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GENETIC ARCHITECTURE OF AN IMPROVED VERSION OF A MAIZE COMPOSITE. I. GENETIC ANALYSIS OF GRAIN YIELD, YIELD COMPONENTS AND SOME AGRONOMIC TRAITS

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ABSTRACT

Improved version (C3) developed from a commercial maize composite (Super-I) was studied to estimate the components of genetic variances for grain yield, yield components, and some agronomic traits during the main season of 1982 and 1983. Design-I of Comstock and Robinson was used to estimate the genetic variances. All the characters except grain yield exhibited greater importance of additive components of variance with dominance in the negligible to partial range; whereas both the components played a major role in the inheritance of grain yield. Dominance variance was, however, highly inconsistant over environments and had significant G x E interaction for almost all the traits.

Key words: Genetic variance, dominance ratio, G x E interaction, residual genetic variability.

Recurrent selection in a population improvement programme is effective only when the base population has high genetic variability created through intermating of divergent gene pools. Substantial residual genetic variability in the improved versions can be maintained when the elite lines are identified for reconstitution in each cycle. Random mating of each reconstituted version for a few generations, before initiation of the next cycle, would greatly help to bring the population near linkage equilibrium, besides creating new genetic variability from potential variability locked in heterozygous polygenic blocks through crossing over [1], and reduce the linkage bias in the estimation of the components of genetic variance.

Continued selection influences the residual genetic variability in maize populations. Increase in the total and additive genetic variance, after a few selection cycles, was reported earlier [2–4], as against a reduction in the additive genetic and dominance variance [1, 5].

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Substantial reduction in the genetic variability was not observed in some maize populations even after many cycles of selection [6–8].

The study reported has estimated the residual genetic variability after three full-sib family selection cycles in a maize composite.

MATERIALS AND METHODS

The Super-I maize composite was developed by intermating divergent gene pools of four composites (Vijay, Kisan, Amber and Jawahar) and four hybrids (Him-123, Ganga-5, VL-54 and Deccan). After thorough random mating of the base population (C_0), elite full-sib families were identified on the basis of their mean performance across geographical locations and improved versions reconstituted from the remaining seeds. The source population (C_3) was developed after three cycles of full-sib selections across locations and random mated for six generations.

The experimental material was developed and evaluated as per the N.C. Design I [9, 10]. Precautions to avoid assortative mating were taken [11]. A large number of random male plants were mated to each of four random female plants. At harvest, 100 male groups (half-sib families) comprising 400 full-sib families were selected on the basis of sufficient seed on each ear. The material was evaluated for two years during the monsoon season in randomised incomplete design. Four male groups were randomly assigned to each set, thus, each set contained 16 full-sib families, which were randomly assigned to each plot and replicated twice within the set, forming a total of 25 sets. One row each of C_0 and C_3 populations were sown at either end of each replication within a set.

Each plot consisted of a single row of 5 m length with the 25 hills spaced at 20 cm and rows at 75 cm. Each hill was planted with 2 seeds and later thinned to one plant, ensuring good final stand in each experiment.

The data were recorded on five competitive plants within each plot for seven quantitative characters. Days to 50% silk were recorded on the total number of plants in each plot. Total plant height and ear height were recorded at dry silk stage. Grain yield per plant and kernel weight were adjusted at 15% moisture.

The mean values for each character in a plot (median value for days to silk) were used for analysis of variance.

The results of two experiments will be referred to as Exp. 1, Exp. 2, respectively, in the present study.

RESULTS AND DISCUSSION

A perusal of the comparative estimates of genetic variance (Table 1) reveals that the magnitude of these components for most of the traits was higher in Exp. 1 as compared to Exp. 2 or combined analysis, possibly due to more favourable environment during Exp. 1.

Inheritance of grain yield per plant exhibited greater magnitude of dominance variance than additive genetic variance in single environment which, however, decreased considerably in the pooled analysis. Judging from the behaviour and relative magnitude of the components of genetic variance for this trait it can be concluded that the trait was greatly influenced by additive genetic variance with dominance within the partial to complete

Table 1. Estimates of the genetic components of variance ($\hat{\sigma}^2A$ and $\hat{\sigma}^2D$), dominance ratio ($\hat{\sigma}^2D/\hat{\sigma}^2A$), and G x E interaction ($\hat{\sigma}^2AL$) for different traits in an improved version (C_3) of a maize composite

Character	Environment	$\hat{\sigma}^2A$	$\hat{\sigma}^2D$	$\hat{\sigma}^2D/\hat{\sigma}^2$	$\hat{\sigma}^2AL$	$\hat{\sigma}^2DL$
Grain yield/plant	Exp. 1	173.4 ± 63.4	269.6 ± 96.4	1.55	—	—
	Exp. 2	83.3 ± 30.9	92.9 ± 48.1	1.12	—	—
	Combined	76.3 ± 36.8	58.4 ± 63.0	0.76	-13.96 ± 31.60	452.92 ± 70.10
Days to silk	Exp. 1	4.6 ± 1.3	3.1 ± 1.8	0.68	—	—
	Exp. 2	1.8 ± 0.7	1.7 ± 1.1	0.95	—	—
	Combined	2.9 ± 0.8	0.4 ± 1.1	0.15	0.28 ± 0.41	2.00 ± 0.87
Plant height	Exp. 1	125.0 ± 32.1	67.1 ± 40.1	0.54	—	—
	Exp. 2	102.2 ± 25.5	65.3 ± 31.1	0.64	—	—
	Combined	89.2 ± 24.6	35.9 ± 29.4	0.40	24.34 ± 9.24	30.38 ± 14.12
Ear height	Exp. 1	58.0 ± 17.2	56.7 ± 23.5	0.98	—	—
	Exp. 2	67.8 ± 16.9	28.7 ± 20.7	0.42	—	—
	Combined	55.7 ± 15.0	24.9 ± 19.4	0.45	-1.84 ± 5.10	62.66 ± 11.34
Ear length	Exp. 1	1.3 ± 0.3	-0.2 ± 0.4	NE	—	—
	Exp. 2	0.8 ± 0.2	0.7 ± 0.2	0.89	—	—
	Combined	0.6 ± 0.2	0.1 ± 0.3	0.16	0.05 ± 0.16	1.90 ± 0.33
Ear diameter	Exp. 1	0.02 ± 0.01	0.04 ± 0.01	1.86	—	—
	Exp. 2	0.02 ± 0.01	0.04 ± 0.01	2.93	—	—
	Combined	0.02 ± 0.01	0.01 ± 0.01	0.59	-0.003 ± 0.002	0.03 ± 0.01
Kernel rows/ear	Exp. 1	0.48 ± 0.14	0.36 ± 0.19	0.75	—	—
	Exp. 2	0.62 ± 0.15	0.22 ± 0.19	0.36	—	—
	Combined	0.43 ± 0.12	0.02 ± 0.17	0.06	-0.01 ± 0.06	0.90 ± 0.14
100-kernel weight	Exp. 1	5.22 ± 1.57	5.60 ± 2.15	1.07	—	—
	Exp. 2	6.69 ± 1.76	2.56 ± 2.26	0.38	—	—
	Combined	5.29 ± 1.45	3.00 ± 1.80	0.58	0.69 ± 0.47	1.03 + 0.90

Note. NE—could not be estimated since dominance variance was negative.
Exp. 1—rainy season 1982; Exp. 2—rainy season 1983; and Combined—pooled analysis of Exp. 1 and Exp. 2.

range. Greater importance of additive genetic variance for grain yield was also reported earlier [5, 11–14]. Many other workers, however, suggested greater contribution of dominance variance [15–17] as well as equal contribution of both additive genetic and dominance variance [18, 19] to this trait.

Table 2. Estimates of relative magnitude of interaction of components of variance (male and female) and genetic components of variance (additive and dominance) with environments

Character	$\hat{\sigma}^2$ml/ $\hat{\sigma}^2$m	$\hat{\sigma}^2$fl/ $\hat{\sigma}^2$f	$\hat{\sigma}^2$AL/ $\hat{\sigma}^2$A	$\hat{\sigma}^2$DL/ $\hat{\sigma}^2$D	$\hat{\sigma}^2$DL/ $\hat{\sigma}^2$AL
Grain yield/plant	–0.18	3.26	–0.18	7.76	NE
Days to silk	0.09	0.68	0.10	4.70	7.16
Plant height	0.27	0.44	0.27	0.85	1.25
Ear height	–0.03	0.75	–0.03	2.51	NE
Ear length	0.08	2.68	0.08	19.75	36.46
Ear diameter	–0.13	0.76	–0.13	2.25	NE
Kernel rows/ear	–0.12	1.95	–0.02	37.33	NE
Kernel weight	0.13	0.20	0.13	0.34	1.54

NE—could not be estimated as $\hat{\sigma}^2$AL was negative.

Yield components (ear length, ear diameter, kernel rows per ear and kernel weight) also exhibited higher magnitude of additive genetic variance than dominance variance in both the environments and combined analysis (except for ear length in Exp. 2 showing equal importance of both these components and ear diameter, which exhibited higher dominance variance in both the environments). Taking into consideration the inconsistencies of dominance variance and the magnitude of additive variance in the combined analysis it could be concluded that these yield components have preponderance of additive gene action. Similar findings were reported earlier for ear length and ear diameter [11, 12, 14] and kernel rows per ear and kernel weight [15, 20].

Plant height, ear length and days to silk also revealed greater importance of additive genetic variance with dominance in the partial range (except ear height in Exp. 1 and days to silk in Exp. 2, where both revealed equal importance of additive genetic and dominance variance). Greater importance of additive genetic variance for these traits was also emphasised by earlier workers [11, 12, 14].

Confounding of the components of genetic variance with G x E interaction in individual environments leads to their biased estimates that subsequently affects the gains realised through selection. A perusal of Table 2 indicates that all the traits exhibited higher values of $\hat{\sigma}^2$fl/ $\hat{\sigma}^2$f as compared to their respective values of $\hat{\sigma}^2$ml/ $\hat{\sigma}^2$m. Unproportional bias in the components of variance ($\hat{\sigma}^2$f and $\hat{\sigma}^2$m) due to interaction with environments and larger values $\hat{\sigma}^2$fl/ $\hat{\sigma}^2$f as compared to their respective $\hat{\sigma}^2$ml/ $\hat{\sigma}^2$m values reveals inflation in the estimates of dominance variance over environments [12]. Likewise, the estimates of relative magnitude of genetic components of variance x environments for all the traits indicated that the magnitude of $\hat{\sigma}^2$DL/ $\hat{\sigma}^2$D ratios in the combined analysis were higher for all the traits indicating inconsistency of dominance variance over environments as compared to the small and negligible values of $\hat{\sigma}^2$AL/ $\hat{\sigma}^2$A. Robinson and Moll [21] have suggested that large magnitude of $\hat{\sigma}^2$DL/ $\hat{\sigma}^2$D and/or $\hat{\sigma}^2$AL/ $\hat{\sigma}^2$A ratio indicates inconsistency of that genetic component of variance over environments. However, Comstock and Moll [22] suggested that larger magnitude of $\hat{\sigma}^2$DL/ $\hat{\sigma}^2$AL ratio for a trait as compared to its respective dominance ratio ($\hat{\sigma}^2$D/ $\hat{\sigma}^2$A) in the combined analysis would indicate inconsistency of dominance variance over environments. The magnitude of $\hat{\sigma}^2$DL/ $\hat{\sigma}^2$AL ratio for days to silk, plant height, ear length, and kernel weight were higher in magnitude as compared to their respective dominance ratios in the combined analysis. This comparison could not be made for other traits since their ^$\hat{\sigma}$AL values were negative though not significantly different from zero. These small negative values actually could also be some small positive values being affected by sampling error. If so, their $\hat{\sigma}$DL/ $\hat{\sigma}$AL values would also be higher in magnitude than their respective dominance ratios in the combined analysis.

Taking into consideration the G x E interaction of the components of genetic variance and their relative stability over environments it can be concluded that the dominance variance for all the traits was highly inconsistent over environments and had a signifciant G x E interaction. On the contrary, additive genetic variance revealed greater consistency, as was reported earlier [2, 14, 23].

Under the temperate weather, the cultivation of newly synthesised high yielding maize composites must fulfil two main objectives, i.e., high yielding potential and early maturity. The long term population improvement programme undertaken for this Super-I composite of maize is to make available improved high yielding versions with early maturity. Even after three selection cycles in the said composite, the residual genetic variability was sufficient for further improvement. Inheritance of grain yield in this improved version was controlled by additive genetic variance with dominance in the partial – complete range, while mainly additive genetic variance was found to be important for maturity. The full-sib selection programme adopted for this composite seems to be appropriate at the present.

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