PLAIN ENGLISH SUMMARY OF PROJECT OUTCOMES

Cotton fibres, or lint, are very long single cells which develop during the weeks after flowering. Fibre development is directed by the ordered expression of genes which make signalling molecules, enzymes and structural proteins. Together with the environment in which the plants grow, they are responsible for determining the characteristics of the fibre.

Genetic manipulation of the cotton fibre requires an understanding of the genes which are important in controlling the commercially desirable characteristics of the fibre, a subject which has been addressed in past CRDC-funded research in our laboratory, as well as in project UA5C. Once this information is gained it may be possible to alter fibre characteristics and yield by specifically changing the level and/or timing of the expression of particular genes.

The aims of this project were two-fold. Firstly, we intended to isolate, characterise and test genetic elements which control genes expressed at very high levels in the cotton fibre but at low levels elsewhere in the plant. We obtained seven such elements, three of which were shown to be fibre-specific in cotton transformation experiments. These important elements are now available for further research and engineering of the fibres, as they allow expression of genes (such as pigment or pest resistance genes) just in fibre cells.

A second aim was to target and isolate genes which had not been isolated from cotton, but which, based on data from other plant systems, we suspected would be important in fibre development. We isolated and characterised several such genes, many of which are regulatory, that is, control the expression of other genes, and may have a role in the initiation of cotton fibre growth. This significant preliminary analysis has put us in a position to test these genes, in order to identify the best candidate(s) for manipulation of cotton fibre characteristics and yield.

BACKGROUND TO THE RESEARCH PROJECT

Project UA5C was designed to capitalise on results obtained during the tenure of a CRDC/APRA PhD scholarship (UA1C) and a CRDC Postdoctoral Fellowship (UA4C). Five classes of abundant messenger (m)RNAs had been identified, which are expressed specifically in cotton fibres. All five were shown to be encoded in cotton by gene families of six or more members, thereby complicating the task of isolating the corresponding genes and their regulatory elements. Nevertheless, three genes showing similarity to one of the cDNAs (pFS6) had been isolated, together with one gene corresponding to a second cDNA, pFS18, by screening a Siokra 1-4 genomic library. The four genes had undergone preliminary sequence analysis and the promoters