



GLEANINGS IN COTTON RESEARCH

OCTOBER 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.

*Chetali Rodge
In charge Library*

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Title: Effects of compound microbial fertilizer combined with potassium fulvic acid on soil physicochemical properties, microbial community structure, and cotton productivity in saline-alkali soil

Authors: Zeyu Wang, Yingjie Ma, Xingwang Ma, Hongbin Liu & Shenghai Pu

Imprint: *Sci Rep* 16, 30520 (2026). <https://doi.org/10.1038/s41598-026-57729-2>

Abstract: To explore the effects of compound microbial fertilizer (containing *Lactobacillus acidophilus* and *Corynebacterium glutamicum*) combined with potassium fulvic acid on cotton growth and soil ecology in Xinjiang saline-alkali soil, a two-year field experiment with seven treatments was conducted in a randomized block design. We analyzed cotton emergence rate, yield components, rhizosphere soil physicochemical properties (pH, water-soluble salts, major ions), and soil microbial community structure using high-throughput sequencing. Results showed that HT5 (150 L·hm⁻² microbial fertilizer + 15 L·hm⁻² potassium fulvic acid) significantly increased cotton emergence rate to 85.00%. HT4 (120 L·hm⁻² microbial fertilizer + 15 L·hm⁻² potassium fulvic acid) achieved the highest yield increase of 13.31% compared with the fulvic acid-only control. Application of microbial fertilizer effectively reduced soil pH, water-soluble salt, Cl⁻, and Na⁺ contents, and the improvement effects were enhanced with increasing application rate. Bacterial diversity was relatively stable among treatments, while fungal diversity and the relative abundance of beneficial fungi such as *Pseudeurotium* and *Mortierella* increased significantly. Overall, compound microbial fertilizer combined with potassium fulvic acid improved soil physicochemical conditions, optimized rhizosphere microbial community structure, and enhanced cotton growth and yield under saline-alkali conditions. The HT4 treatment was identified as the optimal application scheme under the experimental conditions, providing a feasible strategy for high-quality and high-yield cotton production in Xinjiang saline-alkali soils.

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Title: Synergistic impact of cotton-legume intercropping and integrated weed management on soil health and productivity

Authors: Bishan Singh¹, V S Hooda¹, Todar Mal Poonia¹, Ramesh Kumar¹, Harender Dagar^{2*}, Arti Yadav² & Anamika Singh²

Imprint: PLANT SCIENCE TODAY Vol 13(sp5): 01-07
<https://doi.org/10.14719/pst.15324>

Abstract: Cotton is a globally important crop that serves as a major source of fibre and edible oil while supporting millions of livelihoods. With increasing demand for sustainable materials, improving cotton productivity in an eco-friendly way has become essential. One promising approach is the integration of legume intercropping with efficient weed management to reduce the potential yield loss of up to 86 % caused by weed competition. A two-year field experiment during 2021 and 2022 at Agronomy Research Farm, Chaudhary Charan Singh (CCS) Haryana Agricultural University, Hisar, Haryana, India, assessed the impact of various management practices on cotton yield, economic returns and soil health. Using a split-plot design, the study contrasted monoculture cotton with a cotton + green gram (1 : 2) intercropping system under 11 weed management treatments. Results revealed that sole cotton recorded greater plant height (177.05 cm) and dry matter accumulation (427.40 g plant⁻¹). However, intercropping with green grams significantly improved soil fertility, with higher available nitrogen (N) (126.7 kg ha⁻¹) and phosphorus (P) (17.6 kg ha⁻¹) observed at harvest. Among the weed management treatments, the weed-free treatment recorded the highest seed cotton yield (26.64 q ha⁻¹), followed by two hoeings at 25–30 and 40–45 days after sowing (24.20 q ha⁻¹). Notably, the integrated application of pendimethalin (1000 g ha⁻¹, PRE) followed by single hoeing at the 35–40 days proved highly effective, increasing seed cotton yield by approximately 40 % compared with herbicide use alone. Cotton-legume intercropping enhances soil fertility and profitability. Combining chemical and cultural weed management practices ensures better weed control, improved productivity and sustainable soil health.

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Title: Conventional manure and bio-organic fertilizer application improve soil quality and cotton yield through distinct enrichment of beneficial microorganisms in arid saline areas

Authors: Haotian Gong^a, Yunshu Zhang^b, Guangmu Tang^b, Hui Zhai^a, Maoxin Chen^b, Wanli Xu

Imprint: Applied Soil Ecology, Volume 228, 2026, 107495,
ISSN 0929-1393,
<https://doi.org/10.1016/j.apsoil.2026.107495>.

Abstract: Crop yield is significantly influenced by the application of different types of organic fertilizer. However, under equivalent carbon input conditions, the mechanisms through which different organic fertilizer types affect soil properties and cotton (*Gossypium hirsutum* L.) yield in arid saline soils remain unclear. Therefore, this study aimed to investigate the effects of conventional manure and bio-organic fertilizer application on soil properties and cotton yield in severe saline-alkali soil of arid regions. Based on equivalent carbon input, a field experiment was conducted with five treatments (no organic fertilizer application (CK), application of 37.5 t ha⁻¹ (COF1) and 52.5 t ha⁻¹ (COF2) conventional manure, 18 t ha⁻¹ (BOF1) and 25.5 t ha⁻¹ (BOF2) bio-organic fertilizer). Results showed that compared with CK, the COF2 and BOF2 treatments reduced surface soil soluble salt content by 13.77% and 13.17%, respectively, and increased cotton yield by 57.94% and 51.51%, respectively. These improvements were attributed to enhanced soil aggregate stability and promoted leaching of soil salts. Concurrently, fertilization increased the content of soil available nitrogen and potassium. Notably, BOF was superior to COF in improving soil aggregate stability, whereas COF outperformed BOF in enhancing soil available nutrients. This was primarily attributed to the distinct enrichment of beneficial microorganisms in the cotton rhizosphere by COF and BOF treatments. Specifically, the enrichment of Pseudomonadota may promote soil nutrient activation, while the enrichment of Actinomycetota may improve soil aggregate stability. This study provides a theoretical basis for ameliorating saline-alkali soils and enhancing crop yield in arid regions.

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Title: Moderate nitrogen reduction enhances cotton yield and nitrogen use efficiency via early flowering root exudate–rhizosphere interactions

Authors: Zihui Shen, Mengjuan Liu, Yunzhu He, Xiaoxiao Liu, Hushan Wang, Yao Yang, Qian Zhang, Wangfeng Zhang & Xiaozhen Pu

Imprint: Plant Soil (2026). <https://doi.org/10.1007/s11104-026-09169-0>

Abstract: Background and aims: High nitrogen (N) inputs and low nitrogen use efficiency (NUE) remain critical constraints in cotton production. This study aimed to identify an optimal reduced N rate and to elucidate whether early flowering root exudates mediate rhizosphere N transformations to sustain yield.

Methods: A pot experiment was conducted with four N rates: N1 (conventional N, 0.240 g kg⁻¹), N2 (15% reduction, 0.204 g kg⁻¹), N3 (30% reduction, 0.168 g kg⁻¹), and N4 (0 N). Root exudates were collected at early flowering. Soil N transformation

indicators, enzyme activities, microbial biomass, root morphological traits, plant N accumulation, seed cotton yield and root exudate metabolites were measured.

Results: Compared with N1, moderate N reduction (N2) increased seed cotton yield per plant by 14.7%, N partial factor productivity by 34.9%, and N agronomic efficiency by 38.7%. N2 promoted a compact, dense root system with higher root tissue density, reflecting carbon (C) reallocation from elongation to structural reinforcement. Root exudate profiles shifted under N2, with proline and hypoxanthine as the dominant responsive metabolites. These metabolites were associated with altered rhizosphere enzyme activities and enhanced microbial biomass N retention. Such metabolic-functional associations suggest that early flowering root exudates couple yield formation to soil N transformation and plant N acquisition, potentially via microbial N turnover linked to rhizosphere C metabolism.

Conclusion: Early flowering represents a critical window for rhizosphere intervention. Proline and hypoxanthine are key exudate metabolites coordinating N cycling, plant N acquisition and yield formation under moderate N reduction.

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Title: Climate drivers of mesophyll conductance: temperature and water deficit alter CO₂ diffusion and leaf anatomy in cotton

Authors: Demi Sargent^{1,2}, Warren C. Conaty², Kelly Chapman³, Garima Dubey¹, Laurel George⁴, Sue Lindsay⁵, Richard Wuhrer⁴, Susanne von Caemmerer³, John R. Evans³ and Robert E. Sharwood

Imprint: New Phytologist (2026) doi: 10.1111/nph.71602

Abstract: Mesophyll conductance (gm) limits CO₂ delivery to Rubisco, yet its responses to temperature, heat and water deficit are poorly resolved in cotton (*Gossypium hirsutum*). We characterised photosynthetic and gm temperature responses in five *Gossypium* species, then examined cultivated *G. hirsutum* and the Australian native *Gossypium bickii* under combined elevated temperature and soil water deficit to link physiological responses with mesophyll anatomy.

Plants were grown under controlled glasshouse conditions. We quantified gm using simultaneous gas exchange and online stable carbon isotope discrimination (D, &) and measured leaf anatomy.

Across species, photosynthesis and gm exhibited broad thermal optima (33–36°C). In *G. hirsutum*, water deficit at control temperature reduced gm and induced thicker, more porous mesophyll and thicker cell walls, while assimilation declined only under combined heat and water deficit. In *G. bickii*, gm and assimilation remained stable

under combined stress, and gm was stimulated by elevated temperature without anatomical adjustment.

gm emerged as a stress-sensitive trait in cultivated cotton, whereas *G. bickii* exhibited stress resilience, with responses incompletely explained by anatomical acclimation. Further research on gm responses to environmental stresses and on the mechanisms underpinning these responses is required to inform model development and identify traits for climate resilient crops.

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Title: The cotton transcription factor YP positively regulates petal size by enhancing brassinosteroid-dependent cell expansion

Authors: Lingfang Ran a, Nan Zhao a, Weiran Wang a, Meng Wang a, Jianping Li a, Zixin Zhou a, Yifan Wang a, Caixia Li a, Yahui Deng a, Yang Jiao a, Jiahui Zhu a, Zhiqing Liu a, Jie Kong a, Alifu Aierxi a, Yuehua Xiao a b, Yaohua Li

Imprint: Plant Physiology and Biochemistry, Volume 239, 2026, 111841, ISSN 0981-9428, <https://doi.org/10.1016/j.plaphy.2026.111841>

Abstract: Petal size is crucial for both ornamental appeal and reproductive success in flowering plants, yet the molecular basis of its variation in many non-model species, including cotton, remains poorly understood. Here, we defined the period from –1 DPA to 0 DPA (10:00) as the rapid elongation phase for cotton (*Gossypium hirsutum*) petals. Disruption of R2R3-MYB gene GhYP in cotton prematurely arrested petal development (by 06:00 on 0 DPA) and reduced petal size through restraining epidermal cell expansion, whereas ectopic expression of its *G. arboreum* homolog GaYP in tobacco enlarged petals by promoting cell expansion. Transcriptome and metabolome profiling of cotton petals across developmental stages revealed down-regulation of brassinosteroid (BR) biosynthesis genes in ghyp petals, coinciding with markedly reduced levels of bioactive castasterone (CS) and its upstream intermediates. Exogenous application of 24-epibrassinolide (24-EBL), a bioactive BR compound, rescued the small-petal phenotype of the ghyp mutant by significantly enlarging its petal epidermal cells. Furthermore, dual-luciferase (Dual-LUC) and yeast one-hybrid (Y1H) assays demonstrated that GhYP modulates the expression of multiple BR biosynthesis genes without detectable direct promoter binding. Collectively, these findings establish that YP transcription factors (GhYP and GaYP) promote epidermal cell expansion by enhancing BR biosynthesis, thereby increasing petal size. Our work will advance understanding of the genetic basis of cotton petal development.

Title: Co-application of sodium nitroprusside and melatonin enhances root-shoot recovery without additional lint-yield gain in waterlogged cotton

Authors: Lixia Dong a 1, Weitian Kong a 1, Yu Su c, Hongchun Sun a, Guangyu Cheng a, Dongmei Zhang b, Shizhen Xu b, Zhenhuai Li b, Yanjun Zhang a b, Ke Zhang a, Hezhong Dong

Imprint: Plant Stress, Volume 24, 2026, 101580,
ISSN 2667-064X, <https://doi.org/10.1016/j.stress.2026.101580>.

Abstract: Waterlogging during flowering disrupts root metabolism, leaf source activity and reproductive yield formation in cotton. Sodium nitroprusside (SNP), a commonly used experimental nitric oxide (NO) donor, and melatonin (MT) can alleviate waterlogging injury, but whether their co-application provides an agronomic advantage over either regulator alone under field conditions remains unclear. A two-year field experiment was conducted with five treatments: non-waterlogged control, waterlogged control, and waterlogged cotton sprayed with SNP, MT, or SNP plus MT during a 10-d waterlogging episode at early flowering. Waterlogging reduced total dry matter, boll density, seed cotton yield and lint yield by 17.6%, 23.7%, 26.1% and 27.6%, respectively. Relative to waterlogging alone, co-application increased biological yield by 18.5%, exceeding the increases under SNP (9.6%) and MT (10.3%) alone. However, its seed cotton and lint yields were not significantly greater than those under either single treatment. Waterlogging reduced root and leaf NO contents by 57.2% and 47.3%, approximately doubled root hydrogen peroxide (H₂O₂) and malondialdehyde (MDA) contents, and increased root alcohol dehydrogenase (ADH) and pyruvate decarboxylase (PDC) activities by 75.5% and 84.2%, respectively. Co-application increased root and leaf NO contents by 63.1% and 41.5%, increased root MT content by 70.3%, and reduced root H₂O₂, MDA, ADH and PDC by 22.8%, 32.8%, 28.0% and 27.3%, respectively, relative to waterlogging alone. These root responses were accompanied by improved leaf redox status, chlorophyll retention, photosynthetic activity, hormone status and the expression of selected stress-response marker genes. Thus, SNP plus MT broadened root-shoot physiological protection and biomass recovery, but the additional biomass was not proportionally converted into lint. These findings identify an important field-level boundary between physiological stress alleviation, biomass recovery and economic-yield realization, without establishing causal NO-MT crosstalk or a directly demonstrated source-sink mechanism.

Title: Effect of glufosinate-ammonium on weeds, cotton yield and soil microbes

Authors: T .U. Patel*, M.L. Patel, D.D. Patel

Imprint: [10.5958/0974-8164.2026.00051.1](https://doi.org/10.5958/0974-8164.2026.00051.1)

Abstract: The present study evaluated the response of weeds and cotton to different weed management treatments. The weeds predominant in the experimental field were: *Echinochloa crus-galli*, *Echinochloa colona*, *Digera arvensis*, *Amaranthus viridis* and *Cyperus rotundus*. The monocot weeds increased from 48.50% at 25 days after seeding (DAS) to 55.42% at 50 DAS, while dicot weeds increased to 47.00% during that period, probably due to crop growth and canopy development. The weed-free treatment [hand weeding (HW) thrice + inter cultivation (IC) at 20, 40 and 60 DAS] recorded the highest weed control efficiency (WCE) (84.70%) and seed cotton yield. The weedy check recorded cotton yield reduction of 46.53%. Pendimethalin 0.9 kg/ha followed by (fb) quizalofop-ethyl + pyrithiobac-sodium 50 + 75 g/ha and glufosinate-ammonium 350–450 g/ha combined with hand weeding and inter-cultivation at 50 DAS, effectively managed weeds recording weed control efficiency of 71.15-78.90% and cotton yield of 2.158 t/ha. Glufosinate-ammonium applied alone exhibited lower weed control efficacy (41.41-45.49%) and lesser cotton yield. Soil microbial populations showed transient suppression following herbicide application but recovered by 60 days after application indicating short-term and reversible effects. Overall, integrated weed management proved most effective in managing diverse weed flora and recording higher cotton yield.

Title: The small GTP-binding protein GhARAC3 is involved in cotton resistance to *Verticillium dahliae* by regulating lignin metabolism

Authors: Yajie Wu , Jinglong Zhou , Feng Wei , Lihong Zhao , Yalin Zhang , Zili Feng , Yong Song , Yanjun Li , Xinyu Zhang , Feng Liu , Jie Sun , Jun Zhao , Tao Zhang , Qianhao Zhu , Heqin Zhu , Hongjie Feng

Imprint: Plant Physiology, kiag734, <https://doi.org/10.1093/plphys/kiag734>

Abstract: Plant Rho/ROP GTPases act as essential molecular switches in disease resistance. However, how their protein stability is regulated and integrated with lignin metabolism remains poorly understood. Here, we demonstrate that the cotton small GTPase GhARAC3 serves as a positive regulator of resistance against the vascular

pathogen *Verticillium dahliae* (V. dahliae). Genetic analyses reveal that overexpression of GhARAC3 enhances defense responses in cotton and Arabidopsis, whereas its silencing significantly compromises plant immunity. Under normal physiological conditions, the E3 ubiquitin ligase GhKEG acts as a key regulator that targets GhARAC3 for proteasomal degradation by ubiquitinating multiple lysine residues. Notably, the lysine 161 (K161) residue within the conserved G5 motif is identified as an in vivo ubiquitination site. Mutation of this residue (K161R) impairs GTPase activity and compromises disease resistance, without altering its subcellular localization at the plasma membrane and nucleus. Pathogen infection attenuates this ubiquitination to promote the stabilization of GhARAC3. Genetic epistasis analysis indicates that GhARAC3 requires GhLAC14, a transmembrane laccase, to confer effective immunity. Rather than altering GhLAC14 protein stability, GhARAC3 physically interacts with and stimulates the enzymatic activity of the laccase. Additionally, GhARAC3 promotes reactive oxygen species (ROS) production. This dual activation of laccase activity and the ROS burst drives the rapid deposition of guaiacyl lignin to fortify the plant cell wall. Furthermore, transcriptomic profiling reveals that GhARAC3 broadly upregulates downstream defense-related pathways. Collectively, our findings uncover a regulatory module linking ubiquitin-mediated GTPase turnover to laccase activation, providing a mechanistic framework for improving cotton disease resistance.

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Title: Evaluation of Soil Quality and Cotton Productivity in Long-Term Cultivated Fields in the Southern Xinjiang Oasis

Authors: Ning Li Ning Li Songrui Ning, Weiyang Liu, Jiandong Sheng, Yuhui Yang, Tingting Huo and Yusufujiang Yasheng

Imprint: Agronomy 2026, 16(19), 1978; <https://doi.org/10.3390/agronomy16191978>

Abstract: To investigate the effects of long-term cultivation on soil physicochemical properties, cotton production and soil quality dynamics in the oases of southern Xinjiang, uncultivated and unfertilized wasteland was used as the control (CK), and cotton fields with cultivation durations of 7, 12, 21, 30 and 40 years were selected in the Tailan River oasis. Soil physicochemical properties (0–200 cm) and cotton production indicators were measured. A minimum dataset (MDS) and soil quality index (SQI) were constructed, and obstacle-factor diagnosis, partial least-squares structural equation modelling (PLS-SEM), the Mantel test and multiple linear regression were used to identify key drivers. The results indicated that the SQI in the 0–40 cm soil layer showed an increase-then-decrease pattern with different cultivation histories. Organic matter (OM), available phosphorus (AP), pH and electrical conductivity (EC) were identified as major obstacle factors for SQI improvement. PLS-SEM indicated a strong positive association between soil nutrients and SQI, whereas salinity and alkalinity were

negatively associated with SQI; cultivation duration was indirectly associated with SQI through its positive association with soil nutrients. Soil nutrients also had the strongest positive association with cotton yield, whereas salinity and alkalinity were negatively associated with yield. Reproductive organs' dry weight (RDW), available potassium (AK) and OM were the most important predictors of cotton yield. In summary, the SQI showed an increase-then-decrease pattern across sampled fields with different cultivation histories, with the highest mean in 30-year fields and a lower mean in 40-year fields. Insufficient soil nutrient supply emerged as the primary obstacle to SQI and yield in long-term cultivated fields. Synergistic improvements in cotton yield and SQI can be achieved through measures such as optimising the combined application of nitrogen and phosphorus, regulating water and salinity, increasing the application of organic fertiliser and implementing appropriate crop rotation, thereby providing a reference for soil quality management and sustainable agricultural development in arid regions.

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Title: Effects of salt stress on soil water-salt distribution and cotton yield under mulched drip irrigation

Authors: Hong-Wei Yang, Si-En Li

Imprint: Water Saving Irrigation / Jieshui Guan'gai, 2026, No. 9, 25-31 ref. 15

Abstract: Investigating the characteristics of soil water-salt transport, crop yield, and water use efficiency under salt-stressed mulched drip irrigation, and determining the suitable salt concentration of irrigation water for crop growth, are of great significance for improving water resource utilization efficiency. This paper investigated the water-salt dynamics in cotton fields under mulched drip irrigation with different irrigation water salinity concentrations, as well as cotton yield and water use efficiency (WUE), through field experiments. The results showed that the soil moisture content between drippers was significantly higher than that between belts in the 0-100 cm soil layer during the growth period of cotton, with the 40 cm soil layer reaching 32.6%, and soil salt content between drip belts in the 0-100 cm soil layer was higher than that between drippers. The treatment of irrigation water with a salt concentration of 3 g/L formed a diluted zone in the soil layer of cotton roots, with a soil salt content between 0.64 and 0.81 g/kg. The yield and WUE of cotton under the treatment of irrigation water with a salt concentration of 3 g/L were close to those under the treatment of conventional fresh water irrigation, and the yield of cotton under the treatment of irrigation water with a salt concentration of 6 g/L decreased significantly, with only 3 970.1 kg per hectare, compared to conventional freshwater irrigation, the yield reduction is about 23.5%. From the perspective of the soil water-salt environment for cotton growth,

economic benefits, and efficient utilization of saline water resources, mulched drip irrigation with irrigation water salinity not exceeding 3 g/L can ensure that the yield and WUE of cotton reach the optimal levels.

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Title: A Comparative Study of the Specific Surface Area of Some Egyptian Cotton Varieties Before and After Chemical Treatments Under Different Maturity Levels

Authors: Eman A. Bydoon, 2shimaa A. Shahat, 2abeer S. Arafa

Imprint: Textile Science & Research Journal

ISSN: 3059-846X, Volume – 2, Issue – 3, 2026

DOI: <https://doi.org/10.63456/tsrj-2-3-57>

Abstract: Purpose: The specific surface area (SSA) is an important structural feature that affects how cotton fibers interact with dyes, finishing agents, and moisture. Because SSA influences mass transfer, it is closely linked to textile processing efficiency. However, there is limited quantitative analysis of SSA across different cotton varieties, maturity levels, and treatment conditions. This study measures SSA differences among selected Egyptian cotton varieties, looks at how fiber maturity affects SSA, evaluates the impact of chemical treatments on fiber structure, and compares the reliability of two SSA measurement methods.

Design and methods: The study used three Egyptian cotton varieties: extra Giza 93 (extra-long, extra-fine staple), Super Giza 94 (long staple), and Giza 98 (long staple). All samples were homogenized and conditioned under standard conditions ($20 \pm 1^\circ\text{C}$, $65 \pm 2\%$ relative humidity). Maturity ratios were measured and grouped using an image analyzer, and samples were classified as Immature, Medium, or High maturity based on international standards. Fibers underwent scouring and mercerization, and some were dyed. SSA was measured using both the Worley method and methylene blue adsorption. Mechanical and physical properties were tested with standard textile methods. Statistical analysis determined the significance of the results.

Findings: SSA values obtained from the Worley method decreased with increasing maturity, ranging from approximately 0.85 to 1.45 m^2/g . In contrast, methylene blue adsorption yielded higher values (45–120 m^2/g), reflecting internal surface accessibility. Mercerization increased SSA by up to 35% in immature fibers. Mature fibers showed higher strength but lower accessibility. A statistically significant interaction ($p < 0.05$) was observed between fiber maturity and treatment. The results show that there exists a strong correlation between the structure of fibers, specific surface area, and their mechanical properties. A higher specific surface area, especially considering internal surfaces, helps in improving the uptake of dyeing agents and water molecules. But although high crystallinity is good for improving tensile strength, it is also responsible for reducing accessibility.

Originality/value: This study is the first comparative evaluation that integrates structural and surface characterization methods to provide a thorough understanding of SSA behavior in Egyptian cotton. It highlights the importance of selecting appropriate processing conditions based on fiber maturity to improve textile performance. These findings guide the selection of cotton varieties suitable for chemical finishing and dyeing

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Title: Performance Evaluation of Hand-Operated Seeder for Cotton Planting Under Different Tillage Practices in B

Authors: E. D. Dayou^{1,2,3*}, A. Hougni^{1,4}, C. Kanlindogbè^{1,5}, G. F. Tiando⁵, E. Sekloka^{1,5}

Imprint: Nigerian Journal of Technological Development, Vol. 23, No 2, September 2026

Abstract: Cotton farming faces challenges such as climatic variability, labor shortages and high labor costs, and a lack of suitable equipment, particularly for sowing, which prevent successful sowing within the appropriate timeframe. This study, carried out at the research station of Okpara (Parakou), aimed to evaluate the performance of an adapted hand-operated seeder under different tillage practices. A split-plot design was used to compare three tillage practices: Manual Tillage, Tractor Plough, and Strip Tillage, and two sowing methods: Hand-operated Seeder and Manual Sowing. The key indicators assessed were the sowing time, the effective daily capacity, the clogging frequency and the seedling emergence. Descriptive and two-factor analyses of variance with interaction were performed and validated after checking normality and homogeneity of residuals. Tukey's test was used to separate the means in case of a significant difference at the 5% threshold. Results showed that the hand-operated seeder had significantly lower sowing time of 2.6–3.1 h/ha, compared to 14.4–20.4 h/ha for manual sowing. Strip tillage improved sowing regularity with the hand-operated seeder, by reducing the seed hill opener clogging. Furthermore, the hand-operated seeder ensured optimal plant density (60,735–64,732 plants/ha) and emergence rates closer to the recommended two plants per hill, whereas manual sowing yielded lower. Overall, the use of an adapted hand-operated seeder, combined with the appropriate tillage practices, improves sowing efficiency and crop establishment quality in cotton farming

Title: Prevalence of plant parasitic nematodes in cotton (*Gossypium hirsutum*) in New South Wales, Australia

Authors: Duy P. Le, Chi PT. Nguyen

Imprint: Australasian Plant Pathol. 55, 121 (2026). <https://doi.org/10.1007/s13313-026-01196-w>

Abstract: Cotton (*Gossypium hirsutum* L.) is a main fibrous cash crop in New South Wales (NSW) and Queensland in Australia. The Australian cotton industry generated an annual revenue of approximately AUD 1.9 billion in export (CRDC 2018). Fungal diseases are of the major constraint with yield losses commonly reported around 10% (Otto 2020). Unlike fungal diseases, nematodes are not considered a country-wide concern although yield reduction associated directly with reniform nematode infestation of cotton was reported in Theodore, central Queensland (Smith et al. 2024). Reniform nematode (*Rotylenchulus reniformis*) was reported on cotton for the first time in 2012 (Bauer et al. 2014). To date, *R. reniformis* has not been detected outside of central Queensland (Smith et al. 2024). Other plant parasitic nematodes (PPNs) were also reported in Australian cotton fields. For example, low levels of *Tylenchorhynchus ewingi* and *Helicotylenchus dihystra* were reported from cotton in NSW in 2006, but no damage was observed (Knox et al. 2006a, b). An additional detection of a low population of *Pratylenchus* sp. in cotton soil was reported in 2020 (Knox et al. 2020). Knox et al. (2006b) speculated that limited reports of PPNs in cotton in NSW could be attributed to the high clay content of the soil. However, previous studies in NSW were limited to only two fields and were sampled only once (Knox et al. 2006a, b, 2020). Thus, we propose that the occurrence and prevalence of PPNs in cotton fields in NSW may have been underestimated. In this study, we sought to unveil the prevalence and dynamics of PPNs recovered from soil samples that were collected during our annual early and late season disease surveillance in the 2023-24 cropping season in NSW.

Title: Genetic architecture of two-spot cotton leafhopper (*Amrasca biguttula*) resistance revealed by generation-mean analysis, morpho-biochemical traits and explainable machine learning

Authors: Madhu, B., Keerthivarman, K. & Selvaraj, S.

Imprint: *Phytoparasitica* 54, 110 (2026). <https://doi.org/10.1007/s12600-026-01441-4>

Abstract: The two-spot cotton leafhopper (*Amrasca biguttula*) is a major constraint to cotton production, yet the genetic architecture of resistance and the relative contributions of morphological and biochemical defence traits remain poorly resolved. Here, we dissected the genetic basis of leafhopper resistance by integrating biometrical genetics with explainable machine learning. Six generations (P_1 , P_2 , F_1 , F_2 , BC_1P_1 , and BC_1P_2) derived from three contrasting cotton crosses-C1 (TVH002 $\times$ NDH1938), C2 (TVH002 $\times$ Suraksha), and C3 (CO17 $\times$ Suraksha)-were evaluated for leafhopper resistance under field and controlled polyhouse conditions during 2023–2024. Leafhopper abundance (NLTP), injury index (LII), susceptibility index (LSI), trichome density (TD), trichome length (TL), gossypol (GP), total free amino acids (TFA) and total protein (TP) were subjected to generation-mean, segregation, genetic variability, correlation, path and Random Forest (RF)-SHapley Additive exPlanations (SHAP) analysis. Significant scaling tests across crosses and traits revealed extensive epistasis, with dominance (h) and dominance $\times$ dominance (l) effects particularly important for NLTP, LII and LSI; complementary (9:7) and duplicate (15:1) interactions further demonstrated genetic-background-dependent inheritance. F_2 populations consistently fitted a 13:3 susceptible:resistant ratio, confirming inhibitory gene action. C2 showed the highest resistance frequency under both field (33.0%) and polyhouse (45.3%) screening, establishing the resistance ranking $C2 > C1 > C3$. LSI exhibited exceptionally high variability (PCV 93.82%; GCV 93.06%) and genetic advance (GAM 190.13%), while TL and TD recorded 99% broad-sense heritability; genetic variability ranked $C3 > C2 > C1$. TL, TD and GP showed predominantly negative contributions to NLTP, whereas TFA and TP contributed positively. RF-SHAP identified cross-specific leading predictors: TD in C1, TL in C2 and LSI in C3, with C3 achieving the highest predictive performance ($R^2 = 0.830$; OOB $R^2 = 0.863$). These findings establish leafhopper resistance as a multicomponent trait governed by dominance and epistatic interactions and provide a quantitative framework for mechanism-informed selection. C2 offers the strongest resistance background, whereas C3 provides greater segregating variability, supporting their complementary use in cotton resistance breeding.

Title: Advancing integrated pest management for thrips in cotton: integrating biopesticides, host plant resistance, and emerging molecular tools

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Imprint: Entomologia Generalis Open Access

Published online October 2026 DOI: 10.1127/entomologia/4391

Abstract: Thrips management in cotton is increasingly constrained by widespread insecticide resistance. Early-season infestation and associated yield losses have led growers to rely heavily on prophylactic insecticide seed treatments, which further exacerbate resistance development in pest populations. Although natural enemies such as minute pirate bugs and predatory mites offer biological suppression, they rarely provide adequate protection against economically damaging infestation during the seedling stage. This highlights the need for educating growers about integrated pest management (IPM), particularly as many continue to rely on input dealers and remain insufficiently informed about sustainable alternatives and bioagents. This review covers current research progress and key challenges in sustainable thrips management within the cotton-based system. The IPM approach combines cultural and biological controls with technological innovations like transgenic cotton, improved biopesticides, and drone-assisted spraying, offering viable pathways to reduce dependence on synthetic insecticides. Host plant resistance in *Gossypium hirsutum* and *Gossypium barbadense* remains vital, particularly in the context of evolving thrips resistance. Concurrently, next-generation microbial biopesticides, especially those enhanced through nanotechnology, are emerging as promising alternatives. At the molecular level, resistance mechanisms involving cytochrome P450 genes and mutations in the nicotinic acetylcholine receptor have been well documented. Furthermore, RNA interference (RNAi) combined with Bt-based approaches offers potential for disrupting insect development and delaying resistance progression. Advances in precision agriculture, driven by artificial intelligence and predictive analytics, are further improving pest surveillance and decisionmaking. Overall, these developments highlight the transition toward more sustainable, knowledge-intensive pest management frameworks. Emerging genome-editing tools, such as CRISPR/Cas systems, offer additional potential to develop durable host resistance and counter rapid pest adaptation. However, for several emerging technologies (e.g., semiochemicals, RNAi, and CRISPR), direct field validation in cotton remains limited, and this review identifies these gaps as critical research priorities

Title: Histochemical Analysis for Lignin Differences Between Reniform Nematode-Resistant and Susceptible Cotton Genotypes

Authors: Lavanya Mendu 1, Chunda Feng

Imprint: Vis Exp. 2026 Oct 6:(236).

doi: 10.3791/72690

Abstract: Reniform nematodes (*Rotylenchulus reniformis*) are a major constraint on cotton production, particularly in the southern United States. The reniform nematode is the second most important pest among more than 400 nematode species. These nematodes pose a threat to global food security. Increasing environmental and human health concerns and the cost of nematicides have intensified interest in resistant cotton germplasm. The plant cell wall, especially lignin, is a critical biopolymer involved in resistance to biotic stress. Because nematodes infect root tissues, cell wall components such as lignin may contribute to defense; however, lignin-mediated barriers in cotton roots are not well characterized. This study employed a standardized phloroglucinol-HCl histochemical staining protocol to visualize lignin deposition differences in reniform nematode-resistant (A2-514, A2-995) and susceptible cotton (*Gossypium arboreum*) genotypes at the true leaf stage under non-infected conditions. This stain binds specifically to hydroxy cinnamylaldehyde such as coniferyl aldehyde and sinapyl aldehyde of lignin in the presence of acid and generates a pinkish purple color to visualize lignin. Distinct lignin staining patterns were observed between resistant and susceptible genotypes, supporting a potential role for lignin-associated structural defenses.

Title: Changing pest dynamics and pesticide use in cotton: Challenges and sustainable management

Authors: Veeragowtham, V.; Suganthi, A. ; Murugan, M. ; Renukadevi, P. ; Vellaikumar, S. ; Iqra, Ali ; Kousika, J.; Sheela, Venugopal ; Prakash, K. ; Dharani, M.

Imprint: Plant Science Today, Volume 13, Issue sp5,
[10.14719/pst.16195](https://doi.org/10.14719/pst.16195)

Abstract: Cotton (*Gossypium* spp.) is one of the world's most important fibre crops, yet its sustainability is increasingly challenged by evolving pest complexes, intensified pesticide use, climate change and climate variability. The evidence indicates current

knowledge on pest dynamics, pesticide dependence and ecological interactions in cotton agroecosystems, highlighting the shift from bollworm-dominated pest complexes to the increasing prevalence of secondary pests following the widespread adoption of *Bacillus thuringiensis* (Bt) cotton. Although Bt (Cry toxin)-based transgenic cotton technology initially reduced insecticide use against the bollworm complex, primarily lepidopteran species, the emergence of resistance among bollworms and the upsurge of certain sucking pests in recent decades have reinstated insecticide dependence for pest management. This has led to ecological imbalance, non-target toxicity, the decline of pollinator populations and natural enemy communities, biodiversity loss, environmental contamination, accumulation of residues in products and yield challenges, in addition to increased production costs. The review emphasises the critical role of integrated pest management (IPM) strategies that integrate biological control, habitat diversification, resistant cultivars and threshold-based pesticide applications to restore ecological stability. Alternative approaches such as botanical pesticides, nanoformulations and plant volatile-mediated pest regulation are highlighted as promising tools for sustainable pest control. Advances in precision agriculture, including artificial intelligence (AI), machine learning and unmanned aerial vehicle (UAV)-based pesticide delivery systems, have the potential to improve pest surveillance and reduce chemical inputs. Supply-chain procurement, certification, traceability and consumer demand can encourage lower-pesticide production, although these mechanisms require fair price incentives to avoid transferring compliance costs to smallholders. Sustainable cotton therefore requires region-specific, climate-resilient, evidence-based IPM supported by extension, market incentives, resistance monitoring and coordinated policy.

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Title: Time-series transcriptome and metabolome profiling reveals GhWRKY33 as positive regulator in cotton response to *Verticillium dahliae* infection

Authors: Wanli Han, G Gang Wang, Z Zhibin Zhang, F Fuxiang Zhao, X Xuwen Wang, T Tao Yang, Li Liu , J Jinxing Qiao, Aijun Si, Y Yu Yu , X Xianhui Kong

Imprint: [Frontiers in Plant Science](#)

Abstract: *Verticillium* wilt severely limits global cotton production, yet the molecular basis of early resistance in upland cotton remains poorly understood. Here, we integrated time-series transcriptomics and untargeted metabolomics to resolve early defense dynamics in cotton seedling roots of the VW-resistant cultivar Jinken1775 and the susceptible cultivar Junmian1 at 0, 4, 8, 12, 24, and 72 h post-inoculation (hpi) with

Verticillium dahliae. Results revealed distinct early defense dynamics. The resistant genotype exhibited restrained yet sustained transcriptional activation coupled with preferential flavonoid/lipid accumulation, whereas the susceptible cultivar displayed disordered reprogramming. Integrated analysis of DEGs and DAMs resolved resistance circuits enriched in calcium signaling, membrane remodeling, and secondary metabolism. Network inference positioned GhWRKY33 as a central hub connecting early signal transduction with downstream metabolic reprogramming. Virus-induced gene silencing of GhWRKY33 significantly compromised cotton resistance to *V. dahliae*, indicating its positive regulatory role in the defense response. Haplotype analysis across 419 upland cotton accessions further revealed that favorable GhWRKY33 alleles are preferentially enriched in resistant lines. This study provided molecular targets for genetic improvement of disease resistance.

PLANT BREEDING AND GENETICS

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Title: Exploiting combining ability and heterosis for yield and fiber quality improvement in cotton (*Gossypium barbadense* L.)

Authors: Abhilasha G. Priyadarshini* and T. Sabesan

Imprint: Electronic Journal of Plant Breeding,
17(3): 341-350. doi:10.37992/2026.1703.044

Abstract: The present investigation in *Gossypium barbadense* L. using a full diallel mating design involving six diverse genotypes revealed substantial genetic variability in agronomic and fiber quality traits. Additive gene action predominated for ginning percentage, fiber length, and fiber strength, whereas seed cotton yield and days to first flowering were mainly governed by non-additive gene action with significant reciprocal effects. Parents RACT 3790 and RACT 5293 were superior general combiners for yield, whereas RACT 3844, RACT 5293, and RACT 5296 were valuable donors for fiber quality improvement. Hybrids RACT 3844 × RACT 5293, RACT 5293 × RACT 5296, and RACT 3790 × RACT 5296 were identified as promising combinations for yield improvement, whereas RACT 3959 × RACT 5294 was superior for fiber quality traits. These results provide valuable information for identification of parental lines and hybrid

combinations for exploiting both the additive and non-additive gene actions for developing high-yielding cotton cultivars with improved fiber quality.

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Title: PBD 88: A High-Yielding, Desi Cotton Variety (*Gossypium arboreum*) for the Irrigated Zones of North India

Authors: Paramjit Singh, Vineet Kumar, Gomti Grover, Dharminder Pathak, Pankaj Rathore, Harish Kumar & Sunayana

Imprint: Genet. Plant Breed. (2026). <https://doi.org/10.1007/s44489-026-00052-x>

Abstract: Cotton (*Gossypium* spp.) remains a foundational cash crop worldwide, driving rural employment and textile manufacturing industries in developing countries. In India, it supports millions of smallholder farming families. Historically, local diploid desi cotton (*Gossypium arboreum*) varieties were preferred across the subcontinent due to their natural resilience against harsh weather and local pests. The fibre of desi cotton variety is short and coarse fibers that are highly valued for specific industrial uses, including surgical absorbent cotton, denims, handloom textiles and household fillings. Over the past years, the agricultural landscape of North India shifted heavily toward transgenic American Bt cotton hybrids. While initially successful, this monoculture triggered secondary pest outbreaks, specifically the whitefly (*Bemisia tabaci*) and pink bollworm (*Pectinophora gossypiella*). Increasing the use of synthetic pesticides and expensive hybrid seeds has squeezed the profit margins of smallholder cotton farmers. The cultivation of desi cotton variety through elite genetic lines is a practical way to restore ecological balance and economic stability. This highlights the breeding background, morphological characters, yield performance and pest-disease resistance profile of the newly released desi cotton variety, PBD 88.

PBD 88 originated from a targeted breeding program at Punjab Agricultural University (PAU), Ludhiana. It is developed by crossing two genetically distinct lines- LD 694 X RG 8. The resulting segregating generations were carefully advanced using the pedigree selection method. Selection criteria focused on stabilizing high seed cotton yields, increasing ginning outturn and developing a manageable plant structure. Once the genetic traits stabilized, the advanced line tested under multi-location trials. Over a three-year period (2019-20, 2020-21 and 2021-22 cropping seasons), a total of 13 field trials were conducted under the All India Coordinated Research Project (AICRP) on Cotton. These evaluations took place at five distinct research locations across the North Zone, covering the states of Punjab, Haryana and Rajasthan. After testing the genotype for three years and across the locations, the variety was identified by the Varietal Identification Committee in its meeting held on 31st, July 2023 for cultivation in North

zone. It has been released and notified by the Central Sub-Committee on Crop Standards, Notification and Release of Varieties of Agricultural Crops, Department of Agriculture and Farmer Welfare, Government of India, New Delhi vide Notification number S.O. 4388(E) dated 08.10.2024 for cultivation in the states of Punjab, Haryana and Rajasthan under irrigated conditions.

On the basis of thirteen trials conducted under the All India Coordinated Research Project, the PBD 88 variety recorded an average seed cotton yield of 3144 kg/ha. This performance represents a yield superiority of 11.02% over the zonal check variety FDK 124 (2852 kg/ha) and 16.04% over the local checks (2710 kg/ha). The variety expresses its maximum yield potential under normal plant spacing of 67.5×45 cm when managed with the standard recommended dose of fertilizers for desi cotton varieties.

In terms of growth and physical attributes, PBD 88 exhibits an indeterminate plant habit with a height ranging from 160 cm to 175 cm and maturity duration of 160 to 170 days. The plants feature palmate-shaped leaves, sparse hairiness with gossypol glands and they completely lack nectaries. The flowers are white with a distinct petal spot, which develop into medium-sized, elliptical bolls containing white, medium-fuzzed seeds. Economically, PBD 88 offers a superior ginning outturn of 37.9%, outperforming FDK 124 at 36.1% and the local checks at 36.3%. Its fibre quality characteristics are highly comparable to existing checks, demonstrating an upper half mean length of 20.4 mm, a micronaire value of 6.3 and a fibre tenacity of 21.4 g/tex under High Volume Instrument (HVI) mode testing. PBD 88 proved resistant to fungal foliar leaf spots and bacterial blight maintaining a Percent Disease Index (PDI) lower than both the zonal and local checks. Furthermore, the bollworm population stayed completely below the economic threshold level, while incidence rates of major sucking insects like jassids, whiteflies and thrips were lower than or equal to the check varieties under field conditions.

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Title: Genome-wide association study (GWAS) of cottonseed traits using micro-CT and high-throughput phenotyping in upland cotton

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Imprint: Industrial Crops and Products, Volume 252, 2026, 124510, ISSN 0926-6690, <https://doi.org/10.1016/j.indcrop.2026.124510>

Abstract: Cottonseed traits influence cotton yield and its value as a source of oil and feed, yet the genetic basis of three-dimensional internal seed architecture remains poorly characterized. Using high-throughput seed imaging and micro-computed tomography (micro-CT), we quantified six external morphological and six internal structural traits in 309 upland cotton (*Gossypium hirsutum* L.) accessions. A subset of

241 accessions with matched resequencing data was used for a genome-wide association study (GWAS). Cavity volume showed the greatest coefficient of variation (30.99%), whereas seed length-to-width ratio was the least variable trait (3.35%). The first two principal components explained 79.6% of the total variation, with seed area, seed volume, seed index, and perimeter contributing most strongly. GWAS detected 49 single-nucleotide polymorphism (SNP) trait associations exceeding the suggestive threshold, corresponding to 38 unique SNP loci across 14 chromosomes. Consolidation of associations within 1-Mb chromosomal intervals yielded 33 top-associated loci, including loci on chromosome D12 associated with cavity volume and cavity ratio. Within ± 500 kb of these loci, 447 genes were identified. Integration of ovule transcriptome profiles and functional annotations prioritized 28 putative candidate genes, including Gh_D03G164000, Gh_D03G168300, and Gh_A07G090600. By integrating high-throughput external phenotyping, non-destructive three-dimensional internal phenotyping, and association mapping across the phenotyping panel and its genotyped subset, this study extends the genetic characterization of cottonseed architecture and provides testable loci and candidates for validation across environments and through functional studies.

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Title: Functional divergence and stress-specific expression analysis of *Gossypium* PRR genes

Authors: Si-jia Liang, Yi-yuan Liu, Pei-yu Li, Wei-na Zhang, Chuan-ying Zhu, Xue-ke Li, Tian-yu Hu, Yi Zhou, Jun-he Liu, Ming-ju Zhu, Bo Li

Imprint: Guangxi Zhiwu / Guihaia, 2026, Vol. 46, No. 5, 790-801 ref. 36

Abstract: Pseudo-response regulators (PRRs) are key regulators of plant circadian rhythms and flowering time, with their functions having been extensively validated across a wide range of plant species. However, the evolutionary trajectory and biological roles of this gene family in cotton remain poorly understood. To systematically dissect the evolutionary characteristics and potential functions of the PRR gene family in cotton, this study integrated data from BLASTP, Pfam, and NCBI databases to perform evolutionary analyses and expression pattern investigations on 32 PRR genes identified from four cotton species—*Gossypium arboreum*, *G. raimondii*, *G. hirsutum*, *G. barbadense*—as well as the model plant *Arabidopsis thaliana*. The results were as follows: (1) The PRR genes were clustered into three evolutionarily conserved subclasses (A, B, and C), whose origin predated the divergence of monocotyledonous and dicotyledonous plants. All PRR members contained the CCT domain, while the majority possessed a dual CCT-Response_reg domain architecture. (2) Significant heterogeneity was observed in the promoter regions of PRR genes among different

cotton species, those in *G. arboreum* were dominated by stress- and light-responsive elements (e.g., ABRE, ACE), whereas promoters in *G. hirsutum* and *G. barbadense* had expanded to include elements associated with defense mechanisms, hormone signaling, and light signal transduction (e.g., MYB, G14K). (3)PRR genes exhibited tissue-specific expression patterns and divergent stress response profiles. Specifically, Ghir_D12G025960 was highly enriched in fibers and ovules; Ghir_D11G001640 was induced by cold stress but repressed under salt or drought conditions; and Ghir_D12G025960 displayed a unique expression dynamic of initial inhibition followed by recovery under heat stress. This study comprehensively characterizes the structural diversity, evolutionary relationships, and functional differentiation of cotton PRR genes in development and stress responses. These findings provide valuable genetic resources and a theoretical framework for future research on the cotton circadian clock regulatory network and the genetic improvement of stress tolerance in cotton breeding.

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Title: *GhMYB106_D13* coordinates cuticle biosynthesis to build the dual shields for anther protection in upland cotton

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Imprint: Plant J

. 2026 Oct 7;128(1):e71142. doi: 10.1111/tpj.71142

Abstract: The plant cuticle acts as a crucial barrier against abiotic stresses. In this study, the vulnerable anther (*van*) gene on chromosome D13 was map-based cloned in upland cotton and identified as *GhMYB106_D13*. It was demonstrated that the differential distribution of MYB106 between D13 and A13 may represent post-polyploidization convergent evolutionary events. Transcriptome analysis, metabolic profiling, and microscopic examination of anther cuticle in *GhMYB106_D13* over-expression and knockout lines revealed that *GhMYB106_D13* affects the wax and cuticle biosynthesis pathway. GC-MS analysis demonstrated that the loss of *GhMYB106_D13* resulted in an ~27.6% reduction in total wax load, predominantly characterized by a decrease in very-long-chain alkanes, whereas overexpression (OE) led to wax accumulation. Key genes involved in the pathway including *FACR2*, *LACS1*, *HHT1*, and *PXG4* were found to be changed dynamically. Specifically, *GhMYB106_D13* likely activates the expression of *LACS1*, a gene involved in wax synthesis that was downregulated in Stage-8 anthers of the *Ghmyb106_D13* mutant. Meanwhile, upregulation of *FACR2*, *CYP704B1*, and *HHT1* was suggested to be potentially involved in cuticle metabolism, possibly through altered 16-feruloyloxypalmitic acid (16-FA) level. Thus, *GhMYB106_D13* contributes to the formation of the first protective ‘shield’ for the anther against external stresses. Additionally, *GhMYB106_D13* participates in trichome differentiation, which constitutes a second ‘shield’ that encloses the petals and sequesters the anther in the

bud before flowering. Overall, these findings unveil the dual function of GhMYB106_D13 in physical protection of plant propagation and offer valuable insights for future strategies aimed at improving stress tolerance in crops.

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Title: Screening and Identification of Disease-tolerant Genotypes of Parental Bt *G. hirsutum*, *G. barbadense* and HxB Hybrid Cotton with Enhanced Yields

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Imprint: Indian Journal of Agricultural Research. 60(9): 1427-1435. doi: 10.18805/IJAR.A-6541.

Abstract: Background: Host plant resistance is a durable, permanent solution for effective disease management in cotton. It reduces agrochemical use, is eco-friendly and is durable. Field evaluation is a practical method to identify cotton genotypes with natural resistance to diseases, including HxB hybrids with higher yields.

Methods: Parental Bt *G. hirsutum*, *G. barbadense* and HxB cotton hybrids were screened under field conditions for Alternaria leaf spot (ALS), Tobacco Streak Virus (TSV), grey mildew, external boll rot and rust diseases. Pathological data were recorded at monthly intervals and PDI was calculated. Yield levels were compared with disease-tolerant HxB hybrids for selection.

Result: Of sixty-six *G. barbadense* male parents, 19 entries, namely B1, B3, B8, B12, CCB26, ICB53, ICB58, ICB40(B), ICB183(B), CCB141, CB99, ICB284, CCB143(B), CCB25(B), CCB29(B), CCB11A(B), SM14, ICB86 and CCB64, were free from all diseases. Another 14 entries were disease-free, except for ALS. Five entries were free from all diseases except rust. Five entries were susceptible to most diseases. All four female *G. hirsutum* parents were infected with ALS and rust. Among 18 BG II *G. hirsutum* parents, V3 was free of all diseases. Ten entries were free from TSV and grey mildew but infected with ALS and rust. Seven entries were infected with ALS, TSV and rust. Among 50 HxB hybrids of BG I, six crosses, namely GJHV 374 Bt x ICB 28, GJHV 374 Bt x ICB 174, GJHV 374 Bt x ICB 194, Rajat Bt x CCB 141, Rajat Bt x ICB 75 and PKV 081 Bt x ICB 258, were free from all diseases. Four crosses were free of diseases except rust. ALS, TSV and rust were recorded in 14 crosses. Of the 14 BG entries, one entry, 211-437, was found free of all diseases. The entries 211-445 and GJHV 374 Bt were found disease-free, except for rust. Four entries, including 211-431, PKV 081 Bt, Rajat Bt and Suraj Bt, were infected with ALS, TSV and rust. All seven commercial BG II hybrids were infected with ALS and rust. Hybrids Ankur Anish, RCH659 and US7067 were also infected with TSV. The six HxB-F1 BG I cotton hybrids that remained free of all the diseases studied and recorded higher seed cotton yields with improved fibre

parameters. Hybrids, such as GJHV 374 Bt x ICB 264 and Rajat Bt x CCB 141, were free from ALS and TSV but showed rust incidence, yet maintained reasonably good yields and fibre quality.

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Title: Pigment Glands as a Developmental and Metabolic Hub in Cotton: Gossypol Biosynthesis, Biotic Stress Defence, and Breeding Strategies

Authors: Feifei Yi, Dan Xu, Bo Li, Weiqiang Li, Yingfan Cai, Xiao Zhang

Imprint: Plant, Cell & Environment 0: 0. <https://doi.org/10.1111/pce.70905>.

Abstract: The pigment gland is a specialised lysigenous cavity structure that stores gossypol and its derivatives in cotton (*Gossypium* spp.). These secondary metabolites provide an intense colour to the gland cavity, appearing as dark dots on the surfaces of various cotton organs or tissues. Gossypol and its derivatives serve as phytoalexins, contributing to plant defence against pests and diseases. However, the direct roles of pigment glands in responses to biotic stresses still need to be clarified. Recent advances in multi-omics and molecular biology have enabled us to elucidate the mechanisms underlying pigment gland formation and development, gossypol biosynthesis, and the role of gossypol in biotic stress responses in cotton. Morphologically, the pigment gland is composed of a layer of secretory cells surrounded by two to three layers of flattened sheath cells, formed via programmed cell death of gland primordia. Pigment gland formation is governed by numerous glandular genes, which constitute a regulatory network that precisely controls gland morphogenesis, gossypol biosynthesis, and enhanced stress resistance. Rational utilisation of pigment glands could improve the value of cotton fibre and cottonseeds. The multifunctionality of pigment gland formation-related genes, encompassing growth and development, stress responses, and cottonseed edibility, provides a theoretical basis for genetic engineering and future research directions.

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Title: A high-quality chromosome-level genome assembly and annotation of a brown Upland cotton 'Zhongmiansuo 81'

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Imprint: <https://doi.org/10.1038/s41597-026-08132-z>

Abstract: Brown cotton, a naturally pigmented variety, predates conventional white cotton, with roots in ancient American civilizations and early cultivation in China. Its genetic diversity is significant in agricultural history. By eliminating chemical dyeing, brown cotton reduces environmental pollution and is recognized for its skin-friendly, breathable, and anti-static properties. Additionally, it exhibits natural antibacterial effects, offers antioxidant benefits, and provides UV protection, making it a sustainable choice for textiles. This study presents a comprehensive chromosome-level genome assembly and annotation for brown cotton, resulting in a highly contiguous genome of 2.30 Gb. Notably, the assembly features a scaffold N50 value of 108.19 Mb, indicating a significant advancement in genome resolution and continuity. A total of 152 contigs were successfully anchored to 26 pseudochromosomes, resulting in a contig N50 of 108.07 Mb. The genome assembly achieved an annotation of 97.43% for the 79,272 protein-coding genes identified, while repetitive sequences account for 80.34% of the genome composition. Furthermore, the annotation includes 318 miRNAs, 2,653 tRNAs, 17,854 rRNAs, and 301 snRNAs. The chromosome-scale genome offers critical insights that enhance comparative genomic analyses within the Malvaceae family. This advancement is poised to expedite genome-guided breeding efforts and improve germplasm development in brown cotton.

PLANT BIOTECHNOLOGY

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Title: Cotton mutant lines derived from gamma-ray irradiation show reduced lodging risk and multiple-harvest potential

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Imprint: PLANT SCIENCE TODAY Vol 13(sp7): 01–09
<https://doi.org/10.14719/pst.14390>

Abstract: Cotton (*Gossypium hirsutum* L.) is an important cash crop supplying natural fibres for the textile industry, yet the availability of cultivars combining lodging resistance and multiple-harvest capability remains limited. This study evaluated gamma-ray-induced cotton mutant lines under field conditions in Bantaeng, South Sulawesi, Indonesia. Seven genotypes were tested, consisting of one wild type (NIAB 999), two national varieties (Karisma and Kanesia 15) and four mutant lines (CN 4A, CN 2A, CN 2C and CN 1A). The mutant lines were derived from tissuecultured immature embryos of NIAB 999 irradiated with ⁶⁰Co gamma rays at a dose of 20 Gy.

The experiment was arranged in a randomized block design (RBD) with 4 replications. Agronomic traits were recorded at budding and boll stage. The results showed at 90 days after planting (DAP), clear genotypic differences in plant height were observed, with Kanesia 15 exhibiting the tallest stature (166 cm), followed by NIAB 999 (152 cm), whereas CN 1A was markedly shorter (94 cm). Despite continuous wind exposure, mutant lines, particularly CN 4A, combined reduced plant height, internode length and stem diameter with adequate numbers of generative branches and bolls. Moreover, mutant lines initiated harvest earlier (115 DAP) and supported up to three sequential harvests at two-week intervals, whereas the wild-type NIAB 999 matured later (130 DAP) and lacked comparable harvest flexibility. These results demonstrate that gamma-ray irradiation successfully generated cotton mutant lines with reduced lodging risk and enhanced multiple-harvest potential

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Title: Genomic dissection and genomic prediction of essential amino acid content in cottonseed identifies candidate genes and elite germplasm for nutritional quality improvement

Authors: Zhong Wang a b, Kai Zheng a, Hongbing Sun a, Yirong Cao a, Huayuan Liu a, Ying Zou a, Yongjie Zhu a, Yanwen Chen a, Yunlong Zhao a, Qanjia Chen a, Xueying Guan d, Xiaojuan Deng

Imprint: Industrial Crops and Products, Volume 252, 2026, 124497, ISSN 0926-6690, <https://doi.org/10.1016/j.indcrop.2026.124497>.

Abstract: The amino acid composition of cottonseed is a critical determinant of its protein quality; however, the utility of genomic prediction for improving the essential amino acid content remains insufficiently established. In this study, 259 upland cotton (*Gossypium hirsutum* L.) germplasm accessions were evaluated for 18 cottonseed amino acids across five environments by integrating best linear unbiased prediction (BLUP), genome-wide association study (GWAS), haplotype analysis, candidate gene annotation, and genomic selection. The 18 amino acid traits exhibited moderate model-based broad-sense heritability ($H^2 = 0.377\text{--}0.588$), while the first five principal components collectively explained 60.02% of the phenotypic variations. Focusing on the nutritionally limiting amino acids lysine (Lys), methionine (Met), and threonine (Thr), 357 significant SNPs were detected, of which 57 were consistently identified across environments or BLUP-based analyses and consolidated into seven stable candidate intervals. Haplotype analysis identified favorable haplotypes associated with increased Lys, Met, and Thr levels. The integration of nonsynonymous variant screening, GO/KEGG enrichment analysis, homologous functional annotation, and expression profiling prioritized 25 candidate genes, including the transporter-related genes Gh_D09G006500, Gh_A08G006200, Gh_A09G006600, and Gh_A09G007200. Genomic

selection showed moderate prediction accuracies of 0.511, 0.531, and 0.637 for Lys, Met, and Thr, respectively, and identified candidate germplasm accessions with favorable combined genomic breeding values. These findings provide stable genomic regions, prioritized candidate genes, and germplasm resources for the targeted improvement of limiting essential amino acids and nutritional quality of cottonseed meal.

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Title: *GhECA8* positively regulates salt tolerance via maintaining intracellular calcium homeostasis in cotton

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Imprint: Cell Biol Toxicol (2026). <https://doi.org/10.1007/s10565-026-10292-y>

Abstract: Calcium (Ca^{2+}) signaling plays a central role in plant responses to salt stress, and endoplasmic reticulum-type Ca^{2+} -ATPases (ECAs), members of the P-type IIA Ca^{2+} -ATPase family, contribute to cellular Ca^{2+} homeostasis by mediating intracellular Ca^{2+} transport. However, the functions of ECA genes in cotton salt tolerance remain poorly understood. In this study, 24 ECA family members were identified across four cotton species, and GhECA8 was selected for functional characterization because of its strong and sustained induction by salt stress. Virus-induced gene silencing (VIGS) of GhECA8 significantly increased salt sensitivity, as evidenced by severe leaf wilting and chlorosis and reduced biomass. GhECA8-silenced plants exhibited altered Ca^{2+} regulation, characterized by enhanced local net Ca^{2+} influx but reduced salt-induced accumulation of total leaf Ca, together with an increased $\text{Na}^{+}/\text{K}^{+}$ ratio, excessive reactive oxygen species (ROS) accumulation, weakened antioxidant capacity and osmotic adjustment, and increased cellular and tissue damage. In addition, GhECA8 silencing enhanced the expression of endoplasmic reticulum stress-related genes and attenuated salt-induced abscisic acid (ABA) accumulation and ABA-associated transcriptional responses. Collectively, these results indicate that GhECA8 contributes to cotton salt tolerance and is associated with coordinated changes in Ca^{2+} homeostasis, ion balance, redox regulation, osmotic adjustment, and ABA-associated stress responses, making it a candidate for further functional evaluation in cotton.

Title: An Intronic Structural Variant in GhEBS1 Drives Cotton Fruit Size Divergence by Modulating Chromatin Accessibility and Gene Expression

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Imprint: Plant Biotechnol J

. 2026 Oct 7:10.1111/pbi.70761. Online ahead of print. doi: 10.1111/pbi.70761

Abstract: Fruit size is not only a crucial fitness trait in plant evolution but also an important agronomic target in crop domestication and improvement, yet its regulatory mechanisms remain poorly characterized. Here, we identified an F-box E3 ubiquitin ligase gene, GhEBS1 (ENLARGED BOLL SIZE 1), as a positive regulator of cotton boll size via map-based cloning. An 845-bp structural variant in the promoter-proximal intronic region of GhEBS1 alters local chromatin accessibility and histone modifications, specifically H3K27 and H3K9 methylation levels and acetylation, thereby modulating GhEBS1 expression and driving boll size divergence. Overexpression or heterologous expression of GhEBS1 in cotton (capsule), tomato (berry) and Arabidopsis (silique) promoted fruit enlargement, indicating its functional conservation. Further analysis showed that GhEBS1 interacts with GhPPD1/2 and GhKIX8/9 to modulate downstream cell proliferation-related genes to control cell number and boll size. Breeding evaluations confirm that the elite GhEBS1 L allele significantly increases boll size, seed size and boll weight. Haplotype analysis reveals that GhEBS1 L originated from *Gossypium hirsutum* race *latifolium* and underwent artificial selection during cotton domestication. Our findings provide new insights into the regulation of plant fruit size and present a valuable genetic locus for crop yield improvement.

Title: Transcriptome profiling across fifteen cotton pests unveils inter and intra-order gene biomarkers for targeted pest control

Authors: Julie Rebecca Joseph Mathari & Habeeb Shaik Mohideen

Imprint: 3 Biotech 16, 456 (2026). <https://doi.org/10.1007/s13205-026-05051-z>

Abstract: Cotton cultivation faces severe challenges by diverse biotic stresses, such as pests, leading to substantial yield losses and increased production costs. Comparative transcriptomic analyses across multiple cotton pests and orders remain largely

unexplored, restricting the identification of conserved broad-spectrum molecular targets for sustainable pest management. This study uncovers transcriptome dynamics across fifteen economically important cotton pest species representing four insect orders (Hemiptera, Lepidoptera, Orthoptera, and Thysanoptera) to identify inter-species and inter-order differential gene expression patterns and potential candidate biomarkers. Comparative differential expression analysis revealed distinct lineage-specific profiles, with *Nezara viridula* exhibiting pronounced downregulation with 1141 downregulated genes, while *Helicoverpa armigera* exhibited the highest gene expression with 1816 upregulated genes. Order-level clustering highlighted marked transcriptomic divergence within Lepidoptera, contrasting with a tightly unified profile in Hemiptera. Functional annotation identified conserved differential expression of genes associated with reproduction, protein regulation, and stress responses. Core reproductive and development-related genes such as vitellogenin and translationally controlled tumour protein (TCTP) were consistently downregulated across Hemiptera, Lepidoptera, and Orthoptera, whereas Ras, Peptidase, and ThiF gene families were predominantly upregulated in Hemiptera and Lepidoptera. Pathway enrichment analysis reinforced these trends showing biological processes associated with amino acid metabolism, protein processing, and cellular regulation. These findings provide a comprehensive comparative transcriptomic resource for cotton pests and identify conserved candidate hub genes and pathways that may facilitate the development of RNA interference-based and other sustainable integrated pest management strategies.

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Title: Genotype- and biostimulant-dependent organization of the cotton response to salinity: sequential screening and multivariate transcriptional analysis

Authors: Venera S. Kamburova, Ilkhom B. Salakhutdinov, Dmitriy A. Mirzabaev, Farkhod S. Radjapov, Shukhrat E. Shermatov, Dinara I. Tojiboeva, Elena F. Nazarova

Imprint: <https://doi.org/10.21203/rs.3.rs-10914277/v1>

Abstract: Salinity limits cotton growth, development, and productivity. One potential approach to mitigating the negative consequences of salt stress is the application of biostimulants. However, it remains poorly understood how biostimulant application modifies the cotton transcriptional response across genotypes and product identities. We conducted a single blocked experiment evaluated through a sequential analytical framework comprising cultivar screening, comparative evaluation of commercial biostimulants, and multivariate analysis of transcriptional changes. Based on morphological traits and the Multitrait Genotype-Ideotype Distance Index (MGIDI), Ishonch and Porloq-1 were identified as contrasting genotypes, whereas Ravnaq-1 represented an intermediate response to salinity. Rizokom-1, Mikrozim-1, and Serhosil were selected for subsequent analysis. Their effects were evaluated through the

expression of genes assigned to the hormonal regulation, antioxidant defense, and metabolic/osmoprotective functional modules. Rizokom-1 provided the most favorable integrated morphological effect and generated the most pronounced transcriptional response, followed by Mikrozim-1 and Serhosil. The amplitude and functional structure of the response depended on both genotype and biostimulant. Salinity predominantly reduced response amplitude while the direction of the response was generally preserved, and the three functional modules remained strongly concordant across the analyzed genotype $\times$ salinity contexts. These findings support genotype-specific selection of biostimulants and identify promising cultivar $\times$ biostimulant combinations for subsequent physiological, biochemical, and agronomic validation.

SEED SCIENCE AND TECHNOLOGY

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Title: Approaches based on seed and seedling images for classification of the physiological potential of cotton seeds

Authors: Marcelo Augusto Rocha Limão, Daniel Teixeira Pinheiro, Rafaela Stefani Silva, Laércio Junio da Silva, Denise Cunha Fernandes dos Santos Dias

Imprint: J. Seed Sci. 48 • 2026 • <https://doi.org/10.1590/2317-1545v48309023>

Abstract: Rapid and accurate methods for assessing seed quality have been increasingly demanded by the seed industry. In this context, the X-ray test and computerized seedling image analysis are promising alternatives for use in quality control programs. The objective of this study was to evaluate the efficiency of radiographic images and seedling images combined with interactive machine learning for classifying the physiological potential of cotton seeds. Seeds from eight lots were initially evaluated using germination and vigor tests. Radiographic images were acquired, and the following variables were obtained: area, perimeter, filling, relative density, integrated density, and grayscale. Seedling images captured at two, three, and four days of germination were processed using the GroundEye system, yielding the following variables: hypocotyl length, root length, total seedling length, and growth, uniformity, and vigor indices. Using the Ilastik software, data were generated regarding the percentage of strong normal seedlings, weak normal seedlings, abnormal seedlings, and dead seeds. The X-ray technique showed a relationship with the physiological potential of cotton seeds, in addition to providing information on their internal structures. Shoot length, primary root length, and total seedling length, as well as uniformity, growth,

and vigor indices determined by GroundEye, together with data obtained via supervised machine learning using Ilastik, enabled the classification of cotton seed lots (cv. 21065TLP) based on their physiological potential at three days of germination; however, external validation using other cultivars, crop seasons, and regions of the country is required.

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Title: DC-Glow and Microwave Plasma Reactors for Surface Modifications of Cotton Seeds: Advancement in Plasma Agriculture

Authors: Areej Fatima, Aamir Shahzad , Muhammad Kashif

Imprint: DOI: 10.4018/979-8-2600-4669-2.ch012

Abstract: Globally speaking, Pakistan is the 4th largest producer of cotton among India, China, US and Brazil and third largest exporter of raw cotton. One of the most valuable non-food agricultural product, cultivated in south Punjab and Sindh. 10% of the Pakistan's Gross Domestic Product (GDP) and 55% of its foreign exchange earnings come from cotton and its products. Cotton seed oil is a sustainable source of protein and satisfies 18.8% of the public's demand for palatable vegetable oil. Defatted cotton seed meal with protein content of (45-55%) used as cattle feed. Pakistan fulfills 17.7% of its demand for edible oils through cottonseed oil. The king of fibers is the most widely produced in nature. Textile is the largest industry of Pakistan, and cotton is the basic raw material of this industry.

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Title: Revealing dynamic crystalline structure development in cotton fibers using cellulose-specific Rietveld refinement

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Imprint: Industrial Crops and Products, Volume 252, 2026, 124486, ISSN 0926-6690,

<https://doi.org/10.1016/j.indcrop.2026.124486>.

Abstract: The crystalline structure of cotton fibers governs their mechanical and physicochemical properties, yet limitations in reliable characterization methods have hindered detailed insight into their structural development. In this study, a cellulose-specific Rietveld refinement approach was applied to elucidate crystalline structure development in cotton fibers. Using a four-step sequential refinement procedure, X-ray diffraction data collected from fibers between 20 and 66 days post-anthesis (DPA) were analyzed. The calculated diffraction patterns showed excellent agreement with the measured patterns across all samples, yielding low figures of merit. Refined structural parameters—including the a-axis, b-axis, γ -angle, crystallite size, crystalline volume fraction, and March-Dollase preferred orientation coefficient along the [001] direction—exhibited coordinated, multi-step changes with DPA. These variation patterns resolved five mechanistically distinct stages by revealing two-step secondary cell wall thickening and maturation as well as a late stage of crystallite coalescence and lateral growth. Full-pattern Rietveld analysis demonstrates highly sensitivity to dynamic changes in crystalline structure and provides a quantitative approach to resolving structural development in cellulose fibers.

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Title: Cotton classical extensin *GhCEXT1-A* regulates fiber elongation by modulating cell wall structure and composition

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Imprint: Plant Science, Volume 374, 2027, 113489, ISSN 0168-9452,

<https://doi.org/10.1016/j.plantsci.2026.113489>

Abstract: Classical extensins (CEXTs) are hydroxyproline-rich glycoproteins that belong to the extensin superfamily and constitute critical structural components of the plant cell wall. However, the genome-wide characterization and functional role of CEXTs in cotton fiber development remain very limited. Here, we conducted a comprehensive comparative genomic analysis across four *Gossypium* species and identified a total of 30 CEXT genes, which were systematically classified into four evolutionary lineages (Groups A-D) based on analyses of phylogenetic relationship and gene structural organization. Sequence alignment analysis suggested the presence of two ancestral CEXTs in angiosperms, which subsequently expanded in representative dicots, indicating their potential functional diversity. Transcriptomic profiling and quantitative real-time PCR validation showed that GhCEXT1-A was predominantly expressed during rapid fiber elongation stages in *G. hirsutum*. Virus-induced gene silencing of GhCEXT1-A in cotton led to significantly shortened fiber length, confirming its role as a positive regulator of fiber elongation. Further cell wall component detection indicated that in GhCEXT1-A-VIGS cotton plants, soluble pectin content was significantly reduced, while the contents of cellulose, hemicellulose, and lignin were significantly accumulated, coupled with a marked increase in cell wall thickness. These results suggest that GhCEXT1-A affects cotton fiber elongation by regulating the dynamics of major cell wall component and structure. This work establishes a genomic framework for the cotton CEXT family and identifies GhCEXT1-A as an important positive regulator linking pectin-driven cell wall extensibility to fiber elongation, providing a molecular basis for precision breeding of cotton.

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Title: Consequential life cycle assessment of cottonseed as a by- product of cotton fibre production in India with energy and carbon offset evaluation

Authors: Aslesha Ravindranath Bhargava, M. Selvadass

Imprint: [Current Agriculture Research Journal](#), 2026, Vol. 14, No. 1, 184-205 ref. 110

Abstract: Cotton is a major crop in India, and its production yields large volumes of cottonseed as a byproduct with considerable feed and energy potential; however, allocation bias in conventional attributional life cycle assessments (LCAs) often leads to systematic undervaluation of cottonseed. This work evaluates the energy and environmental impacts of cottonseed valorization in India using a consequential life cycle assessment (CLCA) with system extension. One ton of seed cotton at the gin gate and one ton of processed cottonseed were the two functional units that were considered. Secondary Indian data was used to predict cotton cultivation, ginning, seed processing, and replacement pathways. Cottonseed oil for biodiesel production, hulls for biomass-based energy, and meal for soybean meal's protein equivalent were all

assessed. According to the findings, cotton-seed valorization can recover up to 10.5 GJ t⁻¹ of renewable energy and reduce the cradle-to-gate global warming potential of cotton production by 20-35%, allowing for a near or net-positive energy balance. The results show that cottonseed valorization is a practical technique to turn cotton into a multipurpose bioresource that will help India's circular bioeconomy.