381

Means and variances of some characters in base populations, with emphasis on grain yield in soybean

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ABSTRACT

The aim of this study was to evaluate in early generations of self-fertilization the potential of single, double and multiple crosses, as producers of base population for soybean breeding programs. The crosses were made involving eight parents with low coefficient of parentage between them. The experiment with the segregating populations was conducted in a completely randomized design with three replications. The results were subjected to analysis based on plot means and individual plants. For the characters number of days to flowering and to maturity, and plant height at flowering and at maturity, the means obtained with the F_3 populations of single crosses, the F_3 populations of double crosses and the F_2 populations of multiple crosses were similar. The best results for grain yield per plant were obtained with the F_3 populations of double crosses. In general, no change was detected in the values of genetic variance of the segregating populations because of the number of parents used in the crosses.

KEY WORDS: *Glycine max*, plant breeding, recurrent selection.

INTRODUCTION

In the 1960s, most Brazilian soybean (*Glycine max* L. Merrill) cultivars were obtained by plant introduction. New cultivars were later obtained from progenies from biparental crosses. More recently, however, it has become increasingly difficult to continue obtaining success with this system, because genetic variation and recombination potential of the available germplasm are low due to the limited diversity and because the process of biparental crosses followed by self pollination restricts genetic recombination (Vello et al., 1988). Hiromoto and Vello (1986) detected that the genetic base of soybean in Brazil was narrow and that 11 ancestors had contributed 89% of the germplasm in use. These factors have been indicated as accounting for the establishment of yield plateaus and for the vulnerability of the germplasm, mainly to diseases (Vello, 1995).

Programs to increase genetic variability in the base populations should be used to allow the occurrence of further advances in terms of yield potential of the new recommended cultivars. Promising results can be obtained when multiple parents combination followed by recombination of selected individuals is given priority in the breeding program, as in recurrent selection. The recombination of selected individuals is performed to favor breakage of linkage groups and to increase the chances of accumulating favorable alleles. This new population obtained from recombination can be used to start a new selection cycle, which becomes, therefore, a dynamic and continuous cycle process (Geraldi, 1995; Destro and Montalván, 1999).

Recurrent selection programs begin with the formation of the base population that can be derived from multiple crosses. The genotypes which participate in these crosses should possess genetic divergence to allow liberation of enough genetic variation for selection success. The superior lines developed by recurrent selection programs can originate new cultivars or can be useful as parents to improve cultivars in a particular quantitative trait (Fehr, 1987b). Several recurrent selection studies in self-pollinating plant species have been reported. In soybean, Kenworthy and Brim (1979) obtained a significant increase of 134 kg/ha/cycle in three selection cycles. Sumarno and Fehr (1982) obtained responses for yield of 120, -14 and 24 kg/ha/cycle in soybean populations of early, medium and late maturity, respectively. Wilcox (1998) obtained a mean increase of 5.8 g/kg/cycle in protein content in eight recurrent selection cycles and showed that practically all the alleles for high protein content in the seed had been accumulated in individual plants by the fifth cycle.

This study was performed to assess, at the early stage (generations) of self-pollination, the potential of single, double and octuple crosses to form base populations for soybean breeding.

MATERIAL AND METHODS

Genetic material

The selection of parents to form the base population for the recurrent selection program followed the following criteria:

a) High yield: recommended cultivars were preferentially selected, following the Technical Recommendations for Soybean Cropping in Paraná State, Brazil (Embrapa Soybean Center, 1995);

b) Tolerance or resistance to the largest number of key soybean diseases;

c) Minimum mean endogamy ($\overline{F}$) between pair of parents (Table 1), measured by the Malécot coefficient of parentage. The Malécot coefficient between two inbred lines measures the probability of the gametes, one taken from one parent and the other from the other parent, to carry alleles which are identical by descent (Falconer, 1981). In this study the mean endogamy among all the parents was 0.0881 or 8.81%.

d) Preferably from the early or semi-early maturity group.

The eight selected parents were the following:

FT Cometa, BR 36, FT Guaíra, Coodetec 201, Ocepar 13, BR 16, BR 37 e USP 1. The crosses were made between the parents to obtain four simple hybrids (Figure 1):

BR 36 x FT Cometa = 1 (F= 0,00098);

Coodetec 201 x FT Guairá = 2 (F= 0,04395);

BR 16 x Ocepar 13 = 3 (F= 0,13867);

USP 1 x BR 37 = 4 (F= 0,06470).

Aside from these, the crosses for obtaining three double-hybrids were:

1 x 2 = (BR 36 x FT Cometa) x (Coodetec 201 x FT Guaíra);

3 x 4 = (BR 16 x Ocepar 13) x (USP 1 x BR 37);

4 x 3 = (USP 1 x BR 37) x (BR 16 x Ocepar 13).

These two last double-hybrids are differentiated only for be treated as reciprocals.

The double hybrids were also crossed reciprocally, originating four octuple hybrids:

(1 x 2) x (3 x 4) = [(BR 36 x FT Cometa) x (Coodetec 201 x FT Guaíra)] x [(BR 16 x Ocepar 13) x (USP 1 x BR 37)];

(1 x 2) x (4 x 3) = [(BR 36 x FT Cometa) x (Coodetec 201 x FT Guaíra)] x [(USP 1 x BR 37) x (BR 16 x Ocepar 13)];

(3 x 4) x (1 x 2) = [(BR 16 x Ocepar 13) x (USP 1 x BR 37)] x [(BR 36 x FT Cometa) x (Coodetec 201 x FT Guaíra)];

(4 x 3) x (1 x 2) = [(USP 1 x BR 37) x (BR 16 x Ocepar 13)] x [(BR 36 x FT Cometa) x (Coodetec 201 x FT Guaíra)].

Characteristics of the Experiment

The F_1 plants were grown in a greenhouse and all seeds were harvested to form the F_2 generation plants. The F_2 generation was advanced by single pod descent (SPD); a single three seed pod was harvested from each plant and the pods were threshed together to form the next generation. The F_3 generation of the single and double crosses and the F_2 generation of the octuple crosses were assessed in 1999/2000, from 26/Nov/1999 sowings (Figure 1). The experiment was carried out in the experimental area on the School Farm at Londrina State University (Londrina, Paraná, Brazil) located at 23° 22´LS, 51° 10´LW.

The experiment was carried out in a randomized complete block design, with three replications. Eleven segregant populations and the eight parents used as

Table 1. Coefficient of endogamy ($\overline{F}$) among the parents used in the crosses.

	FT Cometa	BR 36	FT Guaíra	Coodetec 201	Ocepar 13	BR 16	BR37	USP 1	F
FT Cometa		0.00098	0.10742	0.00391	0.01465	0.00781	0.00854	0.00830	0.02166
BR 36	0.00098		0.01831	0.00855	0.03345	0.01660	0.18249	0.01941	0.03997
FT Guaíra	0.10742	0.01831		0.04395	0.40527	0.08398	0.13696	0.09912	0.12786
Coodetec 201	0.00391	0.00855	0.04395		0.06933	0.28125	0.06323	0.03516	0.07220
Ocepar 13	0.01465	0.03345	0.40527	0.06933		0.13867	0.21289	0.15918	0.14763
BR 16	0.00781	0.01660	0.08398	0.28125	0.13867		0.18115	0.06152	0.11014
BR37	0.00854	0.18249	0.13696	0.06323	0.21289	0.18115		0.06470	0.12142
USP 1	0.00830	0.01941	0.09912	0.03516	0.15918	0.06152	0.06470		0.06391
Mean									0.08810

controls totaled 19 treatments. Disregarding reciprocal crosses, the segregant populations were formed by four single and double hybrids and one octuple hybrid. Each experimental plot consisted of one five-meter row with approximately 10cm between plants after thinning. The between row spacing was 90cm. Five plants from the ends of each row were taken as plot border. Therefore, each plot consisted of 40 plants and each population was represented for 120 plants. These plants were identified with colored strings to allow individual plant assessments.

The soil was prepared by conventional tillage with one plowing and two disk operations. It was fertilized with 50 grams per linear meter (555 kg/ha) of the 0N-28P-20K formula. After sowing, weeds were controlled by manual hoeing. Insecticide was applied to control the velvet bean caterpillar (*Anticarsia gemmatalis*) and the soybean stinkbug (*Nezara viridula*).

Assessed traits

The plants were assessed for the following traits:

a) Number of days to flowering (NDF): period between sowing and the opening of the first flower (R1 stage on the Fehr and Caviness scale, 1977)

b) Plant height at the beginning of flowering (PHF): mean distance between the plant base and the insertion of the uppermost inflorescence on the main stem assessed at the R1 stage;

c) Number of days to maturity (NDM): period between sowing and the day when approximately 95% of the pods on the plants were mature (R8 on the Fehr and Caviness scale, 1977)

d) Plant height at maturity (PHM): distance (cm) measured between the plant base and the insertion of the uppermost inflorescence on the main stem, assessed at the R8 stage;

e) Individual plant grain yield (GY): assessed after threshing the individual plants by weighting the grains in grams.

Data analysis

Data from individual plants from progenies derived from each cross were collected for each trait and used to estimate the arithmetic mean ($\bar{x}$); phenotypic variance (s^2); genetic variance (s^2_g); range (R) (maximum and minimum values) and heritability in the broad sense (h^2). The phenotypic variance was
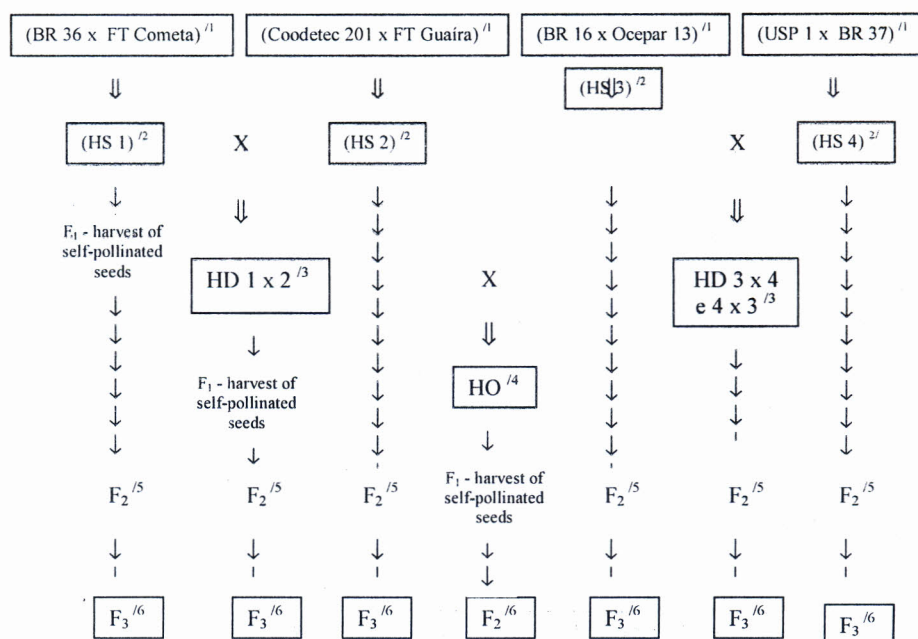

Figure 1. Model of crosses and behavior of progenies. [1] Parents were sown in August and September 1997 in a greenhouse. Simple hybrid seeds harvested in December and January; [2] Simple hybrids (HS) sown to obtain the double hybrids (HD) in January and February 1998 and harvest of double hybrids in May and June; [3] HD sown to obtain the octuple hybrids (HO) in August 1998 and octuple hybrid seeds harvested in November; [4] The four HO (F_1 plant cultivation) sown in December 1998 in a greenhouse; [5] Cultivation of F_2 progeny lines derived from simple and double crosses in the field, 1998/1999 harvest; harvested by the SPD method; [6] Cultivation of F_3 progeny lines derived from simple and double crosses of F_2 progeny lines from octuple crosses and the eight parents in the field, 1999/2000; completely randomized block design, with three replications (40 plants per replication).

estimated from the within plot sum of squares; the three sum of squares were added and divided by the total number of plants minus three. Therefore, the phenotypic variance was an estimate weighted by the degrees of freedom of each plot.

The broad sense heritability was estimated according to Mahmud and Kramer (1951):

$$h^2 = [s^2_g / s^2] = [(s^2 - s^2_E) / s^2].$$

Where,

s^2_E = environmental variance, estimated by the arithmetic mean of the phenotypic variances of the eight assessed parents.

The s^2_g and s^2_E values were used to calculate the variation index (b), which is the ratio of the coefficients of genetic and environmental variation ($b = (s^2_g)^{1/2} / (s^2_E)^{1/2}$). According to Vencovsky (1987), if b is greater or equal to one, there is a very favorable situation for selection of the assessed trait, which facilitates the screening, in the early generations, of crosses with similar means and traits more or less alterable by selection.

The analyses of variance were carried out using the GENES computer program (Cruz, 1997). Four additional analyses of variance were performed using the partition of the degrees of freedom for treatments in contrasts of interest (Banzatto and Kronka, 1989).

RESULTS AND DISCUSSION

Individual plant grain yield analysis

Table 2 shows the means and variances and other genetic parameters of the individual plant yield trait. Considering the cross groups, the largest mean genetic variance was obtained for the double cross F_3 progenies ($s^2_g = 425.9$). This value was almost three times greater than that obtained for the single cross F_3 progenies ($s^2_g = 150.3$), and approximately twice as large that for octuple cross F_2 progenies ($s^2_g = 206.4$). Consequently, the mean variation index ($\bar{b}$) of the double cross F_3 progenies ($\bar{b}_{CD} = 0.8$) was greater than those of the single cross F_3 progenies ($\bar{b}_{CS} = 0.6$) and octuple F_2 ($\bar{b}_{CO} = 0.4$). This suggests that base populations derived from double crosses are more promising for variance generation. Much of the phenotypic variation, in the progenies derived from double crosses, are genetic in nature. Further analysis also detected that the average broad sense heritability of the double cross F_3 progenies is greater that those derived from single cross F_3 or octuple cross F_2 progenies.

For both single and double cross types there was an increase in the genetic variance with the increase in the number of parents involved in the crosses (Table 2). However, the genetic variance diminished when octuple crosses were involved. The fact that the octuple cross populations are in the F_2 generation, while the others are in F_3, may have contributed to this decrease in the genetic variance. The F_2 generation of the octuple crosses should have presented greater amount of dominance variance than the F_3 progenies of the single and double hybrids, and this effect may have hidden part of the genetic variation. One generation of inbreeding ahead, the progenies derived from single and double crosses suffered less influence from the dominance variance and the contribution of the additive variance was greater.

The genetic variance of a given trait of a population, such as grain yield, will increase proportionally to the number of alleles controlling the trait by which the parents differ (Falconer, 1981). Also, it is expected that a decrease in the coefficient of endogamy of the parents will cause an increase in the genetic variance of the derived population (Kisha et al., 1997). Therefore, segregant populations showing greater genetic variance should have greater chances of generating transgressive segregant individuals, i.e, high performing lines, when compared with populations showing less variation. The parents forming the octuple crosses presented a mean endogamy coefficient of 0.0881 (Table 1). This value represents the mean general endogamy which is much smaller than the value of 0.1641 obtained by Vello et al. (1988) with the cultivars recommended for cultivation in Brazil in 1983/1984. According to these authors, this value was 0.25 in the United States where soybean breeding has been practiced for a longer period. In Argentina, where the program is more recent than in the United States or Brazil, the value was 0.09. Gizlice et al. (1993) reported that to maintain the genetic variability in the American soybean germplasm it would suffice to cross cultivars whose parentage coefficient was less than 0.25. In this experiment, the mean endogamy coefficient $(\bar{F})$ (Table 1) of each of the selected parents and other component genotypes varied from 0.02166 to 0.14763. These values were relatively low, suggesting high genetic divergence among parents and guaranteeing presence of variability in the segregant populations.

The plant grain yield data presented in Table 2 show that the greatest mean was obtained in a population also derived from a double cross (4 x 3). This cross also showed the best results for all assessed

parameters. Its reciprocal cross (3 x 4) also presented good results. The presence of the União cultivar in two of the four parents involved in these crosses may have contributed to this. This cultivar has already been extensively used as parent in Brazilian breeding programs and has excellent characteristics.

Another comparative analysis of the progeny means from single, double and octuple crosses was made using the analysis of variance results with four-way partitioning of the degrees of freedom (Table 3). These partitions will now be dealt with individually.

Individual plant grain yield analysis according to each degree of freedom partitioning

The analysis of variance in Table 3 shows significant differences among treatments (parents and progenies from crosses) for individual plant grain yield. The coefficients of variation were at adequate levels, not only for grain yield but also for the other characteristics (Guerra et al. 1999). In the first partitioning of the treatment degrees of freedom, the single cross F_3 progenies, double cross F_3 progenies, octuple cross F_2 generations and inbred parents were considered as individual groups. Significant variation was detected among the grain yield means of at lest two groups (Table 3a). Significant variation was also detected between the means of the progenies within double crosses and parents. However, the single cross F_3 progeny means and the octuple cross F_2 generations were not significantly different. This last result shows that the use of the reciprocal crosses did not influence the grain yield mean.

Partitioning the degrees of freedom in another three

Table 2. Means ($\bar{x}$), phenotypic (s^2) and genotypic (s^2_g) variances, range (R), heritability in the broad sense (h^2) and relationship among the coefficients of variance of genetic and environmental variance (b, variation index), for the grain yield per plant trait, assessed in eight parents and eleven segregant populations derived from simple (CS), double (CD) and octuple (CO) crosses. Soybean, Londrina, Paraná, Brazil. Agricultural year 1999/2000.

Crosses	$\bar{x}$ (g/plant)	s^2	s^2_g	R	h^2 (%)	b
F_3 of CS						
1[/1]	52.4	893.2	421.0	2.7 - 191.0	47.1	0.9
2	45.2	485.2	13.0	2.3 - 101.4	2.7	0.2
3	39.3	394.5	-[/2]	3.8 - 108.8	-[/2]	-[/2]
4	46.7	489.1	16.9	2.7 - 124.6	3.5	0.2
Mean	45.9	565.5	150.3	2.4 - 191.0	17.8	0.4
F_3 of CD						
1 x 2	42.5	511.2	39.0	2.4 - 155.2	7.6	0.3
3 x 4	59.7	807.4	335.1	3.1 - 145.0	41.5	0.8
4 x 3	69.6	1375.9	903.7	2.3 - 176.9	65.7	1.4
Mean	57.3	898.2	425.9	2.3 - 176.9	38.3	0.8
F_2 of CO						
(1 x 2) x (3 x 4)	51.9	983.3	511.1	3.6 - 176.1	52.0	1.0
(1 x 2) x (4 x 3)	43.1	595.6	123.4	3.1 - 110.1	20.7	0.5
(3 x 4) x (1 x 2)	47.9	580.7	108.5	4.2 - 111.8	18.7	0.5
(4 x 3) x (1 x 2)	44.7	555.0	82.8	2.1 - 109.8	14.9	0.4
Mean	46.9	678.7	206.4	2.1 - 176.1	26.6	0.6
Parents						
FT Cometa	48.0	775.0	-	14.6 - 82.1	-	-
BR 36	55.5	725.2	-	14.8 - 110.6	-	-
FT Guaíra	47.4	664.0	-	3.1 - 109.7	-	-
Coodetec 201	35.3	237.2	-	3.3 - 72.0	-	-
Ocepar 13	33.6	267.4	-	3.8 - 73.4	-	-
BR 16	45.7	713.3	-	7.0 - 109.0	-	-
BR 37	40.0	171.4	-	8.8 - 77.2	-	-
USP 1	42.6	224.2	-	11.6 - 77.3	-	-
Mean	43.5	472.2	-	3.1 - 110.6	-	-

[/1] 1: BR 36 x FT Cometa; 2: Coodetec 201 x FT Guaíra; 3: BR 16 x Ocepar 13 and 4: USP 1 x BR 37; [/2] Refers to data with negative sign, not considered.

Table 3. Analysis of variance with the mean squares (QM) and coefficients of variation (R) for five traits, with partitioning of the degrees of freedom of source genotypes (a), and partitioning of the degrees of source freedom among groups (where there are significant differences) for three sets of contrasts of interest (b, c, d), assessed in eight parents and eleven segregant progeny derived from simple (CS), double (CD) and octuple (CO) crosses. Soybean, Londrina, Paraná, Brazil. Agricultural year 1999/2000.

Source of variation	GL	QM[1]				
		GY	NDF	NDM	PHF	PHM
Genotips	18	243.76[1]	8.98[1]	42.94[1]	102.56[1]	195.64[1]
a) Contrast group 1						
Between groups	3	320.89[1]	0.96[ns]	2.40[ns]	52.56[ns]	76.18[ns]
Within CS	3	76.36[ns]	14.48[1]	15.05[1]	99.47[1]	208.60[ns]
Within CD	2	582.90[1]	5.24[1]	24.58[1]	166.83[1]	798.34[1]
Within CO	3	61.93[ns]	1.35[ns]	6.66[ns]	50.50[ns]	137.61[ns]
Within parents	7	263.48[1]	14.41[1]	93.05[1]	129.25[1]	93.94[ns]
b) Contrast group 2						
Parents x progenies of crosses	1	341.78[1]	-	-	-	-
(CS+CD) x CO	1	113.94[ns]	-	-	-	-
CS x CD	1	507.19[1]	-	-	-	-
c) Contrast group 3						
Parents x progenies of crosses	1	341.78[1]	-	-	-	-
CS x (CD+CO)	1	153.32[ns]	-	-	-	-
CD x CO	1	467.81[1]	-	-	-	-
d) Contrast group 4						
Parents x progenies of crosses	1	341.78[1]	-	-	-	-
(CS+CO) x CD	1	620.20[1]	-	-	-	-
CS x CO	1	0.93[ns]	-	-	-	-
Residue[2]	38	55.05	0.64	2.71	26.53	86.46
CV (%)		15.66	1.60	1.42	8.81	11.76

[1] significant at 5% and 1% by the F test, respectively; [ns]: not significant. GY: grain yield per plant (g); NDF: number of days to flowering; NDM: number of days to maturity; PHF: plant height at flowering (cm) and PHM: plant height at maturity (cm); [2] The mean square of the residue was used in the F test for all the contrast groups.

orthogonal contrasts was also performed to investigate which groups (single, double, octuple crosses and parents) were significantly different [Table 3(b, c, d)]. In the second partition, significant differences were detected between the progeny means from the crosses and the mean of the inbred parents (Table 3b). The former were approximately 14% higher than the latter. Probably, the recombination of genes in the crosses resulted in combinations that favorably affected grain yield. However, this statement may not be true if the increase in the mean is basically due to effects of the dominance effects of the genes that control the trait. The mean of the single and double cross progenies did not significantly differ from that of the octuple cross progenies (Table 3b). On the other hand, the mean of the double cross F_3 progenies was 25% larger than the single cross F_3 progenies mean (Tables 2 and 3).

In the third group of contrasts, no significant difference was found between the mean of the double cross F_3 progeny and octuple cross F_2 generations compared with that of single cross progenies (Table 3c). The mean

of the double cross F_3 progeny was 22% higher in absolute values than the mean of the octuple cross F_2. In the fourth group of contrasts, the mean of the double cross F_3 progenies was approximately 23% higher than the mean among the single cross F_3 progenies and octuple cross F_2 (Table 3d).

The mean of the single cross F_3 progenies and the octuple cross F_2 generations were not statistically different (Table 3d). When the means of the populations of the octuple crosses are compared with the best mean of the single cross (Table 2), it is shown that they also were similar. These must be considered good results. The probability of developing high yielding new lines is greater if high yielding elite parents are crossed (Fehr, 1987a). When planning a single cross, the two best parents for the trait to be improved are chosen. In an octuple cross, several parents must be chosen, of which one or some may not be the best for that trait. This can lead to a reduction in the progeny mean. In this case, it is expected that the favorable alleles normally dispersed in different parents can, in their majority, be

Table 4. Means ($\bar{x}$), phenotypic (s^2) and genetic (s^2_g) variances, variation interval (R), heritability in the broad sense (h^2) and relationship among the genetic and environmental coefficients of variance (b, variation index), referent to the traits number of days flowering (NDF) and number of days to maturity (NDM), assessed in eight parents and eleven segregant populations derived from simple (CS), double (CD) and octuple (CO) crosses. Soybean, Londrina, Paraná, Brazil. Agricultural year 1999/2000.

Crosses	NDF						NDM					
	$\bar{x}$	s^2	s^2_g	IV	h^2 (%)	b	$\bar{x}$	s^2	s^2_g	IV	h^2 (%)	b
F_3 of CS												
1[/1]	46.7	4.85	4.06	40-52	79.0	2.2	112.6	24.8	23.1	100-127	93.2	3.7
2	50.4	3.85	2.88	47-56	73.6	1.7	116.1	5.1	3.4	111-124	67.0	1.4
3	51.5	8.38	7.45	45-59	87.8	2.7	117.1	30.5	28.9	102-128	94.5	4.1
4	50.6	5.14	4.08	47-59	80.2	2.0	117.8	12.4	10.7	112-130	86.4	2.5
Mean	49.8	5.55	4.79	40-59	80.1	2.1	115.9	18.2	16.5	100-130	85.3	3.0
F_3 of CD												
1 x 2	49.0	5.30	4.28	42-56	80.8	2.1	113.7	14.9	13.2	96-125	88.7	2.8
3 x 4	50.7	6.26	5.24	44-60	83.7	2.3	116.7	18.7	17.0	103-132	91.0	3.2
4 x 3	51.5	8.95	7.93	44-58	88.6	2.8	119.0	25.1	23.5	104-130	93.3	3.7
Mean	50.4	6.84	5.82	42-60	84.4	2.4	116.4	19.6	17.9	96-132	91.0	3.2
F_2 of CO												
(1 x 2) x (3 x 4)	50.0	6.47	5.45	41-56	84.3	2.3	117.2	25.1	23.4	105-129	93.3	3.7
(1 x 2) x (4 x 3)	49.7	3.48	2.46	45-56	70.7	1.6	116.5	18.5	16.8	104-129	90.9	3.2
(3 x 4) x (1 x 2)	49.9	6.12	5.10	45-62	83.4	2.2	117.0	21.6	19.9	106-130	92.2	3.4
(4 x 3) x (1 x 2)	49.0	4.29	3.27	40-55	76.3	1.8	114.7	18.2	16.5	100-125	90.8	3.1
Mean	49.6	5.10	4.07	40-62	78.6	2.0	116.4	20.9	19.2	100-130	91.8	3.4
Parents												
FT Cometa	45.4	0.62	-	44-46	-	-	104.3	1.90	-	102-106	-	
BR 36	49.5	0.99	-	48-52	-	-	122.7	3.49	-	120-127	-	
FT Guaíra	50.9	1.41	-	49-54	-	-	114.6	1.09	-	113-117	-	
Coodetec 201	49.4	0.68	-	48-51	-	-	115.6	1.03	-	114-118	-	
Ocepar 13	51.5	0.79	-	49-53	-	-	115.9	0.90	-	114-119	-	
BR 16	49.7	1.10	-	48-52	-	-	115.2	0.85	-	113-117	-	
BR 37	52.9	0.56	-	52-54	-	-	118.2	1.69	-	117-121	-	
USP 1	49.4	2.01	-	48-53	-	-	121.0	2.47	-	119-124	-	
Mean	49.8	1.02	-	44-54	-	-	115.9	1.68	-	102-127	-	

[/1] 1: BR 36 x FT Cometa; 2: Coodetec 201 x FT Guaíra; 3: BR 16 x Ocepar 13 and 4: USP 1 x BR 37.

accumulated in one of these progeny derived from octuple or multiple cross. There will then be the need to assess many progeny or families of progenies to identify it. It is known, however, that it is practically impossible to accumulate all the favorable alleles at one single cycle (Fouilloux and Bannerot, 1988). This could only be achieved by stages. A good strategy would be to perform a multiple cross followed by successive selection and recombination cycles, that is, recurrent selection.

Analysis of the number of days to flowering and to maturity traits

In the analyses of the traits number of days to flowering and number of days to maturity based on individual plants showed that the phenotypic variances of the progenies from the crosses were much higher than those of the parents, resulting in high heritability values for these traits (Table 4). The indexes of variation were also high and all close to or greater than two. According to Vencovsky (1987), selection in these traits in the assessed generations will be effective.

For both traits, almost all genetic variance means of the single and double F_3 progenies and octuple cross F_2 generation presented similar values. However, for number of days to flowering, the mean genetic variance of the double cross F_3 progenies had a higher value than that of the single cross progenies and octuple cross F_2. As seen before, this superiority also occurred with the grain yield trait.

The analysis of variance in Table 3 shows differences among treatments for number of days to flowering and number of days to maturity. However, no significant differences were detected among the means of the groups of F_3 progenies derived from single crosses, F_3 progeny derived from double crosses, F_2 generations from octuple crosses or inbred parents (Table 3a). The participation of all the parents in each one of the groups must have contributed to the similarity of these means. For this reason, the degrees of freedom among groups could not be partitioned into three orthogonal contrasts, as to the individual plant grain yield trait.

Significant differences were detected among F_3 progeny and among parent means within single and double cross and parent groups for number of days to flowering and days to maturity (Table 3a). However, the means between octuple cross F_2 generations did not show significant differences, indicating that the use of the reciprocal crosses also did not influence these traits.

Although differences among treatments were detected in the analysis of variance, the cross progeny means for number of days to flowering and to maturity were, in general, similar (Table 4). The parents involved in the crosses belonged to the early and semi-early maturity groups, except for BR 37, which is a medium cycle cultivar. Consequently, all the progenies from the crosses had mean number of days to maturity within the early and semi-early maturity group. This result is important in order to obtain cultivars adapted to the region where the experiment was carried out, because early and semi-early cultivars are the most used. The means of the F_3 progenies from the single cross number one and from the double cross 1 x 2 showed they were the earliest among all progenies, probably because they are derived from FT Cometa, the earliest of all the parents.

Plant height at flowering and at maturity analyses

Table 5 shows the means, variances and genetic parameters of the plant height at flowering and plant height at maturity traits. Taking the cross groups, a small decrease in the genetic variance with the increase in the number of parents involved in the crosses, mainly for the octuple cross F_2 generations, was observed for plant height at flowering. For plant height at maturity, the decrease occurred when moving from single to double crosses, but the reduction was greater in the octuple crosses compared to the double crosses.

For both traits, the heritabilities and variation indexes were greater than for individual plant grain yield.

Although, in some cases, the variation indexes were smaller than one, indicating an unfavorable situation for selection (Vencovsky, 1987), this can be considered a good result because the means of all cross progenies for both traits were considered satisfactory. This reflects the involvement of parents adapted to the region where the experiment was carried out.

For plant height at maturity, single cross number 1 obtained the largest means, variation intervals and, especially, genetic variance (Table 5). This occurred because FT Cometa, one of the parents, had undetermined growth habit, while all the others had determined growth habit. The greatest intervals of variation for plant height at maturity trait showed that the occurrence of plants with undetermined growth habit remained in all the populations where FT Cometa (parent number 1) was involved. The participation of this parent in the F_3 progenies from single crosses, double crosses and F_2 generations from octuple crosses was 50%, 25% and 12.5%, respectively. Therefore, indeterminate plants occurred in greater number in the single cross progenies, at an intermediate number in the double crosses and in a smaller number in the octuple crosses, gradually reducing their genetic variance. These results showed that although the degree of endogamy must prevail in the parental choice, the occurrence of genes with greater effects, such as growth habit, should also be considered, because they may enhance the positive effects of the genetic divergence of the parents.

Significant differences among treatments (parents and progenies from crosses) were detected for plant height at flowering and at maturity according to the analysis of variance in Table 3. The partition of the degrees of freedom of treatments presented similar results to those obtained for number of days to flowering and to maturity. Thus, for the two traits related to plant height, no significant differences were detected among the means of the groups of F_3 progenies derived from single crosses, F_3 progeny derived from double crosses, F_2 generations from octuple crosses or inbred parents (Table 3a and 5).

There was significant variation between F_3 progeny means within single crosses and double crosses and between the mean of the parents for plant height at flowering (Table 3a). For plant height at maturity, differences were only found between F_3 progeny means of double crosses. The largest mean was obtained for the progenies from the 1 x 2 double cross (Table 5). However, for both traits, the means of the octuple cross F_2 generations did not differ (Table 3a).

This result shows that the use of the reciprocal octuple crosses did not influence the plant height at flowering or maturity. The means of the octuple cross F_2 generations also indicated that no reciprocal effects occurred for all assessed traits.

CONCLUSIONS

The base populations derived from double crosses presented greater means and genetic variance for grain yield and were more promising for selection purposes than those derived from single or octuple crosses.

For the plant height at flowering and at maturity traits, the means of the base populations derived from single, double crosses and octuple crosses are equally promising.

RESUMO

Médias e variâncias de algumas características em populações base, com ênfase para produtividade de grãos em soja

Este trabalho objetivou avaliar nas gerações iniciais de autofecundações a potencialidade de cruzamentos simples, duplos e óctuplos, como formadores de população base para programas melhoramento de soja. Os cruzamentos foram feitos envolvendo oito parentais com baixo grau de endogamia entre eles. O experimento com as progênies segregantes foi conduzido em delineamento inteiramente casualizado com três repetições. Os dados foram submetidos a análises com base em média de parcelas e em plantas

Tabela 5. Means ($\bar{x}$), phenotypic (s^2) and genotypic (s^2_g) variances, variation interval (IV), heritability in the broad sense (h^2) and relationship among the coefficients of genetic and environmental variation (b, variation index), for the traits plant height at flowering (PHF) and plant height at maturity (PHM), assessed in eight parents and eleven segregant populations derived from simple (CS), double (CD) and octuple (CO) crosses. Soybean, Londrina, Paraná, Brazil. Agricultural year 1999/2000.

Crosses	PHF						PHM					
	$\bar{x}$ (cm)	s^2	s^2_g	IV	h^2 (%)	b	$\bar{x}$ (cm)	s^2	s^2_g	IV	h^2 (%)	b
F_3 of CS												
1[/1]	55.9	105.4	69.8	21-83	66.2	1.4	90.2	709.4	631.2	41-158	88.9	2.8
2	68.7	92.0	56.4	46-93	61.3	1.3	90.2	147.2	68.9	59-114	46.8	0.9
3	57.0	108.0	72.3	21-83	67.1	1.4	72.5	115.8	37.5	50-96	32.4	0.7
4	59.1	102.4	66.8	35-87	65.3	1.4	75.7	176.5	98.2	52-120	55.7	1.1
Mean	60.2	101.9	66.4	21-93	65.0	1.4	82.1	287.2	209.0	41-158	56.0	1.4
F_3 of CD												
1 x 2	65.6	69.2	33.6	37-93	48.5	1.0	96.0	459.9	381.7	38-173	83.0	2.2
3 x 4	52.4	75.1	39.5	30-88	52.6	1.1	66.2	137.1	58.8	33-105	42.9	0.9
4 x 3	61.9	138.1	102.5	34-97	74.2	1.7	78.8	168.0	89.8	46-115	53.4	1.1
Mean	59.9	94.1	58.5	30-97	58.5	1.3	80.4	255.0	176.8	33-173	59.8	1.4
F_2 of CO												
(1 x 2) x (3 x 4)	58.1	68.4	32.8	22-90	47.9	1.0	72.7	127.0	48.8	26-110	38.4	0.8
(1 x 2) x (4 x 3)	64.9	66.3	30.7	27-84	46.3	0.9	89.4	352.5	274.2	47-167	77.8	1.9
(3 x 4) x (1 x 2)	54.9	93.9	58.4	23-100	62.1	1.3	76.4	231.8	153.5	37-170	66.2	1.4
(4 x 3) x (1 x 2)	63.7	83.0	47.4	26-85	57.1	1.2	86.5	346.2	267.9	33-159	77.4	1.9
Mean	60.4	77.9	42.4	22-100	53.4	1.1	81.2	264.3	186.1	26-170	64.9	1.5
Parents												
FT Cometa	44.6	40.6	-	33-53	-	-	82.3	146.6	-	70-101	-	-
BR 36	57.8	66.5	-	40-76	-	-	71.7	128.8	-	42-94	-	-
FT Guaíra	64.3	42.9	-	46-73	-	-	80.3	107.0	-	46-94	-	-
Coodetec 201	59.1	21.8	-	48-71	-	-	83.2	45.3	-	64-96	-	-
Ocepar 13	58.2	25.8	-	47-68	-	-	75.7	36.9	-	64-93	-	-
BR 16	53.6	40.6	-	36-73	-	-	74.5	82.6	-	58-107	-	-
BR 37	63.7	26.1	-	53-76	-	-	81.2	30.9	-	67-95	-	-
USP 1	49.7	20.4	-	37-60	-	-	66.8	47.8	-	53-83	-	-
Mean	56.4	35.6	-	33-76			76.9	78.2	-	42-107	-	

[/] 1: BR 36 x FT Cometa; 2: Coodetec 201 x FT Guaíra; 3: BR 16 x Ocepar 13 and 4: USP 1 x BR 37.

individuais. As médias obtidas com progênies F$_3$ oriundas de cruzamentos simples, progênies F$_3$ oriundas de cruzamentos duplos e progênies F$_2$ oriundas de cruzamentos óctuplos foram semelhantes para os caracteres número de dias para o florescimento e maturação e altura de planta no florescimento e maturação. Os melhores resultados de média para produtividade de grãos foram obtidos com progênies de cruzamentos duplos. Em geral, não se verificou mudança nos valores de variância genética das progênies de cruzamentos em função do número de parentais envolvidos.

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