COLLABORATIVE DEVELOPMENT OF SNPS FOR COTTON RESEARCH, INTROGRESSION, MAS

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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. Filtering cycles were performed to optimize computational parameters used to determine putative SNPs based on assay success. 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. 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 screening SNPs against their parents and population samples for possible deployment in association and MAS. Individuals potentially interested in participating in a SNP development consortium should contact the authors.