Genetic Mean Analysis of Earliness Among Brazilian and US Upland Cotton

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Introduction

The development of new cotton lines with improved earliness has always been an important breeding goal around the world. In Brazil, the boll weevil (*Anthonomous grandis*) has become a major pest of cotton, causing severe economic damage. The use of early-maturing cotton cultivars has been the major agricultural practice to reduce losses and such practice also allows planting of a second crop such as soybean after cotton in Brazil. The objective of the present work was to study the genetics and heritability for earliness using generation mean analysis (GMA) in cultivars with different maturity from Brazil and United States. These cultivars consisted of BRS 269 (cultivar), CNPA GO 2005-809 (inbred) and CNPA GO 2005-158 (inbred) from Brazil as well as three U.S. cultivars: Tamcot CAMD-E, PSC 355, and Acala 1517-99. Six basic generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each cross were generated and sown in a randomized block design with three replications during the summer of 2011 in College Station, Texas.

Materials and Methods

The present study was carried out during the summer of 2011 growing season at Experimental Station of Texas A&M in College Station–Texas. Six varieties were used for this study namely BRS 269(Cultivar), CNPA GO 2005-809(inbred) and CNPA GO 2005-158(inbred) from Brazil as well three U.S cultivars: as well as three U.S. cultivars: Tamcot CAMD-E, PSC 355, and Acala 1517-99. Six basic generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each cross were generated and sown in a randomized block design with three replications. The row-length was 13.10m in each plot. The number of plants evaluated varied as follows: 5 plants for the non-segregating P_1 and P_2 and F_1 generations; 40 plants for F2 ,BC1 and BC2 generations. The traits assessed were: node first fruiting branch, first white flower, first open boll, vertical flowering interval, horizontal flowering interval, vertical maturation interval, and horizontal maturation interval. The analysis of variance of the six basic generations (P1, P2, F1, F2, BC1 and BC2 was statistically analyzed using (RCDB)analysis of variance. The data was analyzed using SAS 9.2 using PROC GLM.

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Results and Discussion

The means and standard errors of the six generations from three families for NFFB (node for first fruit branch) and DFF (number of days for first flower) are presented on Table 1 and Table 2 respectively. NFFB means for P_1 e P_2 were different ($p \leq 0.05$) in three families studied (Tables 1 and 2). On Table 2, the results indicated for the family 1(BRS 269x BRS 158) that means of the F_1´s were higher than either the highest parent suggesting dominance gene action for DFF. In general, however, the trait mean values for the F_1 and F_2 generations were higher than corresponding values for the BC_1P_1 and BC_1P_2 generation, while the mean performance of the BC_1P_2 segregating generation was lower than that of the BC_1P_1 for all crosses and traits studied (Data not shown). The additive gene effect was predominant for most traits in all populations. The effect AD gene effect was significant only for D.F.O.B in population BRS 158 X CAMD-E. As expected in family 2 (BRS 269 x CAMD-E) crossing contrasting phenotypes for earliness identified additive gene effect indicating that genotypes with improved earliness could be identified through pedigree method and selection methodology.

Conclusions

- Tamcot CAMD-E was the best parent to get earlier materials;
- The additive gene effect was predominant for e traits in all populations indicating that genotypes with improved earliness could be identified through pedigree method and selection methodology;

The effect AD gene effect was significant only for D.F.O.B in population BRS 158 X CAMD-E.

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Table 01 - Means and standard error of P1, P2, F1, F2, BC1P1, and BC1P2 for N.F.F.B per parental combination. College Station -Texas, 2011.

Generation	BRS 269 x BRS158 †	BRS 269 x CAMD-E	BRS 158 x CAMD-E
P1	9.98 ± 1.07 a	9.98 ± 1.07 a	8.65 ± 0.81 a
P2	8.65 ± 0.81 c	6.27 ± 0.59 c	6.27 ± 0.59 c
F1	8.76 ± 1.20 c	8.13 ± 1.19 b	6.73 ± 0.70 c
F2	8.66 ± 0.89 c	7.60 ± 2.32 b	7.55 ± 1.05 b
BC_1P_1	9.53 ± 1.03 b	7.94 ± 2.95 b	7.40 ± 1.31 b
BC_1P_2	8.54 ± 0.79 b	6.84 ± 2.31 c	6.80 ± 1.12 c

†First parent listed is P1, second parent listed is P2.
Means with the same letter are not significantly different by Duncan ($p \leq 0.05$).

Table 02 - Means and standard error of P1, P2, F1, F2, BC1P1, and BC1P2 for D.F.F. per parental combination. College Station -Texas, 2011.

Generation	BRS 269 x BRS158 †	BRS 269 x CAMD-E	BRS 158 x CAMD-E
P1	55.93 ± 3.67 a	55.93 ± 3.67 a	53.13 ± 3.48 a
P2	53.13 ± 3.48 b	46.26 ± 3.48 e	46.26 ± 3.48 d
F1	56.60 ± 3.81 a	50.86 ± 3.81 c	47.46 ±1 .59 cd
F2	56.40 ± 3.67 a	51.27 ± 3.87 bc	47.82 ± 3.34 c
BC_1P_1	54.23 ± 3.56 b	52.45 ± 3.56 b	49.85 ± 3.44 b
BC_1P_2	51.52 ± 3.01 c	48.55 ± 3.02 d	47.82 ± 2.96 c

†First parent listed is P1, second parent listed is P2.
Means with the same letter are not significantly different by Duncan ($p \leq 0.05$).