Abstract No. Poster–23

COMBINING GENETIC AND GENOMICS APPROACHES FOR FIBER QUALITY IMPROVEMENT IN TETRAPLOID COTTON

Jean-Marc Lacape[1], John Jacobs[2] and Danny Llewellyn[3]
[1]UMR-AGAP, CIRAD, France, [2]Bayer BioScience NV, Belgium, [3]CSIRO, Canberra, ACT 2601, Australia

Cotton fibers are the premier natural fibers for textile production. The two tetraploid species, *Gossypium barbadense* and *G. hirsutum*, differ significantly in their fiber properties, the former having much longer, finer and stronger fibers. A better understanding of the genetics and underlying biological causes of these differences will aid further improvement of cotton quality through breeding and biotechnology. In the recent period, the availability of a genetically stable interspecific RIL population (140 $F_{2:8}$ individuals) allowed CIRAD, Bayer Crop Science and CSIRO, to benefit from the financial support of the French National Research Agency (ANR) for a project named "genetic and genomic dissection of cotton fiber quality". The genetic map of the RILs (800 loci, 2044 cM) and more importantly the consensus map resulting from its integration with the BC_1 map (75 BC_1 + 140 RILs, 1745 loci, 3637 cM) now constitutes one of the best basis internationally, as it offers a maximized number of bridge loci in common with other interspecific *G hirsutum x G barbadense* maps (TAG, 2009, 119:281-292). The phenotypic characterisation of the fibers of the RILs on 4 continents and several growing seasons generated 11 independent fiber data sets which served for QTL mapping. The 167 significant fiber QTLs (LOD>permutation based threshold) and 651 putative LOD peaks (LOD>2) from these RIL experiments were integrated with QTLs from the BC_1 and from the literature. The meta-analysis of this large set of QTL data using MetaQTL software indicated that some chromosome regions hosted "confirmed" QTLs. An effective co-localization of unidirectional (similar sign of additivity) LOD peaks from at least 5 independent data sets was observed in at least 26 cases (a given fiber trait and a given chromosome region) where meta-clusters of QTLs were defined (BMC Plant Biol, 2010, 10:132). The fiber trancriptomes of the 2 parents and of a set of 88 RILs were analyzed with focus on 2 key developmental stages (10 and 22 days post anthesis) using 2 profiling techniques, quantitative 3′ targeting cDNA-AFLP and microarray hybridizations. Both platforms showed their utility for the population-wide profiling of the differential expression of an important number of gene transcripts (4,400 and 22,000 respectively). QTL analysis applied to gene expression resulted in large numbers of (>5000) expression QTLs. This is the first report of an application of a genetical genomics approach in cotton.

Abstract No. Poster–24

COMPLETE SEQUENCE OF WILD COTTON (*G. turneri*) CHLOROPLAST GENOME: STRUCTURAL ORGANIZATION AND PHYLOGENETIC RELATIONS TO OTHER ANGIOSPERMS

Farshid Talat and Kunbo Wang
Cotton Research Institute, Chinese Academy of Agricultural Sciences, China

Recently, the complete chloroplast genome sequences of many important crop plants were determined. Economically, cotton is one of the most important crop plants for many countries. Unfortunately, genetically modified cotton has the potential to hybridize with other cultivated and wild relatives, resulting in geographical restrictions to cultivation. However, chloroplast genetic engineering offers the possibility of containment because of maternal inheritance of transgenes. The complete chloroplast genome of wild cotton provides essential information required for genetic engineering. In addition, the sequence data will be used to assess phylogenetic relationships among the major clades of rosids using wild cotton and other completely sequenced angiosperm chloroplast genomes. In this project, we will present the complete sequence of the chloroplast genome of wild cotton, *Gossypium turneri*. One goal of this project is to examine gene content and gene order, and determine the distribution and location of repeated sequences.