotton breeding programs. This study focused on the inheritance of plant productivity and 1000-seed weight in F1 hybrids of *Gossypium barbadense* L., emphasizing the role of dominance effects and cytoplasmic inheritance in hybrid combinations of fine fiber cotton varieties and lines.

**Results:** The inheritance of plant productivity in the F1 hybrids was predominantly influenced by positive super dominance, observed in 14 out of 20 hybrid combinations. Negative super dominance was identified in five combinations, while incomplete dominance was observed in the hybrid L-167  $\times$  Surkhan-14. Reciprocal crosses involving the varieties Surkhan-14, Marvarid, and Guzor exhibited positive super dominance for plant productivity. In contrast, reciprocal combinations of Guzor and Boston displayed negative super dominance with no statistically significant differences in character indicators. Analysis of reciprocal differences revealed that in hybrids involving Marvarid with Guzor, Boston, and L-167, as well as Surkhan-14 with Boston and L-167, both nuclear and cytoplasmic genes played a role in the inheritance of plant productivity. This suggests cytoplasmic inheritance as a contributing factor alongside nuclear genes.

**Conclusions:**The results demonstrate that positive super dominance is the primary mode of inheritance for plant productivity in the F1 combinations of fine fiber cotton studied. The involvement of cytoplasmic genes in certain hybrid combinations highlights the complexity of genetic inheritance in these traits. Varieties such as Marvarid, Surkhan-14, and Guzor show promise for pre-breeding efforts aimed at developing high-yielding cotton genotypes with desirable fiber traits, providing valuable resources for enhancing productivity in fine fiber cotton breeding programs.

Keywords: Cotton, variety, productivity, weight of 1000 cotton seeds, heterosis, inheritance, coefficient of dominance.
## Genome-wide Association Study Discovered Candidate Genes of *Rhizoctonia solani* Kuhn Resistance in Upland Cotton (*Gossypium hirsutum* L.)

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**Background:** Cotton seedling damping-off is caused by the fungus *Rhizoctonia solani*, is a cotton disease during the seedling stage, which can lead to problems such as seed rot, seedling blight, and seedling lodging and death. Currently, research on cotton damping-off mainly focuses on pathogen identification, integrated disease management, with little emphasis on studying the genetic mechanisms of disease resistance.

**Results:** In the field, diseased seedlings were collected for pathogen isolation, identified as the AG4-HG fusion group of *Rhizoctonia solani*. 290 samples of upland cotton natural populations were inoculated with *Rhizoctonia solani* in a greenhouse environment. Using whole-genome association analysis, two significant SNPs were identified on chromosome D03. LD-block analysis identified 16 candidate genes. Virus-induced gene silencing revealed that when the GLUTAMATE RECEPTOR-LIKE (GLR) gene (CG16) was silenced, the resistant material J46 exhibited a susceptible phenotype. Material with glr mutants obtained using CRIS-PR/Cas9 technology showed more susceptible phenotype compared to the wild type after inoculation with *Rhizoctonia solani*.

**Conclusion**: The gene (CG16) encoding the glutamate receptor-like gene may be a candidate gene for cotton resistance to *Rhi-zoctonia solan*. Utilizing this gene to develop cotton materials resistant to Rhizoctonia damping-off could enhance the genetic resources for disease-resistant breeding in cotton.

Keywords: *Rhizoctonia solani*, pathogen, cotton, isolates, glutamate receptor

#### Evaluation of Cotton Lines Obtained With The Participation of Introgressive Forms in Various Soil and Climatic Conditions of Uzbekistan

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**Background:** *Gossypium hirsutum* lines were evaluated for economically important traits under the agroecological conditions of Tashkent, Fergana, and Syrdarya regions in the Republic of Uzbekistan. Twelve accessions were sourced from various cotton breeding institutes to ensure genetic variability. The evaluation examined the effects of genotype and environment on critical traits such as cotton yield, fiber yield, boll weight, seed weight, gin turn-out, and fiber quality parameters, including length, strength, and fineness. Resistance to *Verticillium* wilt and the growing season period were also analyzed to assess the adaptability and performance of these lines in breeding programs.

**Results:** The data analysis revealed that genotypic influence was significantly higher than environmental factors for most traits, highlighting the genetic potential of the evaluated accessions. For fiber turn-out, genotype contributed 22%, while environment accounted for 14%. Boll weight showed a similar trend, with genotypic influence at 39.4% compared to 31.2% for environment. Fiber quality traits, such as length and strength, were predominantly influenced by genotype, with contributions of 35.6% and 62.7%, respectively, while environmental influence was 26.7% and 8.9%. Fiber fineness also showed a strong genotypic contribution (49.6%) compared to the environment (1.6%). Traits related to plant development and disease resistance demonstrated the same pattern. The growing season period was influenced by genotype at 54.8%, compared to 36.0% by the environment. Resistance to *Verticillium* wilt showed 45.3% genotypic influence, while the environment contributed 23.3%. These findings emphasize the genetic stability of the evaluated traits, making the accessions reliable candidates for breeding programs targeting specific production and quality improvements.

**Conclusions:** The study demonstrated that genotype plays a dominant role in influencing most productivity and quality traits in Upland cotton, particularly fiber strength, fineness, and disease resistance. The results underscore the value of these accessions as a genetic resource for developing high-performing cotton varieties. By leveraging this genetic variability, breeders can achieve significant improvements in yield and fiber quality, especially in regions with similar agroecological conditions to Uzbekistan. These findings provide a foundation for advancing breeding strategies and enhancing the resilience and efficiency of cotton production.

Keywords: Gossypium hirsutum, genotype, environment, fiber quality, yield.

# **Scientific Potential of Cotton Breeding**

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**Overview of Cotton Production in Uzbekistan:** Uzbekistan has long been recognized as one of the world's leading producers of cotton and cotton products, and it continues to hold a prominent position in global cotton markets. Cotton growing is a crucial economic sector in the republic, deeply rooted in its agricultural landscape. In 2023, Uzbekistan achieved a historic milestone by producing 3.7 million tons of raw cotton, equivalent to 1.2 million tons of fiber. This achievement highlights the effectiveness of state support for agricultural production and the continuous innovation within the cotton sector. Addressing a video conference in February 2024, the President of the Republic of Uzbekistan emphasized the need to adopt new and previously unused measures to further enhance agricultural productivity. Uzbekistan's cotton production is underpinned by a highly developed breeding science sector, which ensures that local varieties meet not only the demands of the domestic textile industry but also the standards of the global cotton market. This dual focus has allowed Uzbek breeding programs to maintain their competitiveness internationally. Breeding efforts have prioritized precocity and fiber quality, reflecting modern market demands. Thanks to state-supported initiatives, breeding science in Uzbekistan has become an integral, efficient, and powerful component of the cotton industry.

Advances in Breeding Science: The breeding programs in Uzbekistan are designed to develop high-yielding, precocious cotton varieties with superior fiber quality. The diversity of the country's soil and climatic conditions, combined with limited water resources and short vegetation periods, necessitates the selection of varieties that are well-adapted to these challenges. Uzbek scientists have achieved significant progress in creating precocious varieties that exceed older types in economically valuable traits. Modern varieties, such as Andijan-35, Andijan-36, Bukhara-102, and Sultan, are widely cultivated due to their high yield potential and adaptability. These varieties boast yield indices of 50-55%, meaning that over half of the biological mass of the plant is represented by raw cotton. In comparison, older varieties like 108F and Tashkent-1 had yield indices of only 40-45%. The strategic focus on developing intensive-type varieties, characterized by high productivity and limited vegetative growth, has further enhanced cotton yields. Research has also shown that the adaptability of varieties is critical. While Uzbek varieties are specifically tailored to the country's long-day conditions, foreign varieties, such as those from China, India, and the U.S., often require 4-5 years to adapt to local conditions. Even then, breeders must isolate high-yielding and precocious forms from these introductions to ensure their suitability for Uzbekistan's agricultural environments. For example, Sultan, which is now sown in nine regions, has demonstrated its adaptability and consistent performance across diverse agroecological zones.

**Innovations in Seed Technology and Varietal Purity**: Maintaining varietal purity and improving seed quality are vital operations in the breeding and cultivation process. These efforts rely on collaboration between research institutes that originate varieties, elite seed farms that enhance varietal purity, and cotton gins that prepare high-quality seeds for distribution. This integrated approach has been instrumental in ensuring uniformity and consistency in cotton production. Innovations in seed technology have further strengthened the resilience of cotton crops. Encapsulation techniques using chitosan, developed by the Institute of Chemistry and Physics of Polymers of the Academy of Sciences of Uzbekistan, have improved the germination and survival rates of seeds under adverse weather conditions. Field trials conducted in regions such as Andijan, Kashkadarya, Surkhandarya, and Ferghana have demonstrated that encapsulated seeds outperform uncapsulated ones, particularly during prolonged rainfall after sowing. This advancement not only ensures better crop establishment but also contributes to higher yields.

**Contributions to Global Cotton Research:** Uzbekistan's leadership in cotton production extends to its contributions to global cotton research. The country's breeding programs integrate foreign varieties as starting material to enrich the genetic base of local cultivars. Despite the challenges of adapting foreign varieties to Uzbekistan's long-day conditions, they are widely used in the breeding process to introduce new traits. This demonstrates the strategic integration of global resources into local breeding efforts. At the VII International Uzbek Cotton Fair in Tashkent, Mr. Andrei Guitchounts, Director Trade, of the International Cotton Advisory Committee, praised Uzbekistan's scientific advancements in cotton production, particularly in breeding and cultivation. These achievements highlight the country's ability to compete with major cotton-producing nations such as China, India, and the United States. Uzbek breeders have successfully developed varieties with ripening periods as short as 105-115 days, compared to the 120-130 days typical of older varieties. These precocious varieties enable farmers to optimize their use of the growing season, resulting in stable and high-quality yields.

**Conclusion:** Uzbekistan's cotton sector exemplifies the successful combination of state support, scientific innovation, and practical agricultural expertise. The development of modern varieties with high yields, superior fiber quality, and adaptability to diverse conditions has reinforced the country's position as a leader in the global cotton industry. Innovations in seed technology and efforts to maintain varietal purity further strengthen the sustainability of cotton production. With its focus on breeding, technological advancement, and efficient resource use, Uzbekistan is well-equipped to address future challenges in cotton production and maintain its status as a global leader in the industry.

## Development of Allotetraploids (A1A1G2G2) in Australian and Afro-Asian Cotton Species, and Transferring Valuable Genes to Upland Cotton

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Cotton is the leading natural fiber-producing crop in the tropical and sub-tropical regions of the world. Whereas, Upland cotton (G. hirsutum L.) is widely cultivated species globally, because it is known for its high yield potential, adaptability to various environments, ease of cultivation. These features allow the cotton researcher for extensive use for breeding programs aimed for improving its genetic diversity. The primary goal of breeding programs is to enhance its resilience to various diseases and abiotic stresses. Besides, wild cotton species of A1 and G genome are tolerant to various diseases, pests (bollworms, whiteflies), drought, heat, and salinity. These traits are transferable to *G. hirsutum* L. genome ( $2n=4\times=52$ , AADD). Genotypes resulting from this hybridization exhibited valuable characteristics as reported in the literature. Wild Australian cotton species are considered important genetic resources in contemporary cotton improvement. Specifically, introgression of *G. australe* into *G. hirsutum* L. genome has shown enhanced resistance to diseases such as *Verticillium dahliae* and pests. G. nelsonii Fryx is highly resistant and tolerant to various biotic and abiotic stresses, including bacterial blight, Verticillium dahliae, Fusarium wilt, bollworms, high temperatures, and drought. These traits are transferred successfully in upland cotton through inter-specific hybridization. G. herbaceum L., a diploid cotton species, exhibits resistance to pests, leaf curl virus, thrips, and whiteflies. These wild species are considered important germplasm resources for genetic enhancement of cultivated Upland cotton. F1 hybrids obtained by crossbreeding genetically distant species often lose the trait of fertility. To restore their fertility, they are treated with colchicine alkaloid. Their chromosome set is doubled. The hybrids with restored fertility are then crossbred with cultivated varieties.

Keywords: Cotton, polyploidy, interspecific hybrid, introgression, stresses

# Efficacy of Different Intra- and Interspecific Hybridization Methods for Improving of Cotton Fiber Quality

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The prospects of widening the genetic base of Upland cotton is studied by accessing the genetic diversity and fiber quality of as widely cultivated *Gossypium hirsutum* L. by different composite intra- and interspecific hybridization methods. Particularly, this study was conducted to determine quality parameters of new cotton progenies developed by a different method of hybridization. It was determined that there were significant differences among the cotton progenies for all of the investigated fiber quality characteristics. Cotton fibre fineness is a quality parameter associated with fineness and fibre maturity. The fineness is of great importance for yarn quality, as in the case of the rotor spinning method. An equally important parameter, fiber quality, is UHML is the average length of the upper half of the longest fibers when measured on a weight basis i.e. average length of the longest fibers. Experiments have shown that all progenies created on the basis of various hybridization methods have high UHML rates. However, it should be noted that the relatively largest number of progenies with UHML were found during interspecific hybridization. Among these progenies, genotypes appeared that had a UHML of 1.35 (LCG-4/06a), 1.34 (LCG-4/06b), 1.33 (L-69a), 1.31 (MD-02) and 1.30 (L-69b, L-69s, LTSG-4/06s, L-12/0), which confirms the very high efficiency of interspecific hybridization for improving UHML. The results showed that all used methods in research allows developing of new genetically enriched cotton progenies among which comparatively high efficiency for improving of fiber quality properties are composite intra- and interspecific hybridization to improve such important traits as SCI, fibre fineness, UHML and fiber Strength.

**Keywords:** *G. hirsutum* L., *G. barbadense* L., ecologo-heografical, intraspecific and interspecific hybrids, introgressive lines, fiber quality parameters.

## Influence of Nano-Preparations Based on Chitosan *Bombyx mori* on Growth, Development and Yield of Cotton

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**Background:** This study aimed to evaluate the effect of Kuprumchit spray and nano-preparations on key yield components of cotton plants, including the number of bolls per plant, boll weight, number of seeds per boll, and the weight of 1000 seeds. The cotton varieties Andijan-36, S-6524, and AN-Bayaut-2 were treated with nano-preparations PMKCu2+ 7:3, PMKCu2+ 8:2, Nanoascorbate chitosan, and Nanochitosan to assess their impact on improving yield compared to untreated controls and other treatment options.

**Results**: The application of Kuprumchit and nano-preparations led to significant increases in the measured yield parameters across all three varieties. Foliar feeding with Kuprumchit enhanced the number of bolls per plant by 0.7–0.8–0.6–0.7 in Andijan-36, 0.6–0.5–0.4–0.5 in S-6524, and 0.5–0.6–0.8–0.6 in AN-Bayaut-2 compared to the control. Similarly, the boll size, measured as the mass of raw cotton per boll, was consistently higher in plants treated with PMKCu2+ 7:3, PMKCu2+8:2, Nanoascorbate chitosan, and Nanochitosan. For Andijan-36, Kuprumchit spraying increased the number of seeds per boll by 2.0–1.9–1.6–1.8 pieces, and the weight of 1000 seeds was enhanced by 8.5–5.9–4.6–5.2 grams across the treatments. Similar improvements in seed number and seed weight were observed in varieties S-6524 and AN-Bayaut-2, with nano-preparations outperforming the control group in all cases.

**Conclusions**: The results demonstrate that the use of nano-preparations such as PMKCu2+7:3, PMKCu2+8:2, Nanoascorbate chitosan, and Nanochitosan, along with Kuprumchit foliar sprays, significantly improves key yield components in cotton plants. These treatments resulted in higher numbers of bolls, increased boll weight, more seeds per boll, and greater seed weight compared to the control. The consistent performance across all studied varieties highlights the potential of these treatments as effective tools for enhancing cotton yield and productivity.

Keywords: Nano-particles, cottonseed, varieties, production, cottons

#### Development of a Haploid-Inducer Mediated Genome Editing System for Accelerating Cotton (*Gossypium hirsutum*) Breeding

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Doubled haploid (DH) technology was a cornerstone in breeding by shortening the period to achieve homozygous lines used in hybrid breeding, genetic mapping, and fixating desirable traits. However, for over 50 years, DH technology has predominantly been utilized in maize on an industrial scale due to the availability of naturally occurring haploid inducer lines and adequate haploid plant production in field environments. Recent discovery of haploid induction causative genes has paved the way for extending this technology to other crops. Integrating DH technology with gene editing (HI-Edit) represents a significant advancement, enabling precise genome editing in elite cultivars in a single step and accelerating the development of transgene-free varieties without linkage drag. While HI-Edit has shown promising results in maize, ongoing efforts in wheat, rice, and barley indicate its potential in diverse crop species. Our objective is to apply this transformative technology to cotton, a primary global source of natural fiber and a key economic crop in Uzbekistan. Similar to other crops, cotton's haploid production and embryogenesis are highly influenced by genotype. Current breeding practices, involving genetic transformation and backcrossing, typically require 6-7 years to obtain elite variants with desired traits. However, the urgency posed by rapid climate change necessitates the adoption of innovative technologies to expedite the development of stress-resistant cotton varieties. Our proposed approach involves generating a haploid inducer line by silencing the ZmDMP homolog in cotton (Gossypium hirsutum). These inducer lines aim to facilitate the rapid development of new high-yielding, stress-resistant cotton varieties within a two-year timeframe, thus contributing to the sustainability of agriculture.

While our colleagues in China have achieved a haploid induction rate (HIR) of up to 1.06% by targeting specific genes in Gossypium hirsutum, our investigation has identified alternative genes (GH\_D11G0748, GH\_A11G0715) closely related to AtDMP8 and AtDMP9. These findings underscore the need for further research and optimization to enhance the HIR and maximize the potential of this technology in cotton breeding.

### Features of Introgression of Genome of Gossypium barbadense L. in Gossypium hirsutum L.

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**Background:** Chromosome substitution lines in *Gossypium hirsutum* L. represent a valuable genetic resource for enhancing the crop's diversity and breeding potential. The introgression of alien chromosomes, particularly from *G. barbadense*, into *G. hirsutum* has the potential to introduce beneficial traits. To optimize the creation of chromosome-substituted lines, this study investigated the patterns of chromosome introgression and elimination in backcross hybrids across multiple generations. Cytogenetic and molecular genetic analyses were conducted on backcross hybrids derived from crosses between monosomic lines of *G. hirsutum* and hybrids of *G. hirsutum* × *G. barbadense*.

**Results:** The study revealed distinct patterns of chromosome introgression and elimination in backcross hybrids of *G. hirsutum* and *G. barbadense*. In some hybrids, the transmission of alien chromosomes was absent across specific generations. For instance, BC1F1 hybrids involving monosomic lines Mo11, Mo13, and Mo67, which correspond to chromosomes 2 and 6 of the At-subgenome, did not exhibit the presence of alien chromosomes. Similarly, BC2F1 hybrids involving Mo66 (chromosome 6 of the At-subgenome), BC3F1 hybrids with Mo94 (chromosome 12 of the At-subgenome) and Mo17 (chromosome 22 of the Dt-subgenome), and BC4F1 hybrids involving Mo60 (chromosome 4 of the At-subgenome) also lacked evidence of alien chromosome substitution.

In other hybrids, alien chromosomes were eliminated during backcrossing. This elimination was evident in BC1F1 hybrids involving lines Mo27, Mo48, and Mo42, which correspond to chromosomes 7 of the At-subgenome and chromosomes 18 and 21 of the Dt-subgenome, respectively. These hybrids showed alleles only from the *G. hirsutum* parental line L-458, with no detectable *G. barbadense* alleles. A similar pattern was observed in BC1F1 hybrids involving line Mo16, which corresponds to chromosome 2 of the At-subgenome.

Genetic variation was also observed within the same backcross generation in hybrids involving specific monosomic lines. For instance, BC1F1 and BC3F1 progeny derived from Mo95, Mo34, and Mo60 (chromosomes 4 and 6 of the At-subgenome) exhibited different profiles of chromosome-specific microsatellite SSR markers. Some hybrids displayed alleles of *G. barbadense*, indicating the presence of alien chromosome substitutions, while others retained only the alleles of the *G. hirsutum* parental line, suggesting no substitution.

Substitution lines CS-B06 and CS-B07 from the American cytogenetic collection, which were reported to carry substitutions on chromosomes 6 and 7 of the At-subgenome, were also analyzed. These lines exhibited only polymorphic alleles from *G. barbadense*, confirming the absence of substitution on these chromosomes.

Meiotic analysis of backcross hybrids indicated regular chromosome pairing and high meiotic indices in most cases. However, some hybrids displayed abnormalities. For instance, the BC2F1 hybrid (Mo34 × BC1F1(2933)) with substitution of chromosome 6 of the At-subgenome showed a reduced meiotic index (83.66 ± 0.62%) and a higher frequency of tetrads with micronuclei (9.23 ± 0.77%). Pollen fertility was also reduced in several hybrids, with the most significant reductions in viability observed in two hybrids (70.09 ± 1.57% and 75.00 ± 1.66%, respectively).

These findings demonstrate the complexity of chromosome introgression in backcross hybrids, highlighting challenges in maintaining stable alien chromosome substitutions and the associated impacts on meiotic behavior and pollen fertility.

**Conclusions:** This study highlights the complexity of introgressing alien chromosomes from *G. barbadense* into *G. hirsutum.* The observed patterns of chromosome elimination and substitution underscore the challenges in creating stable chromosome-substituted lines. While many hybrids displayed high meiotic indices, reduced pollen fertility remains a concern in certain cases. These findings provide valuable insights for optimizing breeding strategies to enhance genetic diversity in *G. hirsutum.* Future work should focus on understanding the mechanisms underlying chromosome elimination and improving the stability of introgressed traits.

Keywords: G. hirsutum L. pollen viability, backcrosses, genetic gain, polymorphic alleles

# Development of a Set of Monosomic Alien Addition Lines From *Gossypium raimondii* in *Gossypium hirsutum* Toward Breeding Applications In Cotton

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**Background:** *Gossypium raimondii* Ulbr is a diploid wild cotton  $(2n=26, D_5D_5)$  that originated in west-central Peru in South America and has desirable characteristics lacking in the Upland cotton *G. hirsutum*. Many good genes were lost from *G. hirsutum* in the process of domestication, leading to a narrowed genetic base and greater vulnerability to biotic and abiotic stresses. This genetic base can be expanded through distant hybridization using the superior genes of *G. raimondii*.

**Results:** In this study, *G. hirsutum-G. raimondii* putative hexaploid  $F_1$  plants were obtained by interspecific hybridization. Analysis of its mitotic metaphase plates revealed the presence of 78 chromosomes, and each of six chromosome-specific ( $3D_5$ ,  $5D_5$ ,  $6D_5$ ,  $7D_5$ ,  $9D_5$ , and  $10D_5$ ) fluorescence in situ hybridization (FISH) probes of *G. raimondii* exhibited bright and distinct signals on its respective pair of chromosomes. Then, the fertile hexaploid  $F_1$  plants were continuously backcrossed with *G. hirsutum* and a set of *G. hirsutum-G. raimondii* MAALs were developed using SSR markers in successive backcrosses and self-crossing from BC<sub>2</sub>F<sub>1</sub> to BC<sub>4</sub>F<sub>2</sub>, and these MAALs were confirmed by chromosome-specific anchored SSRs and FISH. This set of MAALs showed abundant variation in morphological, agronomic, yield, and fiber quality traits, and in drought and salt resistance. In particular, MAAL\_9D<sub>5</sub> and MAAL\_10D<sub>5</sub>, MAAL\_12D<sub>5</sub>, and MAAL\_13D<sub>5</sub> exhibited drought resistance potential; and MAAL\_8D<sub>5</sub>, MAAL\_9D<sub>5</sub>, MAAL\_12D<sub>5</sub>, and MAAL\_13D<sub>5</sub> showed salt resistance potential.

**Conclusion:** The study developed a first set of MAALs from *G. raimondii* under the *G. hirsutum* background via the use of molecular marker and cytogenetic techniques, and identified favorable agronomic traits for cotton breeding programs. These MAALs will facilitate the introduction of useful genes and traits for cotton improvement. This MAALs will provide important genetic bridge materials for gene transfer from *G. raimondii* as well as for the study of *Gossypium* species genomes and evolution.

Keywords: Gossypium hirsutum, Gossypium raimondii, Monosomic alien addition lines, Fluorescence in situ hybridization (FISH), SSR marker

#### Genetic Regulation of Gene Expression by Genomic Infiltration During Fiber Development in Allotetraploid Cotton

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**Background:** Cotton (*Gossypium* spp.) is grown widely throughout the world. Improving fiber quality is thus an important objective in cotton breeding. It is worth noting that introgression line populations have been widely used in crops, the accuracy of existing methods for mapping genetic loci from exogenous genome fragments in populations remains suboptimal in that it they typically do not fully define the effect of introgression segments on phenotype at nucleotide level.

**Results:** In this study, we used introgressive populations of two allopolyploid cotton species (*Gossypium*) to describe the regulatory perturbations of gene expression with fiber quality during fiber development. The genome of recipient parent (*G. hirsutum* Emian22) was reassembled from de novo and 323 introosmotic lines from donor parent (*G. barbadense* 3-79) were identified. We documented gene expression dynamics by sequencing 1,284 transcriptomes at four stages of fiber development and characterized perturbations in genetic regulation mediated by genome penetration using a multi-site model. Analysis of infiltration events during domestication and improvement revealed clusters of favorable variants are associated with fiber quality, possibly reflecting historical selection. In addition, we identified an introgression line (N182) that improved fiber quality and validated a candidate gene, GhFLAP1, associated with fiber length.

**Conclusion:** This study outlines a framework for understanding introgression-mediated regulatory perturbations of gene expression in polyploids, and provides insights relevant to targeted breeding for superior cotton fiber.

Keywords: Cotton, Introgressive fragment, Genetic perturbation, Fiber quality improvement

## Genome-Wide Association Study and Transcriptome Analysis Reveal Key Genes Controlling Angle of Fruiting Branch in Cotton

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**Background:** Xinjiang is currently the most important cotton-growing region in China, and high planting densities are widely used in the region to obtain high cotton yields. However, to achieve high cotton yields, high density alone is not enough. As a key factor of cotton plant architecture, fruit branch angle affects plant density, photosynthetic efficiency, disease resistance and lodging resistance, and plays an important role in cotton fiber yield.

**Results:** Fruit branch angle (FBA), a pivotal component of cotton plant architecture, is vital for field and mechanical harvesting. However, the molecular mechanism of FBA formation is poorly understood in cotton. To uncover the genetic basis for FBA formation in cotton, we performed a genome-wide association study (GWAS) of 163 cotton accessions with re-sequencing data. A total of 55 SNPs and 18 candidate genes were significantly associated with FBA trait. By combining GWAS and transcriptome analysis, four genes underlying FBA were identified. FBA-associated candidate gene Ghi\_A09G08736, which is homologous to SAUR46 in *Arabidopsis thaliana*, was detected in our study. In addition, transcriptomic evidence was provided to show that gravity and light were implicated in the development of FBA. This study provides new insights into the genetic architecture of FBA that informs architecture breeding in cotton.

**Conclusion:** The QTL loci related to angle of fruiting branch were identified by genome-wide association study, and candidate genes of FBA were identified by combining the transcriptome data, which is conducive to the improvement of cotton plant architecture and the increase of cotton yield in the future.

Keywords: Cotton, Plant architecture, Fruit branch angle, Architecture breeding

#### Genetic Bases of Breeding of Early Maturing, Low-Foliage Cotton Varieties With High Resistance to Diseases in Republic of Uzbekistan

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**Background:** In recent years, cotton cultivation is being worked in terms of generating more income due to having resource efficient. As we know, the environment is polluted due to use chemical for artificial defoliation, which in turn leads to ecological destruction. The issue of developing eco-friendly varieties of cotton is still need of the day. Studies were conducted in cotton hybrids and families on early maturity, productivity, low leafiness, early natural leaf fall, as well as resistance to diseases. As a result of this research, early maturing, high-yielding, less leaved, disease-resistant cotton lines with early maturity, productivity, natural leaf fall up to 60-70%, and IV-type fibre quality were developed.

**Results:** Our research program included investigation of the genetic nature of low leafiness, early natural foliage on the basis of morphophysiological and biochemical parameters in cotton varieties and hybrids, as well as the degree of their resistance to pests and diseases. As a result, the evaluation criteria and the degree of resistance to diseases on the basis of morpho-physiological and biochemical parameters in cotton varieties and hybrids, as well as their interrelation were developed. New criterion have been developed on the basis of morphophysiological and biochemical tests for early maturity, productivity, leafiness and disease resistance. On the basis of attracted genetic donors with high productivity, early maturity, high resistance to agricultural diseases, new lines L-526, L-888, L-717, L-1435 and L-2014 which, possess a complex of useful traits (high productivity, fork resistance, vegetation period 98-115 days, high yield 38-40% and quality of IV-type fiber) and thus correlations between resistance and quick maturity, productivity, leafiness, etc. are broken. traits, which are new in breeding practice.

**Conclusion:** As a result of breeding work, we obtained early maturing, low-pollinated, high-yielding families and lines with vegetative period of 95-115 days, with high yield of 38-40% and IV-type fiber quality, which have complex resistance to diseases. The research showed that lines L-526, L-888, L-717 and L-1435 had higher resistance to diseases than the released variety C-6524.

Keywords: Ecology, cotton, variety, line, family hybrid, disease, resistance, rapidity, low leafiness, foliage, yield, productivity, wilt, black root rot

# Utilizing Genic-Cytoplasmic Male Sterility System in Seed Production of Inter-Specific (ISH) F<sub>1</sub> Hybrid Cotton-Using Bee Pollination

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Tal Yechiel

**Background:** Inter-Specific Hybrids (ISH) between *Gossypium hirsutum* and *G. barbadense* have been recognized since the 1970s for their exceptional agronomic, morphological, and fiber quality traits. These hybrids leverage the genetic diversity of both species, with traits inherited through dominant genes, additive effects, and heterosis. ISH plants are particularly valued for their ability to enhance lint quality in areas predominantly growing Upland cotton. However, large-scale adoption has been constrained by the challenges of hybrid seed production, particularly the high cost and labor-intensive nature of manual pollination in seed production systems.

**Results:** ISH plants exhibit several agronomic advantages, including vigorous early-stage growth under diverse growing conditions and an average growth cycle of 140 days from emergence to 50% boll opening. These hybrids have been developed with an early plant structure, enabling high yields and efficient resource use. ISH plants demonstrate tolerance to soil-borne pathogens, sucking pests, and soil salinity, and exhibit high water-use efficiency, even under saline water conditions. Morphologically, ISH plants combine traits of both parent species, with large squares and flowers reminiscent of Pima cotton and

bolls with 4–5 locules similar to Upland cotton. Fiber characteristics of ISH are comparable to Pima cotton, offering significantly longer and stronger fibers than Upland cotton. This makes ISH a valuable option for upgrading lint quality in Upland-growing areas. To support commercial-scale planting of ISH, large quantities of hybrid seed are required. Traditional manual pollination for hybrid seed production is cost-prohibitive and inefficient, particularly in Asian countries. In 1975, Vesta Meyer released germplasm lines containing a cytoplasmic male sterility (CMS) and fertility restoration system derived from *G. harknessii*. This system was employed to introduce CMS into *G. hirsutum* (female parents) and fertility restoration into *G. barbadense* (male parents). Extensive testing of male sterility and restoration lines under various conditions enabled the selection of stable and efficient parental lines. The use of bees as pollinators facilitated commercial-scale hybrid seed production, reducing costs and increasing seed availability.

**Conclusions:** ISH hybrids offer a robust solution for enhancing lint quality and agronomic performance in Upland cotton-growing regions. Their unique combination of agronomic and fiber traits, such as tolerance to salinity, pests, and pathogens, and superior fiber quality, makes them an attractive option for commercial planting. The introduction of CMS and fertility restoration systems has significantly improved hybrid seed production efficiency, enabling large-scale adoption of ISH hybrids. Continued advancements in parental line selection and hybrid seed production systems will further enhance the economic feasibility and adoption of ISH in cotton production systems worldwide.

Keywords: Pollinators, ISH, inter-specific hybridization, tetraploids, upland cotton

# Selection of Early Maturing Genotypes of Gossypium hirsutum L.

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The soil and climatic conditions of Uzbekistan largely determine the problems facing cotton growing. The peculiarity is that the nature of distribution and intensity of the manifestation of meteorological factors is significantly unstable over the years and during growing season. This research is devoted to evaluation of hybrid material created through hybridization among lines and varieties of different origins in order to create an early maturing feature. Two- and three-genomic hybrids were developed utilizing *G. hirsutum* L., *G. barbadense* L., *G. thurberi* and *G. raimondii*. The results of the research allowed us to establish that among the lines, the following should be highlighted: L-175/276 – F19 (C-2602 x C-6037) and BSG-455-56/07 (F5 [[(F5 BCF1K-28xC-6524) xOMa $\pi$ ]]). At the same time, K-28 was developed with participation of species - *G. thurberi* and *G. raimondii*. In which, respectively, the average value of the "early maturity" trait is 109-111 days. The values of the heritability coefficient (h2) for the trait of early maturity fall within the range from 0.84 for F2 hybrids NShE-19/06 x Namangan-102 to 0.96 for hybrids NShE-19/06 x Namangan-34, which makes it possible to single out individual early maturing plants among the above-mentioned hybrids and, as a result, to create early maturing families starting with F<sub>3</sub>. It was concluded that the created hybrids have an enriched genetic structure for trait of "early maturity", which made it possible to create selection-significant early maturing selection material starting from F<sub>2</sub>-F<sub>3</sub>.

Keywords: Parental species of hirsutum, hybridization, early maternity, heritability coefficient

# ORAL PRESENTATIONS COTTON GENOMICS & MOLECULAR BIOLOGY



## The Latest Community-based Genotyping Resource - Introducing the CottonSNP30K array

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The global cotton community emphasized the need for continued support for a publicly available, standardized genotyping resource with the discontinuation of the technology for the CottonSNP63K array released in 2015. In response, the latest community-based genotyping resource the CottonSNP30K array has been developed. This resource includes selected markers with optimum performance and physical locations from the prior array, along with a new set of high-value markers derived from public research efforts. A group of researchers have contributed samples towards the effort of developing a cluster file for this new resource which enables automated, standardized processing of genotypic data similarly to the past array. Support is provided by the CottonGen database to enable ease of depositing data into the community database. An update will be provided on the development and current availability of the CottonSNP30K array.

Keywords: CottonSNP63K array, upland cotton, CottonGen database, genetic diversity

#### Comparative Transcriptome and Co-Expression Analysis Reveals Key Genes and Pathways Regulating Nitrogen Use Efficiency in Cotton Genotypes

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**Background:** Nitrogen (N) is a critical nutrient for crop production worldwide, yet its availability often limits crop yields. In indeterminate crops like cotton, increasing nitrogen application rates generally reduces nitrogen use efficiency (NUE). Understanding the molecular mechanisms underlying NUE is essential for developing more efficient cotton varieties. This study used Illumina RNA-Seq to investigate the transcriptional responses of two cotton genotypes, CCRI-69 (N-efficient) and XLZ-30 (N-inefficient), under nitrogen starvation and resupply. The goal was to identify the genetic and molecular factors contributing to genotypic variation in NUE.

**Results:** Transcriptomic analysis revealed significant genetic and molecular differences between CCRI-69 and XLZ-30 in response to N availability. Differentially expressed genes (DEGs) associated with nutrient transporters, photosynthetic pathways, antioxidants, transcription factors (TFs), and hormone signaling pathways varied significantly between the two genotypes. In CCRI-69, genes related to N transporters, phytohormones, antioxidants, and photosynthesis were upregulated in both roots and shoots, highlighting its superior N absorption and utilization capacity compared to XLZ-30.

Among the transcription factors, WRKY in roots and AP2/ERF in shoots showed the most differential expression in both genotypes, followed by MYB. These TFs play crucial roles in regulating stress responses and nutrient assimilation. Additionally, CCRI-69 demonstrated higher biomass production and more efficient photosynthetic activity under varying N conditions. Hormone signaling pathways and antioxidant activities also contributed to the superior NUE of CCRI-69.

Co-expression network analysis identified hub genes associated with high N efficiency in CCRI-69, offering insights into potential molecular targets for improving NUE. These genes are involved in key pathways, including N transport and metabolism, stress responses, and hormone regulation.

**Conclusions**: The study highlights the molecular basis of NUE differences between CCRI-69 and XLZ-30. CCRI-69's superior NUE is attributed to its higher expression of N transporters, enhanced photosynthesis, active hormone signaling, and robust antioxidant responses. The identified hub genes and regulatory networks provide valuable insights for breeding N-efficient cotton varieties. Leveraging these findings could help develop cotton genotypes with improved NUE, reducing the environmental impact of nitrogen fertilizers while maintaining high yields.

Keywords: Cotton: N-starvation: RNA-sequence; co-expression network analysis; N use efficiency (NUE)

# RNA Interference of Cotton (*Gossypium hirsutum* L) *HY5* Gene Improves Fiber Quality and Increases Boll Accumulation

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**Background:** Light is a critical factor regulating plant growth and development, influencing all stages from seed germination to the vegetative period's end. It governs morphological and physiological processes, with key regulatory genes such as *ELONGATED HYPOCOTYL5 (HY5)* playing central roles. *HY5* is a bZIP-type transcription factor involved in photomorphogenesis, root development, flavonoid metabolism, nutrient uptake, and stress tolerance. Its conservation across plant species highlights its importance in plant biology.

In this study, modern biotechnological methods, specifically RNA interference (RNAi), were employed to characterize *HY5* function in cotton. Synthetic oligonucleotide-based RNAi duplexes targeting *HY5* were used to create biotechnological cotton lines with improved agronomic traits

Mirzakamol Ayuboy

**Results:** Synthetic RNAi duplexes specific to the cotton HY5 gene (Syn*HY5* RNAi) were developed, resulting in several genetically modified cotton lines. These lines were advanced through self-pollination and crosses with Uzbek commercial cultivars. Morphological traits were analyzed

under greenhouse and field conditions across multiple years and seasons, with statistical evaluation of agronomic performance.

Somatically regenerated Syn*HY5* RNAi lines of Cocker-312 exhibited notable improvements, including increased fiber strength, enhanced root systems, higher boll accumulation, and reduced flowering time. Subsequent hybridization of Syn*HY5* RNAi lines with elite Uzbek commercial upland cultivars yielded significant enhancements in fiber micronaire, vigorous vegetative growth, and high yields. Independent plants across three generations of Syn*HY5* RNAi hybrids (BC3F3) consistently demonstrated superior agronomic traits.



**Conclusions:** This study underscores the utility of RNAi-mediated gene silencing for improving key traits in cotton. The Syn*HY5* RNAi lines exhibited enhanced fiber quality, improved root development, and increased yield, making them promising candidates for breeding programs.

Crossing these lines with commercial upland cultivars further validated their potential to enhance cotton production. These findings provide a foundation for developing superior cotton varieties with robust growth, high productivity, and improved fiber properties.

**Key words:** *Gossypium*, transcription factor, *HY5*, RNA interference, fiber

## Analysis of Heat Tolerant Genes in Anther, Mapping and Molecular Functional in Gossypium barbadense L.

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Background: Cotton production accounts for 90% of China's total in Xinjiang, and it 'is the only region that cultivates Gossypium barbadense in China. High temperature is a critical factor constraining the enhancement of cotton yield and quality in Xinjiang. Enhancing the high-temperature resistance of cotton varieties is a vital direction for future improvements in cotton vield and quality in Xiniiang's cotton yield and quality. However, molecular mechanisms underlying high temperature resistance during the flowering stage of island cotton remain unclear.

**Results:** This study focused on the core germplasm resource population of island cotton, utilizing a high-throughput phenotyping platform and related analysis technologies to identify island cotton ger-

Yang Jing mplasm resources resistant to high temperatures. Genome-Wide Association Study (GWAS) methods were applied to identify six key Quantitative Trait Loci (QTL) and 195 candidate genes controlling the target traits. Thirteen key genes were obtained, including nine genes involved in flavonoid regulation, ARAC3, CYP19, and two GRP2B genes that participate in cell wall and reproductive organs development in stress. A variety of molecular biological methods were applied to analyze gene functions and signal regulatory networks. The study revealed the molecular mechanisms which high temperatures lead to premature degradation of the tapetum layer, reduction of flavonoids and anthocyanin in anther, and subsequent pollen sterility and boll drop in island cotton. This research aimed to create new island cotton germplasm for high temperature resistance and a high boll-setting rate.

> Figure. Transgenic phenotype: Pollen viability of the overexpression F3H material was superior to that of the wild type and the knockout material under high temperature.



**Conclusion:** The results revealed that flavonoid genes can improvement the rate of pollen activity in reproductive organs by increasing the initial accumulation of flavonoids and anthocyanins, thereby enhancing pollen fertility and boll setting, which increasing higher yields. This research provides significant genetic resources and germplasm support for the breeding of high temperature resistant island cotton and provide the foundation for genetic improvement of yield and quality in Xinjiang's island cotton.

Keywords: QTL, High temperature resistance, Flavonoid accumulation, Joint improvement of pollen activity and yield, Gossypium barbadense L.

## Lessons Learned From Cotton Genomics and Molecular Genetics

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John Yu

Cotton (*Gossypium* spp.) is a vital component of global agricultural economy. Genetic improvement of this cash crop is a key to dramatic increase in the productivity and quality of fiber and cottonseed under changing environments. However, the increase has been achieved with a concurrent erosion of commercial cotton's genetic base due in part to largely untapped *Gossypium* germplasm collections that may otherwise contain beneficial alleles for specific traits.

Over the past decade, dozens of *Gossypium* species have their complete genomes sequenced and thousands of accessions re-sequenced. The availability of cotton genome sequences and annotations provides unprecedented means to characterize underlying genetic diversity that is not measurable through phenotypic descriptors. Advanced genomic knowledge and resources have enabled molecular genetic

analyses for gene discovery and problem-solving in cotton. While lessons are learned from these studies to identify and manipulate economically valuable genes or quantitative trait loci (QTLs), more research advances are needed in the areas including plant transformation and synthetic biology to broaden the genetic base with desirable transgenes and/or multiplex gene edits for continued improvement of the cotton crop.

Key words: Upland cotton, genetic diversity, genomics, biotechnology, molecular genetics, synthetic biology

Figure. Development of PCR-based DNA marker for cotton germplasmcharacterization and genetic linkage mapping.



BAC clones randomly selected from the TM-1 *Hind*III BAC library. The cotton nuclear genomic DNA was digested with *Not* I. The average insert size of the *Hind*III library is 152 kb, ranging from 110 to 180 kb, based on 58 random clones.



A high-density clone blot of the TM-1 Hindill BAC library used for screening of SSR loci. The probe was made from four SSR oligos: (CA)<sub>10</sub>, (GA)<sub>10</sub> (TA)<sub>10</sub> and (AA)<sub>10</sub>.





## Genome Characterization, Phylogeny, and Predicted Divergence Time of Cotton Leafroll Dwarf Virus Isolates

#### Judith Brown

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**Background:** Cotton leafroll dwarf virus (CLRDV) is an aphid-transmitted polerovirus with a positive-sense single-stranded RNA genome encoding seven proteins. It has emerged as a significant threat to cotton production globally, with variety-specific impacts on economic damage. Suspected in East Africa initially, CLRDV has since been reported in China, Korea, South America, the United States, and Uzbekistan. Despite its increasing spread, limited information is available on its genetic diversity and evolution. This study aimed to characterize CLRDV isolates in the United States to better understand their genomic structure, phylogenetic relationships, and geographical distribution.

**Results:** Genome sequencing of 103 CLRDV isolates collected from sentinel plots in seven U.S. cotton-growing states during 2020–2021 was performed using probe capture enrichment and Illumina sequencing. Out of 392 samples, 331 (83.8%) were RT-PCR positive for CLRDV, and 180 were sequenced. Complete genome sequences (5,722–5,866 nt) were obtained for 103 isolates, revealing three major phylogenetic clades distributed across Asia, South America, and North America. Within the North American clade, two genome types were identified, one uniquely found in Texas and another widespread across all sampled states.

Pairwise nucleotide identity among global CLRDV isolates ranged from 89% to 100%. Recombination analysis predicted 84 recombinant genomes among 139 available sequences, indicating substantial genetic exchange. Fst analysis showed relatively high genetic admixture within the Asian clades compared to South and North America. Molecular clock analysis and genetic diversity studies suggested the existence of four distinct CLRDV populations in North America, indicating ongoing evolutionary divergence and regional adaptation.

**Conclusions:** This study provides a comprehensive genetic and phylogenetic analysis of CLRDV isolates, shedding light on the virus's global diversity and regional adaptations. The identification of two distinct genome types in the U.S. and the extensive recombination among isolates underscores the complexity of CLRDV's evolution and its capacity for adaptation. These findings are essential for developing region-specific management strategies and understanding the evolutionary dynamics of CLRDV in cotton.

					1 500	1,000	1,500	2,000	2,500	3,000	3,500	4,000 4,500	5,000	5,500 5,866
Predicted recombinant Predicted breakpoints Putative parental isolate(s)						ORF1 gen	e ORF1-O	RF2 gene				ORF4 gene	ne -	
	Begin	End	Minor parent	Major parent	ORF0 gene							-ORF3 gene		
MT800932 GA_40 GA	1884	3673	unknown (KF906261 Delt	21.127-23 AL	subclade 1a			unkr	iown (subcl	ade 2a)				
19.96-14 TX	849	4480	19.96-6 TX	20.126-90 AL	subclade 1a				subclade 1a					
19.96-7 TX	1084	5619	OM 687235   EC4   OK	unknown (19.97-52 AL)	unknown (subclade 1a)					subclade 1a				
19.96-4 TX	1782	5626	OQ300130 Bamberg SC	unknown (22.17-137 SC	subclade 1a						subclade 1a			
20.126-19 FL	892	3435	19.97-52 AL	20.126-39 LA	subclade 1a subclade 1a				1a					
22.17-114 FL	1606	3792	unknown (19.97-52 AL)	21.127-32 AL	subclade 1a			unk	nown (subc	iade 1a)				
19.97-17 AL	1646	4937	21.127-7 AL	unknown (20.126-17 FL)	unknown (subclade 1a)					subci	ada 1a			
MT814776 GA_58 GA	211	3825	unknown (21.127-32 AL)	19.97-52 AL			unkr	nown (subcla	de 1a)			subclade 1a		
22.17-112 FL	1241	4937	20.126-40 LA	19.97-52 AL	subclade 1a					subcla	de 1a			
OQ300126 Orange SC	1601	3825	Unknown (19.97-52 AL)	21.127-32 AL	subclade 1a				subclade 1a					
19.121-13 AL	1934	4277	Unknown (21.127-32 AL)	19.97-52 AL	subclade 1a			subclade 1a						
22.17-136 SC	1552	3579	21.127-32 AL	21.127-7 AL	subclade 1a				subclade 1a					
MT814774 GA_67 GA	164	3793	Unknown (21.127-25 AL)	22.17-5 AL			unkne	own (subclad	ie 1a)			subclade 1a		
21.127-21 AL	2684	5094	21.127-9 AL	Unknown (21.127-7 AL)	unknown (subci	ade 1a)					subclade	14		
19.97-17 AL	415	1645	Unknown (19.96-13 TX)	21.127-31 AL		subclade 1a		subclade 1	la -					
21.127-31 AL	2626	5647	Unknown (19.121-12 AL)	20.126-16 FL	subvisite te					unknown (subsiste ta)				

#### Figure. Evidence for recombination between CLRDV isolates

ORE3a cene

## Mapping of *Verticillium* Wilt Resistance Genes in Cotton Using Chromosome Segment Introgression Lines

#### Jun Zhao, Jianguang Liu, Jianwen Xu, Liang Zhao

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**Background:** Verticillium wilt (VW), caused by the soil-borne fungus *Verticillium dahliae* Kleb, is a significant threat to cotton production in China, resulting in substantial yield losses annually. While *Gossypium barbadense* exhibits high resistance to VW, transferring this trait to G. hirsutum (upland cotton) has proven challenging due to genetic barriers such as linkage drag and segregation distortion in interspecific hybrids. To address this issue, a Chromosomal Segment Introgression Line (CSIL), SuVR043, containing a heterozygous chromosome segment (D04, Chr.22) from *G. barbadense* cv. Hai 7124, was developed. This study aimed to map VW resistance genes, evaluate their function, and assess the potential for incorporating these genes into upland cotton varieties.

**Results:** Using SuVR043 and an F2 population derived from it, resistance to defoliating (*V. dahliae* isolate V991) and non-defoliating (*V. dahliae* isolate Bp2) strains was evaluated in greenhouse experiments. Two major quantitative trait loci (QTLs) associated with resistance to the non-defoliating isolate Bp2, qVW-Bp2-1 and qVW-Bp2-2, were identified. These QTLs were flanked by markers cgr6409-ZHX30 and ZHX57-ZHX72, explaining 16.38% and 22.36% of phenotypic variance, respectively. The QTL regions spanned 254 kb and 140 kb in the *G. barbadense* genome and contained 36 and 19 putative genes, respectively. Expression analysis of these regions revealed significant differences in the expression of three key genes in *G. barbadense* cv. Hai 7124, CSIL SuVR043, and *G. hirsutum* acc. Sumian 8 after inoculation with isolate Bp2. These genes were GbCYP450 (Cytochrome P450), GbTMEM214 (Transmembrane protein 214a), and GbRLK (Receptor-like protein kinase). VIGS (Virus-Induced Gene Silencing) experiments showed that silencing GbCYP450 and GbTMEM214 reduced resistance in Hai 7124 and SuVR043. Overexpression of these genes in Arabidopsis enhanced resistance to Bp2 but not to V991, confirming their specific role in non-defoliating isolate resistance. Using molecular marker-assisted selection, the chromosome segment containing the QTLs was successfully introduced into six susceptible *G. hirsutum* varieties. Progeny carrying the introgressed segment exhibited significantly improved resistance to Bp2 compared to non-carriers.

**Figure.** Mapping of *Verticillium* wilt resistance loci. Using 49 SSRs showing polymorphisms, we genotyped 1100 individuals and constructed a linkage group using MapChart 2.2. contain 32 loci, and spans 11.1 cM. There were 8 loci containing at least 2 co-segregation markers in 32 loci.



**Conclusions:** This study identified and validated two major QTLs, qVW-Bp2-1 and qVW-Bp2-2, conferring resistance to non-defoliating *V. dahliae* isolate Bp2. The functional analysis of candidate genes (GbCYP450 and GbTMEM214) highlighted their importance in enhancing resistance, as demonstrated through gene silencing and overexpression experiments. The successful introgression of the resistant chromosome segment into upland cotton lines underscores its potential in breeding programs. These findings provide a strong foundation for map-based cloning of VW resistance genes and emphasize the importance of targeted strategies in developing VW-resistant cotton varieties.

# Genotyping-by-Sequencing (GBS) Based Mapping for Fiber Quality in a Global Germplasm Collection of Upland Cotton

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Khezir Hayat

**Background:** The genetics of high-quality lint is complex which hinders the breeding progress towards for achieving the high lint yield and quality. Integration of DNA markers for selecting the desirable cotton plants producing the high-quality fiber can accelerate the breeding progress.

**Results:** 289 diverse cotton genotypes developed in different cotton growing countries were characterized for ginning outturn (GOT) percentage and fiber quality traits. Genotyping-by-sequencing (GBS) assay identified 4730 single nucleotide polymorphisms (SNPs) in these genotypes. In total 332 marker-trait associations were found.

A total of 11 significant SNPs were found for GOT percentage. Out of the 41 SNPs associated with staple length, 11 were found the most significant, of these seven were mapped to Chr-19. Out of these, the most significant SNPs 'A8810' and 'A9078' were identified by both the models using GLM and MLM. Out of the 32 QTLs identified, 11 QTLs were novel.

Out of these, four QTLs for fiber length were showing larger impact on the trait, i.e. qFL (P=1.1E-06;  $R^2$ = 0.17875), qFL (P=3.7E-06;  $R^2$ = 0.21967), qFL (P=0.000013;  $R^2$ =0.19023) and qFL (P = 0.00001;  $R^2$ =0.16858). Similarly, for fiber maturity, out of the three novel QTLs, one expressed larger impact on fiber maturity trait (P=0.00003;  $R^2$ =0.1695).

Figure. GBS Methodology (BGI) (Elshire et al. 2011)



LD decay r2>0.1 = 18.5% (10cM) r2>0.2= 14.8% (6-8cM) Figure. Linkage Disequilibrium and LD decay



**Conclusions:** we concluded that SNPs can be used as candidate markers for fiber traits which will ultimately assist in marker-aided selection.

Keywords: Cotton, Fiber quality, Molecular Markers, NGS, GBS, Association mapping

### The Molecular Mechanism and Germplasm Innovation of Cotton Resistance to Soil-Borne Fungal Pathogens, *Fusarium oxysporum* and *Verticillium dahliae*

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Longfu Zhu

**Background:** Soil-borne fungal pathogens such as *Fusarium oxysporum* (Fov) and *Verticillium dahliae* (Vd) are hemibiotrophic organisms that cause significant agricultural losses worldwide. These pathogens are particularly challenging to manage due to their complex infection strategies and persistence in the soil. This study focuses on two key findings: the identification of a gene (Fov7) conferring resistance to *E oxysporum* race 7 in upland cotton and the characterization of molecular and biochemical responses to *V. dahliae*. Innovative approaches, including transcriptomic analysis, quantum dot treatment, and gene editing, were used to elucidate the mechanisms underlying cotton's defense responses and to enhance resistance to these pathogens.

**Results:** *Fusarium oxysporum Resistance:* The Fov7 gene, putatively encoding a GLUTAMATE RECEPTOR-LIKE (GLR) protein (GhGLR4.8), was identified as conferring resistance to *F. oxysporum* race 7. A single nucleotide polymorphism (SNP) (C/A) in GhGLR4.8 caused an amino acid substitution (L/I), which was associated with resistance. CRISPR/Cas9-mediated knockout of Fov7

rendered cotton lines highly susceptible to Fov race 7, confirming its role as a resistance (R) gene. This is the first report of a GLR-encoding gene functioning as an R gene, providing a novel perspective on plant-pathogen interactions.

*Verticillium dahliae Tolerance:* Transcriptomic analysis and comparative genomics revealed that *V. dahliae* virulence-associated genes are induced during the late stage of infection (Stage II). This stage was characterized by a burst of reactive oxygen species (ROS), which is a key component of the plant defense response. While cotton plants activate numerous defense-related genes, excessive ROS accumulation can cause cellular damage. To address this, polyethyleneimine-coated MXene quantum dots (PEI-MQDs) were applied to cotton seedlings. These quantum dots effectively reduced ROS levels, enhanced peroxidase, catalase, and glutathione peroxidase activities, and significantly improved tolerance to *V. dahliae*. In addition, an elicitor protein, VP2, was identified and shown to play a critical role in the cotton immune response to *V. dahliae*. VP2 expression was highly upregulated during early infection by the *V. dahliae* isolate V991 but was barely expressed in interactions with the less virulent strain 1cd3-2. Knockout of VP2 in *V. dahliae* significantly reduced its pathogenicity, while overexpression of VP2 in cotton enhanced resistance to V991 without adverse effects on plant growth and development. VP2-overexpressing cotton showed upregulation of genes involved in jasmonic acid (JA), salicylic acid (SA), and lignin synthesis, further supporting its role in triggering the immune response.



Figure. Resistance of J668 to Fov race 4 isolates is dependent on GLR4.8

Longfu Zhu (unpublished data)

Conclusions: This study provides key insights into the mechanisms of resistance to F. oxysporum and V. dahliae in cotton. The identification of Fov7, a GLR-encoding gene functioning as an R gene, highlights a novel molecular pathway for resistance to Fov race 7. Meanwhile, the use of PEI-MQDs demonstrated the potential of ROS management in enhancing tolerance to V. dahliae. Additionally, the elicitor protein VP2 was found to be a critical component of the cotton immune response, enhancing resistance to V. dahliae through the activation of JA, SA, and lignin synthesis pathways. These findings provide promising tools and molecular targets for developing cotton varieties with enhanced resistance to these devastating pathogens.

# The Transcription Factor MYB106 Regulates Anther Development in Cotton

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Meilin Chen

**Background:** The waxy cuticle on plant surfaces serves as a critical barrier against environmental stresses, protecting tissues such as stems, leaves, flowers, and anthers. In cotton (*Gossypium* spp.), the wax content on anthers is particularly important for maintaining pollen viability and fertility under adverse conditions. In this study, a mutant named M247, exhibiting anther necrosis and reduced pollen fertility, was identified in introgression lines of *Gossypium barbadense*. The study aimed to uncover the genetic basis of this phenotype and investigate the role of the identified gene in cuticular wax biosynthesis and stress tolerance.

**Results:** The M247 mutant displayed significant anther necrosis and decreased pollen fertility under normal cultivation conditions. Genetic mapping revealed that this trait is controlled by a single gene. Further analysis identified a transcription factor, MYB106, as the candidate gene within the mapped region. Gene knockout experiments confirmed that MYB106 is essential for maintaining anther health; knocking out MYB106 resulted in a phenotype identical to the M247 mutant, with

reduced cuticular wax content on anthers and pollen.

To further explore the role of MYB106, overexpression lines of MYB106 were generated. These plants exhibited significantly increased wax content on their anthers and pollen compared to wild-type (WT) plants. Transcriptome analysis supported these findings, demonstrating that MYB106 regulates genes involved in the cutin and wax biosynthesis metabolic pathway.

In addition to enhanced wax deposition, MYB106-overexpressing plants showed improved resistance to ultraviolet radiation and higher pollen viability in in vitro germination experiments. These results indicate that MYB106 plays a vital role in protecting anthers and pollen from environmental stress by regulating cuticular wax synthesis.

**Conclusions:** This study identifies MYB106 as a key regulator of cuticular wax biosynthesis in cotton anthers. The results demonstrate that MYB106 contributes to anther development, stress tolerance, and pollen viability by enhancing wax deposition. The findings provide new insights into the self-protection mechanisms of cotton during anther development and suggest that manipulating MYB106 expression could improve plant resilience to environmental stresses, with potential applications in enhancing crop yields under adverse conditions.

Keywords: Waxy cuticle, overexpressing MYB106, metabolic pathway, mutants, wild forms

Figure. The anthers showed intensified browning in knockout lines



Figure. Fuzz fibers increased in overexpression lines



Figure. Phenotypic observations



# A Reference Genome Sequence of GA230

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Peng Chee

**Background:** Reference-quality genome sequences have transformed the field of genetics, offering unparalleled opportunities for crop improvement. High-quality genome assemblies enable precise mapping of traits, identification of causal genes, and the implementation of genomic prediction, thereby unlocking a crop's full genetic potential. However, developing such assemblies for complex crops like cotton has historically been challenging. Cotton is an allotetraploid with two recently diverged subgenomes and a high proportion of repetitive sequences, which are difficult to resolve using traditional short-read sequencing technologies.

**Results:** This study presents the high-quality genome assembly of GA230, a cotton cultivar developed by the University of Georgia cotton breeding program. The genome was assembled using a combination of cutting-edge technologies, including 116.7X PacBio CLR for long-read sequencing, 55.0X Illumina for polishing, and Hi-C scaffolding to organize the assembly into chromosomal structures. The resulting genome sequence covers the 26 chromosomes of the cotton genome

and is represented by only 201 contigs. The assembly includes 75,412 annotated genes, providing a comprehensive resource for functional genomics and breeding applications.

Comparative genomic analyses of GA230 with other elite cultivars, UA48 and CSX8303, as well as the reference genotype TM-1, revealed important similarities and differences in genome sequence and structure. These comparisons offer insights into the genetic diversity among these genotypes and highlight regions of the genome that may be associated with agronomically important traits.



**Conclusions:** The GA230 genome assembly represents a significant advancement in cotton genomics, providing a reference-quality resource that can be used to accelerate cotton breeding programs. By comparing the genome of GA230 with other elite cultivars and reference genotypes, this study sheds light on the genetic variation underlying important traits in cotton. These findings underscore the power of high-quality genome assemblies in advancing crop improvement and demonstrate the potential for leveraging genomic data to enhance cotton production.

Keywords: GA230, Upland Cotton, Genome, PacBio CLR, 55.0X Illumina

# Development of Multiplex Genome Editing Tools and Their Applications for Cotton Molecular Breeding

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Genome editing tools were developed for cotton: CRISPR/Cas9, Cas12a, Cas12b, Cas13, Off-target analysis, Base editors, dCas9-TV (transcription activation). Cotton (G. hirsutum) is an allotetraploid with a complex genome. Most genes have multiple copies that belong to At and Dt subgenomes. Sequence similarity is also very high between gene homologues. To efficiently achieve site/gene-specific mutation is quite needed. In 2018, we successfully developed CRISPR/Cas 9 system with an average 65-85% efficiency. Then, we performed the whole genome sequencing to investigate the off target in the CRISPR/ Cas9 edited cotton plants. The results showed that of 2000+ potential off-target sites, the WGS data revealed that only four are bona fide off-target mutations suggesting that CRISPR/Cas9 system is highly specific for the editing of genes of polyploid plant species. Then, we further developed a high-throughput genome editing system in cotton. A sgRNAs library (containing 1100 sgRNAs targeted to 600 independent genes) was constructed and cloned into the CRISPR/Cas 9 vector. In this way, we can edit several hundred target genes in one transformation. Recently, CRISPR/Cas12a and Cas12b were developed, and both belong to the class 2 CRISPR/Cas system with features distinct from those of Cas9. Our data showed that both work very well with high efficiency and accuracy in cotton. At the same time, we developed several base editing tools (CBE, ABE8e, Dural base editor) for cotton by fusion of dCas9/nCas9 with activation-induced cytidine deaminase (AID) or engineered adenosine deaminase (TadA), creating specific point mutations. Most recently, several CRISPR/Cas13 systems (13a, b, c, d) were developed in cotton to target the RNA for down-regulating the gene transcription (knock-down). On the contrary, a transcription activation (dCas9-TV) system was established by fusion transcriptional activators VP64, TAL and EDLL with dCas9 to knock-up gene's transcription.

Genome editing tools were used in cotton molecular breeding: The high oleic acid content, non-transgenic allotetraploid cotton was generated by the knockout of GhFAD2 genes with the CRISPR/Cas9 system in our lab. Similarly, by targeting GhPGF with Cas12, we efficiently created non-transgenic and gossypol-free cotton plants. These gossypol-free, high-oleic, non-transgenic mutants provide useful parents in breeding programs to introduce agronomically valuable traits into commercial cotton varieties. Moreover, we have extended the application of base editors to cotton plants by editing the non-coding and coding regions of the GhTFL1 gene in a high-throughput approach to create ideotype cotton germplasm with moderate height, shortened fruiting branches, and compact branches. In addition, an in vivo maternal haploid induction system was developed in cotton by knock out the GhDMP through CRISPR/Cas9 exhibiting a haploid induction rate of 1.06% in F1 progeny as the haploid inducer line. Most recently, the optimized dCas9-TV system was recruited to activate the GhEPSPS to generate glyphosate-resistant cotton with the transcription of GhEPSPS increased by 16-fold, resulting in moderate resistance to glyphosate without growth deficit. Dr. Jin's lab has published 20 peer review papers regarding cotton genome editing (https://www.researchgate.net/profile/Shuangxia-Jin).



# The multiple-gene editing (in one vector) system in cotton

- More than 200 T0 mutants (targeting to edit 9 genes in one vector) have been generated;
- Multi-gene editing that is expected to edit 22 genes (loci) with a singe construct is under way (We are breaking the highest reported record, 16 genes edited simultaneously)

# Involvement of Transcription Factors in the Drought Tolerance of Diploid and Tetraploid Varieties of Cotton

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Uzma Qaiser

**Background:** Cotton (*Gossypium hirsutum*) is a key commercial crop, but its growth and productivity are significantly constrained by drought stress. Understanding the genetic and molecular mechanisms underlying drought tolerance can facilitate the development of more resilient cotton varieties. This study employed bioinformatics methodologies and meta-analysis of whole-genome expression microarray datasets to identify genetic factors and transcriptional responses to drought stress in sensitive and tolerant genotypes of *G. hirsutum* and *G. herbaceum*.

**Results:** Meta-analysis revealed a substantial transcriptional response to drought stress across both species. In *G. herbaceum*, 517 and 896 genes were differentially expressed in drought-tolerant and drought-sensitive genotypes, respectively. In *G. hirsutum*, 3658 genes responded to drought stress, with 148 genes showing differential expression between tolerant and sensitive genotypes.

Gene ontology (GO) enrichment analysis of these differentially expressed genes indicated that similar biological processes, such as responses to stimuli and metabolic processes, were affected by drought in both species. Several transcription factor families were implicated in drought stress response and tolerance, including AP2/ERF-ERF, bHLH, MYB, GRAS, NAC, WRKY, C2C2-GATA, and bZIP.

Notably, the C2C2-GATA transcription factor family exhibited distinct regulatory patterns. In drought-sensitive genotypes, members of this family were predominantly down-regulated, whereas in drought-tolerant genotypes, some genes were up-regulated while others were down-regulated. Validation through qPCR confirmed these expression patterns in *G. hirsutum* drought-tolerant and sensitive genotypes, emphasizing the functional significance of the C2C2-GATA family in mediating drought response.



#### Figure. Transformation of Cotton for Seed-oil Enhancement

**Conclusions:** This study highlights the role of specific transcription factor families, particularly C2C2-GATA, in regulating drought stress responses in cotton. The differential expression of these genes between tolerant and sensitive genotypes underscores their potential as targets for biotechnological interventions. By leveraging these transcription factors, it is possible to develop genetically engineered cotton plants with enhanced drought tolerance, contributing to sustainable cotton production in water-limited environments.

Keywords: Transcription factor, drought tolerance, gene ontology, Gossypium herbaceum, microarray

### Illumina Technologies to Develop Genomic Ecosystem for Plants

#### Xavier David

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In order to address the new challenges of global food demand, such as increasing productivity while maintaining biodiversity, agricultural researchers are adopting a deeper use of genomics and DNA science to optimize new findings. Thanks to its NGS platforms, bioinformatics pipeline, and tools, Illumina has become the largest provider of high-quality sequences worldwide, accounting for more than 70% of the market. This DNA sequencing technology is the starting point for generating highly accurate data for reference genomes, identifying new mutations, and discovering new marker/trait associations for essential phenotypic performances such as drought tolerance, disease resistance, and other productivity-related traits. Once scientifically published, these findings are implemented using Illumina's array-based genotyping technology in high-throughput screening tests relevant to plant breeders, becoming a critical decision-making tool for developing healthier, more resilient, and more productive plants.

## Genomics and Transcriptomics Reveal Cotton Fiber Differentiation and Development

#### **Xianlong Zhang**

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Cotton is a worldwide crop providing natural fiber for textiles, and the most cultivated cotton are tetraploid species (within the AADD genome group, with a genome size of about 2.4 Gb. Cotton fiber is a representative single-cell in plants and undergoes staged differentiation, to understand fiber evolution and genetic regulation is of great significance in improving fiber quality in the coming genomic breeding. We released the reference genome sequences of *Gossypium hirsutum* and *G. barbadense* and identified 10 more QTLs for fiber quality using a RIL population. Then we constructed a pangenome of the two cultivated tetraploid species, and retrieved thousands of genes that were lost during domestication and selection. In 2022, we published a pangenome across all the diploid species and dissected the genetic basis of fiber length by GWAS and TWAS. Recently we used 2215 fiber transcriptomes from 376 *G. hirsutum* (AD1) accessions and identified 53854 ciseQTLs and 23811 trans-eQTLs for 23012 genes, which enriched our knowledge in improving cotton fibers in breeding. We are sure that the data will be effectively used in developing breeding chips to real improve the complex fiber quality traits by genomic selection.







## Exploration and Application of Molecular Breeding System for Drought Resistance of Cotton

#### Xiyan Yang

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Cotton is an important raw material for the textile industry, as well as an important source of oil and protein, which occupies an important position in the world and China's national economy. Drought is the main adverse factor affecting the high yield and quality of cotton in the main producing areas of China. Water-saving and drought-resistant is an increasing demand for the green development of the world. Understanding the genetic and molecular mechanism for drought resistance of cotton and improving the drought resistance ability and water use efficiency of cotton are the main ways for the green and sustainable development of cotton industry. In our study, we established a cotton phenomics platform to achieve high-throughput identification of drought resistance (DR) traits, developed 10 new imaging-based traits (i-traits) for DR, and mapped 179 QTL related to DR traits based on newly developed i-traits and conventional phenotypic traits. We cloned 28 DR related genes in cotton and analyzed the functions and regulatory mechanisms of 12 important genes such as GhCIPK6 and GhM-KK16. A total of 22 SNP-based DR markers were developed, and 8 of them were developed to PCR molecular markers. A total of 18 drought-resistant resources were identified by high-throughput phenotypic selection and water control assays in Xinjiang field, assisted by DR-related molecular markers. And more than 20 drought-related cotton lines were created by genetic modification, and gene editing. A transgenic line with enhanced drought resistant and unaffected cotton yield and quality, developed by overexpressing GhPYL8, entered the third level of transgenic safety evaluation procedure.





Eight DR-PCR markers were developed from genome-wide SNP markers and functional genes.

The drought resistant was improved of Hubei provincial trial variety H3908.



## Genome Sequence of Gossypium anomalum Facilitates Interspecific Introgression Breeding

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Crop wild relatives are an important reservoir of natural biodiversity. However, incorporating wild genetic diversity into breeding programs is often hampered by reproductive barriers and a lack of accurate genomic information. We assembled a high-quality, accurately centromere-anchored genome of *Gossypium anomalum*, a stress-tolerant wild cotton species. We provided a strategy to discover and transfer agronomically valuable genes from wild diploid species to tetraploid cotton cultivars. With a (*Gossypium hirsutum 3 G. anomalum*)<sup>2</sup> hexaploid as a bridge parent, we developed a set of 74 diploid chromosome segment substitution lines (CSSLs) of the wild cotton species *G. anomalum* in the *G. hirsutum* background. This set of CSSLs included 70 homozygous substitutions and four heterozygous substitutions, and it collectively contained about 72.22% of the *G. anomalum* genome. Twenty-four quantitative trait loci associated with plant height, yield, and fiber qualities were detected on 15 substitution segments. Integrating the reference genome with agronomic trait evaluation of the CSSLs enabled location and cloning of two *G. anomalum* genes that encode peroxiredoxin and putative callose synthase 8, respectively, conferring drought tolerance and improving fiber strength. We have demonstrated the power of a high-quality wild-species reference genome for identifying agronomically valuable alleles to facilitate interspecific introgression breeding in crops.

Keywords: wild diploid species, *Gossypium anomalum*, genome, chromosome segment substitution lines, drought tolerance, fiber strength

**Figure.** Causal gene conferring drought tolerance in *G. anomalum*. Overexpression of Goano05G0268 modulates drought response in Cotton. Three overexpression (OE) transgenic lines of Goano05G0268 showed higher drought tolerance than wild-type lines. Goano05G0268 encodes a peroxiredoxin protein, which participates in protection against oxidative damage and plays a role in plant responses to drought stress.



Figure. Abundant phenotypic variations of CSSLs



# Development of Disease Resistance in Plants Using CRISPR/Cas Technology: A Step Forward to Ensuring Food Security

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After ensuring food security for several decades, the green revolution has gained its potential and reaching its biological boundaries which is reflected by the stagnation in yield. Meeting the growing food demands of the masses, due to increasing population, is the biggest challenge for plant scientists. CRISPR-edited crops hold tremendous potential for food security and global agriculture. CRISPR technology has become a new face of genome editing with rapidly increasing applications in academic research (functional genomics and reverse genetics) as well as applied research for developing crop varieties with new or improved traits. After successful deployment of gene editing technology to modify simple traits, more ambitious ventures to combat food security challenges in the wake of growing world population with changing climate are in progress. CRISPR may be used in several ways to develop resistance in plants; targeting host susceptibility genes/factors, inserting resistance genes, activating host immunity, breaking host-pathogen cross-talk/interaction etc. We used CRISPR system against bacterial and viral disease and found promising results. In case of bacterial disease, bacterial leaf spot, we targeted susceptibility gene with CRISPR to enhance plant immunity against the disease in tomato, while in case of viral diseases (caused by Begomoviruses such as CLCuD), we targeted several viral genes to develop resistance against Cotton Leaf Curl Virus Disease. It was found that targeting multiple genes simultaneously may provide resistance up to 70-80%. Moreover, delay in symptoms, low virus titer and attenuated symptoms were observed on the CRISPR plants. Initially, we screened all gRNAs in the model plants; Arabidopsis and Nicotiana benthamiana. Later, we expressed selected gRNAs-CRISPR, transient and stable expression, in tomato and cotton. CRISPR technology has a potential to be used for genetic improvement of plants to ensure food security and safety. Moreover, producing DNA-free, non-GMO plants with CRISPR is an attractive approach for breeders of all regions of the world.

Keywords: Plants Diseases, CRISPR/Cas, GMO, New breeding techniques, Climate-smart crops, Diseases Resistance, Food Security



#### Figure. CRISPR for Resistance against Begomoviruses

# POSTER PRESENTATIONS COTTON GENOMICS & MOLECULAR BIOLOGY



### Introgression of QTL-Hotspot Regions Enhances Drought Tolerance in Cotton Genotypes

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**Background:** Drought is a complex trait to understand the genetics of the trait had a major focus on molecular and physiological traits associated that contributes to drought tolerance.

Results: With an aim of enhancing drought tolerance in cotton, introgression of the QTL-hotspot regions from CNH 28I (drought tolerant genotype) that harbors quantitative trait loci (QTLs) for several drought-tolerance related traits into elite Indian cotton cultivar Suvin which has a superior fiber length.QTL hotspot regions on different chromosomes for drought tolerant traits like osmotic potential, carbon isotope ratio, canopy temperature, root tip, root weight, relative water content, root length, root surface area, root volume were selected for screening the recombinant inbred lines (RILs). The introgression lines were genotyped using a total of 157 SSR markers linked to drought QTLs. Eight QTLs were linked to osmotic pressure (OP) located on chromosome C1, C2, C6 & C25. Four QTLs were linked to canopy temperature (CT) hotspot on chromosome C 6. Fifteen QTLs were linked to carbon isotope ratio (CIR) hot spot located on chromosome C15 & C24, C25, C21. Five QTLs linked to root weight (RW) located on chromosome C11 & C24. Five QTLs linked to root length got distributed on chromosome C5, C13, C14, C21. Four QTLs linked to root tip (RT) on chromosome C13, C19 & C21. Four QTLs linked to root surface area (RSA) on chromosome C1, C13, C21. Five QTLs linked to root volume (RV) hot spot area on chromosome C19. Two QTLs for root weight (RW) linked on chromosome C20 and one locus each on C13, C20, C24 in the cotton genome (http://www.cottongtldb.org). These QTLs were screened with RIL population amplified PCR products of same size like drought tolerant parent CNH 28I showing introgression of QTL-hotspot areas. Sixteen QTLs produced polymorphism among parents and RIL population were five QTLs viz., NAU 2557, CIR 143b, MUSB 0818c, JESPR 0205, BNL 1053 linked to CIR, 5 QTLs viz., NAU 2474, BNL 3594b, BNL 2884, BNL 3259, BNL 1153b linked to OP, four QTLs viz., JESPR 230c, BNL 3347, MUSS 096a, CIR 061b linked to RV, 1 OTL BNL 3173b linked to RWC, one OTL BNL1705 linked to RL. Six improved lines with drought tolerant traits and fiber length were selected by genotyping and phenotyping using the physiological parameters relative water content (RWC), Canopy temperature (CT), Chlorophyll and Proline content.

**Conclusion:** The data generated from this study and the markers identified will be used for marker-assisted selection (MAS) approach in breeding for further utilization in the development of drought tolerant varieties.

Keywords: G hirsutum; G barbadense; interspecific cross; RILs; QTL's.

# Genomic Insights into Fiber Quality: Candidate Genes in Gossypium hirsutum L.

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The quality of cotton fiber is as crucial as its quantity, assessed through key indicators such as fiber length, strength, uniformity, color, and Micronaire. With the growing demand for high-quality cotton fiber, identifying candidate genes involved in fiber development and breeding new varieties based on these genes becomes a primary objective for researchers. This study conducted in-silico analyses of the SSR-marker BNL1666, associated with fiber quality, using the nucleotide sequences of primer pairs across the genome of the tetraploid cotton species *Gossypium hirsutum* (AD1). The virtual PCR analysis revealed that this marker is amplified on the D01 chromosome. Subsequent analyses using AUGUSTUS and NCBI-BLAST identified two potential genes in this chromosomal region: subtilisin-like protease SBT6 and leucine-rich repeat serine/ threonine protein kinase (LRRK2). Both SBT6 and LRRK2 genes are documented in the literature as being involved in the synthesis of secondary cell walls throughout plant development, including in fibers. Further research is currently underway to identify candidate genes that regulate the development of fiber quality.

Keywords: cotton, *G. hirsutum* L., candidate genes

# Analysis of Expression Patterns of Laccase Gene Family Members in Upland Cotton

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Laccases are members of the copper blue oxidase protein family and play an important role in plant lignin synthesis and enhancing plant stress resistance. In this study, 104 laccase genes (GhLAC) family members were identified from the upland cotton genome, and a phylogenetic tree and tissue expression map were constructed. Twenty genes were randomly selected for quantitative PCR analysis to verify the results of the expression heat map. To further explore the role of laccases in cotton, promoter-GUS fusion vectors were used to transform *Arabidopsis*. Through GUS staining of different tissues at various developmental stages of transgenic *Arabidopsis*, the fine expression patterns of six upland cotton laccase gene family members (GhLAC12A, GhLAC14A, GhLAC20A, GhLAC25D, GhLAC59D, GhLAC63D) were analyzed.

To investigate the role of laccases under stress conditions, expression analyses under two types of wounding stress (cutting and puncturing) were performed for these six laccase genes. Fluorescent quantitative PCR analysis was conducted on anthers from two cotton varieties, '84021' (heat-tolerant) and 'H05' (heat-sensitive), under normal and high-temperature stress conditions at different developmental stages.

The results showed that the 20 randomly selected genes were differentially expressed in six tissues: roots, stems, leaves, petals, anthers, and stigmas, with most gene expressions consistent with transcriptome results. The promoters of the six laccase genes could drive GUS gene expression at various stages such as seed germination, two-leaf stage, and four-leaf stage. Wounding treatment results indicated that the promoters of GhLAC12A and GhLAC14A significantly increased the ability to drive GUS protein expression in leaves after wounding, suggesting that these two genes may be involved in wound stress response. Expression of the six GhLACs genes showed a significant downward trend during tetrad stage and anther dehiscence under high-temperature stress in the heat-tolerant cotton variety '84021,' suggesting that GhLACs genes may negatively regulate the heat tolerance of upland cotton anthers. These findings provide a reference for further exploration of the functional roles of the laccase gene family.

# GhUBC10-2 Mediates GhGSTU17 Degradation to Regulate Salt Tolerance in Cotton (*Gossypium hirsutum*)

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Ubiquitin-conjugating enzyme (UBC) is a crucial component of the ubiquitin proteasome system, which contributes to plant growth and development. While some UBCs have been identified as potential regulators of abiotic stress responses, the underlying mechanisms of this regulation remain poorly understood.

Here, we report a cotton (*Gossypium hirsutum*) UBC gene, GhUBC10-2, which negatively regulates the salt stress response. We found that the gain of function of GhUBC10-2 in both Arabidopsis and cotton leads to reduced salinity tolerance. Additionally, GhUBC10-2 interacts with glutathione S-transferase (GST) U17 (GhGSTU17), forming a heterodimeric complex that promotes GhGSTU17 degradation. Intriguingly, GhUBC10-2 can be self-polyubiquitinated, suggesting that it possesses E3-independent activity.

Our findings provide new insights into the PTM of plant GST-mediated salt response pathways. Furthermore, we found that the WRKY transcription factor GhWRKY13 binds to the GhUBC10-2 promoter and suppresses its expression under salt conditions. Collectively, our study unveils a regulatory module encompassing GhWRKY13-GhUBC10-2-GhGSTU17, which orchestrates the modulation of reactive oxygen species homeostasis to enhance salt tolerance.

Keywords: GhWRKY13, salt stress, ubiquitination

## Identification of High Temperature Tolerance Genes and Molecular Functions by GWAS Analysis in *Gossypium barbadense*

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**Background:** Cotton production in Xinjiang accounts for 90% of China's total, and it's the only region that cultivates *Gossypium barbadense* in China. High temperature is a critical factor constraining the enhancement of cotton yield and quality in Xinjiang. Improving the high-temperature resistance of cotton varieties is a vital direction for future improvements in Xinjiang's cotton yield and quality. However, the molecular mechanisms underlying high temperature resistance during the flowering stage of island cotton remain unclear.

**Results:** This study focused on the core germplasm resource of sea-island cotton, utilizing a high-throughput phenotyping platform and related analysis technologies to identify island cotton germplasm resources resistant to high temperatures. Genome-wide association study (GWAS) methods were applied to identify six key quantitative trait loci (QTL) and 195 candidate genes controlling the target traits. Thirteen key genes were obtained, including nine genes involved in flavonoid regulation, ARAC3, CYP19, and two GRP2B genes that are involved in cell wall and reproductive organ development in stress. A variety of molecular biological methods were applied to analyze gene functions and signal regulatory networks. The study revealed the molecular mechanisms which high temperatures lead to premature degradation of the tapetum layer, reduction of flavonoids and anthocyanin in the anther, and the subsequent pollen sterility and boll drop in sea-island cotton. This research aimed to create new sea-island cotton germplasm for high temperature resistance and a high boll-setting rate.

**Conclusion:** The results show that flavonoid genes can improve the rate of pollen activity in reproductive organs by increasing the initial accumulation of flavonoids and anthocyanins, thereby enhancing pollen fertility and boll setting, which increases higher yields. This research provides significant genetic resources and germplasm support for the breeding of high temperature resistant sea-island cotton, and it provides the foundation for the genetic improvement of yield and quality in Xinjiang's sea-island cotton.

#### Evolution and Functional Divergence of CIPK6 Subfamily Genes in Regulating Drought Resistance in Cotton

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**Background:** The occurrence of ancient whole-genome duplication or polyploidization in plants may contribute to increasing plant adaptability to the environment. However, there are few reports of functional differentiation of homologous genes in plants.

**Results:** Here, we clarified the evolutionary relationship of eight GhCIPK6 homologous genes in upland cotton (*Gossypium hirsutum*) through the phylogeny of species. Gene expression and interaction analysis in *Gossypium* indicated that GhCIPK6 homologous genes showed significant changes after polyploidization. Among those, GhCIPK6D1 and GhCIPK6D3 were significantly upregulated by drought stress. Functional studies revealed that GhCIPK6D1 negatively regulates cotton drought resistance, while GhCIPK6D3 is a positive regulator, indicating clear functional differentiation through the course of gene family evolution. Genetic and biochemistry evidence confirmed the synergistic negative/positive regulation of cotton drought resistance through Gh-CBL1A1-GhCIPK6D1 and GhCBL2A1-GhCIPK6D3, where GhCBL1A1 and GhCBL2A1 are calcineurin B-like proteins, which recruited GhCIPK6D1 or GhCIPK6D3 to cell membrane or tonoplast, to further regulate stomatal movement by control the entry and exit of K+ in guard cells.

**Conclusion:** These results reveal regulatory innovation following duplication of the GhCIPK6 genes in upland cotton after polyploidization to regulate drought stress, which provides strong evidence supporting the hypothesis that whole-genome duplication leads to adaptability of plants at the gene level, and also provides a new perspective for exploring in the future the new functionalization and sub-functionalization that is the consequence of plant polyploidization.

Keywords: Cotton, CIPK6, Drought resistance, Evolution, Polyploidization

# Expression Pattern Analysis of Na+/H+ Antiporter From Cotton in Response to Salt Stress

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**Background:** Salinity is one of the most important abiotic stresses that decrease crop production. Cotton (*Gossypium hirsutum*) has a relative tolerance to salinity. NHX1 gene encoded a Na+/H+vacuole antiporter that this antiporter has important roles in cellular pH and Na+, K+ homeostasis. To investigate NHX1 expression pattern, RNA extracted by modified LiCl procedure and Real Time PCR performed. Split-factorial design of time based on randomized complete block design with 3 replications was used. Results: The real-time PCR results for, root, stem, and leaves of 14-day cotton seedlings of tolerant (Sepid) and sensitive (Thermus14) cotton cultivars with salinity levels from 0 to 16 ds.m-1 were analyzed at three time points, namely 0, 7 and 14 days after salinity stress.

**Results** showed that expression pattern NHX1 gene has positively responded to salinity stress and their expression in the root was higher than in stem and leaf.

**Conclusion:** There was significant different between short-time and long-time of stress. also, the expression of tolerant genotype (Sepid) was higher than the sensitive cultivar (Thermus 14) one.

Keywords: cotton, NHX1 expression pattern, Real Time PCR, tolerant and sensitive genotypes

## Intra- and Inter-specific Genetic Diversity for Salinity Tolerant Traits and Symptoms Among Cultivated *Gossypium* species

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**Background:** Among the field crops, cotton is the second tolerant crop after barley. In genus *Gossypium*, diploid species has good tolerance to salinity stress. To evaluation genetic diversity of salinity tolerance in different species and founding tolerant germplasm in cotton, 28 accessions of four cultivated *Gossypium* species were studied in 4 experiments (2 experiments in non-stress and 2 experiments in stress condition). We observed high inter specific and intra specific diversity for salt tolerance.

**Results:** Among the evaluated characteristics, we observed high genetic diversity for K + and K + /Na + in both polyploidy levels but prolin and soluble sugars accumulation especially had low genetic diversity. *G. herbaceum* accessions had high salt tolerance than other species. *G. barbadense* accessions were sensitive than other species. In general, accession which have high K + /Na + ratio will have high seed cotton yield. Among tetraploid cultivars CREMA (*G. hirsutum*) and for diploid cultivars SORKHEH-SEMNAN were best cultivar in stress condition.

**Conclusion:** cultivars with high K+ /Na+ ratios are the best for salinity tolerant.

Keywords: Cotton, salinity stress, Inter-specific diversity, Intra-specific diversity

# Molecular Breeding of Cotton for Salt Tolerance

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**Background:** Cotton plants from existing varieties and collection samples can tolerate salinity up to a maximum of 1%, but no highly salt-resistant varieties currently exist. The advent of agricultural biotechnology, particularly cell breeding techniques, has made it possible to develop salt-resistant varieties in several crop species. In this study, we investigated the potential of cell selection methods to improve salt tolerance in cotton, focusing on the behavior of callus cells under salinity stress and the conditions required for somatic embryoidogenesis and morphogenesis.

**Results:** Callus cells were induced from cotton hypocotyls on Murashige-Skoog medium with low auxin concentrations. Successful long-term sub-cultivation required the absence of phytohormones. While extended sub-cultivation on agar media did not lead to somatic embryoidogenesis, embryogenesis was achieved in the embryogenic variety Coker-312 when callus cells were cultured in a suspension medium with double sub-culturing followed by transfer to a morphogenic agar medium without phytohormones. Somatic embryoids formed in artificial media exhibited diverse shapes and sizes, with abnormalities such as disordered cotyledon leaf formation, disrupted polar organization, and impaired main root development. Under salinity conditions of up to 1.0% NaCl, callusogenesis from cotton hypocotyls was observed, but higher NaCl concentrations inhibited this process. In suspension media, cotton callus cells tolerated relatively high NaCl concentrations, up to 2.0%. Under such saline conditions, cells acquired oval-round shapes, reduced in size and number, and exhibited transparent cytoplasmic contents with accumulated organelles distributed throughout the cytoplasm. Despite these stresses, individual cells retained their normal morphology and division ability. Suspension cultivation allowed the selection of salt-resistant cell lines. When these lines were transferred to a morphogenic agar medium, their morphological structures were restored. However, long-term sub-cultivation did not induce morphogenic development.

**Conclusions:** This study demonstrates the potential of suspension cultivation for selecting salt-tolerant cotton cell lines capable of withstanding salinity levels up to 2.0% NaCl. These selected cell lines can restore their morphology upon transfer to a morphogenic medium but do not progress to morphogenic development with extended sub-culturing. The findings provide valuable insights into the cellular responses of cotton to salinity stress and lay the groundwork for developing biotechnological approaches to create salt-tolerant cotton varieties. Further research is needed to refine these methods for generating morphogenically competent, salt-resistant cotton plants.

Key words: Cell selection, Phytohormones, Salinity, Callus cells, Sub cultivation, Callusogenesis, Somatic embryoids.

# A Male-Sterile Mutant With Necrosis-Like Dark Spots on Anthers was Generated in Cotton

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**Background:** Although conventional hybrid breeding has paved the way for improving cotton production and other properties, it is undoubtedly time and labor consuming, while the cultivation of male sterile line can fix the problem.

**Results:** We induced male sterile mutants by simultaneously editing three cotton EXCESS MICROSPOROCYTES1 (GhEMS1) genes by CRISPR/Cas9. Notably, the GhEMS1 genes are homologous to AtEMS1 genes, which inhibit the production of middle layer and tapetum cells as well, leading to male sterility in cotton. Interestingly, there are necrosis-like dark spots on the surface of the anthers of GhEMS1s mutants, which is different from AtEMS1 mutant whose anther surface is clean and smooth, suggesting that the function of EMS1 gene has not been uncovered yet. Moreover, we have detected mutations in GhEMS1 genes from T0 to T3 mutant plants, which had necrosis-like dark spots as well, indicating that the mutation of the three GhEMS1 genes could be stably inherited. Dynamic transcriptomes showed plant hormone pathway and anther development genetic network were differential expression in mutant and wild-type anthers. And the lower level of IAA content in the mutant anthers than that in the wild type at four anther developmental stages may be the reason for the male sterility.

**Conclusion:** We used gene editing to create a male sterile mutant in cotton. This study not only facilitates the exploration of the basic research of cotton male sterile lines, but also provides germplasms for accelerating the hybrid breeding in cotton.

## Increasing the Level of Suberin in Cotton (G. hirsutum) Tissues Through Genetic Engineering

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**Background:** The rising levels of atmospheric carbon dioxide (CO<sub>2</sub>) emphasize the urgent need for effective strategies to mitigate global warming. Suberin, a hydrophobic polymer primarily synthesized in plant root tissues, is highly resistant to degradation and rich in carbon, making it a viable target for long-term carbon sequestration. Cotton (*Gossypium hirsutum*), an economically important crop, presents significant potential for carbon sequestration through genetic manipulation to enhance suberin production. This study explores the use of RNA interference (RNAi) to upregulate suberin synthesis in cotton tissues, building on insights from *Arabidopsis thaliana*, where disruption of the ESB1 gene led to increased suberin deposition.

**Results:** The orthologous ESB1 gene was cloned from cotton to facilitate targeted genetic modifications. RNAi-mediated silencing of ESB1 in cotton successfully enhanced suberin synthesis, as evidenced by a threefold increase in suberin deposition in RNAi plant tissues compared to controls. Suberin accumulation was particularly prominent in cotton root tissues, aligning with the polymer's natural role in root defense and carbon storage.

This increase in suberin content in RNAi plants underscores the potential of manipulating the ESB1 pathway as an effective strategy for enhancing carbon sequestration. Enhanced suberin deposition not only contributes to long-term carbon storage but also may improve cotton plant resilience to environmental stresses, such as drought and salinity, due to suberin's protective properties.

**Conclusions:** This study introduces a novel genetic engineering approach to enhance suberin synthesis in cotton, with significant implications for carbon sequestration and sustainable agriculture. RNAi silencing of the ESB1 gene in cotton demonstrates the potential to substantially increase suberin deposition, offering a promising avenue for mitigating atmospheric CO<sub>2</sub> levels. Future research should focus on optimizing genetic strategies to maximize suberin accumulation and evaluating the broader agronomic and environmental benefits of suberin-enriched cotton plants. These efforts could establish cotton as a key crop in global carbon sequestration initiatives, advancing efforts to combat climate change.

#### Single-Cell Resolution Analysis Reveals the Preparation for Reprogramming the Fate of Stem Cell Niche in Cotton Lateral Meristem

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**Background:** Somatic embryogenesis is a major process for plant regeneration. However, cell communication and the gene regulatory network responsible for cell reprogramming during somatic embryogenesis are still largely unclear. Recent advances in single-cell technologies enable us to explore the mechanism of plant regeneration at single cell resolution.

**Results:** We generate a high-resolution single-cell transcriptomic landscape of hypocotyl tissue from the highly regenerable cotton genotype Jin668 and the recalcitrant TM-1. We identify nine putative cell clusters and 23 cluster-specific marker genes for both cultivars. We find that the primary vascular cell is the major cell type that undergoes cell fate transition in response to external stimulation. Further developmental trajectory and gene regulatory network analysis of these cell clusters reveals that a total of 41 hormone response-related genes, including LAX2, LAX1 exhibit different expression patterns in the primary xylem and cambium region of Jin668 and TM-1. We also identify novel genes, including CSEF, PIS1, AFB2, ATHB2, PLC2, PLT3, that are involved in regeneration. We demonstrate that LAX2, LAX1 and LOX3 play important roles in callus proliferation and plant regeneration by CRISPR/Cas9 editing and overexpression assay.

**Conclusions:** This study provides novel insights on the role of the regulatory network in cell fate transition and reprogramming during plant regeneration driven by somatic embryogenesis.

Keywords: Cotton, Plant regeneration, scRNA-seq, Gene regulatory network, Gene functional verification

# The GhMYB61-GhMYB3-GhKNAT7 Complex Regulate the Deposition of Secondary Cell Wall in Cotton Fiber

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**Background:** Cotton serves as a vital natural resource for the textile industry. Cotton fiber is highly elongated single cells attached to seeds. The secondary cell wall (SCW) of mature cotton fiber is composed of 90% cellulose. Nevertheless, the regulation of cellulose synthesis in the SCW of cotton remains ambiguous.

**Results:** We report that the R2R3-MYB, GhMYB61 as a transcription repressor in the cellulose synthesis. Its loss-of-function mutants fiber displays thicker walls and higher cellulose content. On the contrary, the overexpression lines of GhMYB61 were delayed into the secondary cell wall thickening and exhibited the longer fiber with thinner walls. Further results show that GhMYB61 could directly bind to different cis elements in the promoter of GhCesA4, GhCesA7 and GhCesA8 and repress GhCesAs. In addition, GhMYB61, GhMYB3 and GhKNAT7 interact with each other. The GhMYB61-GhMYB3-Gh-KNAT7 complex promoted the inhibitory effect of GhMYB61 on GhCesAs.

**Conclusion:** GhMYB61 could form a complex with other genes to bind to the promoter of GhCesAs and regulate the cellulose synthesis, which may provide a strategy for improving fiber quality in cotton breeding.

Keywords: cotton fiber, cellulose synthesis, secondary cell wall, complex, repress

## Cotton Bollworm (*H. armigera*) Effector PPI5 Targets and Inhibits Cyclophilin Gh-FKBP17-2 PPIase and Endoplasmic Reticulum-Mediated Immunity to Modulate Plant JA Responses and Promote Insect Feeding

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**Background:** The cotton bollworm (*Helicoverpa armigera*) is a devastating pest that inflicts mechanical damage on plants during feeding and deposits oral secretions (OSs) at the wound site. While the mechanical damage caused by feeding is well-studied, the role of OSs in plant susceptibility remains poorly understood. In this study, we identified and characterized a novel *H. armigera* effector, Peptidyl Prolyl trans-Isomerase 5 (PPI5), and its interaction with the host protein GhFKBP17-2 in cotton. The study aimed to elucidate the mechanism by which PPI5 modulates plant immunity, making plants more susceptible to cotton bollworm infestation.

**Results:** PPI5, isolated from *H. armigera*, was found to induce programmed cell death (PCD) via the unfolded protein response (UPR) in tobacco leaves. Functional studies revealed that PPI5 is conserved across several lepidopteran species and plays a critical role in facilitating cotton bollworm growth and development on host plants. GhFKBP17-2, a host protein with peptidyl prolyl isomerase (PPIase) activity, was identified as the target of PPI5 in cotton. CRISPR/Cas9 knock-out mutants (CR-GhFKBP17-1/3), VIGS-silenced plants (TRV: GhFKBP17-2), and overexpression lines (OE-GhFKBP17-1/3) were developed to investigate the role of GhFKBP17-2 in cotton immunity. These experiments demonstrated that GhFKBP17-2 positively regulates endoplasmic reticulum (ER) stress-mediated immunity, enhancing plant defenses against cotton bollworm infestation. PPI5 suppresses plant defense responses by repressing jasmonic acid (JA) and salicylic acid (SA) pathways. Gene expression analysis showed that PPI5 downregulates key JA- and SA-associated defense genes, including JAZ3/9, MYC2/3, JAR4, PR4, LSD1, PAD4, ICS1, and PR1/5. This suppression reduces plant immune responses, making plants more susceptible to infestation.

**Conclusions:** This study reveals a novel mechanism by which the *H. armigera* effector PPI5 suppresses plant immunity. By targeting and suppressing GhFKBP17-2, PPI5 represses ER stress-mediated immune responses and downregulates JA- and SA-associated defense pathways, rendering cotton more susceptible to bollworm infestation. These findings provide new insights into the interaction between cotton and its pest and suggest potential targets for developing pest-resistant cotton varieties.

## Multi-omics Identifies Two Homologous MYB Genes Regulating Key Metabolites and Agronomic Traits in Upland Cotton

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**Background:** Understanding the early stages of cotton ovule and fiber development is critical for uncovering the molecular and metabolic factors influencing cell differentiation, organ formation, and agronomic traits. Early cotton ovules exhibit significant up-regulation of gene activity, shaping fiber cell growth and ovule development. Establishing links between gene expression, metabolic patterns, and agronomic traits can provide valuable insights for cotton improvement. This study integrated multi-omics data from upland cotton (Gossypium hirsutum) ovules to identify key regulatory loci and gene networks influencing early developmental processes and agronomic traits.

**Results:** Analysis of 403 upland cotton ovules identified 2,960 metabolic quantitative trait loci (mQTLs) and 24,485 expression quantitative trait loci (eQTLs). A major locus, ME\_A07, was found to regulate 252 known metabolite levels (50.6% of identified metabolites) and 4,293 gene expressions (39.7% of all eQTL-regulated genes). The MYB gene GhMRG (Metabolite Regulatory Generator) emerged as the central regulator of ME\_A07. A 520 Kb-length inversion upstream of GhMRG likely modulates its function, orchestrating transcriptional regulation of primary and secondary metabolite biosynthesis pathways that influence agronomic traits such as fiber quality and yield. Another significant locus, ME\_A06, driven by the MYB gene GhPAR (Proanthocy-anidin Regulator), was associated with proanthocyanin (PA) content. The geographical distribution of ME\_A06 locus haplotypes suggests its role in ecological adaptation. Shared and distinct expression patterns of GhMRG and GhPAR revealed their varying impacts on fiber quality and yield. These findings highlight the complex regulation of cotton metabolic pathways and their contribution to key agricultural traits.

**Conclusions:** This study underscores the pivotal role of MYB genes, such as GhMRG and GhPAR, in regulating early cotton ovule and fiber development. The identified loci ME\_A07 and ME\_A06 integrate metabolic and transcriptional regulation, influencing both primary and secondary metabolite biosynthesis and agronomic traits. The results provide valuable insights into the metabolic mechanisms controlling fiber quality and yield, offering new opportunities for targeted molecular breeding. The multi-omics dataset generated in this study represents a rich resource for future cotton research and genetic improvement efforts.

#### Comprehensive Mining of Long Non-coding RNAs of Gossypoides Based on the Universal Transcriptome

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**Background:** Long non-coding RNAs (lncRNAs) have emerged as key regulators in various biological processes, including growth, development, and stress responses in plants. Despite their importance, the full spectrum of lncRNAs in cotton remains underexplored. Advances in sequencing technology and bioinformatics enable comprehensive mining of lncRNAs to uncover their potential functions. This study aimed to systematically identify and characterize lncRNAs in *Gossypium* using a pan-transcriptome approach, offering new insights into their roles in domestication and stress resistance.

**Methods & Results:** Publicly available RNA-Seq data were comprehensively collected and processed using a uniform pipeline for lncRNA identification. De novo assembly was performed on all datasets to discover potential lncRNAs not present in the reference genome. Clustering was conducted using CD-Hit to create a non-redundant pan-lncRNA library for upland cotton. Multi-omics data were integrated to predict the functions of identified lncRNAs, with a particular focus on those involved in growth, reproductive development, and stress responses. The objectives of this study were to construct a comprehensive lncRNA database for *Gossypium*, investigate the impact of domestication on lncRNA profiles, and identify functional lncRNAs with the potential to enhance stress resistance in upland cotton. The study identified core pan-lncRNAs that exhibited a high number of cis-regulatory elements, suggesting their conserved functions across cotton species. Functional analysis revealed that lncRNA-associated cis-regulatory genes in *Gossypium* were predominantly involved in light response, light collection, and other stress-related processes. These findings highlight the critical role of lncRNAs in mediating plant responses to environmental challenges.

**Conclusions:** This comprehensive mining effort provides a robust pan-lncRNA library for *Gossypium*, uncovering conserved and novel lncRNAs with potential roles in stress resistance and adaptation. The discovery of light-responsive and stress-associated lncRNAs emphasizes their importance in enhancing upland cotton's resilience to adverse conditions. These findings lay a solid foundation for future functional studies and the development of stress-tolerant cotton varieties.