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The Cotton Innovations Newsletter is published twelve times annually. Contributed articles, pictures, cartoons, and feedback are welcome at any time. Please send contributions to the General Editors (see below). The editors reserve the right to edit. The deadline for contributions is one month before the publication date.

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Uzbekistan Host the 8th version of World Cotton Research Conference

The International Cotton Advisory Committee (ICAC) has announced that the World Cotton Research Conference (WCRC-8) will be held in Samarqand, Uzbekistan. The WCRC is organised by the ICAC under the auspices of the International Cotton Researchers Association (ICRA). It brings together the top researchers and cotton specialists from across the globe.

The eighths event held since 1994, the WCRC will serve as a global platform for scientists and experts to share the latest updates in cotton research and development. Internationally recognised experts will be invited to deliver plenary and keynote presentations.

"Given the many challenges that cotton is facing around the world — including soil degradation, inefficient knowledge transfer and lack of access to modern technologies — it is the perfect time to convene many of the world's top cotton scientists to find the path forward," said ICAC Chief Scientists, Dr Keshav Kranthi. "The ability to meet face-to-face with colleagues from all over the world and learn from each other is an opportunity not to be missed." The WCRC is held once every four years in different cotton-growing countries. Previous conferences were held in Australia (1994), Greece (1998), South Africa (2003), USA (2007), India (2011), Brazil (2016) and Egypt (2022).

PROCEEDINGS OF THE GENERAL BODY MEETING

INTERNATIONAL COTTON RESEARCHERS' ASSOCIATION (ICRA)

6 October 2022, Cairo, Egypt

INTRODUCTION

The General Body Assembly meeting of The International Cotton Researchers Association (ICRA) was held on 6 October in the Diamond ballroom of Steigenberger Hotel, Cairo Egypt. A total number of 220 ICRA members participated in the meeting.

The meeting was chaired by Dr Negm, Chairman ICRA; Dr Eric Hequet, Vice-Chair ICRA; Dr Khalid Abdullah, President ICRA Secretariat and Dr Keshav Kranthi, Executive Director ICRA.

AMENDMENTS TO BYELAWS:

The following proposals for amendments to byelaws were discussed and approved unanimously by the General Body Assembly.

1. **ASSOCIATE MEMBERS:** The ICRA Executive Committee is permitted to solicit corporate bodies and private sector organizations to be admitted as Associate members of ICRA. The membership fee would be decided by the ICRA-EC.
2. **TREASURER:** The Vice-Chair or any member of Executive Committees is permitted to officiate as Treasurer until the appointment of a new Treasurer.
3. **NUMBER OF ICRA-EC MEMBERS:** The number of ICRA Executive members (ICRA-EC) will be increased to twenty-five (25) to accommodate adequate geographical representation and to cover majority of the subject-matter disciplines on cotton research. The President of the ICRA-Secretariat and the Chief Scientist of the ICAC will by default be permanent members of the ICRA Executive Committee. The General Body Assembly will elect 15 ICRA-EC members to not exceed a maximum number of two members from any country. The General Body Assembly and/or ICRA-EC will co-opt 3-8 members to facilitate geographical representation and subject-matter disciplines that are not represented by the elected EC members.
4. **ICRA-ADVISORS:** The ICRA-EC will nominate/invite up to three Eminent Scientists to act as Advisors to the ICRA. The ICRA-Advisors will be invited to attend the ICRA-EC meetings to provide guidance on matters of importance as and when they arise.

ELECTION OF ICRA EXECUTIVE COMMITTEE MEMBERS

The Nominating Committee Received 35 applications for election as Executive Committee Members of the ICRA. Seventeen of the 35 candidates attended the WCRC-7 and participated in the elections. Dr Mohamed Negm and Dr Eric Hequet were elected by the ICRA-EC as the Chairman and Vice-Chairman respectively in 2021 and were therefore considered as EC members-designate until the next World Cotton Research Conference.

Voting was held by the General Body Assembly to elect 15 Executive Committee Members of the ICRA. The candidates presented their vision for ICRA before the General Body Assembly. Voting was by show of hands and assessment of majority votes for election.

The following candidates were elected by the General Body Assembly

1	Dr. Akhteruzzaman	Bangladesh	Agronomy & Crop Physiology
2	Dr. Alex Mungai	Kenya	Value Addition & Social Sciences
3	Dr. Bruno Bachelier	France	Plant Breeding and Molecular Genetics
4	Dr. Felix Sawadogo	Burkina Faso	Pest Management
5	Dr. Ghorban Roshani	Iran	Crop Physiology and Soil Science
6	Dr. Ghulam Sarwar	Pakistan	Plant Breeding and Genetics
7	Dr. Jodi Scheffler	USA	Plant Breeding and Molecular Genetics
8	Dr. Marcelo Paytas	Argentina	Agronomy and Crop Physiology
9	Dr. Martin Simasiku	Zambia	Plant Breeding and Genetics
10	Dr. Nazife Ozkan	Turkiye	Plant Breeding and Genetics
11	Dr. Sandhya Kranthi	India	Entomology and Crop Protection
12	Dr. Souzan Sanad	Egypt	Spinning & Fibre Technologies
13	Dr. Tahani Yousif Elagib	Sudan	Agricultural Biotechnology
14	Dr. Venugopalan MV	India	Agronomy & Soil Science

Prof. Ibrokhim Abdurakhmonov, Hon'ble Minister of Innovation, Uzbekistan, was nominated and unanimously approved by the General Body Assembly as the ICRA Advisor.

TERMS OF REFERENCE FOR EC MEMBERS

- ICRA will convene a meeting of the newly elected ICRA-EC at the earliest possible convenience to discuss the future plans for ICRA.
- The newly elected Executive Committee shall co-opt new EC members for Geographical and subject matter representation in the next immediate ICRA-EC meeting.
- Each subject group will develop communication channels and social media networks to connect researchers of their subject area and to explore research collaborations.
- Each of the ICRA-EC subject-groups team will coordinate all activities related to research collaboration, conducting training programmes, certificate programmes, conferences, meetings, seminars, workshops, institution visits, review papers, reports and technical publications in their subject area.
- The EC members and ICRA experts will receive a certificate signed by the ICAC as and when required for their CV.

Mohamed Negm
Chairman, ICRA

Keshav Kranthi
Executive Director, ICRA

6 October 2022

Phosphorus stratification in Australian Cotton farming systems

Authors: Guna Nachimuthu1, Graeme Schwenke2, Clarence Mercer2, Nilantha Hulugalle3 and Mike Bell4

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Phosphorus (P) is an essential nutrient for cotton plant growth. Most Australian cotton-growing soils typically have high clay contents, cation exchange capacities and total P contents, but many also have alkaline pH's (>7.5) that can reduce P availability. Phosphorus deficiency can lead to poor seedling vigour, stunted plant growth, delayed flowering, poor boll retention and consequently reduced lint yield. Most Australian cotton farms are designed as irrigated row cropping systems with the capacity to saturate down to 1 m of the soil profile. Traditionally, this design assists the cotton crop to access soil moisture and nutrients deeper in the profile, although other soil constraints such as compaction and sodicity can limit the root growth into deeper layers. Previous research in the Australian grains industry has highlighted subsoil P depletion and P stratification in topsoil over the long term. Irrigated Vertisols undergo a more intensive crop production cycle than dryland systems and have the potential to deplete soil nutrient reserves at a faster rate. However, scientific information on the long-term changes in soil P in Australian irrigated .cotton growing soils is limited

Soil inorganic P can be assessed using several currently available commercial soil tests that differ in the type of extraction solutions and extraction duration used. These include solution P (readily available for immediate plant uptake), plant available soil P (Colwell P: an extraction that simulates P release over a growing season and includes solution P), and slowly available soil P or reserve P that may become plant available over years. In most soils in the Australian cotton industry, reserve P can be approximated by the difference between BSES P (0.005 M sulphuric acid extract for 16 hours) and Colwell P (0.5 M sodium bicarbonate extract for 16 hours), although the fraction of this P available in any one year can vary with the soil mineralogy and fertiliser use. Quantifying the BSES P and Colwell P at different depths using archived samples from five long-term cropping system experiments (located in New South Wales) should improve the understanding of current soil P status and its stratification and potential implications for future nutrient management strategies in .Australian cotton-growing soils

The long-term trends and comparison with native sites showed a decline in all three measurements

of P (Solution P, Colwell P and BSES P) in most of the locations (average for BSES P presented in Table 1). This suggested a negative P balance in all but one site located in the Macquarie valley (Warren). Phosphorus export in cotton seed (8–34 kg P/ha) over the years is likely to be the main cause of the negative trend at the other four sites. A cotton crop yielding 15 bales/ha would accumulate 58 kg P/ha in crop biomass, with ca. 2/3 of that leaving the field in the seed cotton. Therefore, P fertiliser inputs for each cotton season need to match the P in cotton (and grain) .seed exported since the previous P application

The depth increment BSES P results reveal two key facts. In the experiment in the Namoi valley (Australian Cotton Research Institute (ACRI), Wee Waa and Merah North) (Figure 1A), with high background P fertility throughout the profile, there has been significant P extraction in each soil layer down to at least 50cm, indicating the depths from which roots will extract P. In the Macquarie valley study (Figure 1B), where background soil P was much lower and there has been a history of fertiliser P application into the surface soil, P stratification can be seen to be occurring. The prolonged addition of fertiliser P into the cultivated layer has led to the gradual buildup of P in the surface soil—P stratification—over the years (Figure 1B), although there has been no change to P status in deeper layers (>30 cm) due to the lack of P leaching in these soils. After harvest, the cotton crop is mulched back onto topsoil each season. This practice is an additional factor contributing toward P strati- .fication in the topsoil

Colwell P levels were higher under minimum tillage (soil tilled 10 cm) compared to maximum tillage (soil tilled 30 cm) cotton monoculture. In contrast, there was no difference in BSES P concentrations among the three cropping systems (maximum tillage ~ cotton monoculture, minimum tillage ~ cotton monoculture and minimum tillage ~ cotton-wheat rotation) (Table 2). This suggests an interaction between soil management and the dynamics of P entering or being released from the reserve pool (BSES) to the Colwell P. While the ACRI long-term experiments that were running longer than 13 and 22 years were sufficient to develop clear treatment differences in P decline, the duration of the on-farm experiments was less than 7 years and crop rotation treatments had no measurable effect on soil P levels (0-60 cm average). The ACRI results imply sustainable soil management benefits can be realised after the implementation of best .management practices over many years

While P application to the topsoil will restore the overall P balance in the cotton field, the stratification of available P in this layer will lead to a mismatch over time between remaining available P and where the plant roots access most of their water and nutrients in the soil profile. To achieve a theoretical maximum yield of 22 bales/ha, it was estimated that 83 kg P/ha would need to be available for plant uptake (Constable and Bange 2015). This will be a challenge with the observed trend of the long-term decline in soil P at different depths. While the topsoil P can be supplemented with fertilisers, the decline in subsoil P will further restrict the soil volume available for cotton plant roots to explore for P to achieve maximum yield potential. The self-mulching action of Vertisols may help to transfer some of the topsoil P to the subsoil, although there will be high variability in crack depth and volume, and the quantities involved are dwarfed by annual crop uptake. All options including crop rotation, soil and irrigation management and their interaction with nutrients such as P need to be explored to realise the maximum yield potential of modern cotton cultivars. Short-term changes in soil

P during and between cropping seasons require a more detailed mechanistic understanding under field conditions, particularly with regard to the access of available P by plant roots in irrigated .cotton fields

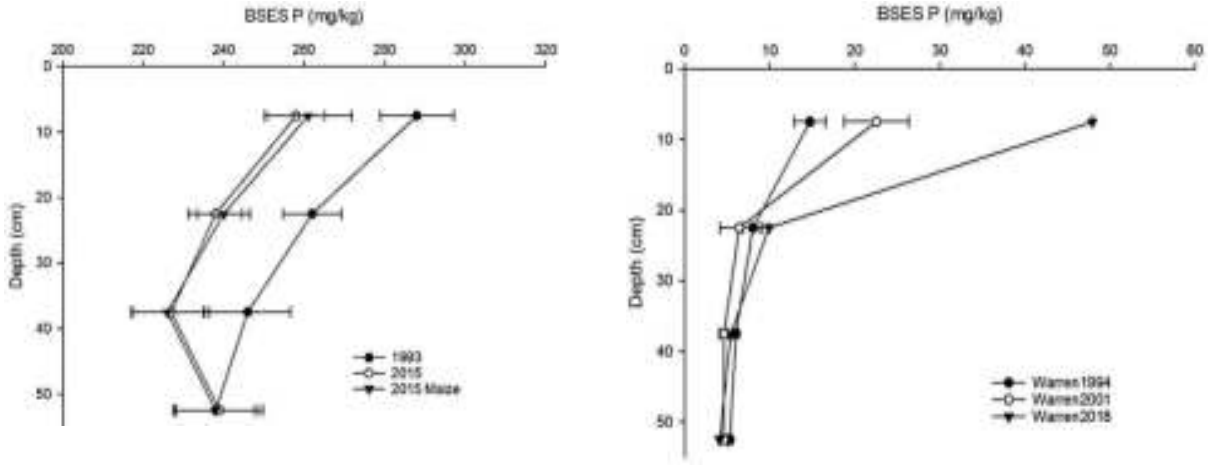
Table 1. Soil BSES P (reserve P status) in long-term cotton systems experiments and adjacent native sites. ACRI is the Australian Cotton Research Institute. All sites except for Warren are located in the Namoi Valley New South Wales (NSW). Warren is located in the Macquarie Valley in NSW

Locations	Depth	Cotton field	Native site	% of Native site
ACRI 1	0–15 cm	259	299	87
	15–30 cm	239	219	109
	30–45 cm	227	239	95
	45–60 cm	238	235	101
ACRI 2	0–10 cm	191	281*	68
	10–30 cm	170	244*	70
	30–60 cm	180	226*	80
Wee Waa	0–15 cm	191	244	78
	15–30 cm	174	143	121
	30–45 cm	185	254	73
	45–60 cm	204	422	48
Merah North	0–15 cm	83	185	45
	15–30 cm	62	220	28
	30–45 cm	75	237	32
	45–60 cm	112	307	36
Warren	0–15 cm	106	15	711
	15–30 cm	39	8	501
	30–45 cm	15	8	177
	45–60 cm	11	10	106

*The values were estimated using the logarithmic relationship as the native paired site for ACRI 1 used a different depth increment.

Table 2. Effect of cropping systems on soil P levels (0–60 cm depth) at ACRI 1

Cropping systems	Solution P (mg/kg)	Colwell P (mg/kg)	BSES P (mg/kg)
Maximum tillage cotton monoculture	0.319a	46.5a	246a
Minimum tillage cotton monoculture	0.457a	65.4b	234a
Minimum tillage cotton-wheat rotation	0.434a	57.8ab	242a



A) B)

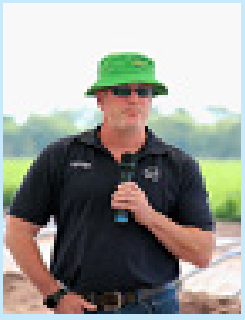
Figure 1. Long-term changes in soil Colwell P in long-term cotton systems experiments at (A) .ACRI, Namoi Valley and (B) Macquarie Valley

Acknowledgement

This research was undertaken as a sub-project of the More Profit from Nitrogen Program, supported by funding from the Australian Government Department of Agriculture, Water and Environment as a part of its Rural R&D for Profit program, Cotton Research and Development Corporation and NSW Department of Primary Industries is gratefully acknowledged. Assistance from various tech-.nical and ACRI farm staff are gratefully acknowledged

A Brief Summary of the Effect of Nitrogen Application Rates on Cotton Fibre Quality

Authors: Marinus (René) van der Sluijs



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Introduction

The importance of the application of nitrogen in the cotton production system in terms of plant growth, health, yield etc. are well understood and has been studied for over a century, with practical guidelines, decision support systems, models and reviews providing information on the importance of providing crops with sufficient supply of nutrients and improving nitrogen use efficiency (NUE). Unfortunately, despite the fact that the financial return to the grower in most crop production systems depends on crop quantity and quality only a limited number of studies have been published on work and knowledge relating to the effect of N application rates on fibre quality. As a consequence, it was considered important to un-.dertake a focussed review of published on this

Fibre Quality Properties

Due to the greater demands of modern spinning, in terms of speed and automation, the cost of raw material and the increasingly competitive global textile market, cotton fibre quality is of utmost importance to the spinner. As a consequence, there are a number of physical properties that have been identified by the cotton trade and spinning industry as the most important which includes fibre length, length uniformity, strength, micronaire (a combination of maturity and fineness), colour and trash. As a consequence, cotton is bought and sold on these fibre properties, with colour having the highest contribution to the price of cotton, followed by cleanliness/trash, .micronaire, length and strength

In terms of fibre length, the majority of studies concluded that increased application rates of N had no significant effect on length, with a few studies finding no clear trend. There were also some studies that found that N application rates either had a positive (i.e., increase) or a negative .(decrease) effect on fibre length

Similarly, the majority of studies concluded that increased application rates of N had no significant effect on strength, with a few studies finding no trend. There were also some studies that found that N application rates either had a positive (i.e., increase) or a negative (decrease) effect .on fibre strength

For micronaire the majority of studies concluded

that increased application rates of N had either no significant effect, or no clear trend. There were also some studies that found that N application rates either had a positive (i.e., increase) or a neg-.ative (decrease) effect on micronaire

On the other hand, there is general agreement that colour in terms of reflectance and yellowness was negatively affected by increased N application rates resulting in the fibre becoming less bright and duller and possibly resulting in a reduction in the colour grade. In terms of lint turn out the majority of studies concluded that N application rate did result in either a significant reduction in lint turn out, no significant effect or with no clear trend. There were however a small number of studies that showed that N application rates did .increase lint turn out

Cotton stickiness, when it occurs, can present a major problem, in terms of textile processing performance and cost and product quality. The main problem related to cotton stickiness is that of the sticky deposit, or residue. The most common and problematic causes of stickiness are those due to excess sugars related to insect secretions, notably aphids and whitefly, referred to as honeydew. This deposit adheres to any machine part or surface encountered by the cotton along the processing pipeline, causing an accumulation of fibres (and even dust or grit), during the ginning and spinning processes but can also cause issues during cotton classification, with deposits on the combs, used in HVI instruments, resulting in incorrect and inaccurate fibre measurements. In addition, a black sooty mould can also grow on honeydew, darkening the lint and adversely affecting grade. Studies have shown that increased N application rates result in increased populations of aphids and whitefly. N also increased their and other pests resistance to standard insecticides, resulting in increased applications and the use of more harmful .products to beneficials

Conclusion

The observed effects of N application rates on fibre quality are rather varied and often inconsistent. This was specifically the case for fibre length and length uniformity, strength and micronaire. This was unsurprising as length and strength are primarily genetic traits with micronaire primarily attributed to weather and management. Of course, the range of different test methods and instruments and at times no indication of the test method and instrument could have contributed to these differences. On the other hand, colour, lint turn out and sticky cotton were very much influenced by the application rate of N. The colour of the fibre becoming less bright and duller, with a reduction in lint turn out and increased susceptibility and insect attractiveness with increased N .application rates

There is no doubt that nitrogen plays a significant role in the production of cotton however, the excess application above NUE has no economical .benefit and could impact on fibre quality

Further assessment to further clarify the effect of N on fibre quality are currently being conducted .in Australia

This summary is an extract from a very comprehensive review published in The Journal of Cot-:ton Research. Details are as follows

van der Sluijs MHJ. Effect of Nitrogen Application Level on Cotton Fibre Quality. Journal of Cotton Research. 2022; 5(9): 35 https://doi.org/10.1186/s42397-022-00116-9

New Insights on Why There are Differences in Micronaire in Cotton Crops

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Summary

Experiments were conducted over eight cotton seasons and varied planting time, fruit load, canopy size and were exposed to water stress.

Final Micronaire was primarily influenced by temperature during the boll filling period.

Average boll size at harvest and leaf area index at flowering moderated crop Micronaire.

This new understanding has been used to successfully developed a mathematical function to predict Micronaire at crop maturity (including crops which have been stressed) which may be used to inform crop management.

Introduction

Environment and crop management can both play important roles in determining fibre quality. Micronaire is an indirect measure of fibre linear density (fineness) and maturity, and it is affected by crop growth and partitioning of available assimilates (from photosynthesis) to cotton fruit. High Micronaire occurs when there is an excess of assimilates due to good growing conditions and/or fruit number is low. Conversely low Micronaire occurs when growing conditions are poor and/or fruit number is high. Too low Micronaire may mean that fibres are immature, leading to breakages in fibres within the yarn and poor dye uptake during textile processing. Too high Micronaire may indicate that fibre is coarse and is undesirable for spinners as it results in too few fibres in yarn cross section, reducing its strength. Consequently, growers may incur price discounts if Micronaire of their cotton falls outside the optimal range (3.5 to 4.9).

Picture: The maturity of fibres in the cotton yarn affects its strength and it ability to take up dye.

Fibre growth and development are affected by most variables which influence plant growth. Since fibre is primarily cellulose, any influence on

crop photosynthesis will have a similar influence on fibre growth. Much research has been conducted that has shown that Micronaire responds independently to variables like temperature and radiation levels during boll filling; leaf defoliation; water stress; and internal competition from bolls for assimilate carbohydrate within the plant. Little research, however, has been conducted attempting to develop an integrated understanding at a crop level of combinations of some of these impacts on Micronaire. This research involved a range of field experiments that generated variability in Micronaire by changing growing temperature conditions at boll filling through changes in planting time; manipulated crop canopy size through use of plant growth regulators and plant tip removal; and changes in the crop demand by the fruit by manually removing a proportion of fruit from the plant at flowering.

To capture our understanding of the response of these variables to Micronaire, we developed a mathematical function from some initial experiments, and then tested it on later experiments to ensure that we had appropriately described the impact. This relationship can also be used to predict crop Micronaire which then can be used to refine management decisions to improve fibre quality before, or at harvest time.

Methods

Experiments were conducted at the Australian Cotton Research Institute (ACRI) at Narrabri Australia over eight seasons. Treatments were applied to experiments with the intent to generate differences in Micronaire at final harvest. Experiments (Exps) had different planting times (to generate effects of temperature on fibre thickening), fruit removal (fruit removed at the start of boll filling and all fruit retained to modify crop fruit demand), canopy modification treatments (tipped, normal, and regulated to modify crop supply), and irrigation (normal and water deficits by missing a single irrigation during boll filling).

Leaf area was measured at the start of the estimated fibre thickening period which was the same day of fruit removal in those experiments. At harvest yield, yield components (boll number (per m2), boll size (g seed cotton per boll), and fibre Micronaire (with HVI) was measured. Average temperatures for each treatment in each experiment for the fibre thickening phase was calculated.

Development of functions to predict Micronaire used leaf area at the start of the fibre thickening period, the calculated mean temperature during the fibre thickening period, the boll size at maturity (g seed cotton per boll), and boll number at maturity (boll per m2). Stepwise linear multiple regression analysis was used to see how all variables together impacted Micronaire. Once the relationship was developed it was validated against independent datasets.

Results

Stepwise linear regression analysis applied to the first two experiments (data combined) to determine how all crop variables together could influence Micronaire. The process of stepwise regression analysis is a process by which variables are added to a regression (that predicts Micronaire) and determines if it is statistically significant (95% confidence) in affecting Micronaire along with estimating the degree of impact (the higher the increase in r2 the bigger the impact). On the basis that temperature had previously been identified as a significant variable affecting Micronaire, it was the first variable added to the stepwise regression analysis. The regression then was significantly improved by adding boll size followed by leaf area. The inclusion of the interaction term in the function that accounted for the temperature during fibre filling and leaf area together, also significantly improved the regression (the stepwise

regression build of function is detailed in Table 1). After all variables were added the regression the r2 was 0.79 which represents excellent ability to explain Micronaire. Boll number was also tested as part of the assessment but did not significantly help understanding of the impacts on Micronaire.

Following on, the understanding generated from these initial experiments the function was then tested on independent data generated from the remaining experiments and the predicion ability was reasonable across the spread of data from these experiments as shown by the plot of predicted versus observed (measured) Micronaire (presented in Figure 1). There was tendency for the function to underpredict Micronaire across this dataset; importantly however, the function was able to capture the variation generated by the water deficit treatments.

To represent the relative effects of the different variables, a sensitivity analysis was undertaken (Figure 3). Micronaire was predicted for three different boll sizes and three leaf areas (leaf area indices) across mean temperatures for the fibre filling period. The sensitivity analysis showed that at lower mean temperatures, leaf area has little influence on Micronaire despite boll size, while boll size has a greater influence. At higher temperatures again the greatest influence on Micronaire was from changes in boll size; however, there was also a substantial effect of leaf area, highlighting the interaction of temperature and leaf area. From a crop physiological perspective, the responses of Micronaire to these variables in this manner are highlighting firstly, the effect of boll size at harvest encapsulating the crop effects on both assimilate supply and demand leading to effects on fibre thickening during boll growth; and secondly that as air temperature increases leading to increases in photosynthesis and subsequent assimilate supply, the effect of increasing leaf area is diminished. Consequently, this suggests that when temperatures are higher this may help to compensate for lower resource capture from a lower leaf area. The sensitivity analysis also emphasized that temperature and boll size were the two dominate factors affecting Micronaire, and that reasonable predictions of impacts could be made with these factors alone.

Conclusions

Considering that there was reasonable ability to capture the different crop and environmental variables we see good opportunities to utilise this approach with some confidence to predict crop Micronaire before harvest. This ability to predict Micronaire will enable improved assessments of the reasons for seasonal and regional differences in Micronaire and assess management opportunities to improve Micronaire in both current and future climates. This understanding could also be linked with crop measurements taken with remote and proximal sensing technologies to improve precision of prediction of fibre quality and capture spatial variability in the field prior to harvest. Such linkages might be useful in the development of harvest strategies using these predictions that allow for segregation of fibre based on quality (with different modules) before being delivered to the cotton gin for processing allowing for improving fibre quality outcomes and potential economic returns growers.

Acknowledgments

This paper is a summary of research published in the journal Crop Science Vol. 62 pages 397 to 409 (2022). Cotton Seed Distributors for provision of cotton seed. The Australian Cotton Catchment Communities Cooperative Research Centre and the Cotton Research and Development Corporation of Australia provided partial financial support for this work.

Table 1: The improvement in predictability of linear regression when all variables were added. The higher the 'r2' value and closer it is to the value 1 the better the functions ability to predict Micronaire.

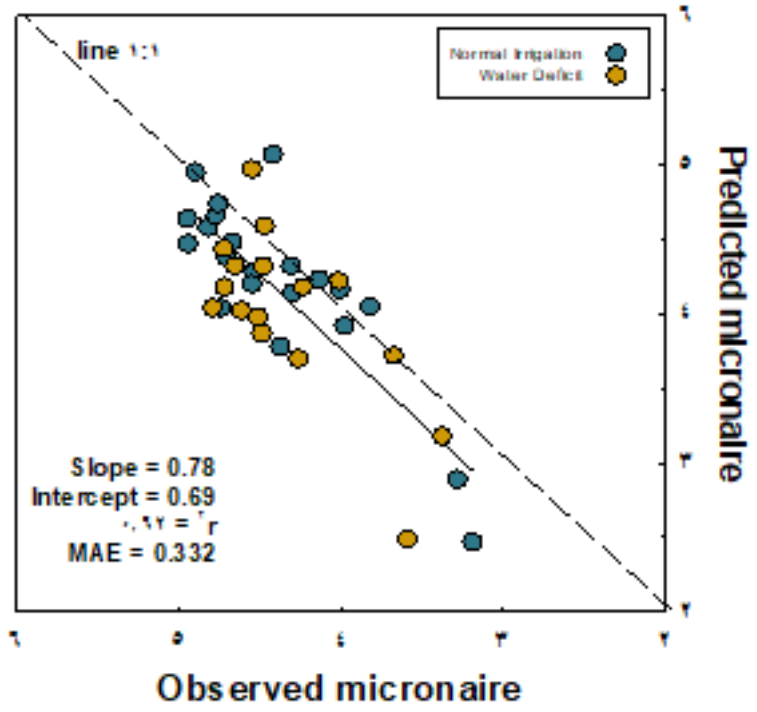

Table 1: The improvement in predictability of linear regression when all variables were added. The higher the 'r2' value and closer it is to the value 1 the better the functions ability to predict Micronaire.

Variable	Improvement in Predictability
Micronaire versus Temperature	**r2 = 0.19**
Add Boll Size	**r2 = 0.72**
Add Leaf Area (LAI)	**r2 = 0.77**
Add Interaction of Temperature and Leaf Area	**r2 = 0.79**

Figure 1. Validation of our functions that predict Micronaire on independent experiments. The graph shows the predicted versus observed Micronaire values generated using datasets collected from five independent experiments. Blue points are those crops that have normal irrigations, whereas brown points are treatments that have had an irrigation omitted causing a water deficit. Solid line is the line of best fit. Dashed line is the 1:1 line. The further data is from the 1:1 line the greater the overall differences from the actual versus predicted values. MAE is the mean absolute error which is the average of the difference between the actual and predicted values.

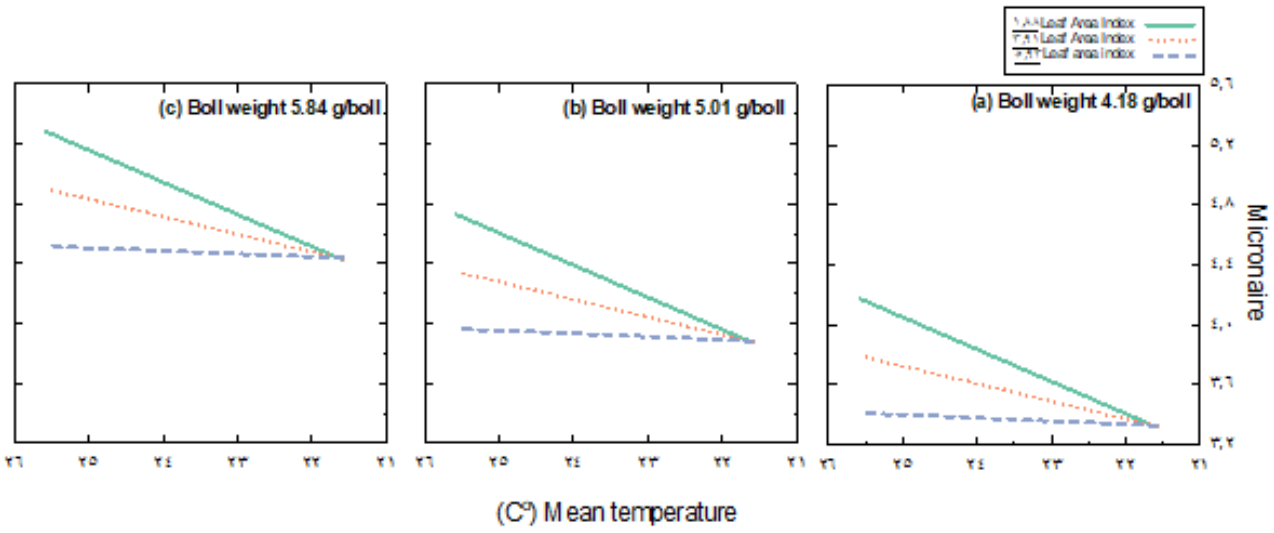

Figure 2. A sensitivity analysis showing the degree of effects of the different variables affecting Micronaire; for three different individual boll sizes and three leaf areas (LAIs) across temperature for the fibre filling period.

Disease in Australian Cotton Systems

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The Queensland Department of Agriculture and Fisheries (QDAF) Pathology Team conducts research funded by the Cotton Research and Development Corporation (CRDC) focussed on providing diagnostic capacity for fungal diseases and reniform nematode, conducting disease surveys to better understand disease issues and trends that direct pathology research, as well as development of management strategies for key diseases and reniform nematode. The 2021/22 season represented the 20th consecutive cotton disease surveys in Queensland. QDAF leads a national project to better understand cotton diseases, soil health and management strategies that support the development of disease suppressive soils in collaboration with Dr Gupta Vadakattu (CSIRO) and NSW DPI pathology team led by Dr Duy Le.

First report of novel Eutypella species causing disease in cotton

Reoccurring wilt is a newly described disease of cotton in Australia. Symptoms associated with the disease are a sudden wilting and dying of plants with leaves remaining on the plant (Figure 1); dead plants with blackened stems (Figure 2); internal reddening of roots and root decay; and in cross section, the infected tissue may possess a wedge-shaped appearance and has a reddish-grey colour (Figure 2). The wilting and death of plants were observed to occur from squaring and at all stages of growth there on, occurring as either single plants or in patches.

Reoccurring wilt is caused by a fungal pathogen in the family Diatrypaceae. Comparison of pathogen isolates from Queensland with reference sequences representing Eutypella species suggests our isolates consist of two novel species (Figure 3). Closest relatives are Eutypella scoparia causing Eutypa dieback on pecan. To our knowledge there are no reports of Diatrypaceous fungi causing disease on cotton worldwide. This research has been published in Australasian Plant Pathology.

Since 2019/20 when the cause of this disease in the Dawson Callide region of Central Queensland was confirmed, disease surveys of cotton across all growing regions in Queensland and New South Wales has confirmed the disease is also present in Emerald, St George, Border Rivers, Mungindi, Walgett/Bourke and Namoi valleys. The disease continues to spread within fields and to new fields.

The Cotton Research and Development Corporation has funded new research by the Queensland Department of Agriculture and Fisheries (QDAF) Pathology Team focussed on understanding the diversity of the pathogen and its lifecycle, to enable management strategies to be developed for the cotton industry.

Figure 1: Plants suddenly wilted and died from squaring and throughout the season to mature plants

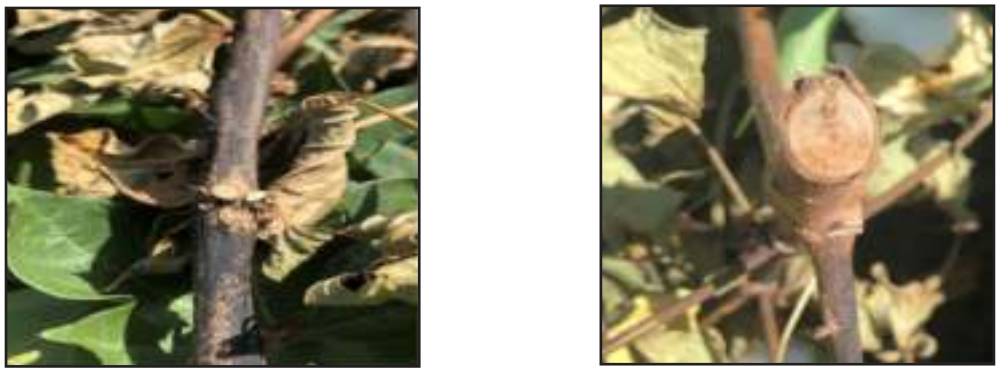

Figure 2: Typical symptoms of reoccurring wilt include blackening of the stem and a redish Internal reddish/grey discolouration of the stem and in cross-section may be wedge shaped.

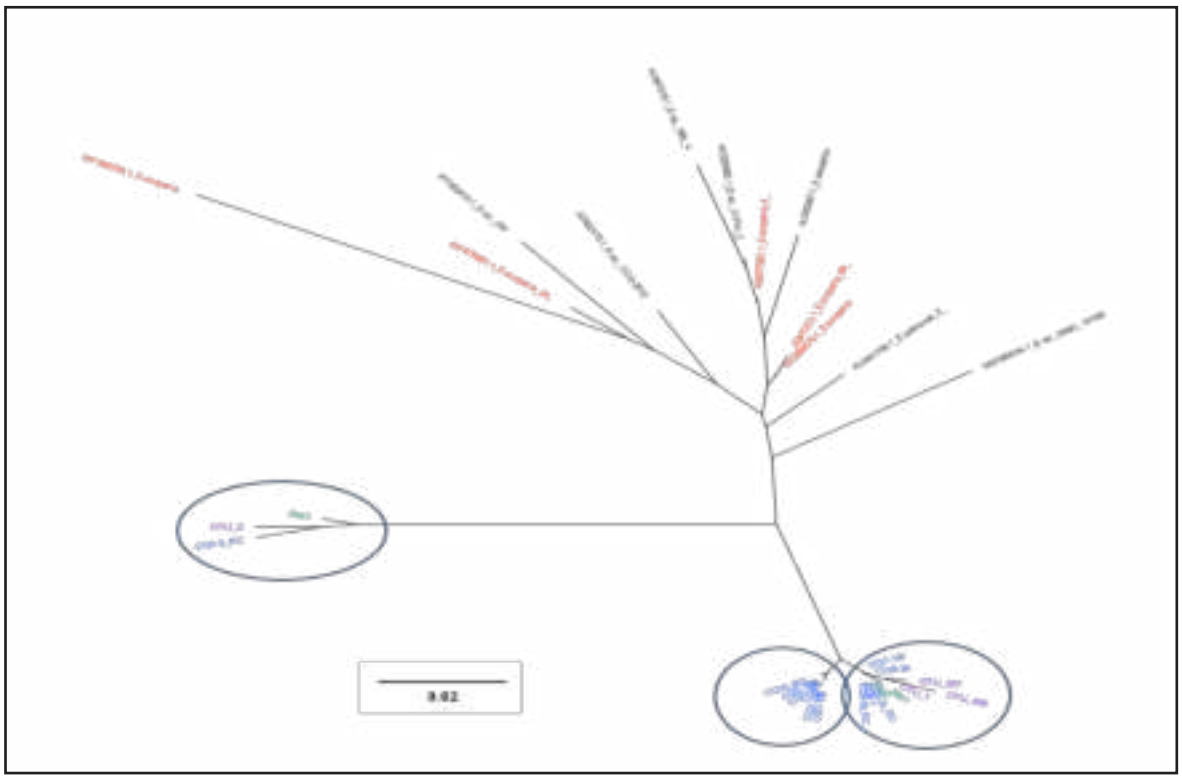

Figure 3: Phylogenetic tree generated based on trimmed ITS1 (amplicons) and ITS1+5.8S+ITS2 (isolates) sequences. The specimens in this study are: Eutypella isolates from diseased cotton plants in blue, Eutypella isolates from diseased cotton roots in green, community Operational Taxonomic Unit (OTU) amplicons in purple and other neighbouring Eutypella species from Genbank in black and red for those identified as Eutypella scoparia

Developing management strategies for Verticillium Wilt

Verticillium wilt is a major economic constraint to cotton production worldwide. Successful control of soilborne plant diseases, such as Verticillium wilt involves management of infection and disease incidence through targeted management strategies. Our research is aimed at reducing the impact of this disease through improved understanding of the intricacies of complex microbiome-pathogen interactions to identify management practices that can promote natural disease suppression capacities of Australian cotton soils, including the influence of rotation crops. Given the ever-expanding host range of Verticillium dahliae, research is identifying disease risks associated with growing alternate crops. Inoculation studies in the glasshouse, using the two prevalent Australian pathotypes (VCG 1A and VCG 2A), have identified symptomatic infection in varieties of mungbean (Vigna radiata), black gram, (Vigna mungo), faba bean (Vicia faba), pigeon pea (Cajanus cajan), soybean (Glycine max), butterfly pea (Clitoria ternatea), cowpea (Vigna unguiculata), chickpea (Cicer arietinum), wheat (Triticum aestivum), barley (Hordeum vulgare), triticale (x Triticosecale), oats (Avena sativa) and canary grass (Phalaris canariensis). Targeted surveillance of these crops grown in commercial fields will begin to fully understand the impact alternate hosts may have on soil inoculum levels and any potential survival carryover on crop residues.

Field trials have shown that sorghum and corn

are good rotation options for reducing inoculum levels and disease incidence, but at least two years of rotation out of cotton is required to begin to significantly reduce disease incidence when the inoculum load is high (Figure 4). Despite two years of bare fallow also resulting in a decline of V. dahliae, evaluation of soil microbial populations indicates that rotation to non-hosts, such as sorghum or corn, result in a greater abundance of fungal populations and general catabolic diversity compared to bare fallow (Figure 5). Thus, non-hosts should aid in improving microbial diversity and maintaining soil biological functions and be better for overall soil biological health compared to a bare fallow. Crop rotation with non-hosts and avoiding fallow is recommended to both reduce pathogen inoculum along with maintaining and improving overall soil microbial diversity and biological health.

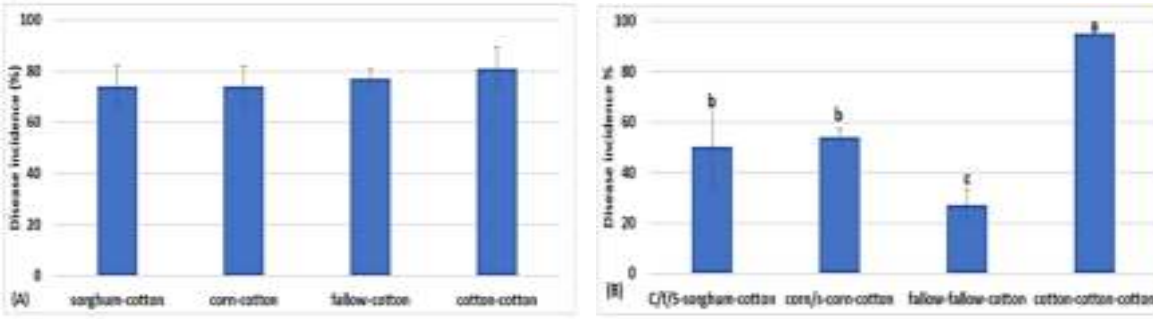

Figure 4: Effect of either one year (A) or two years (B) of crop rotation compared to continuous cotton on Verticillium disease incidence in the subsequent cotton crop. C/f/S indicates corn, fallow or sorghum as the crop in the first year. Corn/s indicates corn or sorghum as the crop in the first year. Bars with different letters are significantly different from each other ($p<0.05$).

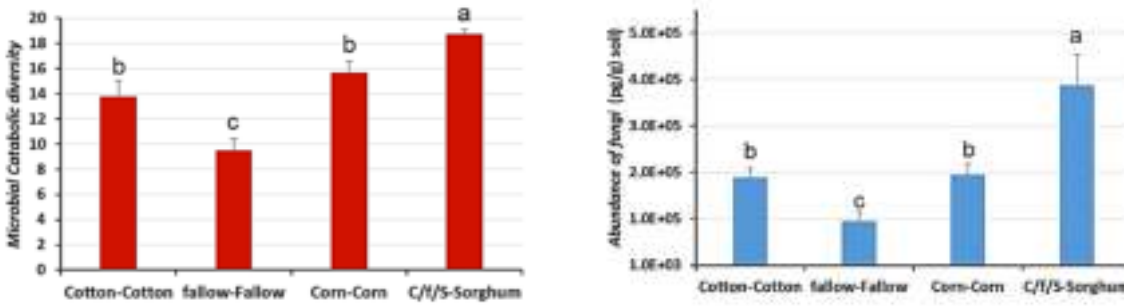

Figure 5: Effect of two years of crop rotation sequences on microbial catabolic diversity (L) and total soil fungal populations (R) in surface 10 cm soil. C/f/S indicates corn, fallow or sorghum as the crop in the first year. Bars with different letters are significantly different from each other ($p<0.05$) (Gupta Vadakattu)

Distribution of reniform nematode in Australian cotton soils

The first detection of reniform nematode (Rotylenchus reniformis) in Australian cotton was recorded in a single field in Emerald, Queensland on Nov 11, 2003. No further detections were made until an investigation of stunted plants led to the identification of reniform nematode in Theodore, Queensland on Nov 23, 2012. A comprehensive soil survey of Theodore cotton fields was commissioned to map distribution of the pathogen. Reniform nematodes were found to be widespread, inhabiting 72 – 75% of fields in the northern districts, 49% of sampled fields to the south of Theodore as well as a limited area in Emerald.

Disease surveys are conducted annually across all cotton growing regions in Queensland and New South Wales to ascertain the incidence and importance of disease early and late season. In Theodore, the high reniform pressure at planting continues to impact seedling development (Figure 7). To determine if reniform nematode has spread to other cotton growing regions, soil samples are collected early season from around the roots of plants being assessed for disease. Soil is collected early season rather than late season for ease of soil collection in heavy clay soils that Australian cotton is commonly grown. Plant-parasitic nematodes are extracted from soil using the whitehead tray method and counted (based on morphology) under the microscope. To date no reniform nematodes have been detected outside of Central Queensland.

It is known however from the spread of reniform nematode to the Lockyer Valley and more temperate zones in Queensland and New South Wales in other crops such as sweet potato, that this plant parasite would happily survive in cotton growing regions south of Central Queensland. Hence the continued surveying and monitoring of reniform nematode is very important for the Australian cotton industry, particularly as there is no host resistance available in Australian cotton or registered chemicals, so management options are limited.

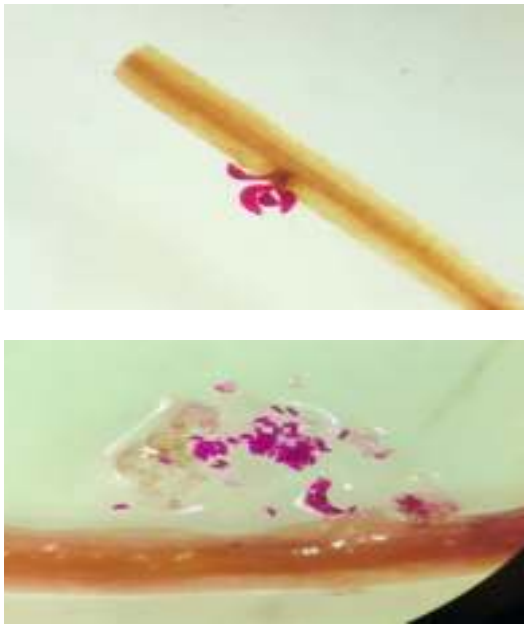

Figure 6: Reniform females and eggs (stained pink) on cotton root

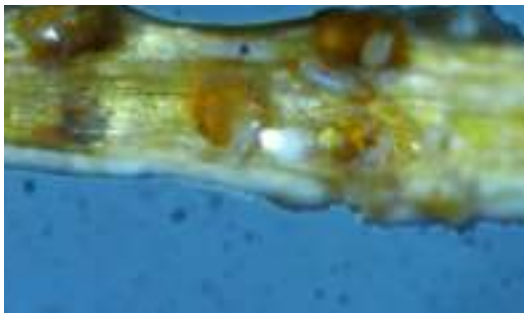

Figure 7. Extensive infection of cotton seedling roots by reniform nematode

The Challenges of Breeding for Verticillium Wilt Resistance in the Australian Cotton Breeding Program

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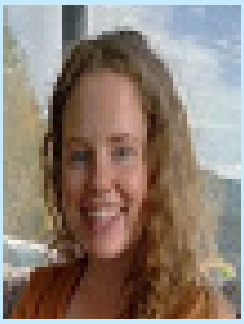
Lucy.Egan@csiro.au



Verticillium wilt (VW) is a critical disease to the Australian cotton industry. It is caused by the soil-borne fungal pathogen Verticillium dahliae Kleb and has two causal pathotypes: non-defoliating (ND) and defoliating (D). In Australia, the D vegetative compatibility group (VCG) is 1A, and the ND VCGs are 2A and 4B. The characteristic symptoms of VW include plant wilting, mottled and reddening of the leaves, defoliation, vascular browning (Figure 1) and reduced yield.

Figure 1. Vascular browning of a cotton stem cause by Verticillium wilt.

The Commonwealth Science and Industrial Research Organisation (CSIRO) cotton breeding program supplies 100% of the varieties to the Australian industry. By world standards, CSIRO cotton varieties have high levels of resistance to VW, but modern high-input management practices aimed at producing very high yields, changing environmental conditions, and the increase in prevalence (and possible virulence) of the disease ensures resistance to VW is a key breeding target. The first CSIRO cultivar with significant VW resistance was released in 1991 and showed higher yields and significantly reduced levels of infection and symptoms. The majority of the CSIRO cultivars now grown commercially have relatively strong resistance to both pathotypes, particularly to non-defoliating VW, but significant yield losses can still occur in seasonal conditions that favour the disease. Nevertheless, several challenges are associated when breeding for VW resistance.

Firstly, our VW disease trials are located at field sites that have a history of heavy disease pressure. Multi-site disease nurseries are critical for the development of resistant germplasm to expose the populations to different isolates of VW. However, within a single field the distribution of inoculum is

often uneven which provides challenges for the placement of field trials. Therefore, knowledge of the field history is important to identify disease 'hotspots' that can aid with decisions about trial placement.

Secondly, when we are breeding for resistance to VW, each pathotype must be treated as a separate breeding target, as we have evidence that resistance to ND doesn't necessarily mean resistance to D, and vice versa. Our current suite of commercial varieties has a similar level of resistance to both pathotypes. However, from a breeding perspective we must increase the level of resistance. Although the ND pathotype appears to be more prevalent within the cotton growing regions of Australia, the breeding program continues to breed for resistance to both pathotypes (Figure 2a and b).

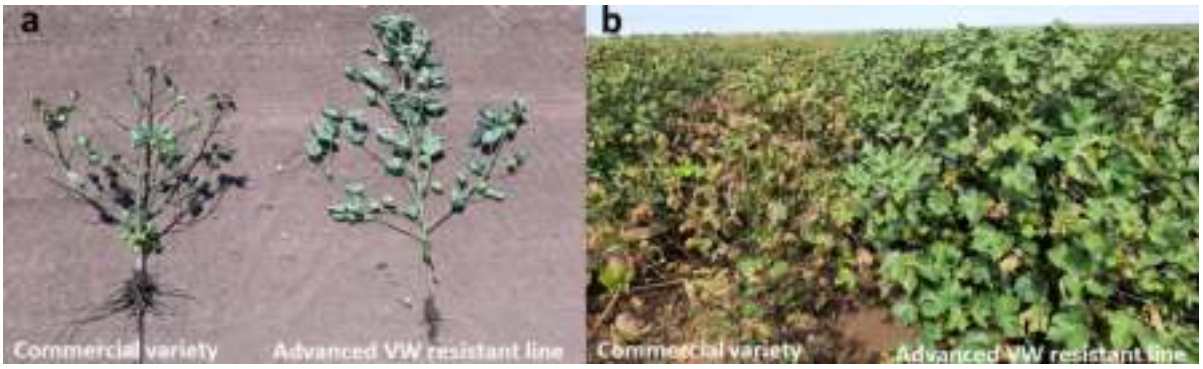


Figure 2. The phenotypic progress of advanced non-defoliating resistant material compared to a commercial variety when planted in a Verticillium wilt disease nursery (a and b).

Lastly, we are continually trying to improve our screening methods to discriminate the levels of resistance to both pathotypes in germplasm. Currently, we use a controlled environment root dip assay. The root dip bioassay is valuable as it is high-throughput, fast and we have results within 6 weeks. However, there are limitations. The process of root dipping involves uprooting the plants which causes significant root damage and is not fully representative of what we see in the field. If we find resistance in the bioassay and this is validated in the field, then we know we have identified a robust source of resistance. However, the problem arises when we find resistance in the bioassay, and it is not present in the field. There are already significant challenges around finding new sources of resistance and genomic regions that control resistance to VW, and without a reliable bioassay, this is complicated further.

In summary, VW resistance has been a key breeding target for the CSIRO cotton breeding program for many decades and is likely to remain critical in the future. We are working to improve our existing screening methods which will aid in identifying new sources of resistance and may enable the identification of the genomic regions controlling said resistance.

Are arbuscular mycorrhiza fungi an exciting new player or misunderstood hero in cotton?

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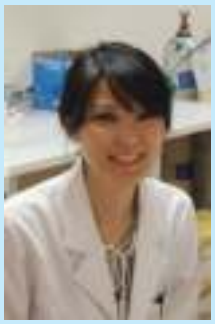

Arbuscular mycorrhizal (AM) fungi form a mutual relationship with many plants, including cotton (Nehl and McGee 2010). They occur in most soils, and form extensive underground networks of hypha that both explore a large volume of soil and access nutrients and other soil resources. They do all this in return for carbon from their host plant. They are also linked to other soil health benefits, such as improving soil structure and soil carbon sequestration and so could be essential for improving nutrient use efficiency, drought tolerance and agricultural sustainability.

With regard to cotton, previous studies into AM benefits are often inconclusive, despite demonstrating root colonisation (Eskandari et al. 2018). One potential reason for this is that the benefit of forming the symbiosis could be costing the plant more carbon than there are benefits from the improved nutrient recovery. However, another possible reason is that the nutrients being studied were perhaps not the most important. Most work looking at the benefit of AM association has focused on the uptake of immobile nutrients, like phosphorus, however, in the majority of Australian cotton systems mobile nitrogen (N) is generally the most growth-limiting nutrient. What if AM have an important role in N uptake?

A field experiment at the Australian Cotton Research Institute was established to test whether AM association improved cotton growth and, if so, what was the mechanism behind it.

To do this, we constructed root containment bags that allowed AM hyphae to grow out of the bags, to explore a greater volume of soil through their extensive hyphal network, while restricting the growth of cotton roots (Figure 1). Lifting the bags was used as a means to disrupt and limit the hyphal network and the field experiment tested whether the effect of AM association on growth differed between normal N and reduced N fertiliser levels. Of the 48 bags established, only 37 made it to the final analysis because cotton had failed to germinated in one of the intact and three of the cutt-off bags and, upon the final recovery, seven bags had failed to contain cotton roots so were exluded.

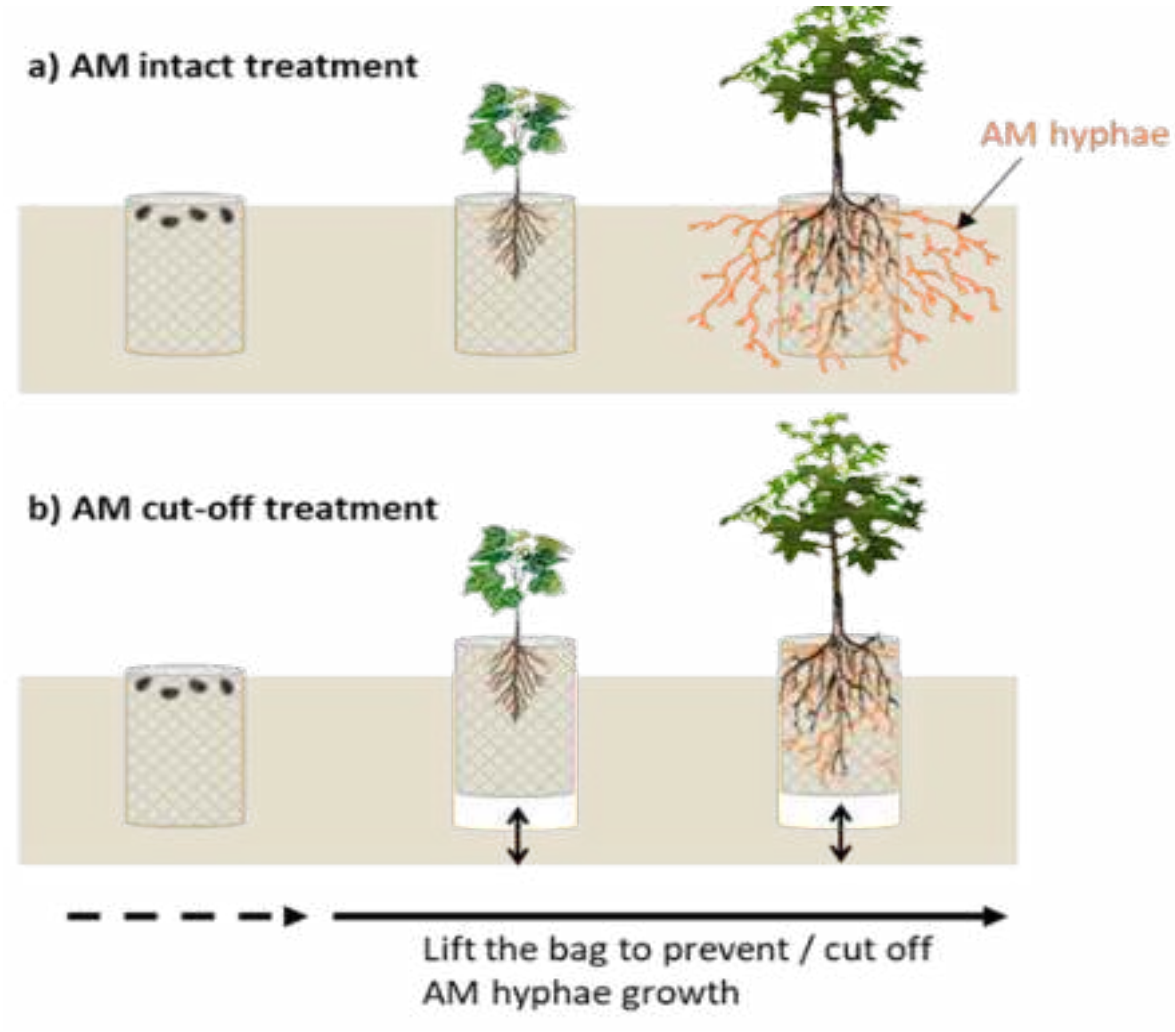

Figure. 1 Schematic diagram of AM root containment bag treatment as applied in field. In the AM intact treatment a), root growth is contained within the mesh bag while AM hyphae are allowed to grow out of the bag. In the AM cut-off treatment b), after three weeks of initial growth, the bag is lifted every week to cut off any AM hyphae that have grown out of the bag.

Lifting the bags and disconnecting the AM network reduced early cotton growth, and this was explained by low N uptake in the cotton, which implied that AM association does benefit cotton growth. The AM benefit in this study was observed to be greater under the normal level of N fertiliser treatments, and was equivalent to the growth benefit provided by the application of N fertiliser.

While this study only focused on early growth of the cotton, it demonstrated that AM association is important in our cotton systems. In addition, this experiment also proved and quantified the growth benefit provided by the local, pre-existing AM communities. Secondly, it proved that the benefit of AM association is not restricted to immobile nutrients, such as phosphorus, and implies that we need to reassess the potential of AM as a misunderstood hero in our cotton systems.

There is a general assumption that soil biology is negatively affected by agricultural practice, such as tillage and agrochemical use (Osanai et al. 2020), so applying AM propagules to soils with reduced soil biology could improve cotton yield.

However, there are more unreliable than reliable AM products on the market (Elliott et al. 2019) as well as differences between different AM species to benefit their host plants. This field experiment revealed that the existing AM communities provide benefits to cotton, so more robust strategies to capitalise on this important soil biological component may simply revolve around improved farm management practices focusing on improved periods of live roots in the system, which is one of the core concepts of the Australian Cotton Industries Soil Health Framework (Figure 2).

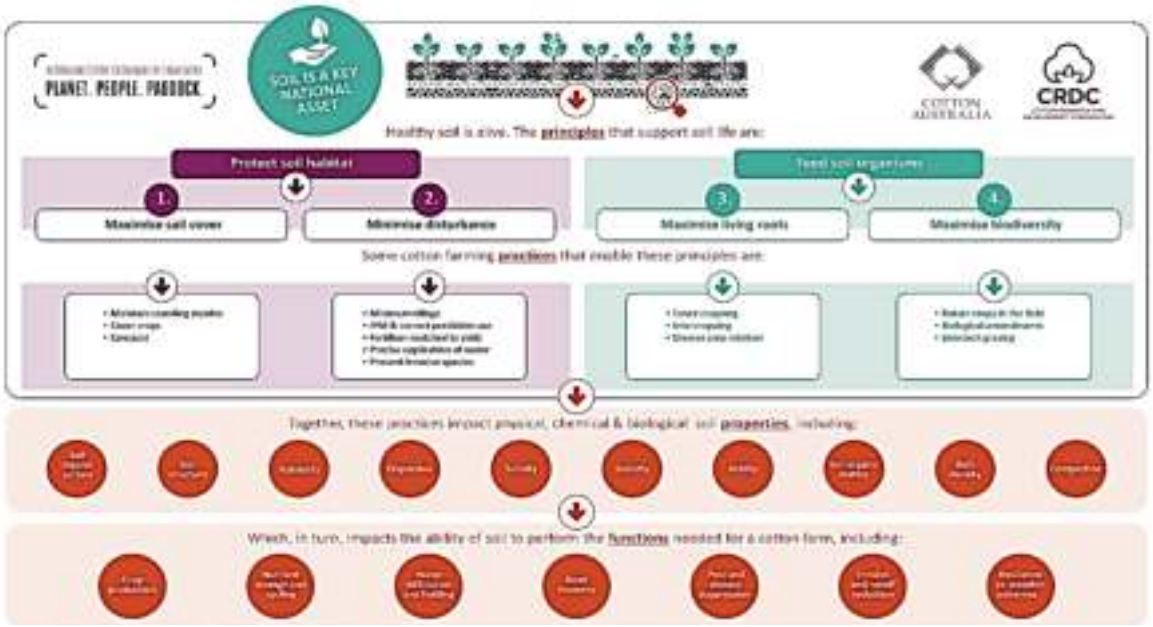

Figure 2. An schematic of the proposed Sustainable Soils Framework for Australian Cotton production, that would fit other production systems. The framework is developed based on the two key principles of protecting soil habitat and feeding the soil biology, which would benefit AM.

Elliott AJ, Daniell TJ, Cameron DD, Field KJ (2019) A commercial arbuscular mycorrhizal inoculum increases root colonization across wheat cultivars but does not increase assimilation of mycorrhiza-acquired nutrients. PLANTS, PEOPLE, PLANET n/a. doi: 10.1002/ppp3.10094.

Eskandari S, Guppy CN, Knox OGG, Backhouse D, Haling RE (2018) Understanding the impact of soil sodicity on mycorrhizal symbiosis: Some facts and gaps identified from cotton systems. Applied Soil Ecology 126: 199-201. doi: https://doi.org/10.1016/j.apsoil.2018.01.008.

Nehl DB, McGee PA (2010) Ecophysiology of arbuscular mycorrhizas in cotton. Physiology of Cotton. Springer.

Osanai Y, Knox O, Nachimuthu G, Wilson B (2020) Contrasting agricultural management effects on soil organic carbon dynamics between topsoil and subsoil. Soil Research 59: 24-33.

Synthetic Biology: The Key to a New Era of Elite Cultivar Development?

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Conventional breeding techniques have been integral to the development of many agronomically important traits in cotton including fibre quality attributes, crop maturity and disease resistance. Modern biotechnology applications such as genetic modification (GM) of crops has enabled trait developments beyond the capacity or efficiency of conventional breeding, such as insect and herbicide resistance (e.g. Bt cotton). However, climatic conditions, insect pests and pathogens continue to hinder cotton productivity, and their incidence is increasing with climate change. These complex challenges would require traits that are more genetically complex than can be developed efficiently through conventional breeding or traditional genetic engineering. Additionally, pressure to generate or tap into new sources of genetic diversity is increasing. Ultimately, more advanced trait development approaches are required to maintain and improve yields and production efficiency. To meet the industry demands of desirable cotton traits, a suite of synthetic biology (SynBio) tools will need to be adopted.

Traditional genetic modification has taken a more straightforward approach with focus on single genes or components of a pathway, whereas developments in SynBio have tapped into a multifaceted approach, expanding the capabilities of genetic engineering. SynBio encompasses approaches that design and construct new biological elements (e.g. enzymes, genetic circuits, cells) or redesign new and improved functions into existing biological systems. Synthetic biology pipelines are beginning to adopt commonly used engineering terms such as ‘switch’, ‘rewire’, and the ‘design, test, simulate, learn cycle’ (Figure 1). A selection of key SynBio technologies are described in Table 1. New opportunities to advance breeding applications through applying modular approaches include the targeted introduction of new genes of known function, complex multi-genic traits through gene stacking, artificial creation of genetic variation, topical application of small RNAs as biopesticides, and faster development of cultivars with sophisticated traits to improve crop productivity.

As genetic engineering has become more sophisticated, it has become seen as a solution for tackling a multitude of issues that are apparent in agricultural industries. For example, modular cloning strategies can rapidly stack and transfer

multiple genes in a single transgenic event, either derived from an organism or synthetically generated. Therefore, more complex traits can be developed more efficiently than through traditional breeding or GM. The uptake of biofoundaries in state-of-art research facilities has enabled the integration of high-throughput molecular biology techniques that incorporate robotics, analysis and data management, therefore consolidating genetic engineering processes.

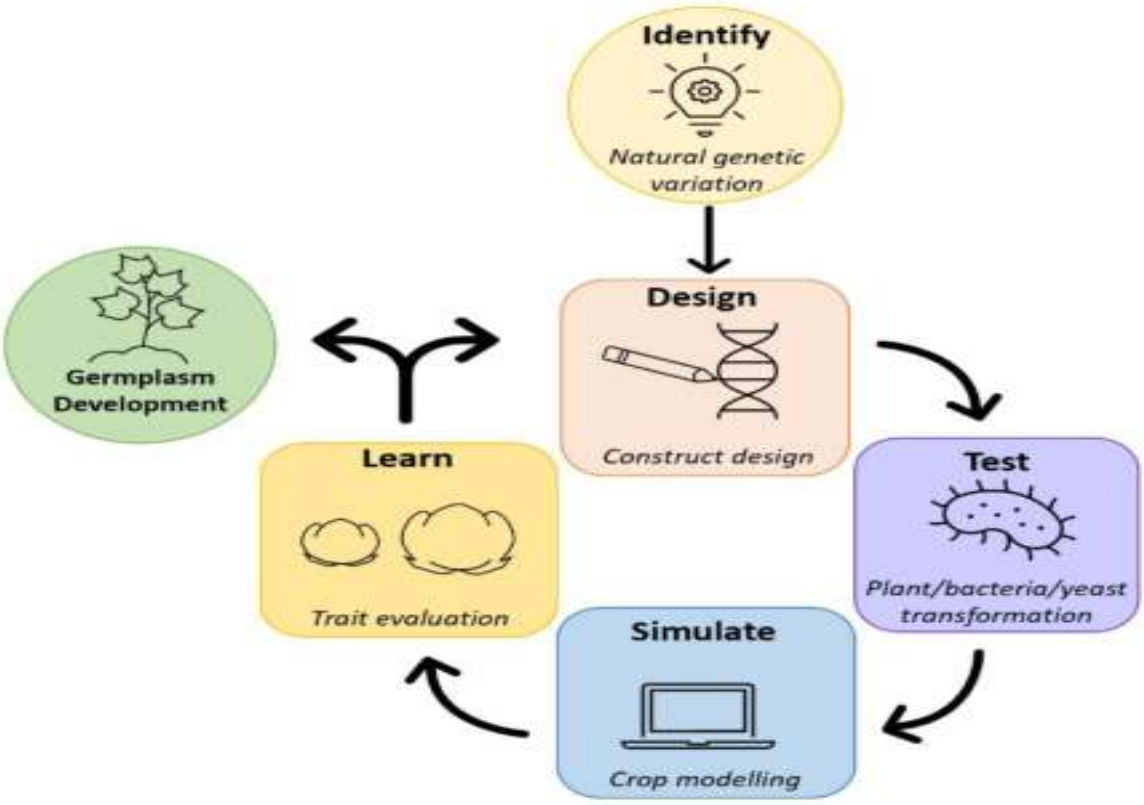


Figure 1. The "Design, Test, Simulate, Learn" cycle of developing a synthetic biology pipeline for developing novel crop traits. Potential traits of interest can be identified from natural variation in crop germplasm. Constructs are carefully designed with the appropriate components (i.e. promoters for targeted expression), and tested using high-throughput plant, bacterial or yeast transformation systems. Crop models can estimate the impact of this transformation on crop yield and resource-use efficiency. From this we learn how to optimise the incorporation of these traits and enhance crop productivity. Traits determined to be of value are carried through for germplasm development

Gene editing using the CRISPR-Cas9 system is one of the fastest, easiest, and cost-effective methods of modifying an organism's genome without introducing foreign genetic material. The simple design and easy construction of components also makes gene editing a promising alternative to traditional breeding and GM approaches. Further, single-gene knockouts or single base-pair mutations that can be achieved by gene editing through CRISPR-Cas9 may not require regulation in a growing number of countries (Waltz, 2017), adding to the appeal of this system. In 2019, the Australian government declared that gene editing techniques that do not introduce new genetic material in plants and animals will not be regulated as Genetically Modified Organisims (GMOs). Regulation by the relevant government authorities will be required where editing techniques incorporate new genetic material.

RNA interference (RNAi) is a post-transcriptional gene silencing (PTGS) mechanism. Gene silencing through RNAi has various potential agricultural applications, such as inducing sterility or mortality in insect pests upon consumption of RNAi-producing plants, modifying seed oil composition, removing toxin production in edible tissues and in supressing fungal and viral pathogens.

Table 1. Summary of SynBio tools with potentially valuable applications in agriculture. Adapted from Sargent et al., (2022)

Technology:	Description:
Gene Editing Techniques	**Targeted in vivo gene silencing or altering sequences in the promoter region to change expression or within the coding sequence to alter function. An efficient tool for site specific editing of genes for desired outcomes.**
Modular Cloning	**Crucial strategy for cloning multiple genes for applications of rewiring metabolic pathways. Examples include Golden Gate, BioBricks and Gibson cloning. Can be intertwined with biofoundaries to select certain genetic parts for expression in certain tissues.**
RNAi	**The plant defence system towards viruses and hence double stranded RNA can be utilised to target insects through the application of siRNAs or their expression from the chloroplast.**
Gene Drives	**Promoting inheritance of deleterious alleles (i.e. lethal or sterile alleles in insect pests).**
Regulated Promoters	**Regulated promoters can temporally control gene expression by activating or deactivating downstream genes under specific conditions, such as environmental stress or phenological development.**

Dr. Mohamed Negm

ICRA, Chairman

Dr. Keshav R. Kranthi

Chief Scientists-ICAC

Dr. Jodi Scheffler "ICAC Researcher of the year 2022, with H. E. Mansoor Bek Ambassador of Uzbekistan in Egypt

H. E. Dr. Ibrokhim Abdurakhmonov

Minister of Innovation and Development, Uzbekistan

Mr. Khaled Schuman

CEO, Cotton Egypt Association-Egypt

Eng. Mohamed Khedr

Chairman of Cotton

Arbitration and Testing general Organization-Egypt

Prof. Dr. Mohamed Soliman

President, Agric. Research

Center-Egypt

Opening from eft to right:

H. E. Mansor Bek, Ambassador Of Uzbekistan In Egypt,

Mr. Khaled Schuman, Dr. Mohamed Siloman, Dr. Keshav Kranthi.

Dr. Khaid Abduah, Cotton Commissioner, Pakistan Government and Dr. Mohamed Negm

Dr. Jodi Scheffler
USA

Dr. Kater Hake, Dr. Jodi Scheffler, and Dr. Eric Hequet Vice President of Texas Tech Univ. For Research

Dr. Marcelo Paytas
Head of INTA, Argentina

H. E. Dr. Ibrokhim and Dr. Mohamed Negm

Dr. Mohamed Negm, Dr. Khade
UNIVERSITY OF AGRICULTURAL SCIENCES DHARWAD, India
And Dr. C D Mayee, President, South Asia Biotechnology Centre

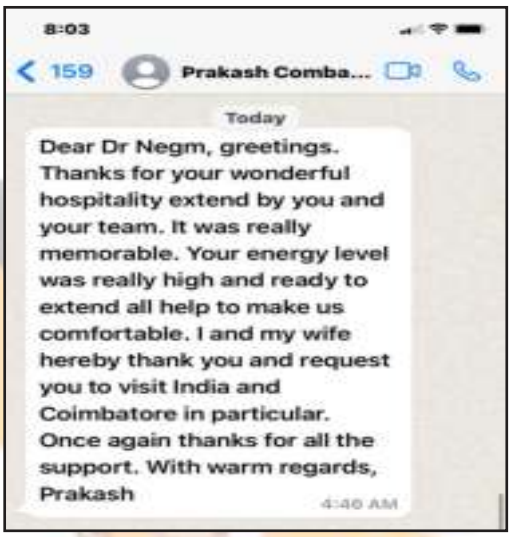
Dr. kater Hake,

Cotton Incorporated

USA


Keshav Kranthi 6:21 PM
to me
Dear Dr Negm,
You are not only an excellent scientist and a superb organizer, but also a great human being and an endearing friend.
With lots of affection
Keshav


Khalid Abdalla Pak
I can not find words to thank you for all you did for me. It was amaizing experience and everything was nicely organized. I must congratulate you and your team for thier efforts. My brother, you are gem. Proud of you. Regards
7:57 pm


8:03
159
Prakash Comba...
Today
Dear Dr Negm, greetings. Thanks for your wonderful hospitality extend by you and your team. It was really memorable. Your energy level was really high and ready to extend all help to make us comfortable. I and my wife hereby thank you and request you to visit India and Coimbatore in particular. Once again thanks for all the support. With warm regards, Prakash
4:46 AM


7:57
118 views
@0:44 · 9 views
ICAC Retweeted
Kaitlyn Bissonnette @kmbiss · 5d
Celebrating #worldcottonday with @Dr_Jaconis by trekking back to the states after an excellent #WCRC7. Great connections and idea development for the time spent in Cairo this week. Thank you @icac_cotton and those of the meeting committee for all their hard work. Until next time!


8:04
159
India@WCRC7
Ajit Mokate, Bala G., Basavaraj...
Bala G.
Dear Dr Negm brother good morning. We (Nagpur group) reached home jus now. Thank you so much for your kind hospitality and all the arrangements made from the day we reached Cairo to back home. It was wonderful trip and sweet memories of WCRC-7
8:30 AM


8:05
159
India@WCRC7
Ajit Mokate, Bala G., Basavaraj...
+91 75880 82184 ~Dr Wasud...
Reached at mumbai airport safely. Thank you for your help Negum sir. Dr. Narkhede W. N.
3:01 AM
Udikire Dharward
We have reached Mumbai safely and timely. Your logistics are very good.
Kind regards
Dr Udikeri, Dr Rajesh Patil, Dr and Mrs Khadi, Dr Prasad Rao
3:46 AM
+91 94814 67772 ~DrA.G.SRE...
Dr.Mohamed Negm sir,
Good morning
We the UAS RAICHUR team (Dr.A.G.Sreenivas & Dr. Hancinal) reached safely Raichur.
Thanks your and your team wonderful support
6:30 AM


8:08
159
India@WCRC7
+91 94488 66474 ~Manjula M...
8:40 AM
View of Mediterranean sea from hotel balcony
8:41 AM
In Alexandria
8:41 AM
Vipin Dagaonkar
9:17 AM
Bala G.


8:07
159
India@WCRC7
Santosh Kedar
Temple of Hatshepsut
11:36 PM
Santosh Kedar
Karnak Temple
11:36 PM
+91 94663 75285 ~Rishi Kumar


4:37
159
India@WCRC7
Rajesh Patil Today
Dr. Negm Sir, myself and Udikeri reached home safely after a memorable WCRC. Thanks again for all kinds of help you personally rendered. We look forward to your visit to Dharwad.
9:41 AM
Udikire Dharward
Dear Dr Negm, we invite yourself to Dharwad
9:42 AM
+91 89756 15439 ~Dr- DV PA...
Respected sir, Dr.Nagam. I reached Nagpur today safely. Thanks for wonderful hospitality and help. Hope expecting same when ever we visit to Cairo. Dr.D.V.Patil.
2:59 PM


8:08
159
India@WCRC7
+91 94498 01645 ~Suresh Ha...
Alexandria trip
7:24 PM
+91 98769 62774 ~Sanam Sin...
7:26 PM
+91 98769 62774 ~Sanam Sin...

Manoj Kumar

Dear Prof. Negm

I am sorry that I was not able meet you since you are engaged in Alexandria tour for hosting guests from almost 32 countries.

I wish to share some of the best experiences in Egypt during WCRC-7. Please take my words as in person. The hospitality started on 3rd October when I reached Cairo Airport and received by team WCRC-7.

The hassle free checkin at hotel cleopatra was great; this helped me to get proper rest before the start of conference. It was wonderful to meet various cotton researchers during welcome party (cotton connect) at Novotel.

I got superb experience by listening to the cotton experts followed by the presenters from various cotton producing countries. Three days during conference and one day for celebration of world Cotton Day were full of knowledge and fun. The gala dinner and dance party at Al-saraya was awesome.

Thank you for giving us a combo of love, knowledge, and to experience the beauty of Egypt.

You are really very kind and generous person who helped all the participants 24 * 7 for a great stay in beautiful country.

I also acknowledge the support from ICAC, ICRA and my mentor Prof. Baihong Zhang from East Carolina University, Greenville, USA.

Thank you again for the great hospitality.

Dr. Manoj Kumar
Visiting Scientist
Department of Biology
East Carolina University
Greenville, USA

12:09 am

4:13

667

SS **Sankaranarayanan...** Tuesday
To: Mohamed Negm >

Greetings

Respected Sir

Greetings!. Here I express my sincere thanks for providing support and blessings in attending WCRC 7 in CAIRO. You are energetic, friendly, organized and workaholic. We reached safely at Coimbatore. We are proud of you and pray to become higher position

Thanking you

Yours sincerely

Dr. K.Sankaranarayanan M.Sc (Ag.), Ph.D
Principal Investigator (Agronomy) – AICRP (cotton) &
Principal Scientist (Agronomy)
Central Institute for Cotton Research, Regional Station,
Coimbatore -641 003 , Tamil Nadu,India
Phone 914222430045 (O),

Congratulations on a very successful WCRC 7

Scheffler, Jodi

Dr. Negm,

I just want to express my appreciation and gratitude to you and the amazing organization team that put together a very successful and enjoyable WCRC 7 as well as an excellent World Cotton Day celebration.

After two years of delays and challenges, it was the first time many of us had the chance to come together and share our research. I believe that coming to Egypt was the perfect country to host the meeting as I felt a real sense of kindness, patience and optimism from my hosts. This was the case from the organizing committee members and hotel staff to the kind women who helped me cross the busy street. In English I don't know how to express this feeling, but I think that the French do it better when they say "joie de vivre". That spirit of optimism and joy was found throughout the conference and I think all of us returned to our home countries newly motivated and grateful for our time together in Cairo.

Regards,
Jodi Scheffler

ICRA

INTERNATIONAL COTTON RESEARCHERS ASSOCIATION

COTTON INNOVATIONS