

Final Report

Capacity & Community | Cotton Research & Development Corporation

Travel Conference Final Report

Part 1 - Summary Details

CRDC Project Number: **CSP179**

Project Title: Dr-L Dennis Travel to attend International Cotton Genome initiative Conference, Brazil Sep 06

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Research Program: Capacity & Community

Part 2 – Contact Details

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Part 3 – Travel Report

1. A brief description of the purpose of the travel.

I attended the International Cotton Genomics Initiative meeting in Brazil on 18,19, 20 September, 2006. I replaced Curt Brubaker who, because he had left CSIRO, was unable to attend. This meeting was attended by approximately 200 cotton molecular researchers world-wide.

I presented our work on microarray analysis of genes involved in early fibre development as a plenary talk. My presentation included work done by the CRDC funded Post Doc and formerly a PhD student, Adriane Machado. As well as presenting our work a further aim of this travel was to participate in any efforts to initiate sequencing of the Cotton Genome, make contacts and learn about work going on in other parts of the work, particularly genes involved in controlling cotton fibre parameters, but also, generally, cotton molecular biology.

2. What were the:

a) major findings and outcomes

My presentation on our work was well received. Our work is progressing well and other laboratories, particularly those in China and the US, are also making big efforts in molecular biology to identify genes important for fibre development. As an international effort, we are attempting to correlate fibre phenotypes with molecular markers and, ultimately, genes. A cross between *hirsutum* and the *barbadense* lines has been made to and continued selfing to the F5 generation. These recombinant inbred lines (RILs) are now having the cotton fibre phenotype determined. Marker analysis of these lines is now underway using SSLP DNA markers. In this way cotton fibre genetic characters (QTLs) will be linked to molecular markers. We are participating in this project with colleagues from France, Belgium and the USA. We will identify genes that are highly expressed in the lines showing superior cotton fibre phenotypes. Scientists involved in this project also met at the ICGI conference and planned the next steps.

The major development from this meeting was the decision to proceed with an attempt to develop a genome sequencing project for cotton. I was elected as one writing committee member on an eight-member committee; Danny Llewellyn is one of approximately fifty consulting members. We have written a draft white paper (attached) outlining the important outcomes for cotton breeding and cotton research with a complete cotton genome sequence. These include enhancing our understanding of fibre, growth and development, the effects of polyploidisation and the practical development of DNA markers for cotton breeding. The topic of cotton genome sequencing has been discussed at several meetings including previous research conferences held by ICGI. At the Brazil meeting there was strong support for organising a community effort on cotton genome sequencing. At the end of this meeting there was a decision to proceed with developing a proposal for cotton genome sequencing which can be supported world-wide.



3. Detail the persons and institutions visited, giving full title, position details, location, duration of visit and purpose of visit to these people/places. (NB:- Please provide full names of institutions, not just acronyms.)

I visited the cotton genome meeting, ICGI, in Brasillia and discussed our work with many scientists there. I also visited EMBRAPA in Brasilia and discussed our research.

4. a) Are there any potential areas worth following up as a result of the travel?

Any relevance or possible impact on the Australian Cotton Industry?

As a consequence of this meeting, the White Paper has now been written and circulated to members of the ICGI. I attended the Plant and Animal Genome meeting in San Diego in January 2007 and spoke about our cotton genomics work. I also attended a meeting of organisers of the cotton genome effort. We accepted the white paper and made recommendations on directions. The first goal is to complete the sequencing of the D-genome. This genome is only half the size of the A-genome and a third the size of the *hirsutum* genome. The D-genome is presently being partly sequenced in the US from funds from the Joint Genome Initiative of the Department of Energy. The meeting decided to seek to complete the sequence to give four-times genome coverage which would give a complete *Gossypium* sequence, although it is D-genome. The next step is to ready the A (*arboreum*) and AD (*hirsutum*) genomes for sequencing. There will be another workshop, probably in China, to discuss details of moving towards the cotton genome sequencing.

A cotton genome sequence would have tremendous impact on the Australian cotton industry. We would have access to all the genes and to the DNA markers. We would gain a much better understanding of the genes involved in cotton development.

We agreed on the goals of the cotton genome project:

Short-term goals

- a. Develop a set of community-wide recommendations for sequencing that is supported by cotton researchers from the majority of countries with an interest in cotton genomics.
- b. Develop workshops and communication methods for planning, coordinating and executing the sequencing and post-sequencing activities. This will involve developing a Web site or utilizing existing resources such as the ICGI website. Coordinate all activities on the same web site or have multiple sites and locations connected.
- c. Evaluate and identify suitable strategies for sequencing the genome of cotton, both in terms of the species chosen and the physical process of generating the sequence.

Some of the Long-term goals

- d. Fully sequence representatives of each of the *Gossypium* clades. Among these, a singularly important goal is to establish the complete genome sequence of allotetraploid cotton (*Gossypium hirsutum*, $2n=52$, ~2.5-Gb), using the progenitor diploid species genomes as frameworks.
- e. Integrate functional and structural genomic resources at molecular and *in silico* levels.



5. How do you intend to share the knowledge you have gained with other people in the cotton industry?

I have already circulated the White Paper to members of the CRDC (Dallas Gibbs and Bruce Finney, also to Danny Llewellyn and Greg Constable. I would be happy to give a presentation as the work processes and outline how we could contribute.

In summary, the meeting in Brazil was very important in helping to establish an international effort towards obtaining the cotton genome sequence.