ABSTRACT

Despite the long history of cotton production and research, little is known about the genes that control the initiation and growth of the cells on the outer surface of the seed that become fibres. The work described in this thesis uses cDNA microarray technology to study global gene expression differences between normal linted cotton and two reduced fibre mutants to uncover the genetic control of lint production. By comparing differences in gene expression between the mutants and the wild-type, a small number of genes that might be important for fibre development were identified, including a transcription factor GhMyb25, which was assumed to be the best candidate for a master fibre control gene. During normal lint production this gene is predominantly expressed in the cells on the surface of the seed at the same time that fibre cells start to grow, but also in the trichomes on the leaf and stem of developing plants.

Over-expression of GhMYB25 in transgenic tobacco led to an increase in the number and branching of multicellular trichomes on the adaxial leaf surface. By contrast, ectopic expression of GhMyb25 in Arabidopsis had no effect in trichome development suggesting that Arabidopsis and tobacco trichomes are regulated differently.

Over-expression and silencing of Myb25 in transgenic cotton was also performed to validate its role in fibre development. Analysis of primary transformants revealed that the RNA interference (RNAi) of GhMyb25 caused a significant reduction in fibre development, as well as, the production of distorted fruits with

aborted seeds. Apparently the suppression of GhMyb25 in the embryo has inhibited the development of the seed entirely. Trichome development on the petiole and leaves of the transgenic lines was also affected by the suppression of the GhMyb25. The inhibition of the trichome development correlated inversely with the over-expression phenotype, where an increase in trichome production on leaves and stems was observed from a preliminary analysis of a number of primary transformants. Further studies will be required to confirm these phenotypes in segregating progeny and to show co-inheritance of the observed phenotypes with the RNAi or overexpression transgenes.

The outcomes of this project will provide a better understanding of the genes controlling fibre development and should enable genetic engineers to design new strategies using biotechnological approaches to genetically improve cotton fibre yield and quality.