Development of EST Based PCR Markers in Cotton. (C07-chee160353-Poster)

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Abstract:

The volume of characterized-genes currently available in the Genbank has now permitted researchers to elucidate the function of an anonymous gene sequence by cross-referencing it with other known gene sequences through a blast database search. The objectives of this project are to conduct a blast search through the Genbank database to identify cotton EST sequences that show homology to well-characterized genes from other species and to map these known-function ESTs onto an anchor RFLP map. We have developed 94 STS primers based on known-function ESTs from the Gossypium arboreum EST library. Of the 42 primer sets that amplified to a single DNA fragment in G. hirsutum and G. barbadense, 20 have been subjected to restriction digest with four enzymes and five show polymorphisms. The observed polymorphism rate of 25% is low, however, they provide a higher return in genetic information as the function of these genes are well understood, and four of the loci are mapped with LOD>4 on an anchor RFLP map. We anticipate that these ESTS markers will be the primary tool for the transition from genetic linkage mapping to a candidate gene mapping approach for important phenotypes in cotton.

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