INTERNATIONAL
cotton genome
INITIATIVE

ICGI: Past, Present, and Future Direction

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The **International Cotton Genome Initiative** (ICGI) is embodied by the spirit of this meeting in Nanjing. The number of participants and scientific papers presented, and diverse geographical representation are impressive and evidence of the importance of this collaborative effort. Several of us have the fortune of being involved in ICGI from the beginning and participating in its development. By the very diverse nature of ICGI, there are delegates attending this International meeting that are not familiar with ICGI and with events that have led up to this meeting. The objective of this paper is to review the history of ICGI, its current status and a brief look into the crystal ball as to where ICGI may be headed in the future. International consortia are common today in the area of plant, animal, microbial, and human genomics. All of them had unique challenges to overcome in their creation and very existence. The fledging ICGI is no different. The exciting part of this meeting in Nanjing is that everyone has an opportunity, *and I would say an obligation*, to become actively involved in ICGI and influence its scientific direction. The opportunity to forge productive foreign collaborative research efforts should not be missed. We are all aware of the many challenges facing cotton production and related industries worldwide. Stagnate yields, declining fiber quality, threats from biotic and abiotic factors, limit the profitability of cotton in many regions of the globe. The competition from man-made fibers presents a formidable challenge for the very future of cotton in the long-term. We shouldn’t lose sight of the true objective of what we do, which is to facilitate the genetic improvements for productivity, sustainability and profitability.

ICGI is only about 2 years old; it has made progress in some areas and lagged or struggled in others. ICGI really began to form as scientists from the USA, France and Australia met at CSIRO Plant Industry in Canberra on February 16-18, 2000 to discuss the status of cotton genetic mapping, DNA markers, genomics, and marker-assisted selection. CSIRO cotton breeders offered examples of critical areas where DNA markers could be utilized in cotton improvement. The program of this workshop is given below:

SYMPOSIUM ON MOLECULAR MARKERS IN COTTON
CSIRO Plant Industry, Canberra, Australia
16-18 February 2000

16 February	***Symposium – Progress with marker research in cotton***
Elizabeth Dennis	Overview of Symposium and Objectives
Roy Cantrell	1) Utility of SSR high throughput DNA markers in cotton. 2) Genetic mapping populations and progress of map construction. 3) Future strategies for application of DNA markers in "germplasm engineering? 4) Update on San Diego meetings.
Bruce Lyon	The Development of DNA Markers for Fungal Disease Resistance in Cotton
Russell Kohel	The ARS genomics program at College Station, Texas
Curt Brubaker	Chromosome inheritance in *G. hirsutum* x *G. australe* chromosome addition lines
Sukamar Saha	Molecular markers in cotton improvement
Robert Wright	Mapping Bacterial Blight resistance genes in cotton
Thea Wilkins	Fiber genomics
Dainis Rungis	Development of molecular markers in cotton
Tony Arioli	Molecular analysis of cellulose biosynthesis in *Arabidopsis*
Marc Giband	CIRAD cotton mapping program
17 February	***Workshop – Research required to develop marker assisted breeding***
	Research and collaboration planning
	Trait and technique discussion
18 February	***Workshop – Research required to develop marker assisted breeding***
	Formalization of future collaborations

Credit needs to go to Greg Constable (CSIRO) for organizing that first meeting and helping lay a vision for future international direction. The efforts and support of CSIRO, Australia Cotton Research and Development Corporation (CRDC) and Aventis were responsible for that first workshop in 2000. The meeting focused on the frustrations many cotton breeders felt at that time and still feel today, mainly that DNA-marker assisted selection has not led to major enhancements in cultivar development for important traits as promised through the 1990's. Several factors were identified that contributed to this problem:

1. Limited DNA intraspecific polymorphism in *Gossypium* spp. for most marker types.

2. Complexity and size of the tetraploid cotton genome.
3. Inadequate number of portable and informative DNA markers.
4. Communication gap and lack of collaboration between breeders and molecular biologists during much of the 1990s.
5. Limited international coordination and collaboration in cotton genetics and genomics compared to other major agronomic crops.

Some of these shortcomings result from chronic lack of research funding and others more simply from lack of motivation and/or lack of opportunities for meaningful research collaborations. The impressive gains achieved in *Arabidopsis*, rice, wheat, and mammalian genomics over the past decade resoundingly demonstrate, however, that the practical and analytical tools are at hand to move cotton genomics to a level that will produce revolutionary insights into the evolution, structure, and function of the cotton genome.

It was obvious to the workshop participants that some form of international consortium could address many of these issues in a productive manner. The timing for this process was appropriate due to the increasing research activity in several countries in cotton genomics and the interest in cotton genomics at both the public and commercial level in all important crop plants. The workshop participants selected Thea Wilkins (USA), Marc Giband (France), Curt Brubaker (Australia), Roy Cantrell (USA), and Bruce Lyon (Australia) to initially constitute an interim International Steering Committee (SC) for ICGI charged with:

1. Coordinating communication among the initial participating scientists and distributing information to cotton researchers in their respective countries or with whom they may have contacts.
2. Developing an electronic forum for the meaningful discussion and exchange of ideas.
3. Organizing a broader meeting/workshop to be held in 2002 with greater representation from cotton growing countries worldwide.

4. Securing modest financial resources for launching ICGI and defraying publication and travel costs.

The objectives of the newly formed ICGI as articulated in mid-2000 were to:

1. Reduce redundancy of research effort and maximize rate of research progress to understand the cotton genome.
2. Foster tool development to begin integrating genetic and physical maps.
3. Accelerate development of portable cotton linkage map.
4. Foster rapid application of new genomic tools to cotton improvement.
5. Develop comprehensive forum for exchange and communication within cotton scientific community and with the *Arabidopsis* model genome community.
6. Develop standardized nomenclature for DNA markers, maps and etc.

These objectives were very ambitious and were articulated to the cotton community in a letter to the Editor in the *JOURNAL OF COTTON SCIENCE* 4: 149-151 (2000) (http://www.jcotsci.org/). To facilitate communication and recruit participants a listserver (http://cottongenomecenter.ucdavis.edu/) was set up and is hosted by the Cotton Genome Center Website. The purpose of this listserver is to foster an active exchange of resources and information and to provide an open forum for discussing emerging technologies. Thea Wilkins maintains the site.

The workshop in Australia provided an overview or snapshot of the “state of the art” of cotton genomics as we enter this new era. It was reported that marker development was making progress, especially in PCR-based markers, such as, Simple Sequence Repeats (SSRs) and Amplified Fragment Length Polymorphisms (AFLPs). Saturated genetic linkage maps were near completion in several labs that provide at least 5cM coverage. The informativeness of DNA markers was still a major limitation. Development of various BAC resources for tetraploid and diploid *Gossypium* were almost in place.

Integration of genetic and physical mapping resources was limited in the tetraploid cotton genome. EST resources were being launched in several labs and large functional genomics projects were underway for fiber development and other key physiological processes. It was recognized that the scientific community would benefit from identification of a core set of <u>framework DNA markers</u> that would begin to provide opportunities for map integration. A framework marker would preferably be:

1- PCR-based and portable from lab-to-lab by sequence databases.
2- Located to a chromosome or chromosome arm utilizing cotton aneuploid stocks.
3- Polymorphism Information Content (PIC) value known for a diverse set of *G. hirsutum.*
4- Genetic map location on one or more genetic maps.
5- Physically localized to a BAC resource.

With framework markers in the public domain, the international scientific community could truly begin to dissect the cotton genome. It would certainly permit focused research on interesting genomic regions. Framework markers could provide a number of Sequence Tagged Sited (STS) that will be critical if localized or large genome sequencing projects are launched in cotton. STS have been an essential launching point for sequencing efforts in human, mouse, *Arabidopsis*, and rice.

Cotton is characterized in the international arena as a “cash crop” as opposed to a food crop. The politics associated with this perception hinders access to international funding resources for collaborative efforts. Public funding sources and national programs were reluctant to support this international effort. Funds for international travel and coordination of ICGI activities in the early stages was a key activity of the ICGI-SC. No funding mechanism was in place to support even the basic activities of sponsoring a workshop or so forth. The goal was to secure modest ICGI support for the first two years from cotton industry stakeholders with a keen interest in cotton genetics and genomics. A total of $60,000US was solicited in a 3-month period from generous donations from the following cotton stakeholders:

1. Monsanto
2. Syngenta
3. Aventis
4. Delta and Pineland Seed Company
5. Stoneville Pedigreed Seed Company
6. Dow Agrosciences
7. US Cotton Foundation
8. Cotton Incorporated
9. CRDC
10. CSIRO

The response to the solicitation was remarkable and indicative of the importance and timeliness of ICGI. Special gratitude has to go to these initial contributors who recognize the importance of this international consortium. These funds were used to support and defray the cost of travel and ICGI publications. It is *very important* for everyone to understand that ICGI was not designed as a funding agency for sponsored research on cotton genomics. How this continues is up to the delegates and the future Steering Committees. ICGI can provide a platform for productive collaborations that can secure external research funding that would be more difficult in the absence of ICGI.

Although the early participants in ICGI recognized that they could not represent the international cotton genomics community at large, it was acknowledged that such an effort must start with a nucleus of people willing to devote significant effort to developing a structure, recruiting broader participation, and organizing ever more inclusive meetings. This process culminated in a second ICGI workshop in Montpellier France (5-7 June 2001), devoted to moving the ICGI to the next level of development. The program of this workshop is given below:

ICGI2001 Agenda

June 5,2001

Introductions and general comments

Welcome	Marc Giband/Jean-Marc Lacape
CIRAD and it's Annual Crops Department	Jean-Luc Khalfaoui
CIRAD's Cotton Program	Jean-Philippe Deguine

Examples of International consortia in plants

Cotton as part of GFAR (Global Forum for Agricultural Research)	Hubert Omont
INIBAP	Jean-Vincent Escalant
ITMI	Philippe Leroy

Current state of research activities on cotton genetics and genomics

Genetic mapping, QTL analysis	Andy Paterson
Physical mapping	Russ Kohel
Functional genomics (including Arabidopsis as a model system)	Liz Dennis
Genetic resources, cytogenetics of Gossypium	Lloyd May & Sukamar Saha
Bioinformatics	Damian Gessler

June 6,2001

ICGI functional business

Summary of Canberra meeting	Curt Brubaker
Public/private interactions	Open discussion
Collaborative efforts	Open discussion
Sharing of resources	Open discussion
ICGI future funding (NSF-RCN, EU)	Roy Cantrell
ICGI global recruitment	Thea Wilkins

June 7,2001

ICGI Structural business

Year one accomplishments	Bruce Lyon
ICGI funding	Roy Cantrell
ICGI Steering Committee membership	Open discussion
ICGI Advisory Committee	Open discussion

Publications (website, newsletter, proceedings)	Thea Wilkins
Planning 2002 meetings and beyond (PAG, WCRC3 and etc.)	Open discussion
Visits and tours	
Tour 1 – CIRAD Cotton Technology Laboratory	CIRAD
Tour 2 – Biotrop	CIRAD

There were approximately 35 participants in the ICGI 2001 workshop. JM Lacape and M Giband of CIRAD provided valuable leadership in hosting that workshop. This workshop significantly expanded the ICGI participation at both the geographic and discipline level. However, it was obvious at the ICGI 2001 workshop that Asia was not represented. The ICGI-SC focused on broadening the effort to Asia by contacting Dr. Tianzhen Zhang of Nanjing Agric. University and inviting him to be a member of the ICGI-SC. This initiated the process for the ICGI 2002 workshop here in Nanjing. The leadership and hospitality of Dr. Zhang is noteworthy.

What lies in the future for ICGI? One very promising aspect of ICGI has already been achieved at this Nanjing meeting! The focus of the ICGI is rightly shifting to scholarly scientific presentations and exchange and beyond discussions on ICGI structure and operations. The latter is important but without sound scientific progress being on display and discussed then the ICGI would simply be busy work for which we all have precious little time. The ICGI-SC hopes that solid working groups can be formed with ICGI that will provide a more likely forum for research collaboration. Working groups should be able to spring from the key topic areas of this Nanjing workshop. A necessary component is one person being identified and able to facilitate the working group. Some working groups within ICGI may be more effective and develop at a more rapid pace than others. The focus of the working groups should be on advancing the science of their respective areas. Participation in working groups or ICGI for that matter is definitely voluntary. Level of participation will vary with individual interest, and some may choose not to be a part of ICGI at all. It should be repeated, that ICGI only has the intent of being a research catalyst. The benefit to an individual scientist will be proportional to their interest and participation.

With determined and focused working groups, the ICGI could begin to make real impacts in the future in the following areas:

1. QTL verification from population to population and over diverse environments. This, by its very nature, requires extensive collaboration and sharing of data.
2. Framework DNA marker development and widespread distribution and utilization.
3. Consensus linkage map construction. Computational tools are now available for merging diverse genetic maps. This has been accomplished in humans, mice, soybean, rice, *Arabidopsis*, and maize. This requires sharing of raw genetic mapping data, which has been a major obstacle in cotton in the past.
4. Identification of major traits tagged with DNA markers suitable for MAS in cotton breeding programs. Various fiber quality traits and pest resistance are good candidates that could have a major economic impact on genetic gains in cotton.
5. Utilizing *Arabidopsis* genomic resource information to further dissect the cotton genome. Further workshops should invite key *Arabidopsis* researchers to pursue common areas of interest with ICGI scientists. This is an area that has developed slowly within ICGI.
6. Develop an appropriate strategy for genomic sequencing in the public domain for ICGI. The success in sequencing the rice genome illustrates the promise of sequencing of all economically important genomes at some level in the future. The ICGI is an appropriate forum for initiating that discussion and planning process. The rapid pace of sequencing technology development means that the cotton genome will be sequenced, the question is not IF but WHEN! Just as important

is by whom? It should be an international effort lead by the public research sector and ICGI can play an important role in scientific direction.

Certainly all of the above research areas require significant financial resources that are lacking in the public sector. The ability to harness resources to make significant gains in cotton genomics can be enhanced by international collaborations and research partnerships. Some of those collaborations can be formed or strengthened during this Nanjing workshop. We look forward to the time when we can look back to this workshop as the “Dawn of a New Era in Cotton Genomics”.