COTTON GENOMICS

Yingru Wu, Caitriona Dowd, Emmanuelle Faivre-Nitschke,
Danny Lleweylln and Elizabeth Dennis.
CSIRO, Plant Industry, Black Mountain Laboratories, Canberra, ACT 2600.

Background

Genomics is the discovery and study of many genes simultaneously on a genome – wide scale. The completion of the genome sequence of *Arabidopsis thaliana* (a model dicot) heralded the beginning of the genome era for plant biology. The development of genomics tools, such as microarray technologies are profoundly changing and accelerating research in many areas of biology including plant biology.

DNA microarrays consist of thousands of target cDNAs robotically arrayed on glass slides. Flourescently labelled cDNA samples, from different tissues or different conditions, are then hybridised to the arrays. By analysing the fluorescence of the hybridised spots on the microarrays we can assess the gene expression changes of 1000's of genes simultaneously. Microarrays provide a powerful tool for discovery of plant genes involved in important biological processes such as growth, development and defence, to name but a few. Genomics-based characterization of plant genomes has the potential to revolutionize plant science.

Aim

At present comprehensive genomics tools are only available for a few plant species, especially Arabidopsis. In order to tap into this new resource and take advantage of the possibilities of this new technology we are developing a general cotton microarray. Our aim is to produce cotton microarrays with a large non-redundant set of up to 10,000 gene clones chosen from a variety of different cotton tissues and treatments. The different tissues and treatments used for the isolation of clones for the arrays should allow researchers to examine a broad range of cotton research areas, such as fibre development, disease defence and growth. Therefore, the aim of this general cotton microarray or cotton chip is to provide a valuable research tool for cotton scientists.

Progress

In CSIRO, Plant Industry, we already have much of the expertise and many of the tools for developing and analysing microarrays. We have produced specific arrays of cotton clones (mostly

unsequenced) to examine specific research areas, such as cotton fibre development (Yingru Wu) and defences against wilt pathogens (Caitriona Dowd).
However, in the longterm, a more extensive and **general cotton array** is needed and this is what we are currently developing in CSIRO, Plant Industry.

Cotton clones have been collected from different cDNA libraries mostly generated within CSIRO, P.I.(**Table 1**). The acquisition of six thousand sequenced cotton clones is being negotiated with Dr. Ben Burr (Brookhaven National Laboratory, Upton, N.Y.,U.S.A.).

Table 1. Collection of cotton cDNA libraries.

Library from different tissues	**Generated by**	**sequenced**	**analysed**
green leaf	Emmanuelle Faiver-nitschke	+	+
Ovules	Yingru Wu	+	+
root and hypocotyl	Caitriona Dowd	+	+
fibre	Ben Burr	+	-
developing embryo	Qing Liu Curt Brubaker	-	-
Libraries from different treatments			
anaerobically induced root	Tony Millar	-	-
pathogen induced root and hypocotyl	Caitriona Dowd	+	+
cycloheximide treated ovule	Yingru Wu	+	+

1-2000 clones are being sequenced from each of the libraries shown in Table 1
Once sequenced, clones will be analysed for redundancy (multiple copies of a clone) and only unique sequences will be chosen for inclusion on the final array. Individual clones are then picked, amplified, checked on gels and prepared in a multiwell format for printing onto microarray slides. Cotton sequence information will be kept in a database which will also be a valuable source of information for cotton researchers.

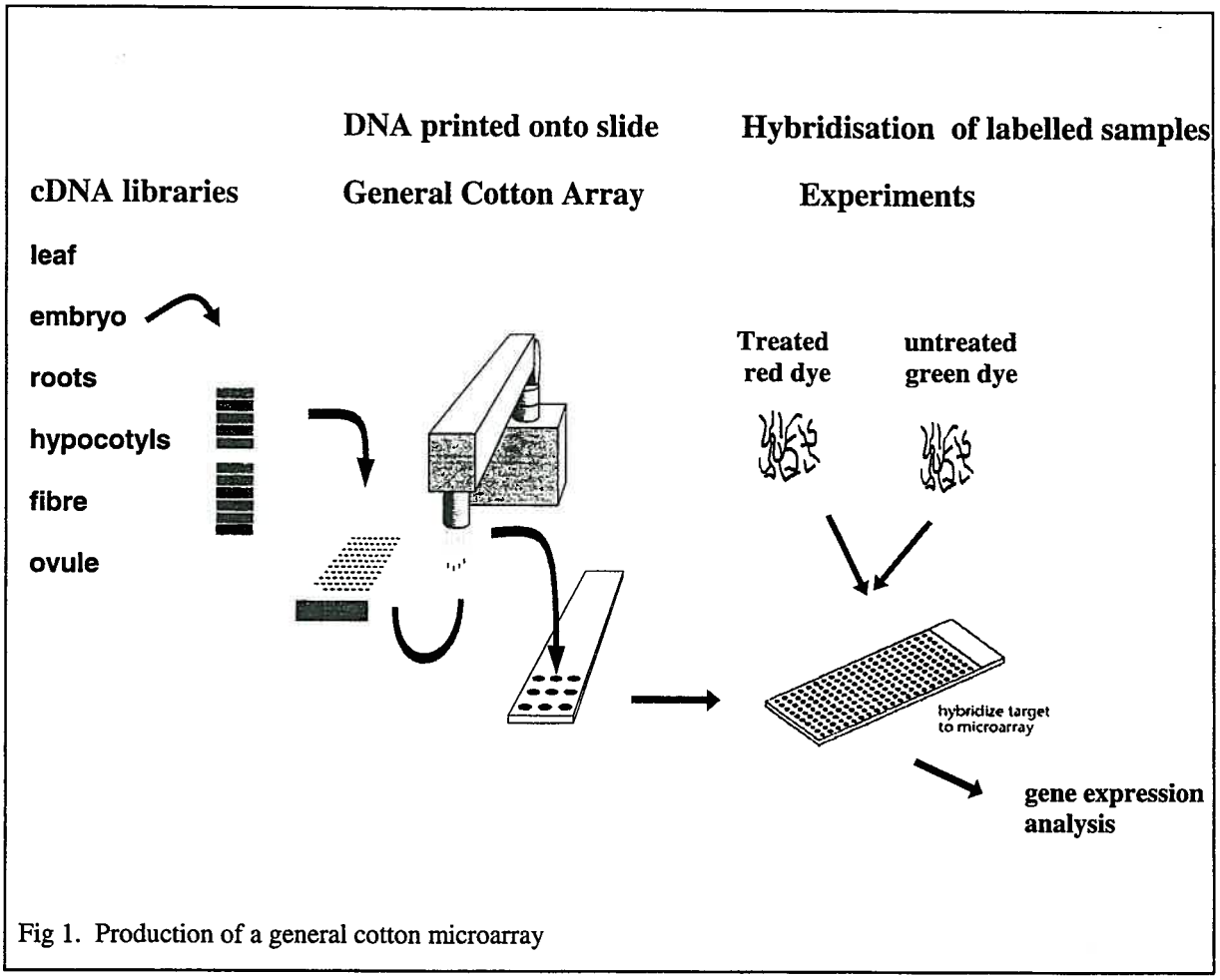

Fig 1. Production of a general cotton microarray

Future Potential

While it will take several years and a concerted international effort to collect all of the genes present in cotton (up to 40,000) and array them, this first draft of a general cotton array (Fig 1) that is being generating in Plant Industry will provide a powerful tool for all cotton researchers. There is no limitation to the range of experiments which can be performed using these cotton arrays and genes involved in many different stress responses or developmental processes can be identified. Cotton genomics should improve and accelerate future cotton research, Australia wide.

Acknowledgements

This project is funded by the Australian Cotton Research and Development Corporation. We thank Adrienne Machato and Robin Chapple for technical assistance.