GLEANINGS IN COTTON RESEARCH

OCTOBER 2023

LIBRARY & DOCUMENTATION CENTRE
ICAR-CENTRAL INSTITUTE FOR COTTON RESEARCH
POST BOX NO. 2, SHANKARNAGAR POST OFFICE
NAGPUR – 440010
E Mail: cicrlib@yahoo.co.in

GLEANINGS IN COTTON RESEARCH

OCTOBER 2023

LIBRARY & DOCUMENTATION CENTRE
CENTRAL INSTITUTE FOR COTTON RESEARCH
Post Box No. 2, Shankarnagar Post Office
Nagpur – 440010
E Mail: cicrlib@yahoo.co.in

Preface

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

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

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

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

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

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

The guidance provided by Dr H B Santosh, Senior Scientist in this venture is highly appreciated.

We duly thank The Director, Dr Y G Prasad for providing the inspiration and support for this publication.

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

Swati Dixit
Incharge Library

Chetali Rodge
Technical Officer (T5)

INDEX

1

Title: Uncovering the dark side of agriculture: How land use intensity shapes soil microbiome and increases potential plant pathogens.

Author: Mohamed Idbella, Giuliano Bonanomi

Imprint: Applied Soil Ecology, Volume 192, December 2023, 105090

Abstract: Soil microbiome plays a critical role in maintaining key soil processes such as litter decomposition, nutrient cycling, and plant productivity. In this study, we aimed to investigate the variability of soil chemicals, microbial diversity, and composition in seven ecosystems i.e., *Fagus sylvatica* and *Quercus ilex* forests, a Mediterranean grassland and shrubland, a vineyard, a horticultural cultivation in open field and under greenhouse, across a gradient of land-use intensity in Southern Italy. Soil chemistry included pH, organic matter, total nitrogen, and C/N ratio, and soil microbiota was characterized by high-throughput sequencing of 16S and ITS genes. Our results showed that greenhouse soils had the highest pH, while *Fagus* had the lowest. Horticultural, greenhouse, and grassland soils had low levels of OM and total N, while shrubland had relatively high levels of OM, total N, and C/N ratio. *Fagus* soils, on the other hand, had the highest levels of OM, total N, and C/N ratio. Bacterial diversity was lowest in horticultural soils, whereas fungal diversity was highest in shrubland soils. Pseudomonadota were the predominant bacteria in *Fagus*, grassland, and vineyard soils, while Actinomycetota dominated in *Quercus*, shrubland, and greenhouse soils. However, Cyanobacteria was predominant in horticultural soils. On the other hand, the Ascomycota was predominant in all ecosystems except *Quercus* soils, where the Basidiomycota was dominant. Our bipartite network analysis revealed that bacteria are often the same in different ecosystems while fungi tend to be specific to a particular habitat. Moreover, in agricultural ecosystems, fungal pathogens belongingto *Alternaria*, *Fusarium*, *Gibellulopsis*, *Stemphylium*, *Acremonium*, and *Curvularia* are more abundant, especially in greenhouse. The findings of this study provide important insights into the variability of soil microbial diversity and community composition in different ecosystems, highlighting the essential role of preserving natural ecosystems while managing agricultural ones, given their higher abundance of pathogens.

2

Title: Long-term nitrogen fertilizer management for enhancing use efficiency and sustainable cotton (Gossypium hirsutum L.)

Author: Yuanqi Ma, Hongchun Sun, Yurong Yang, Zhao Li, Ping Li, Yuetong Qiao

Imprint: Front. Plant Sci. Sec. Plant Nutrition, Volume 14 - 2023 | doi: 10.3389/fpls.2023.1271846

Abstract: Optimal management of nitrogen fertilizer profoundly impacts sustainable development by influencing nitrogen use efficiency (NUE) and seed cotton yield. However, the effect of long-term gradient nitrogen application on the sandy loam soil is unclear. Therefore, we conducted an eight-year field study (2014 to 2021) using six nitrogen levels: 0 (N0), 75 (N1), 150 (N2), 225 (N3), 300 (N4), and 375 (N5) kg/hm2. The showed that: (1) nitrogen fertilizer had insignificantly affected the basic soil fertility but decreased the soil total nitrogen (STN) content by 5.71-19.67%, 6.67-16.98%, and 13.64-21.74% at 0-20, 20-40, and 40-60cm soil layers, respectively. (2) The reproductive organs of N3 plants showed the highest nitrogen accumulation and dry matter accumulation in both years. Increasing the nitrogen application rate gradually decreased the dry matter allocation ratio to the reproductive organs. (3) The boll number per unit area of N3 was the largest among all treatments in both years. On sandy loam, the most optional nitrogen rate was 190 kg/hm2 to 270 kg/hm2 for high seed cotton yield with minimal nitrogen loss and reduced soil environment pollution.

3

Title: Commercial Crops (Jute, Cotton and Sugarcane)

Author: Gouranga Kar, D. Blaise, T. K. Srivastava, Chandan Sourav Kar, P. Verma, A. R. Reddy & Pushpa Singh

Imprint: Trajectory of 75 years of Indian Agriculture after Independence , Chapter First Online: 29 August 2023

Abstract: Jute, cotton and sugarcane are the principal commercial crops in India contributing. While India is the largest producer of jute and cotton; but is the second-largest producer of sugarcane in the world. Research on jute, cotton and sugarcane has long history of research in pre independence era, but more emphasis was given after post-independence period coinciding with the green revolution of India during 1960–1970s. There was a total shift from white jute (Corchorus *capsularis*) to tossa (*C. olitorius*) in jute; from the *desi* (*G. herbaceum*) to the American cotton (*G. hirsutum*) in cotton and hybrid varieties in sugarcane in this period due to high yield and better fibre quality in jute and cotton and higher sugar content and disease resistance in sugarcane. Major path-breaking achievements in jute consist of the introduction of resistance to premature flowering was a *tossa* jute, the development of microbial retting consortium "CRIJAF SONA" comprising pectinolytic bacteria and genome sequencing, while in cotton it was the development of the inter-specific and intraspecific hybrids and the *Bt* cotton hybrids and varieties. Interspecific hybridization through nobilization and improved methods of planting were major achievements in sugarcane. With technological advancement, jute productivity increased from 1.04 to 2.56 t/ha since independence to now. India could take the credit for developing the world's first cotton hybrid (H-4) in 1970. In cotton, productivity which was stagnant at about 300 kg/ha prior to the introduction of *Bt* cotton, now jumped to more than 500 kg/ha. Sugarcane yield also almost doubled from 3.21 to 7.65 t/ha during the corresponding period. There is huge scope in all three commercial crops like diversified use of jute and cotton and alternative source of energy like biofuel or bioenergy from jute and sugarcane. Proper exploration of the untapped potential of this group of crops can not only increase farmers' income but also contribute to the environment and ecology of intensive cropping system.

4

Title: Cotton Emergence Uniformity Assessment Using Remote Sensing and Machine Learning.

Imprint: 2023 ASABE Annual International Meeting 2300471
(doi:10.13031/aim.202300471)

Authors: Fengkai Tian, Jianfeng Zhou

Abstract: Seed emergence uniformity has a significant impact on plant vigor, emergence rate and overall crop health, which ultimately affects fruit production. Identifying the optimal germination rate, taking into account different genotypes and environmental factors, is critical to improving crop yield. This study presents a novel method that uses an unmanned aerial vehicle (UAV) to collect RGB field images and applies deep learning and statistical analysis to evaluate cotton (Gossypium hirsutum L.) uniformity under varying seeding rates. Traditional methods often involve laborious manual plant counting to identify areas of over- or under-emergence that affect lint yield, a time-consuming process for large fields. To address this issue, our study, conducted in southern Missouri, USA, used five different seeding rates. We used a UAV-mounted camera to capture field images two weeks after planting. These images were stitched into an orthomosaic of the entire field and then segmented into smaller blocks. The YOLOv7 object detection algorithm was used to locate each cotton plant within the segmented images. We also used the Hough transform and polynomial regression techniques to identify cotton rows and remove weeds. These methods yielded a mean average accuracy at 50% intersection over the union threshold of 96.8% mAP@50. This study provides valuable insights by developing a pipeline for early-stage cotton stand count and distance estimation using remote sensing techniques. This approach improves the assessment of cotton emergence uniformity, leading to more efficient crop management.

5

Title: Response of Various Intercrops on Growth and Yield Attributes of Cotton (Gossypium hirsutum L.) under Irrigated Situation.

Author: P. Sangameshwari

Imprint: International Journal of Plant & Soil Science Volume 35, Issue 18, Page 1142-1147, 2023

Abstract: Intercropping in cotton is one of the best approachs to improve the food security and soil fertility in addition to that of generating cash income of the rural poor. At present intercropping is common in conventional agriculture to augment the land use and also symbolic in reducing the weeds infestation. But, introducing superfluity population of intercrops without reducing the base crop population is of preeminence. Therefore field experiments were conducted at farmer’s field located at Erode District in Tamil Nadu, India (during 2018-2019) to investigate the compatible, remunerative and best smothering intercrops on the base crop, cotton. The experiment was outlayed in randomized block design with three replications. The treatment encompass of seven treatments viz., Cotton alone (Gossypium hirsutum L.), Cotton + Blackgram (Vigna mungo), Cotton + Greengram (Vigna radiata), Cotton + Cowpea (Vigna unguiculata), Cotton + Coriander (Coriandrum sativum), Cotton + Onion (Allium cepa) and Cotton + Sesame (Sesamum indicum). The study clearly showed that among the treatments Cotton + Cowpea showed superior response in growth attributes like plant height (harvest stage) (153.23 cm), LAI -Leaf Area Index at 70 DAS (6.18), DMP – Dry Matter Production at harvest (6788.01 kg per ha) and yield attributes like number of Monopodial branches per plant (3.22), number of Sympodial branches per plant (19.62), number of squares per plant (48.83), number of bolls per plant (32.23), boll weight (3.98 g) and seed cotton yield (2455.70 t ha-1) and next in order was Cotton + Blackgram. The result evidently proved that Cotton + Cowpea will be an appropriate intercropping system for cotton and it was having considerable increase in growth and yield of cotton.

6

Title: Environmental implication and cancer risk assessment of residual pollutants in cotton crop: a case study of Multan District, Pakistan.

Author: Amna Parveen,Muzammil Anjum, Shahid Mahmood, Rab Nawaz & Azeem Khalid

Imprint: Environmental Monitoring and Assessment volume 195,
Article number: 1100 (2023)

Abstract: Pakistan is the fourth largest yarn producer in the world heavily that relies on cotton crop which receives a substantial 62% of all pesticide applications. The present study was conducted to quantify the levels of pesticides such as bifenthrin, spirotetramat, pyriproxyfen, imidacloprid, and diafenthiuron in soil and plants residue at selected cotton fields of Multan District, Pakistan. In addition to pesticides, the assessment of heavy metal concentration was also conducted in order to determine the overall risks that these compounds to both plants and human population. For this analysis, 20 soil samples and 10 plant samples were collected from 10 selected cotton fields. Pesticides and heavy metals in soil and plant samples were analyzed using high-performance liquid chromatography (HPLC) and Inductively Coupled Plasma-Optical Emission Spectroscopy (ICP-OES), respectively. It was observed that all samples collected from selected fields contained pesticide residue in top soil (0–15 cm). However, no pesticides were detected in the lower soil layer (16–30 cm). In case of heavy metals, the highest concentration of Fe, Pb, and Mn was observed in both soil and plant residue samples. The heavy metals were found in the order of Fe > Mn > Pb > Zn > Cu > Cd in the soil. The total carcinogenic risk values for a few pesticides were found to range from 10−6 to 10−2, indicating that residents of the study area have low to higher chances of developing cancer. A positive correlation was observed among the pesticides (r = 0.18–0.95) as well as in metals related parameters (r = 0.49–0.96), where a weak negative correlation was found among metal to pesticide parameters except Pd where the maximum r value was 0.62. In general, the finding of this study encourages the development and adoption of sustainable agricultural practices that lower the dependence on toxic pesticides and endorse environmentally friendly alternatives.

7

Title: Influence of Plant Geometry and Cultivars on Growth, Yield Attributes and Yield of HDPS Cotton under Rainfed Shallow Soils.

Author: R. Gouthami , U. Nagabhushanam , A. V. Ramanjaneyulu , B. Madhavi

Imprint: International Journal of Environment and Climate Change Volume 13, Issue 10, Page 245-250, 2023

Abstract: A field experiment was conducted at Siddapur research farm, Regional Agricultural Research Station, Warangal, Telangana, India during kharif 2022 to investigate the effect of plant geometry and cultivars on growth and yield of cotton under high plant density system. The results revealed that plant height (102.7 cm) and drymatter production (6499 kg ha-1) were significantly higher at ultra narrow spacing of 90 x 15 cm (74,074 plants ha-1) than medium and wider spacings of 90 x 30 and 90 x 60 cm, respectively but, was on par with narrow spacing of 90 x 20 cm (55,555 plants ha1). Though sympodial branches plant-1 (16.4) and number of bolls plant-1 (24.0) were significantly greater with wider spacing (90 x 60 cm: 18,518 plants ha-1), adoption of high plant density method of 90 x 15 cm spacing (74,074 plants ha-1) (2707 kg ha-1) and 90 x 20 cm (55,555 plants ha-1) (2498 kg ha-1) resulted in significantly higher seed cotton yield. The yield from 90x15 cm was 26.2% and 11.7% higher than that of 90 x 30 cm (2391 kg ha-1) and 90 x 60 cm (1998 kg ha-1), respectively. In case of cultivars, though growth and yield attributes were not significantly influenced, but, the boll weight (5.2) and seed cotton yield (2845 kg ha-1) were significantly higher with NCS 2778 over other cultivars viz., Bt Suraj (2151 kg ha-1), WGCV-79 (2310 kg ha-1) and ADB-39 (2288 kg ha-1).

8

Title: Simulation of root zone soil water dynamics under cotton-silverleaf nightshade interactions in drip-irrigated cotton

Author: Atinderpal Singh, Sanjit K. Deb, Lindsey C. Slaughter

Imprint: Agricultural Water Management, Volume 288, 1 October 2023, 108479

Abstract: The uncontrolled establishment of weeds in upland cotton (*Gossypium hirsutum* L.), especially perennial silverleaf nightshade (*Solanum elaeagnifolium*), reduces lint yield and quality of cotton primarily by competing with cotton to limit essential resources such as water. Quantitative insight into the effects of cotton-silverleaf nightshade interactions on the root water uptake (RWU) in cotton is needed to develop weed management systems, particularly based on the critical periods of competitive water uses. A field experiment was conducted during two consecutive cotton growing seasons (2019–2020) to evaluate root zone soil water dynamics in subsurface drip-irrigated cotton under three treatments: only cotton plants (CP), only silverleaf nightshade plants (SNP), and cotton-silverleaf nightshade plants grown together (CP-SNP). The numerical model HYDRUS (2D/3D) was calibrated and validated using experimental data under the CP, SNP, and CP-SNP systems. The results of numerical simulations suggested that the HYDRUS (2D/3D) provided an effective tool for helping to understand and predict soil water dynamics and RWU under the CP-SNP competitive interactions at different cotton growth stages. Simulations showed that actual RWU (i.e., transpiration) and evapotranspiration rates remained higher under the CP-SNP treatment during two consecutive growing seasons, and RWU and evapotranspiration rates were in the order of CP-SNP > SNP > CP. The temporal variations in cumulative transpiration, evaporation, and drainage fluxes revealed that RWU solely contributed to higher evapotranspiration rates under the CP-SNP system as the magnitudes and patterns of evaporation and drainage fluxes remained similar among all the treatments. The temporal variations in RWU patterns at different cotton growth stages suggested that higher competitive RWU under the CP-SNP system than CP and SNP occurred during cotton’s leaf development and flowering growth stages, indicating critical periods for competitive soil water uses. Weed control measures during these critical periods are essential to minimize competitive water uses under the CP-SNP system in semiarid environments.

9

Title: Genome-wide association study identifies *GhF3'H* affects the spiraeoside biosynthesis in waste cotton (*Gossypium hirsutum* L.) flowers

Author: Xiaomeng Zhang, Ruidan Dong

Imprint: Industrial Crops and Products, Volume 204, Part B, 15 November 2023, 117330
Abstract: Cotton flowers are rich in various flavonoids, exhibiting multiple biological activities, including antioxidant, anti-inflammatory, and anti-tumor effects. The biosynthetic mechanism of flavonoids in cotton flowers remains undefined. In this study, six macro-flavonoids were identified and quantified in the flowers of 373 *G. hirsutum* accessions based on HPLC technology. These flavonoids included quercetin (0–2.94 mg/g), isoquercetin (9.69–33.61 mg/g), hyperoside (2.54–8.78 mg/g), spiraeoside (0.87–7.10 mg/g), quercimeritrin (5.70–20.29 mg/g), and quercetin-3′-O-β-D-glucoside (4.23–21.87 mg/g). Several candidate genes associated with spiraeoside and quercimeritrin were identified through GWAS analysis. The study also revealed a significant upregulation of *GhF3'H* expression and an elevated content of spiraeoside in haplotype II compared to haplotype I. The ectopic overexpression of *GhF3'H* in tobacco led to a significant increase in dihydroquercetin, quercetin, and spiraeoside levels, and a decrease in naringenin content. LUC experiments confirmed

the potential positive regulation of *GhF3'H* by *GhTT2*. This study provides vital insights into the biosynthetic mechanism of macro-flavonoids in the flowers of upland cotton population. The identified elite haplotype and candidate genes hold great promise as valuable tools for enhancing flavonoid content in cotton, thus facilitating the efficient utilization of cotton by-products in the future.

10

Title: Influence of Different Plant Densities on Physiological Parameters Vis-À-Vis Architecture on Bt Cotton (Gossypium Hirsutum L.)

Author: K. Venkatkiran Reddy, Baby Akula, K. Indudhar Reddy, A. Madhavi, K. Supriya and T. Bharath

Imprint: The J. Res. PJTSAU 51(1&2) 25-38, 2023

Abstract: A field experiment was conducted on "Influence of plant density vis-à-vis architecture on Bt cotton (Gossypium hirsutum L.) yield and quality parameters" was carried out on sandy loam soil at College farm, College of Agriculture, PJTSAU, Rajendranagar, Hyderabad during 2021-23. The experiment was laid out in split plot design with three replications. Results revealed that physiological parameters viz., significant on leaf area index and light interception rate were record highest in semi open type. Specific leaf weight was found to be highest in compact type of plant canopy. Among plant densities, leaf area index and light interception rate were observed to be highest in plants planted under 90 x 20 cm (55,555 plants ha-1), while highest specific leaf weight was noticed highest in plant spacing of 90 x 60 cm (18,518 plants ha-1) during two years of study and pooled mean. Nonsignificant statistical differences were observed among canopy temperature and SPAD readings (chlorophyll content in leaves).

11

Title: Enhancement patterns of potassium on nitrogen transport and functional genes in cotton vary with nitrogen levels.

Author: Peng Chen, Linyang Li, Shujie Xia, Runhua Zhang

Imprint: Plant Science, Volume 335, October 2023, 111824

Abstract: The application of potassium (K) in conjunction with nitrogen (N) has been shown to enhance N use efficiency. However, there is still a need for further understanding of the optimal ratios and molecular regulatory mechanisms, particularly in soil-cotton systems. Here, a field trial was conducted, involving varying rates of N and K, alongside pot and hydroponic experiments. The objective was to assess the impact of N-K interaction on the absorption, transport and distribution of N in cotton. The results showed that K supply at 90 and 240 kg ha^{-1} had a beneficial impact on N uptake and distribution to both seed and lint, resulting in the highest N use efficiency ranging from 22% to 62% and yield improvements from 20% to 123%. The increase in stem and root diameters, rather than the quantify of xylem vessels and phloem sieve tubes, facilitated the uptake and transport of N due to the provision of K. At the molecular level, K supply upregulated the expression levels of genes encoding *GhNRT2.1* transporter and *GhSLAH3* channel in cotton roots to promote N uptake and *GhNRT1.5/NPF7.3* genes to transport N to shoot under low-N conditions. However, under high-N conditions, K supply induced anion channel genes (*GhSLAH4*) of roots to promote N uptake and genes encoding *GhNRT1.5/NPF7.3* and *GhNRT1.8/NPF7.2* transporters to facilitate NO_3^- unloading from xylem to mesophyll cell in high-N plants. Furthermore, K supply resulted in the upregulation of gene expression for *GhGS2* in leaves, while simultaneously downregulating the expression of *GhNADH-GOGAT, GhGDH1* and *GhGDH3 genes* in high-N roots. The enzyme activities of nitrite reductase and glutamine synthetase increased and glutamate dehydrogenase decreased, but the concentration of NO_3^- and soluble protein exhibited a significant increase and free amino acid decreased in the shoots subsequent to K supply.

12

Title: Mungari Cotton Strain 274.

Author: K. L. RAMAKRISNA RAO

Imprint: Madras Agricultural Journal Vol: 15, Issue: aug-aug, DOI: https://doi.org/10.29321/MAJ.10.A01388

Abstract: Introduction-Mungari cottons form a part of cottons generally known as Westerns" which is a trade term applied to cottons grown in Bellary District and adjacent Gooty taluk of Anantapur District and Pattikonda taluk of Kurnool District. This cotton, though graded as second class cotton due to shortness of its staple and uncertainty in yield owing to any precariousness of the season, is of no little importance to cotton market as it covers a huge area of nearly 1,150,000 acres. It is grown both on black and red soils, major portion however, being grown on black and loamy soils. It consists mainly of Gossypium Herbaceum but there are traces of Indicums and Neglectums, the latter have, however, spread in recent years with giant strides forming nearly 50 per cent of the bulk crop on red soils. They were first intro- duced in Adoni somewhere about 1900 but their extensive adoption dates from about 1916-17 and from this date these types were a serious rival to local cottons on red and mixed soils. Further, due to their heavy outturn they gain high commendations from the ryots whose main craving is quantity and not quality. In addition to this they are grown with less rainfall and also on lighter soils than the variety of Gossypium Herbaceums formerly grown.

13

Title: Effect of Planting Spaces and Topping Time on Productivity of Cotton Variety Super Giza 97.

Author: El-Sayed; Shaimaa, O.; El-Hendawy, Azza A.

Imprint: Menoufia Journal of Plant Production. Jun2023, Vol. 8 Issue 6, p125-149. 23p.

Abstract: A field experiment was carried out in 2021 season and repeated in 2022 season at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, Egypt to assess the effect of using hill spacing and topping time in addition to their interactions on productivity and quality of cotton cultivar Super Giza 97 (Gossypium barbadense L.). The experimental design was a split-plot with 3 replicates. The main plots were devoted to hill spacing (25, 30 and 35 cm), whereas plant topping time (no topping, manual topping at the formation of 12, 14 and 16 fruiting branches/plant) was allocated in the sub-plots. Data indicated that the widder hill spacing (35 cm) significantly increased total bolls number set/plant and bolls setting%, yield of seed cotton per feddan and its contributory characters as well as fiber length. However, plant height, bolls shedding% and the number of actual plants per feddan at harvest in both seasons were decreased. No topping treatment gave a significant excess in the final plant height and sympodia number/plant in the two seasons of study. Topping when 16 fruiting branches were formed on the plant gave a significant decrease in bolls shedding% and significant increase in numbers of total fruiting points and total bolls set/plant and bolls setting%, yield of seed cotton per feddan and its contributory characters in the two seasons in addition to length in the first season. Sowing cotton at 35 cm between plants interacted with topping cotton plants just after the formation of 16 fruiting branches gave the best results. It could be advised to apply this interaction treatment under Sakha region, to increase cotton productivity of cotton cultivar Super Giza 97.

14

Title: Adoption of Improved Cotton Cultivation Practices among the Farmers in Sriganganagar District of Rajasthan, India .

Author: Jaipal, N. R. Meena , R. K. Doharey , Soniya Rishi and Smita Singh

Imprint: Asian Journal of Agricultural Extension, Economics & Sociology Volume 41, Issue 9, Page 927-930, 2023

Abstract: The study was conducted during the year 2022 in Padampur and Suratgarh blocks of Sriganganagar district of Rajasthan to study the extent of adoption of cotton growers on improved cotton cultivation practices. A sample size of 120 respondents was selected based on proportionate random sampling procedure. Personal interviews with the help of a structured schedule were taken for data collection The study revealed that majority of the respondents (58.34%) had medium level of adoption of improved cotton cultivation practices followed by 30% high and 11.66% low level of adoption of Cotton cultivation practices by the respondents. The study analyzed that high adoption found in time of sowing cotton with 89.30 MPS, and respondents had less adoption of seed treatment in cotton crop with 61.66 MPS.

CROP PROTECTION

15

Title: Effect of Weather Parameters in Relation to Occurrence and Development of Leaf Blight (*Alternaria macrospora*) of Cotton.

Author: R. J. Chaudhari, M. M. Talpada, A. C. Detroja and S. N. Galani

Imprint: Biological Forum – An International Journal 15(8): 488-495(2023)

Abstract: In the present context, cotton farming in India is far from being a sustainable agricultural system. India is the second-largest producer of conventional cotton after China. More than 90% of the cotton is produced from genetically modified, pest-resistant, high yielding Bt cotton varieties. In relation to weather parameters, impact of different meteorological parameters on development of leaf blight on cotton, first leaf blight (Alternaria macrospora) symptoms were appeared on 37th and 39th standard meteorological week during 2020-21 and 2021-22, respectively. In correlation study, maximum temperature was non-significant with negative effect on leaf blight disease development in year 2020-21, while maximum temperature was also non-significant but positive effect leaf blight disease development in year 2021-22. Minimum temperature was non-significant with negative effect in year 2020-21 and 2021-22, respectively. Morning and evening relative humidity was significant and highly significant in both years, respectively and wind speed opposite to RH. Regression study, in year 2020-21 reflect that one per cent increase in morning relative humidity and wind speed led to corresponding decrease in per cent disease index of Alternaria blight in 2020-21 and 2021-22. This study focuses on impact of weather parameters on fungal foliar diseases and tackles the problem as well. Weather parameters play vital and crucial role in

formation, development and multiplication of new virulence pathogen, so its challenges to researchers for identification of responsible different gene for it.

16

Title: The cotton *MYB33* gene is a hub gene regulating the trade-off between plant growth and defense in *Verticillium dahliae* infection.

Author :Hu Guang , Ge Xiaoyang , Wang Zhian

Imprint: Journal of Advanced Research, Available online 28 August 2023

Abstract: Sessile plants engage in trade-offs between growth and defense capacity in response to fluctuating environmental cues. MYB is an important transcription factor that plays many important roles in controlling plant growth and defense. However, the mechanism behind how it keeps a balance between these two physiological processes is still largely unknown. Objectives:Our work focuses on the dissection of the molecular mechanism by which *GhMYB33* regulates plant growth and defense. Methods:The CRISPR/Cas9 technique was used to generate mutants for deciphering *GhMYB33* functions. Yeast two-hybrid, luciferase complementary imaging, and co-immunoprecipitation assays were used to prove that proteins interact with each other. We used the electrophoretic mobility shift assay, yeast one-hybrid, and luciferase activity assays to analyze *GhMYB33* acting as a promoter. A β-glucuronidase fusion reporter and 5′ RNA ligase mediated amplification of cDNA ends analysis showed that ghr-miR319c directedly cleaved the *GhMYB33* mRNA.

17

Title: Upland cotton and nematodes: An analysis of historical resistance, upcoming threats, and coinoculation effects .

Author: Amanda Gaudin Approved by: Seung Joon Ahn (Major Professor) Ling Li Martin J. Wubben Sead Sabanadzovic Natraj Krishnan (Graduate Coordinator) Scott T. Willard (Dean, College of Agriculture and Life Sciences)

Imprint: A Dissertation Submitted to the Faculty of Mississippi State University in Partial Fulfillment of the Requirements for the Degree of Doctor of Philosophy in Biochemistry in the Department of Biochemistry Mississippi State, Mississippi August 2023

Abstract: Upland cotton (*Gossypium hirsutum*) is an important fiber crop grown throughout the southern United States. Plant-pathogenic nematodes are worm-like animals that feed on the roots of most agronomic crops, including cotton. The southern root-knot nematode (Meloidogyne incognita, RKN) and the reniform nematode (Rotylenchulus reniformis, RN) cause significant yield losses in cotton every year. Current sources of resistance are effective but limited, therefore historical screenings of cotton accessions were revisited in search for novel resistance sources. None were identified but many of the screened accessions possessed markers of known root-knot nematode and reniform nematode resistance. The emerging guava root-knot nematode (Meloidogyne enterolobii, GRKN) is a risk for upland cotton production, and identifying host plant resistance would greatly reduce the yield losses for growers. Assays were conducted on the currently available RN and RKN resistance sources inoculated with GRKN. No known nematode resistance gene suppressed GRKN infection, indicating that work must be done to protect crops from the eventual discovery of GRKN in Mississippi fields. Using the same resistance sources, tests were conducted to determine if the currently available resistances to RKN and RN offer any suppression of secondary infection of non-target nematode species for resistance. This is referred to as systemic acquired resistance, which is the induction of non-specific plant defense. Assays found that early inoculation with the nematode targeted by resistance did not effect infection by a secondary nematode species.

18

Title: Dominance of Cotton leaf curl Multan virus-Rajasthan strain associated with third epidemic of cotton leaf curl disease in Pakistan.

Author: Muhammad Arslan Mahmood, Nasim Ahmed

Imprint: Research Square Posted Date: August 11th, 2023 DOI: https://doi.org/10.21203/rs.3.rs-3215589/v1

Abstract: Cotton (Gossypium hirsutum) is an economically potent crop in many countries including Pakistan, India, and China. For the last three decades, cotton production is under the constant stress of cotton leaf curl disease (CLCuD) caused by begomoviruses/satellites complex that is transmitted through the insect pest, whitefly (Bemisia tabaci). Previously, in 2018, we have identified a highly recombinant strain; Cotton leaf curl Multan virus-Rajasthan (CLCuMuV-Raj) associated with the single strain of Cotton leaf curl Multan betasatellite-Vehari (CLCuMuB Veh) that are dominant in cotton-growing hub areas of central Punjab, Pakistan causing third CLCuD epidemic. In the present study, we have explored the CLCuD diversity from central to southern districts of Punjab (Faisalabad, Lodhran, Bahawalpur, Rahimyar Khan) and the major cotton-growing region of Sindh (Tandojam), Pakistan for two years (2020-21). Interestingly, we found same virus strain (CLCuMuV-Raj) and associated betasatellite strain that was previously reported with the third epidemic in the central Punjab region.

Furthermore, we found minor mutations in two genes of CLCuMuV-Raj C4 and C1 in 2020 and 2021 respectively as compared to its isolates in 2018, which exhibited virus evolution. Surprisingly, we did not find these mutations in CLCuMuV-Raj isolates identified from Sindh province. The findings of the current study represent the stability of CLCuMuV-Raj strain and its spread toward the Sindh province where previously Cotton leaf curl Kokhran virus (CLCuKoV) and Cotton leaf curl Shahdadpur virus (CLCuShV) have been reported. The findings of the current study demand future research on CLCuD complex to explore the possible reasons for prevalence in the field and how the virus-host-vector compatible interaction can be broken to develop resistant cultivars.

19

Title: Chitinase of Trichoderma longibrachiatum for control of Aphis gossypii in cotton plants

Author: Waheed Anwar, Huma Amin, Hafiz Azhar Ali Khan, Adnan Akhter, Uzma Bashir

Imprint: Scientific Reports volume 13, Article number: 13181 (2023)

Abstract: Chitinase-producing fungi have now engrossed attention as one of the potential agents for the control of insect pests. Entomopathogenic fungi are used in different regions of the world to control economically important insects. However, the role of fungal chitinases are not well studied in their infection mechanism to insects. In this study, Chitinase of entomopathogenic fungi Trichoderma longibrachiatum was evaluated to control Aphis gossypii. For this purpose, fungal chitinase (Chit1) gene from the genomic DNA of T. longibrachiatum were isolated, amplified and characterised. Genomic analysis of the amplified Chit1 showed that this gene has homology to family 18 of glycosyl hydrolyses. Further, Chit1 was expressed in the cotton plant for transient expression through the Geminivirus-mediated gene silencing vector derived from Cotton Leaf Crumple Virus (CLCrV). Transformed cotton plants showed greater chitinase activity than control, and they were resistant against nymphs and adults of A. gossypii. About 38.75% and 21.67% mortality of both nymphs and adults, respectively, were observed by using Chit1 of T. longibrachiatum. It is concluded that T. longibrachiatum showed promising results in controlling aphids by producing fungal chitinase in cotton plants and could be used as an effective method in the future.

20

Title: Molecular Characterization of Pollinators in Cotton Ecosystem.

Author: Kavita Bajaj, Pardeep Kumar Chhuneja, Bharathi Mohindru and Jaspal Singh

Imprint: Indian Journal of Entomology Online published Ref. No. e23073 DoI. No.: 10.55446/IJE.2023.1073

Abstract: DNA barcoding using cytochrome c oxidase I (mtCO1) for molecular characterization is a taxonomic method that uses a short genetic marker in an insect DNA to identify a species, including an unknown species. The coming-to-light of this identification tool is timely when we are facing perhaps the greatest rate of species loss in recent millennia. This study contributes to increasing the number of published accounts of DNA barcoding and accurately distinguishing the pollinator fauna of cotton in Punjab, India. The mtCOI region of all the samples was amplified, cloned and the nucleotide sequences were determined and analyzed. This study reveals that specimens collected in cotton belong to order Hymenoptera and Diptera. Hymenopterans include Apis dorsata, Apis florea, Xylocopa fenestrata, Sceliphron madraspatanum and Polistes wattii. Dipterns include Eristalinus quinquelineatus and Musca convexifrons.

21

Title: Influence of High Density Planting System (HDPS) on Occurrence of Fungal Foliar Diseases in Cotton.

Author: Ch Yamuna, S L Bhattiprolu, V Prasanna Kumari, Ch Chiranjeevi and P Anil Kumar

Imprint: The Andhra Agric. J 66 (4): 628-631, 2019

Abstract: Optimum plant density is one of the determining factors to reap potential yields in any crop. In cotton HDPS is advocated for varieties to realise maximum yields under rainfed conditions in light soils. Hence, a study was conducted to understand the impact of HDPS on fungal foliar diseases in cotton. Diseases were recorded at different stages of crop viz., seedling, squaring, flowering, boll formation and boll development, boll maturity and bursting and boll bursting and picking stages.Alternaria leaf spot appeared at seedling stage and reached maximum during boll formation and boll development stage. The percent disease index (PDI) ranged from 10 to 21% in different compact genotypes during boll formation and boll development stage. Corynespora leaf spot was observed during boll maturity and boll bursting stage with 3.0 to 5.0 PDI; grey mildew and rust diseases were observed during boll bursting and picking stage with 4.0 to 7.0 and 5.0 to 13.0 PDI, respectively.

22

Title: The colonization of endophytic Bacillus velezensis BHZ-29 in cotton enhances defence enzyme activities against cotton Verticillium wilt.

Author: Yingwu shi, HongMei Yang

Imprint: Research Square, August 29th, 2023 DOI: https://doi.org/10.21203/rs.3.rs-3232137/v1

Abstract: In order to clarify the colonization characteristics and induced disease resistance of endophytic bacteria against Verticillium dahliae, the colonization ability in cotton and the defence enzyme activities of cotton were determined by using the antibiotic labeling method and the greenhouse pot culture method, respectively. The results showed that there was no significant difference in morphological characteristics, antagonistic ability and disease prevention effect between RIF-resistant strains and original strains. The colonization experiment showed that BHZ-29 could be effectively colonized in the roots, stems and leaves of the three varieties of cotton, and the colonization ability was ranked as root > stem > leaf. The colonization dynamics of B. velezensis BHZ-29 in different resistant varieties of cotton showed that the maximum colonization amount of root was 9.13 × 10 5 CFU/g for Xinluzao 61T, 1.82 × 10 5 CFU/g for 9T, and 1.30 × 10 5 CFU/g for Xinluzao 36S. The activities of defense enzymes among three varieties of cotton showed an initial increasing trend after which it decreased, ranked in the following order: BHZ-29 + VD > BHZ-29 > CK > VD. The highest Vc content of Xinluzao 36S inoculated with BHZ-29 + VD was 2281.12 μg/g ·FW, Xinluzao 61T inoculated with BHZ-29 was 2278.30 μg/g ·FW, 9T inoculated with BHZ29 + VD was 2268.43 μg/g FW. The order of MDA content in the three varieties was VD > CK > BHZ-29 > BHZ-29 + VD.

PLANT GENETICS AND BREEDING

23

Title: Characterization of a cotton interspecific hybrid of American cotton with wild species G. armourianum

Author: Debadatta Panda, M. Kumar, L. Mahalingam

Imprint: Environment Conservation Journal. Published Aug 16, 2023, DOI https://doi.org/10.36953/ECJ.19602553

Abstract: Wild species constitute a source of valuable genes for many adverse climatic conditions, disease and pests. To match up the level of quick depleting insect pest and disease resistance and fast evolving pests, it is the urge of the hour to broaden the resistance base. In order to achieve this goal in cotton, wide hybridization was performed between *G. hirsutum* (AADD) cv. MCU5, CO14 and CO17, and *G. armourianum* and interspecific hybrids developed were characterized for several morphological characters for obtaining an idea about the status of the various traits. Interspecific hybrid developed with all three *G. hirsutum* varieties are potential lines for future introgression programs of insect and disease resistance along with other useful traits. The F_1 hybrid displayed intermediate expression for most of the traits. Traits like colour of the stem, leaf colour, position of stigma, nectarines of hybrid completely resembled wild parent-and are considered as dominant in expression. The petal spot was present in the hybrid similar to that wild parent, unlike the cultivated parent; this appeared with different levels of intensity in F_1 along with other characters like colour of the anther, and filament colour. Hybrids had profuse flowering throughout the year with low pollen load and pollen of variable shape and size expressing sterility to partial fertility. Noteworthy differentiation was seen between the leaf size and size of other plant parts of the hybrid.

24

Title: The cotton miR171a-*SCL6* module mediates plant resistance through regulating *GhPR1* expression

Author: Guang Hu, Xiaoyang Ge, Peng Wang

Imprint: Plant Physiology and Biochemistry, Volume 202, September 2023, 107995

Abstract: Plants have developed intricate defense mechanisms in response to fluctuating environmental cues, including the use of microRNA (miRNA) as post-transcriptional regulators. However, the specific mechanisms through which miRNA contributes to disease resistance remain largely elusive. While the miR171-*SCLs* have been investigated in an eclectic array of plants, there has been a notable scarcity of research specifically focused on cotton (*Gossypium hirsutum*). In our previous miRNA-sequencing analysis, we found that ghr-miR171a displayed a differential response to infections by *Verticillium dahliae*. In this study, we further investigated the function of the miR171a-*SCL6* module in cotton during *V. dahliae* infection. The ghr-miR171a was confirmed to direct the cleavage of *GhSCL6* mRNA in the post-transcriptional process, as evidenced by 5′ RLM-RACE, β-glucuronidase (GUS) histochemical staining and enzyme activity assay. Interestingly, we found that overexpressing ghr-miR171a reduced cotton plants' resistance to *V. dahliae*, while suppressing ghr-miR171a increased the plants' defense capacity. The GhSCL6 protein, when fused with green fluorescent protein (GFP), localizes in the cell nucleus, indicating its potential role in gene regulation. This was further corroborated by yeast two-hybrid assays, which verified GhSCL6's transcriptional activation ability. Through quantitative reverse transcriptase PCR (qRT-PCR), luciferase (LUC) fluorescence, and yeast one-hybrid assays, we found that GhSCL6 binds to the GT-box element of the *GhPR1* promoter, activating its expression and thereby enhancing plant disease resistance. Taken together, our findings demonstrate that the cotton miR171a-*SCL6* module regulates Verticillium wilt resistance in plants through the post-transcriptional process. This insight may offer new perspectives for disease resistance strategies in cotton.

25

Title: Genetic diversity among coloured cotton genotypes in relation to their fibre colour and ploidy level based on SSR markers.

Author: Revanasiddayya, Jayaprakash Mohan Nidagundi, Bashasab Fakrudin, Prakash Kushner, Lingappa Neelagiri Yogeesh, Shivanand Hanchinal

Imprint: Czech J. Genet. Plant Breed. X: X | DOI: 10.17221/12/2023-CJGPB

Abstract: Genetic diversity is referred to as any variation at the phenotypic, DNA or genomic level of an individual, population or species. The appraisal of diversity is important to understand its pattern and evolutionary relationships between germplasms or genotypes, which will aid in sampling the genetic resources in a more systematic manner for conservation and crop improvement. The present study employed 50 simple sequence repeat (SSR) markers linked to the yield and fibre quality/colour traits for estimating the genetic diversity in 33 cotton genotypes of diploid and tetraploid species differing in fibre colour. The diversity analysis was performed in GenAlEx (Ver. 6.41) and Powermarker (Ver. 3.25) while DARwin (Ver. 6.0.21) software was used to establish the phylogenetic relationships following neighbour-joining (NJ) and unweighted pair group method with arithmetic (UPGMA) mean method. Markers generated 186 polymorphic loci as genotypic data with an average of 3.72 alleles and an average polymorphic information content (PIC) value of 0.59 per SSR locus. The NJ and UPGMA grouped 33 genotypes into three major clusters I, II and III consisting of 21 tetraploid Gossypium hirsutum, 10 G. arboreum coloured and 2 white cotton genotypes, respectively. In the PCA, the first two components (PC1 and PC2) explained 74.69% of the variation and the biplot plotted the 33 genotypes in three groups. The study established the diverse nature of 33 cotton genotypes based on their fibre colour and ploidy level. With confirmation of the prevalent genetic diversity, we suggest that hybridisation can be planned among diverse genotypes to unleash greater variation in the fibre colour or to derive superior cross combinations.

26

Title: Cotton Variety 20R827B3TXF

Inventor: Dawn E Fraser, Darren G Jones, O. Lloyd May

Current Assignee Monsanto Technology LLC

Abstract: The invention relates to the novel cotton variety designated 20R827B3TXF. Provided by the invention are the seeds, plants, plant parts and derivatives of the cotton variety 20R827B3TXF. Also provided by the invention are methods of using cotton variety 20R827B3TXF and products derived therefrom. Still further provided by the invention are methods for producing cotton plants by crossing the cotton variety 20R827B3TXF with itself or another cotton variety and plants and seeds produced by such methods.

27

Title: Registration of Arkot 1112, Arkot 1114, and Arkot 1115 cotton germplasm lines

Author: Fred M. Bourland, Don C. Jones

Imprint: Journal of Plant Registrations 29 August 2023,
https://doi.org/10.1002/plr2.20320

Abstract: Arkot 1112 (Reg. no. GP-1139, PI 702559), Arkot 1114 (Reg. no. GP-1140, PI 702560), and Arkot 1115 (Reg. no. GP-1141, PI 702561) are conventional cotton (*Gossypium hirsutum* L.) germplasm lines released by the Arkansas Agricultural Experiment Station in November, 2022. The three lines share Arkot 0306 (PI 671966) as a common parent. The second parents for Arkot 1112, Arkot 1114, and Arkot 1115 were 'UA222' (US patent no. 8,859,862), Arkot 0309 (PI 669969), and Arkot 0316 (PI 669970), respectively. The three lines were compared with 'UA48' and UA222 in replicated field tests at four Arkansas sites over 5 years. Over these tests, each of the three lines produced about 11 and 25% higher lint yields than UA48 and UA222, respectively. Lint yields of Arkot 1115 exceeded those of Arkot 1112 and Arkot 1114. Over 10 locations of the 2019 Regional Breeders Testing Network test, lint yields of Arkot 1112, Arkot 1114, and Arkot 1115 were equal to each other and ranked third, fourth, and fifth, respectively, out of 22 genotypes, indicating that the lines have wide adaptation. Leaf pubescence, stem pubescence, and bract trichome density of the lines were higher than UA48 and similar to UA222. All three lines displayed high resistance to bacterial blight. The lines were more resistant to tarnished plant bug than UA48 but were more susceptible to tarnished plant bug than UA222. Fiber quality of Arkot 1115 approached that of UA48 (excellent fiber quality), whereas Arkot 1112 and Arkot 1114 was similar to UA222 (good fiber quality).

28

Title: Cotton variety 11pwpy94

Inventor: Mustafa McPherson

Current Assignee: Phytogen Seed Co LLC

Abstract: The disclosure relates to a cotton variety, designated 11PWPY94, the plants and seeds of the cotton variety 11PWPY94, methods for producing a cotton plant, either varietal or hybrid, produced by crossing the cotton variety 11PWPY94 with itself or with another cotton plant, hybrid cotton seeds and plants produced by crossing the variety 11PWPY94 with another cotton variety or plan, methods for producing a cotton plant containing in its genetic material one or more transgenes, and the transgenic cotton plants produced by that method. This disclosure also relates to cotton varieties derived from cotton variety 11PWPY94, to methods for producing other cotton varieties derived from cotton variety 11PWPY94, and to the varieties derived by the use of those methods.

29

Title: Cotton variety 11pujj24

Inventor: Karl Brauer

Current Assignee: Phytogen Seed Co LLC

Abstract: The disclosure relates to a cotton variety, designated 11PUJJ24, the plants and seeds of the cotton variety 11PUJJ24, methods for producing a cotton plant, either varietal or hybrid, produced by crossing the cotton variety 11PUJJ24 with itself or with another cotton plant, hybrid cotton seeds and plants produced by crossing the variety 11PUJJ24 with another cotton variety or plan, methods for producing a cotton plant containing in its genetic material one or more transgenes, and the transgenic cotton plants produced by that method. This disclosure also relates to cotton varieties derived from cotton variety 11PUJJ24, to methods for producing other cotton varieties derived from cotton variety 11PUJJ24, and to the varieties derived by the use of those methods.

30

Title: Site regression and multivariate analysis for genetic diversity in *Gossypium barbadense* accessions.

Author: K. Baghyalakshmi, S. Manickam, M. Amutha, A. Sampathkumar, M. G. Yamuna and A. H. Prakash

Imprint: Electronic J.of Plant Breeding https://doi.org/10.37992/2023.1403.088 Vol 14(3): 1

Abstract: In India, Gossypium barbadense is cultivated in niche areas in the south and central regions of the country, especially for its quality fibre. Initially, 50 barbadense accessions were screened for their stability across 2 years from the germplasm maintained at ICAR, CICR, RS germplasm, and stable diverse genotypes were selected for further breeding. The results indicated that ICB 262, ICB 174 and ICB 73 were early maturing. ICB 264, CCB 26 and ICB 73 showed tolerance to sucking pests due to their higher trichome density (TD), gossypol glands and epicuticular wax (ECW). G × E interactions were analysed for the 2019–2020 and 2020–2021showed that traits like number of bolls, single plant yield and fibre strength could express better during 2019–

2020, single boll weight and micronaire were dominant in season 2. Traits like ginning percentage and fibre length were stable across environments indicating that their expression is genetically controlled. PCA results indicated that about 91.45% of total variability was explained by PCA1, 2 and 3. Diversity analysis grouped the accessions into four major clusters with two sub-clusters in groups 2, 3 and 4, hence forming seven groups. The minimum distance was observed between ICB 176 and CCB 11 (0.56) and the maximum distance was observed between ICB 174 and ICB 1 (3.11).

31

Title: Trait Correlations and Implications for Yield Potential in Cotton: A Comprehensive Study.

Author: Hussain Z, Muzamil M, Saeed Mr1, Naheed K, Kareem M, Munir A, Haider Mz, Sami A

Imprint: Biological and Agricultural Sciences Research Journal2023: 24. doi: https://doi.org/10.54112/basrj.v2023i1.24]

Abstract: Cotton (*Gossypium hirsutum* L.) yield improvement is a primary objective for breeders and researchers. This study explores trait correlations and their impact on cotton yield potential. Through field experiments and statistical analyses, relationships between traits and yield to provide insights for cotton breeding programs was investigated. Results revealed significant associations between traits and cotton yield. Plant height, number of nodes, monopodial branches and open ball showed positive correlations with yield. Taller plants, increased sympodial branches and more open balls were linked to higher yield potential. SS32 RH-668, NIAB-KIRAN and CIM-599 per form better among 19 genotypes. Further research is needed to establish causality. The study emphasizes that when selecting cotton genotypes for better yield potential, it's crucial to consider traits like sympodial branches, boll weight, open ball and green ball. Understanding their direct and indirect effects can help breeders develop varieties with desired characteristics and maximize yield. Additionally, the study found significant genetic variability among tested genotypes creating opportunities for breeding programs to enhance yield and desired traits. These findings offer valuable insights into trait correlations, paving the way for future research on genetics and developing better cotton varieties to meet global demand.

32

Title: Characterization and fine mapping of a yellow leaf gene regulating chlorophyll biosynthesis and chloroplast development in cotton (*Gossypium arboreum*)

Author: Liqiang Fan, Yan Hou, Lei Zheng

Imprint: Gene, Volume 885, 15 November 2023, 147712

Abstract: Chlorophyll biosynthesis and chloroplast development are essential for photosynthesis and plant growth. *Gossypium arboreum*, a valuable source of genetic variation for cotton improvement, remains poorly studied for the mechanisms regulating chlorophyll biosynthesis and chloroplast development. Here we created a *G. arboreum* etiolated leaf and stuntedness (*els*) mutant that displayed a distinct yellow color of leaves, bracts and stems throughout the whole growth, where chlorophyll accumulation in leaves was reduced and chloroplast development was delayed. The *GaCHLH* gene, which encodes the H subunit of magnesium chelatase (Mg-chelatase), was screened by MutMap and KASP analysis. Compared to *GaCHLH*, the gene *Gachlh* of the mutant had a single nucleotide transition (G to A) at 1549 bp, which causes the substitution of a glycine (G) by a serine (S) at the 517th amino acid, resulting in an abnormal secondary structure of the *Gachlh* protein. *GaCHLH*-silenced SXY1 and ZM24 plants exhibited a lower *GaCHLH* expression level, a lower chlorophyll content, and the yellow-leaf phenotype. *Gachlh* expression affected the expression of key genes in the tetrapyrrole pathway. *GaCHLH* and *Gachlh* were located in the chloroplasts and that alteration of the mutation site did not affect the final target position. The BiFC assay result indicated that *Gachlh* could not bind to *GaCHLD* properly, which prevented the assembly of Mg-chelatase and thus led to the failure of chlorophyll synthesis. In this study, the *Gachlh* gene of *G. arboreum els* was finely localized and identified for the first time, providing new insights into the chlorophyll biosynthesis pathway in cotton.

33

Title: Genome-wide association study reveals novel genes on different chromosomal positions regulating boll weight in upland cotton (Gossypium hirsutum L.)

Author: Zubair Iqbal,Muhammad Shahid Iqbal, Salman Alamery, Khurram Shehzad, Qamar U. Zaman,

Imprint: Genetic Resources and Crop Evolution (2023)

Abstract: The boll weight (BW) is the most decisive yield component character and is utilized as a key index for selection in various cotton improvement programs. In the current study, 1260 accessions of cotton with a diverse genetic background were assessed for boll weight across four different environments (two locations for each environment) in China. A genome-wide association study (GWAS) was performed to mine novel single nucleotide polymorphisms (SNPs) controlling boll weight characteristics. A total of 1,122,352 SNPs were identified in association with boll weight across multiple environments, of which 138 were designated as key SNPs, harboring significantly higher association peaks for the all chromosomes on the basis of log10 P value (− log10 ≥ 6). Among 53 significant associations related to BW development across environments were identified. Six genes in the vicinity of these key SNPs (Pentatricopeptide repeat-containing protein PCMP-E76), Trihelix transcription factor ASIL2, Auxin-responsive protein SAUR50, Floral homeotic protein AGAMOUS (AG), Piriformospora indica-insensitive protein 2 (PII-2), and LOB domain-containing protein 16 (LBD16) exhibited higher expression patterns. These identified BW-related key SNPs and candidate genes could prove to have potential for influencing BW development in upland cotton. The outcome of the current study will serve as a base for further mechanistic research focused on the exploitation of BW for accelerated cotton improvement.

34

Title: Complex Analysis of New Interspecific F1 Hybrids Obtained From Crossing Cotton Monosomic Lines of The G.Hirsutum L. With The Pima 3-79 Line of the Species G.Barbadense L.

Author: F. Sanamyan, Sh.U. Bobokhujayev, Sh.S. Abdukarimov

Imprint: International Scientific Journal”Modern Biology & Genetics” 2023, 2(4)

Abstract: Analysis of F1 hybrids obtained from crossings of five monosomic cotton lines of the species *G. hirsutum* L. with the donor line Pima 3-79 of the species *G.barbadense* L., using SSR markers previously assigned to the chromosomes, revealed monosomic seedlings in seven hybrid families of four variants of crossings (with the participation of lines Mo69, Mo71, Mo76, Mo81), and also confirmed the earlier identification. This analysis contributed to the rapid identification of monosomic cytotypes at the seedling stage and the earlier involvement of hybrids in backcrossing. However, among the hybrid seedlings of one crossing variant (Mo79xPima 3-79), monosomic cytotypes were not found. Analysis of chromosome pairing in F1 hybrid monosomics lacking chromosome 4 of the cotton At-subgenome showed chromosome pairing normal for monosomics with the formation of 25 bivalents and one medium-sized univalent in all studied PMCs. The study of buds at the sporad stage revealed a high meiotic index and the formation of a small number of tetrads with micronuclei, while the study of pollen fertility revealed its variation between high and low, indicating a latent structural interspecific variability not recorded at the metaphase I stage of meiosis, leading to the formation partially unbalanced gametes.

35

Title: Genetic variability exploration in upland cotton (*Gossypium hirsutum* L.) for yield and fiber traits.

Author: Hardik H Patel, Kalpesh V Patel, Vipul L Suthar, Rahul J Parmar and Sunil K Patel

Imprint: The Pharma Innovation Journal 2023; 12(8): 628-634

Abstract This experiment aimed to investigate genetic variability among the all genotypes along with heritability presence, genetic advance per cent over mean, correlation studies and path coefficient carried out for 17 different characters in 16 genotypes, including sixty-four F1 hybrids, and one check G. Cot. Hy. 18 of upland cotton (Gossypium hirsutum L.). The trail was demonstrated during the Kharif season of 2022 at the Regional Research Station (RRS), Anand Agricultural University, India. Variability studies revealed high phenotypic coefficient of variation (PCV) and moderate genotypic coefficient of variation (GCV) for the number of bolls per plant, lint yield per plant and seed cotton yield per plant. Additionally, the number of monopodia per plant exhibited a high estimate of both PCV and GCV. Heritability analysis showed high heritability for various traits, including days to 50% flowering, days to 50% boll bursting, plant height, monopodia per plant, sympodia per plant, number of bolls per plant, boll weight, lint yield per plant, seed cotton yield, seed index, fiber strength, fiber fineness, and seed oil content. Moreover, days to 50% flowering, plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, lint yield per plant, seed cotton yield, fiber fineness, and seed oil content demonstrated both high heritability and significant genetic advance as per cent over the mean. This stipulate significant attributing part of additive gene action in the heredity of these characteristics. During the correlation study, it was found that seed cotton yield per plant showed noteworthy positive correlations with several traits: the number of sympodia per plant (0.29), the number of bolls per plant (0.77), fiber length (0.26), uniformity index (0.37), and lint yield per plant (0.95). Path analysis revealed that seed index and ginning outturn had the highest positive and direct effects on seed cotton yield per plant.

36

Title: Combining ability and gene action studies for yield and fibre traits in *Gossypium arboreum* using Griffings numerical and Haymans graphical approach

Author: Sukrutha Bhimireddy, Rajeswari Sivakami, Premalatha N., Boopathi Narayana Manikanda, Thirukumaran K. & Manivannan A.

Imprint: Journal of Cotton Research Open Access, Published: 08 August 2023
Volume 6, Article number: 12 (2023)

Abstract: For the purpose of utilizing hybrid vigour to produce possible hybrids with a suitable level of stability, the knowledge of gene activity and combining ability is a crucial prerequisite before choosing desirable parents. The present study was carried out with six parents crossed in full diallel fashion and generated 30 F_1 hybrids. These hybrids were evaluated in two replications in Randomized Block Design at Department of Cotton, TNAU for combining ability and gene action. Diallel analysis was carried out according to Griffing's method-I (parents + F_1 + reciprocals) and model-I and Hayman's graphical approach by using INDOSTAT software. Results Analysis of variance for combining ability indicated that mean square values of GCA, SCA and reciprocals were highly significant for all the traits except for the uniformity index. RG763 and K12 showed highly positively significant GCA effects for most of the yield traits while PA838 and K12 for fibre quality traits, so they were found as best general combiners. PAIG379 × K12 and PDB29 × K12 for yield traits, and PDB29 × PA838, RG763 × PA838, and CNA1007 × RG763 cross combinations for fibre quality traits could be recommended for future breeding programms. Conclusion The results of both Griffing's and Hayman's approaches showed that non-additive gene action predominates as SCA variance was bigger than GCA variance, so heterosis breeding is thought to be a more fruitful option for enhancing GCA of many traits.

FIBER AND FIBER TECHNOLOGY

37

Title: GhXB38D represses cotton fibre elongation through ubiquitination of ethylene biosynthesis enzymes GhACS4 and GhACO1.

Author: Qingwei Song, Wanting Gao, Chuanhui Du, Wenjie Sun, Jin Wang, and Kaijing Zuo

Imprint: Plant Biotechnology Journal (2023), pp. 1–15 doi: 10.1111/pbi.14138

Abstract: Ethylene plays an essential role in the development of cotton fibres. Ethylene biosynthesis in plants is elaborately regulated by the activities of key enzymes, 1-aminocyclopropane-1- carboxylate oxidase (ACO) and 1-aminocyclopropane-1-carboxylate synthase (ACS); however, the potential mechanism of post-translational modification of ACO and ACS to control ethylene synthesis in cotton fibres remains unclear. Here, we identify an E3 ubiquitin ligase, GhXB38D that regulates ethylene biosynthesis during fibre elongation in cotton. GhXB38D gene is highly expressed in cotton fibres during the rapid elongation stage. Suppressing GhXB38D expression in cotton significantly enhanced fibre elongation and length, accompanied by the up-regulation of genes associated with ethylene signalling and fibre elongation. We demonstrated that GhXB38D interacts with the ethylene biosynthesis enzymes GhACS4 and GhACO1 in elongating fibres and specifically mediates their ubiquitination and degradation. The inhibition of GhXB38D gene expression increased the stability of GhACS4 and GhACO1 proteins in cotton fibres and ovules, resulting in an elevated concentration of ethylene. Our findings highlight the role of GhXB38D as a regulator of ethylene synthesis by ubiquitinating ACS4 and ACO1 proteins and modulating their stability. GhXB38D acts as a negative regulator of fibre elongation and serves as a potential target for enhancing cotton fibre yield and quality through gene editing strategy

38

Title: Efficient genome editing in cotton using the virus-mediated CRISPR/Cas9 and grafting system

Author: Wei-Feng Guo, Dan-Dan Guo, Fen Li, Shen-Zhai Shang, Ting-Wan Li, Ying-Chao Tang, Man Jiang, Fu-Chun Xu & Wei Gao

Imprint: Plant Cell Reports (2023)

Abstract: The extensive application of CRISPR in cotton was limited due to the labor-intensive transformation process. Thus, we here established a convenient method of CRISPR in cotton by CLCrV-mediated sgRNA delivery. The data that support the findings of this study are available from the corresponding author upon reasonable request.

39

Title: Single-cell resolution analysis reveals the preparation for reprogramming the fate of stem cell niche in cotton lateral meristem

Author: Xiangqian Zhu, Zhongping Xu, Guanying Wang, Yulong Cong, Lu Yu

Imprint: Genome Biology volume 24, Article number: 194 (2023)

Abstract: Somatic embryogenesis is a major process for plant regeneration. However, cell communication and the gene regulatory network responsible for cell reprogramming during somatic embryogenesis are still largely unclear. Recent advances in single-cell technologies enable us to explore the mechanism of plant regeneration at single-cell resolution. Results: We generate a high-resolution single-cell transcriptomic landscape of hypocotyl tissue from the highly regenerable cotton genotype Jin668 and the recalcitrant TM-1. We identify nine putative cell clusters and 23 cluster-specific marker genes for both cultivars. We find that the primary vascular cell is the major cell type that undergoes cell fate transition in response to external stimulation. Further developmental trajectory and gene regulatory network analysis of these cell clusters reveals that a total of 41 hormone response-related genes, including LAX2, LAX1, and LOX3, exhibit different expression patterns in the primary xylem and cambium region of Jin668 and TM-1. We also identify novel genes, including CSEF, PIS1, AFB2, ATHB2, PLC2, and PLT3 that are involved in regeneration. We demonstrate that LAX2, LAX1 and LOX3 play important roles in callus proliferation and plant regeneration by CRISPR/Cas9 editing and overexpression assay. Conclusions: This study provides novel insights on the role of the regulatory network in cell fate transition and reprogramming during plant regeneration driven by somatic embryogenesis.

40

Title: Co-expression of nitrogenase proteins in cotton (*Gossypium hirsutum* L.)

Author: Yimin Shang, Wenfang Guo, Xiaomeng Liu, Lei Ma

Imprint: PLoS ONE 18(8): e0290556. https://doi.org/10.1371/journal.pone.0290556

Abstract: Chemical nitrogen fertilizer can maintain crop productivity, but overuse of chemical nitrogen fertilizers leads to economic costs and environmental pollution. One approach to reduce use of nitrogen fertilizers is to transfer nitrogenase biosynthetic pathway to non-legume plants. Fe protein encoded by *nifH* and MoFe protein encoded by *nifD* and *nifK* are two structural components of nitrogenase. NifB encoded by *nifB* is a critical maturase that catalyzes the first committed step in the biosynthesis of nitrogenase FeMo-cofactor that binds and reduces N_2. Expression of the *nifB*, *nifH*, *nifD* and *nifK* is essential to generate plants that are able to fix atmospheric N_2. In this study, the four genes (*nifB*, *nifH*, *nifD* and *nifK*) from *Paenibacillu polymyxa*WLY78 were assembled in plant expression vector pCAMBIA1301 via Cre/LoxP recombination system, yielding the recombinant expression vector pCAMBIA1301-*nifBHDK*. Then, the four *nif* genes carried in the expression vector were co-introduced into upland cotton R15 using *Agrobacterium tumefaciens*-mediated transformation. Homozygous transgenic cotton lines B2, B5 and B17 of T_3 generation were selected by PCR and RT-PCR. qRT-PCR showed that *nifB*, *nifH*, *nifD* and *nifK* were co-expressed in the transgenic cottons at similar levels. Western blotting analysis demonstrated that NifB, NifH, NifD and NifK were co-produced in the transgenic cottons. Co-expression of the four critical Nif proteins (NifB, NifH, NifD and NifK) in cottons represents an important step in engineering nitrogenase biosynthetic pathway to non-legume plants.

41

Title: Identification and molecular evolution of the GLX genes in 21 plant species: a focus on the Gossypium hirsutum.

Author: Menglin Xu, Dongyun Zuo, Qiaolian Wang, Limin Lv

Imprint: BMC Genomics volume 24, Article number: 474 (2023)

Abstract: The glyoxalase system includes glyoxalase I (GLXI), glyoxalase II (GLXII) and glyoxalase III (GLXIII), which are responsible for methylglyoxal (MG) detoxification and involved in abiotic stress responses such as drought, salinity and heavy metal.Results:In this study, a total of 620 GLX family genes were identified from 21 different plant species. The results of evolutionary analysis showed that GLX genes exist in all species from lower plants to higher plants, inferring that GLX genes might be important for plants, and GLXI and GLXII account for the majority. In addition, motif showed an expanding trend in the process of evolution. The analysis of cis-acting elements in 21 different plant species showed that the promoter region of the GLX genes were rich in phytohormones and biotic and abiotic stress-related elements, indicating that GLX genes can participate in a variety of life processes. In cotton, GLXs could be divided into two groups and most GLXIs distributed in group I, GLXIIs and GLXIIIs mainly belonged to group II, indicating that there are more similarities between GLXII and GLXIII in cotton evolution. The transcriptome data analysis and quantitative real-time PCR analysis (qRT-PCR) show that some members of GLX family would respond to high temperature treatment in G.hirsutum. The protein interaction network of GLXs in G.hirsutum implied that most members can participate in various life processes through protein interactions.ConclusionsThe results elucidated the evolutionary history of GLX family genes in plants and lay the foundation for their functions analysis in cotton.

42

Title: A systematic analysis of the phloem protein 2 (PP2) proteins in *Gossypium hirsutum* reveals that *GhPP2-33* regulates salt tolerance

Author: Fei Wei, Pengyun Chen, Hongliang Jian, Xiaohao Guo, Xiaoyan Lv

Imprint: *BMC Genomics* volume 24, Article number: 467 (2023)

Abstract: Phloem protein 2 (PP2) proteins play a vital role in the Phloem-based defense (PBD) and participate in many abiotic and biotic stress. However, research on PP2 proteins in cotton is still lacking. Results-A total of 25, 23, 43, and 47 *PP2* genes were comprehensively identified and characterized in *G.arboretum*, *G.raimondii*, *G.barbadense*, and *G.hirsutum*. The whole genome duplication (WGD) and allopolyploidization events play essential roles in the expansion of PP2 genes. The promoter regions of *GhPP2* genes contain many *cis*-acting elements related to abiotic stress and the weighted gene co-expression network analysis (WGCNA) analysis displayed that *GhPP2s* could be related to salt stress. The qRT-PCR assays further confirmed that *GhPP2-33* could be dramatically upregulated during the salt treatment. And the virus-induced gene silencing (VIGS) experiment proved that the silencing of *GhPP2-33* could decrease salt tolerance. Conclusions- The results in this study not only offer new perspectives for understanding the evolution of *PP2* genes in cotton but also further explore their function under salt stress.

43

Title: Initiation of Callus and Plant Regeneration in Cotton (*Gossypium hirsutum* L.)

Author: A. KALAMANI

Imprint: Madras Agricultural Journal Vol:81, Issue:nov-nov, DOI:https://doi.org/10.29321/MAJ.10.A01585

Abstract: The hypocotyl explants of MDU 9 cultured on Murashige and Skoog medium supplemented with kinetin (1.0 mg/lit.)+ IAA (1.5 mg/lit.) formed callus in 20 days. The calli on sub culture to media containing benzyl amino purine (2.0 mg/lit.) developed shoots. Multiple shoots were formed from each callus mass. These on further sub culture with reduced level of benzyl aminopurine developed well. Root initiation and growth was promoted by lowering the sucrose concentration and supplementing the culture media with NAA (3.0 mg/lit.).

44

Title: Gossypium hirsutum gene of unknown function Gohir.A03G0737001 encodes a potential Chaperone-like Protein of protochlorophyllide oxidoreductase (CPP1)

Author: Alana N. Osborne, Andrew Osagiede, Amanda R. Storm, Amanda M. Hulse-Kemp, Angela K. Stoeckman

Imprint: MicroPublication Biology. 7/30/2023 - Open Access
10.17912/micropub.biology.000867

Abstract: A gene of unknown function identified in Gossypium hirsutum, Gohir.A03G0737001.1, was studied using sequence and bioinformatic tools. The encoded protein (referred to here as GhCPP1-A0A1U8HKT6) was predicted to function as a Chaperone-like protein of protochlorophyllide oxidoreductase (CPP1), which is involved with initiation of photochemical reactions of chlorophyll biosynthesis. Sequence analysis indicates it is embedded in the chloroplast envelope membrane through four transmembrane regions and contains a J-like domain that is structurally similar to the J domain of DnaJ/Hsp40 “holdase” chaperone proteins.

SEED SCIENCE AND TECHNOLOGY

45

Title: Identification of novel candidate loci and genes for seed vigor-related traits in upland cotton (*Gossypium hirsutum* L.) via GWAS

Author: Libei Li, Yu Hu, Yongbo Wang

Imprint: Front. Plant Sci., 01 September 2023, Sec. Plant Breeding, Volume 14 - 2023 | https://doi.org/10.3389/fpls.2023.1254365

Abstract: Seed vigor (SV) is a crucial trait determining the quality of crop seeds. Currently, over 80% of China’s cotton-planting area is in Xinjiang Province, where a fully mechanized planting model is adopted, accounting for more than 90% of the total fiber production. Therefore, identifying SV-related loci and genes is crucial for improving cotton yield in Xinjiang. In this study, three seed vigor-related traits, including germination potential, germination rate, and germination index, were investigated across three environments in a panel of 355 diverse accessions based on 2,261,854 high-quality single-nucleotide polymorphisms (SNPs). A total of 26 significant SNPs were detected and divided into six quantitative trait locus regions, including 121 predicted candidate genes. By combining gene expression, gene annotation, and haplotype analysis, two novel candidate genes (Ghir_A09G002730 and Ghir_D03G009280) within qGR-A09-1 and qGI/GP/GR-D03-3 were associated with vigor-related traits, and Ghir_A09G002730 was found to be involved in artificial selection during cotton breeding by population genetic analysis. Thus, understanding the genetic mechanisms underlying seed vigor-related traits in cotton could help increase the efficiency of direct seeding by molecular marker-assisted selection breeding.

46

Title: Line X Tester Analysis for Seedling Characters in Cotton (*Gossypium Hirsutum L.)*

Author: P.NAGARAJAN, M.KADAMBAVANASUNDARAM and S.R.SREE RANG

Imprint: Madras Agricultural Journal Vol: 81, Issue: jun-jun

DOI:https://doi.org/10.29321/MAJ.10.A01525

Abstract: A line x tester analysis involving 7 lines and 4 testers of upland cotton was carried out to estimate combining ability for seed in the germination, root length, shoot length and vigour index during winter 1989. The parent TCH 65/8 (Sparsely fuzzed was found to be a good combiner for all the characters studied. Both additive and non-additive genetic affects were operative in the inheritance of these traits.

47

Title: Comparative Transcriptome Analysis of Seed Germination of a Cotton Variety with High Tolerance to Low Temperature.

Author: Genhai Hu; Maoni Chao; Xiuren Zhou; Yuanzhi Fu

Imprint: Phyton (0031-9457). 2023, Vol. 92 Issue 9, p2535-2554. 20p

Abstract: Gossypium hirsutum L. is an important cash crop native to the subtropics and is widely cultivated around the world. Low temperature is an important stress that seriously affects seed germination and emergence during planting. In this study, transcriptomic profiles of low-temperature- and normal-temperature-germinated seeds of Xinluzao 25, a variety with low-temperature tolerance and high germination rates, were analyzed and compared. The following results were obtained. (1) A total of 81.06 Gb of clean data were obtained after transcriptome sequencing and assembly, and 76,931 non-redundant Unigene sequences were obtained after data consolidation and concatenation; of these, 69,883 Unigene sequences were annotated. In addition, 55,463 Unigene transcript sequences (72.2%) were annotated for Gene Ontology (GO) classification, and 26,629 genes were involved in 50 metabolic pathways identified by Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis. (2) Three main pathways related to low-temperature tolerance of seed germination were identified: starch and sucrose metabolism, phenylpropanoid biosynthesis, and cysteine and methionine metabolism. Their main molecular functions involve the regulation of abscisic acid and activities of enzymes such as amylase, peroxidase, and oxidoreductase. During germination at low temperature, more genes were down-regulated than up-regulated genes at the protrusion stage (2 mm), and more genes were up-regulated than down-regulated at the germination stage (30 mm) after protrusion. (3) The enzyme activities at the two stages showed that amylase, peroxidase, catalase, and glutathione reductase had higher activities when the seeds germinated at 15°C. In this study, high expression of amylase, peroxidase, catalase, and glutathione reductase genes may be the main cause of increased tolerance to low temperature.

48

Title: Effect of Hydro and Osmo Priming on the Physiological Qualities of Stored Cotton Seed (Gossypium Spp. L.)

Author: H. Saleh, A.I. Yahaya, H. Abubakar and R.A. Sami

Imprint: Journal of Agriculture and Environment Vol. 19 No. 1, 2023: 165-174

Abstract: Planted seeds require the highest probability of survival and plants need to grow as efficiently as possible to help support improved productivity to meet the increasing demands of society for both food and fiber. However, poor seed germination in field is a major challenge to cotton farmers in the Guinea savanna zone of Nigeria. Therefore, this study seeks to determine the physiological qualities (germination and vigour) of the Nigerian cotton varieties with a view to determine the most efficient cotton seed priming treatment method for the farmers. Six (6) IAR commercial cotton varieties (SAMCOT 8,9,10, 11, 12, and 13) and treatments (polyethylene glycol 6000 20% solution, hot water and a control) were studied in a factorial experiment based on completely randomized design with two replications. Eight parameters were considered for data collection viz germination percentage, percentage of first count, germination rate, root and shoot length, root and shoot fresh weight, and seedling dry weight. The data collected were subjected to statistical analysis using the analysis of variance (ANOVA). The best variety with highest first count germination, total germination and germination index was SAMCOT 8 under 20 hours treatment with polyethylene glycol 20% solution followed by SAMCOT 11. Soaking seeds in hot water for 30 seconds gave the highest first count germination. The Control had the least total germination and germination index. It could therefore be concluded that application of PEG 6000 20% solution for 20 hours is effective for SAMCOT 8 and 10 while PEG treatment for 15 hours is better for SAMCOT 13.

49

Title: Multi-level biological effects of diverse alkyl chains phthalate esters on cotton seedlings (*Gossypium hirsutum* L.): Insights into individual, physiological-biochemical and molecular perspectives

Author: Huijuan Lv, Chunliu Liang, Wenrong Liu

Imprint: Journal of Hazardous Materials, Volume 460, 15 October 2023, 132352

Abstract: Phthalate esters (PAEs) are organic contaminants that pose environmental threat and safety risks to soil health and crop production. However, the ecological toxicity of different PAEs to cotton and the underlying mechanisms are not clear. This study investigated the ecotoxic effects and potential mechanisms of different alkyl-chain PAEs, including dioctyl phthalate (DOP), dibutyl phthalate (DBP), and diethyl phthalate (DEP) on cotton seedlings at multiple levels. The results showed that PAEs significantly hindered the growth and development of cotton. The chlorophyll content decreased by 1.87–31.66 %, accompanied by non-stomatal photosynthetic inhibition. The antioxidant system was activated by the three PAEs in cotton seedlings, while the osmotic potential was boosted intracellularly. Additionally, PAEs significantly interfered with functional gene expression and exhibited genotoxicity. Risk assessment results indicated that the ecotoxicity was DOP >DBP >DEP, with a "dose-response" relationship. The affinity between the three PAEs and catalase increased as the alkyl chain length increased, further supporting the toxicity sequence. Surprisingly, the bioconcentration factors of short-chain DEP were 8.07 ± 5.89 times and 1837.49 ± 826.83 times higher than those of long-chain DBP and DOP, respectively. These results support the ecological risk assessment of PAEs in cotton and provide new insights into determining the toxicity levels of different PAEs.