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Czech J. Genet. Plant Breed.

**X., Liu K., Wang Q.,
Zhang C., Liu C., Zhu
W., Shan G., Chin C.K.,
Fang W.:**

Integration and characterization of T- DNA insertion in upland cotton

Czech J. Genet. Plant Breed., 49 (2013):
51-57

Copy numbers were evaluated by real-time quantitative PCR, and 149 junctions of T-DNA were isolated by thermal asymmetric interlaced PCR from 92 independent transgenic cotton lines transformed by *Agrobacterium tumefaciens* strain LBA4404. Real-time quantitative PCR results showed that 46% had integration of one or two T-DNA copies, 54% had three or more copies. Among 63 amplified products at LB junctions, 51% showed co-transformation of the vector backbone, 30% retained a

portion of LB ranging from 3 to 23 bp, and 19% showed deletions ranging from 1 to 148 bp from the LB inner end. In contrast, all of the cleavage sites were located in the inner region of RB. The distribution of T-DNA insertions in upland cotton genome included coding sequences, transposons, plastid-derived sequences and microsatellites.

Keywords:

cotton (*Gossypium hirsutum* L.); deletion of border; genetic transformation; transgene copy; vector integration

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