

**DNA VARIATION IN TEN INFLUENTIAL
UPLAND COTTON VARIETIES BY RAPDS**
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Abstract

Influential Upland cotton (*Gossypium hirsutum* L.) varieties (lines) are parents that contributed larger proportion of genes to modern cultivars than other germplasms. Our previous research has shown significant differences in general combining ability (GCA) effects for yield, yield components and fiber properties among the influential cotton varieties. In this study, we used random amplified polymorphic DNA (RAPD) markers to evaluate DNA variation of ten influential cotton varieties that had been previously involved in GCA analysis. Of fifty random decamer primers screened for their capability of amplifying DNA via the polymerase chain reaction (PCR), 36 primers generated a total of 154 DNA fragments. Nineteen bands were polymorphic, which showed a low percentage (12.3%) of DNA variation among these influential varieties. Seven varieties were individually identified by variety-specific markers in genetic fingerprinting. One primer, UBC-149 (5'AGC AGC GTG G3'), amplified a special DNA fragment that was absent in five varieties with positive general combining ability (GCA) effects for seed cotton yield and present in five varieties with negative or low positive GCA effects for the same trait. Regression analysis indicated a highly significant linear combination between this fragment and GCA effect for seed cotton yield. This finding, for the first time, identifies a DNA fragment in cotton that is a potential DNA marker linked to yield gene(s) or yield-related gene(s). This DNA marker might also be useful in identifying heterosis in cotton.