INTERNATIONAL COTTON
ADVISORY COMMITTEE

1629 K Street NW, Suite 702,
Washington, DC 20006, USA

78th Plenary Meeting – Brisbane (Australia)

MINUTES

Third Open Session

Germplasm Exchange

11:00 hrs, Tuesday, 3 December 2019
Chair: Jeremy Burdon, Director, Cotton Research & Development Corporation, Australia

The CHAIR invited Mr. Jon Welsh, Partner, AgEcon, Australia to deliver his presentation "Climate Risk Management: Tools, Tips and Barriers."

SPEAKER: Dr KATER HAKE
Dr Kater Hake presented a brief history of cotton diversity. Origin of diversity started with the natural converhence of genome A with genome D. Humans started selecting for long fibres in A and AD Genomes. Optimization of gibberellin and & florigen were used in domesticated varieties in wheat and tomatoes. Selection continued for not too tall and not too short, not too leafy not enough leaves - just right height optimized for harvest. For thousands of years farmers made local selections for improved cultivars. Experiments showed that cotton pollen movement occurred up to 3000 metres at least, thereby indicating the potential of natural crossing in cotton. In the United States of America, cotton breeding was focused on specific regions Delta & south East, Texas Area and Acala. Breeding history of cotton started with the development of varieties such as of Deltapine 16 which was released in 1968 and Deltapine 50 in 1983. DP16 spread to Mexico, Colombia, Australia and China, whereas DP 50 only spread to Greece. Interestingly, seed quality drove breeding innovation. Seed was being produced in Arizona which didn't have heat tolerance. Subsequently, crossings were carried out between elite varieties from different continents to develop new elite varieties, enhance diversity and adaptability. However, several important traits were lost in this process resulting in narrowed genetic diversity. Transportation of varieties from one region to another causes localized problems. Dr Hake concluded that there is a need to enhance diversity of germplasm by investing more in cotton breeding.

QUESTIONS AND ANSWERS:
The delegate of Mali asked if Jassid resistant varieties were available, to combat the severity of damage in the country. Dr Kater said that hairy cotton varieties resisted jassids but that could result in lower fibre quality because of genetic linkage.

The delegate from Burkina Faso asked if Is was possible to breed climate-resilient varieties by changing short cycle or long cycle growth. Dr Kater replied that there was a need to invest in plant breeding to acquire the tools necessary for accelerated molecular breeding for adaptability to climate change.

A cotton breeder from Turkey asked if molecular breeding could replace classical breeding. Dr Hake said that conventional breeding would continue across the world even with Genetically modified crops or with marker assisted breeding. He added that plant breeders first breed conventional classic varieties before converting them to GM crops.

SPEAKER: Dr JOHN YU

Dr John Yu spoke on exploiting genetic variation for Gossypium improvement. He said that there were 10,000 accessions in the USDA which cover 50 species of primary secondary and tertiary gene pools. The collections have been characterized as core collections and working collection in Texas. There is a large genetic diversity in the germplasm pool and new accessions are collected every year. A total of 2516 domestic and 526 international accessions were shared from 2008-2018. The collections are maintained by bagging to ensure self-pollination. Germplasm lines are characterized by examining patterns and structure of species, race and geographic diversity. Morphological diversity is characterized for petal colour, leaf shape etc., for 36 morphological traits. Digital image scales were developed for the morphological descriptors. DNA markers have been developed and analysed for cotton germplasm. Genetic linkage maps have been developed for the 26 chromosomes and QTL maps are now available. ESTs were also developed for functional expression of important genes. A library of 105 core SSR markers have been developed for characterization. Each arm has two markers at least. The SSR markers were used to characterize a total of 2256 accessions. The core set of SSR markers elucidate diversity structure within Gossypium germplasm collection to characterize the diversity reference set of 9 genomes and 33 species. Species specific marker bands have been used to identify misclassification and introgression.

Genome sequence was released for *G. raimondii* in 2012, for *G. arboreum* In 2014 and AD genome in 2015. The genome of Texas marker genetic standard was developed for 78,000 genes. Genome wide variation was elucidated among eight upland lines. Comparative analysis of linkage disequilibrium was carried out across 26 chromosome blocks. Along each chromosome, fibre quality traits were anchored. Gene editing based on genome sequencing was done to create variation. Silencing susceptibility genes of bacterial blight using TALENS showed that seedling growth was not affected by VIGS-GhSWEET10 gene silencing.
Monsanto donated 54 accessions for breeding programmes, containing African landrace accessions, cultivated accessions and African breeding lines. More details of germplasm diversity were available on CottonGen and GRIN-Global.

QUESTIONS AND ANSWERS:

The delegate from Uganda asked as to who should be contacted for germplasm sources and what kind of conditions are imposed on germplasm sharing. Dr John informed that there are standard policies in the United States of America that have been followed successfully for many years, based on which seeds have been distributed for international researchers and domestic researchers. However, very few accessions are received from foreign countries.

The delegate of Egypt asked if it was possible to distinguish all four cotton species through DNA analysis of leaves and green parts. He also enquired if DNA profiling could explain the difference in productivity across the world to link the phenomenon to varietal capacity or environmental variation. Dr John answered that DNA markers are used to distinguish species. Markers for traits need resources. Collaborations between countries is required for phenotypic and genotypic characterization. Diversity profiles are being characterized through genetic analysis.

SPEAKER: Dr MICHEL FOK

Dr Michel Fok spoke on diversity, germplasm information and exchange. Genetic diversity, if exploited, helps to make great progress in the sustainability of growing cotton in a world evolving notably under climate change. This diversity is preserved in several collections managed by public organizations in a handful of countries. The exchange of genetic materials is however of low level. Dr Fok

T: +1 (202) 463 6660 | E: secretariat@icac.org | www.icac.org

emphasized that germplasm exchange is good because new varieties can be developed. He elucidated the example of the development of a new variety CIM-620 resistant to the Cotton leaf Curl Disease (CLCuD) that was released in 2016 in Punjab province. The variety was developed from 74 accessions obtained from Venezuela, which were given to Pakistan by CIRAD in 2006.

There is rationale to move towards a regional/international program for variability creation so that national breeding programs could benefit and be used to finalize locally adapted new varieties. ICRA is making efforts to launch an initiative to overcome this shortfall, but more organizations should join in and financial support is required to meet the ultimate objective. Dr Fok explained how okra traits were exploited in Australia for better light penetration and how high density of gossypol is being exploited in China. He explained that glandless cotton was cultivated in 250,000 hectares in West Africa in 1990, so that seed-meal could be used for monogastric animals. However, the varieties were not evaluated for pest control and did not survive for long. Dr Fok wondered why there was such a low level of germplasm exchange across the world. Was it the lack of information on germplasm or was it because of people who manage germplasm who find it difficult to describe the germplasm accessions? He felt that the main reason of the current problems of germplasm exchange lies in the lack of comprehensive information on existing genetic materials and on the sharing of this information. Another reason is the lack of means and capabilities of breeding teams, to address and integrate genetic variability into breeding programs, notably in developing countries.

QUESTIONS AND ANSWERS:
The delegate from Brazil said that in a tropical environment there was a general problem of variable boll maturity which causes different quality at top and bottom of the plants. He asked if it would be possible to breed for uniform maturity for uniform quality. Dr Fok said that adaptability of varieties could be a general problem but breeding efforts could find answers.

The delegate from Mali pointed out that oil was extracted from cotton varieties which had gossypol, because cotton plants without gossypol were sensitive to insect pests. He asked if it was possible to breed varieties without gossypol in seeds? Dr Fok replied that cotton seed oil across the globe comes from varieties with gossypol and that industrial process neutralizes it. He added that until 1990s Mali had innovative seed-crushing plants but now the processes were different, which may not be as efficient as the previous methods.

The delegate of Pakistan wondered as to why Cotton leaf Curl Disease (CLCuD) was still a problem despite the new varieties that were developed for resistance to the disease. He asked if it was the failure of the variety or mutation of the virus? Dr Fok replied that co-evolution was a common phenomenon, where variations in viruses could be overcoming the variety. This would be a constant battle and cultivation techniques could be used to augment resistance.

SPEAKER: DR IBROKHIM ABDURAKHMONOV
Dr Ibrokhim Abdurakhmonov spoke on cotton germplasm resources, development and exchange. He explained that it is important to combat biotic and biotic stresses using the genetic variability available in the germplasm resources. He described the inventories available in germplasm banks of different countries. He referred to the information available in his edited book 'World Cotton Germplasm Resources'. Dr Abdurakhmonov highlighted the challenges and Issues with redundancy, maintenance and storage, seed renewal period, characterization and evaluation, systematization, cataloguing and data basing. He said that while germplasm sharing, enrichment and exchange was well organized within each of the countries, sharing germplasm between countries presented roadblocks because of the cumbersome and complicated procedures involving written formal application, MTA development, internal Government approvals and intellectual property (IP) issues. He emphasized the need to prioritize expeditions and encourage germplasm exchange. Methods of characterization should be updated through

T: +1 (202) 463 6660 | E: secretariat@icac.org | www.icac.org

molecular techniques while protecting IP through bar-coding. Dr Abdurakhmonov described new trends such as the use of molecular markers; application of Association Mapping; genotyping by sequencing methods; re-sequencing of whole genomes; marker-assisted selection approaches; genomic selection approaches; gene pyramiding; virtual World Cotton Germplasm Center/Database; virtual breeding; personalized agriculture (chemical genomics) and training of scientists. Dr Abdurakhmonov said that over 1000 upland germplasm and 300 ELS germplasm were exchanged with USDA. Main fiber quality traits were evaluated in the two diverse environments of the Uzbekistan and Mexico/California. USDA sent over 700 Upland landrace and wild species, multiplied seeds in Mexico and sent part of the collections to Uzbekistan. Researchers in Uzbekistan received a set of 17 chromosome substitution lines of TM-1/G. *barbadense* from USDA partners. Other Institutions exchanged over 1200 Upland germplasm with USDA-ARS in the past 10 years.

Dr Abdurakhmonov concluded that germplasm evaluation and exchange was important. There was a need to enrich collections continuously, by applying novel methods for cotton improvement. Activities such as sharing knowledge and technologies, wider international collaboration, training and education of new generation cotton scientists and increasing investments to expedite commercialization of new technologies would greatly contribute to germplasm improvement.

QUESTIONS AND ANSWERS:
A plant breeder from Turkey explained that germplasm exchange was difficult because of obstacles and procedures. Some countries do not exchange their germplasm. Turkey opposes GM cotton, therefore seeds received should be without GM traits and that cotton breeders must find solutions to ensure that germplasm must be protected from GM contamination. Dr Abdurakhmonov replied that GM does not destroy germplasm. Since, obstacles are man-made, it would be possible to find solutions.

A scientist from Australia asked if the RNAi target gene details were available. Dr Ibrokhim said that the *phytochrome A1* gene was associated with far-red light reception and gene silencing resulted in fibre length elongation and high yields.