GLEANINGS IN COTTON RESEARCH

JANUARY 2026

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Preface

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

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

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

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

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

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

We duly thank The Director, Dr V. N. Waghmare, for providing inspiration and support for this publication.

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

Swati Dixit
In charge Library

Chetali Rodge
Technical Officer (T5)

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Title: Multi-modal feature integration from UAV-RGB imagery for high-precision cotton phenotyping: A paradigm shift toward cost-effective agricultural remote sensing.

Author:Xiaoyu Zhi , Qiaomin Chen, Yingchun Han, Beifang Yang, Yaru Wang , Fengqi Wu, Shiwu Xiong, Yahui Jiao , Yunzhen Ma, Shilong Shang, Tao Lin , Yaping Lei

Imprint: Computers and Electronics in Agriculture, Volume 239, Part B, December 2025, 111002

Abstract: Cost-effective remote sensing solutions are critically needed to democratize precision agriculture technologies. While hyperspectral and LiDAR systems deliver high accuracy, their prohibitive costs limit widespread adoption. This study demonstrates that systematic multi-modal feature integration transforms standard UAV-based RGB imagery into a powerful phenotyping instrument, achieving crop trait prediction accuracy comparable to systems costing 10–50 times more. We developed a comprehensive framework integrating spectral indices, geometric parameters, and texture metrics from commodity RGB sensors to predict five critical cotton traits: leaf area index (LAI), intercepted photosynthetically active radiation (IPAR), above-ground biomass, lint yield, and seed cotton yield. The progressive integration approach employed Random Forest regression with four feature configurations: baseline color indices (CI_{base}), refined color indices (CI_{ref}), geometric parameters (CI_{ref} + GP), and texture metrics (CI_{ref} + GP + T). Field experiments across three trials over two growing seasons (2022–2023) with varying genotypes, planting densities, and sowing dates provided 2,126 ground truth measurements for model development and validation. The optimal multi-modal model achieved $R^2 = 0.97$ for IPAR (rRMSE = 6 %), $R^2 = 0.91$ for LAI (rRMSE = 15 %), and $R^2 = 0.85$ for biomass (rRMSE = 32 %), with lint yield and seed cotton yield demonstrating R^2 values of 0.92 and 0.77, respectively. Variance partitioning analysis revealed texture features as the dominant contributor (16.2 % ± 7.1 %), followed by spectral indices (9.1 % ± 4.2 %) and geometric parameters (8.0 % ± 2.8 %), with substantial shared variance (45–65 %) indicating strong feature complementarity. Phenological analysis demonstrated that flowering-stage imagery outperformed boll opening stage measurements, while stage-general models showed superior robustness. Cross-temporal validation confirmed model generalizability, with trial-general models achieving R^2 values of 0.91–0.97 for IPAR across diverse environmental conditions. The framework enables sub-meter spatial resolution trait mapping while maintaining operational simplicity and cost-effectiveness,

demonstrating that systematic feature engineering can democratize high-precision phenotyping technologies for broader agricultural applications.

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Title: Optimizing cotton plant architecture and yield through the use of plant growth regulators.

Author: Chen Chen, Gang Wu, Munire Abuduaini, Xinxin Li, Yangqing Tian, Jiahao Zhang, Wenqing Wang, Wenyue Feng, Xinghu Song, Qiang Zhao

Imprint: Crop Science, 18 September 2025, https://doi.org/10.1002/csc2.70131

Abstract: Growth regulation in cotton (*Gossypium hirsutum* L.) is essential for shaping optimal plant architecture and achieving full mechanization in its cultivation. However, the regulators are often poorly controlled when applied individually, leaving plants with poor morphology, which in turn leads to lower yields. Combining regulators is the key to solving these problems. In this study, the effects of spraying 0.1% thidiazuron (TDZ) (T1) individually and TDZ mixtures with 98% mepiquat chloride (T2), 5% prohexadione calcium (T3), and 5% uniconazole (T4), with pure water as a control, were studied. The results showed that the combination of plant growth regulators optimized the cotton plant architecture, and the leaf area index, diffuse not-intercepted area, as well as mean tilt angle of the T4 group increased by 58.4%, 28.1%, and 9.9%, respectively, at the boll-setting period. Net photosynthetic rate, stomatal conductance, intercellular CO_2 concentration, and transpiration rate increased by 27.2%, 20.0%, 6.6%, and 52.4%, respectively, at the peak flowering period. Further, the dry matter accumulation of cotton in reproductive organs increased by 9.6% and 14.3% for 2 years, respectively, and the average seed cotton yield of 2 years was significantly increased by 12.5% under this treatment condition. This study revealed that the combination of 0.1% TDZ and 5% uniconazole could improve the photosynthetic capacity of cotton plants and increase dry matter accumulation through optimizing plant architecture, thus increasing the seed cotton yield. In conclusion, it provides technical guidance for suitable plant architecture and high-yield cotton cultivation in Xinjiang.

3

Title: Cotton boll formation and fiber quality when grown alongside perennial groundcover crops.

Author: Eric D. Billman, Sarah K. Holladay, B. Todd Campbell

Imprint: Crop Science, 12 September 2025, https://doi.org/10.1002/csc2.70160

Abstract: The incorporation of perennial groundcover crops (PGCC) into cotton (*Gossypium hirsutum* L.) systems may provide similar benefits to annual cover crops with fewer associated costs, but their effects on boll production and fiber quality have not been investigated. This study assessed the effects of growing PGCC species on end-of-season boll formation, retention, position, distribution, and fiber quality compared to annual cover crops or fallow systems. Over 2 years, cotton was interseeded and grown in four cover crop treatments as follows: (1) terminated weedy fallow, (2) terminated annual ryegrass (*Lolium multiflorum* Lam.), (3) a living 1:1 mix of perennial red clover (*Trifolium pratense* L.) and white clover (*Trifolium repens* L.), and (4) a living 2:1:1 mix of ryegrass, red clover, and white clover. Post-harvest plant mapping was conducted on plants from outside of harvested rows in each plot to determine final boll set, position, and canopy distribution as well as sympodial and monopodial branching. Fiber quality was also assessed via high volume instrument. Results indicated that the presence of clovers increased boll density lower in the canopy while also increasing the number of position 2 bolls compared to the fallow system, and that growing perennial clovers alongside cotton reduced formation of monopodial shoots. Presence of perennial clovers also reduced the incidence of short fibers in cotton under drought conditions, but did not alter any other fiber quality parameters over the study period. These findings further support the use of PGCC as a mechanism to improve adoption of cover crops in cotton production.

4

Title: No drought memory in cotton despite evidence of drought acclimation.

Author: Ricky S. Kong, Hugh A. L. Henry & Nicholas G. Smith

Imprint: Oecologia , 12 September 2025, Volume 207, article number 156, (2025)

Abstract: Plants are likely to experience multiple cycles of drought. However, physiological acclimation and stress memory may play key roles in reducing the detrimental effects of successive droughts. We investigated drought acclimation in cotton (*Gossypium hirsutum*) fertilized with low or high nitrogen (N) in a greenhouse factorial experiment. The cotton plants were subjected to one of four drought treatments applied during two 15-day periods, where plants were withheld water or were fully watered. We assessed CO_2 assimilation (A_{400}) and stomatal conductance (g_{s400}), maximum rates of ribulose-1,5-bisphosphate (RuBP) carboxylase/oxygenase (RuBisCO) carboxylation (V_{cmax}), maximum rates of electron transport for RuBP regeneration (J_{max}), and biomass at the time of harvest. Droughted and well-watered plants had similar rates of A_{400}, g_{s400}, V_{cmax}, and J_{max} during the first drought under low N. High N plants were larger in size than low N plants, which suggests that the additional N likely increased the severity of the drought, causing stomatal closure and a decline in photosynthesis. However, there were increases in both V_{cmax} and J_{max} for high N plants during the first drought. There was no evidence of drought memory, and plants exposed to both droughts responded similarly to plants exposed to only the second drought. Overall, our results indicate that cotton can acclimate under drought, and additional fertilization may result in severe drought stress.

5

Title: Water footprint, runoff and soil loss assessment of cotton production in central India.

Author: B. Bhargavi a,c , D. Blaise a, , P. Nalayini b

Imprint: Cleaner Water 4 (2025) 100119

Abstract: Cotton the major crop grown on the Vertisols of central India is dependent on the monsoonal rains. Most often the high intensity rains are received in short spells and most of it is lost through runoff. Information on runoff, soil loss and water footprint (WF) of cotton grown under rainfed conditions is meagre. We determined the water runoff, soil loss, and the water footprint in a field study conducted during 2019–2022. During the study period, of the total mean annual rainfall, 47 % was effective rainfall (541 mm), and 51 % was lost through runoff. The soil loss was highest (11.5 Mg ha− 1) in the year 2022. The average annual soil loss was 8.81 Mg ha− 1. It was observed that the mean crop water use was 541 mm and 624 mm under rainfed and drip irrigated conditions, respectively. The WF of rainfed cotton was 11,339 m3 to produce 1Mg of lint. The green (WFgreen) and grey (WFgrey) WF values were 9424 and 1915 m3 Mg− 1, respectively, corresponding to 83 % and 17 % of the total WF (WFtotal). The values obtained for WFgreen, WFblue, WFgrey and WFtotal under drip irrigated cotton production were 7227, 842, 1891 and 9959 m3 Mg− 1, respectively. These values correspond to 73 %, 8 % and 19 % of the WFtotal, respectively. The blue water use in drip irrigated cotton was 50–120 mm during non-monsoon months (October to November), which resulted in 0.18 Mg ha− 1 (28 %) lint yield enhancement and 13 % WF reduction compared to rainfed cotton. Our study indicates scope for enhancing rainfed cotton production by adopting appropriate water and crop management practices making it not only profitable but also addressing the sustainable development goals.

6

Title: Advances in Micronutrients Signaling, Transport, and Integration for Optimizing Cotton Yield.

Author: Unius Arinaitwe, Dalitso N. Yabwalo and Abraham Hangamaisho

Imprint: Posted Date: 9 September 2025

doi: 10.20944/preprints202509. 0684.v1

Abstract: Micronutrients, particularly boron (B), iron (Fe), manganese (Mn), and zinc (Zn), are pivotal for cotton (Gossypium spp.) growth, reproductive success, and fiber quality, yet their roles are often overshadowed by macronutrient-focused fertility programs. This review synthesizes recent advancements in understanding the physiological, molecular, and agronomic roles of B, Fe, Mn, and Zn in cotton production, with a focus on their signaling integration and impact on nutrient use efficiency (NUE). Drawing from peer-reviewed literature, experimental data, and regional surveys, we highlight how these micronutrients regulate critical processes such as photosynthesis, cell wall integrity, hormone signaling, and stress responses, directly influencing root development, boll retention, and fiber quality. Deficiencies, exacerbated by soil pH, redox conditions, and nutrient interactions, contribute to significant yield gaps, even when macronutrients like nitrogen (N), phosphorus (P), potassium (K), and sulfur (S) are adequately supplied. Key genes, including BOR1, IRT1, NRAMP1, and GhZIP3, mediate micronutrient uptake and homeostasis, offering targets for breeding high-yield, nutrient-efficient cotton varieties. Advanced phenotyping using unmanned aerial vehicles (UAVs) and single-cell RNA sequencing (scRNA-seq) provide novel avenues for identifying nutrient-efficient genotypes and regulatory networks. The review also explores synergistic interactions between micronutrients and macronutrients to influence growth and yield of cotton. Future research directions include leveraging microRNAs, CRISPR-based gene editing, and precision nutrient management to enhance B, Fe, Mn, and Zn use efficiency, addressing environmental challenges while closing persistent yield gaps in sustainable cotton production systems.

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Title: Cotton response to row pattern and plant density: Part I—Development and yield.

Author: William J. Rutland, Brian K. Pieralisi, Darrin M. Dodds, Whitney D. Crow, G. Dave Spencer, J. Wes Lowe, Brian E. Mills

Imprint: Agronomy Journal. 2025;117:e70132. wileyonlinelibrary.com/journal/agj2 1 of 11 https://doi.org/10.1002/agj2.70132

Abstract: The ability of cotton (Gossypium hirsutum L.) to compensate for lower plant densities and 2 × 1 skip row patterns has been evaluated by numerous studies. Studies were conducted to determine if cotton yield can be maintained in a 1 × 1 skip row pattern and across plant densities to increase profit margins. Cotton growth, development, and yield were investigated in an irrigated production system in Starkville, MS, on a Leaper silty clay loam (fine, smectitic, nonacid, and thermic Vertic Epiaquepts) and in Stoneville, MS, on a Beulah very fine sandy loam (coarse-loamy, mixed, active, and thermic Typic Dystrudepts). Row patterns consisted of solid planted

and 1 × 1 skip row pattern, and plant density consisted of 37,065, 74,130, 111,195, and 148,260 plants ha−1. Skip row pattern and lower plant density reduced plant height. Total node and nodes above cracked boll were reduced as plant density increased. There was an interaction between location, year, and pattern, as well as year and plant density, with respect to yield. At three of four site years, solid row pattern produced greater yield in comparison to skip row pattern. However, row pattern and plant density had no effect on yield when pooled over location and year. Net returns varied by location and row pattern. Skip row produced a greater net return in Stoneville when compared to solid planting pattern; however, in Starkville, a greater net return was produced with solid planting pattern. Increased plant density did not increase profit margin due to increased seed costs.

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Title: Cotton response to row pattern and plant density: Part II. Boll distribution.

Author: William J. Rutland, Brian K. Pieralisi, Darrin M. Dodds, Whitney D. Crow, G. Dave Spencer, J. Wes Lowe, Brian E. Mills

Imprint: Agronomy Journal, 05 September 2025, https://doi.org/10.1002/agj2.70159

Abstract: Studies have shown cotton (*Gossypium hirsutum* L.) can sustain high yields at various row spacings and plant densities. The ability of cotton to compensate is due to boll distribution. There are numerous studies evaluating the effects of skip-row production and narrow row spacing on boll distribution. However, very little research is available evaluating the effects of wide row spacing and reduced plant density on boll distribution. Studies were conducted to determine how boll distribution is affected by plant density and row spacing. The effects of plant density and row spacing on boll distribution in cotton were investigated in Starkville, MS, on a Leaper silty clay loam (fine, smectitic, nonacid, thermic Vertic Epiaquepts) and in Stoneville, MS, on a Beulah very fine sandy loam (Coarse-loamy, mixed, active, thermic Typic Dystrudepts). Boll distribution was influenced by row spacing and plant density. As plant density increased regardless of row spacing, a greater percentage of bolls by weight are oriented toward the top of the plant. At a wider row spacing, a greater percentage of total yield occurred at positions 2, 3, 4, and 5.

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Title: Diagnosis of Farmers' Sowing Practices of Cotton (Gossypium Hirsutum L.) to Improve Plant Density per Hectare in Mali.

Author: Sissoko, S., Dembele, B., Maïga, A. D., Dembele, M., Rueff, M., & Soumare, M

Imprint: European Journal of Applied Sciences, Vol - 13(05). 80-91. Services for Science and Education – United Kingdom

Abstract: In Mali, cotton production faces a number of constraints that partly limit its yield. The low planting density is the most significant of these constraints. The objective of the study is to identify practices that are more or less suitable for improving cotton planting density in the field. A quantitative and qualitative survey of current sowing densities on farms in Mali's cotton-producing zones was carried out among 300 farmers in 20 villages. Simple descriptive statistics, frequencies or percentages, and analyses of variance were applied to the data collected to determine means, significance of differences between means, and other parameters. The results showed low densities, with an average of 44,200 plants per hectare, well below the recommended density of 83,333 plants per hectare. The best practices identified included using recent generation seed (R1) (57,600 plants/ha), fungicide treatment of the seed before sowing (56,500 plants/ha), sowing after scraping the plot (54,500 plants/ha), and sowing with a drill (53,100 plants/ha). Low densities were recorded with the use of two types of mixed seed (delinted and undelinted) (25,600 plants/ha), the use of the old seed variety NTA 90-5 (25,600 plants/ha), and children removing seedlings (27,400 seedlings/ha). The results show that the low densities are linked more to practices than to the climatic conditions often mentioned.

CROP PROTECTION

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Title: Biochemical defense responses in cotton: secondary metabolite and antioxidant shifts under thrips infestation.

Author: Sunidhi, Sucheta Sharma, Prabhjot Singla, Rimaljeet Kaur & Anju Sharma

Imprint: Phytoparasitica, Volume 53, article number 95, (2025)

Abstract: Thrips are among the most destructive pests of cotton, causing significant losses in yield and fiber quality through direct feeding. This study aimed to investigate the biochemical responses associated with thrips resistance in two cotton genotypes-LH 2107 (susceptible) and LD 491 (tolerant). Key defense-related parameters, including phenolic metabolism, antioxidant activity, and volatile compounds, were analyzed under both uninfested and thrips-infested conditions. Activities of phenylalanine ammonia-lyase and tyrosine ammonia lyase increased significantly in LD 491 during an infestation, indicating enhanced phenolic biosynthesis. Both genotypes exhibited

increased levels of total phenols, *o*-dihydroxy phenols and total flavanols from 15 days post-infestation, with LD 491 showing significantly higher concentrations than LH 2107. Antioxidant assays revealed a marked rise in DPPH free radical scavenging activity, FRAP activity, total reducing power, superoxide anion radical scavenging activity, and hydroxyl radical scavenging activity, with LD 491 demonstrating the greatest enhancement. GC–MS analysis of volatile compounds showed genotype-specific differences, with the compound palmitin, 2-mono- uniquely present in LD 491 under both conditions. These findings suggested that elevated phenolic content, antioxidant activity, and specific volatiles contribute to thrips resistance in cotton. The identified biochemical markers may serve as valuable tools for screening and breeding thrips-resistant cotton genotypes.

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Title: Changes in Cotton Cultivar Maturity, Yield, and Volatile Organic Compound Emissions in Response to Feeding by Sucking Bugs (Hemiptera: Miridae and Coreidae).

Author: Alwedyan, Malek
Imprint: https://hdl.handle.net/1969.1/1595223, 2025-26

Abstract: Cotton fleahopper (Pseudatomoscelis seriatus) and the leaffooted bug (Leptoglossus phyllopus) are key pests in upland cotton (Gossypium hirsutum) production, contributing to yield loss and delayed maturity. Management strategies currently depend on insecticide applications, but alternative control methods are needed. This research investigates how cotton cultivars with different maturation traits and volatile organic compound (VOC) emissions respond to feeding by these sucking bugs. The study assessed the response of cotton cultivars with varying maturity traits to cotton fleahopper feeding. In the no-spray subplots of a natural infestation experiment, cotton fleahopper feeding increased square abscission, resulting in yield loss and delayed boll maturation, particularly in late-maturing cultivars. In contrast, early maturing cultivars displayed higher boll opening ratio and achieved faster maturity. These findings suggest that early-maturing cultivars may be preferable in regions with high cotton fleahopper infestations. Further studies investigated whether cotton fleahopper and leaffooted bug herbivory induced VOC emissions in cotton plant reproductive parts and the role of herbivore-induced plant volatiles (HIPVs) in mediating cotton fleahopper and leaffooted bug behavior. Cotton squares damaged by cotton fleahoppers feeding emitted higher levels of (E)-Beta-ocimene, (E)-Beta-caryophyllene, and (E)-Beta-farnesene compared to the non-damaged squares. Behavioral assays indicated that (E)-Beta-ocimene alone attracted cotton fleahoppers, while volatiles from damaged squares, (E)-Beta-caryophyllene alone, and the combination of (E)-Beta-caryophyllene and (E)-Beta-ocimene repelled cotton fleahoppers. Similarly, leaffooted bug feeding on cotton bolls resulted in higher VOC emissions, including benzaldehyde, Alpha-pinene, Beta-pinene, Beta-myrcene, p-xylene, and (E)-Beta-caryophyllene, compared to non-damaged bolls. Olfactometer assays showed that benzaldehyde, Alpha-pinene, and damaged bolls attracted leaffooted bugs, potentially facilitating aggregation and host selection. Field trials evaluated the use of synthetic (E)-Beta-caryophyllene and (E)-Beta-ocimene, individually and in combination, to assess their effectiveness in attracting or repelling cotton fleahoppers. The trials used different trap designs and concentration levels to increase the effectiveness of the compounds and manipulate cotton fleahopper behavior. However, (E)-Beta-caryophyllene and (E)-Beta-ocimene did not significantly influence cotton fleahopper behavior. Overall trap capture rates were low, which may have resulted from an inconsistent release rate from the dispenser or ineffective trap placement in the field. This research highlights the potential benefits of selecting early-maturing cotton cultivars and presents additional reasoning for their planting. It also explores the use of certain HIPVs as attractants or repellents to manage populations of cotton fleahopper and leaffooted bugs in cotton fields.

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Title: Efficacy of *Metarhizium anisopliae* and *Purpureocillium lilacinum* isolates in the control of *Meloidogyne incognita* race 3 in cotton.

Author: Bruno Scentinela, Jacintho Paes, , Henrique Roberto de Araújo,

Claudio Marcelo Gonçalves de Oliveira, José Eduardo Marcondes de Almeida

Imprint*: Pesqui. Agropecu. Trop.*, Goiânia, v. 55, e83171, 2025

Abstract: Plant-parasitic nematodes such as *Meloidogyne incognita* cause severe damage to the cotton root system, impairing plant development and yield. The use of fungi-based nematicides presents a sustainable and promising alternative for nematode management. Two greenhouse experiments were conducted to evaluate the efficacy of isolates of the *Metarhizium anisopliae* and *Purpureocillium lilacinum* entomopathogenic fungi in controlling *M. incognita*, in TMG91WS3 cotton cultivar. The experiment 1 included 12 treatments: one inoculated control, four *M. anisopliae* isolates and seven *P. lilacinum* isolates, with four replicates. At 162 days after sowing, all treatments significantly reduced the final population of *M. incognita*, except *M. anisopliae* IBCB Ma03. The *P. lilacinum* IBCB Pl06 and *M. anisopliae* IBCB Ma04 isolates were the most effective, with reproduction factors below 1 and efficiency close to 80 %. The experiment 2 included 11 treatments: one control, four *M. anisopliae* and six *P. lilacinum* isolates, with six replicates. After 97 days, only the IBCB Pl06 isolate differed from the control in the final population variable, although all tested isolates, except *M. anisopliae* IBCB Ma03, showed positive efficacy for the *P. lilacinum* (> 90 %) and *M. anisopliae* IBCB Ma04 (85 %) isolates.

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Title: Identifying key meteorological factors influencing density-dependent dynamics of major sucking pests and natural enemies in cotton (*Gossypium hirsutum* L.) fields in India.

Author: Rishi Kumar, Debashis Paul, Satpal Singh & Rupinder Singh Cheema

Imprint: Discover Agriculture, Volume 3, article number 162, (2025)

Abstract: The density-dependant relationship between the pest and their natural enemies is well documented but the regulation process is influenced by other associated meteorological factors as well. Here meteorological factors influencing the interaction of major sucking pests and natural enemies in cotton fields was studied to evaluate the effect of the natural enemies (NEs) and meteorological factors on the major sucking pests (MSP) populations. A study conducted for 10 years to monitor the dynamics of the major sucking pests (Whitefly, *Bemisia tabaci*; Thrips, *Thrips tabaci;* and Leaf hopper, *Amrasca devastans*) and the natural enemies (Ladybirds Beetle: *Coccinella sp*, Lacewings: *Chrysoperla* sp. and Spiders: *Neoscona theisi* as dominant species) particularly the generalist predators on different cotton cultivars showed an interesting relationship notably, As the MSP population increased; there was a corresponding increase in the NE population after a time lag indicating additive impact of climate variables. The increasing trend in the population of NE was recorded 2–3 weeks after the peak attained by MSP during the majority of the years. The overall correlation analysis was based on 10 years of observations; it was noted that the major sucking pest population was positively correlated with minimum temperature, morning relative humidity and evening relative humidity whereas the natural enemies' population showed a significant negative correlation with maximum and minimum temperature. Principal component analysis depicted a close association of natural enemies with morning relative humidity whereas major sucking pest population was closely associated with minimum temperature and evening relative humidity. This study unveiled that the dynamic interaction between the MSP population and the NE population might be influenced by climate factors and also by the interrelationship among major sucking pests and natural enemies.

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Title: Response Mechanism of Cotton GhDMT7 Gene to 5-azacytidine.

Authors: YANG, Zhining; LU, Xuke; FAN, Yapeng; SUN, Yuping; YU, Xin; WANG, Liang; GAO, Yongjian; Habuli, Gulijiayinashen; Nasiyi, Gulishaxi; Abudu, Wumuer; HUANG, Hui; ZHANG, Menghao; WANG, Lidong; CHEN, Xiao; XIAO, Lei; ZHANG, Xinrui; WANG, Shuai; CHEN, Xiugui; WANG, Junjuan; GUO, Lixue

Imprint: Journal of Agricultural Science & Technology (1008-0864), 2025, Vol 27, Issue 8, p28

Abstract: To investigate the effects of 5-azacytidine (5-azaC) on the expression of the GhDMT7 gene and seed germination of cotton (Gossypium hirsutum L.), this paper analyzed the expression level of GhDMT7 and the growth traits of cotton seed. The GhDMT7 gene was cloned and performed comprehensive bioinformatics analysis. The results showed that GhDMT7 protein was a stable hydrophilic protein with no signal peptide and transmembrane domains. Under salt stress conditions, the malondialdehyde content in cotton leaves increased, indicating exacerbated membrane damage. 5-azaC exhibited a dosage effect on GhDMT7 expression with slightly up-regulated expression at low dosage and down-regulated expression at high dosage and decreased 5-methylcytosine (5mC) content. Furthermore, the treatment with 50 μmol ·L-1 5-azaC significantly enhanced seed germination potential and growth parameters, which promoted seed germination. Above results laid a foundation for further studying the function of GhDMT7 on cotton growth and development and provided genetic resources for breeding new varieties of saline-resistant cotton.

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Title: Dominance and Heterotic Effects for Boll Number And Boll Weight in Upland Cotton Hybrids.

Author: A. Azimov, A. Khatamov , S. Nabiev, J. Shavkiev, S. Khamdullaev, Sh. Kuziev, D. Sultonova, and T. Maimaiti

Imprint: SABRAO Journal of Breeding and Genetics 57 (4) 1575-1583, 2025 http://doi.org/10.54910/sabrao2025.57.4.23

Abstract: The succeeding study sought to determine the mean performance of parental cultivars and heterotic effects in F1 hybrids of upland cotton (Gossypium hirsutum L.). Six parental genotypes (Guliston, ANBoyovut-2, Buxoro-102, Yuksalish, Shodlik-11, and Kelajak) underwent crossing to develop 30 complete diallel F1 hybrids and evaluation in comparison with the standard cultivar (Guliston). The experiment layout in a randomized complete block design (RCBD) had three replications. Analysis of variance revealed significant differences among the parental genotypes and F1 hybrids for most traits, except the staple length. The F1 hybrids Guliston × AN-Boyovut-2 and AN-Boyovut-2 × Buxoro-102 produced the most bolls per plant, while the F1 hybrids Guliston × Yuksalish, Guliston × AN-Boyovut2, and Shodlik-11 × AN-Boyovut-2 showed the maximum boll weight. Parental genotype performance individually did not reliably predict hybrid performance, indicating the complex genetic interactions in F1 hybrids. The heterosis analysis showed the hybrids Guliston × AN-Boyovut-2 and AN-Boyovut-2 × Buxoro-102 exhibited relative heterosis exceeding 15%–20% and heterobeltiosis above 10%–15% for bolls per plant and boll weight, respectively. The considerable heterotic effects in the F1 hybrids for bolls per plant and boll weight suggest that utilizing heterosis breeding could be effective.

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Title: Genic Male Sterility in Cotton: Post-Meiotic Microspore Abortion as a Decisive Factor.

Author: V. Deepa Dharsini, A. Subramanian, N. Premalatha, N. Manikanda Boopathi, M. Djanaguiraman & V. P. Santhanakrishnan

Imprint: Russian Journal of Plant Physiology, Volume 72, article number 196, (2025)

Abstract: Hybrid cotton can be effectively developed by exploiting genetic male sterility (GMS). Establishing male sterile (MS) lines is a significant challenge in plant breeding programmes for F_1 hybrid development. A comprehensive look into the cellular mechanism behind GMS is important, since it is still unclear. To better understand the mechanisms of male sterility in a GMS line of *Gossypium hirsutum* (GMS 4), morphological, cytological and histological analyses of anthers were performed. The results indicate that phenotypic differences between fertile and sterile anthers were anther dehiscence and atrophy. Scanning Electron Microscope (SEM) observations indicate concave, atrophied anthers and immature microspores in the sterile anther's pollen sacs. The histological study indicates that in the early uninucleate microspore stage, the microspores were degenerated, leading to no pollen formation. Pollen staining experiments showed that fertile pollens had active mitochondria, dense cytoplasm, high quantities of starch in the cytoplasm and callose in the pollen wall. The primary cause of sterility in the GMS line is post-meiotic delayed callose degradation and microspore degeneration. The cellular level understanding of the GMS presented in this study will be helpful in developing the MS lines for hybrid breeding.

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Title: Cotton Cultivar M-5027 with Agrotechnology and its Relationship with Productivity in the Turkestan Region, Kazakhstan S.

Author: P. Makhmadjanov, B.M. Amirov, L.K. Tabynbayeva, A.K. Kostakov, K.K. Kulymbet , A.M. Tagaev , And D.S. Makhmadjanov

Imprint: SABRAO Journal of Breeding and Genetics 57 (4) 1399-1410, 2025 http://doi.org/10.54910/sabrao2025.57.4.6

Abstract: The cotton (Gossypium hirsutum L.) crop is a priority sector of agriculture in the Turkestan Region, Kazakhstan. An evaluation of the cotton cultivar Maktaaral-5027's response took place for nine variants comprising different doses of nitrogen, phosphorus, and potassium under two soil backgrounds (slightly saline and medium saline). The study occurred at the Agricultural Experimental Station of Cotton and Melon Growing, Turkestan, Kazakhstan. Fertilizers used included ammonium nitrate (34%), double superphosphate (45%), and potassium sulfate (51%), which were applied in one step before sowing the cotton crop for deep cultivation. The fertilizer application revealed some patterns in the formation of seed cotton yield. In the variant combining triple doses of nitrogen with double doses of phosphorus and potassium (N150P100K80) under low soil salinity, the seed cotton yield was higher, reaching 6.49 t/ha of raw cotton. On a slightly saline background, nitrogen fertilizers increased the raw cotton yield to 18.3% and 28.8% in variants with double (N100P100K80) and triple (N150P100K80) doses compared with medium doses of phosphorus and potassium.

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Title: Performance Assessment of Three Cotton Varieties under the Coastal Region of Bangladesh.

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Imprint: Journal of Agroforestry and Environment Volume 18, Issue 2, 2025 Journal DOI: https://doi.org/10.55706/jae

Abstract: Cotton (Gossypium spp.) is an important cash crop in Bangladesh and serves as the primary raw material for the textile industry. Growth and development, yield and fiber quality of cotton production are negatively impacted by excessive soil salinity. To ensure effective cotton production, it is crucial to select varieties that are well-suited to the coastal area. The research was conducted at the farming field of the research field in the Department of Agriculture, Noakhali Science and Technology University, Noakhali, Bangladesh, during the period of November 2024 to May 2025. The main objective was to evaluate the three cotton varieties that are suited for cultivation in coastal areas. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Plant height (169.39 cm), branch number per plant (18.66), initial flower opening (67.43 days) and yield contributing parameters such as balls per plant (23.46), ball length (5.16 cm), ball diameter (15.94 cm), weight of individual cotton ball (4.77 g), yield per plant (111.99 g), yield per plot (2239.82 g) and yield per hectare (7.47 t ha-1) all the studied parameters performed better in the hybrid variety Rupali-1, followed by Shuvra-3. On the other hand, inbred cotton varieties such as CB-15 are inferior to hybrid varieties. Hybrid varieties outperform in traits like ball size, branching, and early flowering, benefiting from genetic diversity and improved physiological efficiency. The findings of the experiment indicated that hybrid varieties performed better in all the parameters than inbred varieties in coastal areas. Therefore, it can be concluded that, hybrid varieties Rupali-1 and Shuvra-3 may be suitable for cultivating in coastal regions of Bangladesh

PLANT BIOTECHNOLOGY

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Title: Genome-wide identification analysis of aldo–keto reductase gene family in cotton and *GhAKR40* role in salt stress tolerance.

Author: Yiman Liu, Qiankun Liu, Yuqing Hou, Guangxing Zhang, Jiangping Han, Zhaoguo Li, Aziz Khan, Zhongli Zhou, Xiaoyan Cai

Imprint: Functional & Integrative Genomics, Volume 25, article number 187, (2025)

Abstract: In this study, a comprehensive genome-wide identification and analysis of the aldo–keto reductase (AKR) gene family was performed to explore the role of *Gossypium hirsutumAKR40* under salt stress in cotton. A total of 249 AKR genes were identified with uneven distribution on the chromosomes in four cotton species. The diversity and evolutionary relationship of the cotton AKR gene family was identified using physio-chemical analysis, phylogenetic tree construction, conserved motif analysis, chromosomal localization, prediction of cis-acting elements, and calculation of evolutionary selection pressure under 300 mM NaCl stress. The real-time qPCR showed that genes encoding members of the aldo–keto reductase (AKR) family in *Gossypium hirsutum* displayed distinct expression patterns various stress treatments. Specifically, the expression levels of certain genes were significantly upregulated under drought and salt stress. Notably, the role of *GhAKR40* gene in salt stress tolerance was validated using virus-induced gene silencing (VIGS) technology in cotton. The *GhAKR40*-silenced plants experienced leaf wilting under salt stress compared with wild-type and null-control plants. In addition, a series of physio-biochemical such as DAB staining and measurement of RWCL (relative water content in leaves) indexes also indicated that silencing of the *AKR40* gene reduced the salt tolerance in cotton. Transcriptome sequencing and analysis of the VIGS-silenced lines suggest that *GhAKR40* may enhance salt tolerance in cotton plants by potentially participating in plant-pathogen interactions and the MAPK signaling pathway, thereby modulating both pathways. These data demonstrate that *GhAKRs* play a significant role in salt stress tolerance. *GhAKR40* functions as a positive regulator with a significant impact on stress tolerance. This study not only establishes a theoretical foundation for the comprehensive utilization of resistant germplasm resources in cotton but also paves the way for further exploration of resistance genes in the species.

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Title: Molecular evolution of the bZIP family in allotetraploid *Gossypium* and GhbZIP017 function under drought stress.

Author: Fangting Ye,Jing He, Zhaowei Li, Huanyu Wu, Ziyou Zhang,Dan Fu, Yanchun Li, Jinwen Huang, Changlan Zhu & Kai Fan

Imprint: Plant Cell Reports, Volume 44, article number 229, (2025)

Abstract: The basic leucine zipper (bZIP) transcription factors are widely distributed in plants, but the evolutionary history is still unclear in allotetraploid *Gossypium barbadense* and *Gossypium hirsutum*. In this study, 203 bZIP members were identified in each *G. barbadense* and *G. hirsutum*. The bZIP members could be further divided into 13 subfamilies. A total of 227 gene duplication events were discovered in two allotetraploid cotton species and mainly occurred in the cotton ancestor. Furthermore, the bZIP family had a conserved evolutionary history in two allotetraploid cotton species. Meanwhile, the bZIP members had tissue-specific expression levels. Moreover, through the RNA-seq analysis, GhbZIP017 from the A subfamily played an important role in drought stress response. GhbZIP017 was localized in the nucleus and acted as a transcriptional repressor. The expression levels of *GhbZIP017* in leaves and roots could be highly induced by drought stress. *GhbZIP017* overexpression in Arabidopsis could enhance drought tolerance with a higher survival rate, lower membrane ion leakage, higher SOD and POD activity, lower MDA content, and higher expression levels of some drought-related genes. Overall, these results could help us uncover the evolutionary history of the bZIP members in cotton and provide a candidate gene GhbZIP017 for drought breeding in *G. hirsutum.*

SEED SCIENCE AND TECHNOLOGY

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Title: Nutritional Composition, Fatty Acid Profile, and Biochemical Characteristics of Six Varieties of Cotton (Gossypium hirsutum L) Seed, and Cottonseed Oil Cultivated in Northern Nigeria.

Author: Dangana, M. C., Falusi, O. A., Daudu, O. A. Y., Abubakar, A., Audu, M. A. I., & Gado, A. A

Imprint: Journal of Applied Sciences and Environmental Management, 29(9), 2884–2891. https://doi.org/10.4314/jasem.v29i9.25

Abstract: Although *Gossypium hirsutum* oil is ranked among the top six vegetable oils globally, however, in Nigeria, *G. hirsutum* oil remains underexploited and underutilized. Consequently, the objective of this paper was to evaluate the nutritional composition, fatty acid profile, and biochemical characteristics of six varieties of cotton *(Gossypium hirsutum* L) seed, and cottonseed oil cultivated in northern Nigeria using appropriate standard procedures. The results revealed notable differences in the characters examined among the six varieties. SAMCOT-8 had the highest ($p < 0.05$) seed protein content (22.17 %), while SAMCOT-12 recorded significantly higher fibre (17.00 %), carbohydrate (60.87 %), and magnesium (72.46 %) contents. SAMCOT-13 revealed the highest arachidic (1.76 %) and palmitic acid (10.74 %) levels, and SAMCOT-11 had the highest ($p < 0.05$) oil content (18.00 %), oxalic acid (5.71 %), and linoleic acid (12.72 %) contents. Significant variability was also observed in the physical properties of the oil across the six cotton varieties, except for specific gravity, which showed no significant difference ($p > 0.05$). These attributes could be exploited for the improvement of various traits by cotton breeders and researchers in future cotton breeding programs.

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Title: Combining Ability Studies for Seed Cotton Yield and Its Components in Desi Cotton (Gossypium arboreum L.).
Author: B Borgaonkar , A.H Rathod , A.B Jadhav , V.N Chinchane , S.N Devkule

Imprint: Journal of Advances in Biology & Biotechnology, 2025, 28 (9), pp.1214-1226. ⟨hal-05249234⟩

Abstract: The present investigation was taken up to study the general combining ability of parents and the specific combining ability of crosses for seed cotton yield and yield contributing traits. Design: In the present investigation, six lines were crossed with five testers to get thirty hybrids in a Line x Tester mating design. The sum total of thirty crosses, eleven parents with one check, were evaluated in a randomized block design with two replications. Place of study: The research work was carried out during Kharif 2024 at Cotton Research Station, Mahboob Baugh Farm, VNMKV, Parbhani. Methodology: The crosses were made using the LineXTester mating design. The analysis was carried out in a randomized block design. The observations were recorded on twelve seed cotton yield and yield contributing and fibre characters viz., days to50 per cent flowering, plant height(cm), number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), days to maturity, ginning outturn (%), Upper half mean length(mm), fibre fineness/micronaire value (g/inch), fibre strength (g/tex) and uniformity ratio Results: Analysis of variance for the mean sum of squares revealed significant differences for all twelve characters examined. The male parental line PA 08 was found to be a good general combiner for the number of sympodia, the number of bolls per plant, boll weight, and seed cotton yield/plant. The male parental line PA 402 was found to be a good general combiner for days to 50 per cent, plant height, boll weight, seed cotton yield/plant, ginning outturn, and fibre fineness. The male parental line PA 812 was found to be a good general combiner for upper half mean length and uniformity ratio, whereas AKA 2016-3 was a good general combiner for upper half mean length and fibre strength. The cross combinations PA 08 X PA 955, PA 812 X PA 950, and JLA 505 X PA 960 exhibited significant and desirable specific combining ability effects for most of the yield and its contributing traits. Conclusion: The hybrid JLA 505 X PA 785 found a superior specific cross combination for fibre quality traits studied, indicating its potential for exploiting specific combining ability for enhancing seed cotton yield in the cotton breeding programme.

FIBER AND FIBER TECHNOLOGY

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Title: Advances in Genetic Mapping of Cotton for Yield, Fiber Quality, and Stress Resistance.

Author: Ayesha Khawar, Ghalib, M. A. B., Asad Sultan, Jareer Abdullah, Waqas Mushtaq, Ashir Masroor, & Ahsan Raza

Imprint: *International Journal of Agriculture Innovations and Cutting-Edge Research (HEC Recognised)*, *3*(3), 95–108. Retrieved from https://jai.bwo-researches.com/index.php/jwr/article/view/159

Abstract: Cotton (Gossypium spp.) is a major global cash crop providing natural fibre and supporting textile and agriculture industries. However, its productivity is negatively impacted by pests, diseases, and abiotic stresses, which are inadequately addressed by conventional breeding. Recent advances in genome sequencing and molecular breeding offer new opportunities to improve fibre quality and stress resistance. This review highlights the role of genetic mapping, quantitative trait locus (QTL) analysis, and marker-assisted selection (MAS) in uncovering genes linked to key traits. High-throughput sequencing and genome-editing approaches, particularly CRISPR/Cas9, enable precise improvement of cotton genomic characteristics. Integration of high-density molecular markers with genomic selection accelerates breeding program by enabling early trait identification. Studies demonstrate that combining traditional breeding with genomics reduces the limitations of polyploidy and genetic bottlenecks, while enhancing yield stability under stress. Future directions include wider adaptability of genome-assisted breeding, functional genomics, and high-throughput phenotyping to strengthen cotton resilience against climate variability and biotic challenges. This review concludes that genomics-integrated breeding can deliver long-term improvements in fibre quality, productivity, and stress tolerance, thereby supporting sustainable cotton production.