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GENOTYPIC DIVERGENCE AMONG SUNFLOWER POPULATIONS[1]

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RESUMO

ESTUDO DA DIVERGÊNCIA GENOTÍPICA ENTRE POPULAÇÕES DE GIRASSOL

O objetivo deste estudo foi estimar a divergência genotípica entre dez populações de girassol, usando a estatística D^2 de Mahalanobis e variáveis canônicas para indicar grupos mais semelhantes e/ou divergentes e, assim, direcionar os cruzamentos nos programas de melhoramento. Foram conduzidos quatro experimentos, em duas épocas (junho/julho e fevereiro), em Goiânia e Goianésia, Estado de Goiás, nos anos de 1995 e 1996. Em todos os experimentos, utilizou-se o delineamento em blocos completos casualizados, com dez tratamentos e quatro repetições. Pelos resultados das análises de variância, verificou-se que existe grande variabilidade genotípica entre as populações, para todos os caracteres avaliados. Já pelas análises de divergência genotípica, dendrogramas e gráficos fornecidos pelos escores das variáveis canônicas, evidenciou-se que, nos quatro experimentos, as populações se agrupam de forma semelhante e de acordo com suas regiões de origem, na maioria dos casos. Ao se compararem os dois métodos, pode-se concluir que ambos conduzem a resultados semelhantes de agrupamento.

PALAVRAS-CHAVE: *Helianthus annuus L.*; agrupamentos; métodos de estimativa da divergência genotípica; Mahalanobis.

ABSTRACT

Genotypic divergence, among ten sunflower populations, was investigated, using the Mahalanobis' D^2 statistic analysis and canonic variables to identify more similar and/or divergent groups, and, thus, better direct crossings in breeding programs. Four experiments were carried out in two seasons (June/July and February), in two localities (Goiânia and Goianésia, Goiás State, Brazil), in 1995 and 1996. A randomized complete block design was used, with ten treatments and four replications. Variance analysis showed great genotypic variability among the four populations, for all traits assessed. The genotypic divergence analysis, dendrograms based on Mahalanobis' distance, and graphs supplied by the canonic variable scores showed that the populations grouped similarly and according to their regions of origin, for most cases. When the two genotypic divergence estimation methods were compared, it was concluded that both led to similar clustering results.

KEY-WORDS: *Helianthus annuus L.*; clusters; methods of genotypic divergence estimation; Mahalanobis.

INTRODUCTION

Sunflower breeders have tried to increase yield and have generally found a great amount of potential parent genotypes, among which only a limited number of crosses can be made to obtain new materials to start a selection program. The choice is generally based on a combination of data, including yield, visual observations of agronomic traits, pest and disease resistance and, more rarely, genealogy. Genetic investigations based on test crosses are usually expensive and, therefore, not common.

Studies on genetic divergence are important to guide breeding programs aiming to obtain hybrid cultivars, so that crosses are made among genetically divergent lines that have contrasting and complementary characteristics. Heterosis exploitation, using genetically different lines, would be an important aspect of sunflower breeding, because it is a predominantly cross pollination crop

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(Anand & Chandra 1979). It is generally assumed that a maximum use of the initial material can be obtained from crosses that release a maximum quantity of variation among parents that are genetically divergent (Vrânceanu & Stoenescu 1986).

Teklewold et al. (2000) studied 16 quantitative characters in 144 sunflower genotypes, at the University of Agricultural Sciences (UAS), Bangalore, India, to determine the extent of genetic divergence, using univariate and multivariate analyses. They confirmed the presence of significant differences among the genotypes and found out that Mahalanobis' D^2 statistics indicated the presence of substantial genetic diversity. Clustering of genotypes resulted in 7 and 14 clusters in the germplasm accessions and inbred lines, respectively. Some clusters were unique, having only a single genotype, while clusters with up to 55 genotypes were also formed.

Subrahmanyam et al. (2003) determined the extent of genetic divergence, with respect to eleven characters in 85 sunflower genotypes, using univariate and multivariate variance analysis, which revealed the presence of significant differences among the genotypes. Potential lines were identified for crossing programs. Amorim et al. (2007) studied twelve agronomic characteristics of fifteen sunflower genotypes, with the objective of developing new superior sunflower cultivars, using univariate and multivariate analyses, and identified three divergent sunflower genotypes clusters.

Thus, the objective of the present study was to investigate the genotypic divergence among ten sunflower populations, from morphological and agronomic variables of plant and grain that might guide the choice of parents for crossings in breeding programs for the crop.

MATERIAL AND METHODS

Ten open pollination populations, from several countries and from the germplasm bank of Embrapa Soybean (1995), in Londrina, Paraná State, Brazil, were used. The populations and their respective numbers, names, countries of origin and/or derivation are shown in Table 1.

Four experiments were carried out, during two seasons (June/July and February), in two localities (Goiânia and Goianésia, Goiás State, Brazil), in 1995 and 1996. Experiment 1 was installed on July 1995, in the experimental area of the Agronomy School, in Goiânia, Goiás State (16°41´S, 49°17´W, altitude 730 m, and Aw climate, according to the Köppen climate classification). The soil was the dark red latosoil type of the Goiânia mapping unit. Experiment 2 was installed in the same area, on February 1996.

Table 1. Relation of the populations used and their respective numbers, names, countries of origin and/or derivation.

Population	Name	Origin	Source
01	Majak	Yugoslavia	Beltsville-USA.
02	Armavirsky	USSR	VIR - Russian Federacy
03	Klein-A	Argentina	Maryland -USA
04	Comangir	Argentina	Fargo University -North Dakota - USA
05	Belenshy	USA	Fargo University -North Dakota-USA
06	Collihuay	-	FAO-Chile
07	Local-Blue	South Africa	Moçambique
08	6B x Ienissei	Russia	EERA-INTA-Argentina
09	Sundak	USA	Fargo University -North Dakota-USA
10	Guayacan	Argentina	CONTIBRAZIL

Source: Embrapa (1995).

Experiments 3 and 4 were installed in an experimental area of the Planagri S/A company, in Goianésia, Goiás State (15°18´S, 49°07´W, altitude 670 m, and the same climatic classification), belonging to the Mato Grosso-Goiás micro-region, 165 km from Goiânia. Experiment 3 was installed on February 1996 and experiment 4 on June 1996.

In all experiments, soil management was conventional and 350 kg ha^{-1} of the 4-30-16 + Zn NPK formula were used as planting fertilization and 400 kg ha^{-1} of urea were used as covering, 30 days after sowing. When necessary, the following cultural treatments were applied: manual weeding, combat to the black lizard (*Lacinia Chlosyne saundersii*), using pyrethroid (Decis) insecticide, and to sauba ant (*Atta* spp), using ant bait (Mirex).

A randomized complete block design was used in the four experiments, with ten treatments (population) and four replications, in a total of 40 plots per experiment. Each plot consisted of four 3.9 m rows, with 0.9 m inter-row spacing, and the spacing between holes was 0.3 m, with two to three seeds per hole, that were thinned to one plant per hill, or 13 plants per line, that corresponded to 37,000 plants per hectare. The total plot area was 14.04 m², but only the assessments of the two inner rows were used, comprising a useful area of 7.02m^2 and the rest served as border.

The following traits were assessed, according to recommendation by Embrapa/CNPSo (1991): initial flowering (IF), final flowering (FF), plant height (PH), stem diameter (SD), head diameter

(HD), head height (HH), weight of 1,000 seeds (WS), number of grains per head (NG), yield (YD), % moisture content (MC), and % oil content (OC).

The individual variance analyzes for the traits assessed were carried out according to the randomized complete block design. Joint analyses were also carried out in the experiments, for both seasons and both localities, thus obtaining information on the population-environment interaction in addition to the main effects.

The Mahalanobis' generalized distance was used as a measure of dissimilarity with standardized data, weighted by the residual covariance matrix (Cruz & Regazzi 1994). The agreement on the value of the Mahalanobis' D^2 statistic, among the different experiments, was ascertained by a matrix correlation coefficient, tested by the Mantel Z statistic (Manly 1991). The clustering analysis was performed from the dissimilarity matrix and the corresponding dendrogram constructed by using the nearest neighbor joining analysis method (Cruz & Regazzi 1994). The cutting point for cluster formation was established as the value corresponding to 60% of the largest distance in all the experiments, according to the discontinuity observed in the dendrogram.

Another procedure adopted was the canonic variable analysis, that consists of an alternative process to assess the degree of genotypic similarity among the populations, taking into consideration the phenotypic covariance matrixes and residual covariance among the traits. This technique has the advantage of maintaining the principle of the clustering process, based on the Mahalanobis' generalized distance, and takes into account the residual correlation among the traits. Analysis by canonic variables aimed to assess the similarity of the populations by graphic dispersion on cartesian axis. The most similar populations from the graphic analysis were clustered by inspection and the results compared with those obtained by the clustering process based on the Mahalanobis' generalized distance. The statistical genetic analyses were carried out using the Genes program (Cruz 1997).

RESULTS AND DISCUSSION

The results of the individual variance analyses pointed out significant differences for the initial flowering, final flowering, plant height, head height, oil percentage, moisture content, and yield, in all the experiments in which these traits were assessed. This indicated that there was great genetic variability among the populations, for those traits. The traits stem diameter, head diameter, weight of 1,000 seeds, and number of grains per head presented differences, which were sometimes significant, sometimes not, indicating that these traits show genotype-environment interaction. The significant differences, regarding grain moisture content, showed mainly that there were cycle differences among the populations, resulting in different moisture contents, when populations are harvested on the same date.

The experimental precision was generally considered good, because the variation coefficient values were within the acceptable range (approximately 20%) for sunflower experiments. Hassan (2001) corroborates this information, since most of the appraised characters is quantitative and highly influenced by environment.

The joint analyses of experiments 1; 2; 3; and 4 showed highly significant differences among populations and among environments, for most the variables common to the four experiments that confirmed expectations, because the experiments were conducted under very different environmental conditions. There was significant population-environment interaction for all traits, except for plant height, indicating that the populations did not alter their relative position, regarding this trait.

The joint variance analyses were carried out with the traits assessed in only three out of the four experiments, because, in the first experiment, some traits wouldn't be available due to a bird attack. The results show that interactions were highly significant for all the traits, indicating that there was differential environment influence on the relative performance of the populations.

Table 2 shows the estimates for distances, for all the populations' pairs, in the four experiments. Those estimates were obtained by using only the variables common to the four experiments, to certify the consistency of the data used in the calculation of the Mahalanobis' D^2 statistic. It was observed that, in general, the populations that were close in one experiment, that is, presented low values for the Mahalanobis' D^2 statistic, were close in the other experiments, while the populations which were distant, were also distant in the other experiments. Exceptions were found regarding experiment 3, that did not correlate with the other experiments (Table 2).

Table 2. Estimates of Mahalanobis' distances between genotypes: Experiment 1(Goiânia, Jul./1995), 2 (Goiânia, Feb./1996), 3 (Goianésia, Feb./1996), and 4 (Goianésia, Jun./1996), considering common variables for all experiments.

Populations	Experiment			
	1	2	3	4
01-02	127.79	72.29	30.65	44.84
01-03	35.60	14.70	40.29	3.42
01-04	44.51	50.18	23.23	46.43
01-05	114.56	67.79	21.10	26.39
01-06	36.90	24.03	67.37	4.20
01-07	36.17	23.17	60.88	12.20
01-08	3.06	12.44	14.54	2.91
01-09	36.13	37.20	46.16	13.86
01-10	38.73	26.40	4.98	12.93
02-03	257.80	130.61	127.09	65.28
02-04	313.57	161.95	23.71	155.36
02-05	3.69	12.23	4.25	4.48
02-06	257.92	123.06	180.87	51.08
02-07	270.69	79.79	161.06	91.83
02-08	154.44	86.90	12.16	66.49
02-09	35.77	7.94	4.36	10.61
02-10	295.87	135.72	29.53	86.45
03-04	10.53	21.09	107.18	33.46
03-05	249.71	137.87	115.19	40.78
03-06	3.90	7.89	9.22	2.04
03-07	0.95	20.93	3.60	4.99
03-08	26.54	14.50	90.75	3.27
03-09	106.10	81.23	164.56	24.18
03-10	6.73	6.94	51.50	5.64
04-05	296.76	194.16	14.47	123.45
04-06	12.13	8.06	142.28	43.04
04-07	6.53	15.97	138.10	13.50
04-08	30.39	18.66	18.25	30.13
04-09	144.56	119.85	28.35	89.19
04-10	1.00	7.99	16.52	15.38
05-06	245.23	143.80	161.47	30.53
05-07	261.46	103.89	149.93	64.90
05-08	139.64	101.89	9.92	44.53
05-09	35.58	15.46	5.77	4.56
05-10	279.29	151.87	18.80	58.76
06-07	6.37	8.23	6.73	9.05
06-08	25.11	10.35	123.82	7.87
06-09	108.84	81.58	221.52	15.58
06-10	7.22	6.50	77.23	10.17
07-08	27.05	7.18	166.28	6.59
07-09	114.79	52.89	203.36	40.96
07-10	4.14	12.31	75.10	2.74
08-09	48.22	54.98	20.57	26.53
08-10	26.35	12.12	12.98	7.47
09-10	132.98	92.65	41.76	38.43

According to the matrix correlation analysis (Table 3), performed to ascertain the existence of correlation among the Mahalanobis' generalized distances, in the four experiments, experiment 3 presented low and non-significant correlation coefficients by the Mantel test, when compared to the other experiments. The other pairs of experiments showed high and significant correlations, showing a good fit by the distances calculated based on their data. It is not uncommon to happen lack of correlation among data from experiments carried out in distinct environment conditions. Some researches show that the lack of correlation among genotypes averages (that is, genotypic value) constitutes the main cause of interaction between plant genotypes and environments. Table 4 shows the Mahalanobis' generalized distances values among the populations studied, considering all the variables assessed in each experiment. The distances between genotypes 1 and 8, and genotypes 3 and 8, were small in experiments 1 and 2 (carried out in Goiânia) and relatively large in the experiments carried out in Goianésia. Populations 1 and 10; 2 and 9; 3 and 10; and 4 and 7 were only similar in experiment 3. The distances among populations 2 and 5; 3 and 6; and 6 and 7 were small in experiments 1 and 3, and relatively large in experiments 2 and 4, indicating that, for some populations, the number of variables and/or the variables themselves, used in the calculation of the distances, must have been important. The magnitude of values gotten in these experiments is different, precisely because of the genotype x environment interaction.

The cluster analysis was carried out based on those results, using the Mahalanobis' generalized distances, calculated from the data of all the variables

Table 3. Matrix correlation coefficients of Mahalanobis' generalized distances for pairs of experiments.

Pair of experiments	Correlation coefficient (r)	p - value (%)[1]
1 and 2	0.9498	0.04
1 and 3	0.2267	11.70
1 and 4	0.8254	0.03
2 and 3	0.1359	21.73
2 and 4	0.8148	0.20
3 and 4	0.0244	41.30

[1] Probability to occur a higher or equal value to the calculated value, by Mantel test.

Table 4. Estimates of Mahalanobis' distances between genotypes: Experiment 1(Goiânia, Jul./1995), 2 (Goiânia, Feb./1996), 3 (Goianésia, Feb./1996), and 4 (Goianésia, Jun./1996), considering all variables for each experiment.

Populations	Experiment			
	1	2	3	4
01-02	127.78	82.45	36.53	139.21
01-03	35.60	17.40	60.06	88.40
01-04	44.51	65.06	73.42	189.20
01-05	114.56	87.96	30.34	39.23
01-06	36.90	34.86	82.53	37.35
01-07	36.17	28.37	82.03	118.81
01-08	3.06	15.63	28.89	36.83
01-09	36.13	76.32	57.05	244.45
01-10	38.73	33.73	13.46	137.99
02-03	257.80	136.21	149.54	89.21
02-04	313.57	168.90	73.55	207.09
02-05	3.69	19.04	8.90	95.58
02-06	257.92	164.70	207.11	69.40
02-07	270.69	82.79	190.48	142.98
02-08	154.44	99.85	24.13	129.90
02-09	35.77	23.08	6.55	58.68
02-10	295.87	153.40	41.86	110.68
03-04	10.53	26.06	191.60	50.52
03-05	249.71	147.99	129.79	141.50
03-06	3.90	28.20	12.76	25.96
03-07	0.95	23.15	6.90	14.08
03-08	26.55	16.57	120.41	48.18
03-09	106.10	109.37	185.02	99.49
03-10	6.73	11.52	62.27	11.11
04-05	296.77	199.90	86.57	268.28
04-06	12.13	50.50	225.43	99.82
04-07	6.53	22.96	207.83	22.25
04-08	30.39	28.84	38.09	86.65
04-09	114.56	142.17	74.45	176.79
04-10	1.00	19.14	66.11	25.49
05-06	245.23	199.60	180.38	62.10
05-07	261.46	109.14	173.81	186.78
05-08	139.65	115.95	29.02	73.66
05-09	35.59	21.58	14.40	247.21
05-10	279.29	166.13	27.21	195.19
06-07	6.37	37.66	9.81	52.86
06-08	25.11	24.88	156.26	28.10
06-09	108.84	169.19	249.26	125.09
06-10	7.22	24.67	88.67	50.48
07-08	27.05	11.79	142.62	49.54
07-09	114.79	68.95	230.05	134.88
07-10	4.14	19.53	85.26	13.53
08-09	48.22	89.12	30.56	188.84
08-10	26.35	12.97	21.86	70.46
09-10	132.98	127.79	55.42	87.82

of three experiments, except for experiment 3, that presented low and non-significant correlation coefficients by the Mantel test, when compared to the other experiments. The other pairs of experiments presented high and significant correlations, showing a good fit by the distances calculated based on their data.

This analysis led to the following clustering of the populations:

Group 1: Populations 10; 3; 7; 4; and 6 (Guayacan, Klein-A, Local Blue, Comangir and Collihuay, respectively);

Group 2: Populations 1 and 8 (Majak and 6B x Ienissei);

Group 3: Populations 9 and 2 (Sundak and Armavirsky);

Group 4: Population 5 (Belenshy) did not cluster with any other populations.

The clustering pattern of the populations corresponded generally to their geographic origin. Among the populations in group 1, three came from Argentina (Guaycan, Klein-A, and Comangir), while the two populations in group 2 came from neighboring regions: Kajak (Yugoslvia) and 6B x Ienissei (Russia). Only in group 3 there was no coincidence of the populations and their origin: Armavirsky (region of the old Soviet Union) and Sundak (USA). Group 4, formed by only one population, Belenshy (USA), naturally did not group with any of the other populations studied. Teklewold et al. (2000), however, found out that factors other than geographic origin seemed to be a potent source of genetic diversity.

A pertinent consideration is which crosses among the populations should be recommended, after this study, to obtain maximum heterosis to start a selection program. The variance analysis indicated highly significant differences among the populations, for most the traits assessed, revealing, therefore, that the material under study had enough diversity for parental populations to be chosen to start a breeding program. In this study, the largest distances were observed when population 2 was compared to populations 3; 6; 7; and 10; population 5 compared to populations 3; 4; 6; and 7; and population 9 compared to populations 3; 4; 6; and 10 (Table 4). The distances between populations 2; 5; and 9 were much smaller for most experiments, indicating that crossings of one of the populations 2 and 9 (group 3), or 5, with populations 3; 4; 6; 7; or 10 (group 1) would probably

generate higher heterosis and would, therefore, be the recommended crossings.

This recommendation makes sense when the means of experiments 2 and 3 are observed, planted in the dry season, that is, the season when sunflower is recommended for planting in the central region of Brazil. The means of these experiments showed that populations 2; 5; and 9 had a shorter cycle, shorter plant and head height (taller in other populations), presented high values for weight of 1,000 seeds (along with populations 3; 6; 8; and 10), and were among the most productive (along with populations 1 and 6). It was further observed that the performance *per se* of these populations was also good. Population 9 was among those that had the greatest head diameter (along with populations 1; 4; 6; 7; and 8), while populations 2 and 5 were among those presenting high oil content (along with populations 1; 6; 8; and 10). Subrahmanyam et al. (2003) show that the contribution of various characters towards the expression of genetic divergence should be taken into account as a selection criterion of parents for crossing programs.

The variables that have contributed the most to the genotypic divergence among the populations differed from one experiment to another: in experiment 1, initial flowering has contributed the most to the variance of the first canonic variables, while, in experiment 2, the initial flowering and head height have contributed the most to the variance of the first and second canonic variables, respectively. In experiment 3, where it seems to have been great population-environment interaction, the variables were number of grains per head and oil percentage, while, in experiment 4, grain yield and moisture content have contributed the most, representing, in this case, the cycle until harvest.

Subrahmanyam et al. (2003) point out that the characteristics number of filled seeds per head, test weight, kernel to hull ratio and seed yield per plant showed high contribution towards genetic divergence among the genotypes they investigated. Similar results were obtained by Amorin et al. (2007), whose studies about genetic diversity among fifteen sunflower genotypes, using twelve agronomic characteristics and univariate and multivariate (Mahalanobis' generalized distance) variance analyses, revealed that initial flowering, 50% flowering, number of leaves and head height were responsible for most of the genetic divergence observed among the genotypes.

A comparison among the Mahalanobis' generalized distances and canonic variables (Table 5) showed that the results were very similar, indicating that the methods were equivalent in determining genotypic divergence, that is, the use of only one of the methods would be sufficient to determine the similarity among the genotypes. Figures 5; 6; 7; and 8 also showed great agreement among the dendrograms shown in Figures 1; 2; 3; and 4, except for the wider dispersion present on population 6, as shown in Figures 2 and 6.

It can be further stated that the clustering based on the dendrogram was more objective, because of the algebraic calculated distances among the populations, while the clustering based on the canonic variables was more subjective, because it was based on a graphic inspection. An alternative for this procedure would be to calculate the distances based on scores, that would permit the elaboration of the respective dendrograms.

Table 5. Comparison among clusters formed from genetic analysis, using the D^2 Mahalanobis' statistics and the canonical variables analysis in all the experiments.

Experiments	Clusters	
	Mahalanobis' distances	Canonical variables
1 (Goiânia - Jul./1995)	(4; 10; 3; 6; and 7)*; (1 and 8); 9 and (5 and 2).	(4; 10; 3; 6; and 7); (1 and 8); 9 and (5 and 2).
2 (Goiânia - Feb./1996)	(10; 3; 7; 8; 1; 4; and 6) and (2; 5; and 9).	(10; 3; 7; 8; 1; 4; and 6) and (2; 5; and 9).
3 (Goianésia - Feb./1996)	(10; 1; and 8); 4; (3; 7; and 6) and (9; 2; and 5).	(10; 1; and 8); 4; (3; 7; and 6) and (9; 2; and 5).
4 (Goianésia - Jun./1996)	(10; 3; 7; 4; 6; 8; 1; 5; 9; and 2)	(10; 3; 7; 4; 6; 8; and 1); 5 and (9 and 2)

* The numbers in parenthesis refer to populations from the same cluster.

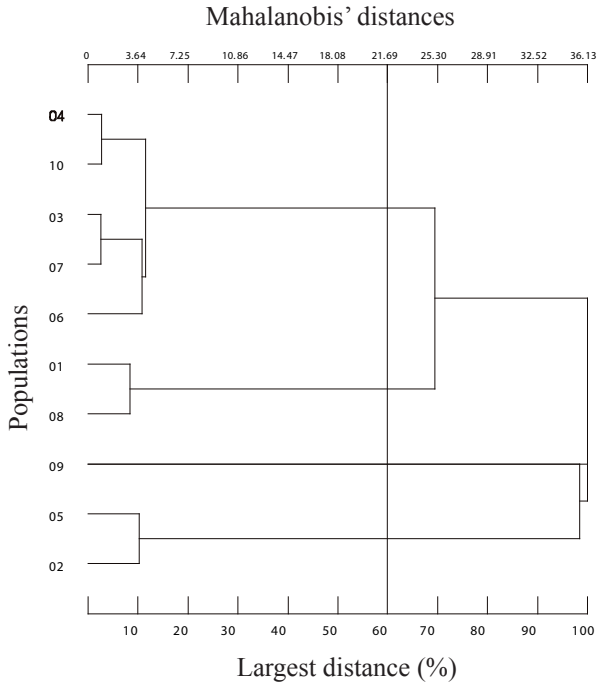

Figure 1. Illustrative dendrogram of similarity between ten populations, from the "next neighbor" method, based on Mahalanobis' generalized distances, corresponding to experiment 1 (Goiânia, Jul./1995).

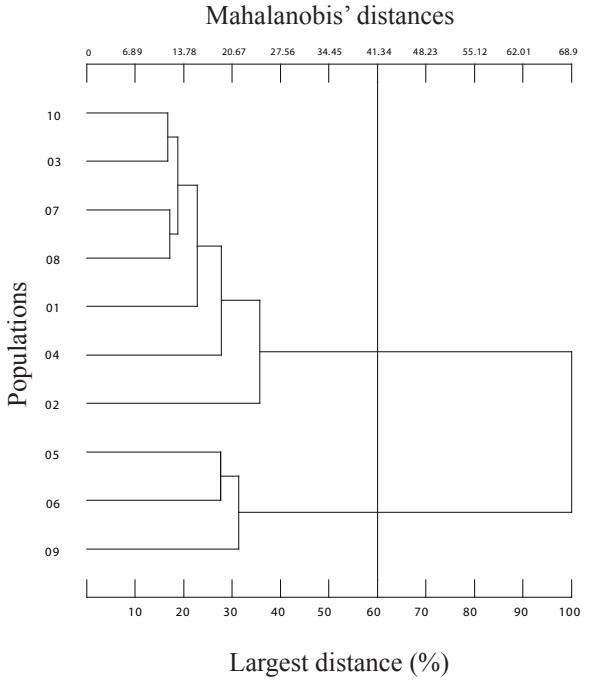

Figure 2. Illustrative dendrogram of similarity between ten populations, from the "next neighbor" method, based on Mahalanobis' generalized distances, corresponding to experiment 2 (Goiânia, Feb./1996).

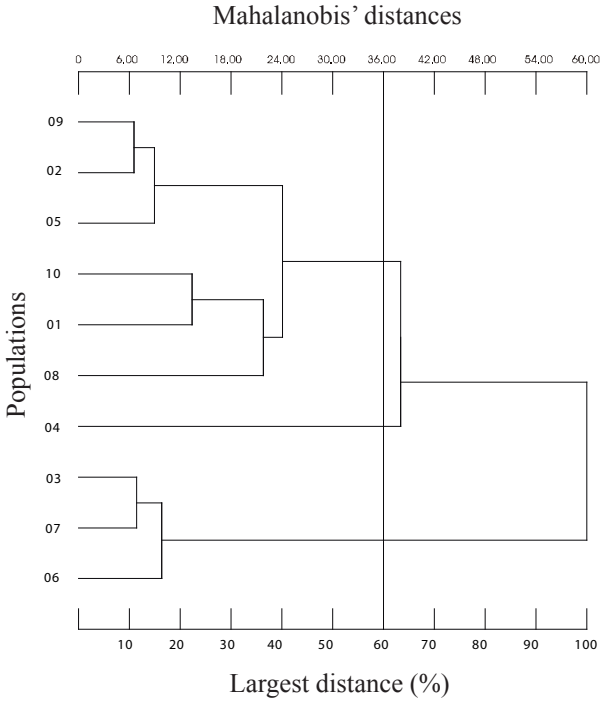

Figure 3. Illustrative dendrogram of similarity between ten populations, from the "next neighbor" method, based on Mahalanobis' generalized distances, corresponding to experiment 3 (Goianésia, Feb./1996).

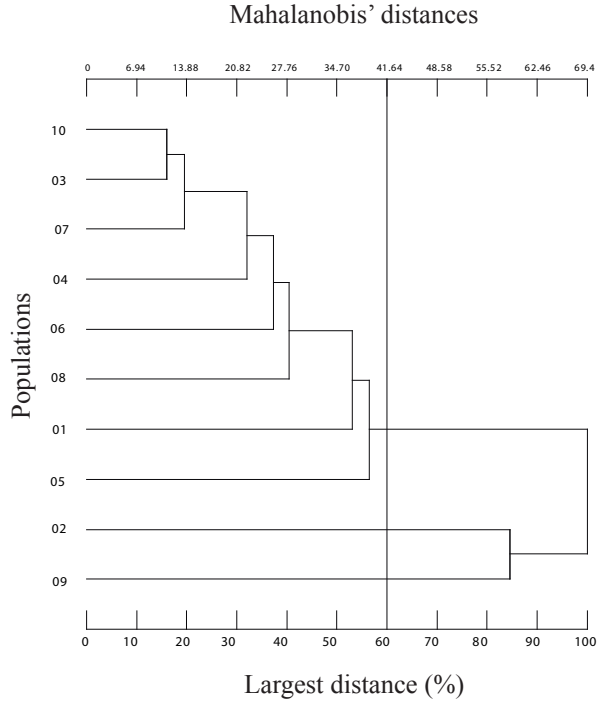

Figure 4. Illustrative dendrogram of similarity between ten populations, from the "next neighbor" method, based on Mahalanobis' generalized distances, corresponding to experiment 4 (Goianésia, Jun./1996).

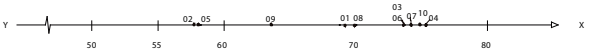

Figure 5. Dispersion of ten populations scores, in relation to the first canonical variables (CV 1), corresponding to experiment 1(Goiânia, Jul./1995).

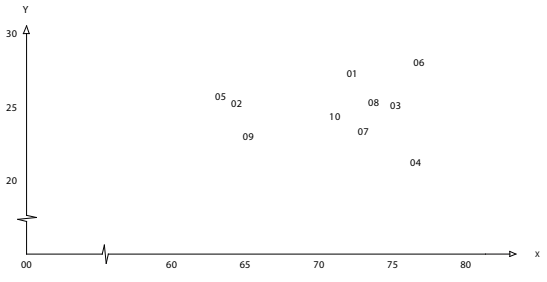

Figure 6. Dispersion of ten populations scores, in relation to the first two canonical variables (CV1 and CV2), corresponding to experiment 2 (Goiânia, Feb./1996).

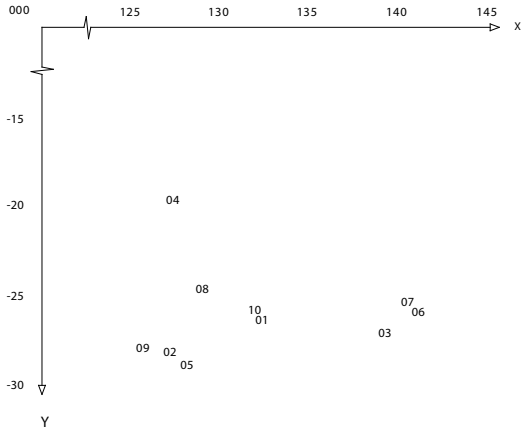

Figure 7. Dispersion of ten populations scores, in relation to the first two canonical variables (CV1 and CV2), corresponding to experiment 3 (Goianésia, Feb./1996).

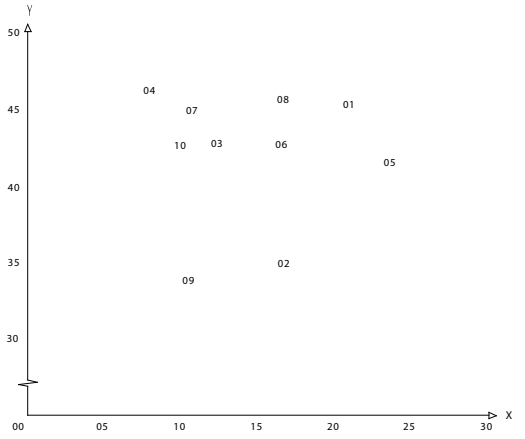

Figure 8. Dispersion of ten populations scores, in relation to the first two canonical variables (CV1 and CV2), corresponding to experiment 4 (Goianésia, Jun./1996).

CONCLUSIONS

1. The methods for estimating genotypic divergence in sunflower populations, from the Mahalanobis' generalized distance or canonic variables, are equivalent and both led to the same clustering results.
2. The populations studied are genotypically divergent.
3. The clustering pattern of the populations generally corresponds to their geographic origin.
4. The recommended crossings are between populations Armavirsky and Sundak (group 3), or Belenshy (group 4), with populations Klein-A, Comangir, Collihuay, Local Blue or Guayacan (group 1).

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REFERENCES

AMORIM, E. P. et al. Divergência genética em genótipos de girassol. *Ciência e Agrotecnologia*, Lavras, v. 31, n. 6, p. 1637-1644, 2007.

ANAND, I. J.; CHANDRA, S. Genetic diversity and interrelationships of oil yielding traits in sunflower. *Sunflower Newsletter*, Zevenaar, v. 3, n. 1, p. 5-8, 1979.

CRUZ, C. D. *Programa genes*: aplicativo computacional em genética e estatística. Viçosa: Ed. da UFV, 1997.

CRUZ, C. D.; REGAZZI, A. J. *Modelos biométricos aplicados ao melhoramento genético*. Viçosa: Ed. da UFV, 1994.

EMPRESA BRASILEIRA DE PESQUISA AGROPECUÁRIA (Embrapa). *Relação de genótipos do Banco Ativo de Germoplasma (BAG)*. Londrina: Embrapa Soja, 1995. (Não publicado).

HASSAN, S. W. *Heritability, genetic correlations and predicted gains from S1 families in two random mated sunflower populations*. 2001. 186 f. Thesis (Doctor of Philosophy)–University of the Punjab, Lahore, 2001.

MANLY, B. F. J. *Randomization and Monte Carlo methods in biology*. London: Chapman & Hall, 1991.

SUBRAHMANYAM, S. V. R.; KUMAR, S. S.; RANGANATHA, A. R. G. Genetic divergence for seed parameters in sunflower (*Helianthus annuus* L.). *Helia*, Novi Sad, v. 26, n. 38, p.73-80, 2003.

TEKLEWOLD, A.; JAYARAMAIAH, H.; GOWDA, J. Genetic divergence study in sunflower (*Helianthus annuus* L.). *Helia*, Novi Sad, v. 23, n. 32, p. 93-104, 2000.

VRÂNCEANU. A. V.; STOENESCU. F. M. Genetic resemblance of sunflower cultivars tested in international trials. *Helia*, Novi Sad, v. 8, n. 1, p. 9-16, 1986.