COMPARATIVE GENE EXPRESSION BETWEEN SEMIGAMATIC AND NON-SEMIGAMATIC PIMA COTTON

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Abstract

The semigamy mutation (*Se*) in Pima cotton was first reported in 1963 by Turcotte and Feaster. It is a type of facultative apomixis in which the egg and sperm undergo syngamy, or cellular fusion, but forgo karyogamy, the fusion of egg and sperm nuclei. As a result, the nuclei develop independently and produce various outcomes, including diploids, haploids, or chimeric embryos. Studies have shown and confirmed that semigamy is controlled by an incompletely dominant gene. Semigamy is an interesting and important phenomenon in that it provides a potential system to study reproductive biology as well as offers an alternative way to generate haploids in cotton breeding. While there is genetic data available concerning semigamy, the molecular mechanism remains to be elucidated.

To analyze the genes and gene products associated with semigamy, we used Affymetrix GeneChip microarray technology to identify differentially expressed genes by comparing semigamatic (57-4) and non-semigamatic (Pima S-1) anthers and ovaries. 57-4 was a doubled haploid semigamy mutant isolated from Pima S-1 in the field. As compared with Pima S-1, 284 differentially expressed genes in semigamatic 57-4 anthers were identified, with 232 being down-regulated and 52 being up-regulated. In the semigamatic 57-4 ovaries, 1,827 differentially expressed genes were identified, with 1,678 being down-regulated and 149 being up-regulated. Upon comparison of the two tissues, we were able to identify 81 common genes differentially expressed in both tissues of the semigamatic genotype and the expression levels between the two tissues were significantly and positively correlated. One common finding upon analyzing the expression data was the down-regulation of genes associated with the production of transcription and translation factors. Additionally, we were able to find several genes associated with embryo growth and development.

Our further studies will be to confirm the microarray results using reverse transcription-PCR (RT-PCR) and quantitative RT-PCR as well as to develop molecular markers associated with the semigamy gene to assist in the molecular breeding and cloning of the semigamy gene. The ultimate goal of our research is to identify the underlying gene(s) and protein(s) associated with semigamy.