

1832 BAC and BIBAC Library Resources of Upland Cotton for Genome Analysis, and Gene and QTL Cloning and Characterization in Cotton

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Large-insert BAC and plant-transformation-competent BIBAC libraries have been proven crucial to advanced genetics and genomics research. To facilitate cotton genomics research, we have constructed two BAC and one BIBAC libraries from two genotypes of the Upland cotton. The first BAC library was constructed from Auburn 623, the root-knot nematode resistance source and a parent of a newly developed RIL mapping population. The library consists of 44,160 clones with an average insert size of 140 kb, representing 2.7 x Upland genome equivalents. The second BAC library was constructed for TM-1 with an average insert size of about 175 kb. The library consists of 76,800 clones, representing a 6.0 x genome coverage of Upland cotton. The third one, BIBAC library, was also constructed with TM-1. The library consists of 76,800 clones with an average insert size of 130 kb and covers about 4.1 x Upland genomes. These libraries have been used in physical mapping of the Upland cotton genome, cloning and characterization of genes and QTLs, and development of DNA markers suited for marker-assisted breeding in cotton.