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COTTON GENOMICS AT CSIRO PLANT INDUSTRY

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Abstract

The concept of genomics as a deliberate research endeavor arises from the realization that traditional genetics, the study of heredity and variation, only encompasses a subset of the biological processes that govern the encoding of heritable information and its conversion into a living organism. Just as Newtonian physics expanded into quantum physics, genetics has expanded into genomics. The conceptual start of genomics is probably coincident with the realization that how (where and when) genes are expressed is as important to determining phenotype, as is allelic variation. Technologically, genomics traces its origins to the discovery of restriction enzymes. With the discovery that natural proteins could be "commandeered" to manipulate DNA and RNA, scientists finally had the tools to examine and manipulate the genome and its expressed products, the transcriptome, with ever increasing levels of precision. CSIRO Plant Industry is an enthusiastic participant in the application of these new tools to agricultural and model systems in the hope that an improved understanding of the evolution, encoding, and expression of plant genomes will allow us to develop new agriculture products that will improve the ecological and economic sustainability of Australian agriculture. Within this broad remit, cotton is an area of notable priority with a wide range of ongoing cotton genomic research initiatives, four of which are highlighted here: (1) Development of cotton chips for studies of gene expression, (2) disease genomics, (3) Germplasm characterization and development, and (4) genome mapping.

Three cotton "chips" are nearing completion--a cotton ovule chip, a cotton leaf chip and the "big" cotton chip. The "cotton ovule" chip comprises 10,000 expressed genes. The chip is designed to identify the genes that condition cotton fibre differentiation and the timing and location of their expression. Armed with a better understanding of the molecular basis of cotton fibre initiation and development, researchers hope to identify critical expression control points that can be manipulated to develop fibres better suited to the current spinning technologies. A cotton leaf chip based on 2,000 cDNAs from late season cotton leaves has been developed to identify leaf-specific promoters that would improve life of crop expression of transgenes. Finally a general application chip, the "big" cotton chip has been developed that incorporates 20,000 cDNAs from a variety of tissues (*e.g.*, ovules, fibres, leaf, hypocotyls, and root). This general-use chip has been developed as a resource for CSIRO scientists to apply to a wide variety of ongoing and future research projects.

Disease genomics has become a research priority with the appearance and spread in Australia of a virulent form of *Fusarium oxysporum* f. sp. *vasinfectum* (*Fov*), the causative organism of Fusarium wilt. Molecular genotyping confirmed that the Australian *Fov* is indigenous and unrelated to the *Fov* overseas. Microarrays that combine cDNAs of infected and uninfected cottons have identified changes in expression in defense, growth, hormone, and stress genes that are correlated with the progression *Fov* in the plant stele. While current work is focused on the response of the cotton plant to *Fov* infection, future research will explore the genetic changes correlated with increasing levels of virulence in the pathogen.

CSIRO Plant Industry also maintains a representative *ex situ* collection of the 17 indigenous *Gossypium* species, which have been characterized for a number of agronomic traits (*e.g.*, fatty acid composition, Fusarium wilt resistance, seed gossypol composition). The Australian *Gossypium* species are diploid species in the C, G, and K genomes, all of which are considered tertiary gene pool species relative to the cultivated cottons. While introgression of genes from tertiary gene pool species into the cultivated cotton is possible theoretically, whether introgression occurs at sufficient levels for cotton breeders is being evaluated in three hexaploid bridging families.

Although direct introgression of genes from the Australian *Gossypium* species to the cultivated cotton is extremely difficult, the C-, G-, and K-genome species may have novel genes of agronomic utility and can serve as simpler genetic models than the tetraploid cultivated cottons. To facilitate the transfer of information, genetic linkage maps are currently being developed the C, G, and K genomes. First generation maps, based on AFLPs, are nearly complete. The AFLP maps will be integrated *inter se* and with the tetraploid map using sequence tagged sites and simple sequence maps that have been mapped in the tetraploid genome.