

Genetic architecture of a heterotic cross between two populations of maize

A. S. Khehra, H. Singh and B. S. Dhillon

Department of Plant Breeding, Punjab Agricultural University, Ludhiana-141 004, India

Received April 17, 1984; Accepted May 1, 1984

Communicated by R. Riley

Summary. The nature and magnitude of variability in the interpopulation cross of 'Mezcla Amarillo Selection' (MAS), an introduction from CIMMYT, Mexico, and 'J607', a population developed in India using indigenous, American, and Yugoslavian germplasm, were studied. Interpopulation progenies developed by following the North Carolina Design I were evaluated at two locations. The additive genetic variance component in interpopulation cross, $\sigma_{A(12)}^2$, and in one population assuming the other population as tester, $\sigma_{A_{12}}^2$ and $\sigma_{A_{21}}^2$, were significant for all the traits evaluated, namely ear length, ear girth, kernel rows and days to silk, with one exception. For kernel rows, the dominance variance component, $\sigma_{D(12)}^2$, was also significant but it was smaller than $\sigma_{A(12)}^2$. The variance component due to dominance \times location interaction, $\sigma_{DL(12)}^2$, was significant for all traits except kernel rows. In the case of ear length and ear girth, $\sigma_{DL(12)}^2$ was greater than the other components. $\sigma_{AL(12)}^2$, $\sigma_{AL_{12}}^2$ and $\sigma_{AL_{21}}^2$ were not significant for any trait. Expected genetic advance indicated a superiority of half-sib reciprocal recurrent selection over full-sib reciprocal recurrent selection.

Key words: *Zea mays* L. – Interpopulation cross – Half-sib reciprocal recurrent selection – Full-sib reciprocal recurrent selection

Introduction

There is a large volume of literature available in maize (*Zea mays* L.) on the estimation of the nature and magnitude of genetic variability within populations (intrapopulation) (Gardner 1963; Moll and Stuber 1974; Sprague and Eberhart 1977; Comstock 1978) but only a few reports are available on genetic variability

in population crosses (interpopulation) (Obilana et al. 1979). Information on the nature and magnitude of genetic variability in an interpopulation cross is useful in formulating a breeding programme based on two populations and their crosses.

'J607', a population developed in India, and 'Mezcla Amarillo Selection' (MAS) an introduction from CIMMYT, Mexico showed a high degree of heterosis (Anonymous 1975). In view of the heterosis and geographic diversity between these two populations, the present study was undertaken to characterise the nature and magnitude of variability in their interpopulation cross.

Materials and methods

The study was based on an interpopulation cross of 'Mezcla Amarillo Selection' (MAS) and 'J607'. MAS is an introduction from CIMMYT, Mexico. 'J607' has been developed at Punjab Agricultural University, Ludhiana as a result of intrapopulation selection in a germplasm complex developed by crossing an indigenous collection, 'Bhodipur Yellow', with two hybrids introduced from USA and one from Yugoslavia. Interpopulation half-sib-full-sib progenies between 'MAS' and 'J607' were produced following the North Carolina Design I (Comstock and Robinson 1948). To generate these materials 100 randomly taken plants from a population were used as males and each male crossed to six plants from the other population. Sixty-four male groups, each having four half-sib interpopulation families, were taken at random from ears having at least 150 grains. 'MAS' and 'J607' were sown at time intervals to facilitate crossing between the two populations and to avoid assortative mating.

The materials were evaluated at two locations, viz. Ludhiana in semi-arid plains and Gurdaspur in humid sub-mountainous region. An incomplete-block design (replications in blocks) with two replications was used. Each family was evaluated in a single row plot of 5 m length with row-to-row and plant-to-plant spacings of 75 and 20 cm, respectively. Data were recorded from 10 randomly taken competitive

plants for grain yield per plant (g), ear length (cm), ear girth (cm), number of kernel rows, plant height (cm) and ear height (cm) and plot averages were used for statistical analysis. The number of days taken from sowing to 75% silking was recorded on a plot basis.

The analysis of variance was carried out following Robinson et al. (1955). Various components, viz. σ_m^2 (variance component due to males), σ_f^2 (variance component due to females within males), σ_{m1}^2 (variance component due to males \times locations) and σ_{f1}^2 (variance component due to females within males \times locations) were obtained by equating observed mean squares and their expectations. These components were translated into genetic components of variance as indicated below (Obilana et al. 1979):

$$\begin{aligned}\sigma_{A12}^2 &= 4\sigma_{m12}^2 \\ \sigma_{A21}^2 &= 4\sigma_{m21}^2 \\ \sigma_{A(12)}^2 &= \frac{1}{2}(\sigma_{A12}^2 + \sigma_{A21}^2) = 2(\sigma_{m12}^2 + \sigma_{m21}^2) \\ \sigma_{D(12)}^2 &= 2(\sigma_{f12}^2 + \sigma_{f21}^2 - \sigma_{m12}^2 - \sigma_{m21}^2) \\ \sigma_{AL12}^2 &= 4\sigma_{m112}^2 \\ \sigma_{AL21}^2 &= 4\sigma_{m121}^2 \\ \sigma_{AL(12)}^2 &= 2(\sigma_{m112}^2 + \sigma_{m121}^2) \\ \sigma_{DL(12)}^2 &= 2(\sigma_{f112}^2 + \sigma_{f121}^2 - \sigma_{m112}^2 - \sigma_{m121}^2)\end{aligned}$$

The suffix 12 denotes population 1 ('MAS') as male and population 2 ('J607') as female whereas 21 denotes population 2 as male and population 1 as female, and (12) denotes inter-population parameters. When gene frequency in the two populations is equal $\sigma_{A(12)}^2$, $\sigma_{D(12)}^2$, $\sigma_{AL(12)}^2$ and $\sigma_{DL(12)}^2$ become σ_A^2 , σ_D^2 , σ_{AL}^2 and σ_{DL}^2 . Standard errors of these components were calculated by using the standard formula. Expected genetic advance using half-sib reciprocal recurrent selection (HSRRS) and full-sib reciprocal recurrent selection (FSRRS) was calculated by using the following formulae (Gardner 1978):

$$\begin{aligned}\text{Half-sib reciprocal recurrent selection} \\ G_c &= \frac{K(\frac{1}{4})\sigma_{A12}^2}{\sqrt{\frac{1}{4}\sigma_{A12}^2 + \frac{1}{4}\frac{\sigma_{AL12}^2}{1} + \frac{\sigma_{12}^2}{r1}}} + \frac{K(\frac{1}{4})\sigma_{A21}^2}{\sqrt{\frac{1}{4}\sigma_{A21}^2 + \frac{1}{4}\frac{\sigma_{AL21}^2}{1} + \frac{\sigma_{21}^2}{r1}}} \\ \text{Full-sib reciprocal recurrent selection} \\ G_c &= \frac{K(\frac{1}{2})\sigma_{A(12)}^2}{\sqrt{(\frac{1}{2}\sigma_{A(12)}^2 + \frac{1}{4}\sigma_{D(12)}^2) + \frac{(\frac{1}{2}\sigma_{AL(12)}^2 + \frac{1}{4}\sigma_{DL(12)}^2) + \frac{\sigma_{(12)}^2}{r1}}}\end{aligned}$$

Table 1. Estimates of components of genetic variance in the interpopulation cross and in one population using the other as tester

| Character | Interpopulation cross parameters | | | | J 607 ¹ × MAS | | MAS ¹ × J 607 | |
|--------------|----------------------------------|--------------------|---------------------|---------------------|--------------------------|-------------------|--------------------------|-------------------|
| | $\sigma_{A(12)}^2$ | $\sigma_{D(12)}^2$ | $\sigma_{AL(12)}^2$ | $\sigma_{DL(12)}^2$ | σ_{A12}^2 | σ_{AL12}^2 | σ_{A21}^2 | σ_{AL21}^2 |
| Ear length | 1.070** ± 0.408 | 0.802 ± 0.634 | -0.802 ± 0.187 | 1.727** ± 0.545 | 0.968* ± 0.394 | -0.485 ± 0.193 | 1.175** ± 0.415 | -0.370 ± 0.170 |
| Ear girth | 0.285* ± 0.125 | 0.319 ± 0.190 | -0.039 ± 0.066 | 0.361* ± 0.159 | 0.218 ± 0.116 | 0.030 ± 0.073 | 0.335** ± 0.132 | -0.106 ± 0.058 |
| Kernel rows | 0.761** ± 0.267 | 0.669* ± 0.331 | -0.026 ± 0.075 | 0.300 ± 0.177 | 0.695** ± 0.262 | 0.035 ± 0.070 | 0.828** ± 0.280 | -0.090 ± 0.072 |
| Days to silk | 3.208** ± 1.211 | 1.368 ± 1.613 | 0.304 ± 0.594 | 2.676* ± 1.203 | 3.483** ± 1.233 | -0.045 ± 0.632 | 2.942* ± 0.168 | 0.650 ± 0.584 |

** * Significant at 5% and 1% probability levels, respectively t indicates tester population

where G_c is expected genetic advance per cycle, K is selection intensity which is standardized selection differential and σ^2 is the error variance. Singh (1981) observed that average gene frequency differed in two populations for grain yield, plant height and ear height whereas for other traits the gene frequency did not differ. Therefore, the results are presented for ear length, ear girth, kernel rows and days to silk.

Results and discussion

The estimates of components of variance in the population cross indicated a greater role of $\sigma_{A(12)}^2$ than $\sigma_{D(12)}^2$ in the inheritance of all the traits (Table 1). Only $\sigma_{A(12)}^2$ was significant for ear length, ear girth and days to silk. For kernel rows both components were significant and $\sigma_{A(12)}^2$ was greater than $\sigma_{D(12)}^2$. The estimates of $\sigma_{AL(12)}^2$ were not significant in any case whereas that of $\sigma_{DL(12)}^2$ were significant for ear length, ear girth and days to silk.

The estimates of components of genetic variance in 'MAS' and 'J607' involving the other population as tester are also presented in Table 1. Only the estimates of additive variance are given as the estimates of dominance variance thus obtained refer to population cross. The estimates of σ_{A12}^2 (estimate of 'MAS' using 'J607' as tester) and σ_{A21}^2 (estimate of 'J607' using 'MAS' as tester) were significant for all traits except the σ_{A12}^2 of ear girth. The estimates of σ_{AL12}^2 and σ_{AL21}^2 were not significant.

For ear length and ear girth, $\sigma_{DL(12)}^2$ was the largest component indicating that the development of hybrids with specific adaptation may prove rewarding if the breeding programme is to be based on 'MAS' and 'J607'. The results also indicated that the expression of variation due to additive gene action is relatively constant over the environments in comparison to variation due to dominance deviation. Similar results have been obtained by Rojas and Sprague (1952); Lonnquist and Gardner (1961) and Dhillon and Singh (1977).

Table 2. Expected gain per cycle (as % of mean of population cross) at different selection intensities (SI) through half-sib reciprocal recurrent selection (HSRRS) and full-sib reciprocal recurrent selection (FSRRS)

| Character | HSRRS (10% SI) | FSRRS (10% SI)* | FSRRS (5% SI)** |
|--------------|-------------------|--------------------|--------------------|
| Ear length | 7.81 | 5.12 | 5.99 |
| Ear girth | 4.52 | 3.21 | 3.76 |
| Kernel rows | 8.85 | 6.00 | 7.02 |
| Days to silk | 3.83 | 1.55 | 1.81 |

* Same selection intensity as HSRRS

** Same resources as HSRRS

The expected genetic advance per cycle assuming 10% selection intensity indicated a distinct superiority of HSRRS over FSRRS (Table 2). However, selection intensity in FSRRS can be twice that in HSRRS without employing additional resources. Therefore, expected genetic advance through FSRRS assuming 5% selection intensity was also estimated. It was interesting to note that expected genetic advance was higher through HSRRS (at 10% selection intensity) than that expected from FSRRS (at 5% selection intensity). This is in contrast with the findings of Jones et al. (1971) who carried out computer simulation studies assuming the same resources (twice the selection intensity in FSRRS than in HSRRS) and an edge of FSRRS over HSRRS. The superiority of HSRRS over FSRRS in the present study may be due to a greater contribution of $\sigma_{D(12)}^2$ or $\sigma_{DL(12)}^2$ in comparison to $\sigma_{A(12)}^2$ than that expected on the basis of the complete dominance model assumed by Jones et al. (1971). However, FSRRS has the advantage that only half as many families are needed to be evaluated in comparison to HSRRS to maintain the same effective size of the population and the natural outflow of hybrids.

References

- Anonymous (1975) Annual Progress Report. Coordinated Maize Improvement Project, New Delhi
- Comstock RE (1978) Quantitative genetics in maize breeding. In: Walden DB (ed) Maize breeding and genetics. Wiley and Sons, New York, pp 191–206
- Comstock RE, Robinson HF (1948) The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. *Biometrics* 4:254–256
- Dhillon BS, Singh J (1977) Combining ability and heterosis in diallel crosses of maize. *Theor Appl Genet* 49:117–122
- Gardner CO (1963) Estimates of genetic parameters in cross fertilizing plants and their implications in plant breeding. In: Hanson WD, Robinson HF (eds) Statistical genetics and plant breeding. NAS-NRC Pub 962, Washington, pp 225–250
- Gardner CO (1978) Population improvement in maize. In: Walden DB (ed) Maize breeding and genetics. Wiley and Sons, New York, pp 207–228
- Jones LP, Compton WA, Gardner CO (1971) Comparison of full-sib and half-sib reciprocal selection. *Theor Appl Genet* 41:36–39
- Lonnquist JH, Gardner CO (1961) Heterosis in intervarietal crosses in maize and its implications in breeding procedures. *Crop Sci* 1:179–183
- Moll RH, Stuber CW (1974) Quantitative genetics – empirical results relevant to plant breeding. *Adv Agron* 26:277–313
- Obilana AT, Hallauer AR, Smith CS (1979) Estimated genetic variability in a maize interpopulation. *J Hered* 60:127–132
- Robinson HF, Comstock RE, Harvey PH (1955) Genetic variance in open-pollinated varieties of corn. *Genetics* 40:45–60
- Rojas BA, Sprague GF (1952) A comparison of variance components in corn yield trials. 3. General and specific combining ability and their interaction with locations and years. *Agron J* 44:462–466
- Singh Harjinder (1981) Genetic analysis of some quantitative characters in two open-pollinated populations of maize (*Zea mays* L.). PhD Thesis, Punjab Agricultural University, Ludhiana, India
- Sprague GF, Eberhart SA (1977) Corn breeding. In: Sprague GF (ed) Corn and corn improvement. American Society of Agronomy Inc, Madison Wis, pp 305–354