ASSEMBLY AND SORTING OF HOMOLOGOUS BAC CONTIGS IN ALLOTETRAPLOID COTTON GENOMES

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Abstract

Upland cotton (*Gossypium hirsutum* L.) is a diploidized allopolyploid species containing At and Dt sub-genomes that have partial homology. Assembly and sorting of homologous BAC contigs into their subgenomes and further to individual chromosomes are of both great interest and great challenge for genome-wide integrated genetic and physical mapping of polyploid crops. As a pilot experiment to test the feasibility of separating the contigs in sub-genome At from the contigs in subgenome Dt, 166 and 128 markers with whole fragment sequences that were genetically mapped to chromosomes 12 and 26 were collected to design Overgo primers to develop an integrated genetic and physical map assembled for one pair of homologous chromosomes 12 and 26 of Upland cotton. Both chromosome-specific and locus-specific markers were used for the contig separation. New SSR markers were developed from both BAC-end sequences and BAC sub-clone sequences for mixed contigs. The results show that about 70% of the contigs were anchored to chromosomes 12 and 26 unambiguously, and 30% of the contigs needed more markers to locate them in the chromosomes. Homologous contigs identified by markers are being sequenced to verify the contigs and the homologous rate between the two chromosomes. Our preliminary data show that the strategy and procedure used for the contig assembly and sorting is capable to separate the contigs to their chromosomes that are partially homologous.