World Cotton Research Conference - 6

Conference 2016

INTERNATIONAL cotton genome INITIATIVE

Official Program and Abstracts

Brazil

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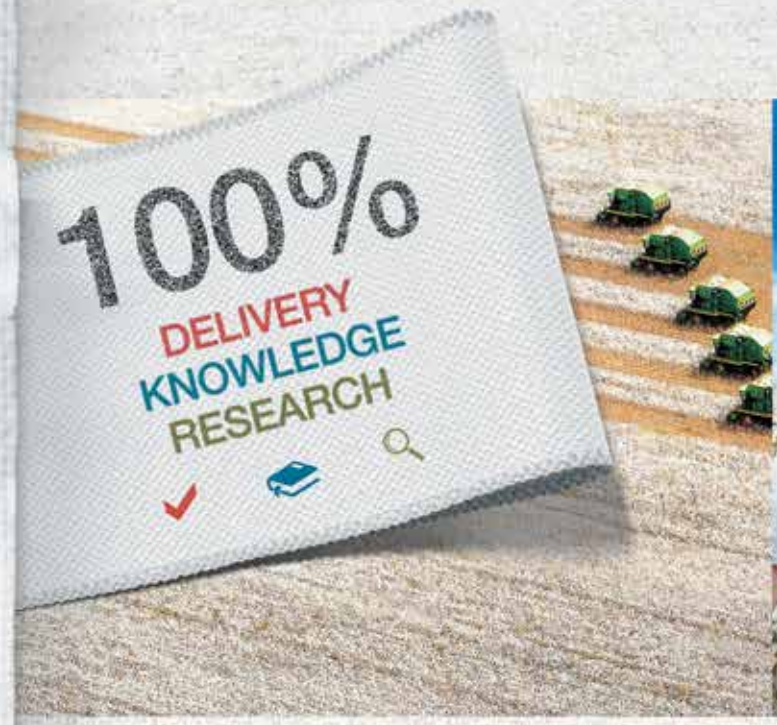

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Index

Opening message from the Institutes Directors

DAVID M. STELLY
Chair of ICGI

The International Cotton Genome Initiative (ICGI) was born conceptually in 2000, based largely out of common desire for molecular markers. The first ICGI Research Conference was held in Montpellier France in 2002, and has met biennially since then at various sites around the world. One decade ago, we met in Brasilia, where we decided collectively as a group to focus initial cotton genome sequencing efforts on a wild non-cultivated relative from Peru, Gossypium raimondii.

Great progress has been made. A high quality genome sequence for that species was assembled and published. Draft genome sequence assemblies for other more complex Gossypium genomes have been published recently, including that of Upland cotton, Gossypium hirsutum. The pace of advances in cotton genomics, genetics, bioinformatics, biotechnology and breeding seems to have incessantly increased, spawning a seemingly ever-expanding labyrinth of data, and swarms of new findings and potential applications.

The International Cotton Genome Initiative (ICGI) will meet jointly in Goiânia - Goiás, Brazil, with the World Cotton Research Conference-6 (WCRC-6) and the International Cotton Researchers Association (ICRA). The joint WCRC-6/ICGI meeting will provide many opportunities for all of us to meet and learn. By indulging in them at WCRC-6/ICGI, we will be better equipped to deliver downstream advances and benefits needed by cotton and the many whose livelihoods are intertwined with it.

As the current Chair for ICGI and thus as a spokesperson for ICGI, I wish to publically acknowledge and thank many who've been involved with the concepts, planning and preparations. I especially want to recognize and thank the local organizers -- preparing such a meeting requires Herculean efforts – thank you all! I would also like to recognize a few individuals with whom I interacted most directly, especially Dr. Alderi Emídio de Araújo, Dr. Marc Giband, Mr. Paulo César da Cunha Peixoto and Dr. M. Rafiq Chaudhary. ICGI appreciates the efforts of ICRA, especially Dr. Greg Constable and Dr. Chaudhary for sharing the vision for a joint meeting, and the rest of the WCRC-6 International Organizing Committee for helping make it happen. I would also like to thank Dr. John Yu, Co-chair of ICGI and all members of our Executive Steering Committee. For more detailed information on the Committee and ICGI, please see https://www.cottongen.org/icgi/home.

GREG CONSTABLE
Chair of ICRA

The International Cotton Researchers Association (ICRA) aims to facilitate communication and collaboration between cotton researchers. World Cotton Research Conferences (WCRC), held every four years in different countries, have established a tradition which ensures increased synergy between cotton researchers. The conference is now a major activity of ICRA. However the ICRA Executive Committee has ambitions to grow the concept to be more than WCRC.

Conferences are an important and special method of sharing information and ideas between people with common interests. Compared with reading a journal article, there can be a better personal connection. The cotton research community is small enough for regular personal contact which ensures synergy and collaboration. In particular there is benefit from meeting peers and discussing ideas. Personally I have gained more ideas, understanding and stimulation from Conference presentations than from papers – often from disciplines other than my own specialisations.

It is good that the International Cotton Genome Initiative (ICGI) is joining with WCRC-6 on this occasion in Brazil. This is a special opportunity for international contact between genomics and other research disciplines in cotton.

On behalf of ICRA I would like to thank and congratulate the WCRC-6 Local Organizing Committee for their hard work in preparation of the Conference. I am confident their efforts will be rewarded by a successful meeting and that all participants will benefit from the experience.

JOSÉ SETTE
Executive Director of ICAC

The International Cotton Advisory Committee and its Members consider the World Cotton Research Conference the most important happening on the calendar for cotton researchers. It is a pleasure to see that the seeds that were sown during the first Conference, held in Australia, in 1994, have borne fruit in the form of this sixth edition of the event, this time in Goiânia, Brazil.

As part of ICAC's commitment to the development and dissemination of information on cotton, one of our strategic goals, we are pleased to support the presence here of dozens of scientists from all over the world. The world cotton research community can count on the backing of ICAC for such worthy initiatives in the future.

The themes that will be discussed in the Conference are of fundamental importance for the future of this crop that we all love so much. Cotton faces immense challenges, above all from the increasing penetration of man-made fibers. During this conference, we will hear from experts from all around the world in such diverse fields as plant biology, entomology, breeding, genomics and agronomic practices about the most modern approaches available to assure that cotton maintains its relevance by remaining competitive in terms of both cost and quality.

I am sure that all of us will be enriched by participating in this landmark event, which will help to guide scientific research in cotton during the coming years and wish all of you a fruitful week of work.

LUIZ RENATO ZAPPAROLI
Chair of the Organizing Committee of WCRC-6

Dear Reader,

Initially, I would like to thank ICAC, ICRA, ICG and specially ABRAPA and EMBRAPA for embracing the possibility to hold this conference in Goiania, Brazil.

The challenge of coordinating the organization of the WCRC-6 was an unique opportunity. This task would not have been possible without my staff, which I would like to thank, as well as all those involved in several committees that have contributed to the success of our conference.

As for my participation and my staff's at the WCRC-6, I would like to highlight how much we have learned by organizing an event in which people from several countries and international organisms were challenged to think of ways to collaborate with the future of cotton in a global perspective, considering that we are used to think locally, or only about Brazilian interests, at most.

When we think about the future of cotton, we see several obstacles and the main one is certainly the market share loss for synthetic fiber and the resulting income loss that directly affects global cotton culture. As part of the cotton chain, I daily wonder where will we be 10 years from now. Maybe I will not be at the front line, maybe in a staff position, since a new generation is already working with me. And what about cotton? Do we like to grow cotton? Certainly yes, but how does one stay in the business without income? In some parts of the world, agriculture helps attach people to the countryside in order to keep cities from over expanding. But how can that be possible without financial feedback?

The world wants cheap food, but it also wishes for cheap fibers and demands farmers to take up part of the responsibility for environmental issues. Thus, we must find methods of grow crops with a reduced environmental impact. In Brazil, agriculture and pasture areas use up 29% of the territory. Natural vegetation, indigenous areas, and conservation parks occupy 68% of the Brazilian territory, while urban areas occupy 3% of the total. Water consumption is also charged on us. Should those charges really be on us? Are the methods to calculate water consumption correct? Whether they are right or wrong, we are being charged and the solution to such problems should guide the future of research so we can pay our share and not the ones attributed to us.

Having said that, I have reported several problems that affect us globally. In Brazil, I did not even mentioned the boll weevil, the diseases and pests that spread in our tropical conditions, once we produce cotton with over 1,800 mm of rainfall per year with rains extending for 9 months almost every year, creating the so-called "green bridge", which provides us with a great number of pests awaiting at each crop beginning.

The agriculturalist must be valued. We need to work with synergy aiming at better income and life conditions so we are stimulated to stay in the countryside managing a business that is at risk of irreparable losses before harvest and storage. I believe global agriculture should improve the overall quality of life of all people involved in the production chain, especially at its base. It is the base that takes higher risks and in general doesn't have access to the advantages of urban centers such as schools, medical assistance, social security, land property and so many others.

Committees

INTERNATIONAL COMMITTEE

Dr. Greg Constable - Chair of ICRA - Australia – CHAIR
Mr. Luiz Renato Zapparoli - AGOPA, Chair of the Organizing Committee of WCRC-6 - Brazil, VICE CHAIR
Dr. Alderi Araújo - Embrapa - Brazil, Member of the Executive Committee of the International Cotton Researchers Association (ICRA)
Dr. Annette Swanepoel - Department of Agricultural and Land Reform, Northern Cape - South Africa, Member of the Executive Committee of ICRA
Dr. C.D. Mayee - Organizing Committee of WCRC-5 (2011) – India
Dr. David M. Stelly - Texas A&M University, Chair of the International Cotton Genome Initiative
Dr. Dean Ethridge - Texas Tech University - USA, Treasurer of ICRA
Dr. Francesca Mancini - Pest and Pesticide Managment Officer – FAO
Dr. Julie Flood, CABI, UK
Dr. Michel Fok - CIRAD – France
Dr. M. Rafiq Chaudhry - ICAC – USA
Mr. Paulo Cesar Peixoto - FIALGO, Brazil
Dr. Sebastião Barbosa - Chief, Embrapa Algodão – Brazil

ORGANIZING COMMITTEE

Chair: Luiz Renato Zapparoli – AGOPA
Co-Chair: Sebastião Barbosa – Embrapa
Organization: Paulo Cesar Peixoto – FIALGO
Organization: Davi Laboissiere Garcia - Fundação Goiás
Organization: Dulcimar Pessatto Filho – AGOPA
Organization: Bruno Coelho Soares - Embrapa
Organization: Janaine Souza Saraiva- Embrapa
Program: Alderi Emídio de Araújo – Embrapa

PROGRAM COMMITTEE

Coordinator: Alderi Emídio de Araújo – Embrapa
Ana Luiza Dias Coelho Borin – Embrapa
Camilo de Lelis Morello – Embrapa
Ciro Antonio Rosolen – UNESP
David Laboissiére E. Garcia - Fundação Goiás
David Stelly - Texas A&M, ICGI
Ederaldo José Chiavegatto - ESALQ-USP
Edivaldo Cia – IAC
Eduardo Massakazu Kawakami - Fundação MT
Fernando Mendes Lamas – Embrapa
Francisco de Souza Ramalho – Embrapa
Francisco José Correia Farias – Embrapa
Jean-Louis Belot – IMAmt
John Yu - USDA-ARS, ICGI
José Ednilson Miranda – Embrapa
Liziane Maria de Lima – Embrapa
Luciano Shozo Shiratsuchi – Embrapa
Marc Giband – CIRAD
Nelson Dias Suassuna – Embrapa
Rafael Galbieri – IMAmt
Renildo Luiz Mion – UFMT
Wanderlei Oishi - Consultor Agropecuário
Yeshwant R. Mehta - IAP

Helpful information

LOCATION OF THE CONFERENCE

Goiânia Convention Center (Centro de Convenções de Goiânia – CCGO)
Rua 30, nº 855 – Portão 1 – Centro – Goiânia-GO
Telephone: 55 (62) 3219-3300
Website: www.ccgo.com.br

FRONT DESK

The reception for the participants and guests will take place at the Front Desk, located on the 1st floor, at the entrance of the Convention Center, on Rua 30.

Front Desk– operating time:

May 1st – Sunday – from 5:00pm to 7:00pm
May 2nd – Monday – from 7:30am to 6:00pm
May 3rd – Tuesday – from 7:30am to 6:00pm
May 4th – Wednesday – from 7:30am to 6:00pm
May 5th – Thursday – from 7:30am to 6:00pm
May 6th – Friday – from 7:30am to 3:00pm

Attendees who have already subscribed can take their badges and material at the secretariat

SCIENTIFIC PROGRAM

All the Scientific Program activities will take place on the 1st floor in the Convention Center: Rooms Auditório Lago Azul, Lago dos Tigres, Rio Araguaia, Serra Dourada, Águas Quentes, Lago das Brisas, Salto de Corumbá e Salto de Itiquira.

The entire Exhibition will be in the Espaço Cerrado in the Convention Center. Check the map of the event for more details.

VIP ROOM

Intended to receive authorities, speakers, and guests. It will be open from May 2nd to May 6th, from 8:00am to 6:00pm, on the 1st floor in the Room Sala Salto de Corumbá in front of the Auditório Lago Azul. Check the map of the event for more details.

MEDIA DESK

The Media Support Desk is located on the 1st floor, in the Room Sala Lago dos Tigres. The Keynotes and Plenary speakers, and Parallel Session speakers must be present at the Media Desk and deliver their presentation file with at least 1 (one) hour before the beginning of the presentation.

LUGGAGE STORAGE

The Luggage Storage is located in the entrance hall, next to the Front Desk. It will be open from May 2nd to May 6th, from 8:00am to 5:00pm. The Luggage Storage will also be the lost and found location. Be aware of the closing time, since we are not responsible for any material left after that time.

MEDICAL STATION

The conference will provide a Medical Station located on the 1st floor of the Convention Center, next to the Front Desk, and with an ambulance on site throughout the event. Check the map of the event for more details.

TRAVEL AGENCY

The official Travel Agency of the conference is the Elite Travel. The Travel Agency will be open from May 1st to May 7th at the booth located next to the Front Desk and the event's entrance.

Elite Travel (Cláudio)
www.elitetravel.com.br
+55 (65) 3023-4242
+55 (65) 8111-4242
+55 (65) 8111-7808

SIMULTANEOUS TRANSLATION

There will be simultaneous translation for the Keynotes and Plenaries that will be held at the Auditório Lago Azul, from May 2nd to May 6th. There will be a booth for collection and return of headphones, located next to the entrance of the Auditório Lago. In order to collect and return your headphone, you will be required to present the event's identification badge.

SHUTTLE

There will be shuttle service from the official hotels to the Convention Center, according to the routes and schedule as listed on the table below.
There will also be transfer from the official hotels to the Conference Dinner that will be held on May 4th at the Infinity Hall.

MOBI SANTA MARTA (PATRÍCIA)
Av. T-6 Setor Bueno
Goiânia - GO
Telephone: (62) 8168-0110

SHUTTLE SERVICE SCHEDULE4317

TRANSFER	
01 MAY - SUNDAY	
CONFERENCE	**04 MAY - WEDNESDAY**
HOTELS > CONFERENCE	**CONFERENCE**
04:30 pm / 05:00 pm / 05:30 pm / 06:00pm	**HOTELS > CONFERENCE**
CONFERENCE > HOTELS	07:45 / 08:00 / 08:15 am
08:30 pm / 09:00 pm / 09:30 pm	**CONFERENCE > HOTELS**
02 MAY - MONDAY	04:30 pm/ 05:00 pm / 05:30 pm / 06:00 pm
CONFERENCE	**CONFERENCE DINNER**
HOTELS > CONFERENCE	**HOTELS > INFINITY HALL**
07:30 / 08:00 / 08:30 / 08:45	07:30 pm
CONFERENCE > HOTELS	**IINFINITY HALL > HOTELS**
05:00 pm / 05:30 pm / 06:00 pm / 06:30 pm	11:30 / 12:00 pm /12:30 pm
03 MAY - TUESDAY	**05 MAY - THURSDAY**
CONFERENCE	CONFERENCE
HOTELS > CONFERENCE	**HOTELS > CONFERENCE**
07:45 / 08:00 / 08:15 am	07:45 / 08:00 / 08:15 am
CONFERENCE > HOTELS	**CONFERENCE > HOTELS**
05:00 pm / 05:30 pm / 06:00 pm / 06:30 pm	05:00 pm / 05:30 pm / 06:00 pm / 06:30 pm
	06 MAY - FRIDAY
	CONFERENCE
	HOTELS > CONFERENCE
	07:45 / 08:00 / 08:15 am
	CONFERENCE > HOTELS
	02:00 pm / 02:30 pm
	CONFERENCE > HOTELS
	05:30 pm / 06:00 pm

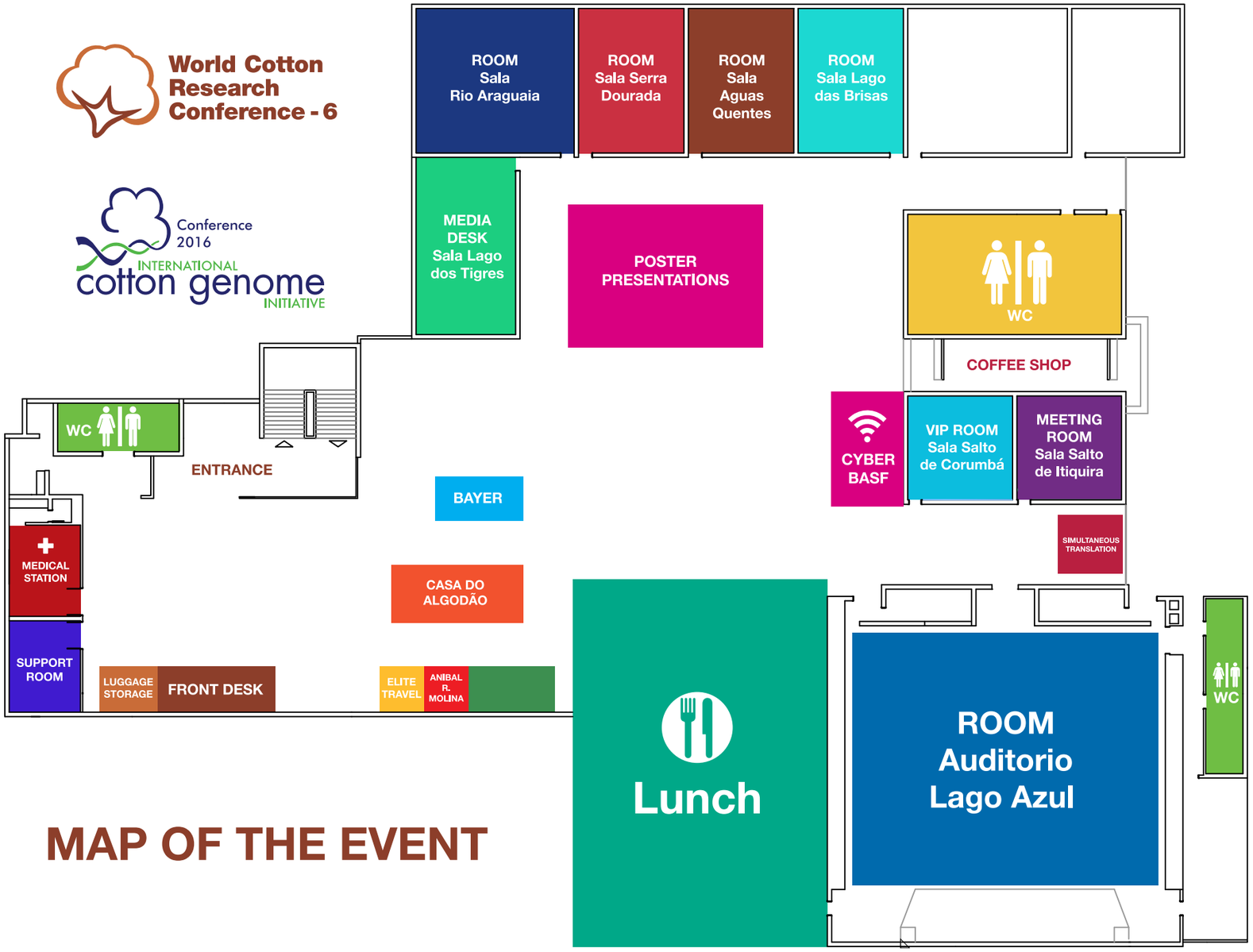
TECHNICAL TOUR

For those who will participate in the Technical Tour, we suggest the use of long pants, hat, boots or closed shoes, insect repellent, sunscreen, and water bottle. The departure location to the Technical Tours will be at the event's official hotels at 7:00am.

Map of the event

World Cotton Research Conference - 6

Conference 2016 INTERNATIONAL cotton genome INITIATIVE



MAP OF THE EVENT

SUNDAY MAY 1	MONDAY MAY 2	TUESDAY MAY 3	WEDNESDAY MAY 4	THURSDAY MAY 5	FRIDAY MAY 6	SATURDAY MAY 7
	7:30 - REGISTRATION & POSTER SET UP	8:30 - 9:15 **PLENARY 1: Cotton Physiology the cornerstone of future cotton science** Speaker: Dr. Michael Bange	8:30 - 9:15 PLENARY 3: Development of GM cotton varieties - challenges for a tropical environment Speaker: Dr. Camilo Morello	8:30 - 9:15 **PLENARY 5: Understanding cotton fiber development based on sequencing data and functional analysis of individual gene** Speaker: Dr. Xianlong Zang	8:30 - 9:15 **PLENARY 7: The first 60 million years of cotton improvement, and what may lay ahead.** Speaker: Dr. Andrew Paterson	OPTIONAL TOUR - REGISTRATION REQUIRED COTTON PRODUCTION AREA (FULL DAY) OR AGOPA FIBER LAB AND EMBRAPA EXPERIMENTAL STATION (FULL DAY)
	9:00 - 10:15 OPENINGSESSION	9:15 - 10:00 **PLENARY 2: Evolution of cotton fiber quality is imperative to fit the future market needs** Speaker: Dr. Eric Hequet	9:15 - 10:00 **PLENARY 4: Addressing the challenges of sustainable cotton production under competition in China** Speaker: Dr. Michel Fok	9:15 - 10:00 **PLENARY 6: Smallholder cotton farming: sustainability matters** Speaker: Dr. Joe C. B. Kabissa	9:15 - 10:00 **PLENARY 8: Integrated pest man agement to compliment GM traits** Speaker: Dr.Keshav Raj Kranthi	
	10:15 - 10:35 COFFEE/TEA	10:00 - 10:20 COFFEE/TEA	10:00 - 10:20 COFFEE/TEA	10:00 - 10:20 COFFEE/TEA	10:00 - 10:30 COFFEE/TEA	
	10:35 - 11:20 **KEYNOTE 1: Innovative Research Solutions to Enhance Cotton Production; how close we are?** Speaker: Dr. Yusuf Zafar	10:20 - 12:15 pm PARALLEL SESSION 3	10:20 - 12:15 pm PARALLEL SESSION 5	10:20 - 12:15 pm PARALLEL SESSION 7	10:30 - 12:15 pm JOINT SESSION / CLOSING	
	11:20 - 12:05pm **KEYNOTE 2: Connecting Growers with Research** Speaker: Dr. Adam Kay					
	12:05 - 01:35 pm LUNCH	12:15 - 01:45 pm LUNCH	12:15 - 01:45 pm LUNCH	12:15 - 01:45 pm LUNCH	12:15 - 01:45 pm LUNCH	
	01:35 - 05:45 pm IAEA Meeting (By Invitation)	01:45 - 05:30 pm IAEA Meeting (By Invitation)	01:45 - 05:30 pm IAEA Meeting (By Invitation)	01:45 - 05:30 pm IAEA Meeting (By Invitation)	01:45 - 05:30 pm IAEA Meeting (By Invitation)	
	01:35 - 03:30 pm PARALLEL SESSION1	01:45 - 03:40 pm PARALLEL SESSION 4	01:45 - 03:40 pm PARALLEL SESSION 6	01:45 - 03:40 pm PARALLEL SESSION 8		
	03:30 - 03:50 pm COFFEE/TEA	03:40 - 04:00 pm COFFEE/TEA	03:40 - 04:00 pm COFFEE/TEA	03:40 - 04:00 pm COFFEE/TEA		
	03:50 - 05:45 pm PARALLEL SESSION 2	04:00 - 05:30 pm POSTER VIEWING -EVEN	04:00 - 05:30 pm POSTER VIEWING -ODD	04:00 - 05:30 pm POSTER VIEWING		
05:00 - 07:00 pm REGISTRATION & POSTER SET UP						
07:00 - 09:00 pm WELCOME RECEPTION			07:30 pm CONFERENCE DINNER			

Program Summary

Detailed Programme

SUNDAY MAY 1

05:00 - 07:00 pm REGISTRATION & POSTER SET UP

07:00 - 09:00 pm WELCOME RECEPTION

MONDAY MAY 2

07:30 REGISTRATION & POSTER SET UP

09:00 **OPENING SESSION**
Room: Auditório Lago Azul

10:15 COFFEE/TEA

10:35 **KEYNOTE 1: Innovative Research Solutions to Enhance Cotton Production: how close we are?**
Speaker: Dr. Yusuf Zafar, IAEA, Pakistan
Chair: Dr. Celestino Zanella, Abapa, Brazil
Co chair: Dr. Ibrokhim Abdurakhmanov, Academy of Sciences, Uzbekistan
Room: Auditório Lago Azul

11:20 **KEYNOTE 2: Connecting Growers with Research**
Speaker: Dr. Adam Kay, Cotton Australia, Australia
Chair: Dr. Gustavo Viganó Piccoli, Ampa, Brazil
Co chair: Dr. Sebastião Barbosa, Embrapa, Brazil
Room: Auditório Lago Azul

12:05 pm Lunch

01:35 - 05:45 pm **IAEA Meeting (By Invitation)**
Room: Sala Lago das Brisas

01:35 pm **PARALLEL SESSION 1**

Room Sala Rio Araguaia
Area **Breeding and Crop Improvement**
Chair **Dr. Todd Campbell**

Oral #	Name	Title	Authors
1	Shahid Mansoor	Engineering Multiple Traits in Cotton	Shahid Mansoor; Imran Amin; Muhammad Saeed; Muhammad Arshad; Zahid Mukhtar; Shaheen Aftab.
2	Mychele Batista da Silva	Effects of Resistance QTLs qMI-C11 on Meloidogyne incognita	Mychele Batista da Silva; Pawan Kumar; Bob Nichols; Richard Davis; Peng Chee.
3	Jack McCarty	Development of Root-Knot and Reniform Nematode Resistant Cotton Lines Using Marker Assisted Selection	Jack McCarty; Johnie Jenkins; Martin Wubben; Frank Callahan; Russel Hayes; Dewayne Deng.
4	Xinlian Shen	Development of Gossypium anomalum-Derived Microsatellite Markers and Their Use for Genome-Wide Identification of Recombination Between the G. anomalum and G. hirsutum Genomes	Xinlian Shen; Caijiao Zhai; Peng Xu; Xia Zhang; Qi Guo; Xinqi Fan; Xianggui Zhang; Wanchao Ni.
5	Thomas Wedegaertner	Elimination of Gossypol in Cottonseed Has the Potential to Satisfy the Protein Needs of Several Hundred Million People	Thomas Wedegaertner

Room Sala Serra Dourada
Area **Cotton Protection**
Chair **Dr. Sebastião Barbosa**

Oral #	Name	Title	Authors
6	Juan Carlos Salerno	Integral Control of the Boll Weevil (Anthonomus Grandis Boheman) in Cotton	Juan Carlos Salerno.
7	José Ednilson Miranda	Influence of the Cotton Cropo Border on the Colonization and Dispersal of the Boll Weevil(Anthonomus grandis)in Brazil	José Ednilson Miranda; Bruna Mendes Tripode; Ismael Ribeiro Rocha Silva.
8	Tina Gray Teague	Zone Management to Reduce Costs for Insecticidal Control of Lygus lineolaris in Midsouth US Cotton	Tina Teague.
9	Megha N. Parajulee	Ecological Management of Lygus bugs in Texas cotton	Megha N. Parajulee.
10	Robert Nichols	Biology and Management of Herbicide-Resistant Palmer amaranth in U. S. Cotton	Robert Nichols; Jim Burton; Nilda Burgos; Stanley Culpepper; Peter Dotray 7; Todd Gaines; Amy Lawton-Rauh; James Norsworthy; Larry Steckel 8; Alan York.

Room Sala Águas Quentes
Area **Measuring Sustainability in Cotton Farming Systems**
Chair **To define**

Oral #	Name	Title	Authors
11	América González Sanabria	Productive Parameters for the Cotton Sector in Paraguay: Baseline Analysis in Rural Family Farming	Claudia Sepulveda Garrido; América Gonzalez Sanabria; Adriana Calderan Gregolin; Beatriz Marciel; Rodrigo Allende; Emilio Valiente;
12	Guy Roth	Measuring sustainability in Australian cotton farming systems	Guy Roth; Angela Bradburn; Jane Trindall; Allan Williams
13	Kater Hake	Quantifying Continuos Improvement in Cotton Production Pratices in the U.S.	Kater Hake; Ed Barnes; Jesse Daystar; Melissa Bastos.
14	Edward Barnes	An Update Global Life Cycle Inventory for Cotton	Edward Barnes; Michelle Wallace; Melissa Bastos; Christy Cagle; Kater Hake; Mary Ankeny; Mike Tyndall.
15	Patrick Filippi	Monitoring the Impact of Irrigated Cotton Production on Soil Condition in a Semi-Arid Landscape in Australia	Patrick Filippi; Stephen Cattle; Thomas Bishop; Inakwu Odeh.

03:30 pm COFFEE/TEA

03:50 pm **PARALLEL SESSION 2**

Room Sala Rio Araguaia
Area **Breeding and Crop Improvement**
Chair **Dr. José Jaime Vasconcelos Cavalcanti**

Oral #	Name	Title	Authors
16	Rajesh S. Patil	Breeding for Productive Compact Cotton Varieties and a Method to Categorise The Plant Type in Gossypium hirsutum L.	Patil, R. S. S.; Khadi, B. M.; Katageri, I. S.; Vamadevaiah, H. M.; PATIL, S. S.
17	Basavaraj Khadi	Introgression Breeding to Address Problems of Bt Cotton-Indian Perspectives.	Basavaraj Khadi; Rajesh Patil
18	Omran Alishah	Cotton Varieties and Seed Production System in Iran	Omran Alishah
19	Mehmet Çoban	Genetic Analysis of Yields and Quality Characteristics in Interspecific Cotton Population (Gossypium hirsutum L. x Gossypium barbadense L.)	Mehmet Çoban; Aydin Ünay; Hakan Çifi; Birnur Ilhan
20	Vendhoti Chenga Reddy	Identification of Donor Parents Containing Favourable Alleles for Improving Target American Cotton Hybrid (NA 1325 × L 604)	Chenga Reddy Vendhoti

Room Sala Serra Dourada
Area **Cotton Protection**
Chair **Dr. Sebastião Barbosa**

Oral #	Name	Title	Authors
21	Oner Cetin	Fertigation Frequency on Cotton Yield and Plant Nutrition	Oner Cetin; Nese Uzen; Mefhar Gultekin Temiz; Sema Basbag
22	Satyanarayana Rao	Management of Leaf Reddening Through Soil and Foliar Nutrition in Irrigated Bt Cotton (Gossypium hirsutum L.)	Satianarayana Rao; Santosh, U.N.
23	Nalayini Periyakaruppan	Beneficial Effects of Structured Water and Pink Pigmented Facultative Methylotrophs for Growth, Yield and Quality of Irrigated Cotton	Nalayini Periyakaruppan
24	Ebadollah Baniani	The Impact of Sewage Irrigation on Morphological Characteristics, Yield Components, and Contain Elements of Seed Cotton in Shahr Ray Region	Ebadollah Baniani; Ebrahim Frahani
25	Sema Basbag	Determination of Some Agricultural and Technological Properties of Cotton Planted as Second-Crop in Wheat-Cotton Cultivation System	Sema Basbag; Remzi Ekinci

Room Sala Serra Dourada
Area **ICGI Conference: Breeding and Applied Genomics**
Chair **Dr. Jodi Scheffler**

Oral #	Name	Title	Authors
26	Todd Campbell	Tracing the Genetic Architecture of High Fiber Quality	Campbell Todd
27	Xianlong Zhang	Understanding Cotton Fiber Development	Lili Tu; Wenxin Tang; Yang Li; Kai Guo; Nian Liu; Xianlong Zhang
28	Zhongxu Lin	Interspecific Recombination Rate, Segregation Distortion and Hybrid Breakdown in Cotton	Zhongxu Lin; Baoshen Dai; Yu Yu; Xianlong Zhang
29	Amanda Hulse	Comparative High-Density Intraspecific Linkage Mapping Using Three Elite Populations from Common Parents	Amanda M Hulse-Kemp; Mauricio Ulloa; David M Stelly; John J Burke
30	Youlu Yuan	High-density Genetic Maps and Their Application to Genetic Dissections of Yield and Fiber Quality Traits in Upland Cotton	Youlu Yuan; Zhen Zhang

TUESDAY MAY 3

08:00 REGISTRATION

08:30 **PLENARY 1: Cotton Physiology the cornerstone of future cotton science**
Speaker: Dr. Michael Bange, CSIRO, Australia
Chair: Dr. Kater Hake, Cotton Incorporated, USA
Co chair: Dr. Md. Farid Uddin, Cotton Development Board, Bangladesh
Room: Auditório Lago Azul

09:15 **PLENARY 2: Evolution of cotton fiber quality is imperative to fit the future market needs**
Speaker: Dr. Eric Hequet, Texas Tech University, USA
Chair: Dr. Iwona Frydrych, Lodz University of Technology, Poland
Co chair: Dr. Mohamed A. E. El-Sayed Negm, Cotton Research Institute, Egypt
Room: Auditório Lago Azul

10:00 COFFEE/TEA

10:20 **PARALLEL SESSION 3**

Room Sala Rio Araguaia
Area **Breeding and Crop Improvement**
Chair **Dr. Jean-Louis Belot**

Oral #	Name	Title	Authors
31	Alison Thompson	Incorporating High-Throughput Phenotyping into Breeding Programs: the good, the bad, and the ugly	Alison Thompson; Kelly Thorp; Matthew Conley; Greg Lohrey; Andrew French; John Dyer.
32	Manzoor Hussain Manj	Improving for Sustainable Cotton Production through Enhanced Resilience to Climate Change with reference to Pakistan.	Manzoor Hussain.
33	Susan Jaconis	Breeding Cotton for a Variable Rainfall Environment	Warren Conaty; Susan Jaconis; David Johnston; Greg Constable.
34	Janagoudar B. S.	Genetic Influence of Root Traits of Cotton (Gossypium hirsutum L.) on Moisture Stress Tolerance	Maruti Laddi; Basanagouda Janagoudar; Ishwarappa Katageri; Basavaraj Khadi.
35	Shiming Liu	Developing Sodium Tolerant Cotton by Exploiting Genetic Diversity Within Two Cultivated Tetraploid Species	Shiming Liu; Greg Constable; Jean-Marc Lacape; Danny Llewellyn.

Room Sala Águas Quentes
Area **Cotton Protection**
Chair **Dr. Allah Bakrhsh (To confirm)**

Oral #	Name	Title	Authors
36	Dean Brookes	Gene Flow and Host Use, Relative to Cotton, in Nezara viridula (the Green Vegetable Bug or Southern Green Stink Bug)	Dean Brookes; James Hereward; Lewis Wilson; Gimme Walter.
37	Adoni Ginnu Sreenivas	Effect Of Elevated Carbon Diozide and Temperature on Tri-Trophic Interaction of Bt Cotton, Aphid, Aphis gossypii Glover and Coccinellid, Cheilomenes sexmaculata Fab.	Adoni Ginnu Sreenivas.
38	José Ednilson Miranda	Determination of the Injury Potential and Economical Threshold of Helicoverpa armigera on Cotton Crop	José Ednilson Miranda; Bruna Mendes Tripode; Laisse Danielle Pereira; Ismael Ribeiro Rocha Silva.
39	James P. Glover	Comparing Boll Injury and EILs for Species of a Boll-Feeding Sucking Bug Complex (Hemiptera: Miridae and Pentatomidae) on Texas Cotton	James Glover; Mike Brewer; Gregory Sword.
40	Syed Zameer Ul Hassan	A Comparative Analysis of Residual Pesticides on cotton Utilizing Biosensor and Tandem Mass Spectrometry	Syed Zameer Ul Hassan; Jiri Militky; Jan Krejci.

Room Sala Serra Dourada
Area **ICGI Conference: Comparative Genomics and Bioinformatics**
Chair **Dr. Alberto Souza Boldt**

Oral #	Name	Title	Authors
41	Jing Yu	CottonGen: Current Functionality and Future Direction	Jing Yu; Sook Jung; Chun-Huai Cheng; Taein Lee; Ping Zheng; Stephen Ficklin; Todd Campbell; Richard Percy, Don Jones; Dorrie Main.
42	Daniel G. Peterson	Getting Bioinformatics Through Its Awkward Adolescence (Featuring Examples from Cotton Research)	Daniel Peterson.
43	John Yu	Recent Developments and Applications of Cotton Genomic Resources for Fiber Improvement	John Yu
44	Qian-Hao Zhu	Genome-wide Identification and Characterization of the Homeodomain-leucine Zipper I Family of Genes in Cotton (Gossypium spp.)	Qian-Hao Zhu; Jian Zhang; Philippe Moncuquet; Danny Llewellyn; Iain Wilson;
45	Dr. Ishwarappa S Katager	Genome wide SNP Marker Survey for Their Utilization in Cotton Breeding	Ishwarappa Katageri; Suresh Handi; Ramesh Metre; Vamadevaiah Hiremat; Biradar D.P.; Khadi B.M.; Reddy Lachagari V.B.

Room Sala Serra Dourada
Area **ICGI Conference: Comparative Genomics and Bioinformatics**
Chair **Dr. Alberto Souza Boldt**

Oral #	Name	Title	Authors
46	Daniel Kean Yuen Tan	Does Wide Row (1.5 m) Cotton Have Better Yield, Fibre Quality and Water Use Efficiency Than Conventional Row (1 m) Cotton?	Timothy Bartimote; John Bennett; Rose Brodrick; Daniel Tan;
47	Jianlong Dai	Evaluation of a Production System in China That Uses High Plant Density and Retention of Vegetative Branches With Reduced Nitrogen Fertilization.	Jianlong Dai; Zhen Luo; Hequan Lu; Shizhen Xu; Xiangqiang Kong; Hezhong Dong;
48	Prem Lal Nehra	Standardization of Nutrient Management for High Density Planting System in Arboreum Cotton	PREM NEHRA.
49	Y R Aladakatti	Performance of Potential Hirsutum Cotton Compact Varieties Under High Density Planting System (HDPS)	Y.R. Aladakatti.
50	Hezhong Dong	The Chinese Way of Achieving High Cotton Yields With Farming Technologies	Hezhong Dong; Jianlong Dai.

12:15 pm Lunch

01:45 - 05:30 pm **IAEA Meeting (By Invitation)**
Room: Sala Lago das Brisas

01:45 pm **PARALLEL SESSION 4**

Room Sala Rio Araguaia
Area **Breeding and Crop Improvement**
Chair **To define**

Oral #	Name	Title	Authors
51	Nelson Dias Suassuna	Sources of Resistance to Ramularia areola and Development of a Resistant Cotton Cultivar	Nelson Dias Suassuna; Taís de Moraes Falleiro Suassuna; Camilo de Lelis Morello; João Luís Silva Filho.
52	Ntjapa Gabriel Lebaka	Development of verticilium wilt and jassid resistant cotton varieties at ARC in South Africa	Ntjapa Lebaka; Antoon Cornellissen; Graham Thompson.
53	Gholamhossein Hosseini	Estimation of Genetic Parameters in Cotton Cultivares (Gossypium hirsutum L. & L.) and New Scaling Test of Epistasis.	Gholamhossein Hosseini.
54	Orawu Martin	Performance of Cotton Genotypes under Diverse Agro-ecologies of Uganda	Martin Orawu; Lastus Serunjogi; Gladys Amoding; George Ogwang; Chris Ogwang.
55	Leonel Domingos Moiana	Screen of us Cotton Germplasm for Completion with African Cotton Germplasm to Ensure Success	leonel Moiana; Dick Auld; Pedro Vidigal-Filho; Maria Celeste Gonçalves-Vidigal; Mendu Venongupal.

Room Sala Águas Quentes
Area **Cotton Protection**
Chair **To define**

Oral #	Name	Title	Authors
56	Mohammad-Amir Aghaee	Characterizing Helicoverpa zea Feeding Damage to Different Cotton Tissue Types and Different Bt Protein Combinations for Use in IRM Modeling	Muhammad-Amir Aghaee; Dominic Reisig; Mike Caprio; Don Cook; Fred Musser
57	Dr.Shashikant S.Udikeri	Tools for Monitoring and Management of Emerging Key Insect Pests Mirid Bug and Flowerbud Maggots in Bt Transgenic Cotton Hybrids	Shashikant S. Udikeri; S.B. Patil; S.T. Prabhu; Vivek Uppar; Siddaling Hugar; Nakul Vandal; Kuberappa Gundannavar.
58	Ashley Tessnow	The Role of Nutrition in Susceptibility of Helicoverpa zea to Cry1Ac	Ashley Tessnow; Carrie Deans; Spencer Behmer; Bill Hutchinson; Marianne Pusztai-Carey; Xianping Wang; Gregory Sword.
59	Tom Walsh	The Old World Bollworm, Helicoverpa armigera: Bt Resistance Mechanisms, Population Genetics and Genomics.	Thomas Walsh; Craig Anderson; Sharon Downes; Karl Gordon; John Oakeshott; Wee Tek Tay.
60	Sharon Downes	Bt resistance in Australian Insect Pest Species	Sharon Downes; Thomas Walsh; Wee Tek Tay.

Room Sala Serra Dourada
Area **ICGI Conference: Functional Genomics**
Chair **Dr. Daniel Peterson**

Oral #	Name	Title	Authors
61	Shuangxia Jin	Transcriptome Analysis Reveals a Comprehensive Insect Resistance Mechanism of Cotton in Response to Infestation by Phloem Feeding Insect-whitefly	Shuangxia Jin; Jianying Li; Xianlong Zhang.
62	Xueying Guan	Small RNAs from Natural Antisense Transcripts of GhMIXTAMYB-like3_A12 Causes the Naked Seed Phenotype in Cotton N1 Mutant	Xueying Guan; Qun Wan; Nannan Yang; Huaitong Wu; Lei Fang; Yan Hu; Wangzhen Guo; Wenhua Zhang; Xiaoya Chen; Tianzhen Zhang.
63	Vasu Kuraparthy	Modifications to a Late Meristem Identity 1-like Gene are Responsible for the Major Leaf Shapes of Upland Cotton (Gossypium hirsutum L.)	Ryan Andres; Daniel Chitwood; Marcela Rojas-Pierce; Candace Haigler; James Holland; Don Jones; Vasu Kuraparthy.
64	Ayyanagouda Mahantgouda Patil	Genome-Wide in Silico Prediction of Putative Transcription Factor Binding Sites (TFBSs) for Cotton Fiber Strength	Ayyanagouda Patil; Dinesh Akula; P. H Kuchanur; J.P Nidagundi; B.S Golsangi; S. S. Gangurde.
65	Uzma Qaisar	Involvement of Wrinkled-1 Transcription Factor in Fiber Development of Extra Long Staple (ELS)	Uzma Qaisar; Fozia Akhtar.

Room Auditório Lago Azul
Area **Agronomy and Sustainable Production**
Chair **To define**

Oral #	Name	Title	Authors
66	Todd Spivey	Comparison of Cotton Tillage Pratices in North Caroline, USA	Todd A. Spivey; Josh L. Heitman; Randy Wells; David L. Jordan; Guy D. Collins; Keith L. Edmisten.
67	Kater Hake	Managing the Diverse Soil Microbiome Most Recently Recognized Benefit of No-Till (Zero-Tillage) to Cotton)	Kater Hake; Diana Vargas-Gutierrez; Kholoud Ghanem; John Zak; Bobbie McMichael; Phil Bauer; Tom Ducey; Gene Stevens; Bob Nichols.
68	Miguel Angel Ken Moriya Roa	Cotton in Direct Seeding in Animal-Drawn Family Farming	Miguel Angel Ken Moriya Roa.
69	Eduardo Enrique Román Gómez	Development of two Pilot Tests of Cotton Fiber Production in Colombia Through Two Systems of Production: Organic and Low Environmental Impact.	Eduardo Enrique Román Gómez; Adriana Calderan Gregolin.
70	Liv Soares Severino	Fluctuation in Storage Carbohydrates in Stem and Root of Cotton Plants	Liv Soares Severino; Julio Cesar Bogiani; Fabiano José Perina; Bruna Santana da Silva Mendes.

WEDNESDAY MAY 4

08:00 REGISTRATION

08:30 **PLENARY 3: Development of GM cotton varieties - challenges for a tropical environment**
Speaker: Dr. Camilo Morello, Embrapa, Brazil
Chair: Dr. Jack McCarthy, USDA-Ars, Mississippi State, USA
Co chair: Dr. Juan Carlos Salerno, Argentina Genetics Society, Argentina
Room: Auditório Lago Azul

09:15 **PLENARY 4: Addressing the challenges of sustainable cotton production under competition in China**
Speaker: Dr. Michel Fok, CIRAD, France
Chair: Dr. Xiongming Du, China Cotton Research Institute, Anyang, China
Co chair: Dr. A. Mohamed Mustafa, Cotton Research Program, Sudan
Room: Auditório Lago Azul

10:00 COFFEE/TEA

10:20 **PARALLEL SESSION 5**

Room Sala Rio Araguaia
Area **Breeding and Crop Improvement**
Chair **Dr. Shahid Mansoor**

Oral #	Name	Title	Authors
71	Ghulam Sarwar	Na Overview of Cotton Leaf Curl Virus Disease in Pakistan: Past, Present and Future	Ghulam Sarwar.
72	Jodi Scheffler	Pakistan and United States partnership project to identify genetic resistance to cotton leaf curl virus and develop resistant cotton for farmers	Jodi Scheffler.
73	Manzoor Hussain Manj	Evolution of NIAB-KIRAN, an early maturing, high yielding, fine quality fiber cotton variety having enhanced resilience against CLCuD & heat under the changed climatic scenario.	Manzoor Hussain.
74	Dharminder Pathak	Identification of new sources of resistance to cotton leaf curl disease and its introgression in American cotton	Dharminder Pathak; Shashi Bala; Pankaj Rathore; Parvinder S Sekhon; Kuldeep Singh.
75	Kalim Ullah	Genetic Diversity of Cotton (Gossypium hirsutum L.) Genotypes for Yield and Quality Attributes and Responses to CLCV Disease	Kalim Ullah khan.

Room Auditório Lago Azul
Area **Agronomy and Sustainable Production**
Chair **Dr. Oner Cetin**

Oral #	Name	Title	Authors
76	Dil Baugh Muhammad	Impact of Potassium Fertilizer on Plant Biomass and Seed Cotton Yield Under Arid Environments	Dil Baugh Muhammad; Muhammad Naveed Afzal; Muhammad Tariq; Abdul Wakeel.
77	Amal Saber Owis	Effect of Different Types of Compost Made From Rice Straw, Cotton Stalk, Bagasse and Their Mixture Compared with Mineral Fertilizers on Cotton Yield and Fiber Quality	Amal Owis; Anwar Eissa.
78	Md. Kamrul Islam	Effect of Organic and Inorganic Source of N and Locations on Cotton Yield	Md. Kamrul Islam; Md. Farid Uddin.
79	Gupta Vadakattu	Does Compost Addition Improve Biological Functions and Microbial Diversity in Cotton Soils?	Gupta Vadakattu; Stasia Kroker; Marcus Hicks; Bhanu Nidumolu; Duncan Weir.
80	Y R Aladakatti	Nutrient response of Bt Cotton in vertisols of Northern Karnataka	Y.R. Aladakatti.

Room Sala Serra Dourada
Area **ICGI Conference: Gerplasm and Genetic Stocks**
Chair **Dr. Xianlong Zhang**

Oral #	Name	Title	Authors
81	Lucia Vieira Hoffmann	Aspects of Cotton Germplasm Maintenance and Evaluation by Embrapa	Lucia Hoffmann; Gildo Pereira Araujo; Francisco Pereira Andrade; Paulo Barroso; Raysa Marques Cardoso. Kalita Cristina Cardoso; Francisco das Chagas Vidal Neto; João Luis Silva Filho.
82	Johnie Jenkins	Introgression of Gossypium barbadense Alleles into Upland Cotton via Random Mating.	Johnie Jenkins; Jack McCarty; Dewayne Deng.
83	Maite Vaslin de Freitas Silva	Functional Genomics Analysis of a Cotton N-end Rule Protein (GhCBD2) Putatively Involved in Viral Resistance in Gossypium hirsutum	Anna Karoline S Fausto; Marianna O Moura; Tatiane S da Franca; Elisson Romanel; Maite F S Vaslin.
84	Dr Muhammad Tehseen Azhar	Response of Wild Relatives of Cotton Against Cotton Leaf Curl Disease	Muhammad Tehseen Azhar; Rana Muhammad Atif; Zahid Iqbal Anjum; Shahid Mansoor.
85	Farshid Talat	Complete Chloroplast Genome Sequences of Three D Genome Cotton Species and Their Evolutionary Implications	Farshid Talat; Kunbo Wang

Room Sala Águas Quentes
Area **Social Dynamics and Technology Transfer**
Chair **Dr. Ivelin Rizov**

Oral #	Name	Title	Authors
86	Mutibo Chijikwa Mushenywa	The Performance of Farmer Field Schools in the Zambian Cotton Production System	Mutibo Chijikwa; Suzanne Philips.
87	Joshua Usha Rani	Front Line Demonstration – Proven Transfer of Technology Approach for Fostering Productivity of Cotton in India	Usharani Joshua; Prakash A.H.
88	Ryan Kurtz	Use of Web-Based Information Delivery by Cotton Incorporated	Ryan Kurtz; Ed Barnes; Phil Bogdan
89	Vlaminck Paiva Saraiva	The Paraiba Cotton Project - A Proposal for Local Integrated Development Within the Scope of Family Farming	Vlaminck Paiva Saraiva; Alexandre Alfredo; José Joacy dos Santos; Dalfran Gonçalves Vale.
90	Ingrid Zabaleta Chaustre	Gender Perspective in the Cotton Value Chain: Challenges and Opportunities in Argentina, Bolivia, Colombia, Paraguay and Peru	Patricia Biermayr- Jenzano; Ingrid Johana Zabaleta Chaustre; Adriana Gregolin.

12:15 pm Lunch

01:45 - 05:30 pm **IAEA Meeting (By Invitation)**
Room: Sala Lago das Brisas

01:45 pm **PARALLEL SESSION 6**

Room Sala Rio Araguaia
Area **Breeding and Crop Improvement**
Chair **To define**

Oral #	Name	Title	Authors
91	Todd Campbell	Simultaneous Improvement of Cotton Fiber and Seed	Campbell Todd.
92	Vendhoti Chenga Reddy	Combining Ability Analysis for Seed Cotton Yield and Quality Traits in Upland Cotton (Gossypium hirsutum L.) Over Environments	Chenga Reddy Vendhoti.
93	Shivaputrappa Tippanna Kajjidoni	Role of Irradiation and Mating Schemes in Enhancement of Variability for Productivity and Fiber Quality Traits in Asian Cotton	Kajjidoni, S.T.; Talawar A.M; Jambulakar S.J.; Wadeyar B. S.
94	Juan Luis Lazo Alvarez	Genetic Inprovement of Extra-Long Fiber Varieties in Peru	Juan Luis Lazo Álvarez
95	Martin Lubinda Simasiku	Evaluation of the Yield Potential and Agronomic Characteristics of Various Cotton Genotypes in Zambia	Martin Lubinda Simasiku

Room Auditório Lago Azul
Area **Agronomy and Sustainable Production**
Chair **To define**

Oral #	Name	Title	Authors
96	Hezhong Dong	Yield and Economic Benefits of Late Planted Short-Season Cotton Compared with Intercropped Full-Season Cotton in a Garlic-Cotton Double Cropping System	Hezhong Dong; Hequan Lu
97	Jianlong Dai	Precision Seeding Without Seedling Thinning Under Double Mulching Improves Stand Establishment and Economic Yield of Cotton in the Yellow River Valley of China	Jianlong Dai; Zhen Luo; Hequan Lu; Zhenhuai Li; Weijiang Li; Shizhen Xu; Dongmei Zhang; Tang wei Xiangqiang Kong 1, Hezhong Dong 1
98	Anibal R. Molina	Due to the Climate Change, Cotton Production (Gossypium hirsutum L.) Has Expanded in Argentina. Now it Can Also Be Cultivated in the Province of Buenos Aires, Proving to Be the Most Southern Cotton Field of South America.	Anibal Ricardo Molina
99	Md. Farid Uddin	Cotton-Rice Intercropping in Chittagong Hill Districts of Bangladesh	Md. Farid Uddin
100	Salihu Adamu Dadari	Cotton Research and Production in Nigeria. Challenges and Strategies for increased Production and Productivity	Dadari, S.A.; Yahaya, A.I; Mohammed, S.M.
100 A	Muhammad Iqbal	Effect of heat stress on cotton (Gossypium hirsutum L.) fruit development and seed physical traits	Muhammad Iqbal, Sami Ul-Allah, Muhammad Naeem

Room Sala Serra Dourada
Area **ICGI Conference: Structural Genomics**
Chair **Dr. David Fang**

Oral #	Name	Title	Authors
101	Joshua Udall	Genome Structure of the Gossypium genome	Joshua A Udall; Thiruvarangan Ramaraj; Aaron Sharp; Christopher Hanson; Carrie Evans; Alex Freeman; David de Amorim; Spencer Hunt; Meghan Crosby
102	Lei Fang	Asymmetric Subgenomic Evolution and Domestication of Allotetraploid Cotton (Gossypium hirsutum L.)	Lei Fang; Yan Hu; Xueying Guan; Jiedan Chen; Christopher Saski; Brian E. Scheffler; David M. Stelly; Wangzhen Guo; Z. Jeffrey Chen; Tianzhen Zhang
103	Brian Scheffler	Subgenome Anchored Physical Frameworks for the Allotetraploid Genome of Upland Cotton (Gossypium hirsutum L.) and an Approach Toward Reference-grade Genome Assemblies for Cotton	Christopher Saski 1, Brian Scheffler 2, David Stelly 3, Jeff Chen 4
104	Xiongming Du	Resequencing of Diploid Cotton (G. arboreum) Revealed the Genetic Basis of Important Agronomic Traits	Xiongming Du; Shoupu He; Xueyan Zhang; Xiongfeng Ma; Junling Sun; Tao Lin; Gaofei Sun; Nan Li; Zhaoen Yang; Yinhua Jia
105	Ye Wuwei	Cotton DNA Methylation and Its Analysis under the Salt-drought Stresses	Wuwei Ye; Xuke Lu; Junjuang Wang; Shuai Wang; Xiaoge Wang

Room Sala Serra Dourada
Area **ICGI Conference: Structural Genomics**
Chair **Dr. David Fang**

Oral #	Name	Title	Authors
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105	Ye Wuwei	Cotton DNA Methylation and Its Analysis under the Salt-drought Stresses	Wuwei Ye; Xuke Lu; Junjuang Wang; Shuai Wang; Xiaoge Wang

Room Sala Águas Quentes
Area **Economics/Cotton Competitiveness**
Chair **Dr. Haroldo Rodrigues da Cunha**

Oral #	Name	Title	Authors
106	Dean Ethridge	Market for Waste Cotton Fibers: Case Study of the United States	Dean Ethridge
107	Joelcio Cosme Carvalho Ervilha	Opportunities for Cotton Development in Paraguay, in the Context of the Analysis of Transaction Costs	Joelcio Cosme Carvalho Ervilha; Adriana Calderan Gregolin; Emilio Valente; America Gonzalez Sanabria
108	Anthony Muriithi	Impact of the Cotton Sub-Sector on Rural Smallholder Livelihoods: Lessons from Kenya	Anthony Muriithi; Alex Mungai; Hesbon Olweny; Naomi Kamau; Lusike Wasilwa
109	Michel FOK-AH-CHUEN	Evolution of Bt Cotton production Costs and Effectiveness in Northern China Over a Decade	Michel Fok; Guiyan Wang
110	Ivelin Rizov	The Approach of European Coexistence Bureau for Sustainable Coexistence of Genetically Modified Cotton Production With Conventional and Organic Farming	Ivelin Rizov; Emilio Rodriguez-Cerezo

03:40 pm COFFEE/TEA

04:00 - 05:30 pm **POSTER VIEWING – ODD**

07:30 pm **CONFERENCE DINNER**

THURSDAY MAY 5

08:00 REGISTRATION

08:30 **PLENARY 5: Understanding cotton fiber development based on sequencing data and functional analysis of individual gene**
Speaker: Dr. Xianlong Zang, Huazhong Agricultural University, China
Chair: Dr. David Stelly - ICGI, USA
Co chair: Dr. Alderi Emidio de Araujo, Embrapa, Brazil
Room: Auditório Lago Azul

09:15 **PLENARY 6: Smallholder cotton farming: sustainability matters**
Speaker: Dr. Joe C. B. Kabissa, Tanzania Cotton Board, Tanzania
Chair: Dr. Graham Thompson, ARC, South Africa
Co chair: Dra. Yelitza Colmenarez, CABI Regional Representative for South America
Room: Auditório Lago Azul

10:00 COFFEE/TEA

10:20 **PARALLEL SESSION 7**

Room Auditório Lago Azul
Area **Cotton Protection**
Chair **Dr. Charudatta D. Mayee**

Oral #	Name	Title	Authors
111	Tyler Jay Raszick	Cotton Boll Weevil (Anthonomus grandis) Genome Sequencing and Population Genomics as Tools for Monitoring and Eradication	Tyler Jay Raszick; Gregory A Sword; Charles P-C Suh; Raul Ruiz-Arce
112	Katherine Parys	Analysis of Tarnished Plant Bug Movement Using Carbon and Nitrogen Isotopes	Katherine A. Parys; Leslie D. Price; Maribel Portilla; Gregory C. Roberts; Bryce D. Blackman; Ryan E. Jackson; Randall G. Luttrell
113	Santam Singh	Extensive Haplotype Analysis of the Whitefly Bemisia tabaci Cryptic Species in Punjab, India	Satnam Singh; Abhishek Sharma; Suneet Pandher; Ramandeep Kaur; Gurpreet Kaur; Judith K Brown; Pankaj Rathore
114	Allah Bakhsh	Towards Better Insect Management Strategy; Restriction of Insecticidal Gene Expression to Insect Biting Sites in Transgenic Cotton	Allah Bakhsh; Emine Anayol; Sebahattin Ozcan
115	Jorge Luis Saavedra Diaz	Native Species of Entomopathogenic Nematodes With Potential for Control of Spodoptera frugiperda Smith. and S. eridania (Stoll) (Lepidoptera: Phalaenidae) in Peru	Jorge Luis Saavedra Díaz; Lito Sigueñas Montalvo

Room Sala Serra Dourada
Area **ICGI Conference: Structural and Functional Genomics**
Chair **Dr. Brian Scheffler**

Oral #	Name	Title	Authors
116	David Fang	Mapping-by-sequencing of Major Genes and QTLs in Tetraploid Upland Cotton	David Fang; Gregory Thyssen; Md islam; Marina Naoumkina; HeeJin Kim
117	Wangzhen Guo	Development of a Genome-wide 90K SNP Array on Allopolyploid Upland Cotton	Wangzhen Guo; Caiping Cai; Tianzhen Zhang
118	Khezir Hayat Bhatti	Molecular Tagging of QTLs for Fiber Quality in Cotton by Using SNPs	Khezir Hayat; Yuksel Bolek; Adem Bardak
119	Vamadevaiah Hiremath	Expression Studies of Transcription Factors under Moisture Stress in Cotton (Gossypium hirsutum L.)	Vamadevaiah Hiremath; Sagar Yadav; Ishwarappa Katageri; Basavaraj Khadi
120	Zhongxu Lin	Interspecific Recombination Rate, Segregation Distortion and Hybrid Breakdown in Cotton	Zhongxu Lin; Baoshen Dai; Yu Yu; Xianlong Zhang

Room Sala Águas Quentes
Area **Fiber Quality and Processing**
Chair **Dr. Dean Ethridge**

Oral #	Name	Title	Authors
121	Iwona Frydrych	Comparison of Utility Properties of Fabrics Made of Cotton and Cotton/PES Blends	Iwona Frydrych; Malgorzata Matusiak
122	Negm Mohamed	Characteristics of Cotton Fabrics Produced from Sirospunand Plied Yarns	Mohamed Negm; Susan Sanad
123	Jean-Paul Gourlot	Is it Possible to Check Microginning Fiber Quality Preservation Performance Using Reference Seed-Cotton?	Mamadou Togola; Jean-Paul Gourlot; Eric Goze; Abdoul Karim Traore
124	Malgorzata Matusiak	Cotton Color Measurement by Means of HVI, Spectrophotometer and Digieye	Malgorzata Matusiak; Anetta Walawska
125	Neima Hamid Osman	Effect of Nitrogen and Phosphorus Fertilizers on Medium Count Cotton Fiber Properties, Barac(67) B	Neima Osman; Ibrahim Mohamed

Room Sala Rio Araguaia
Area **Physiology / Precision Agricultural**
Chair **Dr. Liv Soares Severino**

Oral #	Name	Title	Authors
126	Basanagouda Janagoudar	Impact of Nutrients on Vegetation Index, Canopy Reflectance and Biophysical Parameters in Bt Cotton.	Manjugouda Patil; Basanagouda Janagoudar; Amaregouda Patil
127	Robert Nichols	Quantifying Cotton Cultivar Maturity Across Diverse United States Environments	Robert Nichols; Curtis Schaffer;, Guy Collins; Christopher Main; Jared Whitaker; Craig Bednarz; Glen Ritchie
128	Daniel Kean Yuen Tan	Can Paclobutrazol Improve Vigour and Cold Tolerance of Cotton Seedlings Under Cool Conditions?	Daniel Tan; Marc Freeth, Michael Bange
129	Abdullah Keerio	Influence of Potassium on the Incidence of CLCuV Disease and its effect on seed cotton yield	Abdullah Keerio; Mushtaq Ali Leghari; Vishandas Suthar; Bushra Urooj Panhwar; Allah Dino Kalhoro; Fakhar Imam Khaskheli
130	Luz Angelica Suarez Cadavid	Prediction of Yield Loss in Cotton Crops Caused by Herbicide Drift Through the Analysis of Hyperspectral Data	Luz Angelica Suarez; Armando Apan; Jeff Werth

12:15 pm Lunch

01:45 - 05:30 pm **IAEA Meeting (By Invitation)**
Room: Sala Lago das Brisas

01:45 pm **PARALLEL SESSION 8**

Room Auditório Lago Azul
Area **Cotton Protection**
Chair **To define**

Oral #	Name	Title	Authors
131	Brian Scheffler	Development and Implementation of a Comprehensive Program to Combat Cotton Leaf Curl Virus Through International Cooperation	Brian Scheffler
132	Muhammad Saeed	Characterization of epicuticular wax in cotton (Gossypium hirsutum L.) in relation to Cotton Leaf Curl Disease (CLCuD) resistance	Muhammad Saeed
133	Akhtar Ali	Update on the Virus Diseases of Cotton in the United States	Akhtar Ali
134	Linda Smith	Diseases In Australian Cotton	Linda Smith; Linda Scheikowski; Paul Melloy; John Lehane
135	Gupta Vadakattu	Effect of Crop Rotation and Environment on Fungal Communities in Australian Cotton Soils	Gupta Vadakattu; Linda Smith; Karen Kirkby; Linda Scheikowski; Ian Rochester; Nilantha Hulugalle; Christopher Penton

Room Sala Serra Dourada
Area **ICGI Conference**
Chair **Dr. David Stelly**

Room Sala Águas Quentes
Area **Harvesting and Post-Harvesting Technologies**
Chair **To define**

Oral #	Name	Title	Authors
136	Michael Braunack	Changes in Soil Compaction Due to Cotton Picker Traffic During Harvest on Australian Cotton Soils.	Michael Braunack 1
137	Edward Barnes	Use of Electronic Technologies to Managed Seed Cotton Modules in the United States	Edward Barnes; John Wanjura
138	Gregory Holt	Evaluation of a New Mechanical Delinting System for Cottonseed	Gregory Holt; Tom Wedegaertner; John Wanjura; Mathew Pelletier
139	John Wanjura	Advancements in Cotton Harvesting Research	John Wanjura; Gregory Holt; Mathew Pelletier
140	Prashantkumar Gulabrao Patil	Cotton By-products and its Potential Industrial Applications	Prashantkumar Gulabrao Patil; Sundaramoorthy

Room Sala Rio Araguaia
Area **Physiology / Precision Agricultural**
Chair **To define**

Oral #	Name	Title	Authors
141	Robert Sharwood	Understanding the Photosynthetic Biochemistry that Underpins Cotton Photosynthesis Under Future Climate Extremes.	Robert Sharwood; Bala Sonanwane; Oula Ghannoum; Spencer Whitney; David Tissue; Michael Bange
142	Zhen Luo	Physiological and Molecular Mechanisms of the Improved Root Hydraulic Conductance under Partial Root-Zone Irrigation in Cotton	Zhen Luo; Xiangqiang Kong; Hezhong Dong;, Weijiang Li
143	Stephen Yeates	Balancing Canopy Management Using Mepiquat Chloride With Recovery From Biotic and Abiotic Stress in the Australian Tropics.	Stephen Yeates; Paul Grundy
144	Marcelo Paytas	Developing Management Options for Cotton Grown in Variable Solar Radiation Regions: Yield Recovery in Response to Reduced Radiation During Flowering and Cultivar	Marcelo Paytas; Stephen Yeates; Michael Bange
145	Juan A Landivar	Integration of Ground- and UAS-Platforms for the Evaluation of Cultivar Performance (Phenotyping) and Experimental Treatments	Juan Landivar

03:40 pm COFFEE/TEA

04:00 - 05:30 pm **POSTER VIEWING**

FRIDAY MAY 6

08:00	REGISTRATION
08:30	**PLENARY 7: The first 60 million years of cotton improvement, and what may lay ahead.** Speaker: Dr. Andrew Paterson, University of Georgia, USA Chair: Dr. Shahid Mansoor, NIBGE, Pakistan Co chair: Dr. Basavaraj M. Khadi, University of Agricultural Sciences, Dharwad, India Room: Auditório Lago Azul
09:15	**PLENARY 8: Integrated pest management to compliment GM traits** Speaker: Dr. Keshav Raj Kranthi, Central Institute for Cotton Research, India Chair: Dr. C. D. Mayee, Central Institute for Cotton Research, India Co chair: Dr. (Ms.) Mutibo Chijikwa, Cotton Development Trust, Zambia Room: Auditório Lago Azul
10:00	COFFEE/TEA
10:30 - 12:15 pm	**JOINT SESSION / CLOSING** Room: Auditório Lago Azul
12:15 pm	Lunch
01:45 - 05:30 pm	**IAEA Meeting (By Invitation)** Room: Sala Lago das Brisas

POSTER PRESENTATIONS

AREA: BREEDING AND CROP IMPROVEMENT IN COTTON			
Poster #	Name	Title	Authors
1	José Jaime Vasconcelos Cavalcanti	Expression Of The Serk Gene In Non-Recalcitrant Cotton Genotypes	José Jaime Vasconcelos Cavalcanti; Roseane Cavalcanti dos Santos; Carliane Rebeca Coelho da Silva; Julita Maria Frota Chagas Carvalho; Liziane Maria de Lima; Taiza da Cunha Soares
2	Ghorban Ali Roshani	Comparison Of Successful Cotton Genotypes In Saline Regions Of Iran	Ghorbanali Roushani
3	Matheus Rodrigues Martins	Grouping Of Cotton Genotypes Of Colored Fiber Derived From Different Crosses	Matheus Rodrigues Martins; Michel de Carvalho Reis; Bruna Cardoso Gomes; Cynthia Pereira Gundim; Danilo Araújo Gomes; Elvécio Gomes da Silva Júnior; Guilherme Hugo da Silva Costa; João Felipe Moraes Ferreira; Letícia Teixeira Gold Pereira; Larissa Barbosa de Sousa
4	Matheus Rodrigues Martins	White Fiber Cottonseed And Fiber Yield From Biparental Crossing	Matheus Rodrigues Martins; Bruna Cardoso Gomes; Cynthia Pereira Gundim; Daniel Bonifácio Oliveira Cardoso; Daniel Inserra Bortolin; Elvécio Gomes da Silva Júnior; Guilherme Hugo da Silva Costa; João Felipe Moraes Ferreira; Matheus Araújo Bernardes de Souza; Larissa Barbosa de Sousa
5	Zerihun Desalegn Gebregiorgis	High Ginning Out Turn And The Improvement Of Ethiopian Cotton Production	Zerihun Desalegn Gebregiorgis
6	Omran Alishah	Genetic Study Of Physiological Traits In Inter Varietal Crosses Cotton (G.Hirsutum) In Salinity And Non Salinity Stress Condition	Omran Alishah

7	Daniel Inserra Bortolin	Relative Importance Of Characters In The Study Of Genetic Diversity Of Gossypium Hirsutum Cotton Genotypes	Daniel Inserra Bortolin; Bruna Cardoso Gomes; Daniel Bonifácio Oliveira Cardoso; Elvécio Gomes da Silva Júnior; Guilherme Hugo da Silva Costa; Luccas Marques de Souza Falco; Matheus Rodrigues Martins; Melissa Martins de Araújo; Ana Flávia Oliveira Nascimento; Larissa Barbosa de Sousa
8	Daniel Inserra Bortolin	Plume Yield And Number Of First Position Fruits In Colored Fiber Cotton Genotypes	Daniel Inserra Bortolin; Danilo Araújo Gomes; Cynthia Pereira Gundim; Guilherme Hugo da Silva Costa; Letícia Teixeira Gold Pereira; Matheus Rodrigues Martins; Melissa Martins de Araújo; Michel de Carvalho Reis; Morgana Coelho Mamede; Larissa Barbosa de Sousa
9	Sema Basbag	The Seed Content Of Some Cotton Genotypes	Remzi Ekinci; Sema Basbag
10	Farshid Talat	Multivariate Statistical Analyses Of Earliness In Upland Cotton	Farshid Talat; Sayna Shadparvar; Zarrin Jamshidian; Medhi Badri
11	Manuel Pedro Maleia	Stability And Adaptability Of Cotton (Gossypium hirsutum L.) Genotypes Based On Ammi Analysis In Mozambique	Manuel Pedro Maleia; Afonso Raimundo; Jaime Omar Teca; Fatima Adriano Chale; Edson Jamal; Joaquim Nhacha Dentor; Badrodine Adamuge
12	Larissa Barbosa De Sousa	Phenotypic Correlation Between Agronomical And Morphological Characters Of The Cotton Plant (Gossypium hirsutum L.)	Larissa Barbosa de Sousa; Melissa Martins de Araújo; Daniel Bonifácio Oliveira Cardoso; Daniel Inserra Bortolin; Elvécio Gomes da Silva Júnior; Letícia Teixeira Gold Pereira; Luccas Marques de Souza Falco; Matheus Araujo Bernardes de Souza; Michel de Carvalho Reis; Leandro Yoshiaki Muraoka;
13	Larissa Barbosa De Sousa	Genetic Divergence Among Cotton Genotypes Of Colored Fiber	Larissa Barbosa de Sousa; Daniel Inserra Bortolin; Matheus Rodrigues Martins; Daniel Bonifácio Oliveira Cardoso; Michel de Carvalho Reis; João Felipe Moraes Ferreira; Letícia Teixeira Gold Pereira; Danilo Araújo Gomes; Jenifer Camila Godoy dos Santos; Ana Flávia Oliveira Nascimento
14	S. M. Palve	Genetic Analysis Of Seed Cotton Yield And Fibre Quality In Advanced Breeding Lines Of Upland Cotton (Gossypium hirsutum L.)	Shivaji Palve
15	Camilo De Lelis Morello	Embrapa´S Cotton Improvement Program For The Brazilian Cerrado	Camilo de Lelis Morello; Nelson Dias Suassuna; Murilo Barros Pedrosa; João Luís Silva Filho; Paulo Augusto Vianna Barroso; Tais de Moraes Falleiro Suassuna; Fabiano José Perina; Sidnei Douglas Cavalieri; Fernando Mendes Lamas; Luiz Gonzaga Chitarra
16	Meltem Bayraktar	Somatic Embryogenesis And Plant Regeneration In Gossypium hirsutum L. Cv. Nazilli-143	Sadiye Hayta-Smedley; Nedim Ozbek; Arif Ansiz; Meltem Bayraktar; Aynur Gurel
17	Saulo Muniz Martins	A Root Phenotyping Platform For The Study Of Root System Architecture In Cotton: Features And Validation	Saulo Muniz Martins; Alberto Souza Boldt; Bruna Mendes Diniz Tripode; Washington Conceição Gonçalves; João Batista Duarte; João Luis da Silva Filho; Marc Giband
18	Tekale Pradeep	Genetic Divergence In Multiple Cross Derivatives Of Upland Cotton (Gossypium hirsutum L.)	Pradeep Tekale; Gopala Krishna Murthy Kankati; Radha Krishna, K. V.; Soka Reddy Sallaram

19	Luiz Paulo De Carvalho	Selection For Increased Fiber Lengt In Cotton Progenies From Acala And Non- Acala Types	Luiz Paulo de Carvalho; Francisco Jose Correia Farias; Josiane Isabela da Silva Rodrigues
20	Francisco Jose Correia Farias	Genetic Analyses Of Cotton Maturity Among Brazilian And Us Upland Genotypes	Francisco José Correia Farias; Waine Smith; Camilo de Lelis Morello; Steve Hague; Filipe Cavalcante Farias
21	Francisco Jose Correia Farias	National Cotton Variety Test At Savanna Areas In Brazil - 2013/14.	Francisco José Correia Farias; João Luis da Silva Filho; Camilo de Lellis Morello; Murilo Barros Pedrosa; Nelson Dias Suassuna; Luiz Paulo de Carvalho; José Jaime Vasconcelos Cavalcanti
22	Begüm Akyol	Callus Induction From In Vitro Anther Cultures Of Two Different Cotton (Gossypium hirsutum L.) Cultivars	Begüm Akyol; Meltem Bayraktar; Mehmet Çoban; Aynur Gürel
23	Luiz Gonzaga Chitarra	Resistance Of Cotton Lines And Cultivars To Meloidogyne Incognita Race 3.	Luiz Gonzaga Chitarra; Camilo de Lelis Morello; Murilo Barros Pedrosa; Flávio Dessaune Tardin
24	Aynur Gürel	The History Of Two Naturally Colored Cotton Varieties: “Emirel” And “Akdemir”	Aynur Gurel; Huseyin Akdemir; Meltem Bayraktar
25	Juan Carlos Cousiño Bareiro	Ipta 212 And Ipta 232: Two New Paraguayan Cotton Varieties (Gossypium spp)	Juan Carlos Cousiño Bareiro; Alicia Gonzalez; Francisco Ibarra; Vilma Gimenez;
26	Luz Marina Espinoza De Arenas	Response Of A Tangüis Variety To Inoculation With Selected Strains Of Plant Growth-Promoting Rhizobacteria (Pgpr) Under Controlled Conditions In Ica, Peru	Luz Marina Espinoza de Arenas
27	Remco Van Poecke	Title: Croppedia - Integrated Database & Software Interface For Discovery & Accelerated Breeding	Remco M.P. van Poecke; Rudi L. van Bavel; Jan van Oeveren; Anker P. Sørensen
28	José Jaime Vasconcelos Cavalcanti	Combining Ability Estimates For Agronomic And Morphological Traits In Cotton Under Water Stress	José Jaime Vasconcelos Cavalcanti; Ubieli Alves Araújo Vasconcelos; Walmir Souza Vasconcelos; Roseane Cavalcanti dos Santos; Francisco José Correia Farias; Gildo Pereira de Araújo; José Henrique de Assunção
29	Roseane Cavalcanti Dos Santos	Immunodetection And Feeding Bioassays As Tools To Identifying Gm Cotton Resistant To Insect	Santos Roseane Cavalcanti; Rose Monnerat; Érica Soares Martins;, Liziane Mria de Lima;, Carliane Rebeca Coelho da Silva

AREA: COTTON AGRONOMY AND SUSTAINABLE PRODUCTION

Poster #	Name	Title	Authors
30	Leonardo Quirino De Oliveira	Analysis Of The Production Of Cotton Under Different Doses Of Phosphogypsum In Cerrado Soil	Leonardo Oliveira; Marciana Silva; Itamar Oliveira; Antonio Lima junior; Laiza Rodrigues; Eduardo Miranda; Denise Martins
31	Lucia Vieira Hoffmann	Nitrogen Absorption By Ten Cotton Varieties And Effect Azospirillum Inoculation	Lúcia Vieira Hoffmann; Raysa Marques Cardoso; Michelle Christine Gomes de Moraes; Kálita Cristina Moreira Cardoso; Ana Luiza Dias Coelho Borin; Alexandre Cunha de Barcellos Ferreira
32	Michael Ortigara Goulart	Cotton Selectivity To Diclosulam Applied In Different Soils And Seasons Of Seeding	Michael Ortigara Goulart; Bianca Nathiele Favetti Chagas, Jonnathan de Almeida Marques; Miriam Hiroko Inoue

33	Zhen Luo	Use Of High Plant Density For Increasing Cotton Yield And Water Saving Under Deficit Irrigation In Arid Areas	Zhen Luo; Hezhong Dong
34	Mario Hugo Mondino	Using Winter Crops As A Complementary Source Of Nitrogen For Cotton Production Under Irrigation	Mario Hugo Mondino
35	Mirella Dos Santos Pereira	Growth Regulator Management Under Spacing And Population Densities In Cotton Crop	Mirella dos Santos Pereira; Jailson Vieira Aguilar; Enes Furlani Junior; Igor Cabreira da Silva; Carlos Vinicius Sanches; Amanda Pereira Paixão
36	Julio Cesar Bogiani	Cotton Production Stability Under Different Cover Crops Biomass	Julio Cesar Bogiani; Alexandre Cunha de Barcellos Ferreira; Ana Luiza Dias Coelho Borin; Fabiano José Perina; Francisco Ivanildo Soares da Silva;
37	Julio Cesar Bogiani	Nitrogen Fertilization Management For Cotton Under Corn-Brachiaria Straw In No-Tillage System	Julio Cesar Bogiani; Ana Luiza Dias Coelho Borin; Alexandre Cunha de Barcellos Ferreira Fabiano José Perina 1, Francisco Ivanildo Soares da Silva 3
38	Ana Luiza Dias Coelho Borin	Nitrogen Uptake And Export From A Brazilian Cotton Cultivar	Ana Luiza Dias Coelho Borin; Alexandre Cunha de Barcellos Ferreira; João Luis da Silva Filho; Julio César Bogiani; Michelle Christine Gomes de Moraes
39	Khurshida Narbaeva	An Effect Of Biopreparations With Complex Action Rizokom-1 And Serhosil On Productivity Of Cotton Variety Bukhara-9 On Saline Soils	Khurshida Narbaeva; Anastasiya Babina; Gulnara Djumaniyazova; Makhbuba Ikramova; Bakhtiyor Rakhmatov
40	Khurshida Narbaeva	Nitrate Reductase Activity Of Saline Soil At Application Of The Biopreparation Of Complex Action Rizokom-1 On Cotton	Khurshida Narbaeva; Anastasiya Babina; Gulnara Djumaniyazova; Saidakhon Zakiryaeva;
41	Aynur Gürel	Importance Of Organic Cotton For Turkey	Ülfet Erdal; Meltem Bayraktar; Aynur Gurel
42	Alexandre Cunha De Barcellos Ferreira	Soil Organic Matter After Nine Years Under Crop Rotation, Conventional, And No-Till Cotton Production Systems	Alexandre Cunha de Barcellos Ferreira; Ana Luiza Dias Coelho Borin; Fernando Mendes Lamas; Julio César Bogiani
43	Pius Elobu	Use of Tythonia diversifola to improve cotton productivity under marginal soils in Uganda	Pius Elobu; James Ronald Ocan; John Olinga; Paul Ogabe

AREA: COTTON PHYSIOLOGY

Poster #	Name	Title	Authors
44	Bruna Cardoso Gomes	Effect Of Different Application Timings Of Mepiquat Chloride In Plant Height And Number Of Fruits In Cotton Genotypes.	Bruna Cardoso Gomes; Cynthia Pereira Gundim; Daniel Bonifácio Oliveira Cardoso; Danilo Araújo Gomes; Elvécio Gomes da Silva Júnior; João Felipe Moraes Ferreira; Luccas Marques de Souza Falco; Matheus Araujo Bernardes de Souza; Michel de Carvalho Reis; Larissa Barbosa de Sousa;
45	Bruna Cardoso Gomes	Effect Of Anticipated Application Of Mepiquat Chloride In Chlorophyll Content A And B On Cotton Genotypes	Bruna Cardoso Gomes; Cynthia Pereira Gundim; Danilo Araújo Gomes; Guilherme Hugo da Silva Costa; João Felipe Moraes Ferreira; Luccas Marques de Souza Falco; Matheus Araujo Bernardes de Souza; Melissa Martins de Araújo; Morgana Coelho Mamede; Larissa Barbosa de Sousa;

46	Asia Perveen	Adaptability Of Transgenic Cotton Genotypes To High Temperature Stress	Asia Perveen; Fiaz Ahmad
47	Mirella Dos Santos Pereira	Development, Fiber Quality And Production Of Upland Cotton Genotypes (Gossypium hirsutum L. var latifolium Hutch) Submitted To Mepiquat Chloride	Mirella dos Santos Pereira; Amanda Pereira Paixão; Enes Furlani Junior; Carlos Vinicius Sanches; Simone Silva Hiraki; Luis Henrrique Marani Daruichi Machado
48	Jayant H.Meshram	Phenotyping Of Gossypium hirsutum Germplasm Lines For Drought Tolerance Traits	Jayant Meshram;, J Annie Sheeba
49	Carlos Vinícius Sanches	Application Of Growth Regulator In Cotton By Spraying And In The Seeds	Carlos Vinícius Sanches; Anna Caroline Pelais Queiroz; Enes Furlani Junior; Mirella dos Santos Pereira; Jailson Vieira Aguilar
50	Fábio Echer	Responses Of Cotton Cultivars To Shading	Fábio Echer; Lincoln Araújo
51	Michael Plumblee	Damage Simulation In Early- And Late-Maturing Cotton Varieties In The Mid-South	Michael Plumblee; Darrin Dodds; Tyson Raper; Andrea Jones; Dan Fromme
52	Harel Bacher Juan Piero	How Do High Temperatures Impair Cotton (Gossypium spp.) Productivity?	Harel Bacher; Yehoshua Saranga
53	Antonio Raphael	Cotton Germination And Emergence As Affected By Cultivars And High Diurnal Temperatures	Juan Piero Antonio Raphael; Bruno Gazola; Jesion Geibel da Silva Nunes; Gabrielle de Castro Macedo; Ciro Antonio Rosolem
54	Meltem Bayraktar	The Impact Of Leaf Anatomy On Drought Tolerance And Yield Of Cotton Cultivars	Lale Yildiz Aktas; Bulent Yagmur; Meltem Bayraktar; Aynur Gurel;
55	Roseane Cavalcanti Dos Santos	Initial Growth And Gene Expression In Cotton Genotypes Under Water Deficit	Roseane Cavalcanti dos Santos; Vandre Guevara Lyra Batista; Pedro Dantas Fernandes; Pericles Albuquerque Melo Filho; Liziane Maria de Lima

AREA: COTTON PROTECTION

Poster #	Name	Title	Authors
56	Ebadollah Baniani	Effect Of Seeds Treatment With Fungicides And Insecticides On Germination And Vigurity, Abnormal Root Producing And Protection Of Cotton Seedling	Ebadollah Baniani; Morteza Arabsalmani; Ebrahim Frahani;
57	Edivaldo Cia	Cotton Reaction To Disease And Nematode In Brazil	Edivaldo Cia; Milton Geraldo Fuzatto; Julio Isao Kondo; Rafael Galbieri; Luiz Henrique Carvalho; Fábio Luiz Ferreira Dias; Guilherme A. Ohl; José Carlos Cavichioli; Murilo B. Pedrosa; Rogério Soares de Freitas
58	Alderi Emídio De Araújo	A New Method To Differentiate Colletotrichum gossypii and Colletotrichum gossypii var. cephalosporioides Using The IGS Region of rDNA	A. E. Araújo; F. S. Fernandes; W. M. Coutinho; G. F. Silva
59	Lawrence Malinga	Efficacy Of Organic Nematicides On Meloidogyne javanica For Small-Scale Cotton Farmers In South Africa	Lawrence Malinga
60	Alfredo Riciere Dias	Effect Of Protectant Fungicides And Fertilizers Associated With Azoxystrobin And Cyproconazole Fungicides To Control Ramularia areola and Corynespora cassiicola On Cotton Crop.	Alfredo Riciere Dias; Hugo Manuel de Souza; Eric Fabiano Seraguzi; Juliano Antonio Rodrigues Oliveira; Andrey Carmona Cervigni; José Edson Paschoal; Luis Guilherme Gonçalves da Costa; Rafael Azevedo Borges

61	Hisham Mohamed Mohamed Elbassouiny	Cotton Bollworm Helicoverpa armigera: Control By Conventional And Biorational Insecticides	Hisham Mohamed Mohamed El-bassouiny; Haity M. Tadrose; Aly Zakria El-Nagger;
62	Whitney D Crow	Evaluation Of Timing Intervals Of Foliar Applications For The Control Of Tobacco Thrips (Frankliniella fusca) In Cotton	Whitney Crow; Angus Catchot; Jeff Gore; Darrin Dodds; Thomas Allen; Don Cook; Scott Stewart; David Kerns
63	Tom Walsh	Identifying And Characterising Novel Modes Of Action For Insecticidal Toxins.	Thomas Walsh; Craig Anderson; Lars Jermiin; Wee Tek Tay; Sharon Downes
64	Adam Whalen	Factors Affecting Foraging Honey Bee Exposure To Neonicotinoid Seed Treatments In Midsouthern U.S. Cotton Fields	Adam Whalen; Angus Catchot; Jeff Gore; Scott Stewart; Gus Lorenz; Don Cook; Fred Musser
65	Nick Bateman	Seasonal Occurrence Of Lepidopteran Pest Of Soybean And The Implications For The Natural Refuge	Nick Bateman; Angus Catchot; Jeff Gore; Don Cook; Fred Musser; Trent Irby
66	Benjamin Carroll Thrash	Termination Of Insecticide Sprays For Tarnished Plant Bug	Ben Thrash; Angus Catchot; Jeff Gore; Don Cook; Gus Lorenz; Glenn Studebaker; Nick Seiter; David Kerns; Sebe Brown; Scott Stewart
67	Fábio Echer	Plant Growth Parameters And Cotton Bollworm [Helicoverpa armigera (Hübner)] Survivorship On Water Stressed Cotton Bt Varieties	Fábio Echer; Miguel Soria
68	Antonio Chamuene	Factors Determining The Attack Of Aphis gossypii Glover, 1877 (Hemiptera: Aphididae) On Cotton (Gossypium hirsutum)	Antonio Chamuene; Marcelo Picanço; Paulo Berger
69	Scott Stewart	The Impact Of A New Bt Cotton Trait On Thrips And Their Injury In Seedling Cotton	Scott Graham; Scott Stewart
70	Lucas Xavier Franca	Impact Of Nitrogen Application Rate On Tarnished Plant Bug Populations, Control, And Cotton Yield	Lucas Franca; Chase Samples; Darrin Dodds; Jeff Gore; Bobby Golden; Angus Catchot; Jac Varco; John Riley; Andrew Denton; Drake Copeland
71	João Paulo Ascari	Relationship Between Ramularia Leaf Spot And The Development Of Cotton Crop (Harvest Of 2013/2014)	João Paulo Ascari; Inês Roeder Nogueira Mendes; Rafael Sbruzzi Prieto; Angélica Carmo de Meneses; Marcos Vinícius Foschiera; Danielle Storck-Tonon; Rivanildo Dallacort; Dejânia Vieira de Araújo
72	João Paulo Ascari	Effect Of Fungicide On Ramularia Leaf Spot And Vegetative Characteristics In The Cotton Harvest Of 2014	João Paulo Ascari; Leonardo Diogo Ehle Dia; Inês Roeder Nogueira Mendes; Rafael Sbruzzi Prieto; Marcos Vinícius Foschiera; Thainara Porcher; Danielle Storck-Tonon; Dejânia Vieira de Araújo
73	Vanessa Costa Da Silva	Influence Of Photoperiod On Mycelial Growth And Conidia Production Of Ramularia areola	Vanessa Costa da Silva; Inês Roeder Nogueira Mendes; Jurandir Ambrósio; João Paulo Ascari; Tainara Porcher; Kethelin Cristine Laurindo de Oliveira; Danielle Storck-Tonon; Dejânia Vieira de Araújo
74	Inês Roeder Nogueira Mendes	Sanitary Quality Of Seeds Produced In Different Canopy Layers Of Cotton Cultivars	Inês Roeder Nogueira Mendes; João Paulo Ascari; Vanessa Costa da Silva; Marcos Vinícius Foschiera; Kemely Mara Ramalho Hiega; Danielle Storck-Tonon; Willian Krause; Dejânia Vieira de Araújo

75	Inês Roeder Nogueira Mendes	Morphological Characteristics Of Ramularia areola On Different Culture Media	Inês Roeder Nogueira Mendes; Jurandir Ambrósio; João Paulo Ascari; Vanessa Costa da Silva; Kemely Mara Ramalho Hiega; Kethelin Cristine Laurindo de Oliveira; Danielle Storck-Tonon; Dejânia Vieira de Araújo
76	Idrissa Tereta	Cotton Topping As A Way To Reduce Farmer's Reliance On Insecticides In Mali	Idrissa Tereta; Thierry Brevault; Fagaye Sissoko; François-Regis Goebel; Alain Renou
77	Fabiano Jose Perina	Insecticides Applications To Control Lepidopterans-Pests In Cotton And Soybeans In Western Bahia Region: An Overview	Fabiano Jose Perina; Augusto Guerreiro Fontoura Costa; Luiz Guilherme Rebello Wadt; Aldemir Chaim
78	Ricardo Sequeira	Development Of An Ipm Strategy For Phenacoccus solenopsis (Cotton Mealybug) In Australia	Richard Sequeira; Moazzem Khan; Kristy Byers; Gail Spargo; David Reid
79	Nelson Dias Suassuna	Evaluating Resistance To Ramulosis In Cotton	Nelson Dias Suassuna; João Luís Silva Filho; Taís de Moraes Falleiro Suassuna; Camilo de Lelis Morello
80	Carlos Alberto Domingues Da Silva	Trigona spinipes (Hymenoptera: Apidae, Meliponinae) Damaging Cotton Plants In Paraíba State, Brazil	Thiele da Silva Carvalho; Carlos Alberto Domingues da Silva; Silvia Ramos de Oliveira; Eduardo Domingos Vasconcelos; Antônio L. de Arroxelas Galvão Filho
81	Sandra Maria Morais Rodrigues	Host Weeds Of Bemisia tabaci (Gennadius, 1889) Biotype B (Hemiptera: Aleyrodidae) In Cotton (Gossypium hirsutum L.).	Sandra Maria de Morais Rodrigues; Alexandre Ferreira da Silva

AREA: ECONOMICS/COTTON COMPETITIVENESS

Poster #	Name	Title	Authors
82	Alejandro Valeiro	Fifteen Years Of Gm Cotton In Argentina: A Partial Balance	Alejandro Valeiro

AREA: FIBER QUALITY AND PROCESSING

Poster #	Name	Title	Authors
83	Abdelrahman Hassan Abdellatif	Over View On Sudan Cotton Research: Fiber Quality And Stickiness	Abdelrahman Abdellatif; Elafadil Babiker
84	Negm Mohamed	Relationships Between Hvi And Ccs And Tensile Yarn Strength	Mohamed Negm; Suzan Sanad; Zeinab Ghareeb

AREA: GENETICS AND GENOMICS – ICGI 2016 BIENNIAL CONFERENCE

Poster #	Name	Title	Authors
85	Sukumar Saha	Development And Utilization Of Interspecific Chromosome Substitution Lines In Genetic Analysis And Germplasm Improvement Of Upland Cotton.	Sukumar Saha; David M. Stelly; Johnie N. Jenkins; Jack C. McCarty; Russell Hayes
86	Guillermo Marcelo Gomez	Mapping Of Qtls Identified In A Novel Source Of Resistance To The Root-Knot Nematode (Meloidogyne Incognita Race 3) In Cotton (Gossypium Barbadense L.)	Guillermo Marcelo Gomez; Marcio C. Moretzsohn; Esdras Henrique da Silva; Cleber Furlanetto; Joelma Gardênia P. Silva; Jean-Marc Lacape; Paulo A.V. Barroso; Regina M.D.G. Carneiro; Marc Giband
87	Joshua Udall	Allele-Mining Rna-Seq Data Of Cotton (Gossypium hirsutum L.) Roots	Daojun Yuan; Alex Freeman; Christopher Hanson; Sara Greenfield; Aaron Sharp; Lori Hinze; Richard Percy; Joshua A Udall
88	Maite Vaslin De Freitas Silva	Complete Genome Of The Cotton Anthocyanosis Virus	Rhuana O Santos; Anna Karoline S Fausto; Roberto Andrade; Tatiane S da Franca; Marc Giband; Maite F S vaslin

AREA: MEASURING SUSTAINABILITY IN COTTON FARMING SYSTEMS

Poster #	Name	Title	Authors
89	Nageeb Ibrahim Bakheit	Vision For Reforming Gezira Scheme In Sudan By Strengthening Cotton Smallholders Field-Level Organization And Decision-Making	Nageeb Ibrahim Bakheit
90	América González Sanabria	Economic Parameters For The Cotton Sector In Paraguay: Baseline Analysis In Rural Family Farming	Claudia Sepulveda Garrido; America Gonzalez Sanabria; Adriana Calderan Gregolin; Beatriz Marciel; Rodrigo Allende; Emilio Valiente

AREA: SOCIAL DYNAMICS AND TECHNOLOGY TRANSFER

Poster #	Name	Title	Authors
91	Joshua Usha Rani	Cotton Transfer Of Technology Prospects For Next Decade In India	Usharani Joshua
92	S.M.Wasnik	'E- Kapas': An Ict Model Of Extension For Knowledge Empowerment Of Cotton Farmers In India	Siddharth Wasnik; K.R. Kranthi; Blaise D.
93	Santam Singh	Mobile Phone Based Voice Call : An Efficient Means For Disemination Cotton Protection And Production Technologies	Isha Gaur; Satnam Satnam; Suneet Pandher; Kulvir Singh; Pankaj Rathore
94	Joelcio Cosme Carvalho Ervilha	Communication For Development - Catalyzing Participatory Process For The Transfer Of Technology In The Scope Of Cotton Family Farming: The Case Of Paraguay	Alberto Troilo; Joelcio Cosme Carvalho Ervilha; Adriana Calderan Gregolin; America Gonzalez Sanabria
95	Diana Raquel Piedra	Argentina: Inta And Cotton Research	Diana Raquel Piedra
96	Mutibo Chijikwa Mushenywa	The performance of Farmer Field Schools in the Zambian cotton production system	Mutibo Chijikwa; Suzanne Philips

BREEDING AND CROP IMPROVEMENT

BREEDING COTTON FOR A VARIABLE RAINFALL ENVIRONMENT

Authors: Warren Conaty [1], Susan Jaconis [1], David Johnston [1], Greg Constable [1]

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Abstract:

Australian rainfed cotton is grown in regions with highly variable rainfall. Therefore, crops are not grown every year. Sowing decisions are influenced by cotton prices, availability of stored soil moisture and rainfall outlooks. The aim of this research was twofold. 1. To develop and evaluate a managed stress protocol where 'rainfed' germplasm evaluations are irrigated when yield is expected to fall below the threshold for conducting selections with confidence; 2. To assess the stability of germplasm performance under extreme rainfed conditions and limited water situations, clarifying weather germplasm selected under rainfed conditions has the ability produce high lint yield in seasons with higher than average rainfall. The CSIRO cotton breeding program conducts rainfed germplasm evaluations at its core research site under nominal rainfed conditions- experiments are pre-irrigated to simulate a full soil moisture profile at sowing. Historically, it has been observed that statistical genotype differences can only be reliably resolved at lint yield levels >550 kg/ha. Between 1994 and 2011, four years (22%) had experiments yielding <550 kg/ha. It was hypothesized that applying one furrow irrigation in very dry years could help resolve statistical differences between germplasm lines. As irrigation timing will impact its efficacy, the OZCOT simulation model for cotton crop management was used to determine the most effective irrigation date with respect to soil water deficit and crop growth stage. The simulation, conducted with weather data from a 151 year period, concluded that yields >550 kg/ha were not achieved in 27 years (18%). These 27 years underwent further simulations to determine the most suitable soil water deficit and crop growth stage where yield was increased with a single irrigation. It was determined that for a mid-October sown crop when soil water deficit reached 100mm by peak flowering, an irrigation should be applied to a 'rainfed' experiment. This protocol resulted in only one year (<1%) where simulated crops yield was below 550 kg/ha, and called for irrigation in 98 of the study years (65%). However, in 71 of these years (72% years irrigation is advised) there was sufficient subsequent rainfall to result in rainfed yield >550 kg/ha. In practice, rainfall forecasts can be taken into account for irrigation decisions, reducing the frequency of irrigation required. A paired rainfed and managed stress experiment with 21 genotypes was sown in 2013/14, 2014/15 and 2015/16 to validate the developed protocol. Genotype performance was assessed in terms of lint yield and fibre quality. Soil water deficit (mm) was monitored in the control genotype. Results show that in dry seasons (2013/14) irrigating the 'rainfed' experiments was necessary to increase yields above 550 kg/ha, and resolve differences in genotypes performance at low yield levels. However, once rainfed yield levels increase due to an increased in-crop rainfall (2014/15 and 2015/16), irrigation was no longer necessary to resolve statistical differences between genotypes. As a result of these experiments it has been decided that a managed stress system will be used in future rainfed evaluation of CSIRO cotton germplasm.

Acknowledgments

This study was financially supported by Cotton Breeding Australia. The authors would like to thank the technical staff of the CSIRO cotton breeding group, particularly Alan Thompson and Mark Laird. We also thank Mick Bange, Warwick Stiller, and Shiming Liu for their contributions to this work.

References

Keywords: dryland, OZCOT, genotype selection, water stress, Gossypium

BREEDING FOR PRODUCTIVE COMPACT COTTON VARIETIES AND A METHOD TO CATEGORISE THE PLANT TYPE IN GOSSYPIUM HIRSUTUM L.

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Abstract:

This study began in 2006-07 and the success achieved after nine years has been highly satisfying. Eight intra-hirsustum hybrids were identified in 2006 from the Indian Cotton Improvement Project trials. Remnant seeds were used to produce seven double crosses in 2007-08 which were sown in 2008-09. Individual plant selection was followed till 2013-14, when only 63 progenies were retained. Promising genotypes, especially with regards to the compact plant type, were found. Seed increase was done in 2014-15 (DCHF7) and in 2015-16,sixty-three progenies were evaluated under rainfed situation at ARS Dharwad Farm. Significant differences among the genotypes proved that substantial genetic variability was created. Two facets of the experiment opened up. Firstly, considerable success was achieved in per se superiority of seed cotton yields touching 2900 kg/ha. Secondly, the concept of the plant type under a high density planting situation was explored. The plant type was categorised into 6 classes based on the plant height and diameter as super-compact, compact, spreading, tall-compact, robust and highly-robust. A majority were robust and highly robust. However, 26 were compact types. Fourteen were super-compact with a plant height of less than 77 cm and diameter of less than 45 cm with average seed cotton yield of 1631 kg/ha. The average seed cotton yield of the compact class was the highest (50.4 g/plant) and yields will certainly improve under a higher population with efficient utilisation of the available free space. Twenty-three genotypes were better than the best check with regards to seed cotton yield. The top 5 genotypes had more than 50 per cent yield advantage over the best check. Two super-compact genotypes viz., VJ-5 (74 g/plant) and RJ-5 (72 g/plant), showed more than 50 per cent yield superiority, occupied lesser space than the

super-compact check and had more number of bolls which is the deciding factor in a high density situation. Though the top 2 entries were robust, these 2 super-compacts had more than 10 per cent yield advantage than the best highly-robust genotype. The genetic superiority derived from the original parents and fixed in the genotypes has been exceptional. As for fibre properties, a high of 33.7 mm and 24.0 g/tex of fibre length and tenacity were recorded in a genotype. There were 9 genotypes in the 23 best ones which had a strength to length (S:L) ratio of 0.8, considered the norm for better spinning. The plant categorisation method is easy to apply. Such compact genotypes amenable to mechanical harvesting will be the staple of rainfed cotton growing regions of India where abiotic stress is also routinely encountered. These genotypes can also be used in appropriate intercropping patterns already identified in the country. With the public sector Bt gene round the corner, promising genotypes can be converted to become Bt varieties, a highly viable alternative to the hybrids, especially in a high density planting situation under rainfed conditions. In hindsight, this successful case study has proved the importance of picking the proper F1 hybrids as parents for hybridisation.

Acknowledgments

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Keywords: Gossypium hirsutum, Compact cotton, Plant diameter, High Density Planting, Double-cross hybrid

COMBINING ABILITY ANALYSIS FOR SEED COTTON YIELD AND QUALITY TRAITS IN UPLAND COTTON (GOSSYPIUM HIRSUTUM L.) OVER ENVIRONMENTS

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Abstract:

Cotton (Gossypium spp.) occupies the predominant position in the Indian textile industry, despite stiff competition from the man-made synthetic fibres. It caters to one of the important basic needs of human race, clothing, besides meeting various industrial needs of cellulose and medicated absorbent cotton. Cotton improvement programmes primarily lay emphasis on the development of varieties/ hybrids that have contributed for the improvement of productivity of cotton. The hybrid cotton era in India had started in 1970 with the release of world's first intra-specific cotton hybrid 'H 4' (Patel, 1971). For developing heterotic hybrids, the diallel analysis provides a systematic approach for detection of appropriate parents and crosses in terms of investigated traits. The analysis of diallel crosses contain further information on the nature of predominant gene action in traits of major agronomic importance, besides estimates of general (GCA) and specific combining ability (SCA). Information pertaining to the different types of gene action, relative magnitude of genetic variance and combining ability estimates are important and vital parameters to mold the genetic makeup of the cotton crop (Senthil Kumar et al., 2013). The genotypes or hybrids performing well under a particular environment may or may not perform well over other environments due to genotype-environment interactions (G × E). Hence, the present investigation was under taken to identify good general and specific combiners for different traits over environments. Forty five intra-hirsutum hybrids from a 10 × 10 diallel crossing excluding reciprocals along with their parents were evaluated for combining ability for seed cotton yield and quality traits over three environments during kharif, 2013-14. The pooled analysis of variance for combining ability revealed that, the variance due to SCA was higher than GCA for all the characters except for days to 50 % flowering and 2.5% span length indicating the predominance of non-additive gene action. The estimates of gca effects revealed that the parents, NDLH 1938, RAH 1004 and L 770 were found to be good general combiners for yield and its component traits in desired direction. The crosses, NDLH 1938 × L 604, NDLH 1938 × RAH 1004 and NDLH 1938 × L 770, recorded high per se performance (202.18, 197.99 and 195.54 g) and significant positive sca effects (32.12, 22.82 and 19.46) for seed cotton yield plant-1 respectively and for fibre quality traits like 2.5 % span length (NDLH 1938 × L 604), micronaire (NDLH 1938 × RAH 1004), bundle strength (NDLH 1938 × L 604), uniformity ratio (NDLH 1938 × RAH 1004) and elongation % (NDLH 1938 × RAH 1004).

Acknowledgments

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Keywords: Cotton, seed cotton yield, quality traits, combining ability, stability

COTTON VARIETIES AND SEED PRODUCTION SYSTEM IN IRAN

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Abstract:

Cotton (Gossypium hirsutum L.) is one of the important cash crops in I.R.Iran. it is the main raw materials of textile industry. It plays a pivotal role in the agriculture-based economy of Iran. It is grown on an area of 70-90 thousand hectares with average production of 762 Kg lint per hectare. Cotton cultivation area has drastically been decreased from 325000 ha in 1996/7 to 75000 ha in 2015. The crop is sown on 10 April until 20 May normally and 20 June after harvesting of wheat in double cropping system. In the most regions, fields are often pre-irrigated because of limited rainfall in the spring. IPM project in Iran was developed and started in year 2000. Nowadays, eight commercial cotton cultivars (from 16) are grown in 11 states of country. The only major source of seed supply is CRII, General Office of Cotton and Oil Crops under control of registration and certification of SPCRI institute. Seed production system is based on international standards. with respect to isolation distances 50 meters. The new data showed 10 meter for inter varietal seed multiplication plots. Cotton seed technology (processing and packing) and improvement of cotton harvesting mechanization are priority research in the country.

Acknowledgments

References

Keywords: Cotton cultivation , cultivars, seed multiplication

DEVELOPING SODIUM TOLERANT COTTON BY EXPLOITING GENETIC DIVERSITY WITHIN TWO CULTIVATED TETRAPLOID SPECIES

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Abstract:

Excess sodium (Na) in the soil profile is a key limiting factor of saline and/or sodic soils which significantly affects irrigated cotton production worldwide (Gorham *et al.* 2010). Under saline or sodic abiotic stresses, cotton can take up and accumulate excessive levels of ions which can be toxic to the plant. Although Na can substitute for potassium (K) in cotton, when K is in a short supply, the antagonistic effect of Na can restrict plant uptake of other essential nutrients such as phosphorus (P) and K (Rochester 2010). These phenomena can lead to nutrient imbalance in plants and limit crop productivity. In cotton growing on sodic soils in Australia under high yield levels with high requirements for P and K, excessive Na uptake is regarded as one of the constraints for continued yield progress (Rochester 2010). Among the cultivated tetraploid cotton species, *Gossypium barbadense* is known for being better able to tolerate soil salinity or sodicity (Abul-Naas and Omran 1974). Given the importance of *G. hirsutum* for global cotton production, transferring these attributes through interspecific crosses has been of interest in cotton breeding (Ashraf 2002; Liu *et al.* 2015). We demonstrate Na and K content of mature leaves at peak flowering represented the largest discrete difference in nutrient content between *G. hirsutum* and *G. barbadense*, and leaf Na and K content also showed high genetic variability and moderate heritability within a RIL population derived from a cross between these two species. QTL mapping suggested only a few regions on different chromosomes were behind the phenotypic variation of Na, K and their ratio. Statistical analysis showed that selection would be able to reduce leaf Na and increase K content and increase leaf K/Na ratio in cotton. When backcross-derived sister lines from an interspecific cross were compared in a sodic clay soil, the lines with low leaf Na content (average 652 ppm) showed better yield than the ones with high leaf Na content (average 843 ppm). We conclude that exploiting genetic diversity of tetraploid species would lead to increased tolerance of cotton to sodic soils and would simultaneously improve nutrient status and yield.

Acknowledgments

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Keywords: Sodium tolerance, heritability, QTL mapping, Gossypium hirsutum, G. barbadense

DEVELOPMENT OF GOSSYPIUM ANOMALUM-DERIVED MICROSATELLITE MARKERS AND THEIR USE FOR GENOME-WIDE IDENTIFICATION OF RECOMBINATION BETWEEN THE G. ANOMALUM AND G. HIRSUTUM GENOMES

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Abstract:

To continue to develop improved cotton varieties, it is essential to transfer desired characters from diploid wild cotton species such as Gossypium anomalum to cultivated allotetraploid cotton species. However, interspecific reproductive barriers limit gene transfer between species. In a previous study, we used colchicine treatment to produce a synthesized hexaploid derived from an interspecific hybrid between G. hirsutum and G. anomalum and demonstrated its hybridity and doubled status using morphological, cytological and molecular marker methods. In the current study, to effectively monitor G. anomalum genome components in the G. hirsutum background, we developed 5,974 non-redundant G. anomalum-derived SSR primer pairs using RNA-Seq technology, which were combined with a publicly available physical SSR map. Based on this combined SSR map and segregation data from the BC2F1 population, we identified a set of 230 informative G. anomalum-specific SSR markers that are evenly distribution on the chromosomes, which cover 95.72% of the cotton genome. After analyzing BC2F1 segregation data, 50 recombination types from 357 recombination events were identified, which cover 81.48% of the corresponding G. anomalum genome. A total of 203 recombination events occurred on chromosome 11, accounting for 56.86% of the recombination events on all chromosomes. Recombination hotspots were observed at marker intervals JAAS1148-NAU5100 on chromosome 1 and JAAS0426-NAU998 on chromosome 2. Therefore, all G. anomalum chromosomes are capable of recombining with their counterpart chromosomes in G. hirsutum. This study represents an important step towards introgressing desirable traits into cultivated cotton from the wild cotton species G. anomalum.

Acknowledgments

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References

Keywords: Gossypium hirsutum, G. anomalum, microsatellites markers, recombination, introgression

DEVELOPMENT OF ROOT-KNOT AND RENIFORM NEMATODE RESISTANT COTTON LINES USING MARKER ASSISTED SELECTION

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Abstract:

Southern root-knot nematode (RKN), [Meloidogyne incognita (Kofoid and White) Chitwood] and reniform nematode (RN), Rotylenchulus reniformis Linford and Oliveria, are major pest in U. S. Upland cotton Gossypium hirsutum L. production regions with annual losses > $100 million. Resistant cultivars would be effective in managing these pests. RKN resistance breeding began in the early 1900's. The first line with a high level of resistance, Auburn 623 RNR, was developed by R. L. Shepherd in the early 1970's. Resistant breeding lines were released in 1989 (Shepherd et al. 1996). One of these lines, M-240 RNR, was used as our source of RKN resistance. Gutierrez et al. (2010) reviewed germplasm sources, genes, and SSR markers linked to RKN resistance. Losses associated with RN were noticed in the 1990's and by the early 2000's major damage was reported. Efforts were made to identify RN resistance in wild G. hirsutum and G. barbadense L. accessions. Robinson et al. (2004) identified GB713 (PI 608139), a wild photoperiodic G. barbadense accession, as resistant. Gutierrez et al. (2011) reported significant association of three SSR (GH132, BNL3279, and BNL569) with RN resistance and we used these markers in Marker Assisted Selection (MAS). Our breeding strategy was to transfer RN resistance from GB713 to a day-neutral Upland line, and then combine with RKN resistance. During the winter of 2007-08 we crossed GB713 to Sure-Grow 747 (SG747) and grew the F2 in field plots in 2009. We selected day-neutral plants, genotyped them with three SSR markers, backcrossed selected plants to SG747, and advanced to the BC1F2. MAS plants were backcrossed to SG 747 and advanced to the BC2F2. MAS plants were verified as resistant to RN, seed were increased, and backcrossed to SG747. RN resistant germplasm was released in 2012 and registered (McCarty et al. 2013). Egg production of RN was suppressed ~ 90% on the resistant germplasm lines and fibers were longer, stronger, and finer than the recurrent parent SG747. In 2011 we crossed one RN MAS plant to RKN resistant M-240 RNR, and advanced to the F2 where MAS for both RN and RKN was applied. SSR markers CIR316 and BNL3661 were used to genotype for RKN resistance (Gutierrez et al 2010). The three identified markers were used for RN. We identified 2 plants homozygous for all 5 markers and crossed one plant to a resistant RN line (BC3 to SG747), advanced to the F2 where MAS was applied, RN-RKN plants were selected and crossed to SG747, advanced to the F2, and MAS was used to select plants homozygous for RN and RKN markers. Selected plants were self pollinated. RN-RKN lines were evaluated in field plots for agronomic traits and in a growth chamber in 2015 for RN and RKN resistance. Lines resistant to both RN and RKN, and with agronomic and fiber traits equal to or superior to SG747 were selected. A germplasm release will be in 2016. These lines are a valuable resource for the development of cotton cultivars resistant to RN and RKN.

Acknowledgments

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Keywords: Cotton Breeding, Root-knot Nematode, Reniform nematode, Marker Assisted Selection.

DEVELOPMENT OF VERTICILIUM WILT AND JASSID RESISTANT COTTON VARIETIES AT ARC IN SOUTH AFRICA

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Abstract:

Diseases and pests are major fibre yield and quality limiting biotic factors threatening the cotton production in South Africa. Verticillium wilt has been identified as a major disease in the lower Orange River Valley area causing tremendous yield losses in most of the available cotton varieties. A tolerant cultivar OR3 was developed by collaboration between the staff of the Oranje Kooperasie and Plant breeders of the National Department of Agriculture Technical Services, Forestry and Fisheries. But, the new "pathovar" that emerged in the 1990s was found to be virulent on the cultivar. In response to this researchers from Agricultural Research Council (ARC) developed two new varieties, GariepVT 1 and 2, which are tolerant to the disease. Verticillium wilt has also been reported in other important production areas indicating the likely spread of the disease over time. Almost all cotton cultivars grown in South Africa today are Bt-cotton. As a result, jassids or leaf hoppers have become a major insect pest that causes devastating yield losses on cotton across most of the cotton production areas in South Africa. While there are some chemicals that are used to control the disease there are some challenges in using these. For small scale farmers, one of the major challenges has been inadequate resources such as limited access to water and such chemicals. ARC-Institute for Industrial Crops has developed and registered a variety, Jassid 1 that is resistant to jassid damage. The variety was developed from a single plant selection that was found to exhibit jassid damage resistance from small-holder on-farm trials with inadequate spray regime due to water inaccessibility. The new hairy variety has shown a consistent yield and quality attributes comparable to the normal varieties that are otherwise susceptible to jassid damage. Keywords: Cotton varieties, verticillium wilt and jassid resistant.

Acknowledgments

References

Keywords: cotton varieties, verticillium wilt, jassid resistant

EFFECTS OF RESISTANCE QTLS QMI-C11 ON MELOIDOGYNE INCOGNITA

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Abstract:

The highly resistance source to *Meloidogyne incognita* (Southern root-knot nematode; RKN) in Upland cotton (*Gossypium hirsutum* L), Auburn 634RNR, was derived from Clevewilt and Wild Mexican Jack Jones, and confers resistance QTLs *qMI-C11* and *qMi-C14*, respectively. A genetic mapping analysis has identified epistatic interaction between the two QTLs, and recent studies suggested they have different modes of action. To confirm these observations, we developed near-isogenic lines (NIL) carrying only a single QTL. We observed RKN development in NIL containing both QTLs (M-120), only one QTL (NIL-C11 with *qMI-C11* or NIL-C14 with *qMi-C14*), or neither QTL (Coker 201). Compared to the susceptible Coker 201, NIL-C11 stopped many nematodes from developing beyond the SJ2 stage whereas NIL-C14 limited the development of J3 and J4 into females, and both consequently reduced egg production. NIL-C11 and M-120 reduced early stage (J2 and SJ2) development by about 50% and showed fewer total nematodes in their roots than Coker 201 and NIL-CH14 throughout the experiment. Additionally, almost 50 % of the nematodes in NIL-C11 and M-120 plants remained in stage J2 or SJ2 25 days after inoculation (DAI), which indicates that many nematodes do not develop following penetration. The number of nematodes was not significant on 4 and 8 DAI for all genotypes, which indicates that the lower nematode counts for NIL-C11 and M-120 during the rest of the experiment may be caused by RKN emigration. To better understand the resistance effects of NIL-C11 and NIL-CH14, we evaluated RKN penetration and emigration in an additional study. We hypothesized that on resistant lines, J2s may be failing to establish a feeding site and leaving the roots. To test our hypothesis, two-week-old seedlings in vermiculite were inoculated; two days later, roots were rinsed

and seedlings were transplanted into small cones with fresh vermiculite. Six replicates per genotype and five sampling dates (4, 6, 8, 10, and 12 DAI) were arranged in a completely randomized design. On each sampling date, nematodes that had left the roots were extracted from vermiculite and roots were stained to count nematodes inside of the roots. The number of RKN extracted from the vermiculite peaked 6 DAI for all genotypes. NIL-C11 plants had greater numbers of RKN leaving the roots than Coker 201 on all sampling dates. M-120 had similar results to NIL-C11, except for 12 DAI when the amount of RKN extracted from vermiculite was similar to NIL-C14 and Coker 201. Almost 70% of the RKN that penetrated NIL-C11 plants were recovered from the vermiculite during the study. More than 70% of the nematodes that initially penetrated Coker 201 and NIL-C14 plants stayed in the root. We conclude that NIL-CH11, which is in M-120 plants, causes many J2s to leave the roots or to fail to develop beyond the SJ2 stage.

Acknowledgments

References

Keywords: Root-knot nematode, cotton, QTL

ELIMINATION OF GOSSYPOL IN COTTONSEED HAS THE POTENTIAL TO SATISFY THE PROTEIN NEEDS OF SEVERAL HUNDRED MILLION PEOPLE

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Institutions: [1] CI - Cotton Incorporated (Cary, NC, USA)

Abstract:

Many plants utilize chemical defense mechanisms to reduce or eliminate predation. The cotton plant is no exception. Gossypol, a naturally occurring noxious compound found in pigment glands located throughout the cotton plant, is an effective insect deterrent and a cumulative toxin in monogastric animals. The end result is that all the protein produced by the cotton plant is relegated to ruminant feed, primarily dairy and beef cattle. Ruminant species do not utilize protein as efficiently as monogastric or aquaculture species. Elimination of gossypol allows cottonseed protein to be used much more efficiently by using it in food products for direct consumption by humans. The volume of underutilized cotton protein is not trivial. About 10-11 million tons of cottonseed protein are produced worldwide each year.Without gossypol, this is enough protein to satisfy the daily, basic protein needs (50 grams/person) of more than 600 million people for one year. Since the cotton plant is drought and heat tolerant, it is uniquely suited to serve as a source of both food and fiber for an ever increasing world population. Modern plant biotechnology utilizing RNAi and a seed specific promoter has produced a genetically enhanced plant that has gossypol production silenced in the seed while retaining normal levels in all other plant tissues, allowing the plant to retain its natural defense mechanism. This technology has the potential to greatly improve the utilization of this massive protein resource, thus making a substantial contribution to global food security. For many years, cottonseed meal has been used in catfish, trout, and salmon feeds; however, gossypol has prevented its widespread use in these and other aquaculture species. Many locations worldwide have aquaculture operations and cotton production in close proximity. This will facilitate the logistics of using cottonseed protein in aquaculture feeds. Recent research demonstrates 100% replacement of fishmeal in feeds for shrimp, black sea bass, hybrid striped bass, and pompano, without a decrease in performance. It is anticipated that Ultra-Low Gossypol Cottonseed (ULGCS) can be used in the diets of many economically important aquaculture species. This will help allow for the expansion of the aquaculture industry, contributing to improved food security as the standard of living improves around the globe and demand for farmed seafood increases. Also, food scientists have created a wide range of food products from cottonseed, including humus, plant-based dairy substitutes, chopped nuts, a peanut butter alternative, protein fortified beverages, and protein bars. This biotechnology-based proof of concept provides strong evidence that it is now possible to produce a gossypol-free cottonseed in an otherwise “normal” plant resulting in greatly improved utilization of this valuable, massive protein resource for improving global food security, while improving the sustainability of cotton.

Acknowledgments

The authors would like to express their sincere gratitude to all individuals and institutions whose members have been used in this paper. Special thanks goes to KALRO, EPZ, KIPPRA and CABI. This report has been completed with a lot of reference from Fibre Directorate (formerly Cotton Development Authority) reports.

References

Keywords: cottonseed, protein, gossypol, biotechnology

ENGINEERING MULTIPLE TRAITS IN COTTON

Authors: Shahid Mansoor [1], Imran Amin [1], Muhammad Saeed [1], Muhammad Arshad [1], Zahid Mukhtar [1], Shaheen Aftab [1]

Institutions: [1] ABD - Agricultural Biotechnology Division (Agricultural Biotechnology Division)

Abstract:

Cotton is the backbone of economy of Pakistan and contributes significantly to fiber and food security of the country. Cotton suffers from several biotic and abiotic stresses where genetic engineering can play significant role. Our research work is focused on understanding of major biotic and abiotic stresses that limit cotton production and development of gene cassettes for engineering agronomic traits. New cassettes targeting multiple genes of virus and whitefly resistance through RNA interference technology were developed and transformed in tobacco and cotton. Multiple codon optimized genes for control of bollworms and herbicide tolerance have been assembled in a single cassette and their expression optimized and evaluated in model plants and cotton. Abiotic stresses such as heat, drought, flooding and salt stresses are having major impact on cotton production. We have short listed genes for conferring abiotic stress tolerance and some of these genes have been

tested in cotton under glasshouse conditions. Tools for genome editing of cotton are also being optimized to utilize this emerging technology for engineering novel traits in cotton.

Acknowledgments

References

Keywords: Engineering, traits, cotton

ESTIMATION OF GENETIC PARAMETERS IN COTTON CULTIVARS (GOSSYPIUM HIRSUTUM L. & GOSSYPIUM BARBADENSEL.) AND NEW SCALING TEST OF EPISTASIS.

Authors: Gholamhossein Hosseini [1]

Institutions: [1] Iran - Cotton Research Institute of Iran (Iran)

Abstract:

A complete diallel cross of nine cotton genotypes (Gossypium hirsutum L. & Gossypium barbadense L.) viz Delinter, Sindose-80, Omoumi, Bulgare-539, Termez-14, Red leaf (Native species), B-557, Brown fiber and Siokra-324 having diverse genetic origin was conducted over two years to determine the potential for improvement in yield, its components, oil and fiber quality traits by means of genetic analysis, combining ability, heritability and heterotic effects. The detailed studies were based on F1 generations whereas crossed seed in first year were used for F1 generation in the second year. The successful hybrids recognized and distinguished by morphological markers such as flower color, spot position and it's color in petal, fiber color, seed linter, leaf color and it's shape. Analysis of variance for Simple Square Lattice Design (SSLD) showed more significant diversity ($P \leq 0.01$) among various traits and significant differences allowed genetic analysis by Hayman, Hayman-Jinks and Griffing,s method. Additive- dominance model was adequate for majority of the traits and partially adequate for some traits. Along with the releavent method for Epistasis effects testing of additive-dominance model by means of significant correlation between Wr and Vr also is presented for first time in this study. Majority of the traits were influenced by non-additive gene action in F1 generation. These results are encouraging for practical improvement through combination and hybrid breeding programs and for remaining which exhibited additive gene action through selection method. Significant variation for genotypic general combining ability (GCA) effects, specific combining ability (SCA) effects and high narrow sense heritability ($P \leq 0.05$) was identified for traits studied indicating potential for improvement through selection on the other hand over-dominance gene action, low and moderate rate of narrow-sense heritability for some traits, it is suggesting that improvements should be made utilizing a combination and hybrid breeding approach.

Acknowledgments

References

Keywords: Cotton, Hybrid, Genetics

EVALUATION OF THE YIELD POTENTIAL AND AGRONOMIC CHARACTERISTICS OF VARIOUS COTTON GENOTYPES IN ZAMBIA

Authors: Martin Lubinda Simasiku [2]

Institutions: [2] CDT - Cotton Development Trust (P.O BOX 670057,Magoye,Mazabuka,Zambia)

Abstract:

Abstract Cotton breeders use various approaches to develop improved cultivars. Selection breeding, among other breeding tools, is used to improve the genetic potential of cotton for agronomic and fibre quality characteristics. Multi environment trials assist breeders in selecting stable cultivars. The cotton breeding program in Zambia seeks to maintain the already existing cultivars in addition to developing novel cultivars to meet the needs of the farmers, ginners and other stakeholders. Zambia has three commercially released cultivars. It however, has fifteen elite genotypes under the progeny yield trials, fifteen under the preliminary yield trials, and twelve in national cultivar trials. All the genotypes in the trials have the potential to produce yields that compete with the already released cultivars. The objectives of this study were to assess the potential yields of various genotypes and to compare the performance of unreleased lines with conventionally bred commercial cultivars. The genotypes selected for their favourable agronomic traits were evaluated in randomized complete block trial designs during 2014/2015 season at Cotton Development Trust Research Station and other outstations. Some lines such as MCZA20KR and MCkf40 Kr performed relatively better than controls in a number of traits. Results of this study demonstrate that the various advanced lines have potential in effecting agronomic improvements in Zambia's cotton industry.

Acknowledgments

I would like to thank the entire Cotton Development Trust team for their overwhelming support and guidance in my young career as a cotton Breeder. Likewise, I would like to render my appreciation to Dr Greg Constable, the CSIRO fellow from Australia for reviewing my paper and for his mentorship. Lastly,my family.

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Keywords: Cotton Breeding program, Commercially released cultivars, Potential yields of genotypes, Agronomic traits

EVOLUTION OF NIAB-KIRAN, AN EARLY MATURING, HIGH YIELDING, FINE QUALITY FIBER COTTON VARIETY HAVING ENHANCED RESILIENCE AGAINST CLCUD & HEAT UNDER THE CHANGED CLIMATIC SCENARIO.

Authors: Manzoor Hussain [2,2,2,2]

Institutions: [1] NIAB - Nuclear Institute for Agriculture and Biology (P.O.Box # 128 Jhang Road Faisalabad, Pakistan), [2] NIAB, Faisalabad - Manzoor H*., W. Ishauque**, K. R. Khan*, & K. P. Akhtar*** (PBG Division, PP Division, SS Division), [3] NIAB, Faisalabad - Manzoor H (PBG Division cotton group), [4] NIAB, Faisalabad - W. Ishauque (SS Division), [5] NIAB, Faisalabad - K. R. Khan (PBG Division cotton group), [6] NIAB, Faisalabad - K. P. Akhtar (PP Division)

Abstract:

The author discusses the history of development and breeding methodology involved in the innovation of upland cotton (Gossypium hirsutum L.) variety "NIAB-KIRAN" embodying valuable attributes like; early maturing coupled with its high yielding, wider adaptation potential, lodging resistant, fine quality fiber values as well as enhanced resilience against the prevailing biotic (Burewala strain of CLCuD) and abiotic (high temperature) stresses. The invention also relates to comprehension means involved in assessing its responses against cotton leaf curl virus disease (CLCuD) under the field conditions for the years 2006-2010 at NIAB, using the disease severity index (SI), highly tolerant responses against heat over the years of its seasonal adaptation, higher root shoot length values after its 30 DAS and superior fiber values in comparison with commercial standards. This multi-adversity-resistant (MAR) type cotton variety, possessing harmonious combination of traits was developed at Nuclear Institute of Agriculture and Biology (NIAB), Faisalabad, Pakistan, as part of efforts in accomplishing the ongoing directed breeding objectives of rational importance in the country. The promising mutant line (M-9811) resulting from the irradiation of F0 seed (Cross of Mutant-98 x NIAB-11/CE) at 300 Gy, was consecutively evaluated from 2006 to 2013 in station yield trials and for two years its requisite evaluation in national adaptability yield trials during the years i.e. 2010-11 & 2011-12. This full seasoned cultivar has the ability for bolls retention on early nodes (i.e. 7-8th node), enhanced yielding ability with significantly higher (54 %) seed cotton yield over the commercial standard MNH-786 in national adaptability yield trials during the years 2010-11 and 2011-12. This variety also showed the enhanced lint potential (2400 Kg ha-1; Gin turn out; 40.9 %) and fine quality fiber traits including; length (30.41 mm), fineness (4.4 µg/inch), strength (33.4 g/tex), uniformity index (82.4 %) and maturity (81.1%). Moreover it illustrated lower value for short fiber index (7.9 %) in comparison with other commercial cultivars likes; MNH-886 (11.0), Torzan (10.1) & IR-3701(10.5) depicting its tendency for making higher counts yarn. This released cotton variety for its commercial cultivation during the 2013, also showed resilience against various climatic adversities and will help in sustaining of the cotton production in the country in future environments. Moreover it will prove of an immense value as genetic resource for creating wealth of genetic variability to cope with the emerging issues of changing climate.

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Keywords: Evolution, Early maturing, high yielding, fine fiber, CLCuD and heat stresses

GENETIC ANALYSIS OF YIELDS AND QUALITY CHARACTERISTICS IN INTERSPECIFIC COTTON POPULATION (GOSSYPIUM HIRSUTUM L. X GOSSYPIUM BARBADENSE L.)

Authors: Mehmet ÇOBAN [1], Aydin ÜNAY [2], Hakan ÇIFCI [4], Birnur ILHAN [3]

Institutions: [1] CRI Nazilli - Cotton Research Institute (Cotton Research Institute Nazilli Turkey), [2] ADU University - Adnan Menderes University Department of Crop Science (Aydin), [3] TAGEM - General Directorate of Agricultural Research and Policies (Ankara), [4] SBRI - Sheep Breeding Research Institute (Bandirma)

Abstract:

This study was carried out to determine gene action for yield and yield contributing traits on cotton in one selected interspecific crosses, involving two parents (Gossypium hirsutum L. and Gossypium barbadense L.), including their F1, F2 and back crosses generations. The significant scaling tests (one or more scales in A, B and C) and joint scaling test indicated the presence of epistasis for all the studied traits. Complex genetic behavior was observed in all traits. Since the segregating generations did not follow a simple

inheritance, high selection pressure is expected in later generations due to probable successful exploitation of additive and dominance components. While the additive-additive gene effects was found significant for fiber fineness, additive, additive-dominance and dominance-dominance gene effect were found significant for fiber strength. All gene effects were found significant for fiber length. From these observations it is suggested that the selection for the improvement of all traits, particularly yield per plant with desired fiber characteristics, should be delayed to the later generations of segregating population in these populations. Presence of complementary gene action and prevalence of the high magnitude of non-additive gene effects were found in most of the traits, indicating that heterosis breeding is more effective with high potential in cotton.

Acknowledgments

This study was carried out at Cotton Research Institute Nazilli between 2012 to 2014.

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Keywords: Gene Action, Yields, Fiber Quality, Generation Mean, Scaling test

GENETIC DIVERSITY OF COTTON (GOSSYPIUM HIRSUTUM L.) GENOTYPES FOR YIELD AND QUALITY ATTRIBUTES AND RESPONSE TO CLCV DISEASE

Authors: kalim Ullah khan [1]

Institutions: [1] PCCC - pakistan central cotton committee (PCCC, old shuja Abad Road Multan, Pakistan)

Abstract:

Twenty five cotton genotypes were planted at the Cotton Research Station D.I.Khan, Pakistan during the crop season 2012 and 2013 and were evaluated for genetic diversity regarding various traits viz., plant height, number of bolls plant-1, boll weight, seed cotton yield, ginning out turn, fiber length, strength, micronaire value and infestation of cotton leaf curl virus. Significant genotypic variation was observed for all the studied traits showing a considerable variation among the genotypes. The genotypic variation for all the studied traits was bit smaller than phenotypic variation indicating that the traits were slightly influenced by environment. High heritability estimates was also recorded for the studied attributes. The correlation analysis indicated that there were significant negative correlations between CLCV and number of bolls plant-1, boll weight and seed cotton yield. Whereas number of bolls and boll weight has significant positive association with seed cotton yield. Based on the Euclidian dissimilarity distance, cluster analysis separated the cotton genotypes into five different clusters.

Acknowledgments

Pakistan central cotton committee (PCCC) is highly acknowledged for the financial support of the study

References

Keywords: heritability, genetic diversity, correlation, yield, CLCV

GENETIC INFLUENCE OF ROOT TRAITS OF COTTON (GOSSYPIUM HIRSUTUM L.) ON MOISTURE STRESS TOLERANCE

Authors: Maruti Laddi [1], Basanagouda Janagoudar [1], Ishwarappa Katageri [1], Basavaraj Khadi [1]

Institutions: [1] UASD - University of Agricultural Sciences, Dharwad, Karnataka, Ind (Krishinagar Dharwad 580005 Karnataka India)

Abstract:

In the present study, response of 30 cotton genotypes to water stress were examined in rainout shelter at Agricultural Research Station, Dharwad. Root traits play a major role in water stress tolerance under terminal water stress. Many studies (Basal et al., 2005 and Khalid Iqbal et al., 2010) suggested that increase in tap root of cotton plant permits to survive under stress. Thus, primary and secondary root length, root number, root volume, thickness, dry weight and root: shoot ratio were examined in 30 cotton genotypes at 75 days after planting (15 days after water stress induction) during 2012-13. Study indicated that genotypes RDT 17, CPD 14 - 5 and CPD 14 - 1 recorded significantly longer primary root length (45.9 cm, 44.2 cm and 42.6 cm) respectively than checks Sahana (38.7 cm), Bikaneri Narma (40.0 cm) and MCU 5 (34.9 cm) under water stress condition. Interestingly, they also recorded significantly longer primary root length even in normal conditions. Parameshwarappa et al. (2012) reported that the water stress tolerant genotypes recorded higher root volume than other genotypes in water stress condition. Therefore they may be considered as suitable genetic resource under water stress resistance breeding. In contrast G. cot - 16, RHC 0811, HLS 321729, EC 560392 and CPD 464 showed drastic reduction for these parameters under water stress conditions. Higher broad sense heritability coupled with high genetic advance over mean were observed for secondary root number, thickness and dry weight. They are potential traits for genetic improvement through pedigree breeding method of selection under water stress. Significant positive associations between root traits imparting moisture stress resistance have been reported in several studies (Rezaeieh et al., 2004 and Basal et al., 2005).Thus, any one of such traits can be used as water stress tolerance selection indices in resistance breeding owing to the absence of undesired relationships among these traits.

Acknowledgments

Authors are acknowledged to University of Agricultural Sciences, Dharwad for funding this research.

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Keywords: Water Stress, Root Architecture, Selection Indices, Cotton

GENETIC IMPROVEMENT OF EXTRA-LONG FIBER VARIETIES IN PERU

Authors: Juan Luis Lazo Álvarez [1]

Institutions: [1] AOVA Peru - Asociación de Obtentores de Variedades de Algodón del Perú (Peru)

Abstract:

The production and harvested area of cotton has been declining at an average rate of 1.5% and 5.3%, respectively, in the last 10 years. We must point out that this is mainly due to the loss of productive potential, earliness, fiber quality and lower prices of raw cotton of traditional varieties, with respect to new extra-long fiber cultivars (Pima IPA 59 and Hazera). Raw cotton yields in the period 2001-2009 presented a range of 2,300-3,082 kilos of raw cotton/ ha. In recent years (2010-2013), despite the reduction of the area, a range of 2,852 was observed at more than 4,600 kilos of raw cotton/ha. In this yield increase the variety Pima-IPA-59 has contributed with harvested areas of 3,000 to 5,000 hectares in the last 5 years, along with a higher price of raw cotton at farm gate (3.37 to 3.80 soles per kilo), with respect to lower prices of traditional varieties (2.50 to 2.g83 soles per kilo) which is having a favorable impact on the increased profitability for small farmers. The Peruvian Cotton Institute, created in 1998 as an initiative of representatives of the cotton-textile chain and based on the diagnosis carried out by Peruvian and foreign experts regarding crop difficulties, initiated a genetic improvement program in order to increase the competitiveness of Peruvian cotton fiber; which, after 12 years of research, obtained the first variety of extra-long Peruvian fiber adapted to the different climate and soil conditions of all coastal cotton valleys. The Pima IPA 59 variety (*Gossypium barbadense L.*), has a genetic origin of intra-specific hybridization between a native progenitor Tangüis (LMG-1-72) and an introduced progenitor from Arizona, USA (Pima Line- 8810) and the subsequent selection of lines with recombinant characteristics of both progenitors: resilience, tolerance to drought, pathogens and parasites of the root (Tanguis) and high incidence of earliness, fiber quality and increased growth determinism (Pima Line). The agronomic characteristics of the variety Pima IPA 59 with respect to the traditional varieties are: average resilience, smaller plant with the possibility of mechanical harvesting (1.0 to 1.3 m), greater precocity (5.5 to 6.5 months), high yield (3.680 to 5.980 kilos per hectare), high quality of fiber and yarn (length:. 35.0 to 37.0 mm, strength: 39.0 to 42.0 g / tex, micronaire 3.8 to 4.2, color: bright white, yarn strength: 21.0 to 23.0 rkm). Currently we are continuing with the genetic improvement of cotton, with new IPA lines in a state of advanced experimentation with the following characteristics: Raw cotton yield from 4.094 to 6.210 kilos/ ha and fiber from 1.516 to 2.258 kilos/ ha, fiber quality: length: 36.0 to 41.0 mm, strength: 39.0 to 45 g/ tex, micronaire 3.6 to 4.2 ug/ cm, yarn strength: 21 to 23 rkm, growth cycle: 155 to 170 days and lower plant size: 90 to 110 cm.

Acknowledgments

Comité Directivo del Instituto Peruano del Algodón Instituto Nacional de Investigación Agraria (INIA) Empresa Algodonera S.A. FILASUR S.A. Empresa Algodonera Peruana S.A.

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Keywords: extra-long fiber, varieties, barbadense, improvement

IDENTIFICATION OF DONOR PARENTS CONTAINING FAVOURABLE ALLELES FOR IMPROVING TARGET AMERICAN COTTON HYBRID (NA 1325 × L 604)

Authors: CHENGA REDDY VENDHOTI [1,1,1,1]

Institutions: [1] RARS, Lam, - Acharya N G Ranga Agricultural University (Guntur-522034,Andhra Pradesh, India)

Abstract:

Cotton (Gossypium spp.) popularly called as "White Gold" is a major fibre crop of global importance. India is the largest cotton growing country with an area of 12.65 million hectares and production of 40.0 million bales of cotton (AICCIP, Annual Report, 2014-15). The widespread use of high speed spinning technology in the textile mills has increased the demand for raw cotton fibre with higher strength and length. Hence, cotton fibre productivity and quality must be improved to remain competitive with synthetic fibres and to meet the needs of new spinning and weaving methods (Kohel,

1999).The present cotton fibre quality and quantity requirement changing scenario is limiting the period of cultivation of cotton hybrids. Therefore, they have to be replaced by new hybrids that will exceed the existing ones in their yield performance along with textile mills required fibre qualities with resistance to biotic and abiotic stresses. Ultimately, one of the objectives in cotton hybrid breeding is to improve different traits in the already existing hybrid(s) as well as to improve agronomic traits of parental component without negative effects on lint yield of elite single cross(s). One of the methods of the development of new hybrids is the improvement of existing hybrids, i.e. the improvement of one or both parental lines of the elite hybrid (Dudley, 1984a and Dudley et al., 1996). Hence, the present study was conducted during kharif, 2013, kharif, 2014 and kharif, 2015 at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh, India. The aim of the present investigation was to evaluate four American cotton genotypes and to determine which have the greatest relative values of favourable alleles for the improvement of number of bolls plant-1, boll weight (g), 2.5 % span length (mm), bundle strength (g/tex), seed cotton yield plant-1 (g) and lint yield plant-1(g) in the elite single cross cotton hybrid (NA 1325 × L 604). Based on the estimates of µG' values the genotype SURABHI may be used as source of favourable alleles for improving elite hybrid with respect to quality traits like bundle strength (µG'=1.830*) and 2.5 % span length (µG'=1.325*). This improvement may be possible by transferring favourable alleles from SURABHI to NA 1325 through back crossing as it has high genetic affinity with NA 1325. For number of bolls plant-1 RAH 1004 (µG'=3.230*) and HYPS 152 (µG'=0.302*) for boll weight and both the donors for seed cotton yield plant-1 (µG' RAH 1004 =13.915*and µG' HYPS 152=23.972*) may be used as donors as they recorded significant and positive & µG' estimates.

Acknowledgments

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Keywords: American cotton, elite hybrid, donor parents, seed cotton yield, favourable alleles

IDENTIFICATION OF NEW SOURCES OF RESISTANCE TO COTTON LEAF CURL DISEASE AND ITS INTROGRESSION IN AMERICAN COTTON

Authors: Dharminder Pathak, Shashi Bala, Pankaj Rathore, Parvinder S Sekhon,Kuldeep Singh [1]

Institutions: [1] PAU - Punjab Agricultural University (Department of Plant Breeding and Genetics, PAU Ludhiana, India), [2] PAU - Punjab Agricultural University (Department of Plant Breeding and Genetics, PAU Ludhiana, India), [3] PAU - Regional Research Station (PAU Regional Research Station, Faridkot, India), [4] PAU - Punjab Agricultural University (Department of Plant Pathology, PAU Ludhiana, India), [5] PAU - Punjab Agricultural University (School of Agricultural Biotechnology, PAU Ludhiana, India)

Abstract:

Cotton leaf curl disease (CLCuD) is the major biotic stress threatening American cotton cultivation in the North Western Indian cotton growing states of Punjab, Haryana and Rajasthan as well as Pakistan. The disease causes heavy losses in cotton yield especially if it appears at early stages of crop growth. The causal virus complex is transmitted through whitefly. Among various approaches to combat this menace, incorporation of genetic resistance is the most viable approach. Many Upland cotton cultivars resistant to CLCuD such as LHH 144, F 1861 etc. have been developed through intra-hirsutum crosses and commercialized by Punjab Agricultural University, Ludhiana. However, due to the continuous appearance of recombinant virus strains, all the extant American cotton cultivars as well as established CLCuD resistant stocks of American cotton have become susceptible. Therefore, identification and use of new sources of CLCuD resistance has become a very important research activity. In this context, G. armourianum (DD), a related non-progenitor wild cotton species and a synthetic amphiploid (A2D1) derived from G. arboreum and G. thurberi cross were evaluated for their reaction to CLCuD. Both of these stocks were observed to be free from disease under natural conditions. For artificial screening, whiteflies were initially allowed to suck the sap of CLCuD infected American cotton plants for 24 hours. Then, the viruliferous whiteflies were collected from the diseased plants and were allowed to feed on the plants of synthetic tetraploid and G. armourianum Acc. PAU 1. No symptoms of CLCuD on these stocks were observed throughout the crop season, whereas susceptible variety F 846 manifested severe symptoms of the disease such as vein thickening, curling of the leaves, leaf enation etc. Total genomic DNA from the diseased American cotton plants (positive control), synthetic tetraploid and G. armourianum was isolated. Virus specific primer was used to amplify the viral DNA from the samples. Virus specific bands were observed both in the positive control and the synthetic but not in G. armourianum. Results indicate that the synthetic tetraploid is a symptomless carrier/tolerant, whereas, G. armourianum is resistant to CLCuD. An interspecific hybrid between G. hirsutum cv. F 1861 x G. armourianum was developed. It was observed to be symptomless carrier like the synthetic amphiploid. Crosses between synthetic amphidiploid (as the female parent) and natural allotetraploid G. hirsutum cv. PIL 43 as the pollen parent were attempted. A total of 3158 flowers were pollinated and 28 mature crossed bolls containing 25 F1 seeds were obtained. These F1 hybrids are yet to be evaluated for their reaction to CLCuD. Very useful germplasm have been generated which will help in the development of American cotton varieties resistant/ tolerant to CLCuD.

Acknowledgments

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References

Keywords: Wide hybridization, alien introgression, virus resistance

IMPROVING FOR SUSTAINABLE COTTON PRODUCTION THROUGH ENHANCED RESILIENCE TO CLIMATE CHANGE WITH REFERENCE TO PAKISTAN.

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Abstract:

Cotton has a special significance and plays an important role in the economies of Asia and the Pacific region countries. This leading fiber crop is grown on 20.5 million hectares in three major cotton producing countries i.e. China, India and Pakistan, with their annual contribution in total world cotton production of about 60-65 %. The huge yield gap exist amongst the top three cotton producing countries of the region and being further aggravated due to changing climate conditions i.e. higher temperature and unprecedented rainfalls. The year to year variability in the climatic conditions is adversely affecting the per hectare yield which in turns reduces the development of cotton based industries in the region. Pakistan is amongst one of the most affected countries by climate change, as far as agriculture and cotton productions are concerned. During the cotton growing season 2013-14, the disastrous effects of extreme period of heat stress were prominent in Pakistan due to early termination of crop with 40-50 % fruit abortion. Most recently short fall of about 33.5 % to cotton production in Pakistan up to 15th January, 2016 have been reported due to poor resilience of main grown cotton varieties against changing climatic scenario. Sensitivity of commercial cotton varieties against extreme periods of heat stress coupled with enhanced requirements for inputs like water and fertilizer, poor seed germination are considered as major factors/causes of erratic trend of cotton production. Seeing the impact of global warming and effects of unexpected periodic episodes of extreme heat stress on cotton production, it is the need of time to evolve cotton varieties that can sustain under the changing climatic scenario. Using the approach of induced mutation breeding, NIAB Faisalabad, Pakistan has demonstrated its capabilities in developing cotton germplasm which can withstand to the changing climatic conditions of heat stress. The results of cotton lines showed enhanced resilience against high temperatures, under the field conditions with their significant variations in their rooting length after days of sowing (i.e. 30, 60, 90,120 and 150); other morphological and physiological traits were also studied. For the survival of cotton based industries and associated economic benefits to producers, the results of identified cotton germplasm that can sustain yield under changing climatic conditions will be shared to bridge the big yield gaps.

Acknowledgments

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Keywords: Sustainable, Enhanced resilience, Climate change, Cotton Production, Yield gaps/hac

INCORPORATING HIGH-THROUGHPUT PHENOTYPING INTO BREEDING PROGRAMS: THE GOOD, THE BAD, AND THE UGLY

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Abstract:

High-Throughput Phenotyping (HTP) is quickly becoming a highly desired technique for rapid trait measurements of plants in field and greenhouse settings. With changing sensor technologies, the capabilities of HTP increase each year, opening many opportunities for incorporation into different research programs. One area of research that could greatly benefit from the application of HTP is plant breeding programs, but how best to incorporate this technol-

ogy is unclear. In 2009 a HTP tractor was developed at the US Arid Land Agricultural Research Center in collaboration with the University of Arizona, Maricopa Agricultural Center both in Maricopa Arizona, United States. The HTP tractor, using proximal electronic sensors, measures canopy height, plant canopy temperature, and multi-spectral reflectance to calculate normalized difference vegetative index (NDVI). Since 2012 the tractor has been used to evaluate Upland cotton for heat and water stress tolerance as part of a national breeders testing network funded by Cotton Incorporated and the United State Department of Agriculture. Briefly, 35 cotton breeder lines and checks were planted in 2-row, 12-meter long plots, spaced 1-meter apart. Well-watered and water-limited treatments were applied when 50% of the lines were at first flower and continued until harvest. The objectives of this research were to evaluate tractor based HTP in a breeding program and compare proximal sensing measurements with data from handheld devices. The tractor-based HTP system recorded canopy height, canopy temperature, and NDVI once per week at solar noon. Canopy height and canopy temperature measurements were validated in 2015 using a Fluke handheld infrared thermometer (IRT) and Mobile barcode scanning system (American Barcode). The IRT data was analyzed using a custom-developed processing pipeline. Comparative analyses indicate that tractor-based IRT measurements were best correlated with handheld IRT measurements when the plant width fully covered the planting bed. Three cotton breeder lines were identified as potentially drought tolerant and two will undergo further evaluation. Challenges identified with incorporating tractor-based HTP into a breeding program include tractor logistics and engineering, field design, data processing and management, data validation, and determining the best statistical approaches to analyze large quantities of data.

Acknowledgments

We would like to thank Don Jones at Cotton Incorporated for continued funding of this project, and Ted Wallace for organizing the Regional Breeders Testing Network.

References

Keywords: High-Throughput Phenotyping, Canopy Temperature, Upland cotton

INTROGRESSION BREEDING TO ADDRESS PROBLEMS OF BT.COTTON-INDIAN PERSPECTIVES.

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Abstract:

The Bt technology did its job as an inbuilt pesticide which gave appropriate and timely control against the bollworm thus helping the hybrid achieve its potential. It seemed like a panacea for all the cotton ills which centered around one major pest. The entire cotton world gravitated towards Bt and today we are staring at dangerous times. The productivity increase from 300 kg/ha in the pre-Bt era to 474 kg/ha after its release has largely been attributed only to the Bt technology which is partly wrong. It was also due to farmers shifting to cotton from other crops and irrigation facilities improving. Effective pesticides which came in much before the introduction of Bt cotton were also a major reason. Since 2005, national yields have not risen phenomenally. If Bt were not to be the reason for surging yields then, it certainly is not the only cause for the near stagnant yields seen now which is enough proof that the Bt technology alone is not responsible for the warning bells now. Natural selection had to happen, resistance had to surface and it did, leading to the 'back-to-square-one' situation. Adoption of Bt cotton in sub-optimal conditions and fly-by-night seed operators selling second generation and spurious seed have all led to lower yields. Warning signs have emerged recently in Southern and Central India where Bollgard II, has shown signs of strain under Pink bollworm attack. Another big reason, however, has been the unprecedented resurgence of sucking pests. Some pests like the Mirid bug and Midge emerged anew, causing havoc. Similarly in Northern India problems of White fly and leaf curl have become impediment in production.The gullible Indian farmer always does his best to raise a good crop and he does not understand the science of resistance mechanisms and new pests. The gene technology should have come in with greater social responsibility attached. As for new directions, alternate technologies are needed. Sucking pests now occur throughout the crop cycle making morphological modification of the plant leaf a sure method to sustain tolerance for long. Introgression breeding with Marker Assisted Selection can withstand the pressures of evolution for a longer time. Diploid cultivated cotton traits can thus be introgressed. Abiotic stress tolerant genes are to be introduced with care taken to avoid yield penalty. Only a few successful hybrids today have narrowed down the genetic base exposing allBt cotton to fresh dangers. Another sensible approach would be high density planting of cotton varieties reinforced with the Bt gene cultivated using a continually evolving package of practices, monitored on real time basis. New models incorporating all the interacting factors are to be built and incorporated into predictive software to be used for timely field interventions. Pragmatic use of pesticides coupled with good per-se hybrids, can help sustain satisfactory yields. Notwithstanding the above arguments, the 'Live-and-let-live' principle has to be respected, especially in the evolutionary background. There is a greater need today to find a middle-ground where all components can co-exist.

Acknowledgments

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Keywords: Introgression breeding, Bt.Cotton Hybrid/variety, Genetic Erosion , Sucking Pests, Pink Bollworm

AN OVERWIEW OF COTTON LEAF CURL VIRUS DISEASE IN PAKISTAN; PAST, PRESENT AND FUTURE

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Abstract:

Cotton Leaf Curl virus (CLCuV) disease is a grave disorder of cotton and several other malvaceous plants and is caused by a whitefly (Bemesia tabaci Genn.) transmitted monopartite begomovirus (family Geminiviredae) associated with helper satellites. Infected cotton plants display a range of symptoms including vein thickening, leaf curling, stunting and development of enations on the underside of leaves. Before 1988, CLCuD was not a serious threat to cotton cultivation in Pakistan. In 1988, something changed and this previously insignificant disease became epidemic during 1992-93 which resulted in the withdrawal of high yielding but susceptible hirsutum cultivars. Conventional breeding approaches during the 1990s yielded varieties with excellent resistance to the 'Multan' strain of CLCuD. Widespread cultivation of these resistant varieties across Pakistan returned CLCuD to obscurity. But the inheritance of resistance against CLCuD, whether it is controlled by dominant or recessive genes which may be monogenic or polygenic and nature of these resistance genes and their precise mechanism of action, is still obscure. Despite almost 14 years of effort, since the appearance of the 'Burewala' strain of CLCuD, conventional breeding has not been fully successful in yielding resistance to the disease (Farooq et al., 2011). However, some promising lines with good tolerance have been developed (Rahman & Zafar, 2007). Tolerant lines are a problem as well since they still support virus replication and systemic spread and may thus act as reservoirs for virus transmission. For geminiviruses, numerous pathogen-derived and non-pathogen-derived approaches to achieve resistance in planta have been investigated. Specifically, for CLCuD associated viruses, studies have investigated RNA silencing-mediated resistance. In addition to breeding for disease tolerance against CLCuD, other conventional approaches including controlling the vector, eradication of alternative hosts and various agronomic approaches have proven useful. Evidently globalization of agriculture will increasingly lead to the spread of viral diseases. There are numerous proven examples, just for geminiviruses. All cotton growing areas have environmental conditions conducive for the proliferation of the disease and whitefly. For example African CLCuD-associated begomovirus, CLCuGeV, has been identified in cotton in southern Pakistan (Tahir et al., 2011). Although not a significant problem currently but introduction of a genetically distinct virus is worrying in an area that already is affected by a large diversity of begomoviruses. Far more worrying is the recent outbreak of CLCuD in southern China (Cai et al., 2010), geographically far remote from the affected areas of Pakistan and India. The sequence evidence for the CLCuD outbreak in China indicates that it is the 'Multan' strain that has been introduced. Previous experience teaches us that instead of single mechanism of action, 'stacked' multiple resistances based upon distinct mechanisms of action is desirable (Ilyas et al., 2011). Thus, for example, reinforce the best natural resistance with an RNAi-based transgenic resistance construct and/or one based on the non-pathogen-derived approach. Also strict control over the movement of agricultural products and live ornamental plants that can potentially harbor the viruses and satellites as well as adaption of best management and cultural practices will be helpful to curb the menace.

Acknowledgments

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Keywords: Gossypium hirsutum L., Cotton Leaf Curl Disease, Begomoviruses, Whitefly, Resistance management

PAKISTAN AND UNITED STATES PARTNERSHIP PROJECT TO IDENTIFY GENETIC RESISTANCE TO COTTON LEAF CURL VIRUS AND DEVELOP RESISTANT COTTON FOR FARMERS

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Abstract:

Cotton leaf curl virus (CLCuV) is a devastating disease endemic to Pakistan. CLCuV has the potential to decrease cotton yields by 20 - 40% and is most devastating to small farmers who do not have the resources to tolerate such decreases in yield. The virus was first reported in Africa and has spread to Pakistan where it has more than 60 known hosts. The virus is also causing yield losses in India, has been found in China and has the potential to spread globally. Although CLCuV has not yet been detected in the U.S., the United States Department of Agriculture has listed the disease as one of the top 20 threats to U.S. agriculture. Through a partnership program, U.S. researchers are collaborating with Pakistani

scientists to identify genetic resistance to CLCuV and transfer it to cotton lines adapted to the growing conditions in each country. Here we describe the identification of multiple sources of resistance through multi-year disease screening programs in Pakistan, and the development of resistant cotton lines. The project as a model for multi-national proactive breeding programs is also highlighted. The program not only helps Pakistan mitigate the effects of an endemic virus, but also allows the U.S. to proactively develop CLCuV resistant cotton for U.S. growers and be prepared should the virus become a problem in the U.S.

Acknowledgments

References

Keywords: cotton, cotton leaf curl virus, germplasm, virus resistance, breeding

PERFORMANCE OF COTTON GENOTYPES UNDER DIVERSE AGRO-ECOLOGIES OF UGANDA

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Abstract:

In the cotton production value chain, the farmers require that cotton varieties developed should be high yielding while the ginners require varieties that produce good fibre qualities. Also the modern spinning technologies demand larger volumes of lint coupled with long fibre length that meet the international markets. The objective of the study was to improve cotton varieties with yield potential and good fibre traits so as to contribute significantly to increased and stable yield performance in diverse agro-ecologies of Uganda. Sixteen cotton genotypes were evaluated in two year cycles of 2013/2014 and 2014/2015 in three different agro-ecological zones of Arua (northwest Nile), Lira (northern) and Serere (eastern), and these constitute the major cotton growing areas in Uganda. Parameters considered were boll weight, lint index, seed weight, ginning out turn (% GOT), fibre traits (micronaire, fibre length and fibre strength) and seed cotton yield. Additive main effects and multiplicative interaction (AMMI) and genotype main effects and genotype by environment interaction (GGE) biplots software were performed to determine stability of cotton genotypes for seed cotton yield in different environments, and this is important for breeders when selecting genotypes for wide adaptation. Analysis of variance revealed significant differences among genotype performances for all the traits with exception of % GOT. Some genotypes showed good fibre traits and high seed cotton yield across sites in the two year cycles. In terms of boll weight, lint index, seed weight, fibre length, fibre strength, %GOT and micronaire, it showed that genotypes MS(13)MO.1, MS(13)MO.2, EZAMMAR(13)MO.1, BPAN(13)MO.3, BHGTAMH(O2)1 and BTAM(13)MO.2 had good performance for all the traits assessed compared to the rest of the genotypes. The mean seed cotton yield of the genotypes across sites and years ranged from 1422kg/ha to 1883kg/ha with eight genotypes including the check (BPA2002), attaining yield above the overall mean of 1729kg/ha. Five genotypes BTAM(13)MO.2 (1883kg/ha), MS(13)MO.1 (1838kg/ha), EZAMMAR(13)MO.1 (1839kg/ha), BTAM(13)MO.3 (1824kg/ha) and BHG(13)MO.2 (1818kg) had higher seed cotton yield than the check (177kg/ha). Using AMMI model, the genotype and environment effects revealed significant differences for the seed cotton yield. The Genotype by environment interactions was significant, indicating that there is genetic variability among cotton genotypes for seed yield in the changing environments. The relationships observed among test locations using GGE biplot analysis, revealed that there were three mega-environments: two main ones were represented by three locations and two locations while the minor one was represented by one location. This is an indication that classifying genotypes into mega-environments implies higher heritability and faster progress for plant breeders and higher yields for growers. AMMI analysis revealed six stable genotypes and included BPA2002, BHG(13)MO.2, BTAM(13)MO.3, EZAMMAR(13)MO.1, BPAN(13)MO.2 and BPAN(02)14 which contributed to relatively lowest genotype x environment interaction. However, genotype MS(13)MO.1 though high yielding was unstable thus requiring specific selection in the environment it performed well. Generally, these results showed that genotypes with above average means of seed cotton yield, good fibre traits and stability could be selected for national performance trials before release by national variety release committee.

Acknowledgments

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Keywords: AMM1, fibre traits, GGE, seed cotton yield, stability

ROLE OF IRRADIATION AND MATING SCHEMES IN ENHANCEMENT OF VARIABILITY FOR PRODUCTIVITY AND FIBRE QUALITY TRAITS IN ASIAN COTTON

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Abstract:

Among Asian cotton varieties, Jayadhar occupies a unique position in Karnataka a south Indian state due to its inherent ability to resist major pest and diseases, high ginning outturn and wider adaptability under rainfed situation, but on the contrary this variety has low yield potential and small bolls with short to medium staple fiber length. In order to improve the seed cotton yield and fibre length of Jayadhar variety an attempt was made to generate variability, selected donor parents were crossed with adapted variety. The F1 seeds of four crosses and parental seeds of Jayadhar were irradiated with 50GY gamma rays and further three double crosses were made using four single crosses in different cross combinations. The variability generated in four single cross F2s and their F2M2s, three double cross F2s and M2 has been studied and the results obtained have been summarized based on variability and association parameters. The variability, nature of association and percentage of superior segregants was compared between single cross F2, F2M2 ,double cross F2 and M2 progenies and high variance values was observed in F2M2 progenies of (Jayadhar X 9749) for boll number and seed cotton yield and DC1-F2 and F2M2 progenies of (Jayadhar X DLSA-17) for halo length.The cross (Jayadhar X 9749) X (Jayadhar X MDL-2582) exhibited higher PCV and GCV estimates for number of bolls per plant and seed cotton yield per plant, F2M2 progenies four crosses expressed higher PCV values for halo length except (Jayadhar X MDL-2582) while double cross involving this single cross i.e. (Jayadhar X 9749) X (Jayadhar X MDL-2582) performed on par with that of F2M2 progenies. All double cross F2 progenies recorded higher estimates of heritability for number of bolls per plant and seed cotton yield per plant except for seed cotton yield per plant in DC3 F2 progenies. The association of seed cotton yield and its components was compared between 12 different progenies which revealed that F2M2 and double cross F2 progenies exhibited significant association between seed cotton yield and boll weight while remaining M2 and F2 progenies exhibited non-significant association except F2 progenies of Jaydhar x DLSA-17. Out of 12 progenies only two progenies i.e. F2 progenies of (Jayadhar X 9749) and F2M2 progenies of (Jayadhar X DLSA-17) exhibited significant association between seed cotton yield and halo length traits and only one i.e. DC3 F2 progenies for boll weight had significant association with boll number. The best performing superior segregants for halo length were isolated from F2M2 progenies, whereas for seed cotton yield double cross F2 produced superior progenies.The irradiation of hybrid seeds with gamma rays is more practical approach to enhance favorable association and to isolate superior segregants than double crosses. The evaluation of advance generation progenies for enhancement of productivity and fibre quality traits derived from irradiation and mating schemes has led to identification of superior progenies.

Acknowledgments

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Keywords: ASIAN COTTON, IRRADIATION, MATING SCHEMES, PRODCTIVITY, FIBRE QUALITY

SCREEN OF US COTTON GERMPLASM FOR COMPLETION WITH AFRICAN COTTON GERMPLASM TO ENSURE SUCCESS

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Abstract:

Cotton (Gossypium spp.) is the world's leading textile fiber and a highly profitable cash crop. The SSR markers are considered as an ideal a user friendly tool once they are conducted through PCR, genetically defined, typically co-dominant, uniformly dispersed in the plant genome. The objective of this study was to screen US cotton germplasm for completion with African cotton germplasm using microsatellite markers. Twenty six cultivars belong to Texas Tech University and Institute for Agrarian Research of Mozambique were accessed. From a total of 27 microsatellite (SSR) markers, nineteen markers revealed 65 polymorphic SSR alleles. On the study of 26 north American and African cultivars and inbredlines, the model-based Bayesian clustering analysis using both Structure and InStruct programs as well as Principal Coordinates and Neighbor Joining Tree revealed two distinct genetic clusters. The FST index indicated very great genetic variability among the 26 North American and African cultivars and inbreedlines. In general, the North American cultivars and inbredlines were the most dissimilar in relation to African cultivars. The dissimilarity index ranged from 0.05 to 0.90 and the lowest genetic dissimilarity was observe between SCM 3-7-3 x SCM 3-4-4 and Albar SZ 9314 x Albar FQ 902.

The most dissimilar cultivars were Raider 276 x STAM 42, Acala 1517-99 x ISA-208, Acala 1517-99 x AFIS B FM 958 330, TTU 202 x TTU 0774 and Raider 276 x ISA-208, therefore, this combination can be recommended in order to increase a variability within Texas Tech University cotton germplasm.

Acknowledgments

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References

Keywords: Upland cotton (Gossypium hirsutum), , microsatellite markers, population's structure, germplasm

SIMULTANEOUS IMPROVEMENT OF COTTON FIBER AND SEED

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Abstract:

Historically, cotton breeding programs have primarily focused on improving the quantity and quality of cotton fiber. Due to the added value of cottonseed and its many uses, including a feed and human food source, there is interest in developing cotton breeding programs that focus improvement efforts simultaneously on cotton fiber and seed. Genetic analysis of cottonseed traits such as protein and oil is a prerequisite to building new joint fiber and seed cotton breeding programs. In this study, our objective was to conduct a genetic analysis of a diverse set of elite upland cotton germplasm for cottonseed protein and oil. Environment was responsible for a large portion of the total variation for protein and oil, and genetics accounted for a larger portion of variation for oil than protein. Genotype × environment interactions were significant for oil. We identified a strong, negative relationship between protein and oil. Positive relationships were found for protein and several agronomic traits including lint yield; whereas negative relationships were found between oil and lint yield along with other agronomic traits. Overall, results showed very little association between protein, oil, and fiber quality traits.

Acknowledgments

References

Keywords: breeding, fiber quality, cottonseed

SOURCES OF RESISTANCE TO RAMULARIA AREOLA AND DEVELOPMENT OF A RESISTANT COTTON CULTIVAR

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Abstract:

Ramularia leaf spot (RLS), caused by Ramularia areola causes economic losses due to intense defoliation in Brazil (Suassuna and Coutinho, 2014). To prevent foliar damages, several fungicide sprays are required. In order to develop resistant cotton cultivars it is necessary identify resistant germplasm to RLS. A collection of 350 accessions of Gossypium hisrsutum originating from different origins was screened over eight seasons (from 2003/04 to 2010/11) in field tests for resistance to R. areola. Field trials were carried out in augmented block design. Plots consisted of two 5 m rows, each one containing about 50 plants. The disease severity was recorded at ages varing 62 to 86 days after plant emergence, with a severity grade, ranging from 1 (no symptoms) to 5 (highly susceptible). Fiber was harvested from each treatment and cotton raw data and disease severity were recorded. A mixed model approach was used considering the season effect as fixed and the genotype and genotype x crop effects as random. The block effect within season (B/S) was considered either as fixed or as random. According to AIC and BIC criteria, B/S as fixed had the best fit, however, herdability estimates (0.19) had similar value when B/S was analised as random (0.17). A significant Pearson correlation (0.98) was detected between BLUPs obtained from each analysis (B/S as fixed or random). From 20 most resistant accessions, or 20 most susceptible, when B/S was analised as fixed, there were coincidente selection of 17 and 16 accessions, respectively, when grouped using B/S as a random effect. There was a significant season effect, indicating environmental influences on onset and development of RLS. Accession "C 3" was the most resistant to RLS using both analysis (B/S as fixed or random effect), and had BLUP estimate differing from zero (t test). It was not identified any imune accession. Incomplete resistance was identified in some accessions: "C 3", "Tamcot CAB CS", "SA 1014", "BRS Buriti", "CNPA ITA 96", "CNPA GO 2002-4771", "Plains" and "IAC 25". The most susceptible accessions were "Delta Opal", "CUBQ", "IAPAR 96-1734", "Lambright GL-5", "DPL 50", "CNPA 97-88" and "CNPA 96-39". In another effort, crosses were made using the more resistant accessions identified every year to generate segregating populations for plant selection. Every selected plant had its progeny tested in subsequent season. In 2006/2007 season it was selected a plant (CNPA GO 2007–423) without false mildew symptons. In a progeny test carried out in 2007/2008 season, a imune response to RLS was recorded. During the subsequent seasons, CNPA GO 2007–423 was evaluated in a complete randomized blocks experiments with four replications, at one site in 2008/2009, eight sites in 2009/2010, and twenty sites in 2010/2011 season. Resistance to foliar diseases, including RLS, and higher lint production were recorded. Averaged across the 20 field performance trials in 2010/2011, CNPA GO 2007–423 presented 7.6% more lint yield than control cultivar FMT 701. Due to superior performance and RLS resistance, CNPA GO 2007-423 was launched as a cotton cultivar in 2014, named BRS 372.

Acknowledgments

The authors gratefully acknowledge EMBRAPA and FIALGO for the partial financial support.

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Keywords: Gossypium hirsutum L, Tropical disease, Genetic resistance

GENETICS AND GENOMICS – ICGI 2016 BIENNIAL CONFERENCE

ASPECTS OF COTTON GERMPLASM MAINTENANCE AND EVALUATION BY EMBRAPA

Authors: Lucia Hoffmann [1], Gildo Pereira Araujo [1], Francisco Pereira Andrade [1], Paulo Barroso [1], Raysa Marques Cardoso [2,1], Kalita Cristina Cardoso [3,1], Francisco das Chagas Vidal Neto [1], João Luis Silva Filho [1]

Institutions: [1] Embrapa - Embrapa (Rodovia GO-462, Km 12, CEP: 75375 Santo Antonio de Goiás, Goias, Brazil), [2] UFG - Universidade Federal de Goias (Campus Samambaia - CEP 74690-900 Goiânia - Goiás - Brazil.), [3] PUC Goias - Pontifícia Universidade Católica de Goiás (Avenida Engler, s/n - Jardim Mareliza, Goiás - GO, 74885-460)

Abstract:

Embrapa collects, maintains and evaluates native and naturalized cotton from Brazil. The collection is formed by around 350 genotypes of mocó cotton (Gossypium hirsutum var. marie galante), 300 of Gossypium mustelinum and 700 of Gossypium barbadense. The quality of cotton fiber is available for 110 genotypes of mocó cotton and 397 genotypes of G. barbadense, measured by nine fiber quality parameters in HVI (High Volume Instruments). The fiber length of twenty-six G. barbadense and four mocó genotypes was superior to 32 mm, but it was not so long among the ten genotypes of herbaceous cotton (G. hirsutum L. var latifolium) used for comparison. Five herbaceous, 271 G. barbadenses (68%) and 75 mocós (68%) genotypes presented strength above 33 g/tex. One mocó collected in Roraima in 2004 (RR0407) and twelve G. barbadenses were classified simultaneously with fiber length above 32 mm and resistance above 30 g/tex. The highest values of the two indices were from one G. barbadense collected in Piaui in 2004 (PI0404), and two collected in Ceará in 2004 (CE0422 and CE0468). Count Strength Product, CSP, was superior to 2760 for 225 barbadenses (56%), seven herbaceous (70%) and 56 mocó cottons (51%). Some new populations of G. mustelinum have been localized in coastal region of the states of Paraiba (municipalities of Lucena and Pitimbu) and Pernambuco (Goiana, Sirinhem and Itamaracá) in 2011. Another G. mustelinum population was known in the municipality of Caicó, Rio Grande do Norte state, and composed by only eleven adult plants as related by expeditions in 2003 and 2005. These plants have no longer been found in an expedition in 2015, but plants obtained from its seeds are maintained ex situ.

Acknowledgments

To CNPq for the Institutional Scientific Initiation Scholarship (PIBIC)

References

Keywords: native, fiber , population, mocó

ASYMMETRIC SUBGENOMIC EVOLUTION AND DOMESTICATION OF ALLOTETRAPLOID COTTON (GOSSYPIUM HIRSUTUM L.)

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Institutions: [1] NJAU - Nanjing Agricultural University (1 Weigang, Nanjing, Jiangsu, China), [2] UT at Austin - The University of Texas at Austin (USA), [3] Clemson University - Clemson University (USA), [4] USDA ARS - USDA ARS MSA Genomics Laboratory (USA), [5] Texas A&M University - Texas A&M University (USA)

Abstract:

Upland cotton is a model for polyploid crop domestication and transgenic improvement. Here we sequenced the allotetraploid Gossypium hirsutum L. acc. TM-1 genome by integrating whole-genome shotgun reads, bacterial artificial chromosome (BAC)-end sequences and ultra-dense inter-specific genetics genetic map. By comparing the A and D subgenomes, we revealed the asymmetric subgenomic evolution and domestication of allotetraploid cotton. More common structural rearrangements were characterized in the A subgenome than in the D subgenome. The A subgenome have evolved faster than the D subgenome and the rich transposable elements make nearly twice the size difference between the subgenomes. Consistent with asymmetric structural rearrangement and evolved rate, there were significantly more genes lost and disrupted in the A sugenome than in the D subgenome. On the contrary, the centromeric retro-element sequence of tetraploid cotton derived from the D subgenome progenitor have invade the A subgenome centromeres after allotetrapolyploid formation. Although no genome-wide expression dominace was found between the subgenomes, gene expression bias for homoeologous gene pairs is widespread, frequently 20-40% range, depending on the tissue. The asymmetric domestication is associated with positively selected genes for fiber yield and quality in the A subgenome and for stress tolerance in the D subgenome. Our studies provide valu-

able genomic resource for cotton research and benefit the understanding of the basis of many other allopolyploids in which two or more subgenomes retain sufficient divergence.

Acknowledgments

We thank Xiaoya Chen, Elizabeth Dennis, Danny J. Llewellyn, Daniel G. Peterson, Peggy Thaxton, Don C. Jones and Baoliang Zhou for their valuable criticisms and suggestion to this study.

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Zhang TZ†, Hu Y†, Jiang WK†, Fang L†, Guan XY†, Chen JD†, Zhang JB, Saski C, Scheffler BE, et al., Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology 2015, 33: : 531-537 Wang S†, Chen J†, Zhang W, Hu Y, Chang L, Fang L, Wan Q, Wang Q, Liang W, Mei G, Pan M, Chen S, Cai C, Zhu X, Zhou B, Guo W*, Zhang T*. Structure variations and evolution of allopolyploidy cotton genomes. Genome Biology 2015, 16:108.

Keywords: Allotetraploid cotton, Genome, Asymmetry, Evolution

COMPARATIVE HIGH-DENSITY INTRASPECIFIC LINKAGE MAPPING USING THREE ELITE POPULATIONS FROM COMMON PARENTS

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Abstract:

High-density linkage maps are fundamental to contemporary organismal research and scientific approaches to genetic improvement, especially in paleopolyploids with exceptionally complex genomes, e.g., Upland cotton (Gossypium hirsutum L., 2n=52). Using 3 full-sib intra-specific mapping populations from the cultivars 'Phytogen 72' (PHY72) and 'Stoneville 474' (STV474), including 93 F2s and reciprocal RILs (132 and 104), we developed 3 independent single nucleotide polymorphism (SNP) maps, plus a 4th consensus map or joinmap. The CottonSNP63K array and cluster file provided 7,417 genotyped SNP markers. The F2 population averaged 49.4% heterozygous loci, whereas the recombinant inbred line (RIL) populations averaged 1.51% and 1.92% heterozygous loci. The linkage groups LG12 and LG26 corresponding to homeologous chromosomes 12 and 26 had the highest percentages of heterozygous loci in F2 (0.525 and 0.542) and RIL populations (0.030-0.037 and 0.024-0.021). Using similar cut-offs/thresholds for grouping and linkage between two SNP markers, 7,030 SNPs were mapped in the F2 PHY72 x STV474 (93 individuals) population; 7,059 SNPs were mapped in the RIL PHY72 x STV474 (132 lines) population; and 6,320 SNPs were mapped in the RIL STV474 x PHY72 (104 lines) population. In all populations, these SNPs were assimilated into 26 linkage groups corresponding to the 26 cotton chromosomes. The percentage of similar or common SNPs among the populations ranged from 96 % to 99 %. The high-density genetic joinmap of the Upland allotetraploid comprised 3,824 SNP bins (7,244 SNP markers) and covered 3,537 centiMorgans (cM) (At- subgenome 1,783 bins and Dt-subgenome 2,041 bins) with an average SNP interval between two linked markers of 1.0 cM. Recombination frequencies were similar in the two subgenomes. Lengths of LGs ranged from 87.6 (LG04 F2 population) to 239.3 (LG05 RIL population) cM. The new maps were highly collinear with the previous published F2 maps. Additional analyses are ongoing with available Gossypium genome assemblies to provide further knowledge of chromosome arrangement, recombination frequencies, parental relationships, and gene order. This is the first high-density SNP genetic linkage joinmap developed for G. hirsutum with a core of reproducible Mendelian SNP markers assayed on different intraspecific populations from crosses involving the same parents.

Acknowledgments

References

Keywords: RIL mapping, Recombination, SNP, Array

COMPLETE CHLOROPLAST GENOME SEQUENCES OF THREE D GENOME COTTON SPECIES AND THEIR EVOLUTIONARY IMPLICATIONS

Authors: FARSHID TALAT [1,2], KUNBO WANG [2]

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Abstract:

Chloroplast research have significant advantage of genomics and genome sequencing, and a new picture is emerging of how the chloroplast functions and communicates with other cellular compartments. To further our understanding of this important crop, the chloroplast genome of three Gossypium species were determined in this study. The complete chloroplast genome sequences belong to three diploid species were determined and annotated. Bioinformatic analyses showed that, the chloroplast genomes of Gossypium were highly conserved. The whole genome size ranged between 159,945 bp (G. laxum; D9), 159,973 bp (G. turneri; D10) and 160,122 bp (G. shwendimanii; D11). Differences in the chloroplast genome size of Gossypium were mainly attributed to the length variations of IGS. Four genes viz. infA, ycf68, ORF42 and ORF56, in addition to earlier mentioned genes, were confirmed to be existed in studied genomes. SSRs totally varied from 62 to 64, and the average rate was 0.36 SSRs/kb between the 3 genomes. The predominant mononucleotide repeats were A or T, which accounted for 94.85% to 97.28% of the mononucleotide repeats among the 3 genomes with a definition mononucleotide & #8805;8 bp. This study revealed that wide ranges of expansions and contractions of IR are very common evolutionary events among 14 Gossypium species

which were compared in our research. The phylogenetic analyses based on 50 protein coding genes for 41 angiosperms and four gymnosperm out groups (Cycas, Ginkgo, Pinus and Gnetum) were performed. Our phylogeny tree continued to strongly support that Theobroma cacao as the closest species to Gossypium inside eudicots. Phylogenetic trees with bootstrap values (BS) were built for fourteen Gossypium species.

Acknowledgments

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Keywords: Gossypium , Chloroplast genome, Sequencing, Inverted repeats, Phylogeny

COTTON DNA METHYLATION AND ITS ANALYSIS UNDER THE SALT-DRAUGHT STRESSES

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Abstract:

DNA methylation, an important component offepigenetics induced usually by adversity, plays a vital role in the response to various stresses including drought and salt. A methylation-sensitive amplification polymorphism method based on capillary electrophoresis was used to explore the epigenetic mechanisms of salt tolerance and heterosis in Upland cotton (Gossypium hirsutum L.), and the results indicated that hypermethylation and demethylation could be an important mechanism to resist the stresses. And the demethylation could be the mechanism to explain heterosis in cotton hybrid. The results of whole genome methylation sequencing showed high DNA methylation density usually occurs in promoter regions and transposons areas. Methylated cytosines in different sequence contexts (CG, CHG and CHH) have different functions and methylation levels. And the results also showed methylated cytosines in asymmetric CHH sequence context are dynamic, being mostly related to stresses. Combined with transcriptome data, we found long non-coding RNAs (lncRNAs) may involve in the regulation of DNA methylation in response to drought stress. All these results could provide theoretical reference value for the mechanism research of tolerance in cotton.

Acknowledgments

References

Keywords: cotton, methylation, stress, draught, salinity

COTTONGEN: CURRENT FUNCTIONALITY AND FUTURE DIRECTION

Authors: Jing Yu [1], Sook Jung [1], Chun-Huai Cheng [1], Taein Lee [1], Ping Zheng [1], Stephen Ficklin [1], Todd Campbell [2], Richard Percy [3], Don Jones [4], Dorrie Main [1]

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Abstract:

CottonGen (www.cottongen.org) is a curated and integrated web-based relational database providing access to publicly available genomic, genetic and breeding resources for cotton research discovery and crop improvement. CottonGen contains annotated whole genome sequences, transcripts, markers, trait loci, genetic maps, genes, taxonomy, germplasm, publications and communication resources for the cotton community. In this update we report on new functionality and data including the addition of RNASeq and GBS data viewable through implementation of the JBrowse genome viewer, synteny analysis viewable in GBrowse-Syn, new metabolic pathways available through Pathway Tools, as well as new genome, trait, map and marker data, and new or improved search tools.

Acknowledgments

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References

Keywords: genomics, genetics, breeding, database

List of Oral Presentations Abstracts

DEVELOPMENT OF A GENOME-WIDE 90K SNP ARRAY ON ALLOPOLYPLOID UPLAND COTTON

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Abstract:

NGS technologies enable researchers to rapidly develop large numbers of SNP markers. High-throughput genotyping platforms play important roles in gene cloning, QTL, and GWAS analysis. We have developed the genome-wide CottonSNP90K, an Illumina Infinium array containing assays for 90K intraspecific single nucleotide polymorphism (SNP) markers from sequencing of allotetraploid cotton G. hirsutum acc. TM-1 and re-sequencing of 500+ different cultivars in G. hirsutum with 5× coverage on average. Totally, intraspecific 1,372,195 putative SNPs (MAF>10%) were detected for inclusion on the array. Subsequent filtering steps included the following: genotype accuracy (>99.12%); SNP in repeat regions filtered; no other SNPs or InDels in 50 bp flanking the SNP site; heterozygosity rates <15%; SNPs cluster analysis. After this filter, 175,192 SNPs remained and were submitted through the Illumina Design Tool to determine assay design scores for each marker. The SNP data set was filtered to retain only Infinium II assays for one-bead-type SNPs (A/G, A/C, T/G, T/C). As a result, SNPs in gene region with Illumina design scores >0.7, and SNPs in intergenic region with Illumina design scores > 0.9 were remained. Further, at least intermarker distance flanking SNPs is >2600bp. Altogether, 90K SNP markers were selected for manufacture by Illumina. The final set comprises 14,582 markers with 12,114 genes and a SNP per 23.8Kb in TM-1 genome. The CottonSNP90K array will be used efficiently in high-density genetic mapping, genome-wide association studies (GWAS), genomic selection(GS), complex trait dissection, seed purity and reality identification, molecular breeding by design in cotton.

Acknowledgments

References

Keywords: CottonSNP90K array , upland cotton, SNP markers, High-throughput genotyping platforms

EXPRESSION STUDIES OF TRANSCRIPTION FACTORS UNDER MOISTURE STRESS IN COTTON (GOSSYPIUM HIRSUTUM L.)

Authors: VAMADEVAIAH HIREMATH [1], SAGAR YADAV [1], ISHWARAPPA KATAGERI [1], BASAVARAJ KHADI [1]

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Abstract:

In the last decade, molecular and biochemical studies have been identified many of these ABA and stress responsive genes and transcription factors responsible for their induction in model plants as well as crop plants (Kim and Kim, 2009; Li et al., 2009; Abdeen et al., 2010, Padmalata et al 2012). These genes are the major components of gene regulatory network involved in drought tolerance. Drought tolerance is a genetically complex plant adaptation trait that involves multiple genes and pathways. Many plant genes are regulated in response to abiotic stresses such as drought, high salinity, heat and cold, and their gene products function in stress response and tolerance. The whole process of plant adaptation to these environmental stresses is controlled by orchestration of complex molecular networks. In the present study, the relative quantitation approach was used to measure the expression levels of 6 TF genes in well watered and water stressed leaf tissues of G.hirsutum 27 varieties to know the distribution of these TFs in different genotypes at Agricultural Research Station, Dharwad farm, University of Agricultural Sciences, Dharwad during 2013-14. Six transcription factor genes viz., WRKY 19, LIM, NAC, GeBP, WRKY 70 and C2H2, showing significant difference of expression on exposure to artificial moisture stress in cotton, were selected. The moisture stress was induced by withholding water from 45 DAS. Expression analysis of transcription factor genes in 27 cotton genotypes was done quantitatively using qRT-PCR. The relative expression profiles of all the six TF genes revealed that, all the TF genes were significantly up-regulated in genotypes 5433 A2 A03 N83 (G16) and PH 1009 (G12), which are known to be drought tolerant from the survey of report of the AICCIP, indicating these TF genes have relevance to drought tolerance in these genotypes.

Acknowledgments

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Keywords: Moisture stress, Transcriptome, qPCR, G.Hirsutum cotton, cotton

FUNCTIONAL GENOMICS ANALYSIS OF A COTTON N-END RULE PROTEIN (GHCBD2) PUTATIVELY INVOLVED IN VIRAL RESISTANCE IN GOSSYPIUM HIRSUTUM

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Abstract:

Cotton blue disease (CBD) is a major cotton disease in Brazil. It is transmitted by Aphis gossypii and its causal agent is the Cotton leaf roll dwarf virus (CLRDV). CBD resistance is controlled by one single dominant locus, however nothing is known about it. Previously, we mapped the Cbd resistance locus in Gossypium hirsutum chromosome 10, identifying two ORFs, Cbd1 and Cbd2. Phylogenetic analysis revealed that CBD2 is an arginyl tRNA transferase (ATE) implicated in the N-end rule leading target proteins to the 26S proteasome. Expression analysis of GhCBD2 in a resistant (Delta Opal) and susceptible (FM966) cotton vs during CLRDV infection showed a strong suppression of GhCBD2 after 24 hpi in susceptible cv although a small reduction was observed in the resistant one. Five dpi, however, the expression was strongly induced in susceptible cultivar (280 x), although it was basal to the resistant cultivar. After 15 and 25 dpi GhCBD2 remained induced in both cultivars. Investigation of similar effects in Arabidopsis thaliana Col. under CLRDV infection showed a strongly increase of AtATE1 after virus infection. Arabidopsis ATE1:GUS plants revealed, an increase GUS activity in shoot and root apical meristems as well in young leaves compared with non-infected leaves. 35S:ATE1 plants blocked viral infectivity. These data shed new lights into CBD genetics resistance. Cbd2 seems to be a good putative candidate for achieve CBD resistance, probably leading virus replication essential host proteins for degradation via N-end rule pathway.

Acknowledgments

Fundings: FAPERJ, CNPq and CAPES

References

Keywords: Gossypium hirsutum, N-end rule, Cotton blue disease, ubiquitination, CBD

GENOME STRUCTURE OF THE GOSSYPIUM GENOME

Authors: Joshua A Udall [1], Thiruvarangan Ramaraj [2], Aaron Sharp [1], Christopher Hanson [1], Carrie Evans [1], Alex Freeman [1], David de Amorim [1], Spencer Hunt [1], Meghan Crosby [1]

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Abstract:

The most recent common ancestor of all cotton ancestors lived between 5 and 10 million years ago. Since that time, eight recognized diploid clades and a single allotetraploid clade have diverged, and yet, maintained extensive genomic structural integrity. This makes cotton an excellent model system for genome evolution. However, the proliferation of transposable elements, as well as the complications inherent to polyploidization, have made it difficult to compare the structure of the D_5-genome (*G. raimondii*) to the D_T-genome of *G. hirsutum* as well as the A_1-genome (*G. herbaceum*) to the A_T-genome of *G. hirsutum*. Here we describe our progress with a genome sequence of *G. arboreum* and the use of BioNano for super-scaffolding its sequencings. We also present genome-wide maps of other cotton species created using BioNano high throughput physical mapping. This technology characterizes very long single molecules, 0.15 to 2.0 Mb, long enough to span most transposable elements and other repetitive units, by labeling restriction endonuclease recognition motifs. Our analyses have revealed regions of significant structural homology and identified putative structural variants within and between the A- and D-genomes.

Acknowledgments

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References

Keywords: Cotton, structural variation, genome evolution, Bionano, physical map

GENOME WIDE SNP MARKER SURVEY FOR THEIR UTILIZATION IN COTTON BREEDING

Authors: ISHWARAPPA KATAGERI [1], Suresh Handi [1], Ramesh Metre [1], VAMADEVAIAH HIREMATH [1], Biradar D.P. [1], Khadi B.M. [1], Reddy Lachagari V.B [2]

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Abstract:

Development of genetic and genomic resources enhance crop improvement. Whole genome sequencing, identification of polymorphic SNP markers and their mapping and identification of QTLs for economically important traits has been initiated in cotton. SNP resources from many studies resulted in development 63 K infinium chip etal (Hulse and Kemp 2015). We report here sequencing of two Indian diploid cotton species with 'A' genome, G. arboreum, DLSa17(A2) and G. Herbaceum,Jayadhar(A1). Comparison of G. arboreum, SXY1 (sequenced by Li etal 2014) and , DLSA revealed 1.86 million SNPs and 14.23 million SNPs with Jaydhar indicating significant divergence of Indian germplasm with that of the Chinese germplasm. Between DLSA and Jayadhar 15.5 million SNPs were recorded. About 9.48 million SNP between DLSa 17 andG. raimondii (sequenced by Patterson etal 2012) and 10.05 million between Jaydhar and raimondii were recorded. We utilized 63K SNP chip for

association genetic analysis in 201 lines of cotton hirsutum germplasm and for linkage mapping using 178 RILs of G. hirsutum X G. barbadense cross.These two populations were characterized in 5 different locations for yield, yield components and fiber quality traits and analyzed with the data. Population structure analysis revealed 12 subgroups and diversity analysis with NJ algorithm showed around 10 subgroups in germplasm. Qin et al (2015) determined two sub populations in 241 cotton collections. About 3.13 percent marker pairs showed significant high LD (R2=1). Mixed linear model (MLM) accounting for population structure and kinship has identified 349 significant marker trait associations for yield, yield component and fiber quality traits. Abdurakhmonov et al (2009), Yin-hua et al (2014), Qin et al (2015) and Zhang et al (2014) in their comparative study of GLM and MLM, they reported that associations detected in MLM were more realistic. A total of 68 markers explained more than 10 % phenotypic variation for various yield, yield contributing and fiber quality traits. By mapping about 2188 polymorphic SNPs between parents using RILs, 12 major QTLs associated with economically important traits were identified. Simultaneous improvement for seed cotton yield and fibre qualities was observed in RILs of interspecific tetraploid cross, For example DHBR 20 recorded 1300 Kg/ha kapas with 24 g/tex fibre strength as against 850 kg of best parent for yield (hirsutum,P1) and on par with best parent for fibre strength (barbadense,P2).

Acknowledgments

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Keywords: Genome sequencing, SNP, Association mapping, Genome mapping, QTLs in Cotton

GENOME-WIDE IDENTIFICATION AND CHARACTERIZATION OF THE HOMEODOMAIN-LEUCINE ZIPPER I FAMILY OF GENES IN COTTON (GOSSYPIUM SPP.)

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Abstract:

Homeodomain-leucine zipper (HD-Zip) transcription factors are unique to the plant kingdom and are classified into four subfamilies, HD-Zip I to IV. This gene family has been extensively investigated in several plant species and many members have been shown to play important roles in plant development and in response to abiotic/biotic stresses. In cotton, several HD-Zip IV genes have been identified and their function investigated, but little is known about the HD-Zip I genes. Here, we performed a genome-wide survey and identified 72, 30 and 34 HD-Zip I genes in G. hirsutum, G. arboreum and G. raimondii, respectively. Almost all G. arboreum and G. raimondii HD-Zip I genes were retained in allotetraploid G. hirsutum, and new HD-Zip I genes were evolved in G. hirsutum after polyploidization, probably through tandem and/or segmental duplication. Most HD-Zip I genes were under purifying selection although some could have experienced positive selection. Small indels and nonreciprocal homoeologous recombination (NRHR) events also played a role in shaping the HD-Zip I genes in G. hirsutum. Most HD-Zip I genes were preferentially expressed in certain tissues. Differential expression of homoeologues was observed but the differences were generally less than that between different genes. Three HD-Zip I genes were found to have a consistent response in G. hirsutum and G. barbadense cultivars resistance to Verticillium dahliae (Vd) following Vd-infection. Our results provided a comprehensive view of the cotton HD-Zip I genes and fundamental information for further research towards understanding the role of HD-Zip I genes in cotton.

Acknowledgments

This study was supported by Cotton Breeding Australia, a joint venture between Cotton Seed Distributors Ltd and CSIRO, and a scholarship awarded to Dr Jian Zhang by the China Scholarship Council.

References

Keywords: HD-Zip I transcription factor, Phylogenetic analysis, Gene conversion, Verticillium dahlia

GENOME-WIDE IN SILICO PREDICTION OF PUTATIVE TRANSCRIPTION FACTOR BINDING SITES (TFBSS) FOR COTTON FIBER STRENGTH

Genome-Wide in Silico Prediction of Putative Transcription Factor Binding Sites (TFBSs) for Cotton Fiber Strength

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Institutions: [1] UAS - Department of Molecular Biology and Agricultural Biotechnolo (Raichur, India), [2] UAS - Department of Genetics and Plant Breeding (Raichur, India), [3] IIMR - Department of Biotechnology (Hyderabad, India)

Abstract:

Transcription factors are the early responsive genes which up on receiving stimulus from both biotic and abiotic stress lead to expression of various kind of proteins which can cope up with stress. Furthermore, the expression of genes takes place only when specific transcription factor (TF) binds to 6 to 15 nucleotide region present in upstream of corresponding gene called as transcription factor binding site (TFBSs). In present study, insilico based approach was used to predict the putative TFBSs and their TF responsible for fiber strength in G.barbadense. The data pertaining to differential expression of genes corresponding to fiber strength was retrieved from NCBI GEO database and used for predicting putative TFBSs. A total of 70 significantly up regulated and down regulated ESTs were retrieved and assembled to 5 contigs. The contigs were functional annoted to know its exact role. The upstream sequence of contigs were retrieved from G.raimondii genome. The upstream sequences were then used to find the promoter region. Based on probability of accuracy, estimated using NNPP software, 4 contigs had suitable promoter region in the upstream end. Using position weight matrix (PWM) of experimentally validated TFBSs deposited in JASPAR database was used to predict the TFBS in promoter regions. The newly identified TFBSs were in the range from 6 to 20 nucleotides with multiple binding sites in the promoter region, except for Gucuronosyl transferases gene. Ethylene response factor 1 (ERF1) binds to 6 nucleotide (AGCCGTC) cis- elements of S-adenosylmethionine synthetase present in region starts at -205 and ends -198 has important role in fiber elongation and thickening. With discovery of TFBSs and their TF for fiber strength will lead to better understanding of fiber strength development, which intern may lead to genetic manipulation of TFs and their introgression in G. hirsutum species which could help in achieving high fiber strength in addition to higher yields.

Acknowledgments

References

Keywords: Transcription factor, Fiber strength, Cotton, Expressed sequence tags

GETTING BIOINFORMATICS THROUGH ITS AWKWARD ADOLESCENCE (FEATURING EXAMPLES FROM COTTON RESEARCH)

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Institutions: [1] MS State (USA) - Mississippi State University (Mississippi State, MS 39762, USA), [2] IGBB - Institute for Genomics, Biocomputing & Biotechnology (Mail Stop 9627, Mississippi State, MS 39762, USA)

Abstract:

The field of bioinformatics has been slowed by a number of sociological, historical, and technological factors. Bioinformatics has been limited by use of outdated scripts developed for small machines/clusters, reliance on high-RAM machines for genome assembly and analysis, poor script documentation, the emergence of "closed source" commercial software packages, inadequate long-term investment in biocomputing, loss of bioinformaticians to more profitable fields, and general non-adherence by many bioinformaticians to high performance computing principles. I will discuss these and other issues facing bioinformatics and provide insight into how the field of bioinformatics can be led through its "awkward adolescence" to maturity. When appropriate, examples will be taken from my lab's research on cotton genomes.

Acknowledgments

Cotton genomics, biocomputing, and bioinformatics research in DGP's lab has been funded, in part, through USDA Agricultural Research Service (ARS) Specific Cooperative Agreements 6402-21310-003-18S and 6402-21310-003-20S, and Cotton Incorporated award 13-479.

References

Keywords: bioinformatics, high performance computing, genomics, parallel computing, cotton

HIGH-DENSITY GENETIC MAPS AND THEIR APPLICATION TO GENETIC DISSECTIONS OF YIELD AND FIBER QUALITY TRAITS IN UPLAND COTTON

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Abstract:

Cotton (Gossypium hirsutum L.) is a worldwide grown crop and provides renewable natural fiber resources for the global textile industry and human life. Technological developments in the textile industry and improvement in human living standards have increased the requirement for supplies and better quality of cotton fiber. Upland cotton 0-153 is an elite cultivar harboring strong fiber strength genes. To identify quantitative trait locus (QTL) for fiber quality in 0-153, a population of 196 recombinant inbred lines (RILs) from a cross between 0-153 and sGK9708 was developed. Three methods, SSR marker, CottonSNP63K array and specific locus amplified fragment sequencing (SLAF-seq) were applied to construct high-density genetic maps with the RIL population, named SSR-map, chip-map and SLAF-map respectively. The SSR-map harbored 997 markers with a total genetic distance of 4,110 cM with an average distance of 5.2 cM between adjacent markers. A total of 165 QTLs of fiber quality traits were identified and 47 of them were estimated to be stable which could be detected in at least three environments. Among the stable QTLs, 14 were for fiber length, 8 were for fiber strength, 10

were for fiber elongation, 5 were for fiber uniformity and 10 were for fiber micronaire. The chip-map harbored 2,398 markers including 2,316 SNP markers and 77 SSR ones previously reported by Sun et al based on the same population. It spanned a total distance of 2,856.73 cM with an average marker interval of 1.20 cM. A total of 63 QTLs of fiber strength were identified and 15 of them were estimated to be stable. The SLAF-map harbored 5,521 SNP markers which covered a total distance of 3259.37 cM with an average marker interval of 0.78 cM without gaps larger than 10 cM. A total of 146 QTLs of boll weight were identified and 16 of them were stable ones. Finally, a high-density consensus genetic map was constructed by combining the above markers. The consensus map harbored 8295 markers, spanned a total distance of 5056.96 cM, covering the whole genome of upland cotton, with an average marker interval of 0.86 cM. Based the consensus high density map, the genetic behaviors and the correlation of the fiber quality traits (fiber length, fiber strength, fiber micronaire, fiber elongation, fiber uniformity) and the yield traits (boll weight, lint percentage and seed index) were dissected. Based on these results, further studies including identification of the functioning genes, pyramiding breeding, could be facilitated.

Acknowledgments

References

Keywords: Genetic Maps, Genetic Dissections, Fiber Quality

INTERSPECIFIC RECOMBINATION RATE, SEGREGATION DISTORTION AND HYBRID BREAKDOWN IN COTTON

Authors: Zhongxu Lin [1], Baoshen Dai [1], Yu Yu [1], Xianlong Zhang [1]

Institutions: [1] HZAU - Huazhong Agricultural University (Shizishan 1, Wuhan, China)

Abstract:

Upland cotton and Sea-island cotton are the two tetraploid cultivated cottons with contrasting yield and fiber quality traits. Cotton breeders are trying to introduce elite genes from Sea-island cotton to upland cotton but impeded by segregation distortion and hybrid breakdown. Two SSR-based BC1 genetic linkage maps revealed that the male gamete mainly resulted in a longer genetic distance between markers, and increased the recombination rates; while the female gamete usually resulted in a shorter genetic distance of marker interval, and decreased the recombination rates. A high-density genetic linkage map revealed Chr2, Chr16 and Chr18 were segregation distorted chromosomes; Eight reciprocal backcross populations were developed to detect six SDLs along the chromosome 18 by EM method, male gametic competition, zygotic selection and female gametic selection were the reasons. Two reciprocal F2 populations were developed to study hybrid breakdown in cotton. Hybrid breakdown was found extensively in the two interspecific F2 populations particularly on the reproductive traits because of the infertility and the bare seed. These findings will facilitate the applications of interspecific hybrid heterosis between upland cotton and Sea-island cotton.

Acknowledgments

This work was financially supported by the National Science Foundation of China (No. 31171593)

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Yu Yu, Zhongxu Lin* and Xianlong Zhang. Genome-wide identification of recombination rates of male versus female gametes in inter-specific population of cotton. Pak J Bot, 2012, 44(2): 521-529.

Keywords: Cotton, recombination rate, segregation distortion, hybrid breakdown

INTERSPECIFIC RECOMBINATION RATE, SEGREGATION DISTORTION AND HYBRID BREAKDOWN IN COTTON

Authors: Zhongxu Lin [1], Baoshen Dai [1], Yu Yu [1], Xianlong Zhang [1]

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Keywords: Cotton, recombination rate, segregation distortion, hybrid breakdown

INTROGRESSION OF GOSSYPIUM BARBADENSE ALLELES INTO UPLAND COTTON VIA RANDOM MATING

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Institutions: [1] USDA, ARS - United States Department of Agriculture (810 Hwy 12 E, Mississippi State, MS)

Abstract:

Gossypium barbadense L. has significantly better fiber quality than G. hirsutum L. (Upland cotton). Many attempts have been made over a considerable number of years to introgress fiber quality alleles from G. barbadense into Upland. However, introgression barriers limit these traditional breeding approaches. The use of chromosome substitution lines from G. barbadense (CS-B) as a bridge should provide a more efficient way to introgress alleles from G. barbadense into Upland. We crossed 18 G. barbadense chromosome (or arm) substitution lines to three elite Upland cultivars SG747, PSC355, and FM966, and random mated for 5 cycles beginning with the F1 generation as cycle zero. After 5 cycles of random mating followed by one generation of self pollination we developed the population, RMBUP-C4S1. A random sample of 96 plants in RMBUP-C4S1 was genotyped using 139 SSR specific to the 17 CS-B parental lines. We found 121 of the 139 SSR fragments and 16 of the 17 chromosomes were present in sampled plants. We did assay for any markers specific to CS-B12sh. All 96 C4S1 plants contain at least five G. barbadense chromosome fragments, which indicated a successful introgression of G. barbadense alleles in an excellent Upland cotton background. The study demonstrates that chromosome substitution lines are a valuable genetic bridge pathway for introgression of exotic germplasm of G. barbadense into Upland.

Acknowledgments

References

Keywords: Gossypium barbadense , Gossypium hirsutum, chromosome subsitution , random mated germplasm , cotton breeding

INVOLVEMENT OF WRINKLED-1 TRANSCRIPTION FACTOR IN FIBER DEVELOPMENT OF EXTRA LONG STAPLE (ELS)

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Abstract:

Global transcriptional analysis using microarray or next generation sequencing produce overwhelming amount of data and full utilization of that information is beyond the capacity of a single scientist. We made use of unutilized public microarray raw data produced in cotton fiber development studies and performed meta-analysis using bioinformatics tools in GeneSpring 13.0 -GX (Agilent Technologies). After normalization between experiments, the transcriptome of various varieties of *Gossypium hirsutum* (producing short and long fiber) and *Gossypium barbadense* (producing extra-long fiber) was compared and identified 1431 genes differentially expressed among fibers of different lengths. 574 genes showed upregulation while 844 genes were down regulated in *G. barbadense* as compared to *G. hirsutum*. In order to validate meta-analysis results, expression of 6 genes was studied in local germplasm of *G. barbadense* and *G. hirsutum* along with desi cotton (*G.arboreum*) using RT-real time PCR. The expression of all tested genes validated microarray data. The expression pattern of an ethylene responsive transcription factor *wrinkeled-1* (*wri1*) and a vacuolar processing enzyme (*vpe*) gene completely correspond to fiber lengths in cotton. *Wrinkled-1* is previously reported to be expressed in seed and involved in the seed oil biosynthesis in*Arabidopsis thaliana* [1]. However, present study highlights that *wri1* is expressed in cotton boll and shows significantly higher expression in ELS as compared to *G. hirsutum* and *G. arboreum* during fiber development. Transcription of *wri1* is enhanced in fiber while reduced in seeds during different stages of boll development. As *wri1* shows minimal expression in desi cotton, thus introduction of this gene in desi cotton can lead to improvement in fiber quality trait.

Acknowledgments

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Keywords: Cotton fiber, expression analysis, transcription fator

MAPPING-BY-SEQUENCING OF MAJOR GENES AND QTLS IN TETRAPLOID UPLAND COTTON

Authors: David Fang [1], Gregory Thyssen [1], Md islam [1], Marina Naoumkina [1], HeeJin Kim [1]

Institutions: [1] USDA-ARS - Cotton Fiber Bioscience Research Unit (1100 Robert E Lee Blvd, New Orleans, LA 70124, USA)

Abstract:

The genomic reference sequences available to the cotton community have grown dramatically over the last few years, tracing an arc that many polyploid species can expect to follow. Draft and reference quality genomes for related diploids were released, followed by draft tetraploid genomes. At each step, we employed new strategies to identify candidate genes for the agronomic traits we study. The creation and sequencing of nearly isogenic lines and bulked segregant populations ensures that genetic diversity is largely limited to the regions under phenotypic selection. However, the presence of similar homeologous sequences in polyploid genomes presents an analytic challenge, as does local rearrangements of chromosomes of the studied cultivars relative to the available reference sequences. When suitable sub-genome read sorting and megabase-scale syntenous reference sequences are available for a genetic locus, simple binning of polymorphisms can identify a diverse region that is closely linked to the gene or QTL. We have converted these polymorphisms to genetic markers that facilitated the fine mapping of genetic loci to the kilobase scale, revealing candidate genes. We will present our progress on identification of major cotton fiber property genes and QTLs including short fiber mutants Li1 and Li2, the immature fiber mutant im, and fiber strength QTLs and look forward to the use of a MAGIC population for allele discovery.

Acknowledgments

We thank Dr. Linghe Zeng, Johnie Jenkins, Jack McCarty, and Chris Delhom for their support.

References

Keywords: Fiber Quality, Mapping by sequencing, QTL mapping, Upland cotton

MODIFICATIONS TO A LATE MERISTEM IDENTITY 1-LIKE GENE ARE RESPONSIBLE FOR THE MAJOR LEAF SHAPES OF UPLAND COTTON (GOSSYPIUM HIRSUTUM L.)

Authors: Ryan Andres [1], Daniel Chitwood [2], Marcela Rojas-Pierce [3], Candace Haigler [1], James Holland [4], Don Jones [5], Vasu Kuraparthy [1]

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Abstract:

Leaf shape in tetraploid Upland cotton (< i > Gossypium hirsutum < /i > L.) is an important trait that influences yield, earliness, flowering rate, disease resistance, and the efficacy of foliar chemical application. Developmental aspects of classical leaf shapes of cotton have also been longstanding interest to plant biologists. In Upland cotton predominant leaf shapes normal, sub-okra, okra, and super-okra, with varying levels of lobe severity, are controlled by a multiple allelic series at the D-genome locus < i > L-D1 < /i > . Using positional cloning approach we show that these major leaf shapes of cotton are controlled by the HD-Zip transcription factor < i > Late Meristem Identity1-D1b < /i > (< i > LMI1-D1b < /i >). A 133 bp tandem duplication in the promoter of okra leaf < i > LMI1-D1b < /i > leads to elevated expression while an 8 bp deletion in the third exon of normal leaf < i > LMI1-D1b < /i > causes a frameshift and truncated coding sequence. Virus-induced gene silencing (VIGS) of < i > LMI1-D1b < /i > in an okra variety was sufficient to induce normal leaf formation. An intermediate leaf shape allele, sub-okra, lacks both the promoter duplication and the exonic deletion. Our results indicate that sub-okra is the ancestral leaf shape of tetraploid cotton and “normal” is a mutant heavily selected for in agricultural production. Understanding the genetic mechanism controlling leaf shape could help its proper manipulation to develop a cotton ideotype that maximizes yield while minimizing inputs. This could represent the first reported map based cloning of an agronomic gene in cotton.

Acknowledgments

Our sincere thanks to Cotton Incorporated and NC Cotton Producers Association for supporting this research and all our cooperators at NCSU, Danforth Center and USDA-ARS. Limitations on the total author number in the online abstract submission precluded the inclusion of all the students and post docs who contributed to this research

References

Keywords: cotton, leaf shape, Okra, cloning, genomics

MOLECULAR TAGGING OF QTLS FOR FIBER QUALITY IN COTTON BY USING SNPS

Authors: Khezir Hayat [1,2], Yuksel Bolek [1], Adem Bardak [1]

Institutions: [1] Agricultural Biotech - Kahramanmaras Sutcu Imam University, Faculty of Agriculture (Avsar Campus, 46100 TURKEY), [2] Cytogenetics Section - Central Cotton Research Institute Multan (Old Shujabad Road Multan Pakistan)

Abstract:

Cotton is a crop of immense importance being the main source of fiber all over the world accounting for about 90% of cotton production. With

the development in spinning technology, the improvement of cotton fiber quality is becoming more and more important. Attempts in utilizing deliberate interspecific G. hirsutum and G. barbadense recombination by conventional breeding had a limited impact on cultivar development. The development of molecular markers has made it possible for plant breeders to find a rapid and precise alternative approach for improving cotton lint yield and fiber quality traits. Quantitative trait loci (QTL) mapping of fiber quality traits can be very helpful in revealing the genetic basis of various fiber quality characteristics and providing important information for improving cotton breeding strategies. QTLs conferring fiber quality traits have been identified and mapped using molecular markers in interspecific populations from crosses between G. hirsutum and G. barbadense. SNPs are the most abundant polymorphism type, and have been explored in many crop genomic studies, including rice and maize. Sinlge nucleotide polymorphism markers has been proven very effective, initial efforts to develop single nucleotide polymorphism (SNP) markers were hindered by the co-identification of interlocus SNP variants between the two subgenomes in the tetraploids. The increasing efficiency of next-generation sequencing, improved in silico methods has allowed SNP development at the whole genome level and provide powerful tools for mapping genes of interest for marker-assisted selection in breeding. The main objective of this research is to identify QTL with useful alleles from G. barbadense, which will be helpful in breeding highly productive G. hirsutum cultivars with superior fibre quality.

Acknowledgments

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Keywords: Cotton, Fiber quality, Molecular markers, SNPs, QTL

RECENT DEVELOPMENTS AND APPLICATIONS OF COTTON GENOMIC RESOURCES FOR FIBER IMPROVEMENT

Authors: John Yu [3]

Institutions: [3] USDA-ARS - USDA-ARS (2765 F&B Road, College Station, Texas 77845, United States)

Abstract:

Cotton farmers have experienced a plateau in fiber yield, fiber quality, and other agronomic traits since the late 20th century. Most commercial cotton cultivars lack genetic diversity, making them vulnerable to natural threats. To date, much of the genetic potential of cotton has not been exploited, due to the large and complex genomes of the Gossypium genus. Recent assembly and annotation of the Upland cotton genetic standard TM-1 (AD1), following upon the sequencing of its diploid progenitors (A2 and D5), creates unique opportunities to effectively unlock the genetic potential otherwise buried in all Gossypium species. Decoding the allotetraploid genome (AtDt) and its sub-genomes (At and Dt) provides molecular insights into cotton evolution and genomic resources for fiber improvement. With the possibility of selection for fiber traits discovered in the At sub-genome, the new knowledge and advanced genomic tools will help researchers and breeders develop cotton cultivars with better fiber qualities, higher fiber yields, and more tolerance to biotic and abiotic stresses to meet requirements of the cotton farmers in the 21st century.

Acknowledgments

References

Keywords: Allotetraploid subgenomes, Fiber development, Genetic variation, Upland cotton

RESEQUENCING OF DIPLOID COTTON (G. ARBOREUM) REVEALED THE GENETIC BASIS OF IMPORTANT AGRONOMIC TRAITS

Authors: Xiongming Du [1], Shoupu He [1], Xueyan Zhang [1], Xiongfeng Ma [1], Junling Sun [1], Tao Lin [2], Gaofei Sun [2], Nan Li [2], Zhaoen Yang [1], Yinhua Jia [1]

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Abstract:

Here we report a map of genome variation for Chinese Asia cotton that encompasses the variants of total ~18 million high quality SNPs and ~2 million indels with ~99.69% average genome mapping ratio and ~92.81% genome coverage, generated by deep resequencing of 245 diploid A genome cotton accessions. We found that most of the SNPs were distributed in intergenic regions (~91.5%), only ~1.2% were located in exonic regions, and ~0.7% were non-synonymous SNPs. The complete differentiation SNPs were found among the 12,189 variants with large-effect on coding genes in G. herbaceum and G. arboretum. We performed genome-wide association studies (GWAS) for 15 agronomic traits included 6 categories of morphology, maturity, fiber quality, yield, disease resistance and drought resistance in the population of 215

G. arboreumrac. Sinense. In general, 1,863 significant loci were identified for all traits in different environments, and only 1.9% loci of them were located in exonic regions, most of the strong signals were located at the noncoding regions. By GWAS population and F2 segregation population sequence analysis, the strongest signals of both phenotypes of the leaf hair and the seed fuzz were found to locate at the same location on chromosome 7 in G. Arboretum. We further observed that the SNP and INDEL variations across the genomic regions of these two genes maybe closely associated with the seed fuzz and leaf hair traits in G. arboreum. Comparative analysis based on ~200,000 SNPs suggests that G. arboreum race sinense existed geographical divergence at the genomic level,even thoughG. arboreumrac. sinense underwent narrower bottlenecks during domestication than grain crops. The genome-wide screening of high divergence genomic regions between different pairwise populations indicated the South China was the most germplasm-rich region for G. arboreum race sinense, and the population differentiation among three Asiatic cotton growing area in China were found. Some candidate GWAS loci and previous QTLs mainly related to lint percentage and disease resistance were found to overlap with high divergence genomic regions(Fst > 0.2) in two comparisions of Group-1 vs Group-2 and Group-1 vs Group-3, suggesting the lint percentage and disease resistance are related nature and artificial selection in G. arboreum races inense. A very strong common signal with high divergence regions ranged from ~22.98Mb to ~23.08Mb at chromosome 3 (Ca3)was detected for the disease resistance of Fusarium wilt (FWDI) and Verticillium wilt resistance (VWDI).The strongest signals for FWDI mainly concentrated at the promoter region of a single copy gene encoded Glutathione-S-transferase (GaGST) (Cotton_A_12321) while that of the VWDI at the downstream of GaGST. This implied that the GaGST was a candidate gene for wilt disease of FWDI and VWDI in G. arboreum. We further found the SNPs in this regions showed two typical haplotypes, one type was the possible ancestral allele which mainly existed in disease susceptive genotype in the south China, but it was replaced by another haplotype showed disease tolerance in the Yellow River regions.

Acknowledgments

References

Keywords: G. arboreumrac.Sinense, Cotton, Diploid, SNP, Geographical Divergence

RESPONSE OF WILD RELATIVES OF COTTON AGAINST COTTON LEAF CURL DISEASE

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Abstract:

New resistance breaking strains of begomoviruses viruses are evolving whenever they find suitable and favorable conditions. Due to these resistance breaking strains the resistance sources are becoming susceptible to different cotton diseases. These viruses cause significant loss to cotton as well as to tomato, beans etc. Utilization of wild relative of field crops are one of the method for the development of resistance. Wild species of genus *Gossypium* are rich source of resistance against biotic stresses (diseases, insect-pests) and abiotic stresses like heat, drought, and salinity; besides other valuable breeding traits. These wild relatives are also being used for the development of wide hybrids. One of the largest living herbarium of cotton relatives is being maintained at Central Cotton Research Institute, Multan, Pakistan from four decades. This herbarium is in continuous challenge by begomoviruses in field conditions. There wild species were grafted several times with infected scions of *G. hirsutum* for the induction of diseases and differentiated response is examined. *G. arboreum* has been continuously observed and found to be free of cotton leaf curl disease (CLCuD). Likewise *G. herbaceum* is also free from virus when screened by using diagnostic primers of begomoviruses and Φ29 DNA polymerase. The symptoms of begomovirus were found to be present in *G. thurberii* and *G. aridum* (both species belong to D genome). Interestingly, *G. gossypioides* is among D genome diploid cotton but it showed resistance against CLCuD. The plants of this species were found to be free from symptoms of disease, and cotton leaf curl Multan betasatellites (CLCuMB) were not detected by RCA and Southern hybridization. This species is a valuable resource for developing synthetic tetraploids and for mapping of resistance by developing segregating populations. The betasatellites of the disease were identified in *G. nelsonii*, and *G. bickii* and levels of begomovirus were below the detection limits. The species having AD genome were found to be susceptible to CLCuD due to the presence of both begomovirus and betasatellite. As expected *G. barbadense*, tetraploid species grown commercially in certain parts of the world had higher levels of viral DNA. However, the two wild relatives like *G. anomalum* and *G. somalense* have more viral load and these species were asymptomatic. Two betasatellites i.e. Cotton leaf curl betasatellite, a malvaceous and Chili leaf curl betasatellite, a non-malvaceous betasatellite are associated with these wild relatives of cottons.

Acknowledgments

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and other serious pests in Gossypium species. A review. Indian Society for Cotton Improvement Journal 19, 10-24.

Keywords: Wild species, resistance, susceptible, cotton leaf curl disease

SMALL RNAS FROM NATURAL ANTISENSE TRANSCRIPTS OF GHMIXTAMYB-LIKE3_A12 CAUSES THE NAKED SEED PHENOTYPE IN COTTON N1 MUTANT

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Abstract:

Cotton fiber is a unique plant epidermal cell type derived form cotton seed epidermis. Each of the cottonseed fiber is a single cell organ which facilitates the plant cell fate determination. Therefore, cottonseed fiber is a model system for plant cell differentiation study. The seed fiber patterning may share some similar components such as transcriptional factors in cell fate determination with leaf hair. Given the complexity of cotton genome and physiological feature of seed fibers, we propose a unique regulation machine developed in cotton fiber control. Using a map-based cloning strategy for the first time in tetraploid cotton, we cloned a naked seed mutant gene (N1) encoding a MYBMIXTA-like transcription factor (MML) in chromosome A12, GhMML3_A12, for seed trichome development, revealing a unique transcriptional regulatory network for cotton fiber development different from leaf trichomes. The extremely low expression of GhMML3_A12 in N1 is associated with the natural antisense transcript (NAT) production on the 3' end of gene, driven by its antisense promoter. Therefore, bidirectional transcriptions of GhMML3_A12 form double strand RNAs and generate 21-22nt small RNAs, which, in a fiber-specific manner, mediate GhMML3_A12 mRNA cleavage and result in the production of naked seeds, and further as transNATs inhibit lint fiber development in N1 plants. However, NAT production of GhMML3_A12 in the wild type is greatly suppressed by its CHH methylation at the 3' proximal region, which is associated with the chromatin state alteration. (NATs) are commonly observed in both animal and plant kingdoms, but only a limited number of such genes have been identified as being involved in gene regulation in plants. The present research reports the first observation of gene-mediated NATs and siRNA directly controlling cottonseed fiber development.

Acknowledgments

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Wan Q*, Guan X*, Yang N, Wu H, Pan M, Liu B, Fang L, Yang S, Yan Hu, Ye W, et al., (2016) Small Interfering RNAs from Bidirectional Transcripts of GhMML3_A12 Regulate Cotton Fiber Development, New Phytologist, Accepted

Keywords: Fiber, Naked seed 1(N1), small RNA, Natural antisense transcript (NAT), Epigenetics

SUBGENOME ANCHORED PHYSICAL FRAMEWORKS FOR THE ALLOTETRAPLOID GENOME OF UPLAND COTTON (GOSSYPIUM HIRSUTUM L.) AND AN APPROACH TOWARD REFERENCE-GRADE GENOME ASSEMBLIES FOR COTTON

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Abstract:

The cultivated cotton genome is large and polyploid (~2.5Gb), consisting of two very similar repeat-rich subgenomes, whose size and complexity pose significant challenges for accurate genome reconstruction using whole-genome shotgun approaches. A strategy for accurately partitioning multiple subgenomes of polyploids for contemporary multiplex sequencing can facilitate reference-grade genome quality. A reference-grade genome assembly is the foundation for positional cloning of genes and the acceleration of trait in Upland cotton. We developed high-quality BAC libraries, subgenome specific physical maps, and the development of a new age sequencing approach that will lead to a reference-grade quality genome assembly for Upland cotton (AD1). Three BAC libraries were constructed, fingerprinted, and integrated with BAC-end sequences to produce a de novo whole-genome physical map. The BAC map was partitioned by subgenome through alignment to the D-genome extant relative reference sequence with densely spaced BAC-end sequence anchor points (~179k). The physical map was validated with FISH hybridization and SNP linkage markers derived from BES. Two pairs of homoeologous chromosomes were used to assess multiple sequencing approaches for contiguity and scalability. We report the first subgenome anchored physical maps of Upland cotton, and a new-age approach to whole genome sequencing that will lead to the first reference-grade assembly of cultivated cotton.

Acknowledgments

References

Keywords: DNA Sequence, Genome, BAC fingerprint

TRACING THE GENETIC ARCHITECTURE OF HIGH FIBER QUALITY

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Abstract:

To meet the current and future requirements of processers and users of cotton fiber, there is a great need for high fiber quality. Genetic improvement is one approach used to improve cotton fiber quality as cotton fiber quality properties typically display high heritability. In this study, our aim was to study the genetic variation present in a population derived from multiple sources of high fiber quality. Knowledge of the genetic architecture of improved fiber quality is necessary to effectively design breeding strategies to further improve fiber quality.

Acknowledgments

References

Keywords: fiber quality, breeding, genetics

TRANSCRIPTOME ANALYSIS REVEALS A COMPREHENSIVE INSECT RESISTANCE MECHANISM OF COTTON IN RESPONSE TO INFESTATION BY PHLOEM FEEDING INSECT-WHITEFLY

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Abstract:

The whitefly (Bemisia tabaci) causes tremendous damage to cotton production worldwide. However, very limited information is available about how plants perceive and defend themselves from this destructive pest. In this study, two cotton cultivars exhibited strong resistance (HR) and sensitivity (ZS) to whitefly were compared in transcriptomic difference at different time points (0, 12, 24, and 48 hr after infection) using RNA-seq. Approximately 1,003,930,166 pair-end total reads were obtained by Illumina sequencing technology. Gene ontology and KEGG pathway analysis indicated that many cotton genes involved in responding to whitefly infestation include protein kinases, transcription factors, and genes involved in metabolite synthesis and phytohormone signaling. Further, a weighted gene co-expression network constructed from 16 RNA-seq datasets showed that WRKY40 and copper transport protein are hub genes that may regulate cotton defenses to whitefly infestation. Silencing GhMPK3 by virus-induced gene silencing (VIGS) resulted in suppression of the MPK-WRKY-JA and ET pathways and lead to enhanced whitefly susceptibility, suggesting that the candidate insect resistant genes identified in this RNA-seq analysis were reliable and valuable. Small RNA and their regulatory functions have been extensively characterized in many plant species, but its role in response to biotic stress remains unknown. Eight small RNA and one degradome laboratories of HR and ZR after infestation by whitefly were constructed and sequenced by Illuminum seqfftuencing platform. We indentified 96 conserved and 109 novel miRNAs family, as well as 241 target genes. GO enrichment and KEGG pathway analysis showed that these target genes play important role in cotton response to whitefly infestation. Real-time PCR confirmed the dynamic expression of several miRNAs revealed by RNA-seq in cotton after whitely infestation at different time points. Three target genes were validated by RNA ligase-mediated rapid amplification of 5' cDNA ends. Furthermore, 7 miRNAs precursor were generated by 21 long intergenic non-coding RNA (lincRNA) transcripts. We also performed a genome-wide discovery of phased small interfering RNA (phasiRNA) loci in cotton after infestation by whitefly and identified a total of 122 PHAS loci (21nt). Among these PHAS loci, 49 were from protein-coding genes and 6 miRNA triggers of 8 PHAS gene were detected. These 8 PHAS loci were originated from several miRNA target genes: nucleotide-binding, leucine-rich repeat disease resistance protein (NB-LRR, CC-NBS-LRR), pentatricopeptide repeat superfamily protein (PPR), auxin response factor (ARF) and MYB transcription factors (AP2/B3, MYB 4r), which were distributed in intron, exon-exon and exon-intron junction region. Our data provide new insight into the expression patterns of miRNAs and siRNA in cotton response to biotic stress. Taken together, this study provides comprehensive insights into the cotton defense system to whitefly infestation and identified several candidate genes for control of phloem-feeding pests.

Acknowledgments

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Gao W, Long L, Zhu L-F, Xu L, Zhang X-L. 2013. Molecular & cellular proteomics

Keywords: Cotton, whitefly, RNA-seq, MicroRNA, insect-resisitance gene

UNDERSTANDING COTTON FIBER DEVELOPMENT

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Abstract:

Higher quality fiber equates to a more comfortable textile and better productivity in the spinning mill. So manipulating fiber developmental processes to improve quality is a common target for breeding and biotechnology. We isolated a gene encoding a calcium sensor,GhCaM7, based on its high expression level relative to other GhCaMs in fiber cells at the fast elongation stage. Overexpressing GhCaM7 promotes early fiber elongation, whereas GhCaM7 suppression by RNAi delays fiber initiation and inhibits fiber elongation. GhCaM7overexpression fiber cells show increased ROS levels compared to wildtype, while GhCaM7 RNAi fiber cells have reduced levels. H2O2 enhances Ca2+ influx into the fiber and feedback-regulates the expression of GhCaM7. GhCaM7 can modulate ROS production and can be regarded as a molecular link between Ca2+ and ROS signal pathways in fiber early development. A novel truncated α-expansin, GbEXPATR, was found to be specifically expressed at the fiber elongation stage in Gb. To compare the functions of GbEXPATR and the normal full length form of this gene, GbEXPA2, in fiber elongation, transgenic cotton lines with RNAi and over-expression of these two genes were produced. The cell wall composition and the fiber quality of the transgenic lines were altered with the GbEXPA2 and GbEXPATR expression level changes demonstrating a role for α-expansin in cell wall remodeling. In particular, GbEXPATR, that lacks the carbohydrate binding domain 2, had a strong effect on cell elongation through delaying secondary cell wall synthesis and, as a result, enhanced fiber length, fineness and strength. microRNAs (miRNAs) play important roles in plant development. We constructed seven fiber RNA libraries representing the initiation, elongation and secondary cell wall synthesis stages. A total of 47 conserved miRNAfamilies and seven novel miRNAs were profiled using small RNA sequencing. In addition, 140 targets of 30 conserved miRNAs and 38 targets of five novel miRNAs were identified through degradome sequencing. Histochemical analyses detected the biological activity ofmiRNA156/157 in ovule and fiber development. Suppressing miRNA156/157 function resulted in the reduction of mature fiber length, illustrating that miRNA156/157 plays an essential role in fiber elongation. Ascorbate peroxidase (APX) is an important ROS scavenging enzyme and we found GhAPX1AT/DT encoded one member of the previously unrealized group of cytosolic APXs (cAPXs) which were preferentially expressed during the fibre elongating stage. Suppression of all cAPX (IAO) resulted in a 3.5-fold increase in H2O2 levels in fiber and caused oxidative stress, which significantly suppressed fibre elongation. The fibre length of transgenic lines with over-expression or specific down-regulation of GhAPX1AT/DT did not change obviously. However, fibres of over-expression lines showed higher tolerance to oxidative stress. Differentially expressed genes (DEGs) in 10 DPA fibre of IAO lines identified by RNA-seq were related to redox homeostasis, signaling pathways, stress responses and cell wall synthesis, and the DEGs up-regulated in IAO lines also up-regulated in the 10 DPA and 20 DPA fibre of wild cotton compared to domesticated cotton.

Acknowledgments

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Keywords: Cotton, Fiber development , Ca2+ signaling, ROS, expansin

PRECISION AGRICULTURAL IN COTTON AND COTTON PHYSIOLOGY

BALANCING CANOPY MANAGEMENT USING MEPIQUAT CHLORIDE WITH RECOVERY FROM BIOTIC AND ABIOTIC STRESS IN THE AUSTRALIAN TROPICS.

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Abstract:

Introduction The Australian tropics present biotic and abiotic challenges to cotton production not observed in traditional growing areas. Mepiquat Chloride (MC) is applied as a significant component of canopy management in temperate Australia where cotton is grown as a high yielding high input irrigated crop. The management guidelines for MC in temperate Australia have evolved to ensure balanced vegetative and reproductive growth in a climate where the retention of early fruit is a significant contribution to yield and timely maturity. Cotton grown during the tropical wet or dry season, is exposed to significant biotic and abiotic stresses rarely observed in traditional temperate growing areas. Insects pests are the key biotic constraint and require an integrated approach that includes damage thresholds than minimise pesticide usage and assist in the prevention of resistant pests. Damage thresholds permit full yield compensation with minimal delays to maturity. For dry season production high early season temperatures favour vigorous

growth. This is followed by cold night temperatures during flowering, a key abiotic stress, which can be detrimental to early fruit setting. Yield recovery from cold in is reliant on flowers pollinated late in the dry season when temperatures rise. Similarly for wet season crops extended periods of cloud and rainfall cause shedding of early fruit and compensation also occurs on later developing fruiting sites. Canopy management in the wet and dry growing seasons must achieve a balance between supressing early growth and not inhibiting the production of later fruiting sites for yield compensation following these stresses. Methods Reviewed are 14 machine picked experiments conducted over 8 growing seasons on irrigated cotton grown in the wet and dry season in tropical Australia. The aim was to validate then tailor temperate MC management for compensation from biotic and abiotic stress in the Australian tropics. An important component of the research was to take a participatory approach by including farmers the onset. Results and outcomes: When recovery from biotic or abiotic stress was necessary treatment with MC using management rules based on change in internode length developed in temperate growing areas reduced yield ($p< 0.05$) by up to 26 and 16 % in the wet and dry season respectively. The temperate 'rules' required high rates of MC that prevented compensation from loss of early fruit via additional fruiting sites. Due to irrigation and a long growing season significant yield increases due to the use MC were rare with only four of a total of 88 treatments applied in the 14 experiments. However regular treatment with modest rates of MC (7.6 to 15.2 g ai/ha) significantly reduced plant height and improved operational efficiency (picking and scouting speed) without yield reduction. Crop monitoring systems based on an maintaining an optimum height range for the boll load as the crop developed (node number) using low rates of MC and or other management (e.g. irrigation) were developed and validated with independent data. Educating new growers in the use of MC in these growing conditions was a priority.

Acknowledgments

Australian Cotton Research and Development Corporation Australian Cotton CRC

References

Keywords: Mepiquat Chloride, abiotic, biotic

CAN PACLOBUTRAZOL IMPROVE VIGOUR AND COLD TOLERANCE OF COTTON SEEDLINGS UNDER COOL CONDITIONS?

Authors: Daniel Tan [1], Marc Freeth [1], Michael Bange [2,1]

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Abstract:

Cotton (Gossypium hirsutum) is an economically important fibre crop grown in subtropical and warm temperate climatic zones in Australia. Due to its tropical origin cotton has low tolerance to cold conditions especially during the establishment stages. Any increase in seedling vigour or cold tolerance might benefit cotton management during cool periods. Paclobutrazol (PBZ) is a triazole Plant Growth Regulator (PGR) that inhibits gibberellin and sterol synthesis, hence decreasing shoot growth. Other triazole PGRs have been shown to increase antioxidative enzyme activity associated with reducing chilling injury. The aim of this research is to determine the chilling tolerance of Sicot 74 BRF and the effects of varying concentrations of PBZ on early growth and vigour. Laboratory tests were conducted at the University of Sydney on Sicot 74 BRF (S74) coated with 0, 2, 4, 8, 16 and 64 ml/100 kg PBZ where 50 seeds were placed between wet paper towels rolled up and placed in a controlled-temperature cabinet at 14˚C, 18˚C and 30˚C. Seedling length, shoot and root length and germination percentage were measured on Day 4, 7, 10 for 14˚C and 18˚C and on Day 2, 4 and 10 for 30˚C. Field experiments were conducted at Cobbitty (34˚01'18.46S, 150˚39'47.02"E) and Collie (31˚38'49.66"S, 148˚13'45.76"E) using 0, 2, 4 and 8 mL/100 kg PBZ under cool conditions. No germination was observed at 14˚C. Laboratory tests at 18˚C and 30˚C both showed seedling length decreased logarithmically as PBZ concentration increased ($R^2>0.95$, P

<0.05). The field experiments showed an increase in seedling emergence with the control (0 mL/100 kg) compared with PBZ treatments at 2, 4 and 8 mL/100 kg. Shoot length decreased linearly as PBZ concentration increased in both field sites. The Tuck laboratory test (mean cool-warm seedling length measurement at 18 and 30˚C) was a good predictor of seedling length at Collie after 27 days ($R^2=0.89$, P><0.05). PBZ did not improve cotton S74 vigour or cold tolerance under cool laboratory or field conditions. >Acknowledgments

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Keywords: Cotton, Paclobutrazol, Plant growth regulator, Seed coating, Crop establishment

DEVELOPING MANAGEMENT OPTIONS FOR COTTON GROWN IN VARIABLE SOLAR RADIATION REGIONS: YIELD RECOVERY IN RESPONSE TO REDUCED RADIATION DURING FLOWERING AND CULTIVAR

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Abstract:

Collaborative research in higher rainfall areas of Argentina, tropical Australia where intra-seasonal solar radiation is variable was conducted to investigate cotton growth and in response to periods of low solar radiation. Specifically the objective was to understand cotton growth and recovery in response to reduced radiation at different times during flowering and boll filling of cultivars with both long and short fruiting cycles. Field experiments were located at the Burdekin River (19.4oS) Australia a tropical climate with variable intra-season solar radiation; Reconquista (28.9oS) Argentina a temperate site with variable intra-seasonal solar radiation, and Narrabri (30.2oS) Australia a reference high yielding temperate site with low intra-seasonal variability of solar radiation. A long and a short fruiting cycle cultivar were compared under shading treatments of 30 and 60% radiation reduction imposed for 14 days at 3 growth stages: First flower (FF); Mid Flowering (MD) 14 days after FF; and Cut Out (CO) 4 to 6 weeks after FF. Shade tents covering 9 m2 and at least 4 rows were placed in each plot. Measurements were taken from the centre rows. All experiments were fully irrigated and were conducted in 2013 and 2014 (except Narrabri 2014 only). Unshaded lint yields were reflective of the growing environment each season and averaged 2633 kg/ha at Narrabri, 1992 kg/ha at the Burdekin and 816 kg/ha at Reconquista. Hence to compare sites and seasons, lint yields from shaded treatments were presented as percentages of their respective unshaded control. Not surprisingly 60% 0f incoming solar radiation significantly ($p < 0.05$) reduced lint yield compared to the unshaded control. Interestingly at all locations yields relative to the unshaded control were similar ranging between 60 and 88% for all treatments despite large differences in unshaded yields at each location. Yield reductions were less with 30% shade. At the Namoi site yield reductions equated to 1.7% per day of shading during early or late flower similar to water deficit effects at this location at the same growth stages. Differences in yield recovery between treatments at the Burdekin and Reconquista reflected the solar radiation and temperature following shading. At the Burdekin full yield recovery occurred when radiation reduction was 30% at FF and climatic conditions were favourable for recovery via the production of new fruiting sites (high solar radiation and warm temperatures). At both locations yield reduction following 60% shade during was more variable than 30% shade, with lint yields between 88 and 57% of unshaded; yield loss reflected the interaction between the climatic conditions and length of fruiting cycle of the cultivar prior to or following shading. Shade during MF and CO had lower compensation, higher fruit abortions and smaller bolls, resulting in yield penalty ($P < 0.05$). Knowledge of the mechanisms for crop recovery from shading can provide insight into management practices that could minimise this production risk. These experiments indicate sowing date selection to avoid low radiation periods later in flowering and a mixture of cultivars with short and long fruiting cycles could be beneficial.

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References

Keywords: cotton grown, cultivar, reduced radiation

IMPACT OF NUTRIENTS ON VEGETATION INDEX, CANOPY REFLECTANCE AND BIOPHYSICAL PARAMETERS IN BT COTTON.

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Abstract:

With the advance of precision agriculture and remote sensing, newer methods of N status detection have been developed. These tools are based on the spectral properties, absorption or reflectance of a single leaf or a canopy, and have the potential to sense reflectance change caused by N deficiency. Similarly, Normalized Difference Vegetative Index (NDVI), which is a combination of red and NIR reflectance measurements, is one of the most widely used vegetation indices and has been extensively used to analyze the greenness of plant which is related to the amount of chlorophyll present in plant leaf guided by application of N fertilization. The NDVI values indicate the reflectance of canopy in different wavebands. Hence, with this background the present study was conducted to study the “Impact of Nutrients on Vegetation Index, Canopy Reflectance and Biophysical Parameters in Bt Cotton” during 2013-14 at College of Agriculture, Raichur. Results of the investigation showed that application of N fertilization showed significant differences among the treatments. The treatment with 150 per cent RDF recorded significantly higher NDVI values compared to 150 per cent RDN, 100 per cent RDN, 50 per cent RDN, Zero per cent RDN at all stages of growth except 30 DAS. Similarly, significantly lower NDVI values were recorded with application of STCR (Target 2.00 t/ha). These NDVI values showed the reflectance of canopy i.e., higher the NDVI values, lower is the reflectance. The application of N fertilization is negatively associated with canopy reflectance, It indicates that due to application of nitrogen more chlorophyll is synthesized and leaf appears green, this led to the less reflectance of canopy i.e., higher NDVI values. Similar results of higher NDVI values with application of higher level of N application were obtained by Ansari et al. (2006), Bajwa andMozaffari (2005) and Lee et al. (2007),

Relationship between various growth and yield components versus NDVI has showed positive correlation. NDVI showed significantly higher positive correlations with LAI (0.985), light interception at 90 DAS (0.982), SLW (0.972), LNC (0.972), total chlorophyll content (0.970), RWC (0.953), Light interception at 60 DAS (0.943) and seed cotton yield (0l.927) but high negative correlation with stomatal resistance (-0.946).Thus, canopy reflectance is very useful, non-destructive and reliable tool for applying the nitrogenous fertilizer to the crop for maximizing the yield and Canopy reflectance has good correlation with LAI, light interception, SLW, LNC, total chlorophyll content and plant height. Based on the information generated from the present investigation, it can be concluded that treatment with application of 150 per cent RDF showed lower canopy reflectance, more light interception and higher yield of Bt-cotton.

Acknowledgments

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Keywords: Nitrogen, STCR, Canopy reflectance, NDVI, Cotton

INFLUENCE OF POTASSIUM ON THE INCIDENCE OF CLCUV DISEASE AND ITS EFFECT ON SEED COTTON YIELD

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Abstract:

Low yields of cotton are often an outcome of biotic and abiotic stresses. Among these stresses, cotton leaf curl virus disease (CLCuV) has caused severe threat for cotton production in Pakistan. A field experiment on cultivar Bt. CRIS-508 was conducted in Central Cotton Research Institute, Sakrand for two consecutive years to determine response of potassium (K) nutrition to the infestation of CLCuV and seed cotton yield. Experiment was laid out in randomized complete block design (RCBD) with four replications. Potassium levels were applied 0, 50, 100 and 150 kg K2O ha-1 along with a basal dose of 170:60 kg N:P205 ha-1. Seed cotton yields and its components like boll formation plant-1, boll weight and seed index were significantly improved by the addition of K application and were observed highest with the application of 150 kg K2O ha-1 on both consecutive years. Data for K concentration in different organs of plant differed significantly due to K –fertilization. Potassium concentration increased linearly with increasing K-levels. The absorption of K by various plant parts increased with concurrent increase in varying levels of K-fertilizer. Averaged across levels, the relative K concentration in plant parts was found in decreasing in order of leaves > burs > stem > seed > lint. Results for incidence of CLCuV disease differed significantly due to K levels and seasons. The application of K fertilizer resulted in reduction of spread of disease at its mild infection level.

Acknowledgments

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Dr. M. Rafiq Chaudhry, Head Technical Information Section International Cotton Advisory Committee Dr Muhammad Ali Talpur Director Economic Research at Pakistan Central Cotton Committee, Ministry of Textile Industry, Govt of Pakistan Dr. Khalid Abdullah Cotton Commissioner/Vice president, Pakistan Central Cotton Committee (PCCC), Ministry of Textile Industry Mr. Mushtaq Ali Leghari Director Central Cotton Research Institute Sakrand Sind Pakistan

Keywords: Cotton, Potassium, CLCuV Disease, Seed cotton Yield

INTEGRATION OF GROUND- AND UAS-PLATFORMS FOR THE EVALUATION OF CULTIVAR PERFORMANCE (PHENOTYPING) AND EXPERIMENTAL TREATMENTS

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Abstract:

The purpose of this project is to develop and link components of a remote sensing system oriented at assisting plant breeders and crop management researchers in identifying best performing genotypes or experimental treatments. The component of the system includes; (1) ground- and UAS-based remote sensing platforms, (2) data analysis and visualization, and (3) data interpretation and application. The proper and coordinated operation of these three components is essential to produce tangible agriculture applications. Sensors used in this ground-based platform include an ultrasonic sensor used to determine plant height, a multi-spectral sensor used to estimate Normalized Difference Vegetation Index (NDVI), and an infrared sensor used to measure canopy temperature. Plant height is an important component of canopy cover and interception of solar radiation. NDVI is a parameter that takes into account the reflectance of infrared (~ 0.87 m) and red (~ 0.65 m) wave-

lengths by plants. Healthy vegetation reflects very well in the near-infrared part of the electromagnetic spectrum. Canopy temperature is an important indicator of the current water status of plants. The UAS platform is equipped with multiple sensors that can capture images in 4 spectral bands (Blue, Green, Red, and NIR) and thermal spectrum for canopy temperature measurements. Images acquired from the UAS are processed using Structure from Motion (SfM) algorithm to generate fine spatial resolution orthomosaic images and dense 3D point cloud data. These geospatial data products provided valuable information on two-dimensional canopy cover and three-dimensional vertical profiles of plants, so that these measurements can be used to track the time course of growth rates of plant height, canopy cover, NDVI, and canopy temperatures over the season at spatial and temporal scales that have not been possible via traditional remote sensing methods. When images are acquired at the end of growing season, open cotton boll count analysis enables the estimation of number of open bolls and open boll size, so that these information can be used to estimate lint yield. Preliminary results indicated that (1) canopy cover estimate is an important seed cotton yield component; (2) NDVI and canopy temperature can help fine tune the selection of elite genotypes or the performance of experimental treatments; (3) growth analysis of plant height and canopy cover development appears to be a promising diagnostic tool, and (4) open boll count can be an important variable to help defining cultivar selection or the performance of experimental treatments.

Acknowledgments

References

Keywords: Phenotyping, Unmanned arial systems, remote sensing, precision agriculture

PHYSIOLOGICAL AND MOLECULAR MECHANISMS OF THE IMPROVED ROOT HYDRAULIC CONDUCTANCE UNDER PARTIAL ROOT-ZONE IRRIGATION IN COTTON

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Abstract:

Partial root-zone irrigation (PRI) improves water use efficiency (WUE) via regulating stomatal conductance and increasing water uptake from the hydrated roots (Kang et al., 1997, Kang and Zhang 2004). The regulation of stomatal closure has been extensively studied and it is well known that PRI induces the ABA-based root-to-shoot signaling regulating stomatal conductance and leaf expansion hereby increasing WUE (Dodd, 2007; Wang et al., 2010). However, it is still not clear how the PRI increases the hydrated root hydraulic conductivity (L). A split-root system was established through grafting to simulate PRI (0/30mM PEG6000) to study physiological and molecule mechanism of increased water uptake in the hydrated roots. The results showed that the up-regulated root L related PIP genes (5 PIP1 and 7 PIP2) were possibly involved in the water uptake in the hydrated roots. There was no significant difference of the Pro content, root water content and root water potential (Ψ) between the hydrated roots (0/30-0) and either root side of control (0/0). The expression level of P5CS and late embryogenesis abundant (LEA) protein genes did not change significantly in the hydrated roots (0/30-0) compared with either root side of control (0/0). Since there was no osmotic stress in the hydrated roots (0/30-0), it is thus suggested that hydraulic signal may exclude from the signals regulating the L of the hydrated roots (0/30-0). Girdling on the hydrated side (0/30-0) of PRI plant indicated that there were chemical signals transported via the phloem regulated L of the hydrated roots (0/30-0). The ABA and H2O2 contents in the hydrated roots increased, possibly due to the increased expression of their key biosynthesis genes, NCED and NADPH oxidase, and the decreased expression of ABA catabolic CYP707A genes. Exogenous H2O2 induced the generation of ABA by up-regulating the NCED and down-regulating the CYP707A genes, but ABA content was decreased through up-regulating the CYP707A and down-regulating NCED genes with diphenylene iodonium (DPI) treatment, an inhibitor of H2O2 biosynthesis. Exogenous H2O2 increased the root L by up-regulating PIP genes of the hydrated roots (0/30-0), but these were decreased by DPI. Exogenous ABA increased the root L of the hydrated roots (0/30-0), but this was decreased by fluridone, an inhibitor of ABA biosynthesis, though both exogenous ABA and fluridone did not influence the expression of PIP genes. All the results suggesting that H2O2 is an important signal for increasing root L via up-regulating PIP genes, and ABA may increase root L at the post-transcription level.

Acknowledgments

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Keywords: Partial root-zone irrigation, root hydraulic conductivity, PIP gene, ABA, H2O2

PREDICTION OF YIELD LOSS IN COTTON CROPS CAUSED BY HERBICIDE DRIFT THROUGH THE ANALYSIS OF HYPERSPECTRAL DATA

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Abstract:

Yield loss in crops is often associated with plant disease or external factors such as environment, water supply and nutrient availability. Improper agricultural practices can also introduce risks in the equation. Herbicide drifts can be a combination of improper practices and environmental conditions which inevitably represent a potential yield loss. As traditional assessment of damage is often imprecise and time consuming, the ability of remote and proximal sensing techniques to monitor various bio-chemical alterations in the plant may offer a faster, non-destructive and reliable approach to predict yield loss caused by herbicide drifts. In this study conducted in Queensland, Australia, in situ hyperspectral data were collected to assess the reliability of this technique in the prediction of yield loss caused by herbicide drift. A factorial randomized complete block with dose and timing of exposure as factors were assessed. Three different fallow label rates of the herbicide 2,4-D were applied: nil, 5% and 50% at three timings of exposure of cotton plants: 4-5 nodes, 7-8 nodes and 12 nodes. As expected, the herbicide 2,4-D highly affected cotton crops regardless of the timing of exposure. As the cotton plant matured, yield loss was higher as bolls did not develop properly. When the exposure occurred at the very early stages of the crop, plants tended to replace the main stem with strengthened secondary branches; but even with the best recovery performance and the lowest dose, yield reduction was considerably high between 38% and 98%. The results also showed that cotton fibre quality was not significantly affected. Gin turnout (which may be also associated with quantity) and micronaire were the fibre quality variables affected by dose. However, the variability of micronaire was not considered low quality as any of the samples were lower than 3.52 or higher than 5.0 according to the standard schedule of premiums and discounts of cotton marketers in the region. Four partial least squares regression models (PLS-R) models for predicting yield were developed according to four campaigns of data collection: 2, 7, 14 and 28 days after the exposure (DAE). It was found that 7 DAE was the best time for data collection purposes due to better performance of the model with prediction accuracy of 81.3% (RMSEP = 2.8 and R2 = 0.99), followed by 28 DAE with prediction accuracy of 81.2% (RMSEP = 3.2 and R2 = 0.99). Due to similarities in the parameters of the resulting models, paired t-test were tested to confirm the influence and importance of the time after the exposure for a better yield prediction. With 99% of confidence ($p < 0.01$), we found that there was a significant influence of the time after the exposure in the prediction capabilities of the different models. The main difference between these two models was the higher significance of the red edge wavelength around 762 nm. Results indicated that hyperspectral sensing has the potential to improve the traditional methods for assessing herbicide drift and it is a more precise approach to predict yield loss.

Acknowledgments

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References

Keywords: hyperspectral sensing, herbicide drift, partial least squares regression, cotton

QUANTIFYING COTTON CULTIVAR MATURITY ACROSS DIVERSE UNITED STATES ENVIRONMENTS

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Abstract:

Optimum cotton (Gossypium hirsutum) yields may be achieved by cultivars that set and mature the maximum number of harvestable bolls before crop termination. The objective of this research was to quantify cotton cultivar maturity and thereby provide growers with a means to select cultivars that fully utilize the available degree days in their environment. At present there is a no plant-based protocol for classifying cultivar maturity; rather, planting seed companies designate the maturity of cultivars empirically by referencing their apparent maturity to that of other cultivars. To measure maturity, seven commonly-grown cultivars of diverse nominal maturities were grown for high yields and terminated at nodes above cracked boll = 5; cultivars were grown over a two-year period at two and one location(s) in Georgia, one in Tennessee, and two in the High Plains of Texas - three environments differing in latitude and degree days (nine locations in all). Fruit set was monitored by main-stem node and sympodial fruiting position; lint yields and fiber quality were determined. Under good growing conditions, the main-stem node at which a cultivar accumulated 50% of its total harvestable bolls (N50) served as a reliable (correlated) measure of its productivity within that environment. Within each environment, the relative maturity of each cultivar could be ranked by comparing the node at which it set 50% of its total bolls to that of other cultivars. Between environments, the N50s of cultivars were affected by degree days. For specific cultivars, higher N50s tended to occur at environments with greater degree days. Cultivars at the extremes of the maturity range, whether early or late, tended to be at the same extremes across locations; those with mid-values varied in rank among

locations. N50 is a good measure of relative maturity within location, but is not always conserved across locations by all cultivars. Within an environment, N50 is a measure of the variation in phenotypic maturity among cotton cultivars; compared among locations, N50 is a manifestation of the environmental plasticity of Upland cotton.

Acknowledgments

References

Keywords: Adaptation, Cultivar, Maturity, Plant Mapping, Yield

UNDERSTANDING THE PHOTOSYNTHETIC BIOCHEMISTRY THAT UNDERPINS COTTON PHOTOSYNTHESIS UNDER FUTURE CLIMATE EXTREMES.

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Abstract:

Global climate change resulting in increased drought and higher ambient air temperatures may severely impact future productivity of the cotton industry. Identification of thermo-tolerant and water use efficient (WUE) cotton lines by CSIRO through plant breeding efforts may be utilized to maintain productivity despite unfavorable future climate extremes. Six cotton genotypes, which include DP16 (old genotype), Siokra L23 (WUE), CS50 (decreased WUE), 64224-212 (heat tolerant), SICALA V2 (poor heat tolerance) and Sicot 71, were grown in a sun-lit glasshouse under non-limiting water and nitrogen conditions at mid-day maximum air temperatures of 28 < sup > & #959; < /sup > C and 32 < sup > o < /sup > C. We measured plant growth, photosynthetic capacity, Rubisco catalytic performance and online stable carbon isotope discrimination to calculate photosynthetic WUE and mesophyll conductance of CO < sub > 2 < /sub > (g < sub > m < /sub >). Elevated growth temperature accelerated the onset of flowering and boll formation, and increased plant mass and total leaf area across all genotypes. Analysis of gas-exchange data indicates photosynthetic capacity was increased in all genotypes when measured at 32 < sup > o < /sup > C compared to the identical lines at 28 < sup > o < /sup > C, irrespective of growth temperature. Stomatal conductance (gs) measured under saturating light conditions varied across the genotypes with Siokra L23 displaying lowest gs resulting in improved instantaneous WUE. This was coupled with an improved gm hence CO < sub > 2 < /sub > assimilation remained similar to the other genotypes. In vitro Rubisco catalytic measurements at 25 < sup > O < /sup > C indicated that cotton Rubisco has a high affinity for CO < sub > 2 < /sub > (KmCO < sub > 2 < /sub >) and a slow k < sub > cat < /sub > which was accompanied by a high specificity for CO < sub > 2 < /sub > as opposed to O < sub > 2 < /sub > (S < sub > c/o < /sub >). Analysis of Rubisco content revealed that Rubisco accumulates up to 45% of total leaf soluble protein indicating the significant investment of N into Rubisco synthesis. Therefore, future improvements in cotton photosynthesis could be achieved by improving Rubisco catalysis and reducing content to mitigate against the significant requirement for the large N investment into Rubisco.

Acknowledgments

Funding for this research provided by Cotton Research Development Corporation, Australia and the Department of Agriculture and Water.

References

Keywords: Photosynthetic biochemistry, Rubisco, Climate extremes

COTTON PROTECTION

A COMPARATIVE ANALYSIS OF RESIDUAL PESTICIDES ON COTTON UTILIZING BIOSENSOR AND TANDEM MASS SPECTROMETRY

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Abstract:

This study is a combination of qualitative and quantitative analytical measurements. A rapid, sensitive and low cost method based on AChE-inhibition utilizing biosensor has been developed for the identification of residual pesticides, for qualitative analysis. Mini Thermostat (MT-1) was used for monitoring of changes in bio-electrical signals caused by the interaction of biological substances and residues. The optimization of process parameters involved in AChE inhibition activity has been carried out such as enzyme & substrate concentrations, buffer, pH and incubation time. Real cotton samples collected from different regions (Egypt, Pakistan & India) extracted with different solvents (methanol, hexane & toluene) have been analyzed by the method developed. The sensor exhibited good reproducibility and stability. For quantitative analysis, a multi residue method for analysis of 76 pesticides with different physio-chemical properties was developed. The method includes a rapid and small scale extraction procedure of the real cotton samples with different solvents (methanol, hexane & toluene) from polar to non-polar region, using Ultra Sound Assisted Extraction (USE). Cryogenic Homogenization was being implemented for sample pre treatment. The pesticide residues were determined by Gas Chromatography coupled to tri-

ple quadrupole Tandem Mass Spectrometry (GC-MS/MS). 57 out of 76 pesticides were detected successfully by the method developed. Nineteen (19) pesticides could be analyzed by GC-MS/MS using EI ionization, most often because of incompatibility with evaporation of the intact molecules in the GC injector. Confirmation of pesticide and quantitation was performed in Selected –Reaction Monitoring mode (SRM). The limit of detection (LOD), Limit of quantitation (LOQ), precision and accuracy have been experimentally determined for each individual representative analyte. All validation criteria mentioned by European Commission document SANCO/12495/2011 for 'Method Validation and Quality Control Procedures for Pesticide Residues Analysis in Food and Feed' were fulfilled. The method gave satisfactory analytical performance parameters for the most of the targeted pesticides and measurements on real cotton samples were also compared with the results obtained using biosensor approach.

Acknowledgments

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Keywords: Acetyl cholinesterase (AChE), Mini Thermostat (MT-1), Biosensor, Ultra Sound assisted Extraction (USE), Tandem mass spectrometry (GC-MS/MS)

ANALYSIS OF TARNISHED PLANT BUG MOVEMENT USING CARBON AND NITROGEN ISOTOPES

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Abstract:

Tarnished plant bug, *Lygus lineolaris* (Palisot de Beauvois), is the primary pest of cotton (*Gossypium hirsutum* L.) across the mid-south of the United States. Movement into cotton fields occurs during the late summer from other host plants, both cultivated and wild. Stable carbon isotope (SCI) analysis has been used in other studies to determine the natal hosts of *L. lineolaris* adults, as adults retain an isotopic signature similar to the host plant that they utilized for nymphal development. These insects utilize hundreds of species of plants as food, including both C_3 and C_4 hosts. Collections of *L. lineolaris* were made using a standard set of 500 sweeps on a variety of both wild and cultivated host plants throughout the Mississippi Delta during 2015, and both nymphs and adults were subjected to SCI. The signal obtained from nymphs matches the signal of dominant host plants at the collection location, while adults lacked the same degree of host fidelity observed in nymphs. These host plant signals provide information that can be used to document movement among host plants and potentially identify alternate targets for *L. lineolaris* control measure before damage occurs in cotton.

Acknowledgments

References

Keywords: tarnished plant bug, lygus lineolaris, stable carbon isotope, movement

BIOLOGY AND MANAGEMENT OF HERBICIDE-RESISTANT PALMER AMARANTH IN U. S. COTTON

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Abstract:

Natural and Agricultural Ecology: Palmer amaranth (Amaranthus palmeri) is native to the Neotropic Sonoran vegetation zone of West-Central North America. It's adaption to open niches in conditions of high temperature; high light intensity and low soil moisture enable it to exploit disturbed agricultural habitats, particularly those with intermittent drought. Palmer amaranth was first noted as an agricultural weed in cotton (Gossypium hirsutum) in West Texas. By the mid-20th century, it was found as far east and north as Ontario in Canada. In the Southeast U. S., it was called pigweed or care-

less weed because it was a pest in poorly tended places, especially those disturbed by rooting or overgrazing by life stock. Resistance Mechanisms and Population Genetics: In the late 1980's, Palmer amaranth evolved resistance to the acetolactate synthase mechanism of herbicide action that was widely used for broadleaf weed management in soybean (Glycine max.) Subsequent wide-scale adoption of glyphosate-resistant cultivars of corn (Zea mays), soybean, and cotton enabled multiple post emergence applications of glyphosate on approx. 33 x 106 hectares/year of row crops during the decades of the 2000s. In 2006, a population of Palmer amaranth in Georgia was confirmed resistant to glyphosate at 6-10 X the field labeled rate. The primary mechanism of this resistance is gene duplication (multiplication). The geographic distribution of confirmed resistance shows that glyphosate resistance likely began circa 2005 independently at three centers (AR-TN, GA, and NC). A population genetics analysis of 2009 collections of Palmer amaranth from NC identified five distinct populations in that state alone, with the same resistance mechanism in four of the populations. Impact on Management: Glyphosate resistance in Palmer amaranth has expanded across the U. S. cotton belt as far as AZ, and into the corn belt in IL, MO, and NE. Biological evaluation in MO showed that Palmer amaranth was the fastest growing of six weedy amaranths; thus it has a competitive advantage under post emergence herbicide selection; and it is also capable of prodigious seed production (~ 5.0 x 105 seed/plant in AR). Thus, because glyphosate continues to control may other weed species, Palmer amaranth tends to become the dominant aka 'driver' species in weed management programs. As such, it poses a serious threat to effective weed management. In the Southeast, Palmer amaranth threatened hard-won gains in conservation tillage, and everywhere it increased the use and costs of herbicides in production agriculture. New Weed Management Strategies: Programs now focus on herbicide diversity for resistance management; and in the humid region, on integrating cover crops for early-season suppression of weed emergence in conservation tillage. The failure of programs based solely on post emergence treatment has caused weed scientists to envision a new paradigm based on multi-year management of the soil weed seed bank, use of multiple herbicide mechanisms of action to attain in-season efficacy and to reinforce resistance management, and more purposeful integration of agronomic best management practices for weed population suppression.

Acknowledgments

References

Keywords: herbicide diversity, herbicide resistance, Palmer amaranth, weed management paradigm, weed seed bank management

CHARACTERIZATION OF EPICUTICULAR WAX IN COTTON (GOSSYPIUM HIRSUTUM L.) IN RELATION TO COTTON LEAF CURL DISEASE (CLCUD) RESISTANCE

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Institutions: [1] GCUF - Government College University (Allama Iqbal Road, Faisalabad, Pakistan)

Abstract:

Cotton is an important crop with respect to textile industry worldwide. Cotton production is severely affected by Cotton Leaf Curl Disease (CLCuD) in major cotton growing countries of the world including India, Pakistan, and Sudan etc. Various strategies are suggested to cope this disastrous disease of cotton. Epicuticular wax is reported to impart resistance against various stresses in plants such as drought, mechanical injury and pathogens. In this study, role of epicuticular wax in resistance to CLCuD was investigated. Epicuticular wax load of different varieties/lines of *Gossypium hirsutum*, *Gossypium barbadense* and *Gossypium arboreum* was evaluated. Data for CLCuD infestation was also recorded. There was differential epicuticular wax load in *Gossypium hirsutum*, *Gossypium barbadense* and *Gossypium arboreum*. Epicuticular wax load was found to be associated with CLCuD tolerance. Results of this research will accelerate breeding for development of elite CLCuD resistant *Gossypium hirsutum* cultivars.

Acknowledgments

Author acknowledges the support provided by Cotton Research Institute (CRI), Ayub Agricultural Research Institute, Faisalabad, Pakistan for smooth running of this project.

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Keywords: Epicuticular wax, Cotton Leaf Curl, Disease

COMPARING BOLL INJURY AND EILS FOR SPECIES OF A BOLL-FEEDING SUCKING BUG COMPLEX (HEMIPTERA: MIRIDAE AND PENTATOMIDAE) ON TEXAS COTTON

Authors: James Glover [1,2], Mike Brewer [2,1], Gregory Sword [1]

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Abstract:

Whole-plant caged field experiments were conducted in 2014 and 2015 to characterize the injury of South Texas cotton from a species complex of boll-feeding sucking bugs represented by one plant bug species (Creontiades signatus) and two stink bug species (Euschistus servus, Acrosternum hilare). Field-collected stink bugs and verde plant bug where used to infest cotton maintained free of insect injury. Whole plants were caged (4 plants per cage) with four insect densities: 0 (control), 0.25 bugs per plant (1 bug per cage), 1 bug per plant (4 bugs per cage), and 2 bugs per plant (8 bugs per cage). Each treatment was replicated 12 times across two bloom specific periods mid and late bloom. Bugs remained caged on plants for 7 days then terminated with pyrethrin insecticide. After the infestation period, the whole plants/bolls were allowed to mature inside the cages. Boll response to feeding damage from verde plant bug and both species of stink bug resulted in external and internal boll injury in the form of warts, galls, lint deterioration, and boll rot. Bolls were rated at harvest on a 0 to 4 scale, corresponding to the number of damaged locules. Cotton boll rot was scored by presence or absence visually and the number of diseased locules. Yield data were estimated by the weight of seedcotton/lint. Significant boll injury differences were detected across species, and yield—insect density relationships were used to calculate and compare economic injury levels (EILs). Implications of this work in developing a management program for multiples species will be presented.

Acknowledgments

References

Keywords: Cotton boll rot , Cotton pest mamagment , Miridae, Pentatomidae

COTTON BOLL WEEVIL (ANTHONOMUS GRANDIS) GENOME SEQUENCING AND POPULATION GENOMICS AS TOOLS FOR MONITORING AND ERADICATION

Authors: Tyler Jay Raszick [1], Gregory A Sword [1], Charles P-C Suh [2], Raul Ruiz-Arce [3]

Institutions: [1] TAMU - Texas A&M University (2475 TAMU, College Station, 77843), [2] USDA - United States Department of Agriculture (USDA-Insect Control and Cotton Disease Research Unit, College Station, TX), [3] USDA-APHIS - United States Department of Agriculture (USDA-APHIS, Edinburg, TX)

Abstract:

Despite the success of eradication efforts across most of the cotton-producing regions of the U.S., the cotton boll weevil (*Anthonomus grandis*) remains a major pest of cotton in much of the New World. The area along the Texas border with northern Mexico has been a particularly troublesome area for eradication efforts due to political and environmental constraints, and the fact that the region is the northern edge of the weevil's natural sub-tropical range. In order to improve boll weevil eradication efforts, we aim to develop a powerful suite of genetic markers using next generation DNA sequencing and bioinformatics techniques to determine the genetic relationships and patterns of gene flow among weevil populations along the Texas-Mexico border. These tools will likely enable the identification of source populations for re-introductions in previously eradicated areas (should they occur) and will guide preventative control measures along the border. Furthermore, our markers should be able to discriminate *A. grandis* from morphologically similar, closely related weevil species. Here, we discuss our progress towards developing these genomic tools. The first step towards accomplishing such a task was to sequence and assemble a reference genome, which will act as a scaffold for downstream population genomics and marker development. We have completed the full genome sequence for the boll weevil, and we also present ongoing work towards resolving the population genetic structure for weevils across Mexico and southern Texas.

Acknowledgments

References

Keywords: cotton boll weevil, Anthonomus grandis, genomic sequencing, population genomics

DETERMINATION OF THE INJURY POTENTIAL AND ECONOMICAL THRESHOLD OF HELICOVERPA ARMIGERA ON COTTON CROP

Authors: José Ednilson Miranda [1], Bruna Mendes Tripode [1], Laisse Danielle Pereira [1], Ismael Ribeiro Rocha Silva [1]

Institutions: [1] EMBRAPA COTTON - EMBRAPA COTTON (Embrapa Cotton)

Abstract:

Cotton is worldwide known as one of the most susceptible crops to pest attack, some of them quite harmful. Helicoverpa armigera, a holometabolous insect that whose larval phase causes damage on the reproductive structures, may reduces significantly the yield and quality of the fiber. This study aimed to determine the economical threshold (EC) of H. armigera in Brazilian cotton crops. Second instar larvae of H. armigera were infested in cotton plants cultivar BRS370RF confined in cages at the ages of 80, 120 and 150 days after emergence (DAE). At the same time, H. armigera individuals were prayed with various insecticides and the mortality was checked every 24 hours through three consecutive days for obtaining the agronomic efficiency of insecticides against the pest. There was an 73% reduction of the population by the action of insecticides, hence deriving the value of population decrease rate (k= 0.73). The injury potential of each H. armigera larval individual on cotton plants was set at three times: at 80 DAE (0.0718 kg/m2), at 120 DAE (0.024 kg/m2) and 150 DAE (0.0109 kg/m2). The EC for H. armigera on cotton crop was set at 0.2 larvae/m2 from the beginning of flowering until 80 DAE, 0.6 larvae/m2 from 80 to 120 DAE and 1.2 larvae/m2 from 120 to 150 DAE.

Acknowledgments

References

Keywords: Anthonomus grandis, flowering, behavioral control

DEVELOPMENT AND IMPLEMENTATION OF A COMPREHENSIVE PROGRAM TO COMBAT COTTON LEAF CURL VIRUS THROUGH INTERNATIONAL COOPERATION

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Institutions: [1] USDA ARS GBRU - USDA ARS Genomics and Bioinformatics Research Unit (PO Box 36, Stoneville, MS USA 38776)

Abstract:

Cotton leaf curl virus (CLCuV) is a geminivirus transmitted by whiteflies that was first described in Africa and has subsequently migrated through the Middle East to parts of the Sub-Asia and Asia continents. During this migration, the virus is believed to have mutated numerous times and in two instances within Pakistan such mutations have had a dramatic negative impact on cotton yields. Within Pakistan, yield losses can reach 20-40% and that value could potentially be higher in countries unprepared for the virus. Two highly virulent strains of CLCuV have moved out of Pakistan into India. One of these strains has been detected in additional cotton producing countries including China and Uzbekistan. CLCuV is a multi-tiered threat as the virus can infect more than 60 other species including some vegetable crops. Such a devastating disease cannot be perceived only as a local threat, but represents a potential challenge for all cotton producing countries. As such, the USDA has ranked CLCuV as one of the top 20 threats to USA agriculture. Over the past five years, the USA and Pakistan have developed and implemented a comprehensive program to understand and combat the virus. The program covers increasing of germplasm collections, characterization of the geminiviruses within Pakistan, germplasm screening and germplasm improvement by selecting and breeding for resistance. In addition, the program also covers components such as development of viral detection methods, evaluation of antisense constructs against the virus and vector, improved agronomic practices, capacity building and training of small farmers in best management practices through a farmer field school system. This program represents a model the international community could adapt to combat the virus as it continues to migrate or adapt, or for other emerging disease threats.

Acknowledgments

References

Keywords: cotton leaf curl virus, disease management, international cooperation

DISEASES IN AUSTRALIAN COTTON

Authors: Linda Smith [1], Linda Scheikowski [2], Paul Melloy [1], John Lehane [2]

Institutions: [1] DAF - Department of Agriculture and Fisheries (Ecosciences Precinct, 41 Boggo Road, Qld, 4102, Australia), [2] DAF - Department of Agriculture and Fisheries (203 Tor Street, Toowoomba QLD 4350, Australia)

Abstract:

Australian cotton growers are exposed to and manage a variety of cotton diseases. In Queensland, cotton growers have been successfully managing Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *vasinfectum* (Fov), which was first detected in Queensland in 1993. Fov in Australia is endemic and three strains have been identified. Vegetative Compatibility Group (VCG) 01111 is the most prevalent strain in Australia and in Queensland is present in all cotton growing regions. The tremendous effort to breed varieties with high levels of resistance, as well as develop cultural practices (e.g. residue management, crop rotation, avoid green manure crops and legumes, late planting to avoid cold shock) to manage this disease, has enabled growers to produce profitable cotton in fields infested with Fov. Verticillium wilt caused by *Verticillium dahliae*, although present in Queensland has rarely been detected during annual disease surveys and historically has not caused significant yield reductions. However, in the 2014/15 season, the defoliating strain VCG 1A of *V. dahliae*was detected for the first time, causing significant disease in susceptible varieties. Following molecular characterization and VCG analysis of *V. dahliae* isolates it is known that three strains of the pathogen are present in Australian fields. The defoliating strain VCG1A and non-defoliating strains VCG 2A and 4B were identified using specific primers DB22/DB19/espdef01 (Mercado-Blanco et al. 2003) and VCG analysis (pers. com. R. M. Jiménez-Díaz, Spain). Pathogenicity studies determined that VCG's 1A and 2B are highly pathogenic and VCG 4B is mildly pathogenic on cotton. In 2012 reniform nematode was detected for the first time in the Dawson/Callide region of Central Queensland. This nematode was determined to be widespread in this region causing up to 40% yield reduction. With no host resistance available, research is focused on determining the threshold population of reniform in soil and the benefit of non-host crop rotation to lower soil populations. Data from three seasons suggest that a population of 800 reniform /200 mL of soil post-harvest results in a 10% yield reduction. Deep coring to 100 cm has shown that reniform are present at depth, with populations being greatest in the 30 – 70 cm profile, followed by 0 – 30 cm and lowest in the 70 – 100 cm profile. Corn and sorghum are non-hosts of reniform and significantly reduce soil populations compared to cotton and are therefore good rotation options for growers to manage this pest.

Acknowledgments

Thankyou to the Australian Cotton Research and Development Corporation for funding this research.

References

Mercado-Blanco, J. et al. 2003. Simultaneous detection of the defoliating and non-defoliating Verticillium dahliae pathotypes in infected olive plants by duplex, nested polymerase chain reaction. Plant Disease 87:1487-1494.

Keywords: Fusarium wilt, Verticillium wilt , Reniform nematode

List of Oral Presentations Abstracts

ECOLOGICAL MANAGEMENT OF LYGUS BUGS IN TEXAS COTTON

Authors: Megha N. Parajulee [1]

Institutions: [1] Texas A&M RES CTR - Texas A&M University/ Texas A&M AgriLife Research (1102 East FM 1294, Lubbock, Texas 79403, USA)

Abstract:

Texas leads the cotton production in the United States, with 1.3 million metric ton of lint produced in 2.3 million hectares. Texas High Plains is the largest contiguous cotton growing area in the world, with 4% of the world cotton produced in this region, encompassing 41 counties (≈150,000 sq. km). An ecological approach integrating several management tactics has been used to address pest management issues in the Texas High Plains, consisting of agronomic, cultural, biological, chemical, plant physiological, and spatial (landscape) methods. Western tarnished plant bug, Lygus hesperus, is the primary Lygus species inhabiting cotton and several other crop hosts in this region. In Texas High Plains cotton, Lygus bugs are generally more pestiferous in the boll development stage than in the early squaring stage. Until cotton begins flowering, Lygus prefers to stay in various roadside weed hosts, including mustard, alfalfa, Russian thistle, sunflower, pigweed, and others. As roadside weeds senesce and cotton begins flowering, cotton vulnerability to Lygus infestations increases. Lygus injury to maturing bolls is generally the highest during mid-season (4-5 weeks into flowering). In the Texas High Plains, Lygus can be managed using comprehensive ecologically-based IPM practices, with a focus on non-cotton habitat management. This presentation will highlight the Lygus host utilization behavior and sink-source relationships of non-cotton host habitats, influencing Lygus movement into cotton, and action thresholds and insecticide chemistries.

Acknowledgments

References

Keywords: Lygus hesperus, cropping systems, habitat management

EFFECT OF CROP ROTATION AND ENVIRONMENT ON FUNGAL COMMUNITIES IN AUSTRALIAN COTTON SOILS

Authors: Gupta Vadakattu [1], Linda Smith [2], Karen Kirkby [5], Linda Scheikowski [2], Ian Rochester [3], Nilantha Hulugalle [5], Christopher Penton [4]

Institutions: [1] CSIRO - Agriculture (PMB No 2, Glen Osmond, SA, Australia), [2] DAF Qld - Department of Agriculture and Fisheries (GPO Box 267, Brisbane, Qld 4001), [3] ACRI - Australian Cotton Research Institute (Narrabri, NSW), [4]Arizona State Univ - Center for Functional and Applied Microbiomics (Mesa, Arizona), [5] NSW DPI - Department of Agriculture (Narrabri, NSW)

Abstract:

Fungi are an important component of soil biota playing important roles in a number of plant essential functions. Soil fungal community has the capacity to affect pathogen inoculum levels and their disease causing potential (Penton et al. 2014). Soilborne diseases such as Fusarium wilt, Black root rot and Verticillium wilt have significant impact on cotton production. Currently the management of disease impacts is through the selection of genetically resistant cultivars (where available), agrochemical application and rotation with non-host crops. But even in our current high F-rank cultivars significant losses can occur from disease such as Fusarium under the right environmental conditions. Biological disease suppression mediated by soil microorganisms including soil fungi can assist farmers in reducing the impact of diseases on cotton production through crop management. Soil type based variation in fungal populations in cropping soils has been documented. It is also known that the self-mulching property of Vertosol soils has a significant influence on fungal hyphal matrix in cotton soils and therefore crop residues play a significant role in the dynamics of fungal community in cotton sols. Currently our knowledge about management effects on soil fungi and links to pathogen inoculum levels and their disease causing potential is limited. We analysed surface soils from ongoing field experiments, in New South Wales (ACRI, Narrabri and Cowan) and Queensland (Goondiwindi), monitoring cotton performance and disease incidence in three cotton growing regions, collected prior to 2013 and 2015 planting, for the genetic diversity (28S LSU rRNA or ITS region sequencing) and abundance (qPCR) of fungi as influenced by soil type, environment and management practices and link it with disease incidence and suppression. Samples were also analysed for microbial catabolic diversity, microbial biomass and soil chemical properties. In general, soil type and crop rotation showed a significant effect on catabolic activity and diversity of soil microbial community. Results from the 28S LSU rRNA sequencing based analysis of 2013 samples indicated a total of 370 fungal genera in all the cotton soils and the top 25 genera in abundance accounted for the major portion of total fungal community. There were significant differences in the composition and genetic diversity of soil fungi between the different field sites from the three cotton growing regions, i.e. significantly affected by field location (soil type and environment) and cropping history. Results for diversity indices showed significantly greater diversity in the long-term crop rotation experiment at Narrabri (F6E) and experiments at Cowan and Goondiwindi compared to field sites with long-term disease history (e.g. Biofumigation experiments at ACRI, Narrabri). Diversity was lowest in the soils under brassica crop rotation in Biofumigation experiment. Surface soils from continuous cotton and cotton-fallow rotations showed lowest abundance of fungal populations and overall catabolic diversity of soil microbial communities. Overall, the diversity and abundance of soil fungal community varied significantly by cropping history suggesting that changes in soil fungal community may play a notable role in soilborne disease incidence in cotton. Biological based disease suppression can assist farmers in reducing the impact of diseases on cotton production.

Acknowledgments

Authors acknowledge financial support from the Cotton Research and Development Corporation Australia and all the host organisations.

References

Penton CR, Gupta VVSR et al. (2014) Fungal community structure in disease suppressive soils as assessed by 28S LSU gene sequencing. PLoS ONE 9(4): e93893

Keywords: Fungi, disease suppression, genetic diversity, crop rotation, pathogen

EFFECT OF ELEVATED CARBON DIOXIDE AND TEMPERATURE ON TRI-TROPHIC INTERACTION OF BT COTTON, APHID, APHIS GOSSYPII GLOVER AND COCCINELLID, CHEILOMENES SEXMACULATA FAB.

Authors: ADONI GINNU SREENIVAS [1]

Institutions: [2] UAS, RAICHUR - Shreevani, G. N (COLLEGE OF AGRICULTURE, UNIVERSITY OF AGRICULTURAL SCIENCES, RAICHUR, KARNATAKA), [3] UAS, RAICHUR - A.G.Sreenivas (COLLEGE OF AGRICULTURE, UNIVERSITY OF AGRICULTURAL SCIENCES, RAICHUR, KARNATAKA), [4] UAS, RAICHUR - Beldhadi R.V. (COLLEGE OF AGRICULTURE, UNIVERSITY OF AGRICULTURAL SCIENCES, RAICHUR, KARNATAKA), [5] UAS, RAICHUR - Janagoudar B.S (COLLEGE OF AGRICULTURE, UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD, KARNATAKA), [6] UAS, RAICHUR - Somasekhar (COLLEGE OF AGRICULTURE, UNIVERSITY OF AGRICULTURAL SCIENCES, RAICHUR, KARNATAKA), [7] UAS, RAICHUR - Suhas Yelshetty (COLLEGE OF AGRICULTURE, UNIVERSITY OF AGRICULTURAL SCIENCES, RAICHUR, KARNATAKA)

Abstract:

Information on the effects of enriched CO2 on both biochemical composition of plants (DeLucia et al.,2012) and the consequences of such changes on performance of herbivore and its predator (Aslam et al., 2013) is an important step in understanding the responses of trophic relationships to global environmental change. In future, CO2 concentration is likely to be accompanied by increased temperature (IPCC, 2013), but many studies have revealed only the effects of eCO2 on aphid populations (Sun and Ge, 2011), while the combined effect of elevated temperature and CO2 has received little attention (Murray et al., 2013). Bt cotton- being a C3 and carbon responsive crop, climate change in the form of eCO2 coupled with increased temperature would be helpful for crop per se as such, but, it gets altered in presence of herbivore and carnivore. In this regard, studies were undertaken on tri-trophic interactions of Bt cotton, aphid and coccinellid under Open Top Chambers (OTC's) at Main Agricultural Research Station (MARS) and Department of Entomology, University of Agricultural Sciences, Raichur, Karnataka during 2013 to 2015. Bt cotton (MRC-7351) plants were grown in the open top chambers (OTC's) under different set of climate change treatments viz., eCO2 + etemp. (550 ± 25 ppm with 2°C rise in temperature), eCO2 (550 ± 25 ppm), aCO2 (390 ppm ± 25 ppm 2°C rise in temperature), aCO2 (reference open top chamber) and reference plot (standard check) as control outside the open top chambers in natural conditions. The experiments on phytochemistry of Bt cotton (monotrophic interaction), aphid biology (bitrophic interaction) and tri-trophic interaction with coccinellid was carried out by following standard procedures. Investigations revealed that, the eCO2 and temperature favoured growth and development of Bt cotton which was evidenced by accelerated growth in terms of more plant height, leaves, leaf area and sympodia. This increased growth inturn increased seed cotton yield in eCO2 and temperature treatments which was more compared to reference plot. Biochemical analysis of Bt cotton showed lot of changes in it when subjected to different climate change treatments, wherein, the chlorophyll content, carbon and carbon-based compounds viz., tannins, phenols and sugars significantly increased in eCO2 as compared to aCO2 treatments. On the contrary, nitrogen (N) and N-based compounds viz., proteins and amino acids decreased in eCO2 conditions which inturn altered C: N ratios and hence resulted in decreased Bt toxin production. Further, when aphid biology was studied on such biochemically altered Bt cotton plants, resulted in decreased nymphal period, adult longevity and total life cycle. Whereas, fecundity was increased leading to increased aphid population with reduced fitness and decreased seed cotton yield in eCO2 treatments, in the sense that bi-trophic interaction has negative bearing on host. In tri-trophic interactions, the negative effect posed by aphid on crop was nullified by predator as it devoured the aphids greatly at the cost of its fitness which was slightly affected.

Acknowledgments

Authors are grateful to RKVY, Bengaluru for the financial support and Neo Genesis Engineering, Mumbai for the technical support.

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Keywords: Elevated CO2, temperature, tri-trophic interaction, Bt cotton, Aphid

EXTENSIVE HAPLOTYPE ANALYSIS OF THE WHITEFLY BEMISIA TABACI CRYPTIC SPECIES IN PUNJAB, INDIA

Authors: Satnam Singh [1], Abhishek Sharma [2,2], Suneet Pandher [1,1], Ramandeep Kaur [1,2], Gurpreet Kaur [2], Judith K Brown [3], Pankaj Rathore [1]

Institutions: [1] PAU - Punjab Agricultural University, Regional Station (Faridkot, Punjab-151203, India), [2] PAU - Punjab Agricultural University, Deptt. of Vegetable Science (Ludhiana-141004, Punjab, India), [3] UOA - University of Arizona, Department of Plant Science (Tuscan, AZ-85721 USA)

Abstract:

The Bt-cotton since its introduction in 2005 in North India has witnessed upsurge in whitefly Bemisia tabaci and its transmitted cotton leaf curl disease (CLCuD). This may be attributed to decrease in insecticidal sprays in post-Bt era, susceptibility of the germplasm being introduced as cotton hybrids and the failure of existing spray technology to reach throughout the bushy cotton hybrids. In 2010 there was heavy incidence of whitefly along with cotton leaf curl disease across Punjab. The big blow to cotton production has been reported in 2015 resulting in loss of more than 60-75 % cotton across state. There has been a complete failure of the insecticides to manage the pest and 40-50 percent of the area under cotton has been ploughed in the middle of the cotton season. The whitefly population remained above ETL from July to September. The situation at the farmers' field was worse, the average population at 20 and 15 locations surveyed in July and August was 188.8 and 185.5 whiteflies per leaf, respectively. It is speculated that the emergence of new biotypes in this region may be a major contributing factor to these outbreaks. So the samples were collected from cotton growing as well as non-cotton growing districts of Punjab to amplify the 1kb mtCOI region to from the genomic DNA of single whitefly. The amplified product was cloned susing tandard protocols and bidirectionally custom sequenced. The sequences pertaining to a single population were alligned to form a contig after removing the primer sequences from both ends. The sequences were were analysed along with the reference sequences to form a tree using neighbour joining and maximum likelihood algorithims. Similarly the virus infected plants of cotton, okra, tomato, cucurbits, chilli and weed hosts were also collected from these locations followed by DNA extraction, amplification of DNA A,  BNA and CP gene using specifc primers. The whitefly populations from different host and cotton exhibit a wide diversity, however all the populations fall in two major clades. Most of the North-Indian populations fall in the grooup Asia I and few of them in Asia II. The Asia II is mostly prevelant in the central and southern part and Asia I is predominant in the northern region. The Asia I is close to already reported populations from Pakistan, China and new Delhi, however Asia II is similar to populations reported from Hyderabad, Bangalore, China, Pakistan and Australia. The mixture of Asia I and II is indicative of popultions moments across these regions. The sequence analysis conformed that no new biotype had emerged in the recent times and the population structure was similar to what has been reported earlier. The sequence analysis of CP gene and satellite molecules revealed the association of previously reported virus from different hosts. Some new viruses and hosts were also identified, which were not earlier reported from this region. The satellite molecules sequence analysis showed the association of trans-species beta and alpha satellites along with defective satellites.

Acknowledgments

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Keywords: Bemisia tabaci, Haplotype, Leaf Curl Virus, Cotton, Punjab

GENE FLOW AND HOST USE, RELATIVE TO COTTON, IN NEZARA VIRIDULA (THE GREEN VEGETABLE BUG OR SOUTHERN GREEN STINK BUG)

Authors: Dean Brookes [1], James Hereward [1], Lewis Wilson [2], Gimme Walter [1]

Institutions: [1] UQ - The University of Queensland (Brisbane, Queensland 4072, Australia), [2] ACRI - Australian Cotton Research Institute (Narrabri, New South Wales 2390, Australia)

Abstract:

With the widespread use of Bt cotton, plant-sucking insects have become more significant pests in cotton crops. In Australia, this includes the Green Vegetable Bug or Southern Green Stink Bug (Hemiptera: *Nezara viridula*), an insect pest of global significance. These bugs feed on the developing cotton bolls, potentially reducing yield and staining the lint, but they only occasionally reach numbers that require control. Outside of cotton these insects feed on plants from over 40 families, with the specific host composition varying regionally and temporally, so it is difficult to determine why these insects invade cotton and when they will do so. Our sampling was designed to understand what role, if any, the presence of distinct genetic lineages within *N. viridula* plays in the association of this species with different hosts and in its distribution across continental Australia. We used both phylogenetics and population genetics approaches to assessing gene flow across populations of *N. viridula* from different host plants, as well as across populations from different geographical areas within Australia. Mitochondrial DNA analysis reveals that *N. viridula* arrived in Australia through successive invasions, indicating a complex biogeographical history that resulted in both the Asian and European mitochondrial lineages being present. These lineages are partitioned geographically in Australia, but show no further genetic structure across different host plants within any particular region. Analysis of microsatellite markers indicates, further, that gene flow has occurred across these mitochondrial lineages, in at least some locations. Further analysis on Australian samples is underway. Our current understanding of the genetic diversity within global *N. viridula* populations relies on previous

research that focused on these different mitochondrial lineages. The discordance between the microsatellite and mitochondrial data in our results indicates how the global *N. viridula* populations could be better understood by using microsatellite markers to assess their population genetic structure. This will allow for a more accurate interpretation of the genetic makeup of *N. viridula* populations, which can then be compared with recorded patterns of host use, distribution, and regional population dynamics of this species, and thus inform why and when *N. viridula* invades cotton.

Acknowledgments

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References

Keywords: Australia, phylogenetics, microsatellites, population genetics

INFLUENCE OF THE CROP BORDER ON THE COLONIZATION AND DISPERSAL OF THE BOLL WEEVIL (ANTHONOMUS GRANDIS) IN BRAZIL

Authors: José Ednilson Miranda [1], Bruna Mendes Tripode [1], Ismael Ribeiro Rocha Silva [1]

Institutions: [1] Embrapa Cotton - Embrapa Cotton (Embrapa Cotton)

Abstract:

For nearly two decades cotton production in the Brazilian Cerrado areas coexists with the boll weevil, a major pest of the crop. After the harvest, as food resources will running out, the remnants boll weevil individuals go to refuge areas in order to wait for the new cotton crop. As point of the migration route, the crop perimeter can serve as scale for the insect to feed or reproduce on the latest floral structures. This study aimed to verify the boll weevil behavior in the cotton crop perimeters at the moment of the harvest. The experiment was developed in cotton growing area bordered by native preserved forest. Samplings were made in the first 16 lines of cultivation of 50 plants per row, selected at random. The number of healthy and damaged floral structures, as well as their presence, were recorded through two weeks observation, just before harvest. In the last two weeks before harvest, the remaining individuals (adults and larvae) focused on the crop perimeter where plants produced more floral structures, probably due to less competition for light and water than those situated within the crop. Such comparative ecological advantages of the border plants have enabled the production of floral structures, which favored the establishment of remnants boll weevil individuals, which consequently promoted greater injury on the plants.

Acknowledgments

The authors gratefully acknowledge the Embrapa's partners and supporters: Fundação Goias, SLC Agrícola and Fazenda Macaé.

References

Keywords: Anthonomus grandis, flowering, behavioral control

INTEGRAL CONTROL OF THE BOLL WEEVIL (ANTHONOMUS GRANDIS BOHEMAN) IN COTTON

Authors: Juan Carlos Salerno [1]

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Abstract:

The boll weevil Anthonomus grandis Boheman (Coleoptera: Curculionidae) is the most important cotton pest in Brazil, Argentina, Paraguay and Colombia. The aim of this paper is to provide a framework of action for sustainable integral control of the boll weevil in the region, coupled with management's recommendation, taking into account its impact and increasing aggressiveness and extent of the area of attack. So far, the only possibility of control is with the intensive application of insecticides not be fully effective considering that the weevil is protected inside the flower and makes difficult the entry of agrochemicals to it. The integral control considers the application of different techniques such as the application of myco-insecticides, using bacterium, gene silencing and generation of genetic variability in local germplasm through induced mutations and transgenesis special features for avoiding action and playback the plague.

Acknowledgments

The authors would like to express their sincere gratitude to all individuals and institutions whose members have been used in this paper. Special thanks goes to KALRO, EPZ, KIPPRA and CABI. This report has been completed with a lot of reference from Fibre Directorate (formerly Cotton Development Authority) reports.

References

Keywords: boll wevill, sustainable pest management, control, cotton

NATIVE SPECIES OF ENTOMOPATHOGENIC NEMATODES WITH POTENTIAL FOR CONTROL OF SPODOPTERA FRUGIPERDA SMITH. AND S. ERIDANIA (STOLL) (LEPIDOPTERA: PHALAENIDAE) IN PERU

Authors: Jorge Luis Saavedra Díaz [1], Lito Sigueñas Montalvo [1]

Institutions: [1] UNPRG - Universidad Nacional Pedro Ruiz Gallo (Av. Juan XXIII 391, Lambayeque, Perú)

Abstract:

In the region of Lambayeque, Peru, entomopathogenic nematodes were recovered from the soil of farmers' fields, using *Galleria mellonella larvae* as a sensitive host. Two native species were obtained: *Heterorhabditis baujardi* (Heterorhabditidae) and *Steinernema diaprepesi* (Steinernematidae), which have been studied for their polyphagous nature, regarding their interactions with various important pests. Initial experiments under controlled conditions were carried out with the species *Spodoptera frugiperda* and *Spodoptera eridania*(Fam. : Phalaenidae), key pests such as cotton bollworms and other crops. Different densities of infective nematode larvae on larvae of these species were studied, with the corrected mortality percentage calculated by the formula of Henderson & Tilton. Mortality rates of 92.1% and 84.6% were obtained with *S. frugiperda larvae* of 2nd and 4th stage, and up to 98% and 80% in larvae of 2nd and 4th stage of *S. eridania* with *H. baujardi*, with an average of 40 infective entomopathogenic nematodes per larva on the fourth day of the application. It was noted that mortality began from 48 hours. On the other hand, using *S. diaprepesi*, mortality rates of 38.5% and 12.5% were obtained with larvae of 2nd and 4th stage *S. frugiperda* and up to 46% and 76% with larvae of 2nd and 4th stage of *S. eridania*, respectively, with the same density of nematodes utilized as with the previous species. The observed susceptibility of these species suggests continuing studies under field conditions with these and other cotton pest species that spend part of their larval state in the soil. With this, the tools of biological control of crop pests could be strengthened.

Acknowledgments

The National Institute of Agricultural Research (INIA, for its Spanish acronym) for funding the research.

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Keywords: Earthworms, entomopathogenic nematodes, biological control, pests in cotton, native entomopathogens

TOWARDS BETTER INSECT MANAGEMENT STRATEGY; RESTRICTION OF INSECTICIDAL GENE EXPRESSION TO INSECT BITING SITES IN TRANSGENIC COTTON

Authors: Allah Bakhsh [1], Emine Anayol [2], Sebahattin Ozcan [2]

Institutions: [1] Nigde - Nigde University (Nigde University), [2] Ankara - Ankara University (Ankara University)

Abstract:

Most of the commercialized Bt crops express cry genes under the control of 35S promoter that induces strong foreign gene expression in all plant parts. The constitutive expression of foreign gene (s) has been questioned by many researchers based on various important factors. On the other side, targeted foreign gene expression in plants is esteemed more important as public may likely to accept 'less intrusive' expression of transgene. We developed plant expression constructs harboring cry1Ac gene under control of wound inducible promoter (AoPR1) to confine Bt gene expression in insect wounding parts of cotton plant in comparison with cry1Ac gene under the control of 35S promoter. Both constructs were used to transform four Turkish cotton cultivars (GSN-12, STN-468, Ozbek-100 and Ayhan-107) through Agrobacterium tumefaciens strains GV2260 containing binary vectors p35SAcBAR.101 and AoPR1AcBAR.101 harboring cry1Ac gene under control of 35S and AoPR1 respectively. Phosphinothricin (PPT) was used at concentration of 5 mg L-1 for selection of primary transformants. The primary transformants were analyzed for transgene presence and expression through PCR, real time PCR and enzyme linked immunosorbent assay. The efficacy of introduced insecticidal gene was evaluated using leaf bioassays with larvae of Spodoptera exigua and S. littoralis. The positive plants seeds obtained from T0 progeny were further raised under greenhouse conditions and T1 transgenic progeny was evaluated for cry1Ac gene integration and expression. We found that mechanical wounding of transgenic plant was effective in inducing expression of cry1Ac protein; accumulated levels of cry1Ac protein were recorded during post-wounding period. The transgenic lines in T1 progeny had appreciable level of resistance against targeted pests. We conclude that use of wound inducible promoter to drive insecticidal gene(s) can be regarded as valuable insect resistant management strategy as promoter activity is limited to insect biting sites of plant, no Bt toxin accumulation in unwounded plant organs, seed and crop residues, cotton products and by products, thus minimized food and environmental concerns.

Acknowledgments

The work on development of transgenic cotton in our laboratory was supported by grants from Scientific and Technological Research Council of Turkey TÜB & #304;TAK (Project No. 111O254). The authors acknowledge contribution and support of TÜB & #304;TAK.

References

Keywords: genetic modification, insect resistance, confined expression, comercial

UPDATE ON THE VIRUS DISEASES OF COTTON IN THE UNITED STATES

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Abstract:

Cotton (Gossypium L.) is an economically important agricultural crop and also one of the major sources of food, feed and fiber throughout the world. In the United States (US), cotton is grown approximately 8 million acres annually with an estimated value of more than 50 billion dollars (NASS, 2015). A number of virus diseases have been reported worldwide that infects cotton crops and have significantly affected cotton yield. It is important to know about a particular virus that infects cotton in a locality before formulating control measures against a specific virus. We have initiated surveys for virus-like diseases in cotton crops of Oklahoma and Texas to look for potential virus diseases and determine their relationships with the known viruses reported previously. Various cotton plants showing virus-like symptoms have been collected from the cotton fields. Preliminary data will be presented to update the status of virus diseases in cotton crops of the US.

Acknowledgments

This work was supported by the Cotton Inc. Project number:13-660

References

NASS, National Agricultural Statistics Service–United States Department of Agriculture. 2015. www.nass.usda.gov

Keywords: Cotton, Viruses, Diseases

ZONE MANAGEMENT TO REDUCE COSTS FOR INSECTICIDAL CONTROL OF LYGUS LINEOLARIS IN MIDSOUTH US COTTON

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Abstract:

The carrying capacity of cotton plants will vary with soil physiochemical properties and growing conditions. In the spatially variable agricultural fields common in the Midsouth U.S., crop managers may opt to divide the variable fields into management zones to improve resource use efficiency and reduce production input costs. Zone management practices for agronomic inputs are prevalent on Midsouth cotton [Gossypium hirsutum] farms; however, use of site-specific approaches for insect control are lacking. In this Arkansas researchproject, cotton crop maturity and yield among soil textural zones, with and without irrigation, has been monitored in relation to infestation patterns and feeding injury by Lygus lineolaris (Palisot de Beauvois) (Heteroptera:Miridae). This project has included development and validation of decision guides for crop termination in conjunction with plant monitoring protocols used in the COTMAN™ system (http://cotman.org/). Critical to termination decisions in once-over, machine harvested production systems, is determination of the flowering date of the last effective boll population; this is defined as cutout. As those last effective bolls mature, crop managers use accumulated heat units from date of cutout to identify crop maturity end-points. Earlier maturity means that plants more quickly reach the final stage of crop susceptibility – that late season end-point when a pest species is no longer economically significant. To identify that endpoint can be problematical with indeterminate grow patterns of cotton plants, especially in spatially variable fields. Field stratification into management zones can improve sampling precision and simplify decision-making allowing crop protection tactics to be customized for particular zones. Studies in commercial fields in the Mississippi River Delta region of Northeastern Arkansas, were conducted to gauge cotton plant maturity and yield in management zones across different soil textures, classified using soil EC maps, and in center pivot irrigated fields including irrigated and non-irrigated, rainfed corners. Weekly counts of nodes above white flower (NAWF)) were used to determine date of physiological cutout (NAWF=5) across zones. Lower yielding plants in sandy or clayey soils typically reached cutout 4 to 14 days earlier than plants in sandy loam soils. With low rainfall, non-irrigated plants were lower yielding, and they reached cutout earlier than irrigated plants. Zone management for insecticidal control termination was evaluated in irrigated and rainfed management zones in center pivot irrigated fields in replicated strip trials with three insect control spray treatments (broadcast, zone, or unsprayed) in two management zones (plants under center pivot irrigated “circles” or plants in rainfed “corners”). Final, late-season insecticide applications in broadcast and zone treatments were timed to when last effective bolls had accumulated 250 heat units (DD60s) after cutout (NAWF=5). Over the 4-year study, plants in rainfed zones reached cutout 4 to 21 days earlier than irrigated plants. No yield penalties were associated with following NAWF-based crop termination rules in management zones compared to conventional broadcast control; however, insecticide costs were reduced 14% with zone management. The Fieldprint Calculator tool (https://www.fieldtomarket.org/) was used to evaluate sustainability. Results support the use of zone management in timing insect control termination with both economic and environmental benefits.

Acknowledgments

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Keywords: IPM, Plant Bug, Plant Monitoring, Precision Agriculture, NAWF

COTTON AGRONOMY AND SUSTAINABLE PRODUCTION

BENEFICIAL EFFECTS OF STRUCTURED WATER AND PINK PIGMENTED FACULTATIVE METHYLOTROPHS FOR GROWTH, YIELD AND QUALITY OF IRRIGATED COTTON

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Institutions: [1] ICAR - CENTRAL INSTITUTE FOR COTTON RESEARCH REGIONAL STATI (MARUTHAMALAI MAIN ROAD COIMBATORE 641003)

Abstract:

Water flowing from mountains into river is known to be the purest water and is conditioned by the vortexes formed along its path. Structured water devise is said to create similar effect to water. It breaks up large low energy water molecule clusters into smaller high energy clusters. This gives water a lower surface tension and better hydrating properties. The structured water is different from bulk water and contains more oxygen (Pollack, 2013).The structured water devise marketed by Crystal Blue India based at Mysore, India was used in this study and the bore well water passed through this device is termed as structured water. The experiment was conducted consecutively for two years of 2014-15 and 15-16 cropping season(August-February)atCentral Institute for Cotton Research,Regional Station,Coimbatore to study the influence of structured water and bioinoculants for cotton crop.The design used was split plot design with five replications. The irrigation treatments, structured water irrigation and bore well water irrigation were assigned to the main plot with four bioinoculant treatments in the sub plot.viz., seed treatment of Azospirillum,Phosphorus solubilising bacteria and PPFM each 20g/kg of seeds) ,Seed dressing + soil application of 800 g /ha (each) , seed dressing + soil application + foliar application of PPFM at 1 % concentration twice during flowering to boll development stages were compared with uninoculated control. The soil of the experimental soil was low in Nitrogen, Medium in Phosphorus and high in Potassium.The structured water irrigated cotton were taller in stature, produced more number of leaves, higher chlorophyll , root cation exchange capacity,nutrient uptake and accumulated higher dry matter production. The structured water irrigated cotton produced significantly higher boll numbers (49.9/plant) as against borewell irrigated cotton (40.1bolls/plant).The boll weight also higher(5.83 g/boll) as against 5.66g/boll under bore well irrigation.The enhancement in bolls/plant and boll weight was reflected in seed cotton yield as evidenced from 3173 kgs being recorded under structured water as against 2836 kgs in bore well water irrigation. The fiber quality attributes were better with structured water irrigation. Among the bioinoculants, the subplot treatment which received PPFM as foliar spraying at 1 % concentration twice during flowering to boll development stages combined with seed dressing and soil application influenced the boll numbers significantly over seed dressing alone or seed dressing + soil application. The boll numbers across the irrigation treatments was 41.3 under uninoculated control as compared to 45.1 bolls which received PPFM as foliar spraying combined with seed treatment and soil application of bioinoculants and the yield trend followed as that of bolls/plant with 9.5 % enhanced yield over uninoculated treatment.Pink Pigmented Facultative Methylotrophs (PPFM) influences seed germination and seedling growth by producing plant growth regulators like zeatin and related cytokinins(Holland and Polacco,1994) Compatible with other bioinoculants (Senthilkumar et al.,2002) and bioagents (Nalayini et al,2004) and PPFM could be explored as a potential bioinoculant for cotton nutrition (Nalayini et al.,2010).This study confirmed the beneficial effects of structured water and foliar applied PPFM for cotton crop

Acknowledgments

The author acknowledges with gratitude The Indian Council of Agricultural Research, New Delhi ,The Director, Central Institute For Cotton Research, Nagpur and The Project Coordinator and Head (Cotton) for financial support and facilities provided for conducting this study. The author acknowledgesThe International Cotton AdvisoryCommittee,Washington Dc for the appointment of Research associate

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Keywords: Structured water , PPFM, Bolls, Seed cotton Yield, Fiber quality

COMPARISON OF COTTON TILLAGE PRACTICES IN NORTH CAROLINA, USA

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Institutions: [1] NCSU - North Carolina State University (Raleigh, NC, USA)

Abstract:

Adequate and uniform stand establishment of cotton (< i > Gossypium hirsutum < /i > L.) can be difficult when soil is cool and wet. In years when rainfall in May and June is excessive, stands can be difficult to achieve in reduced tillage cotton. For example, in North Carolina, USA during 2013, rainfall during these months was 84 cm at Rocky Mount resulting in less than optimal stand establishment and poor early season seedling growth. Preparing raised beds in the fall, often referred to as stale seedbeds, is one approach to managing the risk of a poor stand in cool, wet springs. Limited research is available comparing stale seedbed cotton production in North Carolina to conventional and strip-tillage cotton production. The objectives of this study were to evaluate and compare cotton production in reduced tillage systems with conventionally-tilled raised seedbeds as influenced by planting date and wheat (< i > Triticum aestivum < /i > L.) cover crop. A short-term tillage experiment was conducted near Lewiston-Woodville, NC on a Norfolk sandy loam in 2014 and 2015 and at Rocky Mount, NC on an Aycock very fine sandy loam and a Rains very fine sandy loam in 2014 and 2015. Six tillage treatments included combinations of fall and spring conventionally-tilled raised seedbeds and strip-tillage into flat ground in early and late May with and without a wheat cover crop. A long-term study was conducted in 2014 and 2015 near Clayton, NC on a Norfolk sandy loam with six continuous tillage systems of fall and spring raised beds, strip tillage into flat ground, and no-tillage. Soil in continuous no-tillage plots had the greatest resistance to a soil penetrometer and the conventional plots had the least soil resistance both before and after cotton production in 2015. Soil sub-soiled in the fall of 2013 when the experiment was initiated, had soil resistance similar to the conventional plots after two full growing seasons. Response of cotton yield to tillage treatments were observed in five of eight comparisons. Yield of cotton planted in both stale seedbeds and strip-tillage was similar to or greater than conventionally-tilled cotton yield in seven of eight comparisons. These data suggest that cotton grown in stale seedbeds and strip-tillage is comparable to cotton grown in conventionally-tilled systems, especially in years when early season rainfall is not excessive.

Acknowledgments

Funding for these studies was provided by Cotton Incorporated and the North Carolina Cotton Producers Association. Appreciation is expressed to the Central Crops Research Station, the Peanut Belt Research Station, and the Upper Coastal Plain Research Station for assistance with these studies.

References

Keywords: Stale Seedbeds, Strip-Tillage, No-Tillage, Soil Penetration Resistance

COTTON IN DIRECT SEEDING IN ANIMAL-DRAWN FAMILY FARMING

Authors: Miguel Angel Ken Moriya Roa [1]

Institutions: [1] MAG Paraguay - Ministry of Agriculture and Livestock of Paraguay (Yegros nº 437e/ 25 de Mayo y Cerro Corá, Asunción-Paraguay)

Abstract:

Cotton production by small farmers prospered from the 1970s onwards with soils derived from sandstone, which had been recently fortified with a low clay content and acceptable level of organic matter. The systems of soil preparation with moldboard ploughs, the non-use of chemical and/or organic fertilizers, the practice of weed control with high soil removal and the increase of pests that are difficult to control are all factors which have contributed to the gradual reduction in yields, and therefore in the areas of cultivation; aggravated by low international market prices. Starting in 1992, with the expansion of direct seeding in areas of soybean and wheat cultivation, the development of cotton production began with smallholder family farmers and extension workers applying basic principles of conservation agriculture. The lack of equipment and tools for direct seeding in family farming, and especially for cotton production, led to the adaptation and/or development of tools for seeding and crop management. Meanwhile, the validation process carried out by farmers with the species of green manure, which presented improved behavior for a direct seeding system, has allowed cotton to be regarded as a component of a system of recovery for degraded soils since 2006; where the key tools of the system include the use of agricultural lime, chemical fertilizers for system startup, green manure, subsoilers of line seeding, and chemical and mechanical desiccants, with an emphasis on crop rotation. Currently, with the introduction of GM cotton seeds, the yields of the systems of crop rotation in conservation agriculture have presented increases. This work has enabled cotton to be identified as part of a system of recovery for degraded soils, in which a key objective is to increase organic matter while increasing crop productivity; which economically justifies cotton production for the farmers.

Acknowledgments

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Derpsch, R. , Florentín, M. & Moriya, K. Importancia de la Siembra Directa para alcanzar la Sustentabilidad Agrícola. 2006

Keywords: cotton, degraded soils, green manure, direct seeding

List of Oral Presentations Abstracts

COTTON RESEARCH AND PRODUCTION IN NIGERIA CHALLENGES AND STRATEGIES FOR INCREASED PRODUCTION AND PRODUCTIVITY

Authors: S. A DADARI, [1], A.I YAHAYA [1], S. M MOHAMMED [1]

Institutions: [1] IAR - Institute for Agricultural Research, Ahmadu Bello University (Zaria-Nigeria)

Abstract:

Cotton is a major agricultural and industrial crop in Nigeria especially as source of fibre. The crop is also a source of raw material for industries such as the textiles, the oil mills, etc. The country has three cotton growing zones viz, the northern zone which produces about 80 percent; the eastern zone produces about 15 percent while the Southern zone produces the remaining 5%. It remains one of the major cash crop and source of income for the Nigerian farmers. The crop provides job opportunities for between 20-50 million people. The major challenges to cotton productivity includes production constraints, marketing and government policy. For the way forward, there is the need for new set of cotton germplasm, adequate research funding, capacity building, and use of recommended/improved cotton varieties by farmers. The Institute for Agricultural Research Ahmadu Bello University Zaria, has the full mandate for cotton research with reference to variety improvement, purification, seed multiplication, cultural and management practices, crop protection, post-harvest technology and socio-economics of production as well as development of production technologies.

Acknowledgments

The authors would like to express their sincere gratitude to all individuals and institutions whose members have been used in this paper. Special thanks goes to KALRO, EPZ, KIPPRA and CABI. This report has been completed with a lot of reference from Fibre Directorate (formerly Cotton Development Authority) reports.

References

Keywords: Cotton, CHALLENGES AND STRATEGIES, PRODUCTIVITY

COTTON-RICE INTERCROPPING IN CHITTAGONG HILL DISTRICTS OF BANGLADESH

Authors: Dr. Md. Farid Uddin [1]

Institutions: [1] CDB - Cotton Development Board (Khamarbari, Farmgate, Dhaka-1215), [2] CDB - Cotton Development Board (Khamarbari, Farmgate, Dhaka-1215)

Abstract:

Majority of hill population in Chittagong Hill Tracts (CHT) still depends on the hill slope farming for livelihood support. Different forms of intensive to semi-intensive land-use systems have been in practice in the hills of CHT. Among those, slash –and- burn- farming, which is also called shifting or jhum cultivation, is predominant in the hills of CHT. Under Jhum farming generally steep to gentle steep land is cultivated using slash-and-burn techniques. Patches of forest land are first cleared off and subsequent burning of dried vegetation is done before sowing rice, cotton, maize, chilies, sesame, okra, marpha, pigeon pea etc. in the same pit. As a result jhum crops have to compete with each other for nutrient, moisture, sunshine, air and other growth factors. For intra and inter species competition the yield of component crops including cotton, rice are low and unstable. Against this background, Cotton Development Board in Bangladesh has been conducted 120 field trials at the CHT to improve the productivity of the jhum system for three years from 2011 to 2014. The performances of two spatial arrangement viz. (1) 1 row rice +1 row cotton (2) 2 row rice + 1 row cotton were compared with Farmer's practice (Jhum system); the performances of two local varieties of rice viz. Galon, Shere were compared against BRRI dhan-27, a high yield variety of rice; the performances of hybrid and HYV cotton varieties were tested against local hill cotton cultivar and normal planting time was compared with late plantation. Those experiments were carried out in three hill districts of Bandarban, Rangamati and Khagrachari. Results revealed that one row cotton and two rows rice performed better in respect of net income or net profit. Hybrid cotton performed better than hill cotton. Yield of rice varieties did not varied significantly. Sowing at normal time was found better than the late sowing.

Acknowledgments

Krishi Gobeshona Foundation

References

Keywords: Cotton, Intercropping, Hill Agriculture

DETERMINATION OF SOME AGRICULTURAL AND TECHNOLOGICAL PROPERTIES OF COTTON PLANTED AS SECOND-CROP IN WHEAT-COTTON CULTIVATION SYSTEM

Authors: Sema Basbag [1], Remzi Ekinci [1]

Institutions: [1] D.U. Fac. Agri - Dicle University (Dicle University Faculty of Agriculture Field Crops Department 21280Diyarbakir-T)

Abstract:

The opportunity to increase agricultural areas is limited so that increasing demands can be achieved by producing more products from existent agricultural areas. Double cropping is a sustainable practice in which more than one crop is grown and harvested at the same time, on the same ground. This study was carried out to determined fiber technological properties of growing cotton (Gossypium hirsutum L.) as second crop on sttuble of ridge planted wheat in Diyarbak ır. The experiment was conducted of the experimental area of Dicle University Agricultural Faculty as Randomize Complete Block Design with three replications. Eight cotton lines/varieties (Berke, Lachata, BA 119, STV 468, STV 373, Özbek 100, Fantom and DP 396) were used as material. The results indicated

that STV 468, Fantom and Berke in terms of seed cotton yield; Fantom, Berke in terms of fiber length; DP 396 and Berke interms of fiber strength had given highest values. However results showed that whether very early cotton varieties are grown, cotton will be grown as second crop after ridge planted wheat in the stubble seedling under Diyarbak & #305;r ecological condition.

Acknowledgments

This research is supported by Dicle University Scientific Research Projects Cordination Office (DUBAP). We gratefully thanks to for their support.

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Keywords: Cotton, , cultivar, stubble, second crop, yield

DEVELOPMENT OF TWO PILOT TESTS OF COTTON FIBER PRODUCTION IN COLOMBIA THROUGH TWO SYSTEMS OF PRODUCTION: ORGANIC AND LOW ENVIRONMENTAL IMPACT.

Authors: Eduardo Enrique Román Gómez [1], Adriana Calderan Gregolin [1]

Institutions: [1] FAO RLC - Food and Agriculture Organization of the United Nations (Avenida Dag Hammarskjold 3241, Vitacura, Santiago, Chile.)

Abstract:

The project “Strengthening the Cotton Sector through South-South Cooperation,” (South-South trilateral cooperation between the Government of Brazil, FAO and the governments of participating countries), was presented during the ICAC Conference in 2014, as well as in different seminars and workshops. Among the different areas of the project, the issue of sustainability in systems of production is an important strategy. In Colombia, a pilot project was developed in 2013 in two areas: the Departments of Huila (Aipe) and Tolima (Alvarado). The pilot in Alvarado-Tolima was carried out without the presence of cotton in the surrounding area. Half of the plot received organic fertilization (L1T1 -Drycrumbles 300 kg/ha, algae, humic acid, incorporated at 60 days without seed treatment), and the other half received chemical fertilization without seed treatment (L1T2). In Aipe-Huila the plot was located in an area of intensive agriculture; half of the plot received organic fertilization (L2T1 - seed treatment with beneficial microorganisms, COMBOX 750 kg/ha, minor elements and fulvic acids), and the other half received organic fertilizer and chemical fertilizer, treated seeds and microorganisms (L2T2). Conventional soil preparation (disc plough and rake), and manual planting. 100% bio-organic phytosanitary management. Five monitoring stations were established randomly for each treatment and a model of completely randomized design was used. Production and measurements for growth were conducted, along with phytosanitary monitoring, beneficial insects, etc. There were no significant differences in Alvarado or Aipe; neither in the interaction of location or treatment, nor for the interaction location vs. treatment. This could be due to several factors: the plot located in Alvarado presented shading by trees; while in Aipe beneficial microorganisms were used, starting with seed treatment, organic matter was incorporated, reseeding, irrigation and topping were carried out. In both locations the same yield results were found, as the effects of the type of fertilizer and location do not induce a different response in cotton production. It was identified that the variety planted in the zone of commercial agriculture responded well to the organic fertilizer, demonstrating that it could be viable to produce organic cotton in commercial areas in Colombia. Conclusions: Without a premium for sustainable or organic fiber, the activity is not financially appealing to farmers (high use of manual labor is required). Inoculating seeds with beneficial microorganisms is a critical factor to achieve a good crop. Based on the results of these two pilots and analysis of the dynamics of niche markets, it is suggested that projects of organic cotton in Colombia be directed towards family farming schemes. It is recommended that sustainable cotton projects proceed in areas with a low occurrence of the boll weevil. The use of coverage crops and green manure must be included in future projects. Organic and sustainable cotton can be a business opportunity for small producers when they receive technical assistance and rural extension; incorporating technological innovations, and support for adding value. In social terms it is an opportunity for the diversification of systems of production, and to improve the quality of life for family farmers.

Acknowledgments

Banco de comercio exterior de Colombia (BANCOLDEX), Programa de transformación Productiva. Portafolio Verde. Ing. Carlos Brigard Dr. Jorge Cadena (CORPOICA) Asociación Nacional de industriales (ANDI), Cámara de la confección. Algodones del Huila (Ing Luis Fernando Serrano). Empresa algodonera Tolima Norte – EMPRENORTE (Ing. Jairo Palma)

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Keywords: Organic cotton, Antagonist, Biofertilizer, Entomopathogenic, Plant extracts

DOES COMPOST ADDITION IMPROVE BIOLOGICAL FUNCTIONS AND MICROBIAL DIVERSITY IN COTTON SOILS?

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Abstract:

Composts can provide a source of organic carbon and nutrients for soil biota and increase soil fertility as well as provide other biological and structural benefits hence compost addition to cotton soils is seen as a way to improve cotton soil biological health and fertility. We measured the effects of repeated annual application of different compost types, i.e. feedlot, poultry manure and gin trash compost, on microbial populations and activities related to C and nutrient cycling in the surface (0-10 cm) soils from a long-term (after 4 seasons) field experiment located on a Vertosol soil in Queensland, Australia. Additionally, we investigated short-term (6 months) effects in two controlled environment incubation experiments. Generally, there was a significant variation in the chemical composition, e.g. major nutrients and trace elements, between the three compost products. The feedlot compost generally contained higher levels of dissolved organic C, total N and bicarbonate extractable P whereas the Gin trash compost had lower C and nutrient concentrations. In general, the magnitude of effect varied between compost types both in the laboratory and field experiments. Results for the field soils indicated that the addition of various compost materials @ 5 t/ha annually had little or no effect on the microbial biomass and activity measures including the nitrogen mineralization potential of soil. But the catabolic diversity profile data indicated a change in the ability of microbial communities to utilize diverse carbon compounds. Results for the abundances of various microbial groups (i.e. gene abundances) generally showed variable responses suggesting changes in overall microbial community composition. In the incubation experiments, compost addition @ 5 and 10t/ha generally increased microbial activity but the effect was only evident during the first two weeks of incubation. Composts effects on the abundance of total bacteria (16S), nitrifying (amoA), nitrogen fixing (nifH) and denitrifying bacteria (nosZ) and total fungi (ITS gene) varied between different composts. Addition of all three compost materials had no significant effect on the 16S gene abundance, 4 and 24 wks after addition. However, there was a significant increase in the Pseudomonas species population in the soil receiving Feedlot compost. Whereas, the effect of Gintrash and Poultry composts varied in terms of time of change, probably due to the difference in their chemical composition. Populations of soil fungi significantly increased with the addition of Feedlot compost at both rates and Poultry manure @ 5 t/ha. Other changes include, significant increase in chitinase degrading microbial populations in soils receiving Gintrash and Feedlot manure compost and the effect lasted until week 24 in the Gintrash compost treatment. Unlike the Feedlot and Poultry manure composts, Gintrash compost has lower nitrogen and dissolved organic carbon indicating a poor quality in terms of bioavailability or more recalcitrant material. Also, there were lower abundance of denitrifying bacteria in soils receiving Gintrash and Poultry manure composts compared to Control and Feedlot manure compost. Over all, it is important to consider the chemical composition of a compost material to more fully consider its' potential benefits and before application is recommended.

Acknowledgments

Cotton Research and Development Corporation and CSIRO provided the funding for this research. Authors acknowledge the farmer Jan Lefrenz for allowing to conduct the field experiment.

References

Keywords: compost, soil biology, microbial diversity, N mineralization, functional genes

DOES WIDE ROW (1.5 M) COTTON HAVE BETTER YIELD, FIBRE QUALITY AND WATER USE EFFICIENCY THAN CONVENTIONAL ROW (1 M) COTTON?

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Abstract:

Water is the most limiting input in irrigated cotton production. Compaction reduces access to the soil water resource and reduces soil health. Incorporating Controlled Traffic Farming (CTF) in 1.5 m row irrigated cotton improves water use efficiency (WUE). This investigation compared 1.0 m and 1.5 m row-spacing on cotton yield, fibre quality and WUE. The 1.5 m row-spacing cotton was hypothesised to have a similar gross margin and fibre characteristics but greater WUE and yield per plant through access to a larger soil water resource. This replicated study was conducted over two years (2013-14 and 2014-15) and had an RCB design with a field scale whole block experiment which contained nine replicates of 1.0 m and 1.5 m row treatments. The field scale whole block contained two large field blocks of 1.0 m and 1.5 m treatments. The 1.5 m cotton had a greater WUE by producing 0.09 more bales per ML. This reduced the irrigation requirement in the 1.5 m resulting in a higher gross margin than 1.0 m cotton (A$2658/ha and A$2466/ha, respectively). The 1m cotton out yielded the 1.5 m in both seasons by 1.8 bales/ha (16%) and 1.09 bales/ha (6%), respectively. Yield differences in the 1.0 m cotton were only achieved through an increase in inputs. Fibre quality was slightly better in 1.5 m cotton. The 1.5 m row-spacing is more suitable for water limited environments. Furthermore, CTF provides greater water use efficiency by minimising soil compaction.

Acknowledgments

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Keywords: Cotton, Wide rows, Water use efficiency, Yield, Fibre quality

DUE TO THE CLIMATE CHANGE, COTTON PRODUCTION (GOSSYPIUM HIRSUTUM L.) HAS EXPANDED IN ARGENTINA. NOW IT CAN ALSO BE CULTIVATED IN THE PROVINCE OF BUENOS AIRES, PROVING TO BE THE MOST SOUTHERN COTTON FIELDOF SOUTH AMERICA.

Authors: Anibal Ricardo Molina [2]

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Abstract:

So far, and since its inception, cotton has been planted in various parts of the world. This work shows that 20 million more hectares can be planted. In Argentina about 600,000 hectares are cultivated per year in 13 provinces: Formosa, Santa Fe, Santiago del Estero, Corrientes, Córdoba, Salta, Catamarca, Entre Ríos, Jujuy, San Juan, Tucumán, San Luis and Chaco. Cotton production in Argentina now can be extended to a part of the province of Buenos Aires located further south of the traditional planting area due to climate change in recent years in this region. The research was conducted in the district of Bragado, located in the Province of Buenos Aires, https://www.google.co.jp/maps/place/-35.202343,-60.529335, where cotton had never been cultivated. The frost-free period was extended from 160 days in the period 1903/1938 to some 190 days in recent years and the temperature in that period increased, with weeks of 27 to 37 degrees Celsius, which were decisive factors for the expansion of this crop. During the research period, cotton cultivation completely fulfilled its vegetative and reproductive cycle, despite sometimes being exposed to frost in the end of its cycle. Rainfall throughout the growing season, from November to May, are at about 700 mm. The investigations were carried out on a soil with the following taxonomic classification: Typical Hapludoll, loamy fine, mixed, thermal (USDA Soil Taxonomy V. 2006). It is a deep, light, well-drained, non-salty, non-alkaline soil, well provided with the nutrients required by cotton crops. The presence of insects in the crop was very low. Only Aphis gossypii has been for a chemical control. Anthonomus grandis B., considered the most damaging pest in the world for cotton crops, does not exist throughout the region. And possibly this insect never reside in the region. No diseases were presented. During 5 years of research (2011-2015) 5 varieties were planted, 3 genetically modified (NuOpal, Guasuncho 2000 and Delta Pine 402) and 2 conventional (Poirate INTA and Guasuncho 3 INTA). Varying the spacing between rows and sowing period of the crop it was concluded that the bestplanting time is the first week of November and the best distance between rows 1 meter and the distance between plants 12 cm. Parameters were measured as: yield in kg/ha of raw cotton (in the trials ranged from 4,325 kg/Ha and 6,688 kg/Ha) and fiber (fiber yield in those tests was between 1,725 kg/Ha and 2,508 kg/Ha); ginning percentage (between 35.9% and 41.5%) and fiber quality analysis by variety using the HVI Method (performed at the National Institute of Industrial Technology - INTI). Harvest was done manually. With the fiber obtained high quality garments were produced.

Acknowledgments

For my mother Violeta Edelma Font

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Delta and Pine Land – Guía de Manejo para Algodón
El manejo del cultivo del algodón – Guía operativa – Secretaría de Agricultura, Ganadería, Pesca y Alimentación de la República Argentina
Algodón, manual de campo – Instituto Nacional de Tecnología Agropecuaria- Republica Argentina
Programa de asistencia para el mejoramiento de la calidad de la fibra de algodón - Secretaría de Agricultura, Ganadería, Pesca y Alimentación de la República Argentina

Keywords: Climate change, Argentina, Province of Buenos Aires

EFFECT OF DIFFERENT TYPES OF COMPOST MADE FROM RICE STRAW, COTTON STALK, BAGASSE AND THEIR MIXTURE COMPARED WITH MINERAL FERTILIZERS ON COTTON YIELD AND FIBER QUALITY

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Institutions: [1] CRI - Cotton Research Insitute (CRI, ARC, 9 Gamma St., Giza, Egypt)

Abstract:

This research was carried to study the impact of using different types of compost made from rice straw, cotton stalk, bagasse and

their mixture) on Yield, yield components and fiber quality of Giza 90 Egyptian LS cotton variety, to find new source of income for the cotton farmer, because nowadays they face big challenges to cultivate cotton , as you now there is not high benefit to cultivate cotton in all over the world for different reasons, so I thinking to find new and easy technology to help cotton famer to increase their income by recycle the waste or sale the waste. Results indicated that using 50 % compost (3.4 tons *Fed-1) + 50 % (30 kg N fed-1) and 25 % compost (1.7 tons fed-1) + 75 % (45 kg N fed-1) showed means of seed and lint cotton yield, boll weight, lint % seed index and fiber quality very close to those obtained from 100 % N (60 Kg N fed-1) treatment, without statistically significant differences, while using compost alone did not reach their levels of yield and yield components. Rice straw compost and its N combinations proved to be the best one regarding yield and its components followed by the mixture of the three tested compost types and its N combinations, while bagasse and its N combinations ranked as third grade and cotton stalk compost and its N combinations showed the least values of yield and yield components. In most cases the impact of compost and its N combinations on fiber quality was of low magnitude. In spite of the relatively high cost of compost and its combinations with mineral N fertilizer, it is more beneficial to soil structure, fertility and soil minor elements supply. Using compost alone is an important practice in producing organic cotton since the high price of this cotton can compensate the decrease in yield.

Acknowledgments

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References

Keywords: Cotton waste, compost, econmoic impact, cotton yeild, fiber quality

EFFECT OF ORGANIC AND INORGANIC SOURCE OF N AND LOCATIONS ON COTTON YIELD

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Institutions: [1] CDB - Cotton Development Board (Khamarbari, Farmgate, Dhaka-1215, Bangladesh)

Abstract:

Growing concerns about the environmental consequences of inorganic nitrogen use and its future cost perspectives emphasize the need to develop integrated N management technologies combining inorganic and organic sources of nitrogen in cotton production. Field experiments were conducted at three research farms of Cotton Development Board located at Sreepur, Gazipur; Sadarpur, Dinajpur and Jagadishpur, Jessore to determine the effect of various combinations of organic and inorganic source of nitrogen on cotton yield and yield contributing characters in 2013-2014 growing period. The performance of five N sources viz. 100% N from urea, 90% N from urea + 10% N from poultry manure, 80% N from urea + 20% N from poultry manure, 70% N from urea + 30% N from poultry manure and 60% N from urea + 40% N from poultry manure were evaluated. The effect of N sources was found significant for number of primary fruiting branch and number of boll per plant. Besides the interaction effect of location × treatment was found significant for individual boll weight and seed cotton yield. Results revealed that that application of 40% N from poultry manure at Sreepur farm and application of 30% N from poultry manure at Sadarpur and Jagadishpur farm were comparable to 100% of N from urea in respect of seed cotton yield.

Acknowledgments

RAS 5075 Project

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M. K. Islam et al., 2015. EFFECT OF ORGANIC AND INORGANIC SOURCE OF N AND LOCATIONS ON COTTON YIELD, J. Expt. Biosci. 6(1): 47-52, ISSN 223-9626 (Online). ISSN 2077-3358 (Print)

Keywords: Organic fertilizer, Inorganic fertilizer , Cotton yield

EVALUATION OF A PRODUCTION SYSTEM IN CHINA THAT USES HIGH PLANT DENSITY AND RETENTION OF VEGETATIVE BRANCHES WITH REDUCED NITROGEN FERTILIZATION.

Authors: Jianlong Dai [1], Zhen Luo [1], Hequan Lu [1], Shizhen Xu [1], Xiangqiang Kong [1], Hezhong Dong [1]

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Abstract:

Cotton is usually managed intensively by hand pruning and high nitrogen application with a medium plant population density in the Yellow River valley, one of the three major production regions in China (Dai and Dong, 2014). This traditional system characterized with high labor and material input, however, is currently challenged by reduced labor power in countryside and relative low price of cotton in the world. Since vegetative branches can be reduced by high plant density (Bednarz et al., 2000), and increased plant density may compensate for reduced application of nitrogen (Dong et al., 2010, 2012), it is interesting to determine if cotton can be managed by a new production system that uses high plant density and retention of vegetative branches with reduced nitrogen fertilization. Field experiment was carried out from 2013 to 2015 in Linqing (115 42 ′ E, 36 61 ′ N) with a split-split plot design with four replications. The main plot was plant density (5.25 and 8.25 plants m-2), while pruning modes (intensive pruning and retention of vegetative branches only topping) and nitrogen (195 and 255 kg N ha-1) fertilization constituted the sub- and sub-subplots, where intensive pruning was conducted as Dai and Dong (2014). Each sub-subplot contained six rows of cotton, 10 m long with an inter-row spacing of 0.76 m. Results indicated significant interaction effects of plant density with plant pruning or N fertil-

ization on cotton yield, N uptake and N utilization efficiency. At 5.25 plants m-2 density, prunned plants produced 5.2% more lint yield than the retention of vegetative branches, but 9.5% less N uptake. Lint yield in 255 kg N ha-1 was lightly (2.8%) more than in 195 kg N ha-1, and no difference was observed in N uptake and N utilization efficiency. Thus, taking into account of the economic yield only, intensive pruning combined with 255 kg N ha-1 at 5.25 plants m-2 might be the best combination. However, it should be noted that lint yield, N uptake and N utilization efficiency at 8.25 plants m-2 with 195 kg N ha-1 and retention of vegetative branches were relatively comparative to those at 5.25 plants m-2 under intensive pruning and 255 kg N ha-1. The net revenue in the combination of 195 kg N ha-1, 8.25 plants m-2 and retention of vegetative branches was 14% higher than the traditional system and 17-44% higher than other combinations. Therefore, the new system is more competitive than other combinations as result of reducing labor input and fertilizer application without sacrificing yield. It is thus concluded that plant density increased could substitute for more N fertilizer application without reduction in cotton yield under retention of vegetative branches. Retention of vegetative branches combined with less N fertilizer application at high plant density was considered as a new competitive system for cotton production in the Yellow River valley of China.

Acknowledgments

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Keywords: Cotton, pruning, nitrogen fertilizer, plant density

FERTIGATION FREQUENCY ON COTTON YIELD AND PLANT NUTRITION

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Abstract:

The practice of supplying crops in the field with fertilizers via the irrigation water is called fertigation. Best management practices for growing cotton are based on research and experience and apply to cotton under the specified agro-ecological conditions. One important of these is drip irrigation and fertigation. The objectives of this study carried out between 2011 and 2012 in Turkey were to evaluate the effects of drip fertigation frequencies on cotton yield, nitrogen use efficiency (NUE) and the content of some macro and micro elements for cotton. Nitrogen fertigation frequency of every two irrigation cycles (10 days) significantly increased (P & #8804;0.05) cotton yield. The maximum average cotton yield (4120 kg ha-1) for the two experimental years was obtained from the treatment of one lateral for every two rows with one-fifth of the total amount of N during sowing through the soil and equal applications of the remaining N every two irrigations (10 days). The total N content in cotton leaves ranged from 1.66 to 3.05 % in 2011 and from 1.92 to 3.01% in 2012 depending on experimental treatments and growing stages of the plants. The uptake of N increased with an increasing frequency of N application. The maximum NUE (26-38 kg ha-1 kgN-1) was obtained for N fertigation every two irrigation cycles (10 days). The contents of other some macro and micro element in the cotton leaves were: P : 0.19-0.27 %, K: 1.56-1.72 %, Ca: 2.6-5.6 %, Mg: 0.13-0.37 %, Cu: 6.03-8.19 ppm, Zn: 3.55-15.81 ppm, Mn: 43.90-91.92 ppm and Fe: 161-381 ppm. There were no significantly defficiency in terms of micro elemenst except Zn for cotton crop.

Acknowledgments

This study was a part of a research project (Project Number: 10-ZF-166) that was carried out from 2011 to 2012 in the Experimental Station of Agricultural Faculty at Dicle University (Diyarbakir, Turkey).This research project was supported by the Dicle University Scientific Research Projects and Coordination Office.

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Keywords: cotton, lint yield, fertigation, macro elements, micro elements

FLUCTUATION IN STORAGE CARBOHYDRATES IN STEM AND ROOT OF COTTON PLANTS

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Institutions: [1] EMBRAPA - EMBRAPA (Empresa Brasileira de Pesquisa Agropecuária (Embrapa) Campina Grande/PB)

Abstract/:

The total elimination of living cotton plants after harvesting is a challenging requirement in tropical environments because of the perennial nature of this plant. A new approach is proposed for tackling the problem of cotton crop residues destruction. Cotton plants depend on stored carbohydrates to survive along the dry season and sprout when environment conditions become favorable. The plants would not survive without such carbohydrate reserves. Crop management techniques and breeding should be used to develop a cropping system in which cotton plants reach the harvesting time with a low content of carbohydrates. This study was performed with the objective of monitoring the carbohydrate content along the cropping season. Samples were collected in a regular cotton field in the Experimental Farm of Fundação BA (Luis Eduardo Magalhães, BA, Brazil) in the 2014-2015 cropping season. Cotton plants were pulled from the soil (dug when required), and the samples were composed of a 20-cm segment with 10 cm of taproot and 10 cm of the stem. The material was collected every 14 days, from plant emergence to the dry season when the canopy had been pruned. After harvesting, the portion of the stem in the sample was smaller. Crop management was regular with all the practices employed for cotton production in the region. The samples were oven-dried, ground, and the content of starch, sucrose, glucose, and fructose were measured with Megazyme® kits (K-TSTA and K-SURFRG). From seedling up to 56 days after emergence (DAE), which corresponds to the pre-flowering phases of plant development, the total carbohydrates content was stable around 3.2% of the tissue dry weight. From 70 to 140 DAE, corresponding to the phases of flowering and fruit filling the total carbohydrates content increased to approximately 13% of the tissue dry weight. After 154 DAE, corresponding to the phases of crop termination, harvest, and canopy removal, the total carbohydrates had peaks of 15% of the tissue dry weight, and it diminished slowly during the dry season. The harvest occurred around 168 DAE, and from then up to 336 DAE, the plants were exposed to stressful conditions (very hot and dry) and the stored carbohydrates in the cotton taproot and stems remained as high as 11.5% of the tissue dry weight. Soluble sugars (sucrose, glucose, and fructose) are important storing carbohydrates in the early crop development. After 42 DAE, starch is by far the most important carbohydrate stored in the roots and stems. After 70 DAE, starch corresponds on average to 90% of the total carbohydrate stored in that part of the plant. In conclusion, it was found that cotton plants store plenty of carbohydrates, especially starch, to support sprout and regrowth when environmental conditions become favorable. The reserves are enough to endure the dry season and support regrowth of surviving plants in the following rainy season.

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References

Keywords: storage carbohydrates, cotton plants, Fluctuation

IMPACT OF POTASSIUM FERTILIZER ON PLANT BIOMASS AND SEED COTTON YIELD UNDER ARID ENVIRONMENTS

Authors: Dil Baugh Muhammad [1], Muhammad Naveed Afzal [1], Muhammad Tariq [1], Abdul Wakeel [2]

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Abstract:

The transgenic cotton cultivars require higher potassium and its deficiency during peak bloom and boll setting period adversely affects the yield potential. The two years (2014-15) field experiments were conducted at Central Cotton Research Institute, Multan to investigate the potassium requirement of transgenic cotton. In (Set-1) experiment, three potassium doses i.e. 0, 100 and 200 kg K2O ha-1 were applied at sowing and splitted into two equal splits of 100 (pre-plant and 45 DAS) and four equal splits of 200 (pre-plant, 30, 45 and 60 DAS) were tested. While in Set-II, the impact of four foliar sprays of 2% K2O was evaluated in combination with pre-plant application of 0, 100 and 200 kg K2O ha-1 for plant structure, yield components and seed cotton yield. The results revealed that all the potassium levels produced significantly higher seed cotton yield and plant biomass over control. However, split application of potassium irrespective of potassium level was most promising over full pre-plant application for plant structure, total fruit production, number of bolls, boll weight, seed cotton yield and plant biomass. Furthermore, it was also observed that pre-plant application of 200 kg K2O ha-1 along with four foliar sprays of 2% K2O produced the highest figures for plant structure, yield components and seed cotton yield over unfertilized plots. Therefore, it is recommended that cotton must be fertilized with four splits of 200 Kg ha-1 over pre-plant application and four foliar sprays of 2% K2O can further increase the profit margin from pre-plant potassium application.

Acknowledgments

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Keywords: potassium fertilization, foliar feeding, plant structure, seed cotton yield

MANAGEMENT OF LEAF REDDENING THROUGH SOIL AND FOLIAR NUTRITION IN IRRIGATED BT COTTON (GOSSYPIUM HIRSUTUM L.)

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Abstract:

Majority of cotton farmers throughout the India have opined that Bt cotton is very much prone to leaf reddening disorder.Yields can be maximized through integrated nutrition approach. Hence,the field investigation was carried out at MARS Farm, Raichur,India from 2009- 10 to 2011-12 on medium black soil to study the effect of soil and foliar nutrition of NPK and Mg for management of leaf reddening in irrigated Bt-cotton.The experiment comprised of 11 treatments viz., T1: RDF (150: 75: 75 kg NPK/ ha), T2: RDF + Foliar spray (F.S.) of MgSo4 (1%) at 90 and 110 DAS (Check), 125 % RDF incombination with three foliar sprays of 1 % MgSo4 (T3) ,1.0 % 19:19:19(NPK), (T4), 2.0 % KNO3, (T5) , 1.0 % MgSo4 + 2.0 % KNO3 (T6), 1.0 % MgSo4 + 1.0 % 19:19:19(T7), , soil application (S.A.) of MgSo4 at the time of sowing @ 25 kg ha-1 alone (T8) and also with three F.S. of MgSo4 + 19: 19: 19, (T9) , MgSo4 + KNO3 (T10) and MgSo4 +Micro nutrient mixture(T11). In T3 to T11, nutrients solutions as per the treatments were sprayed at flower initiation , boll formation and boll development stages The pooled data revealed that the highest seed cotton yield of 2115 kg ha-1 was obtained with 125 % RDF + S.A .of MgSo4 + 3 F.S. of MgSo4+ KNO3 (T11),followed by 125 % RDF + S.A .of MgSo4 + 3 F.S. of MgSo4 + 19: 19: 19 (T10) (2082 kg ha-1) and 125 % RDF + 3 F.S .of 1.0 % MgSo4 + 2.0 % KNO3 (T6) (2074 kg ha-1) All these treatments were on par and significantly superior over check treatment (T2) (1819 kg ha-1) and RDF (T1) (1773 kg ha-1). The leaf reddening index (LRI) (0-4 scale) indicated that 125 % RDF + S.A .of MgSo4 + 3 F.S. of MgSo4+ KNO3 (T 10) resulted in 42.85 per cent reduction in LRI (0.92) over RDF which recorded significantly higher LRI (1.61) than all other treatments except check treatment (T2) (1.29). Further,the same observations were noticed with respect to total leaf chlorophyll content (SPAD values) at 120 DAS . Data on economics revealed that treatments T 10 and T 9 fetched 12.64 and 12.12 per cent higher net returns over check treatment (T 2) (Rs.61, 028 ha-1). The higher beneficial effects inturns of leaf reddening management, yield and monetary returns were pronounced when foliar spray of MgSo4 was taken in combination with KNO3 or 19:19:19 NPK along with soil application of MgSo4 and 25 % additional NPK dose . Magnesium being associated with maintaining healthy green leaves and higher photosynthesis occupies centre part of the chlorophyll molecule. The foliar nutrition plays an important role in physiology of crop (Weir et al., 2001). In another related study at same location Santhosh ,(2012) and Santhosh et al., (2015) observed lower LRI values and higher cotton leaf N, Mg contents in nutrient management studies.

Acknowledgments

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Keywords: Bt cotton, Leaf reddening, soil and foliar nutririon

MANAGING THE DIVERSE SOIL MICROBIOME - MOST RECENTLY RECOGNIZED BENEFIT OF NO-TILL (ZERO-TILLAGE) TO COTTON

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Abstract:

Cotton growers in North and South America have long been aware of the soil conservation benefits of zero-till (also called no-till). More recently research has demonstrated that zero-tillage benefits organic matter storage, soil structure, soil water availability, and weed seed management with consequent positive impacts on yield and fiber quality. The most recent benefit to be recognized - soil microbiome management and maintenance - was relatively unknown to both growers and agronomists until the techniques to quantify the human microbiomes were developed for soil applications. Besides medical research techniques, other parallels have been noted between healthy soils and healthy humans. Diversity in carbon source, diversity in digestibility, temperature stability and spatial structure are all examples that will be briefly highlighted using field

data across diverse soil and rainfall environments. In addition, suggestions for practical field applications will be presented.

Acknowledgments

References

Keywords: Microbiome, No-till, Zero-tillage

NUTRIENT RESPONSE OF BT COTTON IN VERTISOLS OF NORTHERN KARNATAKA

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Abstract:

Field trial was conducted during 2012-13 and 2013-14 at ARS, Dharwad, Karnataka, India during Kharif season to assess the extent N, P and K nutrients contribution towards the yield of Bt cotton. The trial consisted four treatments viz., T1: Ample NPK (180:70:80 NPK kg/ha), T2: - N (N Omission), T3: - P (P Omission) and T4: -K (K Omission). Deficient micro and secondary nutrients were applied to all four treatment plots wherever necessary based on soil test results. The trial with five replications was laid out on fixed sites during both the years. Quantification of Cry1 Ac and Cry 2Ab at different growth stages was analysed using Quan-T ELISA plate kits from Desi-Gen, Jalna. The data of 2012-13 and 2013-14 indicated that the application of ample NPK recorded higher number of bolls/plant (29.5 & 33.5 respectively), higher seed cotton yield (SCY) (1783 & 3349 kg/ha respectively). N omission resulted in significantly lowest SCY (871 & 1739 kg/ha respectively) followed by K omission (1466 & 2746 kg/ha) and P omission (1594 kg/ha & 2775 kg/ha). The omission of N, P and K resulted in 51 & 48 %, 10.6 & 17.1% and 17.8 & 18% reduction in SCY as compared to application of ample NPK during 2012-13 & 2013-14 respectively. In pooled data, the omission of N, P and K resulted in 49.1 %, 14.8 % and 17.9 % reduction in SCY as compared to application of ample NPK. The extent of reduction in net returns under N, P & K omission treatments were 77.3 %, 25.1% and 26.5 % respectively as compared to the ample NPK treatment. Application of ample NPK resulted in N, P & K uptake of 61.2 kg/ha, 15.6 kg/ha and 60.2 kg/ha respectively. Omission of N resulted in the lowest uptake of N (20.6 kg/ha) as compared to omission of P & K. Similarly omission of P and K recorded a lowest P and K uptake of 8.8 kg/ha and 48.5 kg/ha respectively. Omission of N resulted in lower Cry1 Ac and Cry 2Ab protein content in fresh leaf at different growth stages as compared to the omission of P and K. Application of NPK recorded higher Cry1 Ac and Cry 2Ab protein content in fresh leaf at 60 days after sowing (DAS) and lowest at 120 DAS. Fiber quality parameter like fiber strength and fiber length were reduced in K omission plots (22.6 g/tex & 24.6 mm respectively) as compared to ample NPK (25.5 g/tex & 27.6 respectively). N omission reduced the fiber length (26.4 mm) and matured fiber (55.6 %) as compared to application of ample NPK (27.6 mm & 65.3% respectively). Fiber fineness was reduced in nutrient omission treatments as against the application of ample NPK (3.46 micro g/inch).

Acknowledgments

Authors gratefully acknowledge the financial support and Technical guidance of International Plant Nutrition Institute (IPNI) to undertake this study.

References

Keywords: Net return, Nutrient, Omission, Seed cotton

PERFORMANCE OF POTENTIAL HIRSUTUM COTTON COMPACT VARIETIES UNDER HIGH DENSITY PLANTING SYSTEM (HDPS)

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Abstract:

A field experiment was undertaken to study the performance of potential hirsutum cotton compact varieties under high density planting system in medium deep black soil at the Agriculture Research Station, Dharwad, Karnataka, India, during kharif season of 2014-15. The soil of the site had 0.51 per cent organic carbon with neutral pH (7.01) and 215, 31, and 550 kg ha-1 available N, P2O5, and K2O respectively. The experiment was laid out in Factorial Randomised Block Design with three checks and the treatments were replicated thrice. Four compact varieties were assigned as Factor- I to main plots i.e., V1 : Suraj, V2 : DSC-99, V3: ARBC-64 and V4 : DSC-1351 and four planting geometries i.e., S1 : 45 x 10 cm, S2 : 60 x 10 cm, S3 : 75 x 10 cm and S4 : 90 x 10 cm were assigned as Factor –II to sub plots. Check plots included normal planting of compact variety (C1: 60 x 30 cm), planting of potential Bt cotton hybrid under high density planting system (C2: 60 x 10 cm) and normal planting of Bt cotton (C3: 90 x 60 cm).Farm yard manure @ 5 t ha-1 was applied commonly to all the treatments. All treatment plots of compact varieties received the recommended inorganic fertiliser does of 60: 40:40 N, P2O5, K2O kg ha-1, whereas the Bt cotton hybrid received 100:50:50 N, P2O5, K2O kg ha-1, in check plots. Results indicated that variety DSC-1351 recorded significantly higher seed cotton yield (SCY) of 1721 kg ha-1 which was closely followed by the SCY obtained with DSC-99 (1648 kg ha-1) under high density planting system. DSC-1351 recorded higher boll weight (4.6 g) closely followed by DSC-99 (4.58 g) and Suraj (4.03 g). Planting geometry of 45 x 10 cm resulted in significantly higher SCY (1545 kg ha-1) which was on par with the SCY obtained with planting geometry of 60 x 10 cm (1477 kg ha-1) but higher as compared to the planting geometry of 75x10 cm (1416 kg ha-1) and 90 x 10cm (1330 kg ha-1).This was attributed to the lower boll

weight (3.9 g) recorded under 45 x 10 cm geometry. Bt cotton under recommended practices recorded higher boll weight of 5.5 g while under high density planting of 60 x 10 cm recorded lower number of bolls/plant (14.3) and boll weight (4.5 g) as compared to the normal planting. Variety DSC-1351 with a planting geometry of 60 x10 cm recorded the SCY of 1816 kg/ha which was on par with the SCY obtained with 45x10 cm (1841 kg/ha) and normal planting of DSC-99 (1732 kg ha-1 . Hence, DSC-1351 and DSC-99 were found to be potential hirsutum cotton compact varieties under HDPS with planting geometry of 60 x10 cm in assured rainfed conditions in medium deep black soil.

Acknowledgments

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References

Keywords: Compact, Boll weight, Planting geometry, Seed cotton

PRECISION SEEDING WITHOUT SEEDLING THINNING UNDER DOUBLE MULCHING IMPROVES STAND ESTABLISHMENT AND ECONOMIC YIELD OF COTTON IN THE YELLOW RIVER VALLEY OF CHINA

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Abstract:

Low temperature and rainfall after sowing usually decrease seed emergence and stand establishment, consequently yield reduction (Meryl et al., 1986; Bennett et al., 1966; CRI, 2013). Plastic mulching, widely adopted in China, improves stand establishment through increasing soil temperature, water conservation and preventing adverse effects of rainfall during emergence (Dai and Dong, 2014). In this system, mulching is usually conducted with plastic film (0.6-0.8 um in thickness) after seeding, in which the seedlings should be freed from mulching by cutting film above hills by hand at full emergence. Hand freeing of seedlings in the present system will cost a large amount of labor inputs. Pre-mulching seeding by inserting seeds into the mulched soil can save labor costs of hand freeing of seedling, but emergence and seedling establishment will be reduced in case of rainfall during emergence. Therefore, it is important to design an appropriate seeding method that both avoids the rainfall interference and saves labor costs on hand freeing of seedlings. A two-year experiment was carried out to determine if double mulching can achieve the goal in case of rainfall in the Yellow River valley of China. Field experiment was conducted from 2014 to 2015 in Linqing (115°42′ E, 36°61′ N). A split plot design with four replications was used for the study. The main plot was rainfall treatments (non-rainfall and simulated rainfall of 10 mm), the subplot was modes of mulching including no-mulching, post-seeding mulching, pre-seeding mulching and double mulching. In post-seeding mulching, seedlings were freed from mulch by cutting film above hills by hand at full emergence; in pre-seeding mulching, seeds were inserted into the mulched soil and the film apertures were covered with soil after seeding; in double mulching, seeds were inserted into the mulched soil and recovered by plastic film above the first mulch, and the re-coverage was removed by hand at full emergence. Each subplot contained six rows of cotton, 10 m long with an inter-row spacing of 0.76 m. Results showed that seedling emergence rate, seedling growth and yield were affected by simulated rainfall, mulching and their interaction. Under non-rainfall condition, the emergence rate, seedling dry weight and seed cotton yield of post-seeding mulching, pre-seeding mulching and double mulching was similar, but significantly higher than that in no-mulching. Under simulated rainfall condition, there was no difference in emergence rate, seedling growth and yield between post-seeding mulching and double mulching, while significantly higher than that in pre-seeding mulching owing to the soil hardening of film apertures, the no-mulching was the lowest. While the labor input of removing the upper film in double mulching was lower than hand freeing seedlings in post-seeding mulching. It was concluded that pre-seeding mulching should be advocated in rainless area such as the northwest inland cotton region of China, owing to avoiding seedling freeing and removing film procedure and high yield obtained. Double mulching is an important alternative to improve stand establishment and save labor costs in case of rainfall after seeding in the Yellow River valley cotton region of China.

Acknowledgments

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Keywords: Cotton, plastic mulching, rainfall, emergence rate, yield

STANDARDIZATION OF NUTRIENT MANAGEMENT FOR HIGH DENSITY PLANTING SYSTEM IN ARBOREUM COTTON

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Abstract:

Standardization of nutrient management for high density planting system in arboreum cotton P.L. Nehra and Rajni Gumber Agricultural Research Station (S.K. Rajasthan Agricultural University) Sriganganagar- 335 001, Rajasthan, INDIA ABSTRACT A field experiment was conducted during Kharif 2010-11 and 2011-12 on sandy loam soil low in nitrogen (0.21% OC), medium in phosphorus (18kg P2O5/ha) and high in available potash (325 kg K2O/ha) at Agricultural Research Station, Sriganganagar. The experiment was laid out in split plot design with spacing in main plots and fertilizers in sub-plots. The treatments comprised three spacing, S1- recommended plant population (67.5×30cm), S2- 1.5 times of recommended plant population (67.5×20cm), S3- two times of recommended plant population (67.5×15cm) and three levels of fertilizers (100%, 125% and 150% recommended dose of fertilizer) with four replications. One third dose of nitrogen and full dose of phosphorus were applied at the time of sowing as basal. Remaining one third nitrogen at Ist irrigation and one third at square initiation stage was top dressed. Results revealed that arboreum variety RG-8 gave significantly higher seed cotton yield (2629kg ha-1) under the treatment S2- 1.5 times of recommended plant population (67.5×20cm) over S1 recommended plant population (2410kg ha-1). The higher yield under this treatment was mainly due to increased plant population. Further increase in plant population, two times of recommended plant population (S3) gave statistically at par seed cotton yield (2674kg ha-1) with S2. As regards to fertilizer levels, 100% recommended dose of fertilizer i.e. 90kg N and 20kg P2O5/ha proved as an optimum dose of fertilizer (2565kg ha-1) and further increase in dose could not show its impact on seed cotton yield. Highest nutrient uptake 324kg N, 37kg P2O5 and 173kg K2O ha-1 was recorded under S3- two times of recommended plant population (67.5×15cm). In case of fertilizer treatments 150% recommended dose of fertilizer recorded highest nutrient uptake 314 kg N, 36kg P2O5 and 168kg K2O ha-1. Fibre quality parameters viz., fibre length, uniformity ratio, micronaire value and strength g/tex were not influenced by different levels of spacing and fertilizer.

Acknowledgments

References

Keywords: Arboreum Cotton, Plant spacing, Fertilizer, Seed cotton yield, Fiber quality

THE CHINESE WAY OF ACHIEVING HIGH COTTON YIELDS WITH FARMING TECHNOLOGIES

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Abstract:

Cotton production in China has developed rapidly during the last sixty years. In 2014/15, the planted area and total output in the country were 4.35 million hectares and 6.53 million tons, respectively, and the unit yield was 93% higher than the world average. China currently accounts for about 25% of world cotton production with just over a 12% share of the world area planted to cotton (Dai and Dong, 2014). The high yield is largely due to the country's adoption of intensive farming technologies like double cropping, seedling transplanting, plastic mulching, plant training and super-high plant density (Dong et al., 2007; 2009). (a) Double cropping of cotton with other crops ensures a greater efficiency in the use of soil and solar energy. It also significantly increases multiple crop indexes and reduced competition between cotton and other crops for land resources. Currently the dominant double cropping pattern is of cotton-wheat, cotton-rape and cotton-garlic. (b) Transplanting of cotton seedlings just before or after the wheat harvest can prevent or alleviate the interaction of both crops. It consists essentially of three steps including cultivation of the seedlings in the nursery bed, transplanting seedlings to the fields and field management after transplantation. Compared with direct-seeded cotton after the wheat harvest, the yield of transplanted seedlings was found to be 20 to 30% higher. (c) Chilling, drought and soil salinity stress usually decrease seed emergence and stand establishment.These problems can be solved by plastic mulching. Currently, about 70% of the total cotton area is covered with plastic film, especially in the arid and semi-arid regions of northern China and in saline-alkali soils. (d) Plant pruning mainly involves removal of vegetative branches, topping the plants, and excision of old leaves and empty fruit branches. It can efficiently optimize the relationship between vegetative and reproductive growth, improves the microclimate of plants, reduce boll abscission and rot, thus increasing cotton yield and quality. (e) A "short-dense-early" cultivation pattern has been widely adopted in the Northwest Inland. This pattern is achieved by increasing plant density (20-30 plants/m2), keeping low plant height (60-75cm) and inducing early maturity with the support of drip irrigation under plastic mulching. It is easy for most farmers in northwest to achieve yields of 2,250 kg/ha with the "short-dense-early" scheme. Although these technologies help to meet the needs of a large population with limited arable land, they are labor-intensive and involve large inputs of fertilizers, pesticides and plastic film. The low profitability of cotton production compared to competing crops has inevitably caused the planted area to decrease year after year. Thus, there arose a need to undertake a series of comprehensive countermeasures to increase the benefits of cotton production by simplifying field operations, mechanization, cropping system reform and reduced soil pollution. Cotton production in China can be sustainable and has a bright prospect if supported by new farming technologies.

Acknowledgments

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Keywords: Cotton, intensive farming, double cropping, plastic mulch, transplanting

THE IMPACT OF SEWAGE IRRIGATION ON MORPHOLOGICAL CHARACTERISTICS, YIELD COMPONENTS, AND CONTAIN ELEMENTS OF SEED COTTON IN SHAHR RAY REGION

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Abstract:

To investigate the effects of city sewage on yield and yield components and the contamination balance of heavy metals in Ray Zone , an experiment in form of randomized complete block design with four replications and 5 treatments : Includes Treated domestic wastewater (T1), untreated domestic wastewater raw sewage, (T2) irrigation with well water and treated wastewater as interlaced (T3), irrigation with well water and untreated wastewater as interlaced (T4) and Well water as a control (T5) was conducted . The study showed that the effect of treatments on yield and its components was Significant and best yield performance was achieved from untreated city wastewater. A significant difference at 1% level of earliness was observed among the treatments that the highest percentage of earliness with 75/8% belonged to Control which well water was used and untreated city wastewater had the least percentage of earliness. Significant differences at 1% level of the amount of manganese, copper, iron, nickel, cadmium and lead in cotton seed was observed between treatments. This study showed that the effect of treatments on yield and yield components were effective and the best performance was obtained using untreated home wastewater. The reason is that in this type of wastewater have more nutrients that play an important role in the production of bolls numbers and the performance of final yields. In arid and semi arid regions like Iran reuse of water can be a means to compensate for water shortages.

Acknowledgments

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Keywords: sewage water, Heavy elements, morphological, yield components, cotton

YIELD AND ECONOMIC BENEFITS OF LATE PLANTED SHORT-SEASON COTTON COMPARED WITH INTERCROPPED FULL-SEASON COTTON IN A GARLIC-COTTON DOUBLE CROPPING SYSTEM

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Abstract:

Garlic-cotton double cropping is currently a popular cropping system in China. In this system garlic is sown in late October of the last year and harvested in late May of the year, while cotton seeds are sown in a nursery bed in late March or early April and seedlings are transplanted to garlic fields in late April or early May before harvest of garlic. This labor-intensive and high-input dependent intercropping system, however, is currently challenged with reduced labor power in countryside and relative low price of cotton in China (Dai and Dong, 2014). Direct planting of short–season cotton in late May after garlic harvest may meet the challenges without yield reduction of both crops. The objective of this study is to determine yield and economic benefits of late planted short-season cotton in a garlic-cottondouble cropping system. Three field experiments were consecutively conducted in 2012-2015 in Jinxiang County, China. The first two experiments were arranged in a split plot design with three replications. In the first experiment, main plots were planting patterns including relay intercropping system of garlic with full-season cotton and direct seeding of short-season cotton after garlic. Subplots were four density gradients, in which 1.5, 3.3, 4.5, and 6.0 plants/m2 representing low, middle, high, and super-high plant densities were arranged for full-season cotton, and 3.0, 6.0, 9.0 and 12.0 plants/m2 were arranged for short-season cotton. In the second experiment main plots were planting patterns (intercropped

full-season cotton and direct planting of short season), and subplots were soil fertility (mid and high). The third experiment was arranged in a randomized complete block design in three sites aiming to estimate input, output and gross return of two planting systems. Results indicated that plant density had significant influence on yield in both planting systems. The most suitable planting density was mid-density (3.0 plants/m2) for intercropped full-season cotton, but high plant density (9.0 plants/m2) was the best for short-season cotton based on economic yield. Although yield of short-season cotton at high density was 6.4% lower than that of full-season cotton at mid-density, the gross return of short-season cotton was 69.2% higher because of its lower labor input. There was significant interaction on boll density and boll weight between planting pattern and plant density. High plant density significantly increased boll density, but decreased boll weight and harvest index in both systems. Soil fertility had no influence on yield of short-season cotton but low fertility decreased yield of full-season cotton by 9.1% compared to high fertility. It is suggested that high fertility is essential for the intercropped full-season cotton to gain high yield, but it was not very necessary for short-season cotton. The decreased boll weight was the main reason for reduced yield of full season cotton under low soil fertility. In summary, short-season cotton provides higher gross return with reduced labor and material inputs. Therefore, direct seeding of short-season cotton after garlic can be a new alternative for more benefits in garlic-cotton production areas in the Yellow River valley of China.

Acknowledgments

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Dai, J.L., Dong, H.Z., 2014. Intensive cotton farming technologies in China: Achievements, challenges and countermeasures. Field Crops. Res. 155, 99-110.

Keywords: Cotton, garlic, double cropping, intercropping, short-season cotton

HARVESTING AND POST-HARVESTING TECHNOLOGIES

ADVANCEMENTS IN COTTON HARVESTING RESEARCH

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Abstract:

Cotton harvesting research within USDA ARS is focused on improving harvest productivity, cotton quality, and producer profitability. In recent years, our work has encompassed efforts to improve both spindle picker and brush-roll stripper harvesting systems. Specifically, work with cotton pickers in the Southern High Plains region of the U.S. investigated the application of spindle type harvesters in the traditionally stripper harvested area. New cultivars introduced in the region over the last 15 years have substantially improved yields and fiber quality of the crop. Thus, producers have become interested in identifying new harvesting and processing methods for maximizing the value of the crop. Results from this work indicate that fiber and yarn quality is improved for picker type harvesters but lower harvesting efficiency, relative to stripper harvesters, results in significant lint yield loss that cannot be overcome economically by fiber quality gains. Work with picker type harvesters is ongoing to address design deficiencies which limit their adoption in this region. Current research on improving brush-roll stripper harvester design is focused on minimizing the amount of undesirable vegetative material harvested with the cotton. Modifications to the stripper rolls have been investigated to document the influence of bat/brush sequence on foreign matter content. Previous research on lower yielding cotton with poorer fiber quality indicated that reducing the aggressiveness of the harvesting action by reducing the number of bats used and/or reducing the width of the bats reduces stick content as well as the incidence of bark contamination. Current research efforts on new high yielding cultivars indicate similar results but crop termination and weathering effects may play a more critical role with regard to bark contamination. Additional efforts are focused on improving the cleaning efficiency of onboard field cleaners. Cleaning performance gains have been observed for new grid bar configurations with optimized between-grid spacing around the primary and reclaiming saw cylinders. Additional gains in cleaning efficiency have been observed for cleaner configurations using grid bars with experimental cross-sectional geometry. Yield monitors are an essential tool in site specific management of cotton and can be a useful tool for on-farm research. However, reliable and frequent calibration is needed to ensure the production of accurate seed cotton yield maps, especially when varieties and crop/field conditions change. Calibration data can be costly and difficult to obtain when using mobile scale units for in-field calibration. Moreover, post-calibration techniques can be cumbersome in regard to obtaining and processing multiple gin scale tickets. Recently, a new system was developed by USDA ARS CPPRU for measuring seed cotton weight on the harvester. Information from this system can be used to calibrate yield monitors on the harvester without the need for mobile scales or post-harvest calibration techniques. This system can also be used as a stand-alone system for evaluating the effects of various cultivar, irrigation, fertility, or tillage treatments on seed cotton yield. The authors wish to gratefully acknowledge the financial support of Cotton Incorporated and John Deere in this research.

Acknowledgments

References

Keywords: HARVESTING, PICKER, STRIPPER

CHANGES IN SOIL COMPACTION DUE TO COTTON PICKER TRAFFIC DURING HARVEST ON AUSTRALIAN COTTON SOILS.

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Abstract:

Australian cotton growers have rapidly adopted new picking technology of round module balers on dual tyres. These machines weigh twice that of previous basket pickers, usually on single tyres, being replaced. This raises some concern about implications for subsoil compaction (> 0.4 m depth) from harvest traffic. The objective of this study was to quantify changes in soil strength due to picker traffic during harvest. Measurements of soil strength were undertaken before and after traffic by new round module baler (32 t) and current basket (16 t) pickers during one cotton picking season. Soil cone resistance, water content and Plastic Limit (PL) were measured in the upper 0.6 m depth at eight sites during normal picking operations. Results showed that soil strength increased after traffic of either picker compared with before traffic and increases were detected to a depth of 0.6 m. Despite differences in soils and profile water content, the change in strength was similar under the round module baler and the basket pickers. A zone of greater soil strength (3MPa) occurred closer to the soil surface under the round module baler (0.3 m) compared with the basket picker (0.4 m). Zones of increased soil strength were also detected at 0.6 m depth under both pickers indicating possible subsoil compaction. The OZCOT cotton simulation model was used to determine the frequency at which the soil profile was wetter than the soil PL at harvest for both irrigated and dryland systems. Simulations showed that the soil profile could be expected to be wetter than the PL 75 and 14 % of the time under irrigated and dryland systems, respectively, at harvest over the period from 1960 to 2012. This indicates that cotton picking in irrigated systems has a high probability of occurring when the soil is susceptible to compaction, with the risk of subsoil compaction greater with the roundmodule baler.

Acknowledgments

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Keywords: Round module pickers, Basket Pickers, Soil Strength

COTTON BY-PRODUCTS AND ITS POTENTIAL INDUSTRIAL APPLICATIONS

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Abstract:

India is the largest producer of Cotton in the world with an area of 11.7 million ha and an estimated output of 6 MMT in 2015-16. The estimated cottonseed production is 12.6 MMT and the cotton stalk yield is about 30 MMT. Around 5-7 % of the cottonseed is scientifically processed in India, while the rest are crushed in the expeller with 12 % oil recovery and inferior quality cake/meal. The promotion of scientific cottonseed processing results in production of value added products such as linters, seed hull, oil (with improved oil recovery of 18 %) and protein rich cottonseed meal and an additional benefit of $ 8-9 billion can be generated in the sector. The presence of gossypol in the cottonseed meal render it unsuitable for consumption of non-ruminants. Technology has been developed to reduce the free gossypol content by 80 % and bound gossypol by 60 %. This process improves the protein content by 40 % and lysine content by 25 % enabling it as protein supplement for the poultry and fish feed. Cotton stalk can be effectively used by on-farm value addition as well as for rural industrialization. The cotton stalks contain 60 % holocellulose, 27 % lignin and 7 % ash. A particle board pilot plant with one ton capacity per day was established with the assistance of the Common Fund for Commodities (CFC), Netherlands to demonstrate the utilization of the stalks to produce particle board that confirms IS standard. The plant played a vital role in creating awareness about commercial utilization of the cotton stalks. With more visitors and awareness among the stakeholders the utility of stalks widened to include preparation of briquettes, pellets from the stalks for gasification and energy generation. Around 63 briquetting plants and 10 pelleting plants were established in and around Nagpur region that uses cotton stalk as predominant raw material. This fetched a revenue of Rs. 5000/- per ha ($ 75) for the supply of chipped cotton stalks by the farmers. An accelerated process for composting of the cotton stalks using microbial consortia has been developed that produce bio-enriched compost. The stalks can be used as substrate for growing mushroom with yield of 500 g of edible mushroom per kg of cotton stalks. This provides avenues for the farmers to go for on-farm enterprise development. The value addition to the by-products derived from cottonseed has potential industrial application. Novel energy efficient chemo-bio-mechanical process has been developed to synthesis nanocellulose from the cotton linters that has potential application in the area of agricultural packaging, paper and pulp industries, composite development with superior properties, paint industries etc. A nanocellulose pilot plant of 10 kg production per day has been established at CIRCOT,

Mumbai. There is a need to exploit full potential of the by-produce from cotton for their industrial application. With the dismal market scenario of the cotton sector, these interventionswill promote the cotton economy as a composite economy, ensuring sustainable farm income, rural entrepreneurship development and generate employment to boost the rural economy.

Acknowledgments

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Keywords: cottonseed & stalks, particle board, nanocellulose, briquettes and pellets, Compost

EVALUATION OF A NEW MECHANCIAL DELINTING SYSTEM FOR COTTONSEED

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Abstract:

As research for uses of Ultra-Low Gossypol Cottonseed (ULGCS) has expanded into successful studies evaluating the seed as a protein source for aquaculture and human nutrition, there has arisen a need to process the cottonseed in ways that minimize and/or eliminate potentially hazardous chemicals or methods, such as acid cottonseed delinting. This study evaluated a novel new design of a mechanical delinter for efficacy in lint removal, visible mechanical damage (VMD) to the seed, and germination. The new mechanical delinter was developed to in hopes of being able to produce naked planting quality seed with minimal adverse impact on the seed coat and germination. The primary components of the new mechanical delinter are the cottonseed input and output systems, rotating drum, scrub brushes, and lint removal and cleanout system. The basic principle of operation consists of seed being fed into a counter-clockwise rotating drum lined with an abrasive material. Inside the drum, counter rotating scrub brushes “scrub” the lint from the seed as the seed tumbles around inside the rotating drum. The lint removed from the seed exists the drum through a fan system pulling air from the seed input opening through the drum and out the top-half of the back of the unit. The lint is then removed from the air stream using a cyclone and collected in a catch container. The seed remains in the drum until a predetermined operational time has been reached at which point, the seed is discharged through an opening in the back lower-half of the unit. Critical elements of performance include: 1) Material used - type of abrasive lining the drum and scrub brush material; 2) Rotational speeds - drum and scrub brushes; 3) Spacing - between scrub brushes and between the scrub brushes and the abrasive drum lining; 4) Air volume – the amount of air used to take away the lint removed from the cottonseed. A total of four replications were performed for various treatment combinations with seed and lint collected after each run. The collected seed was sent for analysis to a local lab for germination and VMD measurements. Depending on the variety of cottonseed used, the new mechanical delinting system produced naked seed in 3 to 13 minutes. Based on the recent studies, several modifications have been implemented into the design to improve performance and cleanout.

Acknowledgments

References

Keywords: COTTONSEED, DELINTING, MECHANCIAL

USE OF ELECTRONIC TECHNOLOGIES TO MANAGED SEED COTTON MODULES IN THE UNITED STATES

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Abstract:

Most U.S. farmers and ginners still use paper tags to identify cotton modules along with a large number painted on the side of traditional modules. When the gin gets the module, the paper tag is removed and the information is manually entered into a software program. With RFID technology already used in round modules, every module comes with a unique identifier and all of the data associated with the module can be transmitted or downloaded directly from the picker. Many Australian gins use this technology to manage a majority of their modules. There is growing interest in the U.S. to examine the benefits of electronic module tracking. This presentation provides early examples of attempts to use RFID technologies to track modules at U.S. gins. One effort that will facilitate electronic module tracking in the U.S. is the American Society of

Agricultural and Biological Engineers (ASABE) Cotton Engineering committee's work to develop a voluntary numbering standard for cotton modules which specifies the associated technology required to support electronic data tracking (project number X647). Thus, when an equipment company, tarp manufacturer, or module tag distributor wants to use something like a bar code, QR code, or RFID tag to store a module number, gins will not need multiple hardware and software systems unique to each manufacturer in order to utilize electronic module identification. The current draft of the standard proposes to use a GS1 product code to provide a globally unique identifier for each module. It is hoped that the standard will be balloted and approved in the summer of 2016. One of the key drivers for interest in electronic tracking at this time is the fact that John Deere round modules already have RFID tags embedded in the module wrap. Harvest Identification, Cotton is a process in which the RFID tags are automatically documented for use by the grower, gin, or other trusted advisor to improve traceability of round modules, and simplify the module booking process. In addition to the infrastructure supplied by John Deere, new software tools are also needed to facilitate electronic module tracking. For example, a demonstration application, developed by Cotton Incorporated's Fiber Competition Division, provided a means to read the RFID tags with a hand-held scanner and store the GPS coordinates for the location of that module. The hand held scanner performed well and was able to read modules from about 15-ft away. Several U.S. gins have implemented the RFID system with different levels of automation. Some gins have been able to implement the Australia model where the RFID tag is the only identifier use throughout the life of the module. One gin has modified its module feeder with load cells so that the weight of individual round modules can be recorded. The gin then uses module averaging for each round module (a four lint bale average) so the fiber quality associated with each round module is known. Based on progress to date, additional adoption of electronic module management is expected in the future by U.S. gins.

Acknowledgments

References

Keywords: RFID, tracability, logistics, harvest

FIBER QUALITY AND PROCESSING

CHARACTERISTICS OF COTTON FABRICS PRODUCED FROM SIROSPUN AND PLIED YARNS

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Abstract:

The use of Sirospun yarns eliminates two processing stages in comparison with the two-fold yarns production process and consequently, reduces the cost of production. It is claimed that, it brings many advantages for yarn and fabric quality. However, the benefit of this new concept is still to be investigated extensively. The aim of this paper is to present and analyses the quality parameters of them (Sirospun yarns and conventional two-fold yarns and fabrics) of counts 50/2 and 80/2 In addition, the yarn properties of single yarn counts 25/1 and 40/1. Giza 88 Egyptian cotton combed at 18% noils was used. Yarn physical properties including tensile strength, elongation, unevenness and hairiness were measured and compared. The Sirospun yarn values achieved were superb, with regard to yarn strength, elongation and hairiness. The results indicated that increasing the yarn count within the range of Ne 50/2 to Ne 80/2 decreased the hairiness of Sirospun yarn. It is also shown that the hairiness of Sirospun yarns is significantly less than that of two-fold ring spun yarns. According to results, the structural differences between Sirospun and conventional two-fold yarns had a significant influence on weft direction fabric properties. Weft direction woven from Sirospun yarns were found to have higher tensile strength than fabrics woven from ring two-fold yarns. The test results regarding color reflectance and color strength (K/S) indicated that there is insignificant difference in color reflectance between the fabrics of Sirospun and conventional two-fold yarns in 80/2 and 50/2 Ne. The Sirospun fabrics recorded slightly lower color strength than the conventional two-fold yarn fabrics. This result reveals that much less dye can be used for the fabrics of Sirospun fabric, so their dyeing cost might be lower for the same depth of shade in comparison to fabrics of conventional two-fold yarns.

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Keywords: sirospun yarn, plied yarn, fabric

COMPARISON OF UTILITY PROPERTIES OF FABRICS MADE OF COTTON AND COTTON/PES BLENDS

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Abstract:

Cotton is one of the most important raw material applied in the fabrics for apparel industry. However, in the last decade the chemical fibers, especially the polyester fibers are used the most often in fabrics and clothing. There are used only by themselves or together with natural fibers. Combining the cotton and polyester fibers in one textile product leads to better utilization of both kinds of fibers and to optimal properties of the final products. The paper presents an investigation of the woven fabrics made of cotton and cotton/PES blends of different share of cotton and polyester: CO67/PES33, CO50/PES50 and CO33/PES67 [1]. The plain woven fabrics of the same warp and weft density were measured in the range of their mechanical properties as well as the utility properties such as: stiffness, crease resistance, drapeability, formability, surface friction, air permeability and protection against the UV radiation. According to an expectation it was stated that the share of PES fibers in the blend significantly influences the mechanical properties of woven fabrics. The higher percentage of PES fibers, the higher breaking force and elongation at break of the fabrics in both directions: warp and weft. The same relation was observed for the fabric stiffness. The cotton fabrics are characterized by significantly lower crease resistance than the fabrics made of cotton/polyester blends [2]. The higher share of PES fibers in the fabrics made of the CO/PES blend, the higher crease resistance. The opposite tendency was observed in the case of the drapeability of fabrics [3]. The fabric made of cotton is characterized by much higher drapeability than the fabrics made of the CO/PES blends. The results did not show any clear relationship between the percentage of PES fibers and the drapeability of the cotton-polyester woven fabrics. The formability of fabrics also depends on their rawmaterial composition [4]. The highest formability was stated for fabric made of CO67/PES33 blend. The formability of cotton fabric is at the same level than formability of fabric made of the CO50/PES50 blend. The lowest value of the formability was stated for the CO33/PES67 woven fabric. The investigated fabrics differed significantly in the aspect of their surface friction. The cotton fabric is characterized by the lowest value of the static and kinetic frictional coefficients. The highest values of frictional coefficients were noted for the CO33/PES67 woven fabric. Similarly to the drapeability, obtained results did not show any tendency in the relationship between the share of the PES fibers in woven fabrics made of CO/PES blends and the values of the frictional coefficients. Performed investigations confirmed that the cotton fabric significantly surpasses the CO/PES fabrics in the air permeability. On the other hand, the addition of the PES fibers into the woven fabric structure significantly improves the protection against the UV radiation. On the basis of the presented investigation it was stated that by an appropriate blending the cotton with the polyester there is possible to shape the mechanical, technological and utility properties of the woven fabrics.

Acknowledgments

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Keywords: cotton, polyester, woven fabrics, utility properties

COTTON COLOR MEASUREMENT BY MEANS OF HVI, SPECTROPHOTOMETER AND DIGIEYE

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Abstract:

Color is one of the most important properties of cotton. It is a basic criterion, which decides on the quality classification of cotton raw materials [1]. The color grade of cotton is determined by the degree of the reflectance (Rd) and yellowness (+b). They are measured instrumentally by the HVI. Scientists dealing with cotton make efforts to find an instrumental method of cotton color measurement alternative to the HVI color measurement [2, 3]. The paper presents the measurements of color of cotton samples by means of 3 methods: the HVI, spectrophotometer and DigiEye. 21 cotton samples of different origin were measured in the range of their color parameters. The HVI measured the degree of reflectance (Rd) and yellowness (+b) of cotton. By means of the spectrophotometer Datacolor 650 the following color parameters were determined: the lightness - L* and the chromaticity coordinates: a* – green/red, b* – blue/yellow, C* – chroma, h – hue angle [4]. The DigiEye is a computer-controlled digital camera system for measuring color and capturing high-quality repeatable images. In opposite to the HVI and spectrophotometer the DigiEye measures the color of the sample image captured by the calibrated digital camera. The DigiEye provides complex color data for selected area of the cotton sample image. Colorimetric values X, Y, Z with L*, a*, b* are recorded against a selection of standard illuminants: D65, D50, A, F2, F7 and F11 [5]. The results of measurement by means of the described instruments were analyzed from the point of view of their agreement. Performed analysis confirmed the statistically significant correlation between the results of color measurement by means of the HVI and spectrophotometer. A very strong correlation (Rx,y = 0.947) was stated between the (Rd) from the HVI and L* from the spectrophotometer. Lower value of the correlation coefficient (Rx,y = 0.733) was stated between the (+b) from the HVI and b* color coordinate from the spectrophotometer. Strong correlation (Rx,y = 0.865) was also stated between the (Rd) from the HVI and L* from the DigiEye. However, in all cases the values of the lightness L* form the DigiEye were higher than the values of the degree of the reflectance (Rd) from the HVI. The correlation between the yellowness (+b) from the HVI and b* color coordinate from the DigiEye was weaker

(Rx,y = 0.656) than in the case of the HVI and spectrophotometer. In a majority of cases the values of the yellowness (+b) from the DigiEye were lower than the values of the b* color coordinate from the DigiEye. Performed investigations confirmed that there is statistically significant correlation between the results from the spectrophotometer and DigiEye. In both cases: lightness and b* color coordinate the values of the correlation coefficient between the spectrophotometer and DigiEye were higher than 0.8. It was also stated that an application of the DigiEye in the cotton color measurement requires further investigation in order to elaborate the procedures of sample preparation and precise and repeatable color measurement.

Acknowledgments

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Keywords: cotton, colour, measurement, HVI, DigiEye

EFFECT OF NITROGEN AND PHOSPHORUS FERTILIZERS ON MEDIUM COUNT COTTON FIBER PROPERTIES, BARAC(67) B

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Abstract:

Abstract:- This work is concerned with the investigation of the effect of nitrogen and phosphorus fertilizers on cotton fibre properties. Variety under consideration was Barac(67)B produced at two locations, Wad-Elataya and Hag Abdallah in two consecutive seasons. Different levels of both fertilizers were applied in randomized complete block design and their effects on fibre properties were investigated. Parameters measured were fiber length, uniformity ratio, micronaire value, fibre maturity and fibre bundle strength. All tests have been carried out under cotton fibre laboratory standards which were relative humidity (R.H) 65% ±2%, temperature 25c & #730;±2c & #730;. The results obtained showed that, mostly, high rates of nitrogen gave better values of fibre length, micronaire and maturity .Application of phosphorus at H/Abdallah had a positive effect on fibre bundle strength. In general, cotton produced at W/Elataya location was of more superior quality than that produced at H/Abdallah location.

Acknowledgments

References

Keywords: Fibre length, Micronaire, Maturity, strength

IS IT POSSIBLE TO CHECK MICROGINNING FIBER QUALITY PRESERVATION PERFORMANCE USING REFERENCE SEED-COTTON?

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Abstract:

In sub-Saharian countries, simple micro-gin, without seed-cotton cleaner nor lint-cleaner, is often used as a reference device for characterizing the performance of industrial gin plants for fiber quality preservation. It is however useful to check if this micro-gin itself is properly set and maintained. Reference seed-cotton materials, well homogenized with known variability level, and available in large quantities, may serve the purpose of monitoring the performance of the micro-gin in order to detect any malfunction or any drift. Therefore, it is expected that any deviation in SITC results on ginned reference seed-cotton materials from predetermined data would alert on altered ginning conditions. This experiment demonstrates the feasibility of setting mean values and confidence intervals on measured SITC characteristics on fiber samples, to later detect any malfunction or drift that may occur in practices, settings, or degradation in a micro-gin.

Acknowledgments

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Keywords: Ginning performance, Fiber quality, Reference materials

ECONOMICS/COTTON COMPETITIVENESS

EVOLUTION OF BT COTTON PRODUCTION COSTS AND EFFECTIVENESS IN NORTHERN CHINA OVER A DECADE

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Abstract:

Transgenic cotton made resistant to target pest with Bt gene (Bt cotton) have been used for almost twenty years in a handful of countries to which belongs China. In 1997, Bt cotton has been commercially released in China, firstly in a limited number of Northern provinces and particularly in Hebei province. The use of Bt cotton has given rise mainly, if not exclusively, to short term assessment of its effectiveness and profitability in various countries and particularly in developing countries. In India and in China where most assessment studies were conducted, differences in production costs and profitability were appraised between Bt cotton and conventional cotton few years after the commercial release of Bt cotton and when both types of cotton were still in use. Most studies have provided evidence on Bt effectiveness and profitability, although their scientific rigor was seldom perfect. There are few if any studies to appraise the mid-term effectiveness and profitability of Bt cotton use. One reason is the generalized use of Bt cotton that prevents implementing comparison of Bt and conventional cotton in the same way than in short term studies. Indeed, in most countries having adopted Bt cotton, the short term effectiveness has led producers to stop growing conventional cotton varieties. The generalized use of Bt cotton almost two decades after their commercial launch does not necessarily mean that its short term effectiveness and profitability have been maintained. Varieties of conventional cotton might not be grown for lack of availability of corresponding seeds, as observed in many countries. The effectiveness and profitability have been altered by the phenomenon of pest complex shift, in the sense that some pests have shifted from the status of secondary pests to that of primary ones. The phenomenon is particularly documented for lygus in several countries, including China. This communication is a contribution to mid-term appraisal of Bt cotton use through an alternative method. Since Bt cotton effectiveness and profitability can no longer be implemented through comparison to conventional cotton as long as this latter is absent, they are assessed through the evolution of Bt cotton production costs and profitability over a period, as well as the evolution of cotton producers' perception of Bt cotton use. The alternative method of mid-term appraisal of Bt cotton use has been applied in Hebei province, Northern China, where yearly surveys have been conducted to cover production campaigns dating back to 2002/03. Data collected through surveys encompassed production costs and returns, producers' opinions on Bt cotton effectiveness and profitability as well as their feelings about the changes of pest infestations. Results indicate producers' perceptions of the evolution of pest infestation that are consistent with the phenomenon of pest complex shift. This phenomenon leads producers to less acknowledge Bt cotton effectiveness and profitability, because pest control costs have been increasing and yield stagnating.

Acknowledgments

References

Keywords: China, Cost of production, Bt cotton, Effectiveness, pest complex

IMPACT OF THE COTTON SUB-SECTOR ON RURAL SMALLHOLDER LIVELIHOODS: LESSONS FROM KENYA

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Abstract:

Cotton is an important cash crop that was introduced into Kenya in 1901 by the British colonial Government. This crop is grown in the margin and low productive areas in Kenya. Also, it provides income to smallholder and resource poor farmers. The successive administrations introduced policies that enhanced the production and marketing of cotton. However, the structural adjustment programmes (SAPs) in the 1980s had a negative impact on the production and marketing of cotton in Kenya. A large number of smallholder farmers continue to live under the poverty line. The aim of this paper was to present an overview of the current situation in

the cotton sub-sector in Kenya. This was done to identify the constraints and challenges in order to improve on the production and raise income and livelihoods of smallholder farmers. It is proposed to refocus and enforce the existing policies for improved production of cotton in Kenya.

Acknowledgments

The authors would like to express their sincere gratitude to all individuals and institutions whose members have been used in this paper. Special thanks goes to KALRO, EPZ, KIPPRA and CABI. This report has been completed with a lot of reference from Fibre Directorate (formerly Cotton Development Authority) reports.

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Keywords: Cotton , Smallholders, Margin, Polices, Constraints

MARKET FOR WASTE COTTON FIBERS: CASE STUDY OF THE UNITED STATES

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Abstract:

A significant part of the cotton fiber supply currently operates beyond consideration of the cotton production sector, because it occurs beyond the farm gate. The cotton fibers in this non-farm supply include gin motes, linters from processed cottonseed, USDA classing samples, opening and cleaning waste in spinning mills, comber noils in spinning mills, as well as yarn and selvedge waste from fabric formation. There are also diverse operations for reclaiming the fibers from discarded textile products; however, these activities are beyond the scope of this study, which is targeting the gate-to-gate portion of the supply chain between the farm and the finished textile products. The properties of these waste cotton fibers and the uses to which they may apply are quite diverse. The fibers range from bona fide waste fibers to virgin fibers that are waste only in the sense that these are distributed outside the traditional farm-to-retail market channels. The uses range from pharmaceuticals, to black powder catalysts, to batting pads, to insulation, to diverse nonwoven products, as well as to utilization in traditional yarn spinning operations. Therefore, these fibers constitute a multi-million-dollar component of the total impact of cotton on the economy, which is largely ignored for industrywide planning or policy purposes.

Acknowledgments

This study was funded by the Texas State Support Committee of Cotton Incorporated.

References

Keywords: Waste, Cotton, Motes, Linters, Virgin

OPPORTUNITIES FOR COTTON DEVELOPMENT IN PARAGUAY, IN THE CONTEXT OF THE ANALYSIS OF TRANSACTION COSTS

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Abstract:

Agricultural production, especially regarding a commodity such as cotton, requires an evaluation of the economic behavior between the actors involved in the production chain. The present study aims to analyze the transaction costs in the systems of cotton production within the context of family farming in Paraguay, through data obtained in the scope of the project of International Cooperation between the Government of Brazil, FAO and the Government of Paraguay, “Strengthening Cotton Production Chain in Family Farming Systems in Paraguay” A characterization analysis of the cotton value chain was developed by the project in 2015, with the support of the Institute of Development of Paraguay. The basis for sampling used in the analysis is comprised of a group of 305 cotton family farmers from the 6main cotton-producing provinces in the country, with the number of farmers statistically representative of the country. In addition to the farmers, data was also included from the other links in the production chain: 26 middlemen of the same province, 10 ginning facilities, 5financial entities and 13 technicians of various levels of insertion in the cotton productive chain in Paraguay (academia, government, technical assistance and rural extension, and research). The process of modeling was carried out through the methodology of transaction costs, taking into account essential characteristics to determine the economic value of the crop. Thus it was possible to define models to minimize transaction costs by means of contractual mechanisms, whether formal or informal, which may discourage the current conflicts observed in the productive chain. The main scenario evaluated is based on the strengthening of agricultural activities to minimize dependence on external sources in relation to the provision of inputs and services. For this,

an assessment was made of the technical specifications (productivity, costs of inputs, ease of access to quality inputs, logistics, and the dynamics of the market operators); as well as geographical specifics, due to the physical immobility of cotton processing units, as the majority of the processors were installed in the region over 30 years ago. Therefore, given the situation of decreased dependency, the result identifies the development of strategies for reducing the existing external transaction costs through horizontal integration as a priority; thus optimizing associations and increases on a productive scale, primarily as global prices have declined about 60% in the last 5 years and the increase of scale allows farmers to facilitate transactions between actors of the value chain, increasing the power of local negotiation. Furthermore, it was observed that vertical integration, as opposed to horizontal integration, is not compatible with the productive context in Paraguay, since its inclusion is conditional upon the historical relationship with middlemen, which hinder the development of this process due to the high opportunity cost and capillarity that they possess.

Acknowledgments

Agradecimento especial ao Projeto "Fortalecimento do Setor Algodoeiro, por meio da Cooperação Sul-Sul" (FAO-ABC/MRE), pela disponibilização dos dados. Ao Governo do Paraguai pela gestão na execução do Projeto-País e ao Instituto de Desarrollo pelo levantamento das informações com os produtores algodoeiros familiares.

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Keywords: Transaction Costs, Cotton, South-South Cooperation, Family Farming, Competitiveness

THE APPROACH OF EUROPEAN COEXISTENCE BUREAU FOR SUSTAINABLE COEXISTENCE OF GENETICALLY MODIFIED COTTON PRODUCTION WITH CONVENTIONAL AND ORGANIC FARMING

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Abstract:

Being closely associated with the mankind history from ancient times to now days, the evolution of cotton genus was subject on intensive directional selection for desirable fibre properties, resulting in massive reprogramming of cotton transcriptome and entailing partially a reallocation from stress response pathways toward fibre growth, which in turn explains the pest and drought susceptibility of modern cultivars. As more efficient alternatives to resource and labour intensive conventional production of cotton, with strong impact on environment, biotechnological and organic practices for cotton cultivation were introduced. In this industrial and market situation, without authorization of GM cotton cultivation in European Union (EU), the Technical working group (TWG) for cotton of the European coexistence bureau (ECoB) analysed the possibility for coexistence between GM cotton cultivation and non-GM cotton and honey production by addressing the potential sources of GM cross-pollination and admixture which can occur during the farm scale activities, in the context of European agro-climatic and landscape conditions. Based on the extensive analysis (covering total of 194 references), the TWG for cotton of the ECoB proposes the best management practices and provides an approach for evaluation of their potential economic impact. It was concluded that to limit cross-pollination rates between GM and non-GM cotton fields below a 0.9% or 0.1% admixture threshold the establishment of 10m and 20m of buffer zones between them respectively is sufficient. The efficiency of bare ground for preventing of adventitious admixing is lower compare to buffer zones, because of that to achieve 0.9% and 0.1% limits 30m and 100m is required respectively. The current practices in honey production and marketing in Europe in line with the quality legislation are sufficient to ensure that adventitious presence of GM cotton pollen in honey is far below the legal labelling thresholds and even below 0.1% and the adoption of any additional coexistence measures is not necessary.

Acknowledgments

The authors would like to express their sincere gratitude to all individuals and institutions whose members have been used in this paper. Special thanks goes to KALRO, EPZ, KIPPRA and CABI. This report has been completed with a lot of reference from Fibre Directorate (formerly Cotton Development Authority) reports.

References

Keywords: Sustainable Production, Cotton Agronomy, European Coexistence

SOCIAL DYNAMICS AND TECHNOLOGY TRANSFER

FRONT LINE DEMONSTRATION – PROVEN TRANSFER OF TECHNOLOGY APPROACH FOR FOSTERING PRODUCTIVITY OF COTTON IN INDIA

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Abstract:

The results of Front Line Demonstration, an age old proven Transfer of Technology (TOT) approach adopted in cotton emphasized the potential of increasing the yield in India to the tune of world average through demonstrating the sustainable and profitable technologies-developed by the Indian Cotton Research System. The field demonstration conducted under the close supervision of Scientists of the National Agricultural Research System in India is called Front Line Demonstration (FLD). The objectives of FLD are demonstrating the usefulness of the latest improved crop production and protection technologies to the farmers as well as extension workers with a view to reduce the time gap between technology generation and its adoption. It also enables the scientists to obtain direct feedback from cotton farmers and suitably reorient their research programs, develop appropriate technology packages and to create effective linkage among scientists, extension personnel and farmers. This programme has been implemented for cotton crop through Indian Council of Agricultural Research - All India Coordinated Research Project on Cotton since 1996-97. Until 2015, around eighty four million rupees had been spent by the Ministry of Agriculture, Government of India for conducting 18100 FLDs in the ten cotton growing states of India. "Seeing is believing" is the principle of FLD and "Yield Enhancement" is its major motive. For analyzing the impact of these demonstrations on yield enhancement of cotton, the secondary data pertaining to the number of demonstrations conducted so far on cotton through various centers, the average yield obtained from demonstration and the average yield of local farmers' practices were collected and analyzed. The analysis revealed that all through the 18 years, the major technologies contributed for yield increase under FLD were high yielding new cotton varieties and hybrids, Integrated Weed, Water, Disease and Pest Management techniques, intercropping, growth regulators, agro techniques and cotton farm implements. Analysis on yield enhancement due to FLD revealed that an average of 1631 kg/ha seed cotton yield was obtained in the demonstration which was 18.70 per cent increase over the normal farmers' practices of the locations. The average yield gap observed between the FLD and normal farmers' practices was 257 kg seed cotton yield. In addition a significant reduction in the cost of production was observed in FLD as compared to the farmers own practices. Modernizing this proven TOT approach with new extension innovations will foster the productivity of cotton and thereby the profitability of cotton growers in India.

Acknowledgments

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Keywords: TOT, Front Line Demonstrations, Extension, Technology Dissemination, Cotton

GENDER PERSPECTIVE IN THE COTTON VALUE CHAIN: CHALLENGES AND OPPORTUNITIES IN ARGENTINA, BOLIVIA, COLOMBIA, PARAGUAY AND PERU

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Abstract:

This paper discusses the results of a study conducted in Argentina, Bolivia, Colombia, Paraguay and Peru between May and November 2014, on the roles of women cotton producers, along with the factors affecting their participation and gender equity in the chain cotton value. The study was carried out within the framework of the regional project "Strengthening the Cotton Sector through South-South Cooperation," jointly implemented by the FAO Regional Office for Latin America and the Caribbean and the Brazilian Cooperation Agency (ABC/MRE) in Mercosur and associated countries, and Haiti. The study was developed with a participatory approach, integrating a quantitative and qualitative methodology, including fieldwork with both male and female farmers, conducting focus groups and interviews with key actors in the cotton value chain. The development of the study showed that in practice, there are bottlenecks for the participation of women in the cotton value chain which have an impact on their quality of life, and which influence the extension of cycles of poverty and rural exclusion and hinder an effective participation in the market. Based on fieldwork with cotton farmers, eight factors were identified which influence the scope of gender equality in the cotton value chain and therefore affect the empowerment of men and women: (1) Land Tenure / Ownership / access to leasing of farm plots (land) (2) Power of decision-making regarding the farm / income / themselves / mobility (3) Access to Credits and Benefits (4) Access to Technical Assistance (training, formal and informal or adult/extension) (5) Time (use of time) (6) Market Access (local, regional, international) (7) Representativeness (Power of representation or association) (8) Access to services Based on the areas identified, it was possible to propose a set of indicators to measure gender gaps in the countries in order

to guide the establishment of policies, programs and actions in the sector. The study also identified specific experiences regarding the participation of rural women in the cotton value chain. The following were surveyed: from Bolivia, the Organization of Rural Women Producers and Cotton Artisans of Bolivia- UNIARTE; from Paraguay, the Cooperative of Producers of Ao-po'i in Yataiti, Guaira and the Organization of Women Artisans of the Carapeguá district; and in Peru in the region of Lambayeque, the Association Manos con Talento, Caserío Poma 3 and the Association of Artisans Huaca de Barro. Based on the factors and experiences identified, it was possible to suggest recommendations in the area of public policies at the global and sectoral level, with emphasis on four main themes: 1) instruments and mechanisms to ensure the rights of rural women; 2) records of statistical data disaggregated by gender; 3) inter-agency coordination and response capacity and 4) regulatory programs, subsidies and benefits for the cotton sector. Promoting the issue of gender, including rural youth, in the cotton-producing countries through programs, actions in the field and institutional support is an important opportunity to achieve inclusive rural development.

Acknowledgments

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Keywords: Gender, gaps, indicators, empowerment , value chain

THE PARAIBA COTTON PROJECT - A PROPOSAL FOR LOCAL INTEGRATED DEVELOPMENT WITHIN THE SCOPE OF FAMILY FARMING

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Abstract:

In the mid-19th century, the Northeastern region of Brazil became the most important cotton-producer and exporter in the country. In the State of Paraiba, cotton was responsible for high rates of economic and population growth and the city of Campina Grande stood out for being the world´s second largest cotton trading hub. The Paraiba Cotton Project recovers this part of history of the Northeastern region, and adds to it the value of agroecology and principles of solidary economy. Within the scope of this innovative experience in sustainable local development with a participatory approach to production and trade management, family farmers are supported through technical assistance and rural extension (TARE); in order to make decisions regarding the best planting season and techniques, adapt research demands according to real needs, and directly negotiate with buyers of ginned cotton. The main goal is for the family farmers to participate in the organic cotton value chain, in order to increase production rates and reduce costs, in addition to integrating cotton with beef,milk-cattle and goat production chains. Thus, the project contributes to the discussion on concrete conditions for the insertion of family farming in the global market. In order to make this project viable, it was necessary to build a partnership between many individuals, organizations and markets involved in cotton cultivation. Meetings were held to define the role and responsibilities of each counterpart. This included production with support from TARE, through the Paraiba State Technical Assistance and Rural Extension Enterprise (EMATER-PB); from research, through Embrapa Cotton; and from trade and logistics, through the family farming organizations Coopnatural and NORFIL Textile. In this process, proposals for the improvement of existing public policies and programs in support of family farming were identified. As a result, four production centers were identified and selected: Medio Sertao, Curimatau, Borborema and Agreste. Purchase and sale agreements were signed and a work plan was agreed upon; comprised of the planting season, a capacity development program for farmers, field days and Technical Demonstrative Units. Production estimates for the 2015/2016 harvest are 160 tons of cotton fiber with 300 ha planted, involving 150 farming families on average. In recognition, the Brazilian Cooperation Agency, the FAO and ASBRAER have invited EMATER-PB to participate in and support technical assistance and rural extension activities, through the trilateral technical cooperation project ´Strengthening the Cotton Sector through South-South Cooperation´, jointly carried out by the Brazilian government, FAO and MERCOSUR member states and associates.

Acknowledgments

EMBRAPA Cotton Coopnatural Norfil Textile

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Keywords: cotton, family farming, EMATER-PB, organic cotton, Paraiba

THE PERFORMANCE OF FARMER FIELD SCHOOLS IN THE ZAMBIAN COTTON PRODUCTION SYSTEM

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Abstract:

Many technological innovations have been developed to improve agricultural productivity in Zambia. However, the adoption of these technologies has been low. Appropriate extension models are often seen as the missing link between adoption and the achievement of productivity gains. Integrated Production and Pest Management (IPPM) has long been shown to have reduced production cost due to improved use of pesticides and other input costs. However, its introduction has been met with some resistance with farmers as it is viewed to be more labour intensive to implement. Thus, appropriate extension models have to be identified to integrate this approach into small holder farmer systems. Hence the introduction of Integrated production and pest management using the farmer field school (FFS) approach is needed. After implementing the FFS, an Impact study was conducted using standard questionnaires to asses the farmer perception towards this technology, improve the quality of activities and ensure sustainability of the program through buy in from partners. Evaluations were conducted at group level using focused group discussions for FFS participants and at individual levels between FFS participants and non FFS participants in each area where the schools were set up. Data collected was for two seasons namely 2014/15 and 20015/16 seasons. The results showed that 67% of the farmers who attended the FFS training were satisfied to very satisfied with the training. In the first year of implementation farmers were able to adopt the following practises: gap filling, weekly field observations and reduction of pesticide use. After participating the program for one year, farmers felt that the training should also include food security and budgeting. The experimental plots also showed significant differences in the final cotton yields. In the IPPM plots the average yield was 1301.67 kg per hectare while in the non FFS plots the yields were 767.5 kg per hectares. Farmer field schools can be considered as an extension option for small holder cotton farmers. More work needs to be done to ensure their sustainability in the Zambian cotton sector.

Acknowledgments

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Keywords: Cotton, Extension Models, Farmers, Farmer Field Schools, Integrated Production and Pest Managemen

USE OF WEB-BASED INFORMATION DELIVERY BY COTTON INCORPORATED

Authors: Ryan Kurtz [1], Ed Barnes [1], Phil Bogdan [2]

Institutions: [1] CI - Cotton Incorporated (Cary, NC, USA), [2] PMN - Plant Management Network (St. Paul, MN, USA)

Abstract:

Each year, Cotton Incorporated funds more than 300 research projects with universities, USDA and private cooperators across the United States. The majority of these projects are aimed at improving production efficiency and profitability. To help transfer the research results to the production community as quickly and easily as possible, Cotton Incorporated's Agriculture and Environmental Research Department has developed the Cotton Cultivated website and has partnered with the Plant Management Network to deliver the Focus on Cotton webcast series. The Cotton Cultivated website provides a portal that integrates websites, downloadable documents, social media and real-time news feeds that have been "cultivated" in an effort to reduce the time spent sort through pages of irrelevant search results. Focus on Cotton is an open-access monthly webcast series aimed at keeping producers informed on the latest developments and research findings that impact the management and profitability of their cotton farming operations. These audiovisual presentations from noted cotton industry experts offer practical information and guidance in all areas of crop production. These web-based resources are designed to operate on desktop as well as mobile devices allowing users to stay current on the latest research developments at their convenience anywhere there is an internet or cellular data connection.

Acknowledgments

References

Keywords: online, webcast, website

MEASURING SUSTAINABILITY IN COTTON FARMING SYSTEMS

AN UPDATE GLOBAL LIFE CYCLE INVENTORY FOR COTTON

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Abstract:

Life Cycle Assessment (LCA) allows the holistic examination of the environmental impact and resource utilization of a product, from the raw materials used in its creation to the disposal at the end of life. A fundamental component of LCA is the Life Cycle Inventory (LCI), a quantification of relevant energy and material input and environmental release data associated with the manufacturing process. The primary purpose of this project was to provide robust and recent LCI data for global cotton fiber production and textile manufacturing so that cotton is accurately represented in LCAs and provide an update to a similar study completed in 2010. Additionally, Life Cycle Assessments (LCAs) were performed to evaluate the environmental impacts of three cotton garments: t-shirts, knit casual collared shirts, and woven casual pants. The study was conducted according to the principles of the ISO 14040 series. The LCA was divided into three primary phases: the agricultural production phase (seed to production of a bale of fiber from the gin); textile processing (bale to fabric); and use (cut and sew, consumer use and disposal). Agricultural data were collected from the United States, India, China and Australia to represent average production conditions from 2010 to 2014. These countries represented the top three cotton producing and cotton exporting countries during the study period. In an effort to collect the best quality data, textile mills that have relationships with Cotton Incorporated account representatives were selected based on the products that they manufacture, level of verticality, and, and location. Countries and regions of interest (China, India, Turkey, East Asia, and Latin America) were identified based on world textile manufacturing volume. Consumer use behavior data were collected by Cotton Council International and Cotton Incorporated using an international, third party market research company to survey respondents in the uppermost consuming countries regarding their use and laundering practices for T-shirts, knit casual collared shirts and casual woven pants. The survey was conducted from May through June 2015 in fivecountries including the United States (U.S.), China, Japan, Italy, the United Kingdom (UK), and Germany. Preliminary results indicate that most of environmental impact measures for the agricultural and textile phases have not changed significantly since the 2010 study. The differences that were found were due to improved data sources or updates to methodology since the last study as opposed to changes in practices. In the use phase, there was a reduction in most metrics as the current study characterized a global consumer while the 2010 study was limited to U.S. consumer behavior. For the agricultural phase, many of the impacts such has greenhouse gas emissions and energy consumption could be tied back to nitrogen use. Efforts for precise nitrogen management should be a continued priority to reduce impacts of agricultural production.

Acknowledgments

References

Keywords: LCA, sustainability, metrics

MEASURING SUSTAINABILITY IN AUSTRALIAN COTTON FARMING SYSTEMS

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Abstract:

This abstract reports on the use of the Global Reporting Initiative sustainability reporting framework (GRI 2013) and the principles of International Cotton Advisory Committee Expert Panel on Social, Economic Environmental Performance of Cotton Production (2013) to measure the sustainability of the Australian cotton industry. Measurement of cotton industry sustainability requires consistent approaches across multiple farms, regions and sites, repeated over long periods of time. There are many market driven sustainability initiatives around the globe that expect good data to be available, which is not always easy to achieve. Any ongoing review of selected indicators needs to be balanced by the needs of external stakeholders and challenges of collecting long term data sets. The iterative nature of the process, especially with external stakeholder involvement is time consuming and challenging. An inventory of potential cotton farming sustainability indicators was developed which reviewed the material issues of stakeholders and the literature (Roth 2010). This set of potential sustainability indicators was assessed and updated by the Australian cotton industry's environmental assessment working group, taking into account more recent developments in international supply chain sustainability initiatives such as the Better Cotton Initiative, Cotton LEADS™, and the Expert Panel on Social, Environmental and Economic Performance of Cotton Production of the International Cotton Advisory Committee (SEEP 2013). A list of more than 100 potential sustainability indicators was compiled. These indicators were then prioritised using an objective ranking system which scored indicators against six selection criteria. These criteria included; materiality to cotton industry stakeholders, materiality to external stakeholders, cost effectiveness of data collection, technical difficulty of data collection, data integrity and confidence, and accuracy in the data collection. Forty five indicators were shortlisted as high priority material metrics for the cotton industry to collect, collate and report on. An analysis of data was then compiled from a range of sources including the scientific literature and industry reports. The full report is published

as the Australian Grown Cotton Sustainability Report 2014 (Cotton Australia / CRDC 2014; Roth et al 2015).

Acknowledgments

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Keywords: Sustainability, cotton, economic, environment, social

MONITORING THE IMPACT OF IRRIGATED COTTON PRODUCTION ON SOIL CONDITION IN A SEMI-ARID LANDSCAPE IN AUSTRALIA

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Abstract:

The Australian landscape is ancient and, compared to many other countries in the world, possesses highly weathered and infertile. Combining these soils with the intense nature of irrigated cotton production (large fertiliser/water inputs, constant cultivation) poses some significant challenges in the management of the soil whilst maintaining cotton yields. Some important land degradation issues faced in Australia include salinisation and acidification of the soil, as well as the loss of soil organic carbon (SOC). Of particular interest is the trajectory of change in soil pH, salinity and SOC content as the management of soils intensifies. While cotton has been grown in eastern Australia for many decades, the industry is rapidly expanding further south, away from traditional cotton-growing areas. One such example is the semi-arid area of Hillston in New South Wales, which was previously a dryland cropping/grazing area, but has turned into one of the largest and most intense cotton growing regions in Australia in the last decade. In 2002, an extensive baseline soil survey was conducted in Hillston, with a suite of soil properties analysed to assess the preliminary impacts of irrigated cotton production on the soil. The same area was resampled in 2015, with many of the original sites revisited. The objectives of this study are to estimate the change in soil pH, electrical conductivity (EC), and SOC over the 13-year time period under different landuses, including intensive cotton production. Unlike most monitoring studies that solely focus on the topsoil, this study considers 6 depth increments down the soil profile to a depth of 1.5 m, as the condition of the subsoil proves just as vital in cotton production. Additionally, there are few soil monitoring studies that focus on semi-arid areas that have undergone dramatic landuse change, with studies on temperate areas and the tropics being most dominant. To model the change in soil properties we will use linear mixed models with a range of predictor variables (radiometrics, landuse, terrain attributes). This study shows that irrigated cotton production has a significant role in altering soil in a semi-arid australian landscape, however, it also demonstrates that these changes in soil condition are not always necessarily negative. For example, topsoil acidification trends have been observed, however, pH levels are shifting from alkaline towards neutral. In addition, drops in topsoil salinity have also been observed between the two surveys.

Acknowledgments

Acknowledgements to the Cotton Research & Development Corporation (CRDC) for providing funding to attend this conference.

References

Keywords: Soil monitoring, Soil change, Soil condition, Soil sustainability, Land use change

PRODUCTIVE PARAMETERS FOR THE COTTON SECTOR IN PARAGUAY: BASELINE ANALYSIS IN RURAL FAMILY FARMING

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Abstract:

In 2015 the project of international cooperation “Strengthening Cotton Production Systems in Family Farming in Paraguay,” jointly implemented by FAO and the governments of Brazil and Paraguay, conducted an analysis on the cotton sector. The first phase of the projectcreated a baseline of productive, economic, environ-

mental and social information as an input to design public-private policies to reactivate the cotton sector. Primary data was generated with diagnostic tools (surveys) conducted in 6 provinces representing the cotton-producing areas: Caazapá, Caaguazú, Paraguarí, Concepción, Ñeembucú and San Pedro. Field information was obtained from 305 family farms. The areas were studied using continuous and discrete variables based on the data from Excel, which was systematized by the Institute of Development of Paraguay (IDe). The descriptive analysis used information from 303 units: 11% with a traditional system (conventional seeds) and 89% in the commercial system (GM seeds), with statistics of central tendency and dispersion, provincial segmentation and separated by system of production (traditional-commercial). A comparison of relative frequencies used the goodness-of-fit test $\chi 2$ (P

QUANTIFYING CONTINUOUS IMPROVEMENT IN COTTON PRODUCTION PRACTICES IN THE U.S.

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Abstract:

Of all the agricultural crops, only cotton competes with petroleum based products. Even sugarcane and corn grain used for ethanol have other outlets besides competing with petroleum fuel. Cotton competes with polyester in every textile application and with a severe impediment due to the cost and difficulty of textile processing associated with natural products versus synthetic raw materials. Polyester is both cheaper and easier to process into yarn and finished garments. It is only because of the consumer demand for cotton and the ability of cotton growers to make efficiency advancements that we have a market for our agricultural product. While the majority of consumers consider cotton to be safe for the environment, brands and retailers want data to show that cotton growers are responsible stewards of the environment. To provide this data, global and national level programs have been developed and employed. In 2015 a Natural Resource Survey was conducted by Cotton Incorporated that recorded responses from 10% of the U.S. cotton production. These results show continual improvement in most areas of concern to consumers (water, pesticides, land, energy) but more importantly show the close relationship between resource stewardship, input efficiency, and overall profitability. A summary of U.S. results with an eye on how to push for continual improvement will be presented. Considering the global concerns about energy and reactive nitrogen, these topics will be covered in more detail. A brief mention of other national and global cotton production metrics program will also be included.

Acknowledgments

References

Keywords: stewardship, sustainability, metrics, consumer, improvement

BREEDING AND CROP IMPROVEMENT IN COTTON

EXPRESSION OF THE SERK GENE IN NON-RECALCITRANT COTTON GENOTYPES

Authors: José Jaime Vasconcelos Cavalcanti [1], Roseane Cavalcanti dos Santos [1], Carliane Rebeca Coelho da Silva [2], Julita Maria Frota Chagas Carvalho [1], Liziane Maria de Lima [1], Taiza da Cunha Soares [1]

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Abstract:

The transgenesis techniques have offered great versatility to cotton improvement due to possibility of introducing an exogenous transgene, keeping the whole agronomic properties of varieties. The limitation of this process is in the necessity of plant regeneration by somatic embryogenesis, since some genotypes are recalcitrant, hindering the progress of selection and the time spent on research. Some reports have shown that SERK gene (Somatic embryogenesis Receptor Kinase) is involved in embryo formation and also that overexpression is related to embryogenic competence. In order to prospect a gene marker able to identify no-recalcitrant cotton genotypes, in this study we estimated the expression of SERK in six cotton cultivars, by using RT-qPCR. Further we validate the results by crop tissue procedures. The cv. Coker 312 was adopted as a positive control (not recalcitrant). Total RNA from floral meristems was extracted and used for cDNA synthesis. SYBR Green kit (Ludwig) was used to RT-qPCR, according to manufacturer's instructions. A pair of SERK primer (200 bp) was used in reactions. The PP2A (Protein phosphatase 2A) and Ebf1 (EIN3-F-box binding protein 1) were used as endogenous control. All samples showed expression SERK, but at low levels in BRS 201, BRS Topázio e CNPA Precoce 1. The expression of BRS Rubi was 2X higher than control (Coker 312). To validation assays, hypocotyls were grown in MS medium (Murashige and Skoog) supplemented with naphthaleneacetic acid (NAA) and Kinetin (KIN) and further transferred to MS medium plus glutamine and growth regulators-free, according methodology adopted by our team. We verified that somatic embryos were obtained only to Coker 312, BRS Rubi and BRS Seridó, confirming the results seen in RT-qPCR. We suggest that a SERK probe may serve as a valuable tool for identifying non recalcitrant cotton germplasm, given a valuably contributing to cotton somatic embryogenesis.

Acknowledgments

References

Keywords: Gossypium, somatic embryogenesis, Real time PCR

COMPARISON OF SUCCESSFUL COTTON GENOTYPES IN SALINE REGIONS OF IRAN

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Abstract:

During the years 2012 and 2013, an experiment was carried out to study the effect of soil salinity on morphological characteristics of cotton (Gossypium hirsutum L.) and identifying the salt-tolerant cotton cultivars in Golestan province (in the experimental field of Anbar-oloum Research Station). The experiment was arranged as a factorial by a randomized complete block design with three replications. The treatments were included 12 genotypes of cotton, and measured growth parameters such as: germination, plant height, yield, earliness, number and weight of boll and fiber quality traits. The obtained data were analyzed and compared. The results of combined analysis of variance showed that; among studied genotypes, Golestan produced the greatest seed cotton yield (2624 kg/ha) and the highest earliness (35%). Genotype of Q28 had the lowest yield by 1310 kg/ha.

Acknowledgments

References

Keywords: Cotton genotypes (Gossypium hirsutum L.), Soil salinity, cotton yield

GROUPING OF COTTON GENOTYPES OF COLORED FIBER DERIVED FROM DIFFERENT CROSSES

Authors: Matheus Rodrigues Martins [1], Michel de Carvalho Reis [1], Bruna Cardoso Gomes [1], Cynthia Pereira Gundim [1], Danilo Araújo Gomes [1], Elvécio Gomes da Silva Júnior [1], Guilherme Hugo da Silva Costa [1], João Felipe Moraes Ferreira [1], Letícia Teixeira Gold Pereira [1], Larissa Barbosa de Sousa [1]

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Abstract:

Cotton is considered the most important natural fiber of vegetable origin among the textile fiber. The colorful cotton fiber has instigated the interest of textiles to cater for intolerant consumers to dyes used in the dyeing process. The study of genetic variation and the phenotypic performance of genotypes is important for genetic breeding programs, which is useful for breeders in selecting parents to generate segregating population. The objective of this study was to group colored cotton fiber genotypes of Programa de Melhoramento Genético do Algodoeiro of Universidade Federal de Uberlândia (PROMALG-UFU) based on intrinsic characteristics of the fiber and assess whether they meet the requirements imposed by the textile industry. The experiment was conducted in an experimental area located at Fazenda Capim Branco - UFU belonging to the Universidade Federal de Uberlândia, in Uber-

lândia, Minas Gerais, in the 2014/2015 season. Eighteen genotypes of cotton were evaluated, sixteen lineages (LC) of PROMALG-UFU and two witnesses (BRS Rubi and BRS Topázio). The experimental design was a randomized complete block design (RBD) with four replications. The experimental plot was consisted of five rows of five meters spaced 0.9 meters from each other. Seven intrinsic characteristics of the fiber were evaluated through the HVI (High Volume Instrument): micronaire index (MI), fiber maturity (FM), fiber length (UHM) (mm), length uniformity (CU) (%), short fibers index (SFI) (%), tensile strength (RES) (gf / tex), and elongation at break (along). Data were subjected to analysis of variance (F test) and test group (Scott and Knott test). For all the intrinsic characteristics of the fiber evaluated, the genotypes were assigned to the same group, which demonstrates that there was no genetic variability among them, although all genotypes had mean higher than required by the textile industry. The colored fiber cotton genotypes of the Programa de Melhoramento Genético do Algodoeiro UFU have fiber quality and meet meet the requirements of the textile industry.

Acknowledgments

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Keywords: Gossypium hirsutum, variability, genotypes, breeding, HVI

WHITE FIBER COTTONSEED AND FIBER YIELD FROM BIPARENTAL CROSSING

Authors: Matheus Rodrigues Martins [1], Bruna Cardoso Gomes [1], Cynthia Pereira Gundim [1], Daniel Bonifácio Oliveira Cardoso [1], Daniel Inserra Bortolin [1], Elvécio Gomes da Silva Júnior [1], Guilherme Hugo da Silva Costa [1], João Felipe Moraes Ferreira [1], Matheus Araújo Bernardes de Souza [1], Larissa Barbosa de Sousa [1]

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Abstract:

The major end product from cotton plants is the fiber, which has its use widespread worldwide in the production of fabrics in general. To obtain a better quality tissue, it is necessary for the fiber to have quality standards, which restrict differentials characteristics. The objective of this study was to evaluate the productivity and fiber yield of cotton genotypes. The study was developed in the field, in Fazenda Capim Branco - UFU, in Uberlândia - MG, during the season 2014/2015. It was used as an experimental model a randomized block design (RBD) with four replications and 21 genotypes, 19 strains (LB14-A, LB14-B, LB14-C, LB14-D, LB14-F, LB14-G, LB14-H, LB14-I, LB14-J, LB14-K, LB14-L, LB14-M, LB14-N, LB14-O, LB14-P, LB14-R, LB14-S, LB14-T, LB14-Z) of the Programa de Melhoramento Genético do Algodoeiro UFU (PROMALG-UFU) and two witnesses (DP 555 and FM 966). The experimental plot consisted of five rows of five meters, with spacing of 0.90 meters. The characters evaluated were: cottonseed productivity (kg ha-1) and fiber lint yield (%). Data were submitted to analysis of variance and the means were grouped by the Scott-Knott test (Scott; KNOTT, 1974) ($p<0.05$) using the SISVAR program (FERREIRA, 2011). There was genetic variability among genotypes for cottonseed productivity. The genotype DP 555 showed the best performance and stayed in unit group with an average of 2264.00 kg ha-1, followed by group II, represented by genotypes J and R, with an average of 1759.49 kg ha-1. The genotypes LB14-P, LB14-O, LB14-L, LB14-B, LB14-J, LB14-R, LB14-T, LB14-N were in the same group and had the lowest average, ranging between 998.73 kg ha-1 and 354.48 kg ha-1. As for the plume yield (%), all genotypes were in the same group and had averages between 34.35% and 40.91%. Although even the lower values are within the limits set by the textile industry. Genotype 555 stood out with high cotton productivity in seed and fiber yield, followed by genotypes LB14-J and LB14-R, which are presented as superior to the Programa de Melhoramento Genético do Algodoeiro of Universidade Federal de Uberlândia.>

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Keywords: Gossypium hirsutum, breeding, perfomance, improvement

HIGH GINNING OUT TURN AND THE IMPROVEMENT OF ETHIOPIAN COTTON PRODUCTION

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Abstract:

This paper presents the importance of the improvement of ginning out turn in Ethiopian cotton production. The introduction and registra-

tion of new varieties in 2014, an increase of GOT and lint production is expected to transform Ethiopian lint production. The average GOT of varieties across eight locations was between 43 and 46%. This reaches up to 7.8 % advantage over the current standard variety and contributes 50-83% lint yield increase. Samples were ginned by saw gins and tested by HVI 1000. The varieties are 7 and 15 % better than the standard check for length and strength, respectively. It is highly advisable to adopt the registered technologies across agro ecologies to benefit both small and commercial producers.

Acknowledgments

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Keywords: GOT, lint yield, Cotton, quality, Ethiopia

GENETIC STUDY OF PHYSIOLOGICAL TRAITS IN INTER VARIETAL CROSSES COTTON (G.HIRSUTUM) IN SALINITY AND NON SALINITY STRESS CONDITION

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Institutions: [1] CRII - Cotton Research Institute of Iran (CRII-Agricultural Research, Education and Extension (AREEO)- Gorgan-Iran)

Abstract:

Salinity in topsoil and subsoil is one of the major abiotic environmental stresses to crop production. In order to studying the genetic and physiological traits related to salinity tolerance, five new elite cotton (G.hirsutum) and 10 hybrids were evaluated under greenhouse conditions using a completely randomized block design with three replications. The salinity levels were created with the addition of NaCl in the soil (EC= 2 and 12) through irrigation water in three applications. The result showed that the amount of anthocyanine, proline and glycine betain increased in Cotton plant under salinity condition. Analysis of variance in saline status indicated to genetic differences among the genotypes for 10 charactristics (except chlorophyll a); however, in non-saline condition, all the traits were significant (except sodium) indicating genetic variation. The hybrids BG539 × N2 and Cok349× N2 exhibited higher adaptive potential under salinity stress and non stress condition, respectively. Genetic analysis by Hyman- Jinks method indicated both additive and non additive genetic variances for anthocianin, proline and chlorine in plants in both growth condition. The chlorophyll b, chlorophyll ab, K/Na ratio have non-additive genetic variances. Over dominance effect was seen for all the traits except for glycin betain and K/Na ratio , dominance effect was seen for these two characteristics.

Acknowledgments

References

Keywords: Salinity , hybrids , anthocyanine, additive genetic varian

RELATIVE IMPORTANCE OF CHARACTERS IN THE STUDY OF GENETIC DIVERSITY OF GOSSYPIUM HIRSUTUM COTTON GENOTYPES

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Abstract:

A major part of the expansion of cotton production in Brazil is credited to genetic breeding. Studies on the characteristics that best define the genetic distance between accesses and cultivars is of utmost importance to breeding programs, especially in the selection of genotypes with improved performance, which favor the production of genetically superior populations. The objective was to identify the most relevant characteristics for the study of genetic divergence in white fiber cotton. The study was conducted at field level, at Fazenda Capim Branco UFU, located in Uberlândia, Minas Gerais, in the 2014/2015 season. The experimental design was randomized blocks (RBD), with twenty accesses and four repetitions. The plot consisted of five rows of five meters, spaced 0.90 meters apart. The useful area of the plot was constituted by the three main lines, with 0.5 meter border at each end. The evaluated characters were chlorophyll content A and B; number of reproductive branches; height of the first reproductive branch; number of first, second, third and fourth position fruits; leaf width and length; cottonseed productivity (kg ha-¹) and fiber yield (%). The chlorophyll content was obtained by the electronic chlorophyll meter ClorofiLOG, sampling two leaves of 10 plants in each plot. The characteristics cottonseed productivity and fiber yield were determined from all cotton bolls collected in the useful area of the plot. The other characteristics were assessed at the beginning of the flowering period of the crop, at 80 DAE. Among the 12 characteristics involved in the study, cottonseed productivity had the highest contribution, 40.16% in the study of genetic diversity among genotypes, followed by leaf width (11.40%), 4th position apples (10,29%) and fiber yield (9.03%). Although the characteristic leaf length have been suggested for disposal, leaf width appears to be a very important feature, since it enhances the photosynthetic area, resulting in greater cottonseed and plume productivity. Cottonseed productivity is a characteristic to be prioritized in genetic diversity studies of white fiber cotton genotypes.

Acknowledgments

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Keywords: SINGH, cotton, genetic breeding, genetic distance

PLUME YIELD AND NUMBER OF FIRST POSITION FRUITS IN COLORED FIBER COTTON GENOTYPES

Authors: Daniel Inserra Bortolin [1], Danilo Araújo Gomes [1], Cynthia Pereira Gundim [1], Guilherme Hugo da Silva Costa [1], Letícia Teixeira Gold Pereira [1], Matheus Rodrigues Martins [1], Melissa Martins de Araújo [1], Michel de Carvalho Reis [1], Morgana Coelho Mamede [1], Larissa Barbosa de Sousa [1]

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Abstract:

The seeds and fiber accruing from cotton are extremely important for the world economy, as well as the fiber being currently one of the most valuable textile materials and also one of the oldest ever recorded. The study aimed to evaluate the characters fiber yield (FY) and number of first position fruits (N1PF). Moreover, select cotton genotypes with high performance to offer support to breeding programs. The study was conducted at field level, at Fazenda Capim Branco UFU, located in Uberlândia, Minas Gerais, in the 2014/2015 season. The experimental design was randomized blocks (RBD) with four repetitions. Sixteen genotypes of colored cotton were evaluated, fourteen genotypes belonging to the Universidade Federal de Uberlândia (UFU) Cotton Breeding Program (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13 and G14) and two controls (BRS Rubi and BRS Topázio). The plot consisted of five rows of five meters, spaced 0.90 meters apart. The useful area of the plot was constituted by the three main lines, with 0.5 meter border at each end. The characters evaluated were plume yield (%) and number of first position fruits, determined from all cotton bolls collected, and 10 plants in the useful area of the plot respectively. The characteristics were submitted to analysis of variance and averages grouped by the Scott-Knott test ($p < 0.05$). The genotypes G4, G9, G11, G14 and BRS Rubi obtained the best averages in both PY and N1PF. G5, G6, G10, G12 and G2, G3, G7 obtained high (28.77, 28.8, 29.07, 28.48) and low (27.70, 25.2, 27.94) plume yield averages, respectively. The G9 and G 14 genotype has high PY and N1PF, being a great choice for use in breeding programs.

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Keywords: Cotton, genetic breeding, PROMALG

THE SEED CONTENT OF SOME COTTON GENOTYPES

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Abstract:

Cotton as well as being an important fiber crop in the world is a major source of oil for human consumption. The research was conducted in order to determine seed content of 125 cotton genotypes. These cotton genotypes were evaluated in terms of seed content such as starch, protein, 100 seed weight, oil, seed index, seed yield and seed cotton yield. The trail was established as a randomized complete block experimental design with three replications in Dicle University Faculty of Agriculture, Department of Field Crops Experimental Area in 2014-2015 years. The analysis were carried out using Tekafoss NIR instrument at Agricultural Test and Analysis Laboratory, Dicle University Science and Technology Research and Application Center (DÜBTAM). In the study the differences between all genotypes, was found to be statistically significant in terms of all the investigated properties. It was found positive and significant correlation among the some properties such as between protein content and starch content (r=+0,5765), between oil and starch content (r=+0,8753), oil and protein content (r=+0,5213), seed index and 100 seed weight (r=+0,1501), seed yield and seed index (r=+0,1966).

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Keywords: cotton, seed, oil, protein, starch

MULTIVARIATE STATISTICAL ANALYSES OF EARLINESS IN UPLAND COTTON

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Abstract:

In order to study the relationships between early maturation and morph-phonological traits in cotton six varieties of upland Cotton named varamin , early maturing mutant (Mutagenese), 818-132 , Bul-539 , B-557 and Chirpan-539 were planted and a half diallel mating design included parents performed in Cotton Research Institute , deputy of Varamin . Six parents and 15 hybrids in the next year were planted in a randomized complete block design with three replications. 17 components were collected and analyzed. Through stepwise regression analysis, early maturity was considered as dependant variable and other traits as independent variables. Accordingly, the production rate index, mean maturity data and plant height were responsible for about 75 percent of early maturity changes. Path analysis results revealed that direct and negative effects of the production rate index (-0.6682) was effective in the formation of the correlation with early maturity of (-0.809**). But, the indirect effects of production rate index in the case of mean maturity data and plant height were inconsiderable. Direct effects of mean maturity data in correlation of this factor with early maturity (0.455**) was also significant (0.2462). Estimating the selection index showed that in terms of early maturity, parent plant 1 (539-Bul) and hybrids 1*3, 1*4, 3*5 and 1*6 are superior to other hybrids. Changes in yield of varieties followed approximately 95 percent the maturity changes (r2= 0.946). Overall , results from this study demonstrated that the production rate index , mean maturity data and the plant height could be used as an indicator to select early maturing varieties .

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Keywords: Cotton, Stepwise Regression , Path Analysis, Selection Index

STABILITY AND ADAPTABILITY OF COTTON (GOSSYPIUM HIRSUTUM L.) GENOTYPES BASED ON AMMI ANALYSIS IN MOZAMBIQUE

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Abstract:

Evaluation of the stability and adaptability of genotypes across different environment conditions is important for recommending them as new varieties to ensure high adoption. Plant breeders evaluate their germoplasm in multienvironment trials to study the stability and adaptability of genotypes. Multienvironment trials including 3 seasons in 3 locations for 11 cotton genotypes were carried out in Mozambique. The objective of this study was to assess the G x E pattern and evaluate the stability and adaptability for seedcotton yield of new cotton germoplanm in Mozambique. The experiment was set up in Namialo, district of Meconta, province of Nampula; Namara, district of Balama, province of Cabo Delgado and Nhamatanda, district of Nhamatanda, province of Sofala. The treatments, consisting of the 11 studied varieties, were established in a randomized complete block design with four replications. The graphic analysis of Additive main effect and multiplicative interaction (AMMI) were used to understand the G x E interaction pattern and to study the stability and adaptability. The results showed significant genotype, environment and G x E interaction. The AMMI revealed that genotypes FK 37 and BA 919 were the most adaptable, while BA 2018 and BA 320 were the most stable across the variation of environment.

Acknowledgments

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Keywords: AMMI, Genotype x environment interaction, Seedcotton yield

PHENOTYPIC CORRELATION BETWEEN AGRONOMICAL AND MORPHOLOGICAL CHARACTERS OF THE COTTON PLANT (GOSSYPIUM HIRSUTUM L.)

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Abstract:

Cotton is the natural fiber that is most used by textile industries in the world and, as such, is studied by many researchers in breeding programs. The use of characters associated with these programs is one of the main tools that can increase the efficiency of selecting a character, especially if one of them have low heritability. These characters may be associated positively, being possible to obtain gains for one associated with another character (CRUZ; REGAZZI; CARNEIRO, 2012). This study aimed to evaluate the phenotypic correlation between agronomical and morphological traits in 21 genotypes of cotton. The experiment was conducted at field level, at Fazenda Capim Branco UFU, located in Uberlândia, Minas Gerais, in the 2014/2015 season. The experimental design was randomized blocks (RBD), with four repetitions. The plot consisted of five rows of five meters, spaced 0.90 meters apart. The useful area of the plot was constituted by the three main lines, with 0.5 meter border at each end. The evaluated characters were: chlorophyll content A and B; number of reproductive branches; insertion height of the first reproductive branch; number of first, second, third and fourth position cotton fruit; leaf width and length; cottonseed yield (kg ha-1) and fiber yield (%). The chlorophyll accumulation was obtained by the electronic chlorophyll meter ClorofiLOG, sampling two leaves of 10 plants in each plot. The characteristics productivity and fiber yield were determined from all bolls collected in the useful area of the plot. The remaining characteristics were assessed at the beginning of the flowering period of the crop, at 80 DAE. Data were submitted to analysis of variance ($p < 0.05\%$). The number of reproductive branches, number of first, second and third position fruits did not result in any significant correlation with the other assessed characteristics. Chlorophyll content A showed significant positive correlation with chlorophyll content B ($r = 0.64$), while leaf width had a positive correlation with length and fiber productivity with fiber yield ($r = 0.54$ and 0.44, respectively). The characteristic height of the first reproductive branch obtained a significant negative correlation with the number of fourth position fruits ($r = -0.45$). These results reveal that the most productive genotypes can be selected in the breeding program, resulting in higher yield of fiber. It is also possible to select aiming to reduce the first reproductive branch height, as selected progenies will present more fourth position fruits. The study of correlations is important to facilitate early selection for phenotypic characteristics of agronomical interest in cotton genetic breeding programs.

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Keywords: seletion, breeding, Indirect selection

GENETIC DIVERGENCE AMONG COTTON GENOTYPES OF COLORED FIBER

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Abstract:

The knowledge of genetic diversity among a group of genotypes is important in breeding, especially to identify superior combinations. The cot-

ton colored fiber has been shown inferior to the white fiber in the general characteristics of productivity and quality of the fiber, so it is important that progenies that have the best performance are selected so we can proceed with the breeding improvement program. This study aimed to study the genetic divergence between cotton genotypes of colored fiber, that belong to Programa de Melhoramento Genético do Algodoeiro da Universidade Federal de Uberlândia (PROMALG - UFU). An experimental model a randomized block design (RBD) was used with four replications and the experimental plot consisted of five rows of five meters, with spacing of 0.90 meters. They evaluated 16 genotypes of colored cotton fiber, 14 strains of PROMALG-UFU and two witnesses (BRS Rubi and BRS Topázio). The characters evaluated were: chlorophyll content A and B; number of nodes (NN); number of cotton fruits first (NCF1P), second (NCF2P) and third (NCF3P) positions; width and leaf length (WL and LL); leaf area (LA) and fiber yield (FY). The chlorophyll content was obtained by electronic chlorophyll meter ClorofiLOG, sampling two leafs of 10 plants in each portion. The fiber yield was determined from all bolls collected in the useful area of the plot. The genetic dissimilarity was estimated between all pairs of genotypes, by generalized distance of Mahalanobis (D2ii '). After obtaining the dissimilarity matrix between genotypes, there was clustering of genotypes by the nearest neighbor method. There was genetic variability among cotton genotypes and when doing the cut in dendrogram to 37% dissimilarity, five distinct groups were formed. In group I the LC14-9, LC14-11, BRS Rubi, LC14-14 and LC14-6 genotypes were allocated, which represented 31.25% of all genotypes, and in group II and IV four genotypes were allocated each. Group III was represented by only three genotypes (BRS Topázio, LC14-10 and LC14-1). Genotypes belonging to the same group have low genetic diversity and do not indicate hybridizations between them, once they are very similar, which will reduce the chances of getting larger combinations. Among the groups formed, genotypes of different groups can be selected, but the ones that have high performance in order to obtain genetic variability and higher combinations.

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References

Keywords: Gossypium hirsutum, breeding, performance, genetic

GENETIC ANALYSIS OF SEED COTTON YIELD AND FIBRE QUALITY IN ADVANCED BREEDING LINES OF UPLAND COTTON (GOSSYPIUM HIRSUTUM L.)

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Abstract:

Cotton (*Gossypium hirsutum* L.) is one of the most important natural textile fibre crops in the world. In India, all four species of cultivated cotton *G. arboreum* and *G. herbaceum* (Asiatic cotton), *G. barbadense* (Egyptian cotton) and *G. hirsutum* (American cotton) are grown in three distinct agro-ecological regions of the country. Fibre quality is a complex quantitative trait that is a composite of many other traits, such as fibre length, uniformity index, fibre bundle strength, fibre elongation, and micronaire. Each fibre quality trait is influenced by many genes. In view of importance of fibre quality in textile industry, eighteen breeding lines derived from F2 population of twelve parent diallel cross through pedigree method were evaluated at ICAR-Central Institute for Cotton Research, Nagpur, India in 2014. General combining ability (GCA) and specific combining ability (SCA) effects were highly significant for uniformity ratio, micronaire, fibre bundle strength and significant for boll number and seed cotton yield indicating importance of both additive and non-additive gene action in original hybrid population. Lint yield and yield components were mainly controlled both additive variance and dominance variance. Breeding lines CNH 09-4, CNH 09-5, CNH 09-7 and CNH 09-9 derived using pedigree method exhibited better fibre properties and seed cotton yield and recommended for testing under multilocation trials.

Acknowledgments

References

Keywords: Genetic analysis, combining ability, quality traits, general combining ability, Upland cotton

EMBRAPA´S COTTON IMPROVEMENT PROGRAM FOR THE BRAZILIAN CERRADO

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Abstract:

Upland cotton (Gossypium hirsutum L.) is an economically-important crop for fiber and seed production in Brazil. Recent efforts have been made to develop cultivars specifically for the cerrado region of west-central Brazil (Morello et al. 2010, Morello et al. 2015). In the Brazilian cerrado the favorable soil and climate conditions allow to achieve high yields. During the last cotton season (dryland production system), the yield average was 3,867 kg.ha-1 (cottonseed) and 1,523 kg.ha-1 (cotton lint). However, the hot and wet weather favors the emergence and spread of diseases, contributing to yield losses or reduced fiber quality. The high temperatures combined

with high relative humidity favor foliar diseases, such as ramulosis, bacterial blight (BB) and ramularia leaf spot (RLS). In addition, severe outbreaks of viral diseases are frequent, mainly cotton blue disease (CBD) and cotton yellow mosaic. In addition, the root-knot, reniform and root-lesion nematodes cause yield losses in many cotton farms. Embrapa's cotton improvement program has focused on improving genetic solutions for tropical issues with emphasis on diseases and nematodes resistance. Incorporation of genetic resistance to CBD and BB has become routine in the cotton varieties launched since 2005, such as varieties BRS 269, BRS 286, BRS 336, BRS 368RF, BRS 369RF, BRS 371RF and BRS 372. The use of marker-assisted selection (MAS) for CBD and BB – using markers CIR 246 and DC20027, respectively, at the individual plant level, allows to select a higher number of resistant plants. Resistance is confirmed by subsequent progeny test in field trials. All lines in the latest stages of the cultivar development are resistant to CBD and BB. Searching for resistance to RLS, currently the most important disease in the Brazilian cerrado, we identified several sources of resistance. By exploiting these genes, we released variety BRS 372, with multiple resistance and high-fiber yield in 2014. MAS is also used to select for nematode resistance. The markers CIR 316M and BNL 3661 allowed to select several cotton lines, such as the CNPA GO 2011-473 which displays the desirable allelic composition for both markers. Other lines, such as CNPA GO 2011-160, CNPA GO 2012-943 and CNPA GO 2011-551 possess one locus (CIR316M), while others (CNPA GO 2012-1074 and CNPA GO 2012-677) possess the other resistance locus (BNL3661). Another emphasis at Embrapa's cotton improvement program is fiber quality, aiming at obtaining innovation for fiber length and fiber resistance. Variety BRS 336, released in 2011 (Morello et al., 2012), with the length average of 33,0 mm and the fiber resistance average of 32,5 gf/tex, was the first Brazilian variety with genetic background from Upland cotton with superior fiber quality. Recently we developed lines CNPA BA 2009-2270, CNPA BA 2010-1366, CNPA BA 2011-4964, CNPA BA 2011-4970 and CNPA BA 2012-2329, with this fiber pattern. Many of these lines and varieties are in the introgression program in order to combine resistance to diseases and nematode, higher fiber quality and biotech traits for insect and herbicide resistance.

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Keywords: Gossypium hirsutum L., Improvement, Brazilian Cerrado

SOMATIC EMBRYOGENESIS AND PLANT REGENERATION IN GOSSYPIUM HIRSUTUM L. CV. NAZILLI-143

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Abstract:

Cotton (Gossypium hirsutum L.) is one of the most important fiber and valuable seed oil crops in the world and is planted on a land area of about 32.4 million hectares worldwide. Since biotic and abiotic stresses highly influence the development of the fiber, its quality, and the yield in cotton production, conventional plant breeding methods have been generally used to improve these traits [1]. Even though the conventional breeding programs have made steady improvements in the agronomic traits in cotton, genetic improvement is limited by several factors such as the lack of sufficient genetic variability in the existing germplasm pool and the requirement for long time periods. In vitro selection against different kinds of stress factors and the transgenic technology both require the establishment of an effective plant regeneration system [2]. Some factors restrict the regeneration and the transformation of cotton during the production of bio-engineered cotton as they are genotype dependent, and reproducible protocols have not yet been well established for the most elite cotton varieties [3]. Only a few cultivars of cotton have been successfully regenerated via somatic embryogenesis [2]. Several methods have been used for the regeneration of cotton, but among them somatic embryogenesis is the more preferred method than organogenesis, since the regenerants have a probable unicellular origin and since the somatic embryos have no vascular connections with the maternal tissue [1, 3]. In comparison to many other crops, it is more difficult to obtain somatic embryos and regenerated plants from cotton [2]. The number of commercial cultivars and elite germplasm lines that have better-quality fiber and agronomic traits, which can undergo whole plant regeneration, still remains very low [1]. The present study was designed to develop an efficient and simple protocol for somatic embryogenesis and plant regeneration in G. hirsutum L. cv. Nazilli-143, that have elite agronomic traits. Embryogenic calli were initiated from hypocotyl tissues of 7-day-old seedlings. High induction frequencies (100%) of the embryogenic callus were obtained on medium containing MS salts, B5 vitamins, 30 g L-1 glucose, 0.75 g L-1 MgCl2, 0.1 mg L-1 Kinetin and 0.1 mg L-1 2,4-D [4] and the medium was solidified using 0.7% agar (pH 5.8). Embryogenic calli were placed on hormone-free liquid Murashige and Skoog (MS) [5] medium in order to obtain suspension cultures with a high number of embryoid frequency. Suspensions were sieved and the somatic embryoids were collected and plated onto various types of semi-solid media. Embryoid proliferation and maturation processes were best observed to take place on medium containing 2/3 MS plus 1.3 g L-1 KNO3. Plantlets were recovered from 36% of the embryoids. Plants with a root system and true leaves were removed from the sterile culture and were transferred into a plant growth chamber.

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Keywords: Somatic embryogenesis, Plant regeneration, Suspension culture, Cotton, Gossypium hirsutum L.

A ROOT PHENOTYPING PLATFORM FOR THE STUDY OF ROOT SYSTEM ARCHITECTURE IN COTTON: FEATURES AND VALIDATION

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Abstract:

Cotton production often relies on rainfall patterns. The availability of water during plant development impacts on productivity and fiber quality, and the development of ideal plant phenotypes capable of maintaining yield potential and adequate fiber quality under limited water supply is highly desirable. Tolerance to water stress depends on the complex interaction of a number of mechanisms whose morphological, physiological and genetic bases are still not well understood (Tuberosa, 2012). The root system architecture (RSA) and its functioning play a fundamental role in a number of mechanisms including water and nutrient uptake, and the optimization of RSA is important for increased and stable plant productivity under adverse conditions. RSA is in part under genetic control, and a better understanding of the genetic bases of RSA has been hampered by the difficulty in assessing roots (Meister et al., 2014). Different approaches, ranging from field-based manual evaluations to X-Ray or NMR computer imaging have been used to characterize the RSA of plants. Each one of these approaches has its merit and limitations, but systems that are fairly inexpensive and allow the evaluation of a large number of plants are not common. We have developed a non-destructive rhizotron-based system and present the features and validation of our RSA phenotyping platform (Zhu et al., 2011). The rhizotrons, that have a soil capacity of 4.2kg, are constituted of 50x80cm light-proof Aluminium Composite Material (ACM) plates separated from glass plates by a 1.2cm thick spacer. The sandwich is filled with substrate and clamped, glass plate side down, on a second ACM plate mounted on a cart, ensuring that the roots grow in a light-proof condition while allowing easy visualization through the glass plate. At 18-20 days after emergence, roots are photographed in a dark chamber using a digital camera and the images analyzed using the WinRHIZO software (Regent Instruments Inc.) to determine RSA parameters including total length, diameter, and projected area. Proper plant development was verified by growing a panel of 20 diverse cotton accessions in a randomized blocs design with 4 repetitions, and evaluating plant growth parameters (leaf area, aerial part fresh weight, aerial dry weight and fresh root weight). Significant ($p<0.05$) differences were observed between the genotypes for all parameters, and no significant bloc effect was detected. The coefficients of variation were low, ranging from CV=19.06% for aerial dry weight to CV=24.61% for fresh root weight. In another experiment RSA parameters (total root length, main root length, projected area, root volume) were evaluated (5 accessions, 2 experiment dates, 3 repetitions/date). The CV for the different parameters varied from 21.6% to 26.7%. With the exception of total root length whose measurements were less consistent, repeatability was sufficient to allow collecting accurate data with 1-5 measurements of the different parameters. The non-destructive root phenotyping platform we developed is an inexpensive alternative for the characterization of the RSA of cotton. Our setup allows the evaluation of up to 210 plants, with an estimated hands-on time of 3-4mins/plant to document the root system. >

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Keywords: root phenotyping, rhizotron, root system architecture, water deficit tolerance, cotton

GENETIC DIVERGENCE IN MULTIPLE CROSS DERIVATIVES OF UPLAND COTTON (GOSSYPIUM HIRSUTUM L.)

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Abstract:

Cotton farmers in India were compelled to adopt high density planting system (HDPS) in the recent past owing to its cultivation in unfavourable ecologies. In order to develop varieties suitable for HDPS, hundreds of multiple cross derivates were evaluated and finally 52 genotypes with dwarf to medium plant height and short sympodial branches were identified (Pradeep and Sumalini, 2005). Although these genotypes were found to stable and promising under HDPS (Sree Rekha and T.Pradeep, 2015), a need was felt to involve them for exploitation of hybrid vigour. Accordingly, a comparative study was conducted at Agricultural College, Aswaraopet during Kharif 2013 to assess the genetic divergence among 52 multiple cross derivatives of cotton (Gossypium hirsutum L) through metroglyph analysis (Anderson, 1957) and D2 statistics (Mahalanobis, 1936). The experimental material was sown in RBD replicated thrice and the data was recorded as mean values of 5 plants chosen at random per replication on nine morphological characters. The analysis of variance revealed significant differences among 52 genotypes for nine characters. It was further revealed that, all the 52 genotypes were grouped into 12 groups through metroglyph analysis and 8 clusters through D2 statistics. Group I of metroglyph analysis had highest number of genotypes (11) and Cluster II comprised of 20 genotypes as per the D2 analysis. The clusters viz., I, II of D2 analysis included majority of the genotypes from groups I, II, and V of metroglyph analysis. The genotypes of clusters I & II had medium yield (121.17 – 148.40 g/plant) with medium plant height (85.07 – 91.19 cm) and were similar to the genotypes in the groups I, II and V of metroglyph analysis with low to medium yield and low to medium plant height. Comparison between the results of the two analyses even though revealed striking differences with regard to number of groups and group constellation, majority of the genotypes having similar morphological characteristics fell under a single group in both analyses, which could be due to similar contribution of concerned traits to the total genetic divergence. Index score analysis indicated that, genotypes viz., MC 6-2 and MC 11-1 recorded highest scores of 25 and 24 respectively where as genotypes MC 23-1 and MC 23-2 exhibited lowest index score of 12. Group V and XII recorded highest and lowest index scores of 153 and 18 respectively. Similarly maximum cluster distance was observed between the Clusters VI and VIII of D2 analysis, composed genotypes with contrasting characteristics like high plant height with low yield and low plant height with high yield respectively. Among characters, 100 seed weight had shown highest contribution to genetic divergence (34.77%) followed by plant height (18.85%). Results have clearly established the fact that the multiple cross derivates had significant differences for the characters that determine short and compact plant type. Accordingly, the genotypes of the clusters I & II of D2 analysis and I, II, V of metroglyph analysis having compact plant architecture could be selected for further hybridization programme to develop short and compact hybrids suitable for HDPS.

Acknowledgments

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Keywords: Gossypium hirsutum, multiple cross derivatives, genetic divergence, metroglyph analysis, D2 statistics

SELECTION FOR INCREASED FIBER LENGT IN COTTON PROGENIES FROM ACALA AND NON-ACALA TYPES

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Abstract:

Cotton, Gossypium hirsutum L. r. latifolium Hutch., is one of the crops of greatest economic importance in Brazil. The changes in weaving technology, competition with synthetic fibers, and the globalization of cotton and textile production have increased the demand for better quality fibers. One of the characteristics to be improved is fiber length. Brazil traditionally produced and exported longer cotton fibers through the production of G. hirsutum L. r. marie galante, but this race has not been produced during the last ten years because of its perennial growth habit which hinders control of the cotton boll weevil, Anthonomus grandis. This work studied some genetic aspects of fiber length in segregating generations of

crosses between two upland cultivars, 'Guazuncho 2' (PI 606819) and 'Acala SJ4' (PI 529538). Single seed descent protocol and pedigree breeding procedures were utilized to advance generations. The fibers of the recombinant inbred lines (RILs) and those originated by pedigree procedure were evaluated by high volume instrument for length, lint percent and strength. The results suggest that it is possible to select materials with improved upper half mean length (UHML) that have values approaching a commercial extra long staple upland cultivar. A high percentage of the RILs also exhibited an UHML greater than 32 mm. Genetic gain for fiber length from the F4 to the F5 generation was 6.8%, indicating significant variability for UHML. The result indicates that simple methods of intrapopulational breeding may lead to genetic gains in UHML.

Acknowledgments

References

Keywords: fiber length, selection, cotton

GENETIC ANALYSES OF COTTON MATURITY AMONG BRAZILIAN AND US UPLAND GENOTYPES

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Abstract:

The development of new cotton lines with improved earliness has always been an important breeding goal around the world. In Brazil, the boll weevil (Anthonomous grandis) has become a major pest of cotton, causing severe economic damage. The use of early-maturing cotton cultivars has been the major agricultural practice to reduce losses and such practice allows planting of a second crop such as cotton after soybean in Brazil. The objective of the present work was to study the genetics and heritability for earliness using generation mean analysis (GMA) in cultivars with different maturity from Brazil and United States.The present study was carried out during the summer of 2011 growing season at Experimental Station of Texas A&M in College Station–Texas. Six varieties were used for this study namely BRS 269(Cultivar), CNPA GO 2005-809(inbred) and CNPA GO 2005-158(inbred) from Brazil as well three U.S cultivars: as well as three U.S. cultivars: Tamcot CAMD-E, PSC 355, and Acala 1517-99. Six basic generations (P1, P2, F1, F2, BC1 and BC2) for each cross were generated and sown in a randomized block design with three replications. The number of plants evaluated varied as follows: 5 plants for the non-segregating P1 and P2 and F1 generations; 40 plants for F2 ,BC1 and BC2 generations. The traits assessed were node first fruiting branch, first white flower, first open boll, vertical flowering interval, horizontal flowering interval, vertical maturation interval, and horizontal maturation interval. The analysis of variance of the six basic generations (P1, P2, F1, F2, BC1 and BC2 was statistically analyzed using (RCDB) analysis of variance. The data was analyzed using SAS 9.2 using PROC GLM. The additive gene effect was predominant for most traits in all populations. The effect AD gene effect was significant only for D.F.O.B in population BRS 158 X CAMD-E. Tamcot CAMD-E was the best parent to get earlier materials. The additive gene effect was predominant for e traits in all populations indicating that genotypes with improved earliness could be identified through pedigree method and selection methodology.

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Keywords: Cultivars, Breeding, Fiber quality

NATIONAL COTTON VARIETY TEST AT SAVANNA AREAS IN BRAZIL - 2013/14.

Authors: Francisco José Correia Farias [1], João Luis da Silva Filho [1], Camilo de Lellis Morello [1], Murilo Barros Pedrosa [2], Nelson Dias Suassuna [1], Luiz Paulo de Carvalho [1], José Jaime Vasconcelos Cavalcanti [1]

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Abstract:

Many sources of information are available to growers to help them choose a good variety. The best source of information, of course, is personal experience with a particular variety on the farm, but given the large number of varieties to choose from, it is impossible to try them all. Many growers, therefore, consider performance data from variety trials that are conducted by seed companies and research institutes within the region of interest. Annually, the Cotton Breeding Program of Embrapa evaluates cotton varieties at numerous locations within the cotton-growing regions at Savanna Areas of Brazil. The purpose of the National Cotton Variety Test (NCVT) is to provide an unbiased comparison of varieties across a range of environments. Trial evaluation of standard, commercially available, and

new and upcoming cotton cultivars from different breeding programs provides producers data to make well-informed variety selection decisions based upon how a particular cotton variety performed close to their bases of operation. The National cotton Variety Test is conducted annually at different states: Mato Grosso, Goiás,Mato Grosso do Sul, Piauí, Maranhão and Rondônia. At each location, all varieties entered into the trial are treated identically (Conventional and Transgenic) with respect to herbicide and insecticide input to strive for unbiased evaluation of genetic potential. This experiment aims to identify cultivars from different breeding programs with high yield stability and resistance to major diseases that occur in the region. In the season 2013/14, the NCVT (Middle Early) was conducted in 10 locations. The experiment was a randomized completed block design (RCBD) with 13 treatments and 4 repetitions. The experimental plot consisted of four linear rows of 5m, with a spacing of 0.90m between rows. The variables tested were height (HEI); boll size (BS), cotton seed yield (CSY); lint yield (LY); lint percent (LP); fiber length (LEN); resistance (RES) and micronaire index (MIC). In the joint analysis found that the cultivars that produced lint yield (LY) above the average were IMA 690, DP 555 BG RR BRS 369 RF, TMG 42 WS and TMG 41WS. Regarding the lint percent (LP), it was found that the overall average was 42.06%. The cultivars that produced LP above average values were IMA CV 690 (45%), DP 555 BG RR (43.60%), BRS 369 (42.60%), BRS 368 RF (42.40%) and TMG 43 WS (42.40%). While the varieties NUOPAL (39.80%) and TMG 41WS (40.80%) had the lowest average. With respect to the average values of the technological properties of fibers, it was found that the majority of genotypes showed the fiber characteristics required by the textile industry. The material that stood out mainly in relation to the fiber strength (RES) was the cultivar TMG 41WS with 32,20gf / tex values (RES). The cultivars IMACV 690, DP555 BG RR, BRS 369 RF, TMG 42 WS and TMG 41WS were selected for show high yields and fiber quality.

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Keywords: Cotton Improvement, Fiber quality, Yield, Cotton Breeding Program, Savanna

CALLUS INDUCTION FROM IN VITRO ANTHER CULTURES OF TWO DIFFERENT COTTON (GOSSYPIUM HIRSUTUM L.) CULTIVARS

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Abstract:

Cotton (Gossypium hirsutum L.) is both the world's most important natural textile fiber and a major oil crop and therefore it plays an important role in the global economy. Due to the richest source of fiber, it is the backbone for the textile industry [1]. Since traditional breeding methods are time consuming and take years, producing homozygous doubled haploid lines which shortens the breeding cycle for several years are of great importance [2]. Anther culture is one of the most effective and current method for the producing haploid anddouble haploid plants [3]. The objective of this study was to investigate the effect of cold pre-treatment (+4 °C) and culture medium composition on callus induction from anthers of two different G. hirsutum cultivars (Özbek-100 and Nazilli-143). Initially, the association between floral bud size and microspore developmental stages was investigated and 4.0 mm bud size was found to be more appropriate for the anther culture. Flower buds contain anthers at the appropriate developmental stage were stored at 4 °C for 3 days and the control buds were not exposed to cold pre-treatment and cultured immediately. After the surface sterilization, anthers contain mostly microspores at tetrad stage were isolated from flower buds and transferred to Murashige and Skoog (MS) [4] medium containing different plant growth regulators. No significant differences were observed between cold pre-treated and non-treated anther culture of Nazilli-143 and Özbek-100. The emergence of the callus was observed visually on the 21th day of culture. The highest frequency of callus formation (100%) in Özbek-100 was observed in the cold pre-treated anthers cultured on the MS medium supplemented with 1 mg/L BA + 1 mg/L NAA, while the highest frequency of callus formation in Nazilli-143 was obtained in non-treated anthers cultured on the MS medium containing 0.1 mg/L BA + 1 mg/L NAA (96%). The anthers of Nazilli-143 cultivar showed more browning than Özbek-100 cultivar. Anther browning started in almost all media 7 days after the beginning of the culture and reached 100% in non-treated anthers of Nazilli-143 cultured on the MS medium supplemented with 1 mg/L BA + 1 mg/L NAA. No browning occurred in cold pre-treated anthers cultured on the same medium composition in Özbek-100 cultivar. The percentage of anthers turning brown varied depending on the cultivars, cold pre-treatment and culture medium composition. This research provided a useful protocol on callus induction for further research regarding the anther cultures of Özbek-100 and Nazilli-143 cultivars.

Acknowledgments

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Keywords: Gossypium hirsutum L., Cotton, Anther culture, Callus induction, Browning

RESISTANCE OF COTTON LINES AND CULTIVARS TO MELOIDOGYNE INCOGNITA RACE 3.

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Abstract:

In Brazil, Meloidogyne incognita has widespread occurrence and it is distributed throughout the cotton region of the country. The damage caused by this nematode is greater in sandy textured soils with low fertility. The objectives of this study were to determine lines and cotton cultivars for resistance to nematode M. incognita in a greenhouse. The experimental design was a randomized block with 25 treatments [20 lines : CNPA BA 2007-3447 (414) , CNPA BA 2007-3601 (424) , CNPA BA 2006-88 , CNPA BA 2006-92 , CNPA BA 2006-1478 , CNPA BA 2007-4819 , CNPA BA 2007-3637 , CNPA BA 2008-173 , 2008-214 CNPA BA SB , CNPA BA 2008-481 , CNPA BA 2008-1558 , CNPA BA 2008-2349 , CNPA BA 2008-3952 , CNPA BA - 2008 POP14F , CNPA BA 2009-1511RP40 , CNPA BA 2009-286 RF50 , CNPA BA 2006-2728 , CNPA BA 2009-2270 , CNPA BA 2009-2334 , 2009-2356 CNPA and 5 cultivars - FM 910, BRS 336, BRS 335, BRS Acacia and IAC 25] and 4 repetitions. The isolated M. incognita, belonging to race 3 was obtained from infected cotton roots from the city of Barreiras - BA. The confirmation of the specie was carried out using blades with perineal sections of adult females (Hartman & Sasser, 1985). The identification of the race was done according to the method of Taylor and Sasser (1978), using cotton and tobacco plants as differentials. The seeds of the lines and cotton cultivars were sown in plastic pots (eight seeds per pot) containing sterile substrate (soil:manure:straw of rice:manure:limestone) in the ratio 2:1:1:1:1 After germination three seedlings were kept in each pot. Thirty days after sowing, the plants were inoculated with 1500 eggs and juveniles of M. incognita race 3 in aqueous suspension, which was poured around the seedling, with 10 cm spacing, preventing root injury. The counting of nematode eggs mass extracted from the roots was done 80 days after inoculation using an optical microscope. The data were transformed into $\sqrt{(x+0,5)}$. Analysis of variance showed significant effect for genotypes, for this reason it was carried out a cluster analysis proposed by Scott- Knott ($p < 0.05$) forming two groups. The first group, composed of 4 lines [CNPA BA 2007-3447 (414); CNPA BA 2006-88; CNPA BA 2006-92 and CNPA BA 2006-2728] was considered likely to present the highest average value of 5.78 for the mass of M. incognita eggs. The second group, composed of the remaining lines and five cultivars showed increased tolerance to nematode showing the average value of 1.69 for the mass of M. incognita eggs. The results from this experiment will provide subsidies to cotton breeding program in decision making about release varieties.

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Keywords: Nematodes, Gossypium hirsutum L., Detection

THE HISTORY OF TWO NATURALLY COLORED COTTON VARIETIES: “EMIREL” AND “AKDEMIR”

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Abstract:

In recent years, the awareness in order to protect environment and human health has increased in the developed countries and therefore nowadays natural products become more and more attractive. The demand for environment-friendly products has affected textile product types, and increased interest in natural fiber. White cotton (Gossypium hirsutum L.) is processed with various chemicals, and synthetic dyes can be environmentally hazardous and also cause trace chemical contaminants in textiles harmful to human health

[1]. In many countries, consumer demands began to turn towards "eco-textile" products [2]. Naturally colored cotton has a lot of advantages compared to white cotton such as having no risks to the environment and human health, eliminating the costs of bleaching and dyeing, saving on water and energy [3, 4]. This study aims to inform researchers about the history of two naturally colored cotton varieties developed for Ege Region of Turkey. The genotypes with light and dark brown colored fibers are provided from Nazilli Cotton Research Institute in 1996. Field trials were conducted in Bornova and Ödemiş locations to identify fiber quality, fiber color, and yield parameters. Seed and fiber productions were established from light brown and dark brown colored cotton genotypes determined by investigating hundreds of lines based on single plant selections. The traits such as seed-cotton yield per plant, remaining of the seed-cotton on the boll, resistance to wilting and fiber quality (length, fineness, strength), color fastness values and color intensity changes were considered as mainly selection criteria. Micro-yield trials of 30 lines having good traits and belonging to light and dark brown genotypes were established in 2003 and 2004 years, in these locations. 7 dark brown and 3 light brown lines having high fiber quality and also good agronomical performance were determined according to field and laboratory results. In order to increase the seeds and fibers of these lines, macro-yield trials were established in 2005 with financial supports of Güçbirliği Textile Company, and finally two lines as Light Brown 176 (AKDEMIR) having long fiber length and Dark Brown 171 (EMIREL) having high yield were selected. The fiber quality values of light brown cotton sample for spinning performance were better from the others. In 2006-2007 and 2008 years, region variety trials were established by Variety Registration and Seed Certification Centre in four locations "Nazilli, Beydere, Ödemiş and Söke". As a result of our studies, these naturally colored cotton varieties having fibers with light brown and dark brown pigments called "EMIREL" and "AKDEMIR" have been registered by Variety Registration and Seed Certification Center in 2009. These varieties took placed in the National Variety List of Turkey. These two naturally colored cottons varieties have been used to make clothes (e.g. handicrafts towards producing fabric and clothes, knitting, shirts, T-shirts, hosiery, towels, underwear, blankets and other types of clothes), furniture, and home decoration.

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Keywords: Gossypium hirsutum L., White cotton, Naturally colored cotton

IPTA 212 AND IPTA 232: TWO NEW PARAGUAYAN COTTON VARIETIES (GOSSYPIUM SPP)

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Abstract:

IPTA 212 and IPTA232 are two new cotton varieties (*G. hirsutum*) from the Paraguayan Institute of Agricultural Technology (IPTA), created in the Research Center Hernando Bertoni (CIHB), by the cotton genetics team of the Program for Research and Cotton Experimentation (PIEA). The objective was to obtain promising lines of cotton, analyzing their agronomic and technological characteristics, with the goal of improving productivity and maintaining technological quality. The methodology for selection was a pedigree-massal selection following crossbreeding, regional comparative trials of varieties and trials under current farm conditions. The two varieties improved yields, size, capsule opening and ease of harvest, with favorable behavior while facing bacterial blight, fusarium and blue disease. The fibers are of high technological quality. IPTA 212 is suitable for traditional and mechanized cultivation, with a high rate of fiber for ginning (41%), and its fiber is very long and resistant. IPTA 232 is tall and very strong, corresponding to the requirements of small farmers, with an excellent fiber rate (42%) and superior technological quality; in particular regarding its length, resistance and color. The two new varieties are seen as excellent options to satisfy the needs of both small farmers and those using machinery, and they complete the varietal catalog of IPTA.

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Keywords: cotton, genetics, pedigree-massal, varietal

RESPONSE OF A TANGÜIS VARIETY TO INOCULATION WITH SELECTED STRAINS OF PLANT GROWTH-PROMOTING RHIZOBACTERIA (PGPR) UNDER CONTROLLED CONDITIONS IN ICA, PERU

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Abstract:

Cotton is a crop of socio-economic importance in the country and particularly the region of Ica, therefore it is necessary to seek alternatives aimed at reducing production costs and increasing profitability. This research was conducted to evaluate the response of the cotton variety ICA 805W-63 to the application of strains of growth-promoting bacteria (PGPR), with a drip irrigation system in the middle zone of the Ica valley. Five treatments were tested, isolated and combined: (Azotobacter, Bacillus, Bradyrhizobium, Azotobacter + Bradyrhizobium and Bacillus + Bradyrhizobium), in addition to the control without inoculation, NPK + and NPK-, with four replications in a randomized complete block design. Planting was carried out by inserting three previously inoculated seeds per hole with a distance of 0.50 m between holes and 1.10 m between rows during the month of May, with temperatures decreasing; thus the growth and development of the crop were affected in their physiology and phenology during the plants' early stages. In the quantitative variables such as weight per cotton boll, the number of bolls per plant and the yield of raw cotton per parcel, the combinations which stood out with the highest averages, Azotobacter + Bradyrhizobium, Bacillus + Bradyrhizobium, were very close to the control NPK +, but significantly outperforming the control NPK -; unlike the fiber quality parameters (length, fineness and strength), which did not change the response of the lineage evaluated with none of the treatments applied. The study shows that it is possible to lower the production costs of cotton in the area of chemical fertilizers, as well as contribute to soil conservation through the activity of beneficial microorganisms. It is recommended to assess the next stage in the farmer's fields in a participatory manner.

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Keywords: Cotton, Gossypium barbadense, inoculation, PGPR

TITLE: CROPPEDIA - INTEGRATED DATABASE & SOFTWARE INTERFACE FOR DISCOVERY & ACCELERATED BREEDING

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Abstract:

KeyGene's Croppedia is the leading knowledge platform for fast and effective marker development and lead gene discovery. It is the ultimate software tool to speed up molecular breeding by easily tracking and selecting trait associated leads. As an in-house platform, it allows combining of public and private data and visualizing and integrating public and proprietary tools. You can work together globally and optimize the output of team efforts through the web-based gene discovery platform: let molecular breeders team up with trait specialists and bio-informaticians to share results in dedicated workspaces, thus accelerating breeding. Make your data work for you!

Acknowledgments

References

Keywords: Croppedia, Integrated database, Software interface

COMBINING ABILITY ESTIMATES FOR AGRONOMIC AND MORPHOLOGICAL TRAITS IN COTTON UNDER WATER STRESS

Authors: José Jaime Vasconcelos Cavalcanti [1], Ubieli Alves Araújo Vasconcelos [2], Walmir Souza Vasconcelos [2], Roseane Cavalcanti dos Santos [1], Francisco José Correia Farias [1], Gildo Pereira de Araújo [1], José Henrique de Assunção [1]

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Abstract:

The predictions of climatic changes show that agricultural production around the world can have a dramatic impact in the coming decades caused by global warming. One of the consequences is the effects of drought deficit that may reach the plant in morphological, physiological and molecular level at any developmental stage, affecting directly the growth and plant development. In this context, the identification of adapted cultivars has been a major challenge for breeding programs considering genetic complexity involved in mechanisms of drought tolerance and even the maintenance of productive capacity. In order to attend this demand, the cotton breeding program coordinated by Embrapa has focused on generation of different tolerant lines by hybridization, using top genitors, aiming to broaden the genetic variability and to achieve new tolerant lines to water stress. In this study, we used 20 cotton hybrids, obtained through partial diallel crosses between water stress tolerant and high yield genitors. The general combining ability (GCA) and specific combining ability (SCA) were estimated according to Griffing (1956) method based on agronomic and morphological traits under water stress. The experiment was carried out in semiarid environment (Barbalha, CE), in dry season. It was used two trails: watering and water estressed, where plants were submitted to 23 of water suppression, starting at 45 d after emergence (starting buds). We adopted a randomized completely block design and three replications for each trail. The follows traits were evaluated: plant height, fiber yield, fiber percentage, boll size and rising of first flower. Genetic analyses were performed to estimate the GCA and SCA effects using GENE program. We found that GxA interaction to plant height and fiber yield, indicating that parents had different behavior in the two environments, and so, there are different levels of tolerance for water stress among them. The additive effects were more important to fiber yield, fiber content and boll size, while dominance effects were found to plant height. BRS 286 and CNPA 5M showed higher GCA estimates, while BRS 286 x CNPA 5M and BRS 286 x BRS SERIDO were the more promising hybrids, showing high GCA for, at least, one parent. These lines could provide expressive genetic gains in further selection procedures focusing on drought tolerance.

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Keywords: Cotton, diallel analysis, Genetic analysis

IMMUNODETECTION AND FEEDING BIOASSAYS AS TOOLS TO IDENTIFYING GM COTTON RESISTANT TO INSECT

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Institutions: [1] CNPA - Embrapa Cotton (R: Oswaldo Cruz, 1143, Centenário, Campina Grande-PB - 58428-095), [2] Cenargen - Embrapa Genetic Resource & Biotechnology (Parque Estação Biológica, PqEB, Av. W5 Norte (final), Brasília-DF, CEP 70770-917)

Abstract:

GM crops have become a very important agricultural technology in last two decades and offer several human and environment benefits. The development of GM crops is accomplished by using several molecular tools in order to identify the integration of novel DNA into the plant genome. In this work, cotton plants were transformed by ovary drip-microinjection using a minimal linear cassette, containing a cry1Ia gene, with toxicity to boll weevil and fall army worm. Forty three putative transgenes (T0) were first bioassayed to fall armyworm larvae and further to boll weevil, by using leaves and young buds, respectively, during 7d. Then, selected plants were assayed by Sandwich ELISA and confirmed by immunodetection-microscopy. Cry1Ia antibody was produced by Embrapa team and anti-Cry1Ia IgG was labeled with biotin. The secondary antibody was subsequently detected using an anti-biotin labeled with alkaline phosphatase. Absorbance values were read in ELISA reader at 405 nm. Light microscopy assay was carried out by using midguts from 2nd boll weevil larvae fed on artificial diet plus dried and crushed young cotton buds (25 mg/10 mL-Petri dish). Samples were deparaffined in serial baths of xylene/ethanol, and further incubated in Cry1Ia-biotinylated (30 nM). Then, again incubated in avidin-conjugated horseradish peroxidase and developed with tetramethylbenzidine. PCR assays were carried out in T1 plants order to confirm the results. We found that in resistant lines, mortality of army worm larvae was seen after 48h feeding, increasing at final of assay cycle. Four lines were selected: T0-34 (88%), T0-49 (68%), T0-56 (64%) and T0-57 (64%) and further tested by ELISA. Just one line (T0-34), showed high concentration of Cry1Ia (1,8 µg/g fresh weight). 2nd boll weevil larvae were fed on young buds of T0-34 and epithelial cells of midguts were analyzed by immunodetection-microscopy. An avidin/Cry1Ia binding was verified in midgut cells of confirming the presense of cry1Ia in plant. T1 lines from T0-34 were used in feeding bioassays and ELISA. Mortality rate varied from 19% to 87%, while Cry1Ia proteín varied from 0 to 1,9 µg/g fresh weight. Five T1 line were selected for advance in GM cotton breeding coordinated by Embrapa. In order to validate the results of T1 lines, PCR assays were carried out by using two primer combinations. In both situations, amplicons were verified in eight T1 lines, suggesting a fashion 3:1, confirming the insertion of only a single copy of transgene.

Acknowledgments

References

Keywords: GM lines, insets resistance, Bt genes

COTTON AGRONOMY AND SUSTAINABLE PRODUCTION

ANALYSIS OF THE PRODUCTION OF COTTON UNDER DIFFERENT DOSES OF PHOSPHOGYPSUM IN CERRADO SOIL

Authors: Leonardo Oliveira [1,1,1,1], Marciana silva [1], Itamar Oliveira [1], Antonio Lima junior [1], Laiza Rodrigues [1], Eduardo Miranda [1], Denise Martins [1]

Institutions: [1] FMB - Faculdade Montes Belos (São Luis de Montes Belos/Goias, avenida: Hermógenes Coelho, centro.)

Abstract:

In Brazil, the cotton crop was already known by the indigenous peoples even before the settlers came, because from that promoted the increase in the areas planted to the various existing captaincies. The upland cotton produced in Brazil in the last 15 years has undergone several major changes to the increase in production and produced quality feather in both our country and abroad. The main changes that the cotton has suffered in recent years were in relation to breeding, fertilizers and pesticides and agricultural mechanization. The planting of cotton can generate high production costs because there is a gradual increase and may become unsustainable for the producer. Among the key factors for good production management of land and vital, must know the conditions favorable to the development of culture, in addition we find the ground maintenance through proper handling knowing its characteristics and limitations for agricultural fitness, and thereby generate a plan of cultural practices. Cotton is very picky about the quality of the soil should be fertile, deep and well structured. Given this research generate around the application of gypsum in the soil for cotton cultivation, to raise the base saturation and thus deepening roots in subsurface layers, research shows that Ca, Mg and K exchangeable move the surface layer the basement, then the plaster creates favorable conditions for root growth until the deeper layers and thus only able to absorb these minerals in larger quantities thus generating further growth of the vegetative part resulting in higher productivity. The objective was to observe the plaster dosages in cotton growing and check if there was a significant difference in productivity. In the work of the implementation used the BRS 201 of upland cotton and we work as follows six treatments with 20 repetitions each totaling 120 plots, planting was carried out in 15 liter pails fertilization was done according to soil analysis, within the period of data collection was necessary for the application of fungicides, insecticides and miticides and finally maturing and defoliants. After collecting the feathers and subsequent withdrawal of carosos to estimate productivity, the following results were obtained, the T3 treatment applied 2 t / gypsum ha obtained 449 kg / ha, the T4 with application of 4 t / ha was 435 kg / ha, the worst treatment was the T6 with application of 16 t / ha and got 213 kg / ha, the other treatments showed similar average production T1 351 kg / ha, T2 291 kg / ha and T5 316 kg / there is. We can conclude that with the application of plaster values obtained showed little variation, but the treatment showed higher with T3 was 449kg / ha applied fiber 2 t / ha.

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I would like to thank everyone who might help me in the development of work especially to my teachers, classmates and my family.

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Keywords: essential, productivity, growth, fertilizer, cost

NITROGEN ABSORPTION BY TEN COTTON VARIETIES AND EFFECT AZOSPIRILLUM INOCULATION

Authors: Lúcia Vieira Hoffmann [1], Raysa Marques Cardoso [1], Michelle Christine Gomes de Moraes [1], Kálita Cristina Moreira Cardoso [1], Ana Luiza Dias Coelho Borin [1], Alexandre Cunha de Barcellos Ferreira [1]

Institutions: [1] EMBRAPA - EMBRAPA (EMBRAPA)

Abstract:

Nitrogen is fertilizer used less efficiently due to losses by ammonia volatilization and denitrification, as well as leaching. Ten cotton genotypes were evaluated to the efficiency to uptake nitrogen, inoculated or not by Azospirillum brasilliense (AzoTotal®). The cotton varieties BRS Rubi, BRS Ipê, BRS 336, BRS 368, BRS Verde (green fiber), IAC 25, Auburn 612 RNR, Tashkent II, FM 910 and FM 975 WS) were planted in pots, one plant per pot. Five plants of each variety remained non-inoculated, while other five were inoculated twice with Azospirillum, the first when the seeds were planted and the second 30 days after sowing (DAS). The green color of the leaf was 3% more intense in the inoculated plants both when measured 27 or 42 DAS, considering general average, and for genotypes AUBURN 612 RNR, BRS 368 and BRS IPE. The non-inoculated plants presented greater dry shoot weight (7.01 g compared to 5.99 g of the inoculated plants) and dry root weight (1.63 g compared to 1.11 g of the inoculated plants), when the plants were harvested, 56 DAS. The nitrogen content in shoots obtained by multiplying the nitrogen concentration in leafs by total dry shoot weight was in average higher in non-inoculated plants (0.141mg) than in inoculated plants (0.097 mg) considering the ten genotypes and BRS 336, BRS Verde or IAC 25 alone ($p < 0.05$). Similarly, on average, non-inoculated plants have more nitrogen accumulated in roots (0.024 mg) than inoculated plants (0.020 mg) and this can be observed also when only BRS 336, BRS Verde or BRS Rubi were considered. Cotton varieties showed different levels of nitrogen: IAC 25 showed 96% more nitrogen in shoots and 1.3 times more ni-

trogen in the roots than the minimal nitrogen average among these 10 varieties. The lower vegetative growth may indicate the energy expenditure by plants to develop the association with Azospirillum. Production effect may be evaluated later in larger vessels or field in different soil or fertilization conditions. Genotypes bearing leaves showing more intense green color when inoculated with Azospirillum should have more chlorophyll and greater photosynthetic rate, and possibly increased production in field.

Acknowledgments

References

Keywords: Nitrogen, Cotton varietie, effect Azospirillum

COTTON SELECTIVITY TO DICLOSULAM APPLIED IN DIFFERENT SOILS AND SEASONS OF SEEDING

Authors: Michael Ortigara Goulart [1], Bianca Nathiele Favetti Chagas [1], Jonnathan de Almeida Marques [1], Miriam Hiroko Inoue [1]

Institutions: [1] UNEMAT - Universidade do Estado de Mato Grosso (highway MT-358, km 07, Airport Garden, Tangara da Serra - MT)

Abstract:

The cotton plantation has great economic importance to the cerrado (vast tropical savanna ecoregion of Brazil) mato-grossense. The state of Mato Grosso is responsible for 60.7% of national production of cotton (Conab, 2016). In the current agriculture cotton farmers have been adopting cotton cultivation as second crop, especially in succession to soybeans. Because of the need to manage weeds in soybeans, diclosulam has been used plenty and there are few information from the influence of this herbicide on the second crop cotton. Therefore, the goal was to evaluate the selectivity of the cotton after application of diclosulam in different doses and sowing dates in sandy and loamy texture soils located in Tangara da Serra. The design adopted was completely randomized, in the factorial scheme 3 x 3 , containing three doses of diclosulam (D1 = 0, D2 = D3 = 25 and 35 g a.i. ha-1) and three periods (0, 15, 30 and 45 days between the application of herbicide and seeding cultivation), with three replications. At 20 days after sowing, the evaluations of phytointoxication are made and the dry matter is determined. There was a significant interaction among the factors analyzed for soil loamy and sandy texture. The results indicate that in the clayey soil to zero day between the application and sowing cotton the doses were differed, with averages of phytointoxication 0%, 5.33% and 98.67% for D1, D2 and D3, respectively. From 30 days between herbicide application and sowing of cotton, in clay soil, the doses not presented differences, with 0.00% of phytointoxication. When evaluating the dry weight of soil clay, it was observed that the zero-day between application and seeding was no difference between doses, but at 15, 30 and 45 days D2 and D3 doses differ D1. At the sandy soil, only on zero day between application and sowing the doses showed difference, while the other days evaluated the percentage of phytointoxication for the studied doses was 0.00%. At zero day between application and sowing of cotton there was difference between doses in the amount of dry mass, in sandy soil. At 15 and 30 days the doses of D1 and D2 differed the dose of D3 for the dry matter in sandy soil, at 45 days, both doses showed no significant difference. Therefore, there are smaller phytointoxication values and higher dry matter values as increasing the interval between the application of diclosulam and sowing cotton at both doses and soils studied.

Acknowledgments

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References

COMPANHIA NACIONAL DE ABASTECIMENTO. Acompanhamento da safra brasileira: Grãos. Brasília, 2016. 140 p.

Keywords: phytointoxication, Gossypium hirsutum L., herbicide, pre emerging

USE OF HIGH PLANT DENSITY FOR INCREASING COTTON YIELD AND WATER SAVING UNDER DEFICIT IRRIGATION IN ARID ÁREAS

Authors: Zhen Luo [1], Hezhong Dong [1,1]

Institutions: [1] CRCSAAS - Cotton Research Center, Shandong Key Lab for Cotton Culture (Jinan 250100, PR of China), [2] CRCSAAS - Cotton Research Center, Shandong Academy of Agricultural Sci (Jinan 250100, PR of China), [3] CRCSAAS - Shandong Academy of Agricultural Sci (Jinan 250100, PR of China)

Abstract:

The increasing scarcity of water for cotton production in arid areas has forced researchers to focus on increasing water use efficiency by improving both cotton and water management. The objective of this study was to determine the effects of irrigation regime and plant density on growth, yield, yield components and fiber quality of irrigated cotton. To achieve this goal, two field experiments were conducted at three sites in 2013 and one site from 2014 to 2015. A randomized complete block design with three replications was used to determine the effects of 6 irrigation regimes on seedcotton yield in the first experiment, while a split-plot design was used in the second experiment with the main plots assigned to irrigation regime (saturation, regular and deficit) and the subplots to plant density (high, medium and low). Averaged across the three sites, drip irrigation ranging from 3650 to 4700 m3.hm-2 did not significantly affect cotton yield, but seedcotton yield under 3650 m3.hm-2 in S1 was 6.3% lower than that under 4000 m3.hm-2. Thus, it is quite appropriate to regularly drip-irrigate at 4000 m3•hm2 in the experimental area. Deficit irrigation at high plant density also maintained a relatively higher leaf area index (LAI) and net assimilation rate (NAR), particularly at late stages of plant growth, than saturation or regular irrigation. Plant density ranging from 18 to 24 plant•m-2 pro-

duced more seedcotton than 12 plant.m-2 under regular irrigation. Increasing irrigation to saturation levels had little effects on cotton yield regardless of plant density; saturation irrigation at high plant density even reduced cotton yield compared with regular irrigation at medium plant density. Under deficit irrigation, the high plant density produced 9.1-17% greater yield and 9.3-16.8% higher irrigation water use efficiency (IWUE) than low or medium plant density, and comparable yield to medium or high plant density under regular irrigation. This high yield under deficit irrigation at high plant density was due to increased plant biomass occasioned by high plant population and improved harvest index. Deficit irrigation did not affect fiber quality in 2014, but reduced fiber length and increased fiber micronaire value in 2015. Conclusively, use of high plant density under deficit irrigation can be a promising alternative for water saving without compromising cotton yield under arid conditions.

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Keywords: cotton, plant density, deficit irrigation, yield, water use efficiency

USING WINTER CROPS AS A COMPLEMENTARY SOURCE OF NITROGEN FOR COTTON PRODUCTION UNDER IRRIGATION

Authors: Mario Hugo Mondino [1]

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Abstract:

Cotton requires more N than other soil nutrient. In the Río Dulce Irrigation Area (Santiago del Estero, Argentina) a major problem of cotton production is the low soil organic matter and nitrogen. At least 75 kg ha-1 N, in a single application at the beginning of floral bud (square), are required to achieve high cotton yields in the area (Mondino et al, 2005). The N amount supplied by the soil is influenced by the quantity of nutrients returned either by residues of previous crops and fertilizer applications. The most common way to add N to the soil is the application of chemical fertilizers; however, the ability of legumes to fix N and their residual impact on the soil N status have long been recognized. The literature suggests that Vicia villosa (hairy vetch), a winter legume, is an efficient N-fixer (Rochester and Peoples, 2005). During its growth cycle this species accumulates large amounts of N, providing it to the next crop, thus reducing the nitrogen fertilizer requirements. It is estimated that about 70 % of the nitrogen content of the legume biomass come from nitrogen fixation, while the remaining 30 percent is from soil sources (Kumbhar et al, 2008). The objectives of this study were to assess: (a) the influence of Hairy vetch on cotton yield and biomass, and (b) the potential reduction of requirements of N fertilizer. Research was performed during 2013-14 and 2014-15 in the Santiago del Estero Agricultural Station. We used a randomized complete block with split-plot design with four replications per year. Main plot treatments were: (i) cotton conducted under a conventional-tillage system, used as control (no winter crop); and (ii) cotton conducted in the same way, but with hairy vetch a previous winter crop. The split treatment was fertilizer application in cotton with rates of nitrogen of 0, 25, 50 and 75 kg ha-1, respectively. Before cotton seeding, hairy vetch as well the weeds were burned using herbicides and then disked. Fertilizer was applied after seeding, at the first week of pinhead, being broadcast UAN (urea ammonium nitrate) the nitrogen source. The sequence of treatments was the same for all plots during the experiment. Winter crops were reestablished every season after cotton harvest. The N dose of 75 kg ha-1 got the highest cotton yield and biomass production in both treatments. Comparing the same dose of N fertilizer, plots with hairy vetch as previous winter crop produced greater lint yields and biomass than the non-legume system. The use of winter legumes as a cotton predecessor required less N fertilizer for the same yields in the treatment without winter crop. Growing hairy vetch also reduced cotton requirements of N fertilizer, improving soil fertility. Additional benefits of winter crops are soil protection in fallow periods, improvement of soil structure and the breaking soil compacted layers, and also allowed a rotation in a monoculture system that can be used for weed and pest control

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Keywords: winter crop, N fertility, cotton yield and biomass

List of Poster Presentations Abstracts

GROWTH REGULATOR MANAGEMENT UNDER SPACING AND POPULATION DENSITIES IN COTTON CROP

Authors: Mirella dos Santos Pereira [1], Jailson Vieira Aguilar [1], Enes Furlani Junior [1], Igor Cabreira da Silva [1], Carlos Vinicius Sanches [1], Amanda Pereira Paixão [1]

Institutions: [1] UNESP - Universidade Estadual Paulista (Passeio Monção, nº 226 - CEP 15385-000 Ilha Solteira – SP)

Abstract:

Installed himself two field trials with growth regulator applications at 50 and 70 d.a.e. (days after emergency) and 20; 30; 40; 50; 60 e 70 d.a.e., ministering to dose 1000 mL ha-1 the spacings (0,38; 0,45; 0,76 e 0,90 m) and population densities (6; 8; 10 e 13 plants m-1). Was conducted an experimental design in randomized blocks in a factorial scheme 4x4x2, with three replications, used to cultivate FMT 701. The study aimed to evaluate the influence of the fragmentation of the growth regulator application on cotton, and different sowing configurations in agronomic characteristics and crop yield in two agricultural years. Were carried out periodic reviews of cotton growth (height, number of nodes and stem diameter, length of branches and number of reproductive structures of the fifth, seventh, ninth and eleventh reproductive branch) and the yield per area. Growth regulator management alone does not influence the agronomic characteristics of cotton plants, as well as its productivity. The spacings of 0.45 and 0.90 m provided the highest cotton yields in core.

Acknowledgments

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Keywords: densification, mepiquat chloride, Gossypium hirsutum

COTTON PRODUCTION STABILITY UNDER DIFFERENT COVER CROPS BIOMASS

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Abstract:

In recent years, the Western Bahia region is facing severe problems of extended drought periods with substantial cotton yield falls. When these drought periods arise in high water demand stages in the plant, the losses are even larger. Alternatives such as the use of biomass for cover the soil can potentially reduce these problems, since they can reduce water loss by evaporation and therefore increase the efficacy of soil water use by crops. In Face of this reality, this study aimed to evaluate the cotton production stability grown under different soil cover conditions with dry biomass. The study was carried out in in Luís Eduardo Magalhães, BA, Brazil, using an experimental design in randomized block with four replications. Soil covering plants species were seeding in succession to soybean harvest. The Treatments used were: cotton crop on soil without cover crop (T1); soil cover with soybean residue after harvest (T2); and the following as biomass cover: Braquiária ruziziensis (T3); sorghum (T4); millet (T5); Braquiária brizantha cv. Paiaguás (T6) and Braquiária ruziziensis + Crotalaria ochroleuca (T7). In the treatment without cover crop, the plots was prepared using disk harrow while; the other treatments were prepared using a desiccation by herbicides followed by seeding cotton in no-tillage system under the different dry biomasses. The plants emergence occurred on Dec. 3rd , 2014. It was used the cotton cultivar BRS 368 RF with a plant density of 10 plants/linear meter. At sowing, it was used 400 kg ha-1 of the formulated 05-34-00; and two cover fertilization with150 kg ha-1 and 200 kg ha-1 of KCl and urea respectively, at 25 and 55 days after emergence. All other crop managements were proceeded following the recommendations for Western Bahia cerrado region. The crop harvest was performed on Jul.10th 2015. The means among the treatments were compared using LSD test ($P < 0.05$). The dry biomass quantity on soil, at the cotton seeding, were zero, 3.8, 6.3, 6.1, 6.0, 6.7 and 7.3 ton ha-1, for the treatments T1, T2, T3, T4, T5, T6 and T7 respectively. For the same treatments interval, the cotton seed yield were 3659, 4014, 4100, 4207, 4192, 4134 and 4402 kg ha-1. The results showed no difference among treatments with respect to fiber quality and yield. In conclusion, the presence of dry biomass over the soil provided an increase of seed and fiber productivity on cotton. The dry biomass of Braquiária ruziziensis + Crotalaria ochroleuca grown in intercropping system provides the better covering soil as well as the higher seed and fibber productivity on cotton.

Acknowledgments

References

Keywords: Soil covering plants, No-Tillage, Crop Rotation

NITROGEN FERTILIZATION MANAGEMENT FOR COTTON UNDER CORN-BRACHIARIA STRAW IN NO-TILLAGE SYSTEM

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Abstract:

Conventional tillage (CT) is the cotton crop system predominant in Western Bahia. In this system, the soil is prepared using disk harrow and there are no straw presence. However, the cotton crop in no-tillage system (NT) is growing over the years in the region, especially with the use of cotton seeding under covering soil with corn-brachiaria (plants grown in consortium at the previous season), residues of which have high C:N ratio. In these conditions, cotton nitrogen (N) deficiency can appear due to probable soil microorganism mobilization. As a result, cotton plant might have a delayed initial growth, which often is not compensate during the cycle, resulting in lower fibber productivity compared to cotton in CT. Such situations requires a different nitrogen fertilization management to overcome this initial mobilization. Thus, this study aimed to evaluate different early nitrogen fertilization managements in order to avoid the problem of nitrogen deficiency and consequent productivity reduced. The study was carried out in Luís Eduardo Magalhães, BA, Brazil, using experimental design in randomized block factorial 4x4, with four replications. It were used four nitrogen rates (0-80-160 and 240 kg ha-1) and four early N fertilization under corn-brachiaria straw at 25 days before cotton seeding. The N fertilization was applied 100% in advance, 50% in advance with the remaining in two covers of 25%, 25% in advance with the remaining in two covers of 37.5%, 0% in advance with the remaining in two covers of 50%. The plants emergence occurred on Dec. 3rd, 2014. It was used the cotton cultivar BRS368RF. As fertilizer management, it was used 400 kg ha-1 of the formulated 05-34-00 at sowing; and two cover fertilization with150 kg ha-1 of KCl, while N amount (ammonium sulfate) were made according to the proposed treatments. All other crop managements were proceeded following the recommendations for Western Bahia region. The means among the treatments were compared using LSD test (P<0.05). All other crop managements were proceeded following the recommendations for Western Bahia cerrado region. The treatments were compared using Tukey test (P><0.05). It was used polynomial regression analysis for N rates. At cotton seeding, the amount of straw on corn-brachiaria was 8.9 ton ha-1. Cotton seed yield in treatments with early N fertilizer of 100%, 50%, 25% and 0% were 3797, 4201, 4093, 4013 kg ha-1, respectively, with no statistical difference. There was an increase of cotton seed yield due to increase of N rate, with maximum yield (4470 kg ha-1) at N rate of 226 kg ha-1. It was observed no difference between treatments on the quality and yield fiber. It was no interaction of N rates with types of early N fertilization managements. In conclusion, the early N fertilization applied before the cotton seeding did not provide significant increase in cotton seed yield. However, the N management with 25% to 100% of N in advance, under corn-Brachiaria straw, before cotton seeding is a cost-effective alternative to the N fertilization management.>

Acknowledgments

References

Keywords: Soil covering, Nitrogen deficiency , Early nitrogen fertilization

NITROGEN UPTAKE AND EXPORT FROM A BRAZILIAN COTTON CULTIVAR

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Abstract:

Under Brazil's Cerrado cotton production system, fertilizers account for 25-30% of the production costs, while only 50% of the amount applied is removed from the soil through harvest. A better understanding of nitrogen uptake and allocation by cotton cultivars would help in optimizing nitrogen fertilization while helping reduce environmental damages due to excessive application. This work aims at measuring daily and total nitrogen uptake, as well as nitrogen export in cultivar FiberMax975WS grown under rain fed conditions. Planting took place on December 19, 2013, in a no-tilling system under millet straw. Sowing aimed at a final plant population of 100,000 plants per hectare, with a 0.76 m row spacing. All plots were fertilized with 300 $kg.ha^{-1}$ of monoammonium phosphate and 120 $kg.ha^{-1}$ of potassium chloride. Side-dressed fertilization was split in two applications, the first one, with 90 $kg.ha^{-1}$ of N and 60 $kg.ha^{-1}$ K2O, supplied respectively as urea and chloride potassium, at 37 days after emergence (DAE) and the second one was applied at 58 DAE with 100 $kg.ha^{-1}$ N, supplied by urea. Field experiment was carried out using a randomized complete block design with four repetitions, and included twelve sampling dates: 10, 20, 30, 40, 50, 60, 70, 81, 91, 111, 132 and 197 DAE. The highest daily nitrogen uptake occurred between 81 and 91 DAE, reaching 3.52

kg.ha^{-1}.day^{-1}. At 85 DAE, half of total N had already been accumulated. Vegetative nitrogen accumulation (in stem and leaves) occurred until 111 DAE, after which nitrogen was translocated from leaves and stems to reproductive structures (squares, flowers and bolls). From 111 DAE onwards, daily nitrogen uptake in vegetative parts became negative. Models showed that the highest total nitrogen accumulation was 324 kg.ha^{-1} at 154 DAE, for a final seed cotton yield of 4,753 kg.ha^{-1}. This value represents 68 kg of nitrogen per ton of seed cotton, or 15.5 kg of nitrogen per 100 kg of lint. We conclude that under our experimental conditions, nitrogen side-dressing fertilization in cultivar FM975WS should be applied until 60 DAE. Furthermore, under high soil fertility, nitrogen fertilization could be recommended at a rate of 16 kg nitrogen per 100 kg of expected lint produced.

Acknowledgments

References

Keywords: Gossypium hirsutum, FiberMax975WS, Plant nutrition, Nitrogen allocation, No-tilling system

AN EFFECT OF BIOPREPARATIONS WITH COMPLEX ACTION RIZOKOM-1 AND SERHOSIL ON PRODUCTIVITY OF COTTON VARIETY BUKHARA-9 ON SALINE SOILS

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Abstract:

Salinity is one of the most brutal environmental factors limiting the productivity of crop plants and the area of land, affected by it, is increasing day by day. Biological methods for salinity control can play a significant role because microbial inoculation alleviate the stress in plants and may be cost effective and environmentally friendly option which may become available in the near future (1). Cotton is one of main technical cultivars in Uzbekistan. The cotton variety of Bukhara-9 is considered as a potentially perspective variety for cultivation of organic cotton (biocotton) as since it is gossypol-free. Cultivation of this variety on saline soils with application of ecologically safe biological fertilizers is very actual approach (2). The environmentally safe bioagrotechnology that based on the joint application of the two biopreparations RIZOKOM-1 and SERHOSIL at the department of soil microbiology has developed. Biopreparation RIZOKOM-1 is based on cotton rhizobacteria that have the following polyfunctional properties: tolerance to high concentrations (15-20%) of chloride and sulphate toxic salts; phosphorus mobilizing activity; destructive activity to organochlorine pesticides; antagonistic activity against phytopathogens of cotton; rhizogenic and growth promoting activity. The biopreparation Serhosil is based on the green microalgae, which improve photosynthetic activity and plant nutrition by leaves (3). The aim was to study the effect of the biopreparations RIZOKOM-1 and SERHOSIL on productivity and fiber quality of the cotton variety Bukhara-9 without application of mineral fertilizers, in field conditions. We conducted our field experiments at the Bukhara Scientific Experimental Station of the Research Institute of Breeding, Seed Production and Agrotechnologies for Cotton Production on moderate-saline sierozem soils by common accepted methods in three-fold replications (4). RIZOKOM-1 was used for pre-sowing treatment of cotton seeds while SERHOSIL for foliar nutrition of cotton. The variants without application of fertilizers were used as a control group. Fiber quality was evaluated at the Uzbek cotton fiber Certification Center «SIFAT». The experiment data was statistically treated using Student's criteria, $P \leq 0.05$ (5). The application of Rizokom-1 and Serhosil resulted in the increase of yield and fiber quality of cotton. On average, the quantity of cotton bolls in experimental groups was higher by 9.2 pieces than in control variants (without fertilizers). In the experimental variants an average weight of fiber in a bull was higher by 1 gr, the average weight of 1000 seeds was higher by 8.5 gr compared to the control variants. On average, the oil content of seeds in variants without the application of fertilizers was 21.6±1.0%, in variants with the application of the biopreparations - 23.1±2.3%, the average yield of 3 harvests was 39.6±3.8 c/ha (in the control group - 19.5±1.7 c/ha), that is higher by 20.1 c than the control variants. Thus it was established that application of RIZOKOM-1 and SERHOSIL, on gossypol-free cotton variety Bukhara-9 on saline soils, increased productivity of cotton, yield of fiber, and oil content of seeds. It was concluded that, proposed bioagrotechnology may be applicable for cultivation of organic cotton on saline soils of the Bukhara region.

Acknowledgments

This research was conducted within the frame of project AS-A6-T111 "Creation of semi industrial production of biopreparations with complex action Rizokom-1 and Rizokom-2".

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Keywords: gossypol-free cotton, cotton productivity, biopreparations, yield of fiber, saline soils

NITRATE REDUCTASE ACTIVITY OF SALINE SOIL AT APPLICATION OF THE BIOPREPARATION OF COMPLEX ACTION RIZOKOM-1 ON COTTON

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Abstract:

Nitrogen is one of the limiting nutrients for plant growth. Higher plants acquire nitrogen from soil, either as nitrate or ammonium ions. Nitrate is converted to ammonium by the sequential action of the cytosolic nitrate reductase (NR) and the chloroplastic nitrite reductase (NIR). Nitrate reductase (NR, EC 1.6.6.1) is a substrate inducible enzyme being subjected to regulation by a number of nutritional and environmental factors (1). We have developed a biopreparation of complex action RIZOKOM-1 on the basis of salt-tolerant phosphorus mobilizing rhizobacteria of cotton plant. Salt-tolerant phosphorus mobilizing rhizobacteria actively develop in saline soil and stimulate the growth of microorganisms of the nitrogen cycle. This is especially true for nitrifiers (nitrifying bacteria) when RIZOKOM-1 introduced into the soil by pre-sowing treatment of cotton seeds (2). The purpose of this research was to study the effect of biopreparation of complex action RIZOKOM-1 on the dynamics of changes of nitrifying and nitrate reductase activity of saline soils during growing season of cotton in field conditions. Field experiments were carried out at the Sirdarya Scientific Experimental Station of the Research Institute of Breeding, Seed Production and Agricultural Technologies for Cotton Production on moderate-saline sierozem soils in a three-fold replication. We conducted microbiological analyzes of soil 5 times per phase of growing season of cotton by conventional in soil microbiology methods of limiting dilution (3). Nitrate reductase activity was determined by Khaziev methods (4). We conducted agrochemical analyzes of soil by generally accepted methods in agrochemistry (5). We analyzed the composition of the initial soils, salinity was of sulphate type, & #931; of salts - 1.12%, pH - 7.9, ECe – 8.68 dS/m, solid residue 1.09%, the content of N- NH4 - 9.5 mg/kg of soil, the number of nitrifying bacteria – 4.2 lg CFU/g soil, nitrate reductase activity - 6.12 mg NO2-/10 g soil/24 h. The population of nitrifiers decreased by one degree, nitrate reductase activity remained virtually unchanged, content of N-NH4 increased by 7.3 mg/kg soil in the phase of budding in experimental variants (with application biopreparation RIZOKOM-1) in comparison with control group. Also in experimental variants the number of nitrifiers increased by 2 degree, nitrate reductase activity increased by 1.03 mg NO2-/10 g soil/24 hours, the content of N-NH4 reduced by 13.7 mg/kg soil in the phase of flowering-fruiting, that testifies intensive assimilation of nitrogen by plants in comparison with the control. At the end of growing season of cotton the nitrate reductase activity decreased by 1.99 mg NO2-/10 g soil/24 h, the content of N-NH4 increased by 7.3 mg/kg of soil, the content of N-NH4 practically unchanged and was 11.5 mg/kg of soil (in the control 11.8 mg/kg of soil). Obtained results indicate that application of RIZOKOM-1 activated the nitrogen cycle, increased nitrate reductase activity, reduced mobile forms of nitrogen (N-NH4). This led to improvement of nitrogen nutrition of cotton plants on saline soils.

Acknowledgments

This research was conducted within the frame of project AS- & #1040;6- & #1058;111 “Creation of semi industrial production of biopreparations with complex action Rizokom-1 and Rizokom-2”.

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Keywords: cotton plant;, saline soils;, biopreparation;, nitrogen of soil; , nitrate reductase.

IMPORTANCE OF ORGANIC COTTON FOR TURKEY

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Abstract:

Cotton production has been improved in respect to amount and quality with contributions of scientific and technological innovations. Increased sensitivity to health and environmental issues has caused development of new subjects such as organic agriculture. Organic production systems are based on specific standards that combine tradition, innovation and science. It sustains human and animal health and maintains ecosystem and soil quality. The goal of the organic cotton production system is to sustain human and animal health and maintain ecosystem and soil quality by the producing the cotton without synthetic chemical fertilizers, herbicides, insecticides, growth regulators, growth stimulators, boll openers or defoliants [1]. It is a consistency approach since natural fertilizer (usually from animal husbandry) and natural pesticides (Neem-based pesticides, Biosoap, Vegetable oils etc.) are used and it thus represents a circular economy in the agricultural sector [1]. Turkey has a good knowledge on organic farming and is one of the leading countries in this regard. Organic cotton is grown in 19 countries around the World. India, Tanzania, Uganda, China, Burkina Faso can be seen in the rank of the countries related with organic cotton production in 2014. Textile Exchange Organic Cotton Farm and Fiber Report in 2014 announced that organic cotton production 147.971 farmers, 116.974 MT fiber (1.1 million bales)

grown on 258.648 hectares (1.14 million acres) in 2013-14 in the world. Organic cotton now represents approximately % 4.4 percent of global cotton sector [3, 4, 5]. In the future, it is anticipated that demand for organic cotton fiber will be greater than supply. Organic cotton is considered as a niche product or niche-market product up to now, but textile sector relevant to organic cotton with the effects of consumer awareness has started to move from a niche market to mainstream with contributions of many clothing companies. In Turkey, organic cotton production faced with fluctuations from year to year due to several difficulties such as pest and disease intensity, marketing and contracting problems, demand and supply balance, etc. Taking into consideration demands of producers and consumers of cotton and also textile manufacturers, several product types including organic and also natural colored cottons have to be grown in order to provide progress in this field [1].

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Keywords: Organic Cotton, Turkey, Textile

SOIL ORGANIC MATTER AFTER NINE YEARS UNDER CROP ROTATION, CONVENTIONAL, AND NO-TILL COTTON PRODUCTION SYSTEMS

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Abstract:

Despite of its negative impacts on environment, the system based on monoculture and conventional tillage predominated for many years in Brazilian cotton production. A sustainable cotton cropping system requires the adoption of conservation tillage practices that increase the soil organic matter, which is the best indicator of soil quality in tropical conditions. Studies on soil tillage cotton, crop rotation, and long-term are rare in the Midwest Brazilian Savannah (cerrado), the most important cotton producing region in this country. This study aimed to evaluate the influence of soil management and crop rotations on the soil organic matter (SOM) content after nine years under several cotton production systems. The study was made continually from 2005 through 2014 in the State of Goiás. The treatments were as follow: (1) conventional tillage by tractor plowing and continuous cotton (MC); (2) conventional tillage and cotton-soybean-cotton rotation (CSC); (3) conventional tillage and cotton-soybean-corn rotation (CSCORN); (4) no-tillage cotton (NTC) system - [soybean (main crop) + Urochloa ruziziensis (second crop) / maize (main crop) + U. ruziziensis (second crop) / cotton (main crop)], and (5) native cerrado vegetation (NCV). The experiment was designed in a randomized block, with four replications. Soil samples were collected in October 2014, after nine years of treatments, in the layers 0-5, 6-10, 11-20, 21-30, 31-60, and 61-100 cm for evaluation of SOM content. The soil under native vegetation had significant higher soil organic matter than all cropping systems. The difference between native and cultivated soils is smaller in deep layers. In the most superficial layer, the soil organic matter was 23.3, 23.4, 24.5, 34.1, and 63.3 g kg-1 in the treatments MC, CSC, CSCORN, NTC, and NCV, respectively. No-tillage cotton increased by 46% the soil organic matter content in the surface layer (0-5 cm) compared to conventional tillage and continuous cotton, while in deeper (6-100 cm) layers, a non-significant increase of approximately 10% was observed after 9 years. No-tillage system increase SOM content in the most superficial layer.

Acknowledgments

References

Keywords: Soybean, Corn, Urochloa ruziziensis , Brazilian Savannah , Soil management

USE OF TYTHONIA DIVERSIFOLA TO IMPROVE COTTON PRODUCTIVITY UNDER MARGINAL SOILS IN UGANDA

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Abstract:

Surface and subterranean application of five Tithonia (Tithonia diversifolia) rates (0.6, 1.0, 1.6, 2.0 and 2.5 t/ha) was made to cotton at NaSARRI in 2014 and 2015. Surface application was accomplished by spreading the different Tithonia rates on the soil under the cotton crop. Subterranean application was done by making trenches in the ground under the cotton crop followed by burying of the Tithonia in the trenches besides the cotton rows. Under surface application in 2015, seed cotton yields obtained from the five different rates were 2071.1, 2151.3, 2257.7, 2275.3 and 1846.7 kg/ha respectively compared to 1846.7 kg/ha from the control. As for the subterranean application in the same year, yields were 2295.3, 2361.7, 2375.2, 2913.2 and 2504.7 kg/ha respectively compared to 1289.7 kg/ha from the control. Yields of 2014 were lower but

the trends were similar. Yield responses under surface Tithonia increased linearly with increased rates of application, while under subterranean method, the peak was at 2.04 t/ha rate. All the Tithonia application rates under subterranean method were more profitable during the 2015 season compared to the no fertilizer control, the most profitable being 2.04 t/ha which gave a net income of Uganda Shillings 3,349,800 compared to 1,934,550 from the control. Subterranean Tithonia application in 2014 significantly increased cotton fibre micronaire values, length and strength compared to the controls. The longest (27.12 mm) and strongest (29.7 g/tex) fibres were recorded from cotton that received 2.04 t/ha of Tithonia compared 25.47 mm and 25.8 g/tex respectively from the no-fertilizer controls. Analysis of soils after cotton harvest showed significantly higher amounts of residual P and K in the soils where different Tythonia amounts were applied compared to the controls.

Acknowledgments

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Keywords: Tithonia diversifolia, subterranean application, surface application, Cotton, Gossipium hirsitum

COTTON PHYSIOLOGY

EFFECT OF DIFFERENT APPLICATION TIMINGS OF MEPIQUAT CHLORIDE IN PLANT HEIGHT AND NUMBER OF FRUITS IN COTTON GENOTYPES.

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Abstract:

One of the major challenges in the cotton crop is to adjust the ratio between vegetative and reproductive plant growth. In adverse conditions, cotton plants prioritize its vegetative growth, reducing the setting of flower buds and increasing premature abortion rate of fruit (ECHER et al., 2013). Growth regulators, such as mepiquat chloride, are synthetic substances that reduce the concentration of gibberellic acid, and therefore the elongation and cell division without reducing productivity (TEIXEIRA et al., 2008). The objective was to evaluate the effect of different application timings of mepiquat chloride in plant height and number of fruits in cotton genotypes. The experiment was conducted in a greenhouse located at Fazenda Capim Branco, which belongs to the Universidade Federal de Uberlândia, in Uberlândia, Minas Gerais, from july to november 2015. The experimental design was randomized blocks (RBD) with four repetitions in a 5 x 2 factorial scheme. Treatments were five genotypes of colored cotton fiber (LC 14-11, LC 14-15 and LC14-16: lineages of the Programa de Melhoramento Genético do Algodoeiro of Universidade Federal de Uberlândia - PROMALG / UFU; BRS Safira and BRS Topázio: witnesses) with four application timing of mepiquat chloride (commercial product PIX HC), at 10, 20, 30 and 40 days after seedling emergence. The experimental plot consisted of two vases of 10 liters, with one plant per pot. The evaluated characteristics were plant height (cm) and number of fruits per plant, counted 100 days after seedling emergence. Data were subjected to analysis of variance (F, & #945; = 0.05 test), with subsequent application of Tukey test (p < = 0.05). The plant height and number of fruits on each genotype depends on the time of application of mepiquat chloride. The use of mepiquat chloride 10 days after the emergence of the plants was more efficient to reduce the final height and provide increased number of fruits, regardless of the genotype. The cultivate BRS Topázio and LC 14-16 lineage performed well in all application timings, maintaining reduced plant height and high number of fruits.

Acknowledgments

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Keywords: Gossypium hirsutum, mepiquat chloride, number of fruits, plant height

EFFECT OF ANTICIPATED APPLICATION OF MEPIQUAT CHLORIDE IN CHLOROPHYLL CONTENT A AND B ON COTTON GENOTYPES

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Abstract:

Recent trends in cotton cultivation in Brazil include increase in the number of plants per hectare, either by reducing the spacing or

the increase in the number of plants per linear meter. This requires more compact and precocious plants, which is made possible by anticipating the use of growth regulators in the culture. The cotton plant needs regulatory substances to reduce vegetative growth and achieve a balance with reproductive growth. The combination of the use of mepiquat chloride with densified cotton crops is beneficial to the utilization of light by the culture, especially for the production of photoassimilates (MAO et al., 2014). This study aimed to evaluate the effect of anticipating the application of mepiquat chloride in chlorophyll content A and B in cotton genotypes. The experiment was conducted in a greenhouse located at Fazenda Capim Branco, belonging to the Universidade Federal de Uberlândia, in Uberlândia, Minas Gerais, from july to november 2015. The experimental design was randomized blocks (RBD) with four repetitions in a 5 x 2 factorial scheme. Treatments were five genotypes of colored cotton fiber (LC 14-11, LC 14-15 and LC14-16: lineages of the Programa de Melhoramento Genético do Algodoeiro of Universidade Federal de Uberlândia - PROMALG / UFU; BRS Safira and BRS Topázio: witnesses) with two application timing of mepiquat chloride (commercial product PIX HC), at 10 and 40 days after seedling emergence. The experimental plot consisted of two vases of 10 liters, with one plant per pot. The evaluated characteristics were chlorophyll content A and B 100 days after the emergence of the plants, through the clorofiLOG CFL1030 model unit. Two readings were done in the leaves of the middle third of each plant. Data were subjected to analysis of variance (F, & #945; = 0.05 test), with subsequent application of Tukey test (p < = 0.05). The application of mepiquat chloride did not affect the levels of chlorophyll a and b of the genotypes. The witnesses BRS Safira and BRS Topázio presented high levels of chlorophyll a in relation to the lineages of PROMALG / UFU. Among the lineages, LC14-15 and LC14-16 showed high levels of chlorophyll a, although chlorophyll b had no differences between genotypes. Early application of mepiquat chloride does not affect the contents of chlorophyll a and b in colored fiber cotton genotypes.

Acknowledgments

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Keywords: Gossypium hirsutum, mepiquat chloride, chlorophyll a, chlorophyll b

ADAPTABILITY OF TRANSGENIC COTTON GENOTYPES TO HIGH TEMPERATURE STRESS

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Abstract:

Twelve transgenic cotton genotypes, collected from different research centers of the country, were evaluated for high temperature stress based on agronomical and physiological characteristics under field conditions during 2014-15 where temperature exceeded 40°C in June and July. The trial was laid out in RCBD in four replications with a plot size of 12.5×30 sq ft keeping plant to plant distance of 30 cm and row to row distance of 75 cm. Sowing was done in mid-April so that fruiting phase faces the highest temperatures of the summerseason. Fertilizer, irrigation and crop management practices were applied according the recommendations. Data on different agronomic and physiological parameters revealed that the genotypes had a variable response. For example there were statistically significant differences in percent boll set on 1st and 2nd positions along sympodia, boll weight, and seed cotton yield. Moreover, the relative cell injury level (RCIL) varied from 39 to 77%, electrical conductivity (EC) of leaves from 204 to 487 & #956;S cm-1 and pollen viability from 34 to 90%. Associations between investigated traits indicated that there were some positive and negative correlations. These data indicated that pollen viability, cell membrane thermostability (CMT) and electric conductivity (Ec) can reliably be used as heat tolerance indicators to improve/sustain cotton production under thermally stressed environments. Nevertheless, among these measurements CMT and EC are more practical indicators for screening in large breeding trials. The results of the present study revealed that cotton genotypes CYTO-178 and CIM-616 of CCRI, Multan had comparatively more thermal stress tolerance as these varieties maintained lower relative cell injury levels (higher cell membrane thermostability) and higher seed cotton yield than the other investigated varieties.

Acknowledgments

The authors are highly thankful for Central Cotton Research Institute & Pakistan Central Cotton Committee, Multan to provide funds for the study and Ministry of Textile Industry, Islamabad & ICAC to provide financial support for participating in the WCRC-6.

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Dr. Mohammad Ali Talpur Director Marketing and Economic Research PCCC
Mr. Sajid Masood Shah Director CCRI, Multan
Dr. Fiaz Ahmad, Head Physiology/Chemistry Section CCRI, Multan

Keywords: Cotton, Heat tolerance, Physiological traits, Cell membrane thermostability, Seed cotton yield

DEVELOPMENT, FIBER QUALITY AND PRODUCTION OF UPLAND COTTON GENOTYPES (GOSSYPIUM HIRSUTUM L. VAR LATIFOLIUM HUTCH) SUBMITTED TO MEPIQUAT CHLORIDE

Authors: Mirella dos Santos Pereira [1], Amanda Pereira Paixão [1], Enes Furlani Junior [1], Carlos Vinicius Sanches [1], Simone Silva Hiraki [2], Luis Henrrique Marani Daruichi Machado [1]

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Abstract:

The herbaceous cotton genotypes FMT FiberMax 701 and 966 have different morphological and physiological characteristics due to its unique genetic make-up, so you can have that response differences in the application of increasing doses of growth regulator, featuring the main hypothesis of this study. The objective of this study was to evaluate the influence of increasing doses regulator growth mepiquat chloride (MC) on the growth, yield and fiber quality in upland cotton genotypes FMT 701 and FiberMax 966. The project was installed in the city of Selviria- MS in December 2012. The experimental design was a randomized block design in a 5x2 factorial scheme totaling 10 treatments with 4 repetitions, totaling 40 installments. The CM was applied foliar installments in three applications performed at 50, 60 and 70 days after emergence (DAE), whose treatments were constituted by four doses of CM (500; 1,000; 1,500; and 2,500 mL / ha) and a witness. With the results, it was found that the application of CM in genotypes was efficient in terms of growth limitation in height, number of reproductive branches and changed some technological properties of the fiber, however did not affect the production of components. The FMT 701 showed greater maturity fiber. Overall the quality of the fiber obtained is within the standard required by the Brazilian domestic textile industry.

Acknowledgments

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Keywords: plant growth regulator, growth, agronomic characteristics, productivity

PHENOTYPING OF GOSSYPIUM HIRSUTUM GERMPLASM LINES FOR DROUGHT TOLERANCE TRAITS

Authors: Jayant Meshram [1], J Annie Sheeba [1,1]

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Abstract:

Drought is the major limiting factor for cotton production in the rainfed vidarbha region of India. Wilting and red leaf problem associated with moisture stress are also getting more pronounced in recent years. A field experiment was conducted under rain-fed condition at ICAR-CICR, Nagpur during 2013-14 to study drought tolerance traits in two thousand cotton genotypes on the basis of various physiological stress indices for yield and yield attributing characters. The physiological changes induced due to water stress were quantified by withholding irrigation for continuous 25 days to 45 days old cotton plants. All measurements and samples were collected under typical hot a dry summer with high air temperature above 40 °C. Over a month of no rain and maximum air temperatures above 40-43 °C hourly air temperature, relative humidity and solar radiation were acquired with a handheld weather station and used to calculate vapor pressure deficit. In all 350 genotypes comprise of susceptible and drought tolerant genotypes were evaluated in 2014-15 in dry and irrigated condition and selected 108 lines based on leaf area, relative water content, noon water potential, plant height, number of bolls per plant, boll weight (g) and correlate with weather and soil parameters as sown during normal season. Preliminary identified 17 drought tolerant, 15 moderately drought tolerant and 12 susceptible lines based on RWC (%), Mid-day leaf water potential, epicuticular wax content and stay green character of the plants. Selection for stable carbon isotopic discrimination in germplasm lines were also evaluated from 1500 germplasm lines cotton leaf samples. As per data analysis indicated good genotypic variability among cotton germplasm accessions in the range of 17.061-23.730 (δ13C). The differences in leaf shape and vein density in terms of drought tolerance as preliminary observed in cotton and other relevant physiological traits such as CID, epicuticular wax content, RWC and earliness will enable to augment cotton productivity under water limited environments but required to combine these traits with high yield potential.

Acknowledgments

References

Keywords: Drought tolerance, Relative water content, Water potential, Epicuticular Wax , germplasm

APPLICATION OF GROWTH REGULATOR IN COTTON BY SPRAYING AND IN THE SEEDS

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Abstract:

Cotton is included among the most important fiber crops in the world. Every year, an average of 35 million hectares of cotton is cultivated across the planet. Cotton is included among the most important fiber crops in the world. Every year, an average of 35 million hectares of cotton is planted across the planet. When grown under conditions without limitation, cotton has excessive vegetative growth, which impacts negatively on productivity. Thus, the use of plant growth regulator applied on the culture is essential. The objective of this study was to evaluate the behavior of the cotton grown in the Cerrado, where it was subjected to treatment with plant growth regulator dosages by seeds and different application forms by foliar product. The experimental design was a randomized complete block in a factorial 5x3 with 15 treatments and 4 replications, consisting of: 5 doses of mepiquat chloride (CM): 0, 4, 6, 8 and 10g iakg-1seeds, applied directly in cotton seed; The management of the plant growth regulator by foliar with 250 ml ha-1: subdivided in four applications (35, 45, 55 and 65 days after emergence (dae)); single application 70 d.a.e.; and without product application. The application of increasing doses of growth regulator in seeds afforded a linear reduction of the height of cotton plants until 50 days after emergence. There is a reduction of stem diameter, number of nodes and length of 5, 7 and 11 branch with the use of the highest growth regulator doses by seeds. The application of growth regulator in installments increases Ca, Mg and S leaf. The application via growth regulator seed provides an increase in the levels of P, K and S in the leaves to peak at a dose of 6 g iakg-1. The largest cotton seed productivity was observed for the dose of 6g i.a. kg-1 seeds.

Acknowledgments

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Keywords: Gossypium hirsutum, growth regulator, seeds treatment

RESPONSES OF COTTON CULTIVARS TO SHADING

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Abstract:

The effects of shading on cotton yield and fiber quality are known, but most of these studies were conducted in temperate regions where the growing season is short and yields cannot be recovered with an eventual lengthening in cotton growing season. In tropical areas, where the temperature window and rainy season are longer, the plant growing season can be lengthened by adjusting the planting time or cultivar type in a attempt to avoid yield loss. The aim of this work was evaluate the performance of cotton cultivars under artificial shading at field conditions. The experiment was carried out at field conditions in Primavera do Leste, MT – Brazil, in a 4x2 factorial allocated in a ramdomized block design with 4 replications. Cotton cultivars included IMA5675B2RF (early), IMA5672B2RF (mid-early), IMA5822B2RF (mid –early) and TMG 82WS (late) under shaded and no shaded conditions. A black net with 50% of light reduction was displayed over the plant canopy for 2 weeks. There is no diference among cultivars for node number under no shade conditions. However, the late cultivar TMG 82 WS yielded more nodes (14,91) than IMA5822B2RF (10,91), but similar to IMA5675B2RF (13,08) and IMA5672B2RF (12,5) under light restriction. Additionally, boll number was higher on cultivar TMG82WS as compared to IMA5822B2RF under no shade, with no diferences among the others cultivars. The boll number was reduced (36% in average) on cultivars IMA5675B2RF, IMA5672B2RF and IMA5822B2RF as comapred to TMG 82 WS on shaded treatment. There is no diference on seed cotton yield among cultivars in no shade treatment, with an average of 3878 kg ha-1. Under shading the yield reduction compared to no shade treatment in the early (IMA5675B2RF) and mid-early cultivars (IMA5672B2RF and IMA5822B2RF) was in average 18.6%, while in the late cultivar (TMG82WS) only 0.3%. The seed cotton yield under shading was 4111 kg ha-1 for TMG82WS and 3264, 2958 and 3041 kg ha-1 for IMA5675B2RF, IMA5672B2RF and IMA5822B2RF, respectively. In conclusion, the late cultivar had better performance under shading conditions than early and mid-early cultivars. Despite late cultivars are not recommend for relay crops, in situations of extension of rainfall window, as observed in this experiment, late cycle cultivars can avoid yield loss.

Acknowledgments

References

Keywords: Shedding, boll number, yield

DAMAGE SIMULATION IN EARLY- AND LATE-MATURING COTTON VARIETIES IN THE MID-SOUTH

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Institutions: [1] MSU - Mississippi State University (Mississippi State, MS), [2] UT - University of Tennessee (Jackson, TN), [3] MU - University of Missouri (Portageville, MO), [4] LSU - Louisiana State University (Alexandria, LA)

Abstract:

With over $5 billion in crop and property damages occurring in the United States from hail and wildlife each year, it is crucial for farmers and insurance companies to understand cotton response to crop damage. Cotton, a major commodity in Mississippi, has an indeterminate growth habit allowing for it compensate for damage better than other crops; however understanding it's response may also be more complicated. In order to assist with better management decisions and recommendations, the objective of this research was to evaluate the impact of damage intensity and timing on cotton yield in early- and late-maturing cotton varieties. Experiments were conducted in 2015 at the R.R. Foil Plant Science Research Center in Starkville, MS (irrigated) and the Black Belt Branch Experiment Station in Brooksville, MS (non-irrigated). Phytogen 222 WRF, a passive early-maturing variety and Phytogen 499 WRF, an aggressive late-maturing variety were planted on May 8 in Starkville and May 21 in Brooksville. Plots were 2-rows 1.9 m wide x 12.2 m long which were replicated four times in a randomized complete block design. Damage was simulated by counting the number of nodes on each plant per plot and then removing nodes mechanically with scissors. Damage was simulated at four different growth stages, 4-leaf (4 nodes), pinhead square (8-10 nodes), 1st Bloom (12-14 nodes), and 1st Bloom + 4 weeks (18-22 nodes). At the 4-leaf growth stage, 2 or 4 nodes were removed from the plant. At all other growth stages 2, 4, 6, or 8 nodes were removed from the plants. Untreated plots where no damage was simulated were also incorporated for comparison purposes. No chemical plant growth regulators were applied to any cotton in this experiment. Cottonseed yield was collected October 12 in Starkville and October 19 in Brooksville. Data were subjected to analysis of variance using the PROC Glimmix procedure in SAS 9.4 and multiple pairwise T-tests were used to separate means at p = 0.05. The results of this experiment indicate that removal of 8 nodes at pinhead square (8-10 nodes) and at 1st Bloom (12-14 nodes) resulted in significantly lower yields compared to all other removal timings in PHY 499 WRF at both locations. Node removal at 1st Bloom + 4 weeks did not have a significant effect on yield in either PHY 222 WRF or PHY 499 WRF in Starkville. Early maturing cotton (PHY 222 WRF) produced similar yields in Brooksville (non-irrigated) regardless of node removal or growth stage. Overall, PHY 222 WRF was shorter in height than PHY 499 WRF at the end of the season. Cotton maturity at the end of the season was delayed when 8nodes were removed at pinhead square in both PHY 222 WRF and PHY 499 WRF.

Acknowledgments

References

Keywords: Cotton, Damage, Maturity

HOW DO HIGH TEMPERATURES IMPAIR COTTON (GOSSYPIUM SPP.) PRODUCTIVITY?

Authors: Harel Bacher [1], Yehoshua Saranga [1]

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Abstract:

How do high temperatures impair cotton (Gossypium Spp.) productivity? Harel Bacher and Yehoshua Saranga Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem, Israel (harel.bacher@mail.huji.ac.il) Cotton (Gossypium spp.) originates from high temperature climatic regions; however, the optimal temperature range for yield accumulation is rather moderate, 20-30 C°. High temperatures during reproductive stage reduce cotton yield production, a phenomena that is expected to accentuate with the ongoing global climatic change. This study was aimed to characterize the physiological mechanisms by which high temperature impairs productivity of various cotton species, G. barbadense (Gb), G. hirsutum (Gh) and interspecific hybrid (ISH, Gh x Gb). Four cotton cultivars, Goliath 4 (Gb), Goliath 9 (Gb), RavOn (Gh) and Acalpi (ISH), were tested across two years in a phytotron. Plants were grown during summer time under natural radiation and day length in 8 L pots with two plants per pot. Experiment 1 (2014) consisted of four temperature regimes: 2822 C° (day ight, control) 2828 C° (hot night), 3422 (hot day), 34/28 (hot day and night), and 4 replicates. Experiment 2 (2015) consisted of two temperature regimes, 2822 C° (control) and 34/28 (hot day and night) and 5 replicates. Analysis of variance for plant productivity in Experiment 1 revealed a significant difference between cultivars, with Gh and ISH showing greater productivity than Gb cultivars, similar to field grown plants. Genotype * Day temperature interactions had significant effect on most variables, and high day-time temperature was associated with significant reduction in dry matter and seed cotton production. Among the yield components, boll number was not affected by high day temperatures, thus revoking damage to fruit set. As opposed to this, seed cotton per boll decreased significantly under high temperatures, suggesting heat induced assimilates deficiency during boll development. Nevertheless, the rates of photosynthesis and night respiration, as well as leaf carbohydrate contents were even enhanced by high temperatures. The two temperature regimes tested in Experiment 2, confirmed the results of Experiment 1 with respect to productivity, photosynthesis and respiration (carbohydrates were not assessed). In addition, photosynthetic rates of the same (tagged) leaves throughout 50 days in Experiment 2, did not show any reduction with time, suggesting that leaf senescence was not affected by the tested temperature regimes. In conclusion, our results suggest that high temperatures during reproductive stage induce assimilate deficiency which leads to reduced productivity of cotton plants, with no major differences between species. The direct cause for this assimilates deficiency was yet not discovered. The hypothesis that high temperature increase assimilates allocation to roots and thus causing deficiency in the plant canopy and the developing bolls is currently investigated.

Acknowledgments

References

Keywords: cotton, high temperature , productivity

COTTON GERMINATION AND EMERGENCE AS AFFECTED BY CULTIVARS AND HIGH DIURNAL TEMPERATURES

List of Poster Presentations Abstracts

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Abstract:

In Brazilian's Cerrado region, high soil temperatures during cotton-planting season may impair seedling emergence, resulting in poor stand establishment. The limit temperatures established in the literature (Wanjura and Buxton, 1972) are not compatible with what has been observed in Brazilian cotton fields, so, modern cotton cultivars seem to have a higher tolerance to high diurnal temperatures. The aim of this study was to evaluate germination and emergence of modern cotton cultivars under high day temperatures. Six cotton cultivars (TMG 81 WS, FM 975 WS, TMG 41 WS, FM 940 GLT, TMG 11 WS and FM 966 LL) and four diurnal cycles with maximum temperatures of 20 (T20), 30 (T30), 40 (T40) and 50 (T50) °C were tested in three experiments conducted in seed germination chambers. Seed imbibition curve (Experiment I), germination (Experiment II) and emergence (Experiment III) tests were performed. The exponential model fit to imbibition data between 0 and 33 hours indicated that initial water absorption rate by cottonseed was maximum with T50 and up to 13-17 hours. Radicle emergence was observed 33 h with T30 and T40 cycles, and 49 h with T20 and T50 after commencement of imbibition, which showed a delay of seed germination at the highest temperature. The diurnal cycle T30 resulted in the highest germination and emergence rates, and the largest root and shoot length of seedlings, although T40 did not differ frequently. The seed exposure to diurnal temperatures between 45 and 50 °C for only 5.5 hours a day (T50) was enough to damage cottonseed germination and prevent seedling emergence. When the maximum diurnal temperatures were maintained between 35-40 °C in germination and emergence tests (T40), cultivars with increased seed weight were the lowest sensitive, and positive correlations of seed weight with seedling shoot length (r = 0.64), total seedling length (r = 0.57) and seedling dry mass (r = 0.56) were found. The germination and emergence of seeds of modern cultivars developed by cotton breeding programs in Cerrado region showed higher temperature (40 °C) tolerance as compared to the optimal temperatures found in the literature.

Acknowledgments

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Keywords: Imbibition, Seedling development, High temperature stress

THE IMPACT OF LEAF ANATOMY ON DROUGHT TOLERANCE AND YIELD OF COTTON CULTIVARS

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Abstract:

Drought is the most important environmental constraint reducing crop yield. Modern cotton agriculture commonly uses the high yielding genotypes which are lack of drought tolerance. In this study, the impact of distinguished anatomical parameters of leaf on drought tolerance and yield potential of cotton cultivars was evaluated. One drought tolerant (Sahin 2000) and the other drought sensitive (Nazilli 84-S) cultivars were grown in field conditions in the Aegean region of Turkey (Tire-Izmir) at field capacity (normal) and limited (1/3 field capacity) water supply. Among searched anatomical parameters of leaf, drought tolerant cultivar was distinguished by decreasing stomata index, increasing leaf thickness and upper cuticle thickness compared with the sensitive cultivar. Constitutive lower stomata opening and stomata size was observed in the tolerant cultivar under normal irrigation regime. The contribution of constitutional and drought induced anatomical structure in the drought tolerant cultivar was not accompanied by yield parameters such as boll number and seed cotton yield in comparison with the higher yield of the sensitive cultivar. Although anatomical superiority of leaves significantly contributed to drought tolerance capacity of the Sahin 2000 genotype which also had better antioxidant capacity, higher photosynthetic rate and stomatal conductance compared with the sensitive cultivar under limited water supply, the parameter may not be used as selection criterion without assessing yield parameters in cotton.

Acknowledgments

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References

Keywords: Cotton, Drought, Cultivars, Anatomical parameters

INITIAL GROWTH AND GENE EXPRESSION IN COTTON GENOTYPES UNDER WATER DEFICIT

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Abstract:

The cotton crop is a very important economically agricultural activities at worldwide. The management is often prone to environmental stresses that influence in fiber yield, especially drought. Several studies involving genetic improvement have been carried out in order to select genotypes tolerant to drought, aiming further use as parents in diallelic crossings. In this study, we use growth traits and molecular tools in order to identify drought tolerant genotypes, by submission of plants to water suppression. Four genotypes (Delta Opal and Precoce 1, sensitive, and Mocó 1 and Mocó 2, drought tolerant) were grown in pots (288 ml) containing commercial substrate, and submitted to 25 d of water suppression, started when plants were 20 d after emergence. The experimental design adopted was randomized block with factorial 4 (genotypes) x 2 (water treatment: control and stress) with 4 repetitions. Plants were evaluated as to gas exchange, when the stomata closure reached 50% and 3 d after (90%), by using IRGA, and agronomic traits, in the end of water suppression. ANOVA was performed by using SISVAR program, version 5.3. In order to estimate the gene expression of genotypes as to drought tolerance, the Myb60 and Gusp1 genes were used in RT-qPCR assays, using leaves collected in same phases than physiological assays. Three endogenous control was used actin, ubiquitin and PP2A gene. Drought influenced all water-stressed genotypes as to stomata conductance and agronomical traits (number of leaves, stem diameter, dry weight of stem, roots and leaves). Mocó 2 was less affected in growth, but Delta Opal showed the same behavior, probably due both were evaluated at early phase of growth. Then, these agronomical traits were not responsive to differentiating early genotypes, in this situation. As to molecular level, expression of Myb60 gene was higher in all water-stressed genotypes in 50% stomata closure treatment, especially in sensitive genotypes. These results agree with the function of Myb60 gene, which is positively regulated in response to drought. Gradual level of expression was found to Gusp1 in all genotypes and treatments, with peak levels to tolerant genotypes, especially Mocó 2. The information of the Gusp1 function is still limited but some reports indicate its involvement in abiotic stresses. These results suggest that both genes can contribute to selection procedures of materials to drought tolerance, at molecular level.

Acknowledgments

References

Keywords: Gossypium hirsutum, drought tolerance, RT-qPCR, IRGA

EFFECT OF SEEDS TREATMENT WITH FUNGICIDES AND INSECTICIDES ON GERMINATION AND VIGURITY, ABNORMAL ROOT PRODUCING AND PROTECTION OF COTTON SEEDLING

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Abstract:

Abstract In order to evaluate the effect of insecticides, Larvin, Gaucho and fungicides Carbendazim, Carboxin - thiram and Baytan alone or mixed together, by using seed treatment on germination, vigurity, rhizogenesis and potential protecting cotton seedling, seeds treatment with different doses of insecticides and fungicides were plated in Petri dish, pot and field with natural infection to the causal agent of seedling pathogens. Percentage of germination rate, emergence percentage, and percentage of damping off, plant height, root length and number of abnormal lateral roots were measured. Analysis of variance and mean comparison using Duncan's multiple range test. The results showed that the use of 1/25 to 1/5 in thousand of Baytan is the most suitable dose for cotton in dry regions. This dose can protect the seedling from disease agents and reducing dumping off in the field. The root length density did not decline and did not produced adventitious roots of plants. While more dose causes abnormal main root and decrease and increases abnormal secondary root and decreases the length of root. The use of these fungicides in wet areas such as Golestan province is not recommended or if it is used the dose must be 0.5 per thousand. This study showed that in cold and wet regions with planting low quality seed must avoid using it or use with low concentration less than 0.5 in thousand. In dry regions with high quality seeds or in regions where seeds emergence faster and with late planting the possibility use of these fungicides are existence. In addition Larwin insecticide and Gaucho with rate of 7per thousand and Carboxin-thiram with rate of 4 to 6 per thousand can be used alone or in combination for cotton seed treatment for disinfection. Results also showed that Larvin insecticide and carbendazim fungicide with rate of 7 in thousand and Carbanzaim fungicide with ratio of 2 to 2/5 in a thousand can be used alone or in combination with the seed for disinfection. The priority is used for disinfection of seed cotton in arid regions, respectively, are Gaucho and Carboxin - thiram,Larvin and Carboxin - thiram, Gaucho and carbendazim, carbendazim and Larvin, Baytan and Gaucho, Baytan and Larvin, recommended. Key words: carbendazim, Larvin, Gaucho. Carboxin - thiram and Baytan Part of the results of the research project No. 041-80 - 11 - 24-100 of Agricultural Research, Education and Extension-Organization

Acknowledgments

. we express our thanks to Dr. Jafarei and Dr. Bayat Assadi who gave us this opportunity to do this research in a practical approach and the Agricultural Research and extension organization and cotton research institute of Iran to guided us and gave us valuable suggestions and budget.

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Keywords: carbendazim, Larvin, Gaucho, Carboxin , thiram and Baytan

COTTON REACTION TO DISEASE AND NEMATODE IN BRAZIL

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Abstract:

The aim of this study was to evaluate the reaction of eighteen cotton genotypes (cultivars and promising lines), from public and private breeders programs, to different diseases and nematodes that occur in Brazil. Twenty five fields trials were conducted in different regions in São Paulo, Minas Gerais, Goias, Mato Grosso and Bahia states. The disease/nematode evaluate were: Fusarium wilt (Fusarium oxysporum f. vasinfectum), nematodes (Meloidogyne incognita and Rotylenchulus reniformis), ramulosis (Colletotrichum gossypii var. cephalosporioides), Ramularia spot (Ramularia areola), bacterial blight (Xanthomonas citri subesp. malvacearum), Alternaria spot (Alternaria macrospora) and virus (recognized with cotton reddish "vermelhao"). The experimental designs was in randomized blocks, with fivereplications. The plots were formed by 5 meters long rows, spaced 0,90 m apart. Most of disease occurred naturally, except ramulosis (in Piracicaba-SP) and bacterial blight (in Campinas-SP), wich was make field inoculation. The diseases severity were evaluated accord scores (1 to 5), increasing with plant symptoms. The scores were transformed into index related to resistant check. Any genotype were resistance to all the pathogens evaluated. The majority of genotype showed susceptibility at least three disease. The most of genotypes were susceptible to: Fusarium wilt (72,2 %), nematodes (47,2%), ramulosis (58,3 %) and ramularia spot (69,2%). On the other hand, the best results it were obtained for bacterial blight and virus with 16.7% and 22.2% of the genotypes susceptible, respectively. There are few numbers of genotypes with a good level of resistance/tolerance to Fusarium wilt, nematode and ramularia. This is a problem, because these pathogens have been increase a lot in Brazil, above all in center-west regions.

Acknowledgments

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Keywords: cotton, multiple resistance, diseases and nematodes

A NEW METHOD TO DIFFERENTIATE COLLETOTRICHUM GOSSYPII AND COLLETOTRICHUM GOSSYPII VAR. CEPHALOSPORIOIDES USING THE IGS REGION OF RDNA

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Abstract:

The Ramulosis is one of the most important disease of cotton in Brazil. It is caused by a variation of Colletotrichum gossypii, causal agent of damping off and anthracnose, known as C. gossypii var. cephalosporioides. There are no reports of ramulosis in other traditionally cotton producing countries, although there are reports in Venezuela and Bolivia (Lima et al., 1984). The last pathogen has the same morphological characteristics, but induces different symptoms those caused by anthracnose. The symptoms of ramulosis is mainly the overgrowth induced by breaking the apical dominance, which causes excessive vegetative growth. The pathogens are transmitted by seeds and while the damage caused by C. gossypii are easily controlled by chemical treatment, the infection by C. gossypii var.cephalosporioides is not always controlled, and the level of tolerance required in seed health testing is zero, because the epidemiological implication of sowing of infected seed.

The purpose of this study was to define a safe molecular method to distinguish C. gossypii from C. gossypii var. cephalosporioides, which can be used in seed health testing without error probability, which normally occurs using morphological methods. The isolates were maintained in medium for rapid growth (2 g peptone, 10g dextrose, 1.5 g Casein, 2g of yeast extract and 16 g of agar in 1 L of H2O). To obtain mycelial mass for the extraction of DNA, the isolates were grown in bottles of 250ml with 50 ml of the medium described above, under 150 rpm of agitation for approximately three days at 250C. The total DNA was extracted following CTAB extraction procedure (Doyle and Doyle, 1990). The quantification of the extracted DNA was done through the NanoDrop 2000 spectrophotometer and 0.8% agarose gel to analyze the quantity and quality of the samples. The samples are diluted to a concentration of 50 ng & #956;L-1. For molecular differential diagnosis between CG and CGC was used the IGS region of rDNA. A fragment of 3.3 kb of CG and another of 2.7 Kb of CGC were completely sequenced and the gaps between CG and CGC were located to design a primer set that allow molecular diagnosis via PCR. Primers IGS detect F2-5'GAAAAGTAAGTACCCCCGAA3' and IGS detect R- TGGCGGCGGTGAGTCGGGGTGC amplify a fragment of 432 bp to 148 bp in CG and CGC. PCR reactions were performed in 20 uLusing 50 ng of total DNA; 1X buffer (100 mM Tris-HCl (pH 8.8 at 250C), 500 mM KCl, (0.8% v / v) with 2 mM MgCl2; 0.4 mM dNTPs; 1U Taq DNA polymerase (DNA Express Cat. No. 0300.0003.0500) and 0.2 µM of each primer. The conditions for amplification were initial denaturation at 940C for 3 minutes, 40 cycles of denaturation at 940C for 15 seconds, annealing of primers at 650C for 15 seconds, synthesis at 720C for 30 seconds. Finished the cycles one extension of 72 0C for 10 minutes was performed. The results confirm that the region IGS is effective for molecular diagnostic for both GC and CGC, with amplification of 432 and 148 base pairs respectively

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Keywords: Fungus, Genetic, Molecular Method, Diagnosis

EFFICACY OF ORGANIC NEMATICIDES ON MELOIDOGYNE JAVANICA FOR SMALL-SCALE COTTON FARMERS IN SOUTH AFRICA

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Abstract:

Meloidogyne javanica is one of the serious parasitic nematodes in the tropics causing root-knot in cotton. The input costs of small-scale cotton farming are high due to, amongst others, the synthetic chemical costs for nematode control. Synthetic chemicals that have nematicidal properties do not break down as easily as the natural products. Thus they can build-up and cause environmental degradation. Natural chemicals (organic products) that have nematicidal properties are bio-degradable and safe for the environment. A study was conducted in Vaalharts, Northern Cape to evaluate the efficacy of different plant extracts against Meloidogyne javanica under field conditions. Tobacco (Nicotiana tabacum), thorn apple (Datura sp.) and castor oil (Ricinus communis) plants were incorporated in the soil while the marigold (Tagetes erecta) was planted as an intercrop. These treatments were compared to Temik® (Aldicarb) and an untreated control. At 6 weeks after planting, no significant differences between the treatments were found in the number of Meloidogyne in the cotton roots. At 12 weeks after planting, treatment with thorn apple provided significant reduction on the number of Meloidogyne in the roots. None of the treatments had significant effect on the number of Meloidogyne in the soil during the experimental period. Thorn apple gave significantly higher seed cotton yield (5.29 ton/ha) than all the treatments except the Temik®. Treatment with castor oil gave the lowest seed cotton yield of 3 ton/ha. Generally, the organic and chemical nematicides had demonstrated potential in reducing the numbers of Meloidogyne in roots and can be used as a basis for integrated management of the pest with better understanding on their application protocols and other properties that could optimize efficacy.

Acknowledgments

I would like to thank the ARC for funding my research.

References

Keywords: Cotton, Meloidogyne javanica, Nematode, Organic

EFFECT OF PROTECTANT FUNGICIDES AND FERTILIZERS ASSOCIATED WITH AZOXYSTROBIN AND CYPROCONAZOLE FUNGICIDES TO CONTROL RAMULARIA AREOLA AND CORYNESPORA CASSIICOLA ON COTTON CROP.

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Abstract:

The Ramularia blight (Ramularia areola) and target spot (Corynespora cassiicola) are diseases that have reached an important level

at cotton crop scenario in Brazil causing serious damage to production. The main control for these diseases are systemic fungicides, which, in some cases it has been losing efficiency. The protectant fungicides and copper-based fertilizers association with systemic fungicides could be an alternative control for these diseases. The objective of the work was to evaluate the association of protectant fungicides and fertilizers to azoxystrobin and cyproconazole fungicides to control ramularia blight and target spot under field conditions. The experiment was carried out at the experimental area of Fundação Chapadão, located in Costa Rica - MS during the 2014/2015 harvest. The cotton cultivar used was the FM 975WS. Treatments consisted of: a Check, another treatment with azoxystrobin + cyproconazole isolated and associated with Mancozeb, Copper oxychloride, Metiram, Fluazinam, Benzalkonium chloride and Copper sulfate. The applications started at the first bud, followed by five other subsequent applications within 14 days apart, in which were used a constant pressure backpack sprayer (CO2) and volume spray of 150 L.ha-1. The statistical design adopted was random blocks (RBD) with 4replications and plots with 21,6 m². Twenty randomly chosen leaves both from bottom half and top half of the 2 center lines were used for evaluations on each plot, estimating the disease severity according to the percentage of leaf area damaged proposed in diagrammatic scale Aquino et al. (2008) to ramularia blight and Dias et al. (2015) to target spot. Then, it was determined, for the entire plant, the area under the disease progress curve to ramularia blight (AUDPCR) and target spot (AUDPCT) according to Campbell & Madden (1990), the number of rotten bolls, boll weight in top half and bottom half of the plant and the cotton yield. Data were analyzed by variance teste F, and means were compared by the Scott-Knott test at 5% probability, with statistical program MSSA-Agri (Canteri, et al. 2001). The usage of copper sulphate and copper oxychloride associated to azoxystrobin + cyproconazole provided the lowest AUDPCR. The lowest AUDPCT was seen when with Mancozeb fungicide, Copper oxychloride, Metiram, Benzalkonium Chloride and Copper Sulfate associated to azoxystrobin + cyproconazole. All treatments were able to reduce the number of rotten cotton bolls. The highest yield was resulted of the application of azoxystrobin + cyproconazole isolated and associated to Copper oxychloride, Copper sulphate and Fluazinam. The other variables were not enhanced by the use of fungicides. The other variables were not enhanced by the use of fungicides. Under the conditions of this work, there are differences between azoxystrobin + cyproconazole fungicide control associated to protectant fungicides depending on the disease.

Acknowledgments

References

Keywords: Ramularia blight, Target spot, Chemical control

COTTON BOLLWORM HELICOVERPA ARMIGERA: CONTROL BY CONVENTIONAL AND BIORATIONAL INSECTICIDES

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Abstract:

The persent work was devotedto study the impact of some recent insecticides pertaining to biorational insecticides group that have low mammalian toxicity i.e, [chlorantraniliprole, spinetoram, methoxyfenozide, thiamethoxam and lambda-cyhalothrin]which were sprayed individually and/or mixed with each other against the American bollworm ABW Helicoverpa armigera during the consequent growing cotton seasons of 2014 and 2015 at Al Zeiny - Abohoms, El-boheira Government, Egypt. Results of the study showed that the admixed different compounds [Voliam Flexi® 40 WG (Clorantraniliprol 10%+ Thiamethoxam 20 %, Engeo® %24.7 SC (Thiametoxam 14,1%+ Lambda-cihalotrina 10,6%, Radiant® 12% SC (Spinosyn J and L) + Runner® 24% SC methoxyfenozide] gave the highest efficient activity upon the population of H. armigera larvae. It could be also said that, the mixing of each of these different compounds together had a strong effect on the annihilation of the population of ABW H. armigera larvae more than their use individually.

Acknowledgments

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Keywords: El-bassouiny H. M., Haity M. Tadros, A. Z. El-Nagger

EVALUATION OF TIMING INTERVALS OF FOLIAR APPLICATIONS FOR THE CONTROL OF TOBACCO THRIPS (FRANKLINIELLA FUSCA) IN COTTON

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Institutions: [1] MSU - Mississippi State University (Mississippi State, Mississippi USA), [2] UTK - The University

of Tennessee (Jackson, Tennessee USA), [3] LSU - Louisiana State University (Winnsboro, Louisiana USA)

Abstract:

Tobacco thrips, Frankliniella fusca (Hinds), are a consistent and predictable pest of cotton production systems in the United States because of their potential to delay maturity and reduce crop yields. On average, there is an increase in lint of 128 kg ha-1 when treated with an insecticide seed treatment. With the decline in efficacy of thiamethoxam, it is vital that we determine other non-neonicotinoid seed treatment options for effective Tobacco thrips control. Therefore, the objective of this study is to determine the best management strategy for controlling Tobacco thrips by evaluating various foliar insecticide timing intervals. Studies were conducted in 2015, in Mississippi, Louisiana, and Tennessee (USA) using a randomized complete block design with four replications. Treatments included foliar applications at the following intervals: cotyledon, cotyledon followed by two weeks after emergence, cotyledon followed by two and three weeks after emergence, only week two and only week three after emergence, an average of one thrips per plant, and if plants scored an average injury rating of two. All treatments were compared to an untreated check and an imidacloprid seed treatment. At the first sampling, treatment applications made at cotyledon followed by week two and cotyledon followed by week two and three reduced adult thrips below the untreated control, while imidacloprid and cotyledon followed by week two timings had fewer immature thrips than the one thrips per plant and average injury rating of two treatments. Thrips damage ratings were reduced to a 1.25 score when applications where made at cotyledon followed by week two and three. At the second sampling, all treatments reduced adult and immatures thrips densities below the untreated control. In respect to cotton yield, there were no differences among any treatment.

Acknowledgments

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Keywords: Cotton, Tobacco Thrips, Timing Intervals

IDENTIFYING AND CHARACTERISING NOVEL MODES OF ACTION FOR INSECTICIDAL TOXINS.

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Institutions: [1] CSIRO - Commonwealth Scientific and Industrial Research Organisation (Black Mountain Laboratories, Canberra, ACT, Australia)

Abstract:

Insecticidal proteins derived from the bacteria Bacillus thuringiensis (Bt) have been introduced to several agricultural crops to control insect pests. In particular, the crystalline toxin families, Cry1 and Cry2 have been widely used to control Lepidopteran pests, including in cotton. In recent years Vip3 toxins have also been deployed individually and in 'stacked' plant varieties. However, for lepidopteran pests, these three families of insecticidal toxins represent just three modes of action as there is significant evidence of cross resistance between toxins from the same family. Globally, the number of cases of practical resistance to Bt crops (one or more populations with > 50% resistant individuals and reduced crop efficacy) increased from one in 2005 to nine in 2013. Therefore, there is a need for novel insecticidal proteins with novel mechanisms. One method of quickly identifying novel mechanisms is to test candidate proteins against resistant insect lines. Resistant insect lines enable rapid and cost effective testing for these novel mechanisms and also provide insight into how existing toxins work. Since the mid-1990's CSIRO has been tracking resistance frequencies in Australia as part of the Cotton Industry's plan to prolong the life of Bt cotton and has isolated Cry1A, Cry2A and Vip3 resistant insect lines in two different Lepidopteran species, Helicoverpa armigera and H. punctigera. These insect lines, together with the experience with bioassay and molecular identification of resistance mechanisms that CSIRO has developed over two decades, represent a valuable resource that can be used to rapidly screen large numbers of candidate insecticidal toxins.

Acknowledgments

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References

Keywords: Bt, resistant lines, Helicoverpa

FACTORS AFFECTING FORAGING HONEY BEE EXPOSURE TO NEONICOTINOID SEED TREATMENTS IN MIDSOUTHERN U.S. COTTON FIELDS

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Abstract:

There have been recent reports of declining honey bee populations around the world. One suspected cause is the widespread use of pesticides in agriculture. Foraging honey bees can utilize agronomic crops as both pollen and nectar sources. Honey bees have been reported foraging on cotton nectar from extra-floral nectaries during vegetative growth and from floral nectaries during reproductive growth. Experiments were conducted to examine potential exposure routes of neonicotinoid seed treatments to honey bees in Midsouthern U.S. cotton fields. Neonicotinoid seed treatment compounds were studied to determine the rate at which they diminish in crop tissue during cotton development. Tissue samples were collected during plant development from the newest growth on the plant and analyzed for neonicotinoid compounds from seed treatments applied before planting. There was a considerable reduction in neonicotinoid compounds from seed treatments found in plant tissue during development. Little to no neonicotinoid compounds were found in cotton tissue from samples taken at the start of reproductive growth. Another area of research included the observation of honey bee foraging activity in Midsouthern U.S. cotton fields. Cotton fields were scouted for foraging honey bees at three time intervals during the day in both vegetative and flowering cotton. More honey bees were observed in flowering cotton than in vegetative cotton, and more honey bees were observed foraging in vegetative cotton during the mid-day than in other times during the day. There were no differences in honey bee foraging behavior for different times of day for flowering cotton. Therefore, foraging honey bees in the Midsouthern U.S. are not exposed to high concentrations of neonicotinoids from seed treatments through cotton pollen or nectar. Although nectar available during reproductive growth could potentially contain neonicotinoid compounds from seed treatments, foraging activity is not as prevalent at that stage of cotton development than during reproductive growth stages.

Acknowledgments

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References

Keywords: Neonicotinoid, Honey Bee, Exposure

SEASONAL OCCURRENCE OF LEPIDOPTERAN PEST OF SOYBEAN AND THE IMPLICATIONS FOR THE NATURAL REFUGE

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Abstract:

Dual gene Bt cotton was first introduced in 2003, and with this introduction of these dual gene cottons, the natural refuge system was implemented and took the place of a structured refuge system. This system used the surrounding landscape as refuge for the cotton bollworm. With the possibility of Bt soybean being introduced to the United States, the role soybean in the natural refuge needs to be evaluated. Past research has shown that C4 plants play the largest role in the natural refuge, but soybean are also playing a role in the natural refuge. Surveys were conducted throughout Mississippi across early, normal, and late planted soybean. Surveys were done weekly using a standard fifteen inch diameter sweep net, from the R1 growth stage through the R7 growth stage. The object of this study was to determine the distribution of the cotton bollworm in soybeans and when soybeans play the largest role for these pest. Cotton bollworm were highest in normal planting dates with a mean number of 76.8 million cotton bollworm larvae being contributed from these planting dates. Late planting dates had 4.25 million cotton bollworm larvae. When cotton bollworm larvae were corrected for percent positive samples for cotton bollworm, the means13.06 and 2.12 million cotton bollworm larvae for normal and late planting dates respectively. Bt soybeans will be a good fit in late planting dates since these late planting dates are not playing as large of a role in the natural refuge as normal planting dates.

Acknowledgments

The authors would like to thank the Mississippi Soybean Promotion Board for their generous funding of this project.

References

Keywords: Natural Refuge, Lepidotera, Bt Soybean

TERMINATION OF INSECTICIDE SPRAYS FOR TARNISHED PLANT BUG

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Institutions: [1] MSU - Mississippi State University (Mississippi State, Mississippi, USA), [2] U of A - University of Arkansas (Fayetteville, Arkansas, USA), [3] LSU - Louisiana State University (Winnsboro, Louisiana, USA), [4] UTK - The University of Tennessee (Jackson, Tennessee, USA)

Abstract:

Tarnished plant bugs have the highest control cost of any insect in Mid-South cotton with many fields requiring multiple close interval sprays to obtain adequate control. The tightening budgets of growers has fueled the need to cut all unnecessary expenses. The objective of this study was to determine the point in the growing season when tarnished plant bug applications can be terminated without significant yield losses. Tests were conducted in 8 locations across the Mid-South. Treatments consisted of a second, third, fourth, fifth, sixth, and seventh week of flowering insecticide termination, as well as an untreated control and a season long control. Prior to first flower tarnished plant bugs were controlled across the entire test area to maintain at least 80% square retention. Analysis of means across all locations indicated that insecticide applications

occurring after the 5th week of bloom did not result in yields different than the season long control. Tests will be repeated in 2016 and may result in a variable tarnished plant bug threshold depending on crop growth stage.

Acknowledgments

References

Keywords: Tarnished Plant Bug, Lygus lineolaris, Insecticide, Termination, Threshold

PLANT GROWTH PARAMETERS AND COTTON BOLLWORM [HELICOVERPA ARMIGERA (HÜBNER)] SURVIVORSHIP ON WATER STRESSED COTTON BT VARIETIES

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Abstract:

Brazilian cotton crops have been cultivated as a relay crop sowed late in the planting window. As a result plants are exposed to drought since squaring, leading to a favorable reduction of insecticide proteins expressed on Bt cotton plants. Thus, control failures of target pests, such as of the cotton bollworm (CBW), can occur. Water stress was studied on growth parameters, as well as on CBW attack and survivorship on Bt cotton varieties. Plants were grown in pots arranged in a 4x2 complete randomized factorial with four replications during the 2013/2014 growing season in Mato Grosso, Brazil. Treatments included varieties [FM975WS (Cry1Ac+Cry1F), IMA5675BGII (Cry1Ac+Cry2Ab), NuOpal (Cry1Ac) and IMACD6001 (non-Bt)] and, water regimes (well watered and water stressed). Water stress was imposed at pinhead square stage by reducing irrigation in 70% for three weeks followed by plants infestation with CBW neonates for three days. Signs of CBW attack on squares were assessed in planta. A foliar disc bioassay was carried out to assess the survivorship of CBW neonates up to 96h of the infestation. Plant growth was reduced on water stressed treatment. Stomatal conductance did not change under drought stressed varieties, but on well-watered conditions, it was higher on cultivar IMA5675BGII. Plant dry weight and reproductive structures number decreased under water stress, but no differences were observed among them. Under stress there is no difference among cultivars on dry weight of a single reproductive structure (RSDW), but with no water limitation the RSDW was increased on cultivars IMACD6001 and IMA5675BGII. Water stressed plants showed a significant higher number of flower buds with CBW attack signs. The percentage of flower buds attacked was significantly lower on IMA5675BGII and NuOpal varieties. Almost 60% less survivors were observed on IMA5675BGII after 48h of infestation. Varieties under stress had larval mortality reduced from 30 to 42%. Water stress was able to affect the development of Bt plants and their control performance on CBW.

Acknowledgments

References

Keywords: drought, relay crops, larval mortality

FACTORS DETERMINING THE ATTACK OF APHIS GOSSYPII GLOVER, 1877 (HEMIPTERA: APHIDIDAE) ON COTTON (GOSSYPIUM HIRSUTUM)

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Abstract:

The *Aphis gossypii* Glover, 1877 (Hemiptera: Aphididae) is a highly polyphagous and is considered important pest of cotton (*Gossypium hirsutum*). Determination of factors that affect population dynamic, critical life stages and key factors of mortality is crucial for planning of appropriate management strategies and tactics to control this insect pest. However, so far no studies that determine critical stages and key factors of mortality for *A. gossypii* on cotton have been conducted. The aim of this study was to determine the key factors and the critical stages when *A. gossypii* attack cotton. A field ecological life table experiments were conducted at Federal University of Viçosa, Brasil in 2013 and 2014 using randomized complete block design with 12 replications. Each replication consisted of cotton plant containing a cohort of 100 first instar nymphs of aphid. Data were collected from insecticide-free plots within 600 m2 on each entire experimental plant at vegetative, flowering and fruiting stages of cotton cultivar FM910. The mortality and its causes were monitored daily until the individuals had died or became adults. The mortality by predation were determined by observation of predators preying on aphids. The aphids not found on the plants considered eaten by predators. Aphids that disappear after a rainfall have been considered dead by rainfall. The mummified aphids were considered dead by parasitoids. Mummified aphids were removed from the plants for identification of parasitoid species emerged. Life table construction and analysis obtained by calculating and estimation number of individuals dying in nymph and adult stages of aphids. In total 72 ecological life tables were constructed for *A. gossypii*. The total mortality of *A. gossypii* ranged from 83.4 to 84.8%, 77.9 to 94.3%, and 80.2% to 82.2 on plants at vegetative, flowering and fruiting stages for the first and second years, respectively. Nymphs were the mortality critical stage of A. gossypii on each plant stage in the first and second years ($F = 33.79$; $P = 0.0002$). The predation and rainfall were the key mortality factors of *A. gossypii* ($P < 0.05$). The mortality caused by predation was 22.5%, 90.9% and 75.3% on plants at vegetative, flowering and

fruiting stages, respectively. The mortality by rainfall on the same plant stages was 59.1%, 0.17%, and 4.5%. Thus, the population size of this pest can be regulate by the mortality of nymphs caused by the predators and rainfall. The predators and rainfall determine the population size of *A. gossypii*. This suggests adoption of agronomic practices that preserve natural enemies. The rainfall should be monitored to predict locations and times of greater attack of *A. gossypii* for timely implementation of management tactics.

Acknowledgments

Agriculture Research Institute of Mozambique, Brazilian CAPES Foundation, Cotton Institute of Mozambique, Federal University of Viçosa (UFV), Ministry of Science and Technology of Mozambique, and Researchers from Entomology Lab of UFV.

References

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Keywords: Aphis gossypii, key factor of mortality, pest management, predation, rainfall.

THE IMPACT OF A NEW BT COTTON TRAIT ON THRIPS AND THEIR INJURY IN SEEDLING COTTON

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Abstract:

There is a demand for new technologies to help combat thrips in the southeastern United States due to several factors including the loss of aldicarb (Temik 15G), developing resistance to key insecticide seed treatments (IST), and the limited effective alternative treatments. Monsanto has been developing and evaluating a Bt trait for the control of plant bugs. In 2014, some effects on thrips injury were also noticed. In 2014 and 2015, internal and external trails were done to investigate this Bt trait's impact of thrips control. The paper reports the effects of this new Bt cotton trait on thrips and their injury for seedling cotton grown in Tennessee during 2015. Two identical small-plot tests were planted on different planting dates (May 5 and 12, 2015) at the West Tennessee Research and Education Center in Jackson Tennessee. Each test was designed as a randomized complete block with four replications of each treatment. Treatments were all combinations of three factors including 1) Bt trait or non-Bt cotton, 2) an insecticide seed treatment of imidacloprid or no seed treatment, and 3) a foliar application of acephate and the second-leaf stage or no foliar insecticide. At the third-leaf stage, visual estimates of thrips injury (on a 0-5 scale) and thrips counts were made in each plot. Data were analyzed with AOV procedures, and mean separation was done using Fisher's Protected LSD (α = 0.05). For both planting dates, the Bt trait without the use of any insecticides had significantly less thrips injury than non-Bt cotton treated with an insecticide seed treatment and a foliar insecticide. In the absence of insecticides, the Bt trait reduced thrips numbers by approximately 60% compared with non-Bt cotton. These data suggest that this new Bt technology will provide as good or better protection from thrips than the standard best management practice of using an insecticide seed treatment and a foliar insecticide application.

Acknowledgments

The authors wish to express their appreciation to Monsanto for their support.

References

Keywords: Cotton, Thrips, Bt

IMPACT OF NITROGEN APPLICATION RATE ON TARNISHED PLANT BUG POPULATIONS, CONTROL, AND COTTON YIELD

Authors: Lucas Franca [1], Chase Samples [1], Darrin Dodds [1], Jeff Gore [2], Bobby Golden [2], Angus Catchot [1], Jac Varco [1], John Riley [1], Andrew Denton [1], Drake Copeland [1]

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Abstract:

The tarnished plant bug (Lygus lineolaris P) is the primary insect pest of cotton (Gossypium hirsutum L.) in Mississippi. Nearly 95% of these acres received an average of six insecticide applications for tarnished plant bugs during the growing season. Insecticide resistance has complicated the control of tarnished plant bugs. Snodgrass (1994) reported that tarnished plant bug populations in the Mississippi Delta were 54-fold more tolerant to permethrin and 35-fold more tolerant to bifenthrin than other populations from other areas of Mississippi. It has been observed that tarnished plant bugs are attracted to vigorous growing cotton (Willers et al. 1999). Excessive N application to cotton can result in increased plant height as well as increased vegetative growth that can alter maturity (Varco et al. 1999). Given the status of tarnished plant bug resistance to insecticides and the cost required to control this pest, adjusting N rates could make cotton less attractive to tarnished plant bug and allow the crop to mature faster, while maintaining yield, resulting in economic benefits for many growers across the mid-southern

growing region. Experiments were conducted in 2012 and 2013 at the Delta Research and Extension Center located in Stoneville, Mississippi. Plots consisted of sixteen rows spaced 1 m and 23 m long. All plots were replicated 4 times. Stoneville 5288 B2F was planted on 1 May 2012 and 14 May 2013. 32% UAN was side dressed at pinhead square at four application rates which included: 0 (untreated check), 45, 90, 134, and 179 kg N/ha. For each nitrogen application rate as well as the untreated check, one set of plots were managed for tarnished plant bugs based on thresholds developed by the Mississippi State University Extension Service. In pre-blooming stages, 25 sweeps/plot were taken. Once treatment averaged 2 plant bugs per 25 sweeps applications were made. In blooming cotton, 2 drop cloth samples were taken per plot using a black drop cloth. Insecticide applications were made when treatment averaged 3 plant bugs per drop. All data were subjected to analysis of variance and means were separated using Fishers Protected LSD at p = 0.05. Nitrogen application rate had a significant effect on the mean number of plant bugs present across each sampling period. Significantly more plant bugs were present in the presence of N versus were N was not applied in the unsprayed portion of the test. Cotton yield was maximized in the sprayed portion of the test in plots receiving 90 kg N/ha. These results agree with the findings of McConnell et al. (2000) and Main et al. (2013) that as N application rate increased, the number of applications made for plant bug management also increased. Plots receiving 134 and 179 kg N/ha received more insecticide applications across both years to manage plant bug populations. Mean profit was maximized in plots that were managed for plant bugs, when they received 90 kg N/ha. Less risk was also associated with plots receiving 90 kg N/ha when compared to plots receiving 134 and 179 kg N/ha.

Acknowledgments

References

Keywords: Tarnished Plant Bug, Cotton, Nitrogen

RELATIONSHIP BETWEEN RAMULARIA LEAF SPOT AND THE DEVELOPMENT OF COTTON CROP (HARVEST OF 2013/2014)

Authors: João Paulo Ascari [1], Inês Roeder Nogueira Mendes [1], Rafael Sbruzzi Prieto [1], Angélica Carmo de Meneses [1], Marcos Vinícius Foschiera [1], Danielle Storck-Tonon [1], Rivanildo Dallacort [1], Dejânia Vieira de Araújo [1]

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Abstract:

Cotton is a very important crop in the Brazilian agricultural scenario and Brazil is the fifth world largest producer of this crop. The aim of this study was to evaluate the effects of ramularia leaf spot (*Ramularia areola*) on the development of vegetative and productive characteristics of the cotton crop, harvest of 2013/2014. The study was carried out at Mato Grosso State University, Campus of Tangara da Serra city. The experiment was conducted in randomized block design arranged in a triple factorial scheme (4x3x2), with four cultivars (FM 951 LL., FMT 705, FMT 709, IMA CD 05-8276), three layers of the plant (lower, middle and upper canopy), two conditions (treated and non-treated with fungicides) with four replications. Plots were 5m long and 3.8 m wide, spaced 0.76 m apart. Line sowing was carried out at January of 2014 in properly limed and fertilized soil and the thinning was done at 20 days after sowing (DAS), leaving eight plants per linear meter. Fungicides applications were initiated at 75 DAS and performed weekly in treated plots. Assessments of ramularia leaf spots were initiated at 75 DAS and, using the severity values, the area under the disease progress curve (AUDPC) was calculated per canopy layer. The variables number of leaves (NL), number of aborted leaves (NAL), number of bolls (NB) and weight of bolls (WB) were assessed at 150 DAS considering the canopy layers. All assessments were made in six plants randomly marked in the useful area of the plot. Once a crop reaches physiological maturity the bolls were harvested manually, the weight of the plume with cottonseed was obtained and productivity was extrapolated to kilogram per hectare (kg ha-1), considering each canopy layers. AUDPC was higher and the interaction significant in the plots with no fungicides applications, in the lower canopy of the plants and in the cultivars IMA CD 08-8276 and FM 951 LL. The cultivar FMT 705 was less affected by disease in all treatments. The variables NB and NL showed the highest values in the upper canopy in the treatments with fungicides control, with 2.06 bolls plant-1 and 17.34 leaves plant -1, respectively. Due to higher AUDPC, NAL was higher in the lower canopy, being the cultivar IMA CD 05-8276 the most affected by defoliation. Bolls were heavier in the plots treated with fungicides and also in the middle and upper canopy of the plants. IMA CD 05-8276 cultivar despite the high value of AUDPC showed the highest average values of WB, with 28.01 g bolls-1. Cottonseed productivity showed no significant interaction, however, showed differences between factors in an isolated way, where in the condition treated with fungicides and in the middle canopy occurred the highest average, being 1,039.33 kg ha-1 e 1,076.80 kg ha-1 of cottonseed, respectively.

Acknowledgments

References

Keywords: Ramularia areola, Disease severity, Vegetative and reproductive characters

EFFECT OF FUNGICIDE ON RAMULARIA LEAF SPOT AND VEGETATIVE CHARACTERISTICS IN THE COTTON HARVEST OF 2014

Authors: João Paulo Ascari [1], Leonardo Diogo Ehle Dias [1], Inês Roeder Nogueira Mendes [1], Rafael Sbruzzi Prieto [1], Marcos Vinícius Foschiera [1], Thainara Porcher [1], Danielle Storck-Tonon [1], Dejânia Vieira de Araújo [1]

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Abstract:

In Brazil, ramularia leaf spot (*Ramularia areola*) is the most important disease of cotton resulting in large production losses. The aim of this study was to evaluate the effect of fungicide on vegetative and productive characteristics of the second season crop and severity the of ramularia leaf spot. The study was carried out at Mato Grosso State University, Campus of Tangara da Serra city. The experiment was conducted in randomized blocks arranged in a double factorial scheme (4x2), with four cultivars (FMT 709, FM 951 LL, FMT 705, IMA CD 05-8276) submitted to the effect of fungicide application and the non-application of fungicides. Sowing was carried out at January of 2014 in properly limed and fertilized soil and the thinning was done 20 days after sowing (DAS) with density of eight plants per linear meter. The plots were formed by four 5 meters long rows, spaced 0.90 m apart. Fungicides applications in treated plots were initiated at 25 DAS and performed every seven days. Six plants from the useful area of the plots were chosen randomly and after 94 DAS were assessed the disease severity, number of fruiting branches (NFB), number of fruiting branches with bolls (NFBB), weight of bolls (WB) and number of bolls (NB). There was no significant interaction between factors in all the analysed variables. For the variables NFBB, NB and WB the applications of fungicides provide better results than the average of the non-treated with fungicides, with 8.2 branches plant -1, 7.7 bolls plant-1 and 103.7g plant-1, respectively. However, there was no significant difference for the variable NFB and between cultivars. The severity of ramularia leaf spot was 4.9% higher in the plots not treated with fungicides and showed no significant difference between cultivars. Therefore, the application of fungicides caused a reduction in the severity of disease providing better development of vegetative and productive characteristics of cotton plants.

Acknowledgments

References

Keywords: Gossypium hirsutum, Ramularia areola, Chemical control

INFLUENCE OF PHOTOPERIOD ON MYCELIAL GROWTH AND CONIDIA PRODUCTION OF *RAMULARIA AREOLA*

Authors: Vanessa Costa da Silva [1], Inês Roeder Nogueira Mendes [1], Jurandir Ambrósio [1], João Paulo Ascari [1], Tainara Porcher [1], Kethelin Cristine Laurindo de Oliveira [1], Danielle Storck-Tonon [1], Dejânia Vieira de Araújo [1]

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Abstract:

Ramularia leaf spot is one of the most important cotton diseases and responsible for severe economic losses. Therefore, it is very important to understand the development of Ramularia areola in laboratory in order to obtain the pathogen inoculum for studies under controlled conditions. The aim of this study was to evaluate the effects of photoperiod on mycelial growth and conidia production of Ramularia areola. The pathogen isolated was obtained from cotton plants with symptoms of the disease. The experiment was carried out in the Laboratory of Phytopathology at Mato Grosso State University, Campus of Tangará da Serra City. Four photoperiod were tested, using as reference light/dark periods in 24 h. Treatments were: continuous dark (0h/24h), three hours light (3h/21h), three hours darkness (21h/3h) and continuous light (24h/0h). Discs of mycelium (2 mm) were transferred to petri dishes containing 20 mL of potato dextrose agar medium (PDA) and kept in the photoperiods used in this study and adjusted temperature (24°C ±1°C). Every 24 hours, the diameter of the colonies was measured in two orthogonal axes and the mycelial growth index (MGI) was calculated. At the end of the measurements, when one or more dishes showed complete growth, the number of conidia (NC) was counted using a camara of Neubauer. For the variables MGI there was no significant difference between photoperiods, and these showed MGI average of 10.61 mm day-1, completing growth in 9 days. Photoperiod of 0h/24h showed higher NC (2.12x105 conidia mL-1), followed by photoperiod of 24h/0h (3.56x104 conidia mL-1). Photoperiods of 3h/21h and 21h/3h had lower production of conidia and showed no significant difference between them, with 1.85x104 conidia mL-1 and 9.7x103 conidia mL-1, respectively. These results indicated that the growth of Ramularia areola was not influenced by the light condition; however, conidia production was highly favoured by continuous periods of light or dark. This result highlight that to produce large amounts of Ramularia areola conidia, the stress condition is necessary, thus the absence of light is a key factor for development of reproductive structures of this pathogen.

Acknowledgments

References

Keywords: *Light/Dark condition, inoculum, reproductive structures*

SANITARY QUALITY OF SEEDS PRODUCED IN DIFFERENT CANOPY LAYERS OF COTTON CULTIVARS

Authors: Inês Roeder Nogueira Mendes [1], João Paulo Ascari [1], Vanessa Costa da Silva [1], Marcos Vinícius Foschiera [1], Kemely Mara Ramalho Hiega [1], Danielle Storck-Tonon [1], Willian Krause [1], Dejânia Vieira de Araújo [1]

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Abstract:

Cotton (Gossypium hirsutum L.) is a very important crop for Brazilian agriculture. However, there are many fungi that infect plants and cottonseeds. In this context, the aim of this study was to evaluate the sanitary quality of cottonseeds harvested in different canopy layers of cotton plants. The experiment was conducted in a triple factori-

al scheme (8x3x2), being evaluated eight cotton cultivars (IMA CD 8276, FMT 705, FMT 709, FM 951 LL, FM 940 GLT, FM 944 GL, TMG 42 WS e TMG 43 WS), three canopy layers (lower, middle and upper) and two management strategies of disease (with and without fungicide application), with eight repetitions of 25 seeds. The harvest was performed in each canopy layer and bolls were ginned by hand, then seeds were delinted with sulfuric acid. Sanitary quality of seeds was assessed using paper substrate moistened with distilled sterile water, agar-water + 2.4D (5ppm) and placed in petri dishes of 15 cm diameter. Dishes with seeds were incubated for 7 days at 24ºC ±2ºC and 12h photoperiod. Seeds were analysed using a stereoscopic microscope and the percentage of seeds infected by fungi was recorded. There was a significant interaction between cultivar and canopy layer. For the fungus Botryodiplodia theobromae the upper canopy layer showed the lowest average of seeds infection (27.56%) when compared with the lower canopy layer (42.26%). The cultivar FM 940 GLT was less affected by this fungus (15.83%). Fungi Aspergillus flavus and A. niger showed lower infection on cultivar FM 944 GL, being A. flavus with 4.00% and 4.25% and A. niger with 4.00% and 3.75% in the lower and upper canopy layer, respectively. On the other hand, Fusarium verticillioides showed lower average of infection in the cultivar FM 951 LL (0.33%) and in the lower canopy layer (2.13%). Significant interaction was also observed between cultivar and management strategy. Fungi B. theobromae, A. flavus and A. niger treatments without fungicides application were more affected, with 38.07%, 6.14% and 19.78%, respectively. In the cultivar FM 944 GL, seed infection was lower by A. flavus (4.47%) and A. niger (5.44%), while the cultivars FM 940 GLT and FM 951 LL had the lowest incidence of fungi B. theobromae (15.58%) and F. verticillioides (0.33%). Finally, there was a significant interaction between management strategy and canopy layer. Seeds from treatments without fungicides showed higher incidence of B. theobromae (42.44%), F. verticillioides (1.96%), A. flavus (3.13%) and A. niger (19.72%). It can be seen that seeds from the lower canopy were more infected by B. theobromae (42.47%) and F. verticillioides (2.13%), while the middle canopy showed higher infection by A. flavus (6.81%) and A. niger (20.22%). In general, there was a wide variation in infection between cultivars, with the highest infection average in the lower canopy and treatments without fungicides applications.

Acknowledgments

References

Keywords: Gossypium hirsutum, Seed health, Fungi in seeds

MORPHOLOGICAL CHARACTERISTICS OF RAMULARIA AREOLA ON DIFFERENT CULTURE MEDIA

Authors: Inês Roeder Nogueira Mendes [1], Jurandir Ambrósio [1], João Paulo Ascari [1], Vanessa Costa da Silva [1], Kemely Mara Ramalho Hiega [1], Kethelin Cristine Laurindo de Oliveira [1], Danielle Storck-Tonon [1], Dejânia Vieira de Araújo [1]

Institutions: [1] UNEMAT - Universidade do Estado de Mato Grosso (Curso de Agronomia, Rod. MT-358, Cx Postal 287, Tangará da Serra, CEP 78300-000)

Abstract:

The objective of this study was to evaluate morphological characteristics of *Ramularia areola* colony, etiological agent of ramularia leaf spot, in seven culture media. The evaluated culture media were: potato dextrose Agar (PDA), V8 agar (V8), malt extract agar (MEA), vegetable extract agar (VEA), modified Kirchoff›s (MK), modified Rice Agar (RA) and dextrose peptone agar (DPA), with six repetitions each. Discs of 2 mm diameter, removed from *Ramularia areola* colonies grown on PDA, were transferred to petri dishes (9 mm) containing 20 mL of each culture media and placed in 12h photoperiod and temperature of 24°C ±1°C. For the mycelial growth index (MGI), diameter of the colony was measured daily. Conidia production (CP), assessed using a Neubauer chamber, and colony morphology (coloration, mycelium height and formation of sectors) were determined at six days of incubation, when observed the overall growth of the colony in one or more dishes. MGI and CP varied depending on the culture medium and a wide range of appearance and coloration were observed. The highest MGI was found in (RA) (14.33 mm day-1), V8 (13.82 mm day-1), VEA (13.52 mm day-1) and PDA (13.27 mm day-1) and the lowest MGI in MK (8.66 mm day-1) and DPA (11.28 mm day -1), respectively. PDA was the culture medium that showed higher production of conidia (4.33x104 conidia mL-1), followed by V8 (2.33x104 conidia mL-1). All the other culture media showed lower production of conidia, varying between 5.69x103 and 4.84x103 conidia mL-1, and were not statistically different among them. Colony morphology varied in mycelia height, coloration and number of sectors. The culture media VEA, RA and MK showed lower production of conidia and the formation of sectors was not verified. PDA and MEA showed, on average, two and three sectors, respectively. While DPA and V8 formed five sectors each. Regarding colour, culture media were grouped into three groups: white (PDA, MEA, VEA and RA), pinkish-white (V8, DPA) and pink (MK). This last is one of the culture medium with lower mycelial growth and conidia production. The topography of the colony was classified according to mycelium growth as dense and high (PDA and YDA), low and thin (VEA, RM and MK) and intermediate growth and thin, with sectors of mycelium high (V8 and MEA). PDA medium, despite showing one of the lowest MGI, produced the highest number of conidia. In these experimental conditions, MK is not suitable for growing *Ramularia areola*. This fungus showed variation in colony morphology when grown on different culture media.

Acknowledgments

References

Keywords: Ramularia leaf spot, mycelial growth, conidia production

COTTON TOPPING AS A WAY TO REDUCE FARMER'S RELIANCE ON INSECTICIDES IN MALI

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Abstract:

Bollworms such as Helicoverpa armigera, Diparopsis watersi and Earias sp., are a major constraint for cotton production in Mali. Up to now, their control has primarily relied on chemical sprays. Finding ecologically-based alternatives to control those pests is a strategic issue for cotton production. We, here, report results from field experiments on cotton topping, as a promising technique to control bollworms. In 2014, effect of cotton topping on bollworm abundance was investigated at 3 locations in 5 farmer fields per location and 3 replications per field. Each replication consisted of one 10 m long topped row. Abundance of bollworms was recorded weekly on 10 topped plants, 10 non- topped plants located 10 m from topped plants and 10 non-topped plants on rows adjacent to the topped row. In 2015, 100% (T100) and 20% topping (T20) of cotton plants associated with threshold based-sprays and diverse crop management practices were compared to farmer practices (FP) at 5 locations. Insecticide sprays, damage and seed-cotton yield were recorded. In 2014, bollworm abundance was significantly lower (-60.7% for all species) on topped plants vs non-neighboring non-topped plants, except for D. watersi. Bollworm abundance was also lower (-37.2% for all species) on neighboring non topped plants vs non-neighboring non-topped plants, but this was only significant for H. armigera. In 2015 compared to farmer practices (FP), 64.4 and 62.4% of sprays were saved with T100 and T20, respectively. Proportion of plants with freshly damaged squares or bolls was greater with FP (3.4%) compared to T100 (2.4%) and T20 (2.6%). Except at one location, bollworm control was significantly improved regardless of the villages and the agronomical improvements. Seed-cotton yield was significantly improved with T100 and T20 in 3 and 2 out of 10 location x agronomical improvements, respectively. These results show a significant effect of topping on the incidence of bollworms, not only on topped plants, but also on neighboring non-topped plants. They also underline the potential of topping to reduce insecticide use in cotton in Mali.

Acknowledgments

We are thankful to AFD (French Agency for Development) to have allowed the implementation of these studies

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Keywords: Topping-cotton, bollworm, insecticide use

INSECTICIDES APPLICATIONS TO CONTROL LEPIDOPTERANS-PESTS IN COTTON AND SOYBEANS IN WESTERN BAHIA REGION: AN OVERVIEW

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Abstract:

The lepidopteran pest management in cotton and soybean is one of the main factors that had significantly increased the production costs in such crops in Brazil. The Bahia Western region comprises 13 million hectares of agriculture arable land, which in turn, comprises 18% of the new Brazilian agricultural frontier - MATOPIBA, composed by arable lands on the states of Maranhão (MA), Tocantins (TO), Piauí (PI) and Bahia (BA). The caterpillar that affects cotton and soybeans fields (*Helicoverpa* spp.; *Chrysodeixis includens* and*Spodoptera* spp.) is paramount among the main phytosanitary problems in the region. In order to overcome this problem, several cultural management techniques are employed. However, the key control technique currently employed still remains the insecticide applications. Aiming to assure an environment safety and the sustainability of these crops in Brazil, it is important to ensure an efficient use of those insecticides and an effective control of the application technology employed. Thus, Embrapa Cotton is leading an application technologyproject, where the main concern is to support the progress of caterpillars control through the application technology. This study was conducted in order to diagnostic the current situation of application technology (AT) used to control lepidopteran pests. It was performed a survey in 66 cotton and soybeans farms from Bahia Western region. The survey was performed on farms by both in site (80%) and through electronic surveys (20%), which was sent directly to the farmers and farms managers. The survey included questions about farm employees training, entomology and biological control, besides technical and practical questions. It was possible to infer that 79% of the famers workers are trained in AT, and regularly, take courses to update the knowledge; It was also observed that 35% of the farms, make calibrations, on every application needed, while 30%, 27% and 8% make calibrations monthly, weekly and annually respectively; However, only 21% of the farms implement equipment regulations based on calibrations results. The majority of farms (73%) use self-propelled land for caterpillar control while 26%, use tractor with self-propelled in 50% of applications needs and the other 50% of applications needs, after canopy closure, make use of aerial applications. Among the most used insecticides group, highlights the diamide and benzoate; even though, the majority of farms (83%), also make regular use of the biological products besides the insec-

ticides applications; it was also observed that, 74% of Bahia western farms, make area sampling to determine the control based on control levels; The study allowed to designing the current situation of the application technology, providing basic-to-specific information about conditions for the control of lepidopteran pests on Bahia western region; including knowledge about areas closely related to the project objectives. The survey allowing for the adaptation of interdependent activities involved in the project as well as for support future projects in the region concerning application technology, pest management, precision agriculture and correlate areas.

Acknowledgments

The authors thanks to the Bahia western region farmers and employees that friendly contributed to this survey and other research locally developed

References

Keywords: application technology, lepidopteran, control, insecticides

DEVELOPMENT OF AN IPM STRATEGY FOR PHENACOCCUS SOLENOPSIS (COTTON MEALYBUG) IN AUSTRALIA

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Abstract:

The cotton mealybug (CMB hereafter) – Phenacoccus solenopsis - is a highly polyphagous and invasive global insect pest of cotton that poses a significant threat to the world's major cotton industries in Australia, the USA, Argentina, Brazil and the sub-continent (India & Pakistan). CMB was first reported from cotton growing areas in the USA in the early 90s. It has since spread to all major cotton producing countries and continues to grow in pest status (threat level and damage). Damage caused to cotton by this pest includes limiting yield potential (plant stunting and/or mortality) and marketability through effects on lint quality (boll characteristics and lint contamination). Reports from Indian and Pakistan indicate that outbreaks of CMB between 2007 and 2009 increased the cost of crop protection (insecticide application) by US $625- $900 per hectare, over and above direct crop injury and yield loss. In Australia, economically damaging outbreaks of CMB on cotton were reported from the Burdekin and Emerald regions of Central Queensland in the 2009-10 cotton season; it has since been found in southern regions of Queensland and continues to spread further south. Previous research done in Australia and elsewhere has shown that most newly developed "soft" (selective) chemical insecticides currently approved for use within cotton production systems vary in control efficacy from ineffective to having only suppressive effects. Some older organophosphates such as methidathion (eg. Supracide®) are effective but highly hazardous from an environmental and user safety perspective which makes this option incompatible with modern IPM-friendly cotton production systems. Here we report on the preliminary findings of a project currently underway, jointly funded by The Australian Cotton Research & Development Corporation (CRDC) and the Queensland Department of Agriculture and Fisheries, to develop and implement an integrated pest management (IPM) strategy for CMB. The project has three main objectives: (a) To characterise the in-field distribution, survival and inter-seasonal relationships of CMB with a particular focus on understanding the phenomenon of population aggregation or so-called "hot spots", (b) To develop IPM-friendly and cost-effective control options based on chemical/biological insecticides so as to give cotton growers options to treat either entire paddocks or to target "hot spots" and prevent them from growing and multiplying, and (c) To identify practical options for integrating naturally occurring or mass-released predatory insects with compatible chemical control tactics to achieve environmentally responsible and commercially satisfactory CMB management outcomes. Glass house and field evaluations of chemical insecticides done to date have shown that (1) spirotetramat and buprofezin offer good potential for the development of metabolically distinct (alternative) approaches to managing field populations of CMB, (2) new generation neonicotinoids and new molecules such as sulfoxaflor can effectively supplement field control when used in combination with spirotetramat and buprofezin, (3) the addition of emulsifiable crop oils can increase CMB mortality by 10-30% when added to certain insecticide tank mixtures, and (4) a sequential application tactic (two applications 10-14 days apart) is critical for commercially acceptable control of CMB using new-generation, selective insecticidal products.

Acknowledgments

Financial support for this research was provided by the Queensland Department of Agriculture &Fisheries, and the Australian Cotton Research & Development Corporation

References

Keywords: Phenacoccus solenopsis , cotton , mealybug , IPM , Australia

EVALUATING RESISTANCE TO RAMULOSIS IN COTTON

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Abstract:

Brazil is a major cotton fiber producing and exporting country in South America, mostly because the acreage increase that occurred in the cerrado region of west-central Brazil. In this region, the hot and wet weather favors the development of foliar diseases. Ramulosis, caused by the fungus Colletotrichum gossypii var. cephalosporioides (Cgc), is an important disease throughout the growing season. Cotton plants can be infected along all developmental

stages, and disease symptoms includes the shortening of internodes and excessive development of branches and leaves, causing witch's broom type of symptom (Suassuna and Coutinho, 2014, Thaxton and El-Zik, 2001). Currently, the management of ramulosis is based on crop rotation to reduce initial inoculum, the use of cultivars with partial resistance, and fungicide sprays (Suassuna and Coutinho, 2014). Nevertheless, these practices are not always integrated, and, in most cases, application of fungicides is the only control measure used. Over the past decade, a coordinated effort was made to screen sources of resistance to cotton ramulosis. A collection of 347 accessions of Gossypium hisrsutum from di□erent countries was screened over eight seasons (from 2003/04 to 2010/11) in field tests for resistance to Cgc. Field trials were carried out in augmented block design using two cultivars checks as common treatments and cotton accessions as regular treatments. Plots consisted of two 5 m rows, each one containing approximately 50 plants, planted 0.76-0.8 m apart. Plants were artificially inoculated at flowering with a suspension (5 x 104 conidia mL-1) prepared with three isolates of the pathogen. Severity was evaluated at the cutout stage, assessing 20 plants of each plot based on the grade scale (Oliveira et al., 2010) varying from 1 (no symptoms) to 5 (highly susceptible). From the grades recorded, a disease index (DI) was calculated (Czermainski, 1999). A mixed model approach was used considering the season effect as fixed and the genotype and genotype x crop effects as random. The block effect within season (B/S) was considered either as fixed or as random. According to Akaike Information Criterion and Baysian Information Criterion, B/S as fixed had the best fit, however, heritability estimates (0.27) had similar value when B/S was analyzed as random. A significant Pearson correlation (0.98) was detected between BLUPs obtained from each analysis (B/S as fixed or random). There was a significant season effect, indicating environmental influences, although artificial inoculations had been performed. Accessions "C 3", "A 71" and "BRS Antares" were most resistant to ramulosis using both analysis (B/S as fixed or random effect) with BLUP estimates differing from zero (t test). Taking cultivar BRS Facual as a resistance reference, eight accessions were identified with higher resistance level: "C 3", "A 71", "BRS Antares", "CNPA GO 2002-1689", "Coodetec 404", "FMT 701", "IAC 25" and "IAC 23". On the other hand, two accessions were the most susceptible, with BLUP estimates differing from zero (t test): "CNPA CO 99-11612" and "BRS PERO-BA". Despite eight years of effort, conventional breeding has not been fully successful in yielding resistance to the disease.

Acknowledgments

The authors gratefully acknowledge EMBRAPA and FIALGO for the partial financial support.

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Keywords: Gossypium hirsutum L, Colletotrichum gossypii var. cephalospor, Genetic resistance

TRIGONA SPINIPES (HYMENOPTERA: APIDAE, MELIPONINAE) DAMAGING COTTON PLANTS IN PARAÍBA STATE, BRAZIL

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Abstract:

Trigona spinipes (Fabricius, 1793) (Hymenoptera: Apidae, Meliponinae) damaging cotton plants in Paraíba state, Brazil. This bee is commonly found in Brazil damaging crops, but without been reported on cotton. The objective of this research was to record the occurrence of *T. spinipes* on cotton plants grown organically and describing its injuries. *Trigona spinipes* adults partially or totally destroyed cotton bolls, what reduced the production. The information generated may be useful to formulating management tactics for *T. spinipes* on cotton grown organically, especially in agricultural environments of the Brazilian semiarid region.

Acknowledgments

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Keywords: Gossypium hirsutum, hymenopteran, pest

HOST WEEDS OF BEMISIA TABACI (GENNADIUS, 1889) BIOTYPE B (HEMIPTERA: ALEYRODIDAE) IN COTTON (GOSSYPIUM HIRSUTUM L.).

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Abstract:

The aim of this study was to identify which floristic composition of weeds occurring in cotton crops are host of whitefly (Bemisia tabaci biotype B). In a cotton field in Sinop-MT, assessments were made fortnightly during the reproductive stage of the crop. The inventory square (0.25 x 0.25m) was released 15 times within cotton rows. The weeds were cut close to the ground, packed and taken to the laboratory to identify the family and species, and to quantify eggs and nymphs of whiteflies. Eleven families were detected, being the most frequent Amaranthaceae (16.67 %), Convolvulaceae (12.5 %), Rubiaceae (12.5 %) and Poaceae (12.5 %). The most frequent species were Amaranthus spp. (13.79%) and Alternathera tenella, Ipomea spp., Richardia brasiliensis, and Eleusine indica with 10.34 % each. From the 15 species collected only in Portulaca oleracea and E. indica the presence of eggs or whitefly nymphs was not identified. The highest incidence of B. tabaci occurred in Euphorbia heterophylla. Therefore, the occurrence of these weeds should be monitored so the population of whiteflies do not affect cotton fiber quality.

Acknowledgments

References

Keywords: host plants, whitefly, management

ECONOMICS COTTON COMPETITIVENESS

FIFTEEN YEARS OF GM COTTON IN ARGENTINA: A PARTIAL BALANCE

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Abstract:

After 15 years, GM technology has succeeded in terms of its wide adoption by the Argentinean cotton growers. However, questions about the real benefits and risks of GMOs are continuously raised by the society. Ten years after their first approval in 1998, RR and Bt cotton varieties reached 100% of the crop area. The main reasons of this wide adoption were their easier and initially effective control of weeds provided by glyphosate, and the possibility of reduced soil tillage allowing direct planting and lower crop costs. The resistance to Lepidoptera, however, represented only a short term advantage of GM cotton, as it became useless when the boll weevil appeared as a new pest requiring intensive insecticides´ usage. In terms of productivity the GM influence was negligible: only 100 kg/ha more in the national average. On a world basis GM cotton has contributed to a 43% reduction in pesticide consumption. However, in Latin America the trend is the opposite: between 1999 and 2009 the herbicides ´sales have doubled and insecticides´ ones are four times bigger. In Argentina, far from decreasing with the adoption of insect-resistant and herbicide-tolerant varieties, management practices of GM cotton led to an increase in their use. Glyphosate application rates increased with consequences on soils and water contamination, increasing resistance in some weed species, and appearance of herbicide´s residues cases in cotton final products. Indeed, the appearance of tolerant and resistant weeds, led the growers to the use of higher glyphosate doses, and/or increases in the number of applications, and/or to apply additional herbicides with different active principles. While in 1998 2 l/ha of glyphosate were enough for a good weed control, in 2008 the growers used an average of 4 l/ha, reaching in 2015 up to 13 l/ha. Argentina is delayed, if compared with neighbor countries, in terms of de-regulating new GM varieties. The reason could be the high rate of black market seeds, which constitutes a disincentive for seed technology companies. Although there are no official statistics, estimates indicate that between 65% and 90% of the cotton seed market is actually illegal. While public institutions as INTA continue to develop their breeding programs, without genetically engineered seeds their influence in this kind of market is very limited.

Acknowledgments

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Keywords: genetically engineered cotton, agricultural biotechnology, seed industry, research and development, pesticide use

List of Poster Presentations Abstracts

FIBER QUALITY AND PROCESSING

OVER VIEW ON SUDAN COTTON RESEARCH: FIBER QUALITY AND STICKINESS

Authors: Abdelrahman Abdellatif [1], Elafadil Babiker [2,2]

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Abstract:

Abstract: Cotton “Gossypium in Sudan, is one of the main cash crops;. It forms a source of life hood for more than 200,000 of its growers. Cotton in Sudan is grown under irrigation and rainfed. The irrigated system forms the bulk of production. This production covers wide range and nearly full spectrum of cotton qualities, from the extra long (33-36 mm) to short staple cotton (25-26 mm). This wide spectrum since the beginning back by strong research program carried out by the Cotton Program of the ARC. The framework of the cotton research is pillared mainly upon:-Variety improvement, Stickiness and Agronomy. The released varieties and registered lines to date totaled above 50.Promising fibre characteristics to replace the long and extra long current varieties were reported. Improvement of Ginning Out Turn (GOT).were indicated. Better results and practical knowledge on avoiding stickiness were clearly achieved. The main objective of this paper is to focus on the goals and achievements of Sudan cotton program mainly on fibre quality as well as stickiness.

Acknowledgments

References

Keywords: Fibre, Stickiness, GOT

RELATIONSHIPS BETWEEN HVI AND CCS AND TENSILE YARN STRENGTH

Authors: mohamed negm [1], suzan sanad [1], Zeinab Ghareeb [1]

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Abstract:

Prediction of the mechanical properties of cotton yarns has been studied by numerous authors. Theoreti¬cal and mathematical models have been proposed in these studies Five Egyptian cotton varieties and two Upland cottons from Uzbekistan and Burkina Faso based on a wide range of fiber properties i.e., fiber length, HVI fiber strength, fiber elongation and micronaire reading measured by HVI “as High Volume Instrument” they also tested in addition to absolute fiber strength with new device Cotton Classification System (CCS-Textechno) “as Medium Volume Instrument” were analyzed and Using Statistical software APSS forward stepwise multiple linear regressions were performed between yarn strength, yarn elongation (dependent variables) and HVI and CCS fiber properties (independent variables).

Acknowledgments

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Keywords: HVI, CCS, yarn quality

GENETICS AND GENOMICS

DEVELOPMENT AND UTILIZATION OF INTERSPECIFIC CHROMOSOME SUBSTITUTION LINES IN GENETIC ANALYSIS AND GERMPLASM IMPROVEMENT OF UPLAND COTTON

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Abstract:

The tetraploid species Gossypium barbadense, G. tomentosum, and G. mustelinum are useful genetic resources for improvement of Upland cotton. However, derivation of successful new cultivars with introgressed germplasm has been constrained by genetic incompatibilities between the species. To help overcome barriers to effective introgression, we have developed a “platform” for introgression, genetic analysis and breeding, the basis of which includes a number of alien chromosome substitution (CS) lines from G. barbadense (CS-B), G. mustelinum (CS-M) and G. tomentosum

(CS-T). Most of the CS lines are nearly isogenic to the inbred 'Texas Marker-1' (TM-1, G. hirsutum). Comparative analysis of the CS lines have provided means to identify and associate important traits with specific substituted chromosome or chromosome segments. We released a set of 17 disomic CS-B lines through hypoaneuploid-based backcrossing in a near-isogenic genetic background of TM-1 line. By creating and analyzing various types of CS-derived near isogenic families, the chromosome-specific quantitative genetic effects were determined for various agronomic and fiber properties. The results collectively showed that the chromosomal substitution lines constitute important genetic resources opening a new paradigm in Upland cotton breeding. Results have validated CS-B11sh, CS-B16, and CS-B17 harboring RKN, FOV1 and FOV4 resistance genes associated with SSR markers, respectively. Preliminary results based on various morpho-physiological traits suggest that CS-T04 has higher tolerance against drought and low temperature. CS-B25 was associated with improved fiber traits including high fiber strength, length and low micronaire. Affymetrix microarray analysis detected four RING-type ubiquitin ligases (GhRING2-5) genes that are differentially expressed in 10-DPA CS-B25 fiber. We also developed near-isogenic chromosome-specific recombinant inbred lines (CS-RILs) by crossing specific CS lines with the common recurrent, inbred TM-1, then inbreeding via single-seed decent. Analysis of CS-RILs for traits and SSR and/or SNP markers enable markers to be associated with genes with marked effects on important fiber traits. Results demonstrate that chromosome substitution lines are valuable genetic resources in Upland cotton improvement and the value can be amplified by combining their application to breeding with molecular marker analysis.

Acknowledgments

References

Keywords: Interspecific Chromosome, Genetic Analysis, Germplasm Improvement

MAPPING OF QTLS IDENTIFIED IN A NOVEL SOURCE OF RESISTANCE TO THE ROOT-KNOT NEMATODE (MELOIDOGYNE INCOGNITA RACE 3) IN COTTON (GOSSYPIUM BARBADENSE L.)

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Abstract:

The root-knot nematode (RKN) *Meloidogyne incognita* is a serious pest of cotton, causing direct damages and increasing the severity of other root diseases. Host plant resistance and the development of resistant varieties have the potential to efficiently contribute to RKN management in cotton. High levels of resistance has been identified in a breeding line (Auburn 623 RNR) derived from a cross between two moderately-resistant accessions, and this source of resistance has recently been used to develop highly-resistant adapted lines. Nevertheless, continuous exposition to the same source of resistance may lead to the selection of virulent RKN isolates, and the identification of new sources of resistance is important for a durable resistance. We have previously demonstrated that *G. barbadense*accession CIR1348 (Mota et al. 2013; Da Silva et al. 2014) shows the same high level of resistance as the Auburn 623 RNR source, and in this work we describe the mapping of QTLs associated to RKN resistance in this novel source of resistance. An interspecific F_2population of 174 plants, constructed from a cross between the resistant accession CIR1348 and the susceptible Upland cotton variety FiberMax 966, was genotyped using SSR markers and plant reaction to inoculation with *M. incognita* race 3 was evaluated under controlled conditions. RKN resistance was scored using the following criteria: galling index (GI), egg mass index (EMI), number of eggs per gram roots (E/GR) and reproduction factor (RF). A genetic map was constructed using a set of 271 microsatellite markers, and a total of 262 loci assembled into 29 linkage groups at LOD ≥4. The total length map was 4,294 cM with an average distance of 15.1 cM between adjacent loci. QTL mapping identified four chromosomal regions harboring significant QTLs for one or more of the scored traits. Two QTLs (for GI on c2 and for EMI, E/GR and RF on c9) had a positive contribution from the susceptible parent FM966. A major QTL, with a positive contribution of the resistant parent CIR1348 was identified on c11, in the interval flanked by SSR markers CIR316 and CIR069. This major QTL mainly influences nematode egg production, and acted in conjunction with minor QTLs to confer the high level of resistance in cotton accession CIR1348. This same interval has been identified as harboring a major RKN resistance locus in other sources of resistance, including in M-315 RNR (Gutiérrez et al. 2010; Jenkins et al. 2012), and this region of c11 has been shown to be rich in disease resistance genes (Wang et al. 2015). Similarly to other sources, the resistance in accession CIR1348 fits a two-genes model, but in contrast to the M-315 RNR line, resistance in CIR1348 is partially recessive. CIR1348 constitutes a new source of RKN resistance loci, and the identification of markers associated to major QTLs will facilitate the introgression of resistance into desirable genetic backgrounds.

Acknowledgments

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Keywords: Gossypium hirsutum L., microsatellite markers, introgression of resistance, Marker-assisted selection, reproduction fator

ALLELE-MINING RNA-SEQ DATA OF COTTON (GOSSYPIUM HIRSUTUM L.) ROOTS

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Abstract:

Cotton genomic resources and nucleotide polymorphism information is useful to understand germplasm diversity, crop domestication, and crop improvement. There are many publicly available resources of cotton; however most resources of gene expression are from fiber tissue and roots have been less studied. In this study, we report individual transcriptomes of 108 G. hirsutum accessions of root tissue, including 41 improved (domesticated) and 67 wild accessions from the USDA Germplasm collection. More than 3.0 billion clean reads were generated. Of the 37,505 genes in the diploid cotton G. raimondii reference genome, 61.4% were expressed in root tissue. Of these, 1,648 and 1,487 genes in improved and wild accessions respectively which were differentially expressed between the two subgenomes. The RNA-seq data was mined for alleles that were polymorphic among the diverse germplasm. The AT-genome had 234,266 SNPs in 25,993 genes, while the DT-genome had 169,123 SNPs in 25,836 genes (5x coverage). After a stricter filtering (**<50% missing; 5% MAF), 31,513 and 23,585 high-confidence SNPs were used for population genomics analyses of AT and DT-genomes, respectively. Germplasm diversity, population structure and domestication sweeps were analyzed in each genome of polyploid cotton. These genic SNPs from root tissue will complement with the expanding genomic resources of cotton and provides a valuable resource to future genetic analyses and breeding programs. >Acknowledgments** We thank Cotton Inc. and the Plant Genome Research Program (NSF 0817707) for their financial support of this work. We thank the Fulton Supercomputing Lab (FSL) at BYU for their invaluable computational resources and technical support.

References

Keywords: Cotton, RNA-seq, Genetic diversity, SNP discovery, wild cotton

COMPLETE GENOME OF THE COTTON ANTHOCYANOSIS VÍRUS

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Abstract:

Small RNAs or siRNAs (interfering RNAs) are small RNA molecules originated when plants and animals are infected by viruses. After virus entry into the cell, its genome is released and recognized by cellular proteins called Dicer-like. These proteins fragment viral genome producing small interfering viral RNA (sivRNA), sequences that exhibit at approximately 20-26 nucleotides (nts). The sequences of the siRNA are complementary to the viral genome. Total siRNA from Cotton anthocyanosis virus (CAV) infected plants were sequenced by deep sequencing in order to obtain the complete sequence of the CAV genome. The disease caused by CAV is restrict to Brazil, where is called “Vermelhão do algodoeiro”. Symptoms are the intense reddening of leaves and stems. Until now, its agent causal was not known at molecular level. CAV was describing in Brazil in 1961 at Brazil by Santos and collaborators as belonging to the Luteoviridae family, Polerovirus genus. Polerovirus have ssRNA + genomes with seven ORFs. In a previous work we sequenced part of CAV genome corresponding to viral capsid (ORF3) and part of its replicase (ORF2) and observed a a high homology between these ORFs and ORFs 2 and 3 from Cotton leafroll Dwarf Virus (CLRDV) responsible for Cotton blue disease, reaching more than 90% identity. UsingsiRNA libraries obtain through deep-sequencing performed in Illumina platform at Fasteris Co., Geneva, Switzerland, almost complete genome of CAV was mapped using SearchSmallRNA software. The analyzes showed that siRNA generated during the process of infection range from 18-26 nts, with siRNA of 22 nts as the most abundant, followed by 24 nts. Some small genomic portions were not covered by mapping (gaps) corresponding to less than 5% of the genome. For gaps sequencing, sets of primers were design for reverse transcription followed Reaction Polymerase Chain (RT-PCR) and subsequent sequencing by Sanger. CAV genome has about 6000 nucleotides. Mapping results were validate by Sanger nucleotide sequencing. Alignment of the CAV ORFs nucleotide and amino acids sequences with other members of Luteoviridae family confirmed that it is a Polerovirus.

Acknowledgments

Fundings: FAPERJ, CNPq and CAPES

References

Keywords: Cotton anthocyanosis virus, CAV, cotton , virus disease

MEASURING SUSTAINABILITY IN COTTON FARMING SYSTEMS

VISION FOR REFORMING GEZIRA SCHEME IN SUDAN BY STRENGTHENING COTTON SMALLHOLDERS FIELD-LEVEL ORGANIZATION AND DECISION-MAKING

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Abstract:

A case study was conducted on the 'North Group' of the Gezira Scheme in Sudan. The latter was famed for the biggest cotton farm in the world under single management (about .92 m ha) and the backbone of Sudan economy since the 1st quarter of the last century. But the smallholders' roles in decision-making were not always accounted for, without any real representation in the Board and they had almost abandoned cotton farming for the last 3 decades or so. Recently there was a comeback to farming particularly with Bt. Cotton, but alas after infrastructure for cotton had been sold or privatized and field staff paid- off. Both quantitative and qualitative social research methods were used. Descriptive statistical measures for socio-economic characteristics of smallholders were obtained as well as 'Repeated Measures T-Test' for significance of results. The paper ended with recommendations to the Policy-makers of some institutional changes on the field.

Acknowledgments

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Keywords: smallholders, vision, reform, organization, decision-making

PRODUCTIVE PARAMETERS FOR THE COTTON SECTOR IN PARAGUAY: BASELINE ANALYSIS IN RURAL FAMILY FARMING

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Abstract:

In 2015 the project of international cooperation "Strengthening Cotton Production Systems in Family Farming in Paraguay," jointly implemented by FAO and the governments of Brazil and Paraguay, conducted an analysis on the cotton sector. The first phase of the projectcreated a baseline of productive, economic, environmental and social information as an input to design public-private policies to reactivate the cotton sector. Primary data was generated with diagnostic tools (surveys) conducted in 6 provinces representing the cotton-producing areas: Caazapá, Caaguazú, Paraguarí, Concepción, Ñeembucú and San Pedro. Field information was obtained from 305 family farms. The areas were studied using continuous and discrete variables based on the data from Excel, which was systematized by the Institute of Development of Paraguay (IDe). The descriptive analysis used information from 303 units: 11% with a traditional system (conventional seeds) and 89% in the commercial system (GM seeds), with statistics of central tendency and dispersion, provincial segmentation and separated by system of production (traditional-commercial). A comparison of relative frequencies used the goodness-of-fit test $\chi 2$ (P

SOCIAL DYNAMICS AND TECHNOLOGY TRANSFER

COTTON TRANSFER OF TECHNOLOGY PROSPECTS FOR NEXT DECADE IN INDIA

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Abstract:

Technological innovations fostered the production of cotton in India but the challenge of keeping pace with world's average productivity is still being unattained. Among the various reasons cited for stuck up cotton productivity in India, low adoption of innovations in the sector of Transfer of Technology (TOT) fetch an important rank. This paper makes an attempt to foresee the next possible ways to utilize the extension innovations by analyzing the changes and challenges faced by the present cotton TOT programs. Analyzing the past cotton TOT programs in the country revealed the conventional nature of information and communication support, manual nature of technology diffusion through limited number of extension personnel and low capacity building initiatives for the grass root level cotton extension functionaries. Even though the present TOT programs viz., demonstrations and Mobile and web based advisory services impact the technological adoption level of cotton growers in the country, there are still ways to intensify them with new extension innovations in the near future. The past and present cotton TOT programs excluded many extension innovations and attempted very less initiatives on technology forecasting. They have not given a significant place for the Market intelligence surveys for commercializing ourtechnologies and institutional arrangements for freeing indebtedness. They had a meager impact on Media utilization and efforts to organize the cotton growers for better bargaining. Hence, the future of cotton TOT must be a synergistic approach keeping the Information and Communication Technology (ICT) as platform for forecasting and disseminating the environment friendly, sustainable and profitable technologies to the organized cotton farmers associations with gender and youth friendly tools by foreseeing the weather and price situations. This paper suggests a conceptual TOT model for the future prospects of cotton in the next decade in India.

Acknowledgments

Author hereby acknowledges the Director, ICAR-CICR, Nagpur for the opportunity to review the past TOT approaches in cotton under TMC MM 1.6 project and conceptualize a new one.

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Keywords: TOT, Cotton, Extension Innovation, ICT, Technology Dissemination

'E- KAPAS': AN ICT MODEL OF EXTENSION FOR KNOWLEDGE EMPOWERMENT OF COTTON FARMERS IN INDIA

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Abstract:

In the present ICT era, Agricultural Extension in Rural as well as Urban areas is mediated through ICT. This comprises Decision Support System, Management Information System and Expert System by impregnating the User Interface and Knowledge Management System. So, 'e-Kapas', therefore, describes an emerging field focussed on enhancement of cotton development through improved information and communication process that delivers appropriate cotton technologies to farmers, aiming to improve the efficiency of current manual system by saving time, money and making technologies available 'anywhere & anytime' to users. The main objective is to provide an Interface to farmers, consumers, extension workers and linking them with research system. 'e- Kapas Network' - an ICT based Extension Model was initiated by ICAR - CICR Nagpur in 2012 across country with involvement of scientists of 18 participating centres in eleven cotton growing states of India has gained a much popularity within a short span of time. The 'e- Kapas' components include farmers' database, FAQs (Frequently Asked Questions) on cotton, content development, recording voice messages, information delivery as voice calls on mobiles, kapas panchang and cotton apps. Providing vast amount of relevant information to around 200,000 registered rural populations in a timely and cost effective manner helped an average Indian farmer to get information about the production package right from seed to the crop harvest. Information was also provided on aspects such as agro-inputs, marketing, price policies and weather conditions. Thus, farmers living in remote areas received immediate solution in their local language about problems faced in cotton production system. The paper attempts to explain how 'e- Kapas Network' helped cotton farmers in information delivery and knowledge empowerment.

Acknowledgments

References

Keywords: e -kapas, mobile voice messages, technology dissemination, ICT, cotton

MOBILE PHONE BASED VOICE CALL : AN EFFICIENT MEANS FOR DISEMINATION COTTON PROTECTION AND PRODUCTION TECHNOLOGIES

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Abstract:

Central Institute for Cotton Research, Nagpur has executed an extension mechanism called E- kapas network for effective knowledge transfer to cotton growers. The voice call alerts are disseminated in local language to farmers registered with E- kapas network. This system has been executed because India has been struggling with challenges with regard to increasing productivity for decades and the lack of information about yield enhancing cotton technologies among farmers contributes to this in a major way. The extension personnel have many limitations in spreading technologies to all the cotton farmers of the region. So with a view to spread latest knowledge to all cotton farmers, this system has been set up to reach even a single farmer. Punjab Agricultural University, Regional station, Faridkot, Punjab as a cooperating centre for e-kapas has been actively participating in this project. The farmers from various cotton growing districts of Punjab were registered with their address and mobile number during University extension activities like kisan mela ,kisan divas, training camps, field visits and field days. The centre documented the frequently asked questions (FAQs) in cotton and collected from nearby Kisan Call Centres and conducted Focus Group Discussions among cotton growers at regional level. Using software named Unicel, voice SMSs related to cotton cultivation, protection technologies, weather, production and Integrated Pest Management (IPM) have been timely sent to the registered farmers. Till date, 16,000 cotton growers belonging to Punjab state have been registered with Regional Station, Faridkot (Punjab). So far, 43 voice SMSs have been sent to cotton growers which were recorded in Punjabi Language and lasts for 30 seconds. Until December 2015, a total of 1,36,983 voice SMS alerts on cotton production have been sent. The target is to register 5000 farmers in the year 2016-17. Information has been sent about the pest monitoring, countering pest epidemic situation, diseases and disorders with the timely use of recommended chemicals for protecting the crop more than once. The information regarding Refugia has been given to farmers which is indispensable to transgenic cotton technology. Farmers have been informed about the spray technology to deal with serious insect vector e.g. whitefly. Importance of IPM to reduce pesticide load and input costs has been emphasized through this network. The overall success rate of voice SMSs was 77.6%.. Success rate was limited to less than 80% because problems were faced in implementation w.r.t. sending of voice call like invalid numbers and wrong numbers or frequent change in the number by the farmers. However the ystem has received the positive feedback from the farmers and has been appreciated by the majority of them. The mobile is a good means of effective and efficient disseminatoion of technologies from lab to land.

Acknowledgments

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Keywords: mobile phone, voice call, technology transfer, cotton production, IPM

COMMUNICATION FOR DEVELOPMENT - CATALYZING PARTICIPATORY PROCESS FOR THE TRANSFER OF TECHNOLOGY IN THE SCOPE OF COTTON FAMILY FARMING: THE CASE OF PARAGUAY

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Abstract:

Paraguay is principally an agricultural country, whose economy is rooted strongly in primary production and the export of commodities. Soy and beef are of great importance, along with family farming crops such as sesame and cotton. Cotton was the main source of income for family farmers in the 1990s and early 2000s, covering 340 thousand hectares (2002/2013). However, the area currently under cultivation has been drastically reduced to only 20 thousand hectares in the 2014/2015 harvest (USDA, 2016). Nevertheless, the 15 thousand farmers who continue to grow cotton maintain an important part of the area under cultivation, as identified by the project of International Cooperation of the Government of Brazil, FAO and the Government of Paraguay, “Strengthening Cotton Production Chain in Family Farming System in Paraguay” in which a characterization analysis of the cotton value chain was carried out in the country in 2015, with the support of the Institute for Development. According to this survey, it was observed that 43% of arable farmland is planted with cotton (1.8 ha of 4.2 ha). In addition, this crop was identified as the main source of household income for families, representing over 60% of income generated in the productive area, exclusively from the sale of cotton. Given cotton’s important role in the composition of family income, and after analyzing the intrinsic development potential for the crop, based on its low fiber yield (approximately 400 kg per hectare) which is significantly lower than the global average (713 kg per hectare in 2015); the need to improve the productive conditions and technical empowerment of the farmers was identified. Thus, improving the process of technology transfer to technical extension agents, researchers, technical assistants and cotton family farmers was identified as a necessity, by creating a plan for information and communication for development. Communication for Development is a social process based on dialogue and consensus and which makes use of a wide range of strategies, methods and tools. It promotes

and implements the habit of listening, participation, agreement and reaching consensus. The Plan contains the following objectives: 1. Create awareness among cotton farmers and technical extension agents regarding opportunities for improving productive conditions. 2. Generate a solid knowledge base on cotton production systems in the context of family farming, based on content which is complemented and adjusted as the field experiences are developed. 3. Establish mechanisms for the efficient use of Technical Demonstration Units and Technology and Training Centers, in order to increase the active participation of cotton producers. 4. Generate indicators and tools which can assist with monitoring the results, follow-up on the processes and, in general, with the advances of the plan for information and communication for development. Through Communication for Development, the project contributes to the strengthening and improvement of institutional and professional capacities, and thus creating processes of appropriation of information and generating knowledge among the various actors in the cotton value chain in Paraguay.

Acknowledgments

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Keywords: Communication for Development, Cotton, South-South Cooperation, Family Farming, Technology Transfer

ARGENTINA: INTA AND COTTON RESEARCH

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Abstract:

In Argentina, the socio-economic relevance of the cotton sector has been based on activities related to textile production, and has historically represented one of the main sources of income and employment in the northeastern and northwestern regions. Starting in the 1990s, as a result of higher international prices, the cotton sector in Argentina experienced a series of changes. This was reflected in the more than 1 million ha planted, production volumes and export records in fiber. At the end of the decade, however, the combination of a decrease in international prices, increased market volatility, technological positioning of competing crops; in addition to the occurrence of adverse weather conditions in major cotton-producing provinces, caused a slowdown and eventual paralysis and reversal of the Argentinian cotton sector. Argentina was a relevant exporter during some growing seasons, while for others it was forced to supply its spinning industry with imported cotton; characterized by periods of extreme instability, which has affected the competitiveness of this agroindustrial chain. With the overall objective of contributing to enhancing the productive, environmentally and socially sustainable competitiveness of the agribusiness cotton chain, as a component of territorial development through the consolidation of a network that would integrate and strengthen various disciplinary capacities; INTA, through a National Cotton Project, intends to coordinate institutional actions and resources aimed at generating and validating technologies for breeding, plant protection, crop management and quality of fiber and seeds. The project involves the research activities of 45 professionals from the Experimental Agricultural Stations of INTA in Sáenz Peña, Las Breñas, El Colorado, Colonia Benitez, Reconquista, Santiago del Estero and Corrientes. Achieving a good cotton harvest (quantity and quality) depends on the right combination of variables (choice of planting date, handling of biological adversities such as weeds, diseases and insects, the regulation of crop growth and a timely harvest. Thus a number of research projects have been initiated, aimed at generating technological information to be made available to the productive sector. The development of a system of narrow or ultra-narrow rows demanded the advancement and validation of new technologies and adaptation for the conventional system. With the aim of obtaining new cultivars of cotton, INTA carries out the selection of: 1) lines with resistance to diseases of major economic impact in Argentina, under natural and controlled infection and 2) improved crop density of plants and other lines of production.

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Keywords: INTA, COTTON, RESEARCH, development, technology

THE PERFORMANCE OF FARMER FIELD SCHOOLS IN THE ZAMBIAN COTTON PRODUCTION SYSTEM

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Abstract:

Many technological innovations have been developed to improve agricultural productivity in Zambia. However, the adoption of these technologies has been low. Appropriate extension models are often seen as the missing link between adoption and the achievement of productivity gains. Integrated Production and Pest Management (IPPM) has long been shown to have reduced production cost due to improved use of pesticides and other input costs. However, its introduction has been met with some resistance with farmers as it is viewed to be more labour intensive to implement. Thus, appropriate extension models have to be identified to integrate this approach into small holder farmer systems. Hence the introduction of Integrated production and pest management using the farmer field school (FFS) approach is needed. After implementing the FFS, an Impact study was conducted using standard questionnaires to asses the farmer perception towards this technology, improve the quality of activities and ensure sustainability of the program through buy in from partners. Evaluations were conducted at group level using focused group discussions for FFS participants and at individual levels between FFS participants and non FFS participants in each area where the schools were set up. Data collected was for two seasons namely 2014/15 and 20015/16 seasons. The results showed that 67% of the farmers who attended the FFS training were satisfied to very satisfied with the training. In the first year of implementation farmers were able to adopt the following practises: gap filling, weekly field observations and reduction of pesticide use. After participating the program for one year, farmers felt that the training should also include food security and budgeting. The experimental plots also showed significant differences in the final cotton yields. In the IPPM plots the average yield was 1301.67 kg per hectare while in the non FFS plots the yields were 767.5 kg per hectares. Farmer field schools can be considered as an extension option for small holder cotton farmers. More work needs to be done to ensure their sustainability in the Zambian cotton sector.

Acknowledgments

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