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Parent selection for intercrossing in food type soybean through multivariate genetic divergence

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ABSTRACT. Soybean for human consumption shows high genetic variability in relation to nutritional traits. Genotypes can be crossed to obtain inbreed lines adapted for a region, with high yield and nutritional qualities. In the multivariate analysis, the multiple information of an experiment are combined, based on a complex of variables, to select the best parents with high divergence. One hundred and four genotypes were analyzed for 12 characters of agronomic importance to select food type soybean parents, using the multivariate analysis based on Mahalanobis generalized distance (D^2) and on Tocher's classification method. Seven groups were formed trough clustering. The traits that most contributed to this classification were plant height at flowering (19.50%) and plant height at maturity (22.35%). Fifty-five crosses were recommended among genotypes with high genetic divergence and high yield. Eleven genotypes were selected from cluster I to be crossed with five genotypes from cluster III.

Key words: genetic divergence, *Glycine max*, multivariate analysis, soybean.

RESUMO. Seleção de parentais para intercruzamentos em soja tipo alimento por meio da divergência genética multivariada. A soja para a alimentação humana apresenta alta variabilidade genética em relação às características nutricionais. Os genótipos podem ser cruzados para a obtenção de linhagens puras adaptadas para uma região, com alta produtividade e qualidade nutricional. Na análise multivariada, as múltiplas informações de um experimento são combinadas com base em um complexo de variáveis, para selecionar os melhores parentais com alta divergência. Cento e quatro genótipos foram analisados para doze caracteres de importância agronômica para selecionar parentais de soja tipo alimento, usando-se a análise multivariada com base na distância generalizada de Mahalanobis (D^2) e no método de agrupamento de Tocher. Pela aglomeração, foram formados sete grupos. O caráter que mais contribuiu para esta classificação foi altura da planta no florescimento (19,50%) e altura da planta na maturidade (22,35%). Cinqüenta e cinco cruzamentos foram recomendados entre os genótipos com alta produtividade e alta divergência genética. Onze genótipos foram selecionados do grupo I para serem cruzados com cinco genótipos do grupo III.

Palavras-chave: divergência genética, *Glycine max,* análise multivariada, soja.

Soybean [*Glycine max* (L.) Merrill] cultivars are composed by pure lines, and hybridization is carried out to combine genes taken from genetically different parents into a new derived line with desired characteristics. The parents for hybridization are chosen according to some criteria: a) high and relatively stable grain yield in different environments (locations, years and cultivation periods); b) presence of special genes mainly related to insect and disease resistance, late flowering in shorter days, similar cycles, growth type and marker traits; and c) genetic diversity to assure transgressive segregation (Vello, 1992b).

Genetic diversity has been analyzed on the basis of combining ability in the F_1 and F_2 generations (Freire Filho and Vello, 1989) and on average performance of F_2 and F_3 generations (Toledo, 1987). These two procedures provide valuable information about the potential of each crossing, although it is necessary to carry out crosses and obtain F_2 and F_3 generations (Destro, 1991).

Other methods for prediction of genetic divergence are based: on yield and on multivariate analysis of parent traits; on the application of molecular markers (RFLP - Restriction Fragment Length Polymorphism, RAPD - Random Amplified DNA Polymorphism, and DAF - DNA Amplified Fingerprint); on the use of electrophoresis of isoenzyme; on Malècot parent coefficient method; on the dialell crosses analysis method; and on crosses in circulating chain method (Destro, 1991).

The use of multivariate genetic divergence technique is very important when there is a high number of parents to be studied and the amount of necessary crosses is impracticable. Genetic divergence allows parent selections based on a certain group of variables, so that, when crossed, they give a better heterosis effect in the progeny and a higher probability of obtaining superior genotypes in segregating generations (Cruz, 1990).

The multivariate genetic divergence technique has been used in several crops. Wang and Pan (1990) observed a high degree of heterosis in crosses among groups of cotton cultivars, when compared to crosses within groups. Maluf et al. (1983) found a positive and highly significant correlation between hybrid tomato heterosis and the parent genetic divergence. Singh e Ram (1985) studied 50 soybean lines (parents and lines derived from their crosses) and nine groups were found using Tocher's method. With a few exceptions, lines derived from a cross tended to be included in the same group together with the parents. Annappan et al (1989), studying geographically divergent soybean genotypes, found an absence of association between geographic distribution and genetic divergence.

This study was carried out to measure the genetic potential of food type soybean genotypes through Mahalanobis multivariate distance, identify crosses with higher potential for cultivar development, and select most productive food type soybean pure lines.

Material and methods

The 104 soybean genotypes used in the experiment are listed in Table 1. Eighty-eight of these are food type soybean genotypes (with large seeds, either vegetable or Edamame type), eight are food type soybean genotypes (with small seeds, natto or sprout types), and eight are grain type soybean cultivars adapted to Brazilian cultivation conditions. The latter were used as control treatments.

The experiment was conducted in Londrina, in 1991, in a soil classified as *terra roxa estruturada eutrófica* according to Brazilian soil classification. A randomized complete block design was used, with 104 treatments and four replications. Each plot was made up of a 3.0m single row, with up to 12 plants per plot, with an average distance of 0.25m between plants and 0.95m between plots. The following quantitative traits were evaluated:

NDF: Number of days to flowering. Corresponds to the period between sowing and the first flower anthesis - R_1 stage on Fehr and Caviness (1977) scale.

PHF: Plant height (cm) at the beginning of flowering. The distance measured between the soil and the farthest inflorescence insertion from main stem, analyzed on R_1 stage.

NDM: Number of days to maturity. The period of time between sowing and the day in which approximately 95% of the pods are mature- R_8 stage on Fehr and Caviness (1977) scale.

PHM: Plant height (cm) at maturity. Measured distance between the soil and the farthest inflorescence insertion from main stem, analyzed on R_8 stage.

AV: Agronomic value. Visually analyzed at maturity, the grade scale varied from 1 to 5, where 1 corresponded to an inferior plant and 5 to an excellent plant. AV represents a visual value of the plant's global merit for a series of adapting characters such as: number of pods, plant strength and health, resistance to lodging, shattering resistance and lower leaf retention after maturity (Hiromoto, 1990).

NIM: Number of internodes during maturity. Counted from cotyledon node to main stem top.

IPP: Individual plant productivity (g), evaluated by weighing the threshed seeds of the individual plant.

HSW: One hundred seed weight, calculated taking the weight of 100 seeds per individual plant, from four random plants per plot. The HSW arithmetic mean of these four plants was used for analysis.

RP: Reproductive period represents the number of days between flowering and maturity. (RP= NDM-NDF).

%RP: Reproductive period percentage. Represents the value, in percentage, of the number of days between flowering and maturity, in relation to the number of days to maturity. [%RP= (RP/NDM) x 100].

RG: Reproductive growth after flowering represents the plant growth (cm) between flowering and maturity. (RG = PHM-PHF).

%RG: Reproductive growth percentage represents the value, in percentage, of plant growth after flowering, in relation to its height after maturity. [%RG = (RG/PHM) x 100].

After the univariate analysis of variance, the means were grouped based on the method of Scott and Knott (1974). This method allows the separation of treatments into classes, which are represented by one letter per treatment for each analyzed trait. Therefore, the means followed by distinct letters differ among themselves at 1% significance level ($P<0.01$). As IPP is one of the main traits in parent selection for crosses, treatments with higher yield (letter 'A') were chosen for this trait. The coefficient of genotypic determination (H^2_g) was determined by:

$$H^2_g = (\hat{\phi})/(\hat{\phi}_g + \hat{\delta}^2/r)$$

where: $\hat{\phi}_g$: estimated variability of the fixed set of genotypes;

$\hat{\delta}^2$: error mean square; r : number of replications.

The Mahalanobis distance (D^2) (Mahalanobis, 1936) was applied to measure the genetic divergence of the genotypes and clustering was done according to Tocher's method (Rao, 1952). A canonical analysis was carried out to confirm the D^2 analysis as well as to provide a graphic representation of the parent divergence (Cruz and Regazzi, 1997). The genetics and statistics analyses were done by the Genes Program. This program was developed in the UFV by Cruz (1997).

Results and discussion

The genetic distances between genotypes were obtained by the Mahalanobis multivariate analysis and genetically high divergent parental to crosses were selected. The 104 soybean genotypes used in the experiment are listed in Table 1 and the means of the analyzed agronomic traits are showed in Table 2.

Table 1. List of the analyzed soybean genotypes. Londrina, PR, Brazil

Adapted soybean genotypes:			
1 BR-27	3 IAC-12	5 DOKO PRETA	7 PARANÁ MARROM
2 EMBRAPA-4	4 IAC-100	6 DAVIS MARROM	8 IAC-4 MARROM
Food type soybean genotypes, with large seeds:			
09 DELSTA	31 F83-7959	53 NANDA	75 NIMAME
10 FAZ.PROGRESSO	32 F83-7977	54 PI-133.226	76 PI-80.441
11 F80-3309	33 F83-7999	55 PI-157.440	77 PI-91.725-3
12 F80-6717	34 F83-8000	56 PI-423.909	78 PI-165.672
13 F80-6933	35 F83-8012	57 SOJA FEIRA 86-13	79 PI-165.676
14 F81-9136	36 F83-8017	58 SOJA FEIRA 86-14	80 PI-229.320
15 F82-5628	37 F83-8058P	59 ALIANÇA PRETA	81 PI-230.977
16 F82-5630	38 F83-8117	60 ARAÇATUBA	82 PI-230.977/S
17 F82-5721	39 F83-8119	61 BILOXI 252n	83 PI-243.514
18 F82-5722^A	40 F83-8175	62 CHEROKEE	84 PL-1
19 F82-5722P	41 F83-8185	63 FC 31-665	85 PLUTO
20 F82-5767	42 F83-8192	64 HAMPTON	86 STWART
21 F82-5769	43 F83-8203P	65 HOGYOKU	87 TADACHA
22 F82-5782	44 F83-8207AB	66 IVAI	88 TAMBA
23 F82-5783	45 F83-8211	67 JAPÃO-1	89 TARHEEL BLACK
24 F82-5803	46 F83-8240	68 JAPÃO-2	90 TMV
25 F82-5812	47 F85-11346	69 KS#3xAKIYOSHI-F7-2	91 TK#5xUNKNOWN-F7
26 F82-5813	48 KANRICH	70 KS473 x SJ2-F7	92 TN#4xPI-230970 F7-1
27 F83-8202	49 KANRO	71 KURAKAKE	93 TN#4xPI-230970 F7-4
28 F83-7843	50 L81-4590	72 MAJÓS	94 YAMAGATAKEN
29 F83-7864	51 LATE GIANT	73 MAMMOTH YELLOW	95 WOLVERINE
30 F83-7931	52 MENDOTA	74 MIYASHIPOKEN	96 64.64 x KS473
Food type soybean genotypes, with small seeds:			
97 EASYCOOK	100 EASYCOOK PRETA	103 IMPERIAL	
98 EASYCOOK MARROM 4	101 ALIANÇA PRETA/SEL.	104 PI-80.459	
99 EASYCOOK MARROM 4-A	102 IAC STA.MARIA-702		

Table 2. Average of 12 quantitative characters of 104 soybean genotypes with grouping mean test of Scott & Knott (1974). Londrina, PR, Brazil

N.	NDF	NDM	RP	%RP	PHF	PHM	NIM	HSW	IPP	AV	RG	%RG
1	73.6 C	166.0 B	92.4 D	55.6 F	83.8 C	103.3 E	21.5 D	22.5 E	68.6 B	3.56 B	19.5 E	19.0 G
2	50.7 H	137.3 H	86.7 E	63.1 C	41.9 H	54.4 I	15.3 G	20.9 F	75.2 B	2.36 E	12.5 F	22.9 F
3	56.1 G	140.5 H	84.4 E	60.1 D	49.9 G	63.9 I	18.1 F	14.1 G	81.1 A	2.86 D	13.9 F	21.8 F
4	58.9 F	133.0 I	74.1 G	55.7 F	39.1 H	58.9 I	17.4 F	11.8 H	61.8 B	2.58 E	19.8 E	33.4 E
5	84.6 A	162.6 C	78.0 F	48.0 H	97.9 A	100.9 E	22.2 D	16.0 G	47.0 C	3.18 C	3.04 H	2.98 I
6	53.1 G	141.3 G	88.2 D	62.3 D	38.3 H	46.3 J	15.0 G	19.1 F	91.0 A	2.46 E	7.97 G	17.3 G
7	49.0 I	119.7 K	70.7 G	59.0 E	38.2 H	47.9 J	14.2 G	16.5 G	60.4 B	2.12 F	9.73 G	20.3 F
8	70.4 D	157.8 D	87.4 D	55.3 F	64.6 E	74.6 H	20.3 E	14.7 G	66.4 B	2.84 D	10.0 G	13.3 H
9	55.4 G	146.4 F	91.0 D	62.2 D	38.4 H	48.6 J	15.9 F	31.0 C	74.5 B	2.33 F	10.2 G	21.0 F
10	77.1 B	167.1 B	90.0 D	53.8 G	75.3 D	82.5 G	23.7 D	30.2 D	99.5 A	3.51 B	7.23 G	8.71 H
11	51.2 H	150.2 F	99.0 B	65.9 B	38.3 H	45.9 J	13.3 H	24.1 E	49.5 C	2.39 E	7.64 G	16.7 G
12	64.2 E	168.3 B	104.1 B	61.9 D	63.0 E	72.6 H	16.2 F	32.1 C	77.7 B	3.17 C	9.66 G	13.3 H
13	45.4 J	136.4 H	91.0 D	66.7 A	34.2 I	38.3 K	11.3 H	36.2 B	66.5 B	2.07 F	4.07 H	10.7 H
14	50.8 H	158.3 D	107.5 A	67.9 A	37.0 H	49.8 J	14.4 G	34.1 C	70.4 B	2.29 F	12.8 F	25.6 F
15	53.9 G	154.9 E	101.0 B	65.2 B	42.7 H	58.2 I	16.0 F	34.5 C	55.4 C	2.70 D	15.5 F	26.3 F
16	50.8 H	157.7 D	106.9 A	67.8 A	34.6 I	46.9 J	13.7 H	35.8 B	40.7 C	2.12 F	12.3 G	26.4 F
17	52.5 H	153.5 E	101.0 B	65.7 B	41.4 H	49.3 J	13.9 G	34.3 C	83.8 A	2.48 E	7.86 G	16.0 G
18	47.8 I	157.3 D	109.5 A	69.4 A	46.0 G	59.8 I	16.4 F	38.9 B	88.5 A	2.83 D	13.8 F	23.1 F
19	57.6 F	157.0 D	99.4 B	63.3 C	46.7 G	60.1 I	16.0 F	42.0 A	90.9 A	2.91 D	13.3 F	22.0 F
20	52.1 H	154.1 E	102.0 B	66.2 B	40.0 H	42.3 K	11.9 H	42.8 A	71.2 B	2.29 F	2.34 H	5.29 I
21	52.0 H	152.1 E	100.1 B	65.8 B	40.7 H	51.2 J	14.7 G	36.9 B	92.4 A	2.52 E	10.5 G	20.4 F
22	58.1 F	149.5 F	91.4 D	61.2 D	49.4 G	64.1 I	17.1 F	38.3 B	112.3A	2.70 D	14.7 F	23.0 F
23	48.8 I	152.8 E	104.0 B	68.1 A	26.6 I	35.2 L	12.5 H	36.5 B	67.2 B	1.98 G	8.52 G	22.1 F
24	53.5 G	152.3 E	98.8 B	64.9 B	39.3 H	48.3 J	14.0 G	33.2 C	91.0 A	2.56 E	8.98 G	18.5 G
25	50.3 H	153.2 E	102.9 B	67.2 A	34.2 I	40.9 K	12.5 H	35.4 B	67.3 B	2.19 F	6.66 G	15.8 G
26	50.1 H	145.3 G	95.1 C	65.5 B	33.3 I	41.7 K	14.2 G	29.4 D	90.0 A	2.40 E	8.35 G	20.0 F
27	62.2 E	165.0 B	102.8 B	62.3 D	59.4 F	88.9 F	20.9 E	30.1 D	79.6 B	3.23 C	29.6 D	33.2 E
28	54.1 G	151.1 E	97.0 B	64.2 C	41.8 H	50.4 J	15.4 G	31.3 C	84.5 A	2.53 E	8.58 G	16.9 G
29	54.4 G	157.5 D	103.1 B	65.4 B	42.4 H	50.0 J	15.0 G	33.0 C	58.3 C	2.25 F	7.55 G	15.1 G
30	44.4 J	136.5 H	92.1 D	67.5 A	28.8 I	34.8 M	11.7 H	24.7 E	30.5 D	1.74 G	6.04 H	17.1 G
31	55.1 G	158.2 D	103.0 B	65.1 B	36.2 H	42.5 K	14.6 G	31.4 C	39.8 C	2.03 G	6.29 H	14.8 G
32	53.1 G	151.9 E	98.8 B	65.0 B	42.0 H	49.7 J	14.6 G	35.2 B	67.9 B	2.41 E	7.70 G	15.4 G
33	52.1 H	151.2 E	99.1 B	65.5 B	38.3 H	45.3 J	14.1 G	34.1 C	64.0 B	2.33 F	7.00 G	15.5 G
34	53.4 G	161.5 C	108.2 A	66.9 A	36.8 H	43.6 K	14.0 G	33.5 C	53.8 C	2.21 F	6.86 G	15.6 G
35	70.3 D	166.7 B	96.4 C	57.8 E	78.6 C	96.6 E	23.6 D	37.0 B	103.5A	3.71 A	18.0 F	18.5 G
36	55.9 G	147.8 F	91.9 D	62.2 D	51.5 G	65.7 H	17.6 F	36.4 B	83.0 A	2.89 D	14.1 F	21.5 F
37	49.4 I	148.3 F	99.8 B	67.2 A	34.0 I	39.4 K	13.2 H	36.5 B	76.0 B	2.32 F	5.44 H	14.2 H
38	78.4 B	172.8 A	94.4 C	54.6 G	83.7 C	89.2 F	19.1 E	42.3 A	69.8 B	3.40 B	5.41 H	6.07 I
39	59.2 F	162.6 C	103.4 B	63.6 C	44.7 H	61.5 I	16.9 F	39.0 B	79.0 B	2.78 D	16.8 F	27.3 F
40	78.6 B	174.3 A	95.8 C	54.9 F	84.9 C	93.9 F	20.4 E	36.8 B	46.8 C	2.91 D	9.08 G	9.47 H
41	78.4 B	170.3 A	92.2 D	54.1 G	80.8 C	84.0 G	17.1 F	42.8 A	85.5 A	3.32 B	3.23 H	3.96 I
42	79.5 B	170.7 A	91.3 D	53.4 G	87.0 C	92.8 F	19.3 E	43.0 A	86.7 A	3.57 B	5.85 H	6.27 I
43	47.2 I	145.3 G	97.8 B	67.4 A	32.1 I	39.6 K	12.7 H	31.5 C	56.6 C	2.02 G	7.53 G	18.6 G
44	53.0 G	149.3 F	96.5 C	64.6 B	39.5 H	47.4 J	14.2 G	35.9 B	72.7 B	2.42 E	7.95 G	16.8 G
45	50.2 H	155.1 E	104.8 B	67.6 A	36.8 H	44.6 J	13.4 H	31.5 C	72.5 B	2.29 F	7.80 G	17.5 G
46	54.8 G	154.5 E	99.6 B	64.5 C	49.0 G	61.9 I	15.3 G	32.3 C	70.9 B	2.52 E	12.9 F	20.8 F
47	57.0 F	169.5 A	112.5 A	66.4 B	51.8 G	65.2 H	16.5 F	37.2 B	63.3 B	3.03 C	13.3 F	20.4 F
48	31.8 L	105.3 L	73.5 G	69.7 A	20.2 J	46.1 J	15.5 G	31.7 C	29.4 D	1.77 G	25.9 D	56.1 C
49	34.1 L	96.9 M	62.7 H	64.6 C	18.5 J	19.7 M	8.4 J	27.7 D	17.8 D	1.23 H	1.17 H	5.86 I
50	31.2 L	96.3 M	65.0 H	67.5 A	17.4 J	45.0 J	15.5 G	19.9 F	42.4 C	1.97 G	27.6 D	61.4 B
51	45.0 J	146.7 F	101.7 B	67.8 A	24.9 J	31.6 L	11.0 I	39.3 B	53.1 C	1.95 G	6.77 G	21.5 F
52	32.3 L	96.5 M	64.2 H	66.5 B	14.6 J	26.1 M	11.4 H	22.5 E	24.7 D	1.36 H	11.4 G	43.0 D
53	53.0 G	140.0 H	86.5 E	61.8 D	38.2 H	52.0 I	14.8 G	23.1 E	36.1 D	2.17 F	13.8 F	25.7 F
54	72.6 C	150.8 E	78.2 F	51.8 G	100 A	116.0 D	22.2 D	19.8 F	55.2 C	2.97 D	16.1 F	13.9 H
55	47.6 I	120.7 K	72.0 G	59.6 D	37.6 H	40.3 K	12.1 H	21.6 F	57.9 C	1.94 G	2.66 H	6.52 I
56	59.8 F	153.8 E	94.1 C	61.2 D	52.2 G	109.2 D	26.8 C	31.8 C	60.8 B	3.52 B	57.0 B	52.2 C
57	47.8 I	138.0 H	90.2 D	65.3 B	30.8 I	85.4 G	20.5 E	37.8 B	70.5 B	2.44 E	54.7 B	64.0 B
58	72.5 C	155.5 D	83.0 E	53.4 G	80.8 C	86.4 G	22.3 D	28.1 D	61.7 B	3.11 C	5.68 H	6.53 I
59	69.8 D	161.0 C	93.0 D	57.8 E	79.6 C	98.7 E	21.3 D	32.7 C	37.9 D	3.17 C	19.2 E	19.4 G
60	73.7 C	153.3 E	79.6 F	51.9 G	81.6 C	137.1 B	28.8 B	23.9 E	62.7 B	3.62 A	55.5 B	40.5 D
61	73.5 C	150.0 F	76.5 F	51.0 H	73.6 D	126.1 C	30.4 B	21.4 F	47.5 C	3.22 C	52.5 B	41.5 D
62	69.3 D	151.9 E	82.6 E	54.3 G	57.7 F	82.1 G	22.6 D	29.1 D	49.0 C	2.90 D	24.4 D	29.7 E
63	44.6 J	117.3 K	72.7 G	62.0 D	29.0 I	35.0 L	13.1 H	31.9 C	58.4 C	1.88 G	5.97 H	17.0 G
64	48.9 I	143.7 G	94.7 C	65.9 B	37.5 H	39.2 K	13.9 G	31.0 C	60.0 B	2.03 G	1.72 H	4.35 I
65	53.4 G	153.7 E	100.3B	65.2 B	39.6 H	47.1 J	16.2 F	25.5 E	36.5 D	2.08 F	7.50 G	15.8 G
66	53.6 G	141.6 G	88.0 D	62.1 D	47.3 G	60.8 I	17.0 F	24.4 E	74.6 B	2.54 E	13.5 F	22.1 F
67	38.2 K	105.7 L	67.5 H	63.8 C	21.3 J	24.3 M	10.1 I	33.5 C	24.4 D	1.37 H	3.01 H	12.2 H

Continua

Continuação

68	43.9 J	124.0 J	80.1 F	64.5 C	31.0 I	38.2 K	12.1 H	36.1 B	47.1 C	1.77 G	7.24 G	17.5 G
69	52.2 H	124.3 J	72.1 G	58.0 E	38.6 H	43.5 K	13.6 H	27.7 D	42.2 C	1.83 G	4.85 H	11.1 H
70	57.0 F	135.4 H	78.4 F	57.8 E	48.3 G	59.4 I	16.6 F	24.1 E	45.4 C	2.33 F	11.1 G	18.5 G
71	38.0 K	106.0 L	68.0 H	64.1 C	23.3 J	24.9 M	10.7 I	32.4 C	23.1 D	1.38 H	1.55 H	6.27 I
72	51.9 H	145.0 G	93.0 D	64.2 C	40.1 H	45.3 J	15.3 G	35.8 B	97.3 A	2.46 E	5.19 H	11.5 H
73	48.3 I	117.8 K	69.2 G	59.0 E	35.7 H	38.1 K	12.8 H	28.2 D	41.9 C	1.75 G	2.35 H	6.20 I
74	45.2 J	121.7 J	76.6 F	62.9 C	32.7 I	38.8 K	12.3 H	32.5 C	43.3 C	1.83 G	6.16 H	15.8 G
75	34.4 L	109.1 L	74.7 G	68.4 A	28.5 I	32.5 L	10.3 I	34.5 C	28.5 D	1.47 H	4.01 H	11.6 H
76	34.4 L	105.4 L	70.9 G	67.1 A	19.3 J	20.0 M	8.9 J	29.6 D	13.4 D	1.07 H	0.78 H	3.69 I
77	57.8 F	138.9 H	81.0 F	58.2 E	48.4 G	59.2 I	16.8 F	26.4 E	32.0 D	2.38 E	10.8 G	18.4 G
78	49.6 I	118.9 K	69.4 G	58.3 E	45.6 G	66.8 H	16.0 F	33.1 C	55.2 C	2.51 E	21.2 E	31.5 E
79	53.8 G	144.5 G	90.6 D	62.7 D	39.6 H	59.2 I	16.7 F	33.0 C	44.7 C	2.37 E	19.6 E	33.0 E
80	46.9 I	118.9 K	71.9 G	60.5 D	33.1 I	36.6 L	11.8 H	26.8 E	50.1 C	1.76 G	3.53 H	9.51 H
81	47.0 I	131.1 I	84.1 E	64.1 C	26.8 I	30.1 L	12.3 H	40.1 A	68.0 B	1.96 G	3.22 H	10.6 H
82	53.3 G	145.8 G	92.5 D	63.5 C	43.1 H	68.2 H	17.7 F	36.5 B	45.0 C	2.52 E	25.1 D	36.6 D
83	42.9 J	120.3 K	77.3 F	64.3 C	24.9 J	28.2 M	11.8 H	31.2 C	56.3 C	1.62 G	3.35 H	11.3 H
84	70.6 D	150.3 E	79.7 F	53.0 G	75.4 D	87.6 G	21.4 D	29.3 D	68.5 B	3.05 C	12.2 G	14.0 H
85	44.8 J	117.7 K	73.0 G	62.0 D	35.5 H	40.9 K	12.8 H	23.4 E	37.8 D	1.80 G	5.47 H	13.3 H
86	63.0 E	152.7 E	89.7 D	58.7 E	71.2 D	93.9 F	22.2 D	19.7 F	85.7 A	3.49 B	22.7 E	24.1 F
87	41.7 J	112.0 L	70.3 G	62.6 D	25.0 J	27.6 M	10.4 I	26.6 E	18.6 D	1.39 H	2.62 H	9.61 H
88	56.5 F	153.2 E	96.7 B	63.1 C	50.9 G	75.1 H	20.2 E	27.3 D	51.5 C	2.58 E	24.2 D	31.9 E
89	47.4 I	130.9 I	83.5 E	63.8 C	37.7 H	41.8 K	13.1 H	36.7 B	57.4 C	2.06 F	4.02 H	9.65 H
90	72.5 C	153.1 E	80.6 F	52.6 G	85.4 C	91.8 F	21.8 D	25.6 E	100.3A	3.41 B	6.36 H	6.87 I
91	49.6 I	128.7 I	79.1 F	61.4 D	42.4 H	64.8 H	16.6 F	34.2 C	42.4 C	2.46 E	22.5 E	34.6 E
92	61.0 F	153.7 E	92.6 D	60.3 D	68.3 E	81.8 G	18.0 F	23.9 E	46.2 C	2.60 E	13.5 F	16.4 G
93	54.4 G	139.9 H	85.6 E	61.1 D	45.3 G	55.7 I	15.4 G	28.1 D	35.4 D	2.00 G	10.4 G	18.7 G
94	44.1 J	123.6 J	79.5 F	64.3 C	29.7 I	33.8 L	12.0 H	31.9 C	61.3 B	1.85 G	4.14 H	12.2 H
95	44.0 J	116.8 K	72.8 G	62.3 D	26.5 I	31.5 L	11.9 H	23.8 E	52.8 C	1.72 G	5.02 H	15.7 G
96	52.2 H	138.8 H	86.6 E	62.4 D	49.9 G	59.6 I	15.6 G	23.6 E	56.3 C	2.22 F	9.69 G	16.1 G
97	40.3 J	126.6 I	86.4 E	68.2 A	23.0 J	90.6 F	22.1 D	18.4 F	69.3 B	2.23 F	67.6 A	74.5 A
98	73.5 C	148.0 F	74.5 G	50.3 H	90.6 B	147.1 A	29.4 B	15.7 G	65.0 B	2.99 D	56.5 B	38.1 D
99	69.2 D	148.8 F	79.6 F	53.5 G	85.0 C	149.7 A	28.2 C	17.9 G	71.0 B	3.22 C	64.7 A	43.2 D
100	75.4 B	150.9 E	75.5 G	50.0 H	105 A	157.9 A	29.9 B	15.4 G	69.8 B	3.28 B	52.7 B	32.9 E
101	82.2 A	162.0 C	79.9 F	49.3 H	1022 A	152.7 A	33.3 A	12.0 H	68.7 B	3.84 A	50.4 B	33.0 E
102	82.3 A	161.6 C	79.3 F	49.0 H	1004 A	142.0 B	32.8 A	10.8 H	61.8 B	3.78 A	41.5 C	29.3 E
103	68.5 D	141.2 G	72.8 G	51.5 H	55.3 F	72.0 H	22.1 D	8.96 I	57.0 C	2.43 E	16.7 F	23.1 F
104	65.9 E	142.6 G	76.7 F	53.8 G	51.2 G	72.2 H	22.1 D	7.97 I	53.3 C	2.51 E	20.9 E	29.2 E

[1] Means with different letters differ at 1% level of probability

Table 3. Summary of variance analysis of 12 agronomic traits and their respective averages, coefficient of variance (CV) and coefficient of genotypic determination (H^2_g). Londrina, PR, Brazil

Sources of		Mean Squares											
Variation	Df	NDF	NDM	RP	%RP	PHF	PHM	NIM	HSW	IPP	AV	RG	%RG
Blocks	3	8.17	38.33	45.33	6.21	77.10	200.3	3.60	68.97	1399.6	0.28	41.77	48.76
Treat.**	103	606.4	1380.9	593.7	119.8	1908.0	3833.8	109.6	264.4	1674.5	1.55	889.9	690.9
Error	309	5.98	11.88	16.24	3.28	21.02	34.92	1.15	4.10	256.19	0.04	14.79	24.30
Average		55.56	143.19	87.64	61.38	48.19	62.88	16.85	29.07	60.67	2.47	14.69	20.86
CV(%)		4.40	2.41	4.60	2.95	9.51	9.40	6.37	6.96	26.38	8.57	26.18	23.63
H^2_g(%)		99.01	99.14	97.26	97.25	98.90	99.09	98.95	98.45	84.70	97.12	98.34	96.48

** indicate significance at 1 % level of probability for all traits

Table 4. Food and grain type soybean genotypes clusters through Tocher's grouping method based on Mahalanobis generalized distances (D^2). Londrina, PR, Brazil

Cluster	Genotypes													
I	32,	44,	33,	21,	17,	24,	25,	37,	28,	45,	29,	14,	46,	15,
	16,	23,	34,	31,	43,	09,	72,	26,	64,	18,	79,	22,	36,	65,
	93,	11,	39,	19,	20,	82,	53,	88,	77,	66,	13,	96,	70,	51,
	89,	30,	02,	47,	92,	69,	81,	91,	06,	94,	27,	74,	68,	80,
	73,	55,	83,	63,	78,	85,	95,	62,	84,	07,	03,	12,	86,	04.
II	67,	71,	76,	49,	75,	87,	52,	48,	50.					
III	38,	42,	41,	40,	59,	35,	58,	10,	90,	1,	54,	5,	8.	
IV	103,	104												
V	101,	102	100,	98,	99,	60,	61.							
VI	56,	57.												
VII	97.													

Maximum distance D^2 = 1,215.10 between genotypes 41 and 50; Minimum distance D^2 = 1.07 between genotypes 32 and 44

The analysis of variance showed significant differences ($P<0.01$) among parent means for all analyzed traits (Table 3). The estimations of the coefficient of genotypic determination (H^2_g) varied from 84.7% for individual plant productivity (IPP) to 99.1% for number of days to maturity (NDM) (Table 3). This shows a favorable situation for food type soybean improvement and suggests a possibility for a reasonably efficient discrimination among parents, with a superior genotype constitution in the analyzed genotypes. The high values of H^2_g observed resulted from the large number of treatments used in this experiment (104 pure lines), from the extremely high genetic variability among genotypes and from the plot value used, which was the mean of the observed values for the plants in each plot.

Genetic divergence. The maximum distance between genotypes, as measured by D^2 values, were for F83-8185 and L81-4590, and the minimum distance were for F83-7977 and F83-8207AB (Table 4). Seven groups were formed using Tocher's method (Rao, 1952). A total of 70 genotypes belonged to group I, which corresponded to 67.31% of the treatments. In group II there were nine genotypes (8.65%), thirteen in group III (12.5%), two in group IV (1.92%), seven in group V (6.73%), two in group VI (1.92%) and only one genotype in group VII (0.96%).

Table 5 shows the averages of 12 agronomic traits within these seven groups. Group I had a high IPP (62.9 g/plant). The high RP value favored grain filling and increased the IPP. Group II had the lowest IPP (24.7 g/plant), as a consequence of the low PHF and NDF. The PHM and the NIM were also low, since they showed a determined growth type and, consequently, the lowest AV of the experiment. Group III presented the highest IPP (71.5 g/plant). The high PHF was due to the high NDF, which caused a high PHM and the highest NDM and AV. The HSW in this group was also high (an average of 30.1 g/100 seeds). Group IV differed from the others because of the low HSW (an average of 8.47 g/100 seeds) for Imperial and PI-80.459 genotypes. In group V the NDF, NDM, PHF, PHM, NIM, RG, %RG, IPP and AV traits were all high, with an HSW mean of 16.7 g/100 seeds. Group VI showed a low PHF and a high PHM, which led to a high RG and %RG, indicating an undetermined growth type and a high HSW (a mean of 34.8 g/100 seeds) for PI-423909 and *Soja Feira* 86-13 genotypes. Group VII was formed by a single genotype, the Easycook, which showed a low NDF and PHF, different from group V. It also showed a high PHM, causing higher RG and %RG, indicating an undetermined growth habit, but with an HSW of 18.4 g/100 seeds, differing from group VI. As for quantification of genetic divergence through the analysis of canonical variables, the first two variables retained 73.24% of the total available variability. This value was considered near to adequate to represent the total variability in bi-dimensional graphics according to Cruz (1990) and Cruz and Regazzi (1997). Figure 1 shows the score graphic of the first two canonical variables and the representation of the seven groups formed by Tocher's method.

Relative contribution of the traits to the genetic divergence among genotypes. The PHM was the trait that most contributed to the classification of the 104 genotypes into seven groups, with 22.35% (Table 6). When the PHM contribution was added with the PHF(19.50%), RG(12.67%), NIM (4.69%) and with the %RG (0.53%) contributions, a total of 59.74% was obtained for traits related to plant development. Other important contributions for the identification of genetic divergence were RP (15.49%), NDF (11.25%) and HSW (9.27%). The %RP and %RG characters contributed in smaller proportion to genetic divergence (0.95% and 0.53%, respectively).

Table 5. Average within groups of 12 agronomic characters in 104 soybean genotypes. Londrina, PR, Brazil

	Quantitative Characters											
Cluster	NDF	NDM	RP	%RP	PHF	PHM	NIM	HSW	IPP	AV	RG	%RG
I	52.4	143.5	91.0	63.3	41.3	51.7	15.0	30.7	62.9	2.34	10.4	18.9
II	35.1	103.7	68.5	66.0	20.9	29.6	11.2	28.7	24.7	1.45	8.68	23.3
III	75.3	163.8	88.7	54.1	83.2	93.1	21.1	30.1	71.5	3.28	9.90	10.4
IV	67.2	141.9	74.8	52.6	53.3	72.1	22.1	8.47	55.2	2.47	18.8	26.1
V	75.7	153.5	77.8	50.7	91.2	144.6	30.4	16.7	63.8	3.42	53.4	36.9
VI	53.8	145.9	92.2	63.3	41.5	97.3	23.6	34.8	65.6	2.98	55.8	58.1
VII	40.3	126.6	86.4	68.2	23.0	90.6	22.1	18.4	69.3	2.23	67.6	74.5

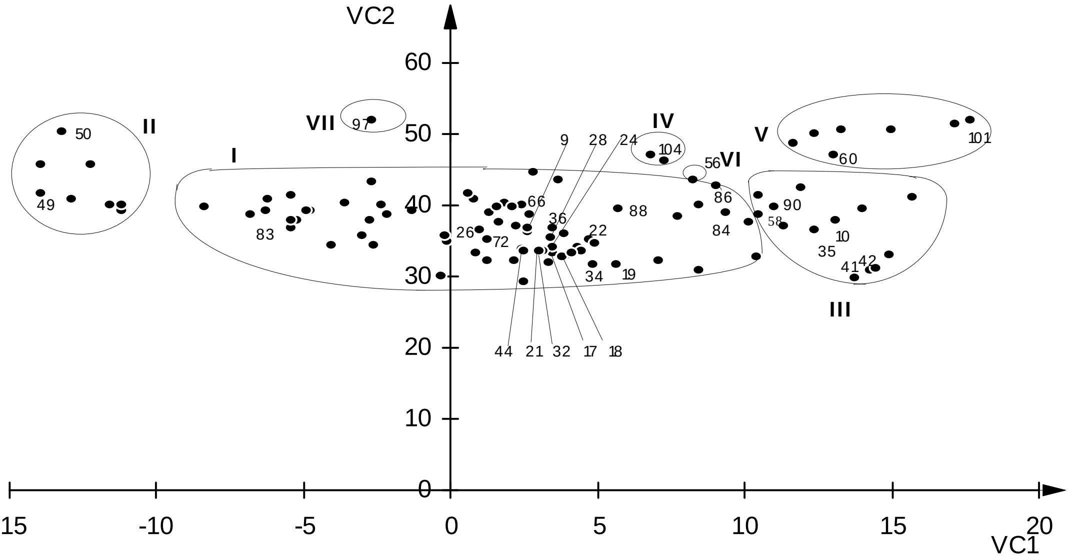

Figure 1. Score graphic of food type soybean genotypes related to the first two canonical variables (VC_1 and VC_2) and representation of the seven analyzed groups. Londrina, PR, Brazil

Table 6. Relative contribution of agronomic characters to the classification of 104 food type soybean genotypes into seven groups by Tocher's method. Londrina, PR, Brazil (Singh, 1981)

Character		Contribution (%)
NDF	Number of days to flowering	11.25
NDM	Number of days to maturity	1.45
RP	Reproductive period	15.49
%PR	Reproductive period percentage	0.95
PHF	Plant height (cm) at the beginning of flowering	19.50
PHM	Plant height (cm) at maturity	22.35
NIM	Number of internodes during maturity	4.69
HSW	A hundred seeds weight (g)	9.27
IPP	Individual plant productivity (g)	0.88
AV	Agronomic value	0.97
RG	Reproductive growth after flowering	12.67
%RG	Reproductive growth percentage	0.53

Annappan *et al.* (1989), while analyzing genetic divergence in 40 geographically divergent soybean genotypes, observed that the weight of 100 seeds (50.64%) and the plant height (20.76%) were the most important traits for divergence evaluation. Destro (1991), however, observed that NDF contributed most to the genetic divergence in 46 grain and food type soybean genotypes. These contradictory results may be explained by the different sowing periods of the experiments or by the different germplasms used. Shwe *et al.* (1972) while studying 16 soybean cultivars, based on D^2 statistics and canonical analysis, observed the traits which contributed most to differentiation and formation of five groups were the total number of nodes, determined by photosensitivity, and plant height.

Reduction in the amount of time and work, increased efficiency and genotypes in the offsprings are expected, when using the selection of parents through multivariate genetic divergence. Arunachalan (1981) studied the genetic distance applied to plant breeding and concluded that parents are genetically divergent when heterosis occurs, which does not mean that heterosis will occur when parents are divergent. Some of the reasons for this are: the inappropriate choice of trait number and nature, the wrong observation of environment influence on trait expression and unsatisfactory field experiment, and sample size for recording the trait values. The same was observed by Destro (1991) in a study with food type soybean lines. He reported that genetic divergence is a parameter that may not be used separately for parent selection for crosses, since high D^2 are not always associated with high productivity.

Some authors have indicated special procedures for autogamous plants, including soybean (Rangel *et al.*, 1991; Vello, 1992a; Destro, 1991). As a first step, one must carry out productivity tests for grain yield and some other agronomic traits, together with genetic divergence studies. This way, parents with satisfactory genetic divergence and superior agronomic development may be identified. A diallel analysis among the parents selected in the first step should be carried out, so those crosses would be performed only between divergent parents. Partial dialells (factorial or chain crosses) (Jensen, 1970) are more interesting for this procedure. Miranda *et al.* (1988) described the circulating chain crosses method for soybean, where for ‘p’ parents only ‘p’ crosses are necessary.

Estimated number of crosses. From 96 food type soybean genotypes, 16 parents, which presented an

'A' classification for IPP (Table 7), were selected from among 88 large seed soybean genotypes. There were 11 parents from cluster I and five from cluster III. As crosses among genotypes from different groups are recommended, only 55 crosses and their reciprocals should be carried out. The amount of work should be lower and more objective, when compared with the 120 possible crosses, plus the reciprocal ones, for the 16 selected genotypes [p = n x (n-1)/2], or the 4,560 possible crosses, plus the reciprocal ones, for the 96 studied genotypes. Therefore, the genotypes F82-5721, F82-5722A, F82-5722 *Preta*, F82-5769, F82-5782, F82-5803, F82-5813, F83-7843, F83-8017, *Majós* and Stwart, selected from cluster I, should be crossed with *Fazenda Progresso,* F83-8012, F83-8185, F83-8203P and TMV, selected from cluster III.

Table 7. Sixteen selected food type soybean parental genotypes to be crossed between cluster I and III, grouped by Tocher's method through the genetic distance multivariate technique. Londrina, PR, Brazil

Cluster		Genotype		Genotype		Genotype		Genotype
I	17-	F82-5721	21-	F82-5769	26-	F82-5813	72-	MAJÓS
	18-	F82-5722A	22-	F82-5782	28-	F83-7843	86-	STWART
	19-	F82-5722P	24-	F82-5803	36-	F83-8017		
III	35-	F83-8012	41-	F83-8185	42-	F83-8192	90-	TMV
	10-	FAZENDA PROGRESSO						

The study of genetic divergence through multivariate analysis is frequently applied in parent selection by researchers involved in breeding programs of several crops, leading to a reduction in the number of crosses. Singh e Ran (1985), studying genetic divergence in 40 new soybean lines plus 10 sample controls, suggested that only seven crosses should be made, among the 780 possible ones, by limiting the crosses between genetically divergent lines, with high productivity and resistance to yellow mosaic. Similarly, Rangel *et al.* (1991), with the multivariate analysis of 72 rice cultivars, obtained four groups using Tocher's method, based on Mahalanobis generalized distance. They recommend crosses among six cultivars from cluster I and seven from cluster II, selected for superior performance for grain yield per plot.

The multivariate analysis using Mahalanobis generalized distance (D^2) and Tocher's grouping method gives a chart where similarities and differences are confirmed and easily interpreted, when the work involves a great number of genotypes without genealogy knowledge and with high genetic variability. Groupings associated with agronomic important traits, especially yield, allow the selection of genetically divergent parents for programs in which hybridization is necessary. These increases the probability of having transgressive genotypes among descendants, saving time, work and costs.

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