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Identification and characterisation of cotton boll wall-specific promoters

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The cotton boll contains the seeds of the plant to which long, white fibres are attached. The cotton industry takes advantage of these fibres to spin yarns for textile production. A major challenge facing the cotton industry is that of crop loss to insect attack. The primary insect pests of cotton preferentially attack the boll, causing damage to the commercially important fibres. The recent introduction of *Bt*-transgenic varieties, containing genes with anti-pest properties from the soil bacterium *Bacillus thuringiensis*, has had positive impacts on pest control and pesticide usage. These transgenes are under control of constitutive promoters, resulting in endotoxin expression in all parts of the plant. This constant high level transgene expression may have several detrimental effects, such as placing strong selective pressure on pest populations to develop resistance, non-target effects of the transgene on other organisms, a yield penalty to the plant, and the presence of transgenic protein in secondary commercial products. For these reasons, this project aims to identify promoters that could be used for tissue-specific expression of anti-pest molecules in only the boll wall of the plant. A differential screening approach was used to identify several boll wall-specific mRNAs and the temporal and spatial abundance of these transcripts was determined using Northern analysis. The promoters corresponding to these transcripts were identified using Genome Walker[®] PCR and isolated from genomic DNA by PCR. Transient transformation of various cotton tissues with these promoters driving reporter expression resulted in predominant boll wall expression. The cotton promoters identified here provide an alternative tool to constitutive promoters for use in future transgenic varieties.