

INTRODUCTION

SYMPOSIUM ON MOLECULAR MARKERS IN COTTON FEBRUARY 16-18, 2000 CSIRO; PLANT INDUSTRY; AUSTRALIA

In February 2000, about twenty cotton genome researchers and industry representatives gathered in Canberra, Australia to, "review progress with research into identifying markers in cotton and to identify further research to develop markers to the point where they

can be used in a breeding program." The meeting had two components. The first day featured a series of talks detailing progress in molecular marker development in cotton. These presentations provided a framework for the discussions the following day.

SYMPOSIUM ON MOLECULAR MARKERS IN COTTON <i>CSIRO Plant Industry, Canberra, Australia</i> <i>16-18 February 2000</i>	
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 <i>G. hirsutum</i> x <i>G. australe</i> 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 <i>Arabidopsis</i>
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

The primary purpose of this symposium was to identify better strategies for incorporating molecular markers into cotton breeding programs, but after a wide-ranging discussion, the group identified the lack of a formal mechanism for collaborating and exchanging information as a key limitation to molecular marker development in cotton. While a number of short term projects were identified that could address specific issues, the workshop participants all agreed that the long-term solution was to instigate an international organization that would facilitate communication and collaboration among cotton researchers involved in breeding, evolutionary studies, gene discovery, cytogenetics, functional genomics, genetic linkage mapping, physical mapping, QTL mapping, genetic resources management, and bioinformatics.

The group identified a saturated and fully integrated physical and genetic map of the cotton genome that existed in the public domain as a priority. In seeking to achieve this goal, four key considerations were identified.

1. A consensus map should be constructed by the analytical amalgamation of current maps using framework PCR-based DNA markers.

The rationale for a consensus map originates from the realization that currently there is no immortalized segregating family available for cotton, and, more importantly, no single population would be universally applicable. While developing a single immortalized reference population would be a useful long-term goal, a number of segregating families have been mapped and are available for immediate use.

2. A physical map should be constructed using a single large-insert library.

In contrast to segregating families, using a single large-insert library as a basis for the physical map was seen as the best way forward. A single library is easily duplicated and distributed, and is more universally applicable. Focusing on a single library provides for more efficient means of constructing the physical map, as the workload can be efficiently split among cooperating labs.

3. The bioinformatic tools for securely storing, analyzing, and disseminating data must be developed.

Genetic and physical maps are not an end in themselves but tools to prise open and manipulate the cotton genome. The data gathered from mapping efforts are complex, overwhelming in size, and only useful to the extent they are soundly analyzed and readily available for downstream applications.

4. This must be a collaborative effort, open to all interested parties internationally.

The lack of international collaboration was identified as a principal reason cotton genomics lagged behind other crop species. Ambitious goals are most efficiently achieved by the coordinated efforts of many groups that reduce redundancy, increase the diversity of funding sources, and importantly facilitate the cross-fertilization of ideas.

As the rest of this document will demonstrate, these initial objectives already have been and will continue to be expanded and refined, and thus should not be read literally. They do illustrate, however, that the underlying concern among cotton genomics researchers around the world is that the lack of collaboration and communication is limiting cotton genomics research and must be redressed.

CREATING THE INTERNATIONAL COTTON GENOME INITIATIVE (ICGI)

Successful international collaboration in pursuit of ambitious goals requires direction and structure. Accordingly, the workshop participants agreed that a formal organization was needed to facilitate and direct cotton genomics research internationally, and thus the International Cotton Genome Initiative (ICGI) was instituted.

To drive this nascent organization forward, a Steering Committee was organized, comprising Thea Wilkins (USA), Marc Giband (France), Curt Brubaker (Australia), Bruce Lyon

(Australia), and Roy Cantrell (USA). The initial Steering Committee was charged with:

- Coordinating communication among the participating scientists, distributing information, and developing an electronic forum for discussion;
- Developing a set of by-laws for consideration at the next international meeting; and
- Organizing a second international meeting.

JOURNAL OF COTTON SCIENCE LETTER

The first concrete outcome of the ICGI Steering Committee was an open letter to the cotton genomics community published in the JOURNAL OF COTTON SCIENCE 4: 149-151 (2000): <http://www.jcotsci.org/> (reprinted below, with permission).

This letter was designed to announce to the cotton genomics community that an initiative was underway and to elicit support. It represented a first important step in distributing information and recruiting new participants.

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components of the cotton genome that specifies the unique characteristics of this crop plant.

International collaborative projects are underway to map and characterize the genomes of rice, wheat, maize, soybean and other agronomic crops. Cotton, however, lags significantly behind other crops in the application of DNA technology to the genetic and physical mapping of the genome. Clearly, the scientific and technological effort required to study the complex cotton genome is immense and, realistically, should be addressed by a coordinated, multi-disciplinary endeavor.

With this concept in mind, a small group of scientists from USA, France and Australia met at CSIRO Plant Industry in Canberra, Australia on February 16-18, 2000 to discuss the current status of cotton genetic mapping, DNA markers, genomic research and marker-assisted selection. It was a general agreement of the workshop participants that a public International Cotton Genome Initiative (ICGI) should be formed to facilitate the development of a saturated and fully integrated genetic and physical map of cotton.

The last decade has seen unprecedented advances in the use of DNA technology to unravel the genetic secrets of plants and animals, and to genetically engineer hybrid or transgenic organisms. The power of such technology is best seen in the current goal to interpret the human genome at the DNA level. A massive scientific effort is underway to identify, map and characterize all of the genes in the human genome. The impact of this epic venture on human health and well being will be profound and long-lasting.

DNA technology is being applied to a range of agricultural crops. Cotton has been a leader in the research and commercialization of transgene technology, and the consequences for agronomic properties such as insect and herbicide resistance have been momentous. The future of cotton improvement not only depends on the addition of such traits, but also on the understanding of fundamental

The proposed genetic or linkage map of cotton would be comprised of PCR-based DNA framework markers (such as DNA microsatellites) that are steadily becoming available in the public domain. A consensus linkage map would be produced by analysis of an amalgamation of genetic maps generated around the world by public scientists using a

common set of framework markers. This approach is essential because no single mapping population will segregate for all of the genes controlling the many important traits of the cotton plant. The framework DNA markers will be anchored to cytogenetic maps to identify chromosomal linkage groups, and bacterial artificial chromosomes (BAC) libraries will be employed in the construction of the physical map.

Fortunately, some of the requisite genetic mapping data already exists and simply needs to be compiled and analyzed. The principal role of the ICGI will be to coordinate the integration of the genetic and physical maps of cotton within the public domain. Major objectives include the generation of a transportable suite of PCR-based framework markers that can be mapped in any segregating population, the development of the bioinformatic and analytical resources to create a virtual consensus linkage map, and the physical mapping of these PCR markers in public domain BAC resources.

The International Cotton Genome Initiative is designed to advance the integration of the genetic and physical maps of cotton in the public domain. ICGI is open to all scientists globally who are willing to collaborate, share data, and disseminate materials. An initial International Steering Committee (ISC) has been formed to guide this effort. Members of the ISC are Curt Brubaker (CSIRO-Australia), Roy Cantrell (NM State University, USA), Marc Giband

(CIRAD-France), Bruce Lyon (University of Sydney, Australia) and Thea Wilkins (UC-Davis, USA). The ISC is charged with the role of coordinating communication among scientists participating in the ICGI and distributing information about the initiative to cotton researchers.

It is recognized that the ICGI will evolve and be refined as more scientists participate. Consequently, the ICGI will provide physical and electronic forums for the discussion of research objectives and the promotion and exchange of ideas. It is intended that the founding meeting of the ICGI will be held in California in January 2001, with the exact time and place to be widely publicized

The members of the ISC wish to make all interested scientists aware of the International Cotton Genome Initiative and to sincerely invite participation. We believe it will be exciting to be a part of a global effort that will yield fundamental genomic information, which can impact cotton genetic improvement for many years to come.

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PLANT AND ANIMAL GENOME CONFERENCE IX COTTON WORKSHOP

To promote an international cotton genomics consortium and to elicit broader participation, the final session of the Cotton Workshop was set aside for an open discussion of the ICGI. The session started with general discussion of the ICGI and its objectives. It was agreed that the next important step was a workshop devoted entirely to the organization and development of the ICGI. Roy Cantrell volunteered to

approach industrial representatives for monetary sponsorship. Russ Kohel and John Yu agreed to establish an ICGI recruitment site. The initial page was included under the Genomics Workbook of the CottonDB homepage. The site provided background information on ICGI and included a form to sign up for participation. This has subsequently moved to an independent ICGI site (<http://algodon.tamu.edu/icgi>)

ORGANIZING A SECOND INTERNATIONAL MEETING

Recognizing that progressing the ICGI required a more formal structure, it was important to organize a second workshop dedicated entirely to the ICGI. Previous venues, although productive, were not designed specifically around the ICGI. The Steering Committee felt strongly that a more formal structure was critical to the future success of the

ICGI. The only means of doing this was bring interested parties together in a room and iron out the details. CIRAD offered to host this workshop and Jean-Marc Lacape and Marc Giband volunteered to organize the meeting, which became the **ICGI 2001 Workshop**.