

GENETIC DISTANCE AMONG COTTON CULTIVARS USED IN THE DEVELOPMENT OF RANDOM MATING POPULATIONS BASED ON SSR MARKERS AND COEFFICIENT OF PARENTAGE

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Abstract

Simple sequence repeats (SSR) and coefficient of parentage have been used as measures of genetic diversity within crops. Association between genetic distance (GD) estimated by molecular markers and coefficient of parentage (CP) has not been studied in cotton (*Gossypium hirsutum* L.). The objectives of this study were to estimate GD among selected cotton genotypes based on SSR markers used in the development of a random mating population, and to investigate the relationship between genetic distance and coefficient of parentage. Nine U.S., one Australian cultivars, and a root knot nematode resistance line (M240) were genotyped using 296 SSR primer pairs providing 156 polymorphic markers. Genetic distance between genotypes ranged from 0.11 to 0.26. The highest GD (0.26) was observed between Acala Ultima and M240 and Deltapine 90 and Pyramid. The lowest GD (0.11) was estimated between cultivars Stoneville 474 and Phytogen 355 and Stoneville 474. and Stoneville 825. The GD between M240 and others cultivars ranged from 0.19 to 0.26. Among the commercial cultivars GD ranged from 0.11 to 0.26, indicating a narrow genetic base. CP ranged from 0.00 to 0.43 for the 11 genotypes. The lowest CP (0.00) was observed between Phytogen 355 and Coker 315, Phytogen 355 and M240 and Phytogen 355 and Stoneville 825. The highest CP (0.43) was obtained between SureGrow747 and Stoneville 474. Correlation between $GS=(1-GD)$ and CP was 0.35, which was significant. Based on SSR markers, GD revealed a lack of genetic diversity among all genotypes and it provided better information than the coefficient of parentage.