# Agronomy, Soil Science and Plant Physiology

## 1

**Title**: Impacts of Nitrogen Fertilizer Application and Mulching on the Morpho-Physiological and Yield-Related Traits in Cotton

**Author**: Khalid Hussain, Ayesha Ilyas, Saqib Ali, Irshad Bibi

**Abstract**: Cotton is a global cash crop with a significant contribution in the world economy. Optimum nutrient and water supply are most important for sustainable cotton production under warmer and dry environments. Field experiments were carried out to evaluate the cumulative impacts of various nitrogen doses and mulches on sustainable cotton production under semi-arid conditions during 2018 and 2019. Four nitrogen doses; 0, 70, 140, and 210 kg ha$^{-1}$ and three types of mulch: control (without mulch), natural mulch (5 tons/ha wheat straw), and chemical mulch (methanol (30%). Nitrogen 210 kg ha$^{-1}$ with natural mulching increased 40.5% gunning out turn, 30.0% fiber length, 31.7% fiber strength, 32.6% fiber fineness, 20.8% fiber uniformity, and 34.0% fiber elongation. Shoot nitrogen, phosphorous, potassium, calcium, and magnesium contents were maximum where 210 kg ha$^{-1}$ nitrogen and mulch was applied. Natural mulch reduced the soil temperature as compared to chemical and no mulch conditions. The soil temperature was 0.5 to 1.8 °C lower in mulching treatments as compared to the control. Maximum economic yield was around 90% higher in natural mulch with the 210 kg ha$^{-1}$ nitrogen application. It is concluded that optimum nitrogen application with natural mulch not only enhanced plant growth and development but also induced sustainability in quality cotton production under semi-arid conditions.

## 2

**Title**: Gossypol and related compounds are produced and accumulate in the aboveground parts of the cotton plant, independent of roots as the source

**Author**: Devendra Pandeya, LeAnne M. Campbell, Lorraine Puckhaber, Charles Suh & Keerti S. Rathore

**Abstract**: Gossypol and related terpenoids, derived from the same basic biosynthetic pathway, are present in the numerous lysigenous glands in the aboveground parts of a cotton plant. Roots, with sparse presence of such glands, do produce significant amount of gossypol and a different set of terpenoids. These compounds serve a defensive function against various pests and pathogens. This investigation was undertaken to examine whether gossypol produced in the roots can replenish the gossypol content of the cottonseed-glands that are largely devoid of this terpenoid in a genetically engineered event. Graft unions between a scion derived from the RNAi-based, Ultra-low gossypol cottonseed (ULGCS) event, TAM66274, and a rootstock derived from wild-type parental genotype, Coker 312 (Coker), were compared with various

other grafts that served as controls. The results showed that the seeds developing within the scion of test grafts (ULGCS/Coker) continued to maintain the ultra-low gossypol levels found in the TAM66274 seeds. Molecular analyses confirmed that while the key gene involved in gland development showed normal activity in the developing embryos in the scion, two genes encoding the enzymes involved in gossypol biosynthesis were suppressed. Thus, the gene expression data confirmed the results obtained from biochemical measurements and collectively demonstrated that roots are not a source of gossypol for the aboveground parts of the cotton plant. These findings, combined with the results from previous investigations, support the assertion that gossypol and related terpenoids are produced in a highly localized manner in various organs of the cotton plant and are retained therein.

# 3

**Title**: Modeling and predicting the effects of climate change on cotton-suitable habitats in the Central Asian arid zone

**Author**:  JianfengMai, GuilinLiu

**Abstract**: Climate change has significantly affected global agricultural production, particularly in arid zones of Central Asia. Thus, we analyzed changes in the habitat suitability of cotton in Central Asia under various shared socioeconomic pathway (SSP) scenarios during 2021–2060. The results showed that the average minimum temperature in April, precipitation seasonality, and distance to rivers were the main environmental factors influencing the suitable distribution of cotton. Suitable habitats expanded toward the north and east, reaching a maximum net increase of $10.85 \times 10^4$ km$^2$ under the SSP5–8.5 scenario during 2041–2060, while habitats in the southwestern area showed a contracting trend. The maximum decreased and increased habitats were concentrated at approximately 68°E and 87°E, respectively. In addition, their latitudinal distributions were concentrated at approximately 40°N and 44°N. The longitudinal and latitudinal dividing lines of increased and decreased habitats were 69°E and 41°N, respectively. Habitats at the same altitude showed an increasing trend, excluding the elevation range of 125–325 m. Habitat shifts could exacerbate spatial conflicts with forest/grassland and natural reserves. The maximum spatial overlap between them was observed under the SSP5–8.5 scenario during 2041–2060. These findings could provide scientific evidence for rational cotton cultivation planning in global arid zones.
# 4

**Title**: Domestication reduces leaf water use efficiency associated with the abaxial stomatal anatomy in cotton.

**Author**: Zhangying Lei, Yang He, Xiafei Li, Ziqi He, Yujie Zhang, Wangfeng Zhang, Fang Liu, Yali Zhang

**Abstract**: Crop domestication appears to alter the adaxial and abaxial stomatal features for increasing growth rate and yield. However, its effect on leaf water use efficiency (WUE) has not been experimentally verified under domestication. In this study, we characterized stomatal anatomy and carbon isotope ($\delta$ $^{13}$C) in 32 wild and 36 domesticated genotypes of cotton grown under agricultural field. The results showed that domesticated genotypes possessed lower WUE as indicated by low or more negative $\delta$ $^{13}$C compared with wild genotypes. Higher maximum theoretical stomatal conductance ($g_{smax}$) was underpinned by more stomata rather than significantly enlarged stomata after domestication. Specifically, abaxial stomatal density was higher but no change in adaxial stomatal density following domestication, while both adaxial and abaxial stomatal size were greater due to larger guard cell without the contribution to stomatal pore size. However, there was a negative relationship between $\delta$ $^{13}$C and SS, especially the abaxial SS across wild and domesticated genotypes, because enlarged stomata resulted in a lower stomatal response rate to fluctuating canopy light, consequently excessive water loss. In conclusion, cotton domestication has triggered substantial variation in stomatal anatomy. WUE and drought tolerance in cotton can be improved by decreasing abaxial stomatal size for faster stomatal response and reducing unnecessary water loss in future cotton breeding.

# 5

**Title**: Use of plant growth regulators to reduce 2-methyl-4-chlorophenoxy acetic acid-Na (MPCA-Na) damage in cotton (Gossypium hirsutum)

**Author**: Quan-Cheng Zhang, Jing Wang & Jun-Gang Wang

**Abstract**: 2-methyl-4-chlorophenoxy acetic acid-Na (MPCA-Na) is a phenoxy carboxylic acid selective hormone herbicide that is widely used in the crop fields. However, drift of MPCA-Na during application is highly damaging to cotton (Gossypium hirsutum) and other crop plants. This study was carried out from 2019 to 2020 to determine the effects of different concentrations of MPCA-Na on physiological and metabolic activities besides growth and yield of cotton plants at seedling, budding, flowering and boll stages. Moreover, we evaluated the different combinations of 24-epibrassinolide, gibberellin (GA$_3$), phthalanilic acid and seaweed fertilizer to ameliorate herbicide damage.

# 6

**Title**: Recent advances and future perspectives in early-maturing cotton research

**Author**: Hang Zhao , Yanli Chen , Ji Liu1, Zhi Wang , Fuguang Li and Xiaoyang G

**Abstract**: Cotton's fundamental requirements for long periods of growth and specific seasonal temperatures limit the global arable areas that can be utilized to cultivate cotton. This constraint can be alleviated by breeding for early-maturing varieties. By delaying the sowing dates without impacting the boll-opening time, early-maturing varieties not only mitigate the yield losses brought on by unfavorable weathers in early spring and late autumn but also help reducing the competition between cotton and other crops for arable land, thereby optimizing the cropping system. This review presents studies and breeding efforts for early-maturing cotton, which efficiently pyramid early maturity, high-quality, multiresistance traits, and suitable plant architecture by leveraging pleiotropic genes. Attempts are also made to summarize our current understanding of the molecular mechanisms underlying early maturation, which involves many pathways such as epigenetic, circadian clock, and hormone signaling pathways. Moreover, new avenues and effective measures are proposed for fine-scale breeding of early-maturing crops to ensure the healthy development of the agricultural industry.

# 7

**Title**: Chemical topping with 1,1-dimethylpiperidinium chloride increases lint yield and defoliation of cotton by improving canopy development

**Author**: ShiYuTian, XiaojuanShi, XianzheHao, NannanLi, JunhongLi, HongxiaZhang, YingChen, QiLiang

**Abstract**: Chemical topping with 1,1-dimethylpiperidinium chloride (DPC) has been considered a promising measure to inhibit apical dominance in cotton (*Gossypium hirsutum* L.). However, knowledge of the plant growth and canopy development of cotton under chemical topping with DPC remains limited, and the effect of this practice on lint yield and defoliation is unclear. A two-year (2019–2020) field experiment was conducted with two varieties, Xinluzao 60 (L60, DPC-insensitive) and Jinken1402 (JK1402, DPC-sensitive), and four topping methods, manual topping (MT), no topping (NT), DPC+ (fortified DPC) and DPC. We found that the lint yields of L60 and JK1402 treated with DPC were equivalent to those of L60 and JK1402 treated with DPC+ but were enhanced by 0.9–4.7% in L60 and 6.7–11.8% in JK1402 relative to those under MT and NT, with no significant difference in fiber quality. This was mainly due to the change in plant growth and canopy structure. In particular, compared with MT, application of DPC shortened the upper branches and extended the duration of the leaf area index peak. Moreover, in the late reproductive period, DPC application increased the number of upper leaves and reduced diffuse noninterceptance. Notably, the light transmittance rate (LLR) of JK1402 treated

with DPC was higher than that of MT in the middle and lower parts of the canopy. Furthermore, there was positive correlation between LLR and defoliation rate. Therefore, chemical topping with DPC provided an effective alternative for manual topping.

# 8

**Title**: Effect of irrigation technology and plant density on cotton growth, yield, yield components, and water use efficiency

**Author**: Komlan Koudahe

**Abstract**: Limited water resources and insufficiently developed infrastructure provide challenges to sustainable production of cotton (Gossypium hirsutum L.) in Western Kansas. This study aimed to (i) assess the effect of irrigation technology and plant density on cotton growth, yield, and yield components, and (ii) determine the actual evapotranspiration, water use efficiency, and grassreference crop coefficients of cotton under different irrigation technologies and rainfed conditions. Four irrigation technologies, which were Low Energy Precision Application (LEPA), Low Elevation Spray Application (LESA), Mobile Drip Irrigation 1 (MDI1 with 3.79 L/hour), Mobile Drip Irrigation 2 (MDI2 with 7.57 L/hour), and rainfed treatments were evaluated under two crop densities (135,908 and 160,618 plants/ha) in a split plot design with three replications using cotton variety PHY 205 W3FE in 2021. The results indicated that the MDI2 had the highest growth characteristics, such as plant height, leaf area index (LAI), and canopy cover, while the rainfed treatment registered the lowest growth performance. There is a significant positive relationship .

# 9

**Title**: Evaluation of Water Stress Memory in Compensation Response of Cotton (Gossypium hirsutum L.) during Subsequent Water Deficiency .

**Author**: M. Habibi1 , E. Faghani, M. Rezaei , M. A. Mahmood Janlou , and M. H. Razzagi

**Abstract**: This research was carried out to provide suitable cotton seed for seed propagation in dryland. In this study, the potential of cotton seeds that have been stressed for the third consecutive year was investigated to evaluate water stress memory responses. The experiment was arranged in split-plot factorial design with four irrigation levels of W0 (No- irrigation), W1 (33% FC), W2 (66% FC), and W3 (100% FC), as the main factor, and five seed treatments (four third-stressed seeds, i.e. S21 to S24, and registered seed), as a sub-plot. Seeds of cotton were grown under different levels of water-stress exposure for three crop-seasons. As results showed, S32 received water stress signal in both W0 and W3 conditions through physiological

mechanisms change. Seeds of S32 accumulated the lowest ABA and the highest calcium in exposure to W0 and W3 . Enhancement to superoxide dismutase and Aspartate peroxidase activity in leaves of S32 in exposure to W0 and W1 is another memorial stress mechanism for scarce water acclimation. The highest-potential thirty-boll weight, thirty-fiber weight, and first-harvesting yield were obtained from S32 against W0 , W1 , and W2.. Also, the seeds of S32 had the most seedling vigor and germination percentage in exposure to W0 , W1 , and W2 . It can be concluded that stress memory, via modification of physiology and morphology of plant behavior, helps plants to tolerate water deficiency when subjected to recurrent drought.

# 10

**Title**: HEAT-RESPONSIVE PROTEIN regulates heat stress via fine-tuning ethylene/auxin signaling pathways in cotton

**Author**: Muhammad Abdullah, Furqan Ahmad, Yihao Zang, Shangkun Jin, Sulaiman Ahmed, Jun Li, Faisal Islam, Mudassar Ahmad, Yaoyao Zhang, Yan Hu

**Abstract**: Plants sense and respond to fluctuating temperature and light conditions during the circadian cycle; however, the molecular mechanism underlying plant adaptability during daytime warm conditions remains poorly understood. In this study, we reveal that the ectopic regulation of a HEAT RESPONSIVE PROTEIN (*GhHRP*) controls the adaptation and survival of cotton (*Gossypium hirsutum*) plants in response to warm conditions via modulating phytohormone signaling. Increased ambient temperature promptly enhanced the binding of the phytochrome interacting factor 4 (GhPIF4)/ethylene-insensitive 3 (GhEIN3) complex to the *GhHRP* promoter to increase its mRNA level. The ectopic expression of *GhHRP* promoted the temperature-dependent accumulation of *GhPIF4* transcripts and hypocotyl elongation by triggering thermoresponsive growth-related genes. Notably, the upregulation of the GhHRP/GhPIF4 complex improved plant growth via modulating the abundance of *Arabidopsis thaliana* auxin biosynthetic gene YUCCA8 (*AtYUC8*)/1-aminocyclopropane-1-carboxylate synthase 8 (*AtACS8*) for fine-tuning the auxin/ethylene interplay, ultimately resulting in decreased ethylene biosynthesis. *GhHRP* thus protects chloroplasts from photo-oxidative bursts via repressing *AtACS8* and *AtACS7* and upregulating *AtYUC8* and the heat shock transcription factors (*HSFA2*), heat shock proteins (*HSP70* and *HSP20*). Strikingly, the Δ*hrp* disruption mutant exhibited compromised production of *HSP/YUC8* that resulted in an opposite phenotype with the loss of the ability to respond to warm conditions. Our results show that *GhHRP* is a heat-responsive signaling component that assists plants in confronting the dark phase and modulates auxin signaling to rescue growth under temperature fluctuations.

# Crop Protection

## 11

**Title**; Early Season Growth Responses of Resistant and Susceptible Cotton Genotypes to Reniform Nematode and Soil Potassium Application.

**Author**:  Bhupinder Singh  , Daryl R. Chastain  , Salliana R. Stetina  , Emile S. Gardiner  and John L. Snider

**Abstract**: A greenhouse study was conducted to investigate the roles that host plant resistance and soil potassium (K) levels play in affecting Rotylenchulus reniformis Linford and Oliveira (Tylenchida: Hoplolaimidae) (RN) populations and early season cotton (Gossypium hirsutum L.) growth. Two upland, RN-resistant cotton lines (G. barbadense introgressions: 08SS110-NE06.OP and 08SS100), a genetic standard (Deltapine 16) and a commercially available susceptible cultivar (PHY 490 W3FE) were evaluated at four different levels of K [100% of recommended rate, 150% of recommended, 50% of recommended, and a base level] from seeding until harvesting, 60 days after sowing (DAS). Quadratic functions (r2 = 0.82 to 0.95) best described the early season growth response of cotton genotypes to soil K. The base K level was associated with the lowest values for most morphological variables, including plant height (PH), mainstem nodes (MSN), leaf area, and dry weight at 30 DAS and 60 DAS. However, soil K did not affect RN population counts (RC). Additionally, soil K did not influence the rate of change in growth variables among genotypes. The resistant genotype 08SS110- NE06.OP showed greater growth in terms of time to first true leaf, PH, MSN, and above-ground dry weights compared to the commercially available susceptible genotype. No interaction between K and RN or genotype and RN was found in early season cotton growth. However, RC in pots of resistant genotypes was less than in pots of susceptible genotypes. Our research on the early season growth response to soil K by novel, RN-resistant genotypes and susceptible genotypes contributes to the development of improved RN resistance and fertilization management in cotton.

## 12

**Title**: Multiplex molecular marker-assisted analysis of significant pathogens of cotton (*Gossypium* sp.)

**Author**: R.L.Chavhan, S.Sable, A.V.Narwade, V.R.Hinge, B.B.Kalbande, A.K.Mukherjee, P.K.Chakrabarty

**Abstract**: Plant pathogens diminish crop quality and yield, leading to economic losses.

Molecular markers have the potential for early and accurate detection of pathogens. DNA

markers based on ITS regions, *pthN* gene, and CP gene were designed to detect strains of

fungal, bacterial, and viral pathogens, respectively. The pRS and pRB primers were found specific to strains of *R. solani* and *R. bataticola.* Four strains of *R. areola* isolates from each cultivated cotton species were detected using the primer pRARE. Further, CAPS markers, *Bst*6I, and *Dra*RI specific to the strains of *Alternaria macrospora* were developed, which could differentiate from other fungal pathogens. Furthermore, we developed a multiplexed assay to detect six pathogens simultaneously. These diagnostic markers could help assess the prevalence of cotton infecting pathogens in the field (from plant tissue or soil). Consequently, the diagnostic assay could be used for undertaking judicious disease control measures in commercial agriculture.

# 13

**Title**: Interaction estimation of pathogenicity determinant protein βC1 encoded by Cotton leaf curl Multan Betasatellite with *Nicotiana benthamiana* Nuclear Transport Factor 2.

**Author**: Ammara Nasim, Muhammad Abdul Rehman Rashid, Khadim Hussain, Ibrahim Mohammed Al-Shahwan, Mohammed Ali Al-Saleh

**Abstract**: Begomovirus is one of the most devastating pathogens that can cause more than 90% yield loss in various crop plants. The pathogenicity determinant βC1, located on the betasatellite associated with monopartite begomoviruses, alters the host signaling mechanism to enhance the viral disease phenotype by undermining the host immunity. The understanding of its interacting proteins in host plants to develop disease symptoms such as curly leaves, enations, vein swelling, and chlorosis is crucial to enhance the disease resistance in crop plants. The current study was designed to reveal the contribution of βC1 in disease pathogenicity and to unveil potential interacting partners of βC1 protein in the model plant *Nicotiana benthamiana.*

# 14

**Title**:  Reduced insecticide applications can enhance natural enemies of Bemisia Tabaci in cotton
**Author**: JAVARIA NAZIR1, MUHAMMAD ARSHAD SHAKEEL, MUHAMMAD ASAD SALEEM, MIRZA ABDUL QAYYUM

**Abstract**: Excessive amount of insecticides destroys natural enemies of cotton pests and consequently the population of whitefly flares up. The present research focused on the use of PB ropes to reduce application of insecticides and to investigate the ecological impact on Bemisia tabaci and beneficial fauna in cotton fields. Two cotton varieties (BS-15 and NIAB-878)

were sown in research area of MNS University of Agriculture, Multan during 2018 on 30 acres. PB ropes dispensers (PB-ropes L®) were installed at 120/acre at pin head square stage of cotton. It was observed that application of PB ropes reduced need for insecticide applications, thus helped conservation of beneficial fauna in cotton fields throughout the season, which kept whitefly populations below EIL. Population of whitefly nymph was reduced after application (0.9/leaf-seasonal average) in PB ropes treated fields as compared to untreated check (8.1/leaf-seasonal average). Furthermore, higher population of green lacewing (4.00/plant) was observed in PB ropes treated field. It was concluded that populations of whiteflies were kept below EIL due to conservation of green lacewing. This positive effect of PB ropes is presumably due to increasing the number of cotton insect pest biological agents. This indirect effect of mating disruption (PB ropes) is of great value within the framework of IPM in cotton.

# Plant Genetics and Breeding

## 15

**Title**: GhAAO2 was observed responding to $NaHCO_3$ stress in cotton compared to AAO family genes.

**Author**: Xiaoyu Liu, Yupeng Cui, Ruiqin Kang, Hong Zhang, Hui Huang, Yuqian Lei, Yapeng Fan

**Abstract**: Abscisic acid (ABA) is an important stress hormone, the changes of abscisic acid content can alter plant tolerance to stress, abscisic acid is crucial for studying plant responses to abiotic stress. The abscisic acid aldehyde oxidase (AAO) plays a vital role in the final step in the synthesis of abscisic acid, therefore, understanding the function of AAO gene family is of great significance for plants to response to abiotic stresses.

## 16

**Title**: Registration of 17 upland cotton germplasm lines with improved resistance to Fusarium wilt race 4 and good fiber quality .

**Author**: Mauricio Ulloa1 Robert Hutmacher, Jinfa Zhang, TariLee Schramm, Philip A. Roberts, Margaret L. Ellis

**Abstract**: With Fusarium wilt (Fusarium oxysporum f. sp. vasinfectum W.C. Snyder & H.N. Hansen) race 4 (FOV4) formally identified in proximity to the High Plains of west Texas—the

largest upland cotton (Gossypium hirsutum L.) producing region in the United States—the need to develop cultivars resistant to FOV4 has become urgent. Currently, there are no commercial upland cultivars available claiming FOV4 resistance. Fusarium wilt race 4, a soil-borne fungus, has affected the cotton crop in the San Joaquin Valley of California for two decades. The primary purpose for the release of the upland PSSJ-FRU01–PSSJ-FRU17 (Reg. no. GP-110– GP-1126, PI 699966–PI 699982) germplasm lines is to provide cotton breeders with urgently needed sources for FOV4 resistance in upland cotton. The lines were derived from six different cross-combinations using 10 parental lines with different genetic backgrounds (e.g., 'DES 920' [PI 536522], 'NM12Y1004' [NuMex COT 15 GLS, PI 678371], 'MARS ROSE CLUSTER' [PI 528483], 'AUBURN M' [PI 529214], and 'SA-3208' [LIAO MIAN 7 HAO]). Several cycles of selection were applied to these developed lines based on an asymptomatic single plant selection after greenhouse FOV4 inoculations or infested field evaluations from F1 to F4. In 2019–2021 evaluations, germplasm lines showed enhanced resistance to FOV4 with significantly lower percentage mortality and vascular root staining as compared to resistant controls ('Pima-S6' and 'PHY 881 RF') and improved fiber strength and some long fibers. These released lines will help to reduce the vulnerability of upland cotton to this fungal pathogen and advance efforts to broaden the resistance genetic base which is critical for the upland cotton industry.

# 17

**Title**: Estimation genotypic environmental interaction by using GGE Biplot analysis of cotton genotypes (G.Hirsutum L)

**Author**:  Dawood S. MADAB,  Suaad M. HASSEN

**Imprint**: VI.International Scientific Congress of Pure,Applied and Technological Sciences MINAR CONGRESS 6

**Abstract**: Seven cotton genotypes were grown in a different environmental conditions (as a combination among plant densities: 15, 20, and 25 cm under salt and non salt stress irrigation) to estimate genetic behavior in different environments of cotton genotypes (Ceebro, W888, Pac-cot189, Lashata, Cocker310, Montana, and Ik259).Analysis of variance for the interaction environments with the genotypes according to Randomized Completely Block Design with three replications were used, furthermore GGE biplot analysis for the seed cotton yield. Results Showed : Environments affected high significant in seed cotton yield for studied genotypes. Genotypic and genotypic environmental interaction contribute of 14.7 and 32.2% of variation respectively. PC1 and PC2 interpreted 53.9 and 26.5 % respectively of differences in GGE variances.IK259 Genotype the most productive and stable than others for high PC1 and low absolute value of PC2.E6 environment correlated significant and positive with other environments that means the effect of salt water stress in a wide distance among plants (25cm). Better performance of IK259 genotype was under un salt stress conditions in narrow distances among plants(15 cm). While Pac-cot genotype was favorable in most salt stress conditions. Consequently IK259 and Pac-cot189 genotypes are productive and desirable in studied environments.

**Title**: Flavanone and flavonoid hydroxylase genes regulate fiber color formation in naturally colored cotton.

**Author**: HongliZheng, BailinDuan, BoYuan, ZhengbinChen, DongliangYu, LipingKe, WenlongZhou, HaifengLiu, YuqiangSun

**Abstract**: Using naturally colored cotton (NCC) can eliminate dyeing, printing and industrial processing, and reduce sewage discharge and energy consumption. Proanthocyanidins (PAs), the primary coloration components in brown fibers, are polyphenols formed by oligomers or polymers of flavan-3-ol units derived from anthocyanidins. Three essential structural genes for flavanone and flavonoid hydroxylation encoding flavanone-3-hydroxylase (F3H), flavonoid 3′-hydroxylase (F3′H) and flavonoid 3′5′-hydroxylase (F3′5′H) are initially committed in the flavonoid biosynthesis pathway to produce common precursors. The three genes were all expressed predominantly in developing fibers of NCCs, and their expression patterns varied temporally and spatially among NCC varieties. In *GhF3Hi*, *GhF3′Hi* and *GhF3′5′Hi* silenced lines of NCC varieties XC20 and ZX1, the expression level of the three genes decreased in developing cotton fiber, negatively correlated with anthocyanidin content and fiber color depth. Fiber color depth and type in RNAi lines changed with endogenous gene silencing efficiency and expression pattern,the three hydroxylase genes functioned in fiber color formation. *GhF3H* showed functional differentiation among NCC varieties and *GhF3′H* acted in the accumulation of anthocyanin in fiber. Compared with *GhF3′H*, *GhF3′5′H* was expressed more highly in brown fiber with a longer duration of expression and caused lighter color of fibers in *GhF3′5′H* silenced lines. These three genes regulating fiber color depth and type could be used to improve these traits by genetic manipulation.

**Title**: Systematical Characterization of the Cotton Di19 Gene Family and the Role of GhDi19-3 and GhDi19-4 as Two Negative Regulators in Response to Salt Stress

**Author**:Lanjie Zhao 1,, Youzhong Li , Yan Li , Wei Chen , Jinbo Yao , Shengtao Fang , Youjun Lv , Yongshan Zhang and Shouhong Zhu

**Abstract**: Drought-induced 19 (Di19) protein is a Cys2/His2 (C2H2) type zinc-finger protein, which plays a **crucial** role in plant development and in response to abiotic stress. This study systematically investigated the characteristics of the GhDi19 gene family, including the member number, gene structure, chromosomal distribution, promoter cis-elements, and expression profiles. Transcriptomic analysis indicated that some GhDi19s were up-regulated under heat and salt stress. Particularly, two nuclear localized proteins, GhDi19-3 and GhDi19-4, were identified as being in potential salt stress responsive roles. GhDi19-3 and GhDi19-4 decreased sensitivity under salt stress through virusinduced gene silencing (VIGS), and showed significantly lower levels of $H_2O_2$, malondialdehyde (MDA), and peroxidase (POD) as well as significantly increased superoxide dismutase (SOD) activity. This suggested that their abilities were improved to effectively reduce the reactive oxygen species (ROS) damage. Furthermore, certain calcium signaling and abscisic acid (ABA)-responsive gene expression levels showed up- and down-regulation changes in target gene-silenced plants, suggesting that GhDi19-3 and GhDi19-4 were involved in calcium signaling and ABA signaling pathways in response to salt stress. In conclusion, GhDi19-3 and GhDi19-4, two negative transcription factors, were found to be responsive to salt stress through calcium signaling and ABA signaling pathways.

**20**

**Title**: Genome-wide analysis of zinc finger-homeodomain (ZF-HD) transcription factors in diploid and tetraploid cotton

**Author**: Linxue Xing,Ke Peng, Shuang Xue, Wenfei Yuan, Baoqi Zhu, Pengju Zhao,

**Abstract**: ZF-HD (zinc finger-homeodomain) gene family plays important roles in plant growth, development, and various stress responses. In the present study, 49, 50, 22, and 32 ZF-HD genes were identified in Gossypium hirsutum, Gossypium barbadense, Gossypium arboretum, and Gossypium raimondii genomes, respectively. According to their phylogenetic features, the ZF-HD genes were classified into six groups. Segmental duplication, whole genome duplication, and transposable elements provides major forces for the expansion of cotton ZF-HD gene family during the divergence of Gossypium species and the divergence between monocots and dicots. The Ka/Ks ratios of the ZF-HD segmental duplication pairs were mainly distributed around 0.12, which indicated that they have experienced strong purifying selective pressure during evolution. Transcriptome analysis showed that 6 Gossypium hirsutum and 4 Gossypium barbadense ZF-HD genes were expressed in all tested tissues. Further, expression profiles under abiotic stress exhibited that the ZF-HD genes were differentially regulated in response to various stresses. Taken together, our findings provide a valuable information on the characterization of ZF-HD gene family and lay foundation for their further function investigations in cotton.

# Fiber and Fiber Technology

## 21

**Title**: A brassinosteroid transcriptional regulatory network participates in 4 regulating fiber elongation in cotton.

**Author**: Le Liu, Guoquan Chen , Shengdong Li , Yu Gu , Lili Lu , Ghulam Qanmber , Venugopal Mendu , Zhao Liu, Fuguang Li, Zuoren Yang

**Abstract:** Brassinosteroids (BRs) participate in the regulation of plant growth and 7 development through BRI1-EMS-SUPPRESSOR1 (BES1)/BRASSINAZOLE-RESISTANT1 8 (BZR1) family transcription factors. Cotton (Gossypium hirsutum) fibers are highly 9 elongated single cells, and BRs play a vital role in the regulation of fiber elongation. 10 However, the mode of action on how BR is involved in the regulation of cotton fiber 11 elongation remains unexplored. Here, we generated GhBES1.4 over expression lines and 12 found that overexpression of GhBES1.4 promoted fiber elongation, whereas silencing of 13 GhBES1.4 reduced fiber length. DNA affinity purification and sequencing (DAP-seq) 14 identified 1531 target genes of GhBES1.4 (GBST), and 5 recognition motifs of 15 GhBES1.4 were identified by enrichment analysis. Combined analysis of DAP-seq and 16 RNA-seq data of GhBES1.4-OE/RNAi provided mechanistic insights into GhBES1.4- 17 mediated regulation of cotton fiber development. Further, with the integrated approach of 18 GWAS, RNA-seq, and DAP-seq, we identified seven genes related to fiber elongation 19 that were directly regulated by GhBES1.4. Of them, we showed Cytochrome P450 84A1 20 (GhCYP84A1) and 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (GhHMG1) 21 promote cotton fiber elongation. Overall, the present study established the role of 22 GhBES1.4-mediated gene regulation and laid the foundation for further understanding 23 the mechanism of BR participation in regulating fiber development.

## 22

**Title**: Tissue specific expression of bacterial cellulose synthase (Bcs) genes improves cotton fiber length and strength.

**Author**: SidraAkhtar, Ahmad AliShahid, SanaShakoor, MukhtarAhmed, SehrishIftikhar, MuhammadUsmaan, SaharSadaqat, AyeshaLatif, AdnanIqbal, Abdul QayyumRao

**Abstract**: Fiber growing inside the cotton bolls is a highly demandable product and its quality is key to the success of the textile industry. Despite the various efforts to improve cotton fiber staple length Pakistan has to import millions of bales to sustain its industrial needs. To improve cotton fiber quality Bacterial cellulose synthase (Bcs) genes (acsA, acsB) were expressed in a local cotton variety CEMB-00. *In silico* studies revealed a number of conserved domains both in the cotton-derived and bacterial cellulose synthases which are essential for the cellulose

synthesis. Transformation efficiency of 1.27% was achieved by using *Agrobacterium* shoot apex cut method of transformation. The quantitative mRNA expression analysis of the Bcs genes in transgenic cotton fiber was found to be many folds higher during secondary cell wall synthesis stage (35 DPA) than the expression during elongation phase (10 DPA). Average fiber length of the transgenic cotton plant lines S-00–07, S-00–11, S-00–16 and S-00–23 was calculated to be 13.02% higher than that of the non-transgenic control plants. Likewise, the average fiber strength was found to be 20.92% higher with an enhanced cellulose content of 22.45%. The mutated indigenous cellulose synthase genes of cotton generated through application of CRISPR/Cas9 resulted in 6.03% and 12.10% decrease in fiber length and strength respectively. Furthermore, mature cotton fibers of transgenic cotton plants were found to have increased number of twists with smooth surface as compared to non-transgenic control when analyzed under scanning electron microscope. XRD analysis of cotton fibers revealed less cellulose crystallinity index in transgenic cotton fibers as compared to control fibers due to deposition of more amorphous cellulose in transgenic fibers as a result of Bcs gene expression. This study paved the way towards unraveling the fact that Bcs genes influence cellulose synthase activity and this enzyme helps in determining the fate of cotton fiber length and strength.

# 23

**Author**: CuicuiWu, ShuipingXiao, DongyunZuo, HailiangCheng, YoupingZhang, QiaolianWang, LiminLv, GuoliSong

**Abstract**: The heavy metal-binding domain is involved in heavy metal transporting and plays a significant role in plant detoxification. However, the functions of HMAs are less well known in cotton. In this study, a total of 143 GhHMAs (heavy metal-binding domain) were detected by genome-wide identification in *G. hirsutum* L. All the GhHMAs were classified into four groups via phylogenetic analysis. The exon/intron structure and protein motifs indicated that each branch of the GhHMA genes was highly conserved. 212 paralogous GhHMA gene pairs were identified, and the segmental duplications were the main role to the expansion of GhHMAs. The Ka/Ks values suggested that the GhHMA gene family has undergone purifying selection during the long-term evolutionary process. *GhHMA3* and *GhHMA75* were located in the plasma membrane, while *GhHMA26*, *GhHMA117* and *GhHMA121* were located in the nucleus, respectively. Transcriptomic data and qRT-PCR showed that *GhHMA26* exhibited different expression patterns in each tissue and during fiber development or under different abiotic stresses. Overexpressing *GhHMA26* significantly promoted the elongation of leaf trichomes and also improved the tolerance to salt stress. Therefore, *GhHMA26* may positively regulate fiber

elongation and abiotic stress. Yeast two-hybrid assays indicated

that *GhHMA26* and *GhHMA75* participated in multiple biological functions. Our results suggest some genes in the GhHMAs might be associated with fiber development and the abiotic stress response, which could promote further research involving functional analysis of GhHMA genes in cotton.

## 24

**Title**: An Approach for Detecting Noise in Cotton Fiber Properties Data Using Nearest Neighbor Algorithm

**Author**:  Mona Shalab

**Abstract**: The purpose of the current study is to decrease noise of cotton fiber properties data using one of methods for machine learning such as K Nearest Neighbor (KNN). The present investigation was carried out at Egyptian & International Cotton Classification Center (EICCC). The first data was for Giza 87, Giza 88, Giza 86, Giza 90 and Giza 95 each one separately and the second data was for combination of all previous cotton varieties. A wide range of lint cotton grades used in this work. The studied traits were basic fiber properties; length, strength and micronaire value. The highest classification accuracy were 117.65 % for G 87 and 149.25 % for combined data. The integrated statistics among fiber length, strength and micronaire value concluded that spinning consistency value (SCI) which is the most intrinsic technological value were in acceptable range for Giza 87, Giza 88, Giza 86, Giza 90, Giza 95 separately and combined data. For instance, SCI values were 163.74 and 174.85 for G 86 of data treated without KNN and with KNN, respectively. Therefore, any study of cotton fiber properties plays a crucial role in determining spinning performance.

## 25

**Title**: A Comparative Study between Trait Selections and Marker-assisted Selections to Improve Fiber Strength in Upland Cotton

**Author**: Linghe Zeng, David D. Fang, Ping Li, Christopher D. Delhom

**Abstract**: A determination of efficiency in the use of marker assisted selection (MAS) for improving cotton (*Gossypium hirsutum* L.) fiber quality is critical for a successful utilization of MAS in cotton breeding. This study was designed to determine selection responses and realized heritability ($h_2$) of fiber strength selected by MAS in comparison with phenotype selections by

traditional breeding. Previously identified SSR markers, CGR6764 and DPL0852, flanking a fiber strength QTL on chromosome A07, were used in MAS. Two genetic populations, MD15/TAM98D-99ne (Pop 1) and TAM98D-99ne/UA48 (Pop 2), were developed. $F_2$ plants were selected by three methods based on (1) phenotype, (2) combined marker-genotype and phenotype (MAS-1), and (3) marker-genotype alone (MAS-2) in Pop1 and two methods based on phenotype and MAS-1 in Pop 2. $F_3$ progeny rows derived from the selected $F_2$ plants were planted with two replicates in 2019. In Pop 1, the fiber strength mean of the selected $F_3$ progenies was in an order of MAS-1 > MAS-2 > phenotype selection. In Pop 2, there was no significant difference in strength between $F_3$ progenies derived from selections by MAS-1 and phenotypic breeding. In Pop 1, $h_2$ of MAS selections was higher than phenotype selections. In Pop 2, $h_2$ of MAS selections was similar to the phenotype selections. The results indicate selection efficiency by MAS for fiber strength is better than or equivalent to phenotype selection.

## 26

**Title**: GhAP1-D3 positively regulates flowering time and early maturity with no yield and fiber quality penalties in upland cotton

**Author**: Caixiang Wang, Juanjuan Liu, Xiaoyu Xie, Ji Wang, Qi Ma, Pengyun Chen, Delong Yang, Xiongfeng Ma, Fushun Hao, Junji Su

**Abstract**: Flowering time (FTi) is a major factor determining how quickly cotton plants reach maturity. Early maturity greatly affects lint yield and fiber quality and is crucial for mechanical harvesting of cotton in northwestern China. Yet, few quantitative trait loci (QTLs) or genes regulating early maturity have been reported in cotton, and the underlying regulatory mechanisms are largely unknown. In this study, we characterized 152, 68 and 101 loci that were significantly associated with the three key early maturity traits—FTi, flower and boll period (FBP) and whole growth period (WGP), respectively, via four genome-wide association study methods in upland cotton (*Gossypium hirsutum*). We focused on one major early-maturity-related genomic region containing three single-nucleotide polymorphisms on chromosome D03, and determined that *GhAP1-D3*, a gene homologous to *Arabidopsis thaliana APETALA1 (AP1)*, is the causal locus in this region. Transgenic plants overexpressing *GhAP1-D3* showed significantly early flowering and early maturity without penalties for yield and fiber quality compared to wild-type (WT) plants. By contrast, the mutant lines of *GhAP1-D3* generated by genome editing displayed markedly later flowering than the WT. GhAP1-D3 interacted with GhSOC1 (SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1), a pivotal regulator of FTi, both in *vitro* and *in vivo*. Changes in *GhAP1-D3* transcript levels clearly affected the expression of multiple key flowering regulatory genes. Additionally, DNA hypomethylation and high levels of H3K9ac affected strong expression of *GhAP1-D3* in early-maturing cotton cultivars. We propose that epigenetic modifications modulate *GhAP1-D3* expression to positively regulate FTi in cotton through interaction of the encoded GhAP1 with GhSOC1 and affecting the transcription of multiple flowering-related genes. These findings may also lay a foundation for breeding early-maturing cotton varieties in the future.

# Plant Biotechnology

## 27

**Title**: A novel tasi RNA-based micro RNA-induced gene silencing strategy to tackle multiple pests and pathogens in cotton (*Gossypium hirsutum* L.)

**Author**: Kesiraju Karthik, Alkesh Hada, Akansha Bajpai, Basavaprabhu L. Patil, Bheema Paraselli, Uma Rao & Rohini Sreevathsa

**Abstract**: Cotton (*Gossypium hirsutum* L.), an important commercial crop grown worldwide is confronted by several pests and pathogens, thus reiterating interventions for their management. In this study, we report, the utility of a novel *Arabidopsis* miRNA173-directed trans-acting siRNA (tasiRNA)-based micro RNA-induced gene silencing (MIGS) strategy for the simultaneous management of cotton leaf curl disease (CLCuD), cotton leaf hopper (CLH; *Amrasca biguttula biguttula*) and root-knot nematode (RKN, *Meloidogyne incognita*). Cotton transgenics were developed with the MIGS construct targeting a total of 7 genes by an apical meristem-targeted *in planta* transformation strategy. Stable transgenics were selected using stringent selection pressure, molecular characterization and stress-specific bio-efficacy studies. We identified 8 superior events with 50–100% resistance against CLCuD, while reduction in the root-knot nematode multiplication factor in the range of 35–75% confirmed resistance to RKN. These transgenic cotton events were also detrimental to the growth and development of CLH, as only 43.3–62.5% of nymphs could survive. Based on the corroborating evidences obtained by all the bioefficacy analyses, 3 events viz., L-75-1, E-27-11, E-27-7 were found to be consistent in tackling the target pests. To the best of our knowledge, this report is the first of its kind demonstrating the possibility of combinatorial management of pests/diseases in cotton using MIGS approach. These identified events demonstrate immense utility of the strategy towards combinatorial stress management in cotton improvement programs.

## 28

**Title**: Phylogeny, gene structures, and expression patterns of the auxin response factor (GhARF2) in upland cotton (Gossypium hirsutum L.)

**Author**: Maoni Chao, Jie Dong, Genhai Hu, Yanyan Li, Ling Huang, Jinbao Zhang, Jihua Tang & Qinglian Wang

**Abstract**: Auxin response factors (ARFs) are a class of transcription factors that regulate the expression of auxin-responsive genes and play important functions in plant growth and development. To understand the biological functions of the auxin response factor GhARF2 gene

in upland cotton, the coding sequence (CDS) of GhARF2 gene was cloned, and its protein sequence, evolutionary relationship, subcellular localization and expression pattern were analysed.

# 29

**Title**: A glutathione S-transferase GhTT19 determines flower petal pigmentation via regulating anthocyanin accumulation in cotton .

**Author**: Qichao Chai1, , Xiuli Wang1, Mingwei Gao1 , Xuecheng Zhao , Ying Chen , Chao Zhang , Hui Jiang , Jiabao Wang , Yongcui Wang , Meina Zheng , Ahmedov Miraziz Baltaevich , Jian Zhao and Junsheng Zhao

**Abstract**: Anthocyanin accumulations in the flowers can improve seed production of hybrid lines, and produce higher commodity value in cotton fibre. However, the genetic mechanism underlying the anthocyanin pigmentation in cotton petals is poorly understood. Here, we showed that the red petal phenotype was introgressed from Gossypium bickii through recombination with the segment containing the R3 bic region in the A07 chromosome of Gossypium hirsutum variety LR compared with the near-isogenic line of LW with white flower petals. The cyanidin-3-Oglucoside (Cy3G) was the major anthocyanin in red petals of cotton. A GhTT19 encoding a TT19- like GST was mapped to the R3 bic site associated with red petals via map-based cloning, but GhTT19 homologue gene from the D genome was not expressed in G. hirsutum. Intriguingly, allelic variations in the promoters between GhTT19LW and GhTT19LR, rather than genic regions, were found as genetic causal of petal colour variations. GhTT19-GFP was found localized in both the endoplasmic reticulum and tonoplast for facilitating anthocyanin transport. An additional MYB binding element found only in the promoter of GhTT19LR, but not in that of GhTT19LW, enhanced its transactivation by the MYB activator GhPAP1. The transgenic analysis confirmed the function of GhTT19 in regulating the red flower phenotype in cotton. The essential light signalling component GhHY5 bonded to and activated the promoter of GhPAP1, and the GhHY5-GhPAP1 module together regulated GhTT19 expression to mediate the light-activation of petal anthocyanin pigmentation in cotton. This study provides new insights into the molecular mechanisms for anthocyanin accumulation and may lay a foundation for faster genetic improvement of cotton.

# 30

**Title**: The GhMAP3K62-GhMKK16-GhMPK32 kinase cascade regulates drought tolerance by activating GhEDT1-mediated ABA accumulation in cotton

**Author**:  LinChen, BingZhang, LinjieXia, DandanYue, BeiHan, WeinanSun, FengjiaoWang, KeithLindsey, XianlongZhang, XiyanYang

**Abstract**: Drought is the principal abiotic stress that severely impacts cotton (*Gossypium hirsutum*) growth and productivity. Upon sensing drought, plants activate stress-related signal transduction pathways, including ABA signal and mitogen-activated protein kinase (MAPK) cascade. However, as the key components with the fewest members in the MAPK cascade, the function and regulation of *GhMKKs* need to be elucidated. In addition, the relationship between MAPK module and the ABA core signaling pathway remains incompletely understood.

# Seed Science and Technology

## 31

**Title**: Effects of phosphorus application on carbohydrate metabolism in cottonseed kernel during the key development period provided a new insight for phosphorus management in cotton production.

**Author**: lJiaweiWang, HuijieLi, QinWang, XiaolinHuang, WeiHu, ShanshanWang, ZhiguoZhou

**Abstract**: Cottonseed provides abundant and high-quality raw materials for biodiesel, fine chemical, and other industries due to its rich oil, but phosphorus-deficient farmland and finite phosphate resource hinder its production. Cottonseed development is based on its carbohydrate, and exploring the response of cottonseed carbohydrate metabolism to phosphorus could contribute to optimizing phosphorus management in cotton production and continuously obtaining high-quality cottonseed. Here, the experiment on phosphorus rates [0 (phosphorus deficient), 100 (phosphorus critical), and 200 (phosphorus excess) kg $P_2O_5$ ha$^{-1}$] was conducted using Lu 54 (low-phosphorus sensitive) and Yuzaomian 9110 (low-phosphorus tolerant) in a field containing 16.9 mg kg$^{-1}$ available phosphorus to assess the effects of phosphorus on cottonseed yield, cottonseed total phosphorus, ash, and oil contents, carbohydrate metabolism related carbohydrate contents, and enzymes activities. The results showed that phosphorus application increased cottonseed yield and oil content by 32.4%−54.2% and 14.8%−20.1% on average, respectively, which could be attributed to the improvements in sucrose transport and hydrolysis in cottonseed kernel during 18–26 days post anthesis induced by higher total phosphorus content (17.1%−26.7%). During the key development period of cottonseed kernel, phosphorus application increased sucrose content (13.0%−19.4%) by

increasing the expression of sucrose transporter genes, and promoted sucrose hydrolysis by elevating enzymes activities, especially sucrose synthase (11.2%−19.1%) in cottonseed kernel. Consequently, phosphorus application increased hexose levels in cottonseed kernel and thus provided more substrates for its development, which promoted the formation of cottonseed kernel biomass (6.2%−10.6%), cottonseed and oil yields. Additionally, carbohydrate metabolism in Lu 54 was more sensitive to phosphorus than Yuzaomian 9110 during the key development period, resulting in greater increases in cottonseed kernel biomass, cottonseed yield, and oil content for Lu 54. Notably, the increments generated by unit phosphate fertilizer on the above indicators attenuated markedly with phosphorus application. Based on sucrose content, the key substance, the critical phosphorus concentration in the subtending leaf to cotton boll (LPC) needed by the efficient operation of the key carbohydrate metabolic pathway was 0.38% for Lu 54 versus 0.34% for Yuzaomian 9110. This report first unveiled the key carbohydrate metabolic pathway regulated by phosphorus for cottonseed and oil yield formation and its demand for LPC during the key development period, providing a new insight for diagnosing and regulating phosphorus in cotton production.

**32**

**Title**: Efficiency of Selection for Seed Cotton Yield under Newly Reclaimed Lands Conditions
**Author**: Salem, M. A,  H. Mahrous,  H. K. Hussien and M. M. Abd El Majeed

**Abstract**: Selection for seed cotton yield plant-1 was applied in F2, F3 and F4-generations of a population of cross Giza 80 X Giza 90 cotton. The experiment was carried out during three successive summer seasons; 2019, 2020 and 2021 at farm west of Minia, El Minia under new reclaimed lands conditions. Entries mean squares of the selection criterion; seed cotton yield were significant or highly significant in F3 and F4-generations. Reduction was observed in the phenotypic and genotypic coefficients of variability from F3 to F4 compared to the phenotypic variation in F2 for the most studied traits as a result the selection for seed cotton yield/plant and reduction the genetic variation. Moreover, increasing the homozygosity. The four selected families of no. 13, 17, 18 and 26 were showed highly significant increase compared to both bulk and better parent for the two traits seed cotton yield and lint yield plant-1 . Seed cotton yield /plant was showed positive genotypic and phenotypic correlation coefficients with bolls weight, lint yield /plant-1 and number of bolls plant-1 . While, negative correlations were observed for Seed cotton yield / plant with each of lint percentage and lint index on genotypic and phenotypic level.

**Title**: Response to Selection for Seed Cotton Yield of (Giza 95 x Super Giza 86) Egyptian Cotton Cross under Newly Reclaimed Lands Conditions .

**Author**: Salem, M. A H. Mahrous and H. K. Hussien

**Abstract**: Selection for seed cotton yield plant-1 in a segregating population of cotton of cross Giza 95 x Super Giza 86 was applied under new reclaimed lands conditions for three summer season, 2019, 2020 and 2021 at Mallawy Agriculture Research station, west of El Minia. The wide range of seed cotton yield/plant in the F2-generation from 16.40 to 186.00 gm. Indicating ability effective selection for seed cotton yield. Entries mean squares of the selection criterion; seed cotton yield and lint yield/plant and number of bolls/plant were high significant in F4-generation. Estimates higher than 82.71% of heritability for the seed cotton yield, lint yield/plant and branches/plant. Two families; No. 6 and 9 were higher than the better parent Giza 95 and bulk sample in each of seed cotton yield, lint yield/plant and number of bolls /plant in the F4-generation. Four selected families no. 2, 6, 9 and 20 were showed significant (p≤0.05 or 0.01) increase compared to the bulk in seed cotton yield/plant by 19.26, 50.03, 32.16 and 64.26%, respectively. The seed cotton yield per plant showed strong positive genotypic and phenotypic correlation with each of lint yield per plant by 0.99 and bolls number/plant 0.97 and 0.95, respectively. Moreover, low positive correlation with boll weight, seed index, fiber length and uniformity index, with negative correlation with each of lint percentage, fiber fineness, lint index and fiber strength.