GENOME-WIDE *GOSSYPIUM* SNP DEVELOPMENT AND VALIDATION

Fei Wang
Amanda M. Hulse
Kevin Hoegenauer
David M. Stelly
Texas A&M University
College Station, TX
Hamid Ashrafi
Allen Van Deynze
University of California
Davis, CA
John Z. Yu
USDA-ARS-SPARC
College Station, TX

Abstract

Extensive use of genome-wide analyses requires that molecular markers be highly abundant, informative and, once developed, extremely cost-effective to use, such as single-nucleotide polymorphisms (SNPs). Public efforts toward development of cotton SNPs have been few and small-scale. We report here on SNP development from novel cotton fiber ESTs from a few *Gossypium* species. Normalized non-clonal cDNA libraries were deep sequenced by high-throughput sequencing technologies, 454 and Illumina. Protocols and parameters were established to identify hundreds of thousands of putative SNP markers relative to Upland cotton, including inter-cultivar SNPs, as well as interspecific SNPs for two diploid species, *G. longicalyx* and *G. armourianum,* as well as three tetraploid species, *G. barbadense, G. tomentosum* and *G. mustelinum*. The Kaspar Assay from Kbiosciences was used to assess putative SNPs by screening TM-1, 3-79, F1 euploid and hypoaneuploid cytogenetic stocks, radiation hybrids and certain 2x and 4x wild species. As part of the informatic pipeline development, more than 1,253 SNPs were tested. Putative SNPs (*G. hirsutum* vs. *G. barbadense*) are currently being validated by linkage mapping. To contend with the extreme complexity of the cotton genome, which exhibits diploid, tetraploid and even octaploid-like features, we are using cytogenetic stocks, linkage mapping and radiation hybrid mapping as independent assessments of structure. SNP maps will be used to associate valuable complex traits, such as fiber characteristics, disease resistance, improved yield potential and stress tolerance with specific markers and render them amenable to marker-assisted selection (MAS). We solicit other researchers and breeders to inquire about a Cotton SNP Consortium.