

An Integrated Genetic, Physical and Transcript Map of Homoeologous Chromosomes 12 and 26 in Upland Cotton (*Gossypium hirsutum* L.)

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While Upland cotton (*Gossypium hirsutum* L.) represents 95% of the world production, its genetic improvement is hindered by the shortage of effective genomic tools and resources. The complex allotetraploid genome of the Upland cotton presents a unique challenge to such research efforts including integrated genome mapping and sequencing, which are considered highly experimental. Here, we report an integrated genetic, physical, and transcript map of homoeologous chromosomes 12 and 26 based on BAC/BIBAC clones, DNA markers, and EST unigenes. The map consists of 220 and 115 physical contigs, estimated to span 73.49 Mb and 34.23 Mb of chromosomes 12 and 26, respectively. Approximately one half of the 220 contigs were anchored to At sub-genome, while 48 of the 115 contigs were sorted to Dt sub-genome. Between the two sub-genome chromosomes, 67 contigs were shared with an overall physical similarity at 40%. A total of 401 fiber unigenes plus 214 non-fiber unigenes were located to chromosome 12, and 207 fiber unigenes plus 183 non-fiber unigenes were located to chromosome 26. Anchoring was accomplished through an Overgo hybridization approach, and all anchored ESTs were functionally annotated via blast analysis. The results revealed four and five gene-rich islands in chromosomes 12 and 26, respectively. This integrated genome map describes the first pair of homoeologous chromosomes of an allotetraploid genome in which BAC contigs were identified and separated through the use of chromosome-specific probes and locus-specific genetic markers. The approach used in this study was proven useful in the construction of genome-wide physical maps for polyploid plant genomes such as Upland cotton. The identification of gene-rich islands in the integrated map provides a platform for many studies including targeted sequencing of specific genomic regions in Upland cotton.