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EST–SSR: USEFUL MARKERS FOR MOLECULAR MAPPING IN COTTON

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Abstract

Selection of suitable marker is one of the key for the success of marker assisted selection program (MAR) in cotton breeding. The primary limitations in the application of MAR are the limited number of available informative molecular markers and information about the association of these markers with important traits. Here we present a preliminary progress report on (1) the identification of a set of EST-SSR markers and (2) developing a linkage map of agronomic and fiber traits with EST-SSR markers. We identified about 133 putative EST-SSR sequences data by mining ***Gossypium hirsutum*** EST databases. The interspecies polymorphism rates of these EST-SSR markers among ***G. hirsutum*** cotton cultivars were 26% and inter specific polymorphism between ***G. hirsutum*** and ***G. barbadense*** was 49%. We also discovered about 1900 sequences containing an SSR motif of at least 18 bp length from ***G. arboreum*** EST database. In the past, SSRs have been developed in cotton based on isolating and sequencing clones containing putative SSR traits, together with designing and testing flanking primers. These methods are typically costly, time-consuming and labor-intensive. Here we report a cost-effective, rapid and efficient strategy of developing EST-SSR markers in cotton by exploiting EST database of GeneBank. We analyzed agronomic and fiber data of 192 upland cotton recombinant inbred (RI) lines in replicated plot, over two years period. Currently work is in progress in developing a linkage map of QTLs and EST-SSR markers using these RI lines. These markers will provide for the first time information about DNA markers, that may give more direct estimate of diversity in functional genome and identify relation of the transcribed region with important QTLs.