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Genetic divergence among sunflower genotypes based on morphoagronomic traits in Parana State

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This work aimed to evaluate the genetic divergence among 16 sunflower hybrids. Experiment was developed in Umuarama County, Parana State, Brazil, in 2010/2011 cropping season. Experimental design used was randomized complete block with four replications. The characteristics evaluated were: Final stand, plant height, chapter curvature, chapter size, grain yield, weight of 1000 achene's and oil content. Significant differences were detected for grain yield, chapter size and chapter curvature (1%). For final stand and oil content, significant differences (5%) was observed, suggesting that evaluated characters are important for genetic divergence characterization. Based on Mahalanobis Generalized Distance it was established that genetic dissimilarity measures, SULFOSOL and SYN 045 genotypes were the most dissimilar with $D^2_{ii'}$ of 134.54%. Clustering by Tocher method by using $D^2_{ii'}$ divided hybrids into two groups. Grain yield and chapter size contributed significantly in genetic divergence observed between hybrids and it was possible to identify divergent genetic materials for obtaining lines and/or formation of new populations.

Key words: Genetic variability, plant breeding, *Helianthus annuus* L., $D^2_{ii'}$ analysis.

INTRODUCTION

Cultivation of sunflower (*Helianthus annuus* L.) has proved to be a cost-effective option in rotations systems with other grain crops, and it is arousing the interest of farmers, agriculture professionals and companies, due to the possibility of using its oil as raw material for manufacturing biodiesel (Castro and Farias, 2005; Backes et al., 2008). In order to ensure the crop development, researches in genetic and breeding are being held for obtaining and evaluation of genotypes contemplating important aspects in the production process (Messetti and Padovani, 2004). According to Oliveira et al. (2005), efforts are needed for the

development of genotypes that presents, in the same genetic material, high oil content, early cycle, reduced height, resistance to biotic and abiotic factors, besides high grain yield.

The incorporation of these characteristics of interest depends on the existence of genetic variability in germplasm available for the crop breeding programs. From this variability, it is possible to implement the selection process for the most several characteristics, searching the development of lines for hybrids constitution or to obtaining varieties of open pollination (Amorim et al., 2007). According to Barelli (2004), studies on genetic divergence have great importance in crop breeding programs since reporting parameters for identifying parents that, when hybridized, offer greater heterosis effect in progeny and a higher probability of

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Table 1. Sunflowers genotypes used in the experiment, obtaining company and origin country (Umuarama, PR/2011).

Genotype	Obtaining company	Origin
M 734 (T)	Dow Agrosience	Argentina
HELIO 358 (T)	HELIAGRO	Brazil
HN 5218	Nidera	Brazil
PARAÍSO 65	Nidera	Brazil
HLA 44-49	HELIAGRO	Brazil
HLA 05-62	HELIAGRO	Brazil
HLA 44-63	HELIAGRO	Brazil
HLA 11-26	HELIAGRO	Brazil
V 60415	Advanta	Argentina
V 70153	Advanta	Argentina
QC 6730	Quality Crops	Argentina
SULFOSOL	Quality Crops	Argentina
SYN 034 A	Syngenta	Brazil
SYN 039 A	Syngenta	Brazil
SYN 042	Syngenta	Brazil
SYN 045	Syngenta	Brazil

superior genotypes recovery in segregating generations, as well as facilitate the knowledge of population genetic basis. Several works that evaluated the genetic divergence in sunflower crop were conducted by using morphoagronomic characters (Subrahmanyam et al., 2003; Messetti and Padovani, 2004; Amorim et al., 2007; Mohan and Seetharam, 2005; Arshad et al., 2007).

Evaluation of genetic divergence is performed through methods based on agronomic, morphology and molecular characteristics. In the case of quantitative variables this variability may be accessed by using dissimilarity measures, outstanding Generalized Mahalanobis Distance (D^2_{ii}), that considers variances and residual covariance's existing between the measured characteristics (Cruz and Carneiro, 2003). Visualization and interpretation of distances may be facilitated by the use of a clustering method and/or graphical dispersion. Clustering methods objectify to separate a group of original observations on different subgroups in order to obtain homogeneity within and heterogeneity between subgroups. Among these methods, optimization and hierarchical ones are employed on a large scale by plant breeders (Bertan et al., 2006). Genetic divergence estimation between different sunflower genotypes has been studied, aiming to develop parents for hybrids constitution or even the formation of new segregating populations, from the intercross of divergent genotypes with complementary agronomic characteristics (Amorim et al., 2007).

In this way, the work aimed to characterize the genetic variability available in different sunflower hybrids, promising in biodiesel production, and identify which agronomic characters, contribute significantly to this divergence.

MATERIAL AND METHODS

The experiment was conducted at the Regional Campus of Universidade Estadual de Maringa, Umuarama County, northwestern region of Parana state, with geographic coordinates: S 23°47'20.4", W 53°15'25.2" and altitude of 396 m. Climate is classified as mesothermal subtropical with average annual temperatures around 19°C. Local soil is represented by Oxisol Dystrophic (Embrapa, 2006), with sandy texture.

Sixteen sunflower genotypes (hybrids) from the National Assessment of Sunflower Genotypes belonging to Embrapa - Soybean Research National Center (Ending Experiment – First Year) were evaluated (Table 1), in an experimental design conducted in randomized complete blocks, with four repetitions. Each genotype was seeded in a plot constituted of four lines of 6.0 m long, spaced 0.70 m. The distance between plants was 0.30 m, totaling 21 hills per line. Each hill contained three and seeding density ranged between 40,000 to 45,000 plants per hectare. Roughing was conducted, seven days after emergency, resting only 21 plants per line.

In addition to the recommended fertilization (40 to 60 kg per hectare of N, 40 to 80 kg per hectare of P_2O_5 and 40 to 80 kg per hectare of K_2O , it was applied one fertilizer containing boron (B), 2.0 kg per hectare in the soil, mixed with coverage nitrogen fertilization, 25 days after plants emergence. Control of weeds, insects and diseases was developed according to crop needs, by using the recommended chemical products for the crop. The harvest of each plot was performed manually.

Two central lines were harvested (useful area), eliminating 0.50 m from each edge. Chapters were covered with TNT protection sacks to prevent birds attack.

The following characteristics were analyzed:

- (1) Final stand (STD): Number of plants in the useful area in the harvest period
- (2) Plant height (PH): Measure from soil base up to chapter insertion (cm), in five competitive plants in useful area
- (3) Chapter curvature do capítulo (CC): Visual assessment, conducted by two appraisers using the classification scale proposed by Knowles (1978)
- (4) Chapter size (CS): Obtained through the average of competitive plants (20%), in plot useful area, measure at physiological maturation stage
- (5) Grain yield (GRAIN): Grain yield ($kg\ ha^{-1}$), through the harvest of grains in each useful plot, with data corrected for moisture content around 11%
- (6) Weight of 1000 achene's (WTA): Achene's weight, in grams, obtained by the ratio between grains total weight from each one of the five chapters in the useful plots to grain total number, later corrected by 1,000 grains
- (7) Oil content (OIL %): Expressed in dry basis (after storage in cold chamber), through Soxhlet methodology.

Data recorded from morphological characters were submitted to analysis of variance by F test and means compared by Scott and Knott (1974) test ($p < 0.05$), considering genotypes effects as fixed. Multivariate analysis was used to evaluate divergence between genotypes, employing Canonical Variables Analysis and clustering based on Mahalanobis Generalized Distance (D^2_{ii}).

In the analysis with canonical variables it was evaluated the progenitor similarity through a graphical dispersion, while agglomerative methods are dependent on the dissimilarity measures estimated through Mahalanobis Generalized Distance (D^2_{ii}) (Cruz and Regazzi, 1994). Genotypes clustering was performed by using Optimization Method proposed by Tocher, cited by Rao (1952), according to Cruz and Carneiro (2003), and Oliveira et al. (1998), where individuals belonging to the same group are more homogeneous than individuals of different groups, and

Table 2. Analysis of variance (ANOVA) for the evaluated characteristics in 16 sunflowers hybrids (Umuarama, PR/2011).

SV	DF	Mean of squares						
		GRAIN	WTA	CS	STD	PH	CC	OIL
Replication	3	33709.89	139.35	41.50	39.56	3114.43	0.29	0.54
Genotypes	15	842130.72**	60.51 ^{ns}	23.06**	44.46*	713.39 ^{ns}	0.68**	19.40*
Error	45	28236.56	66.72	3.99	19.69	383.95	0.19	8.12
Mean		2632.94	55.15	23.86	22.53	199.11	4.31	50.30
CV (%)		9.30	14.81	8.37	19.70	9.84	10.15	5.67

** , * , Significant at 1 and 5% probability level, respectively by F test; ^{ns} , non-significant; SV = source of variation; DF = degrees of freedom; GRAIN = grain yield; WTA = Weight of 1000 achene's; CS = chapter size; STD = final stande; PH = plant height; CC = chapter curvature; OIL = oil content (%).

Table 3. Means of seven agronomic characteristics evaluated in 16 sunflowers genotypes (UEM, Umuarama – PR, 2011).

Genotype	Agronomic characteristics						
	GRAIN	WTA	CS	STD	PH	CC	OIL
M 734 (T)	3135.0 ^b	56.9 ^a	23.3 ^c	22.8 ^a	189.3 ^a	4.5 ^a	53.6 ^a
HELIO 358 (T)	2761.0 ^c	54.4 ^a	22.3 ^c	23.8 ^a	174.8 ^a	5.0 ^a	52.5 ^a
HN 5218	2920.0 ^c	59.8 ^a	27.4 ^a	18.8 ^a	201.0 ^a	4.0 ^b	50.8 ^a
PARAÍSO 65	2128.0 ^d	58.9 ^a	25.2 ^b	18.3 ^a	198.5 ^a	4.0 ^b	52.4 ^a
HLA 44-49	1803.0 ^e	51.1 ^a	22.5 ^c	24.3 ^a	176.5 ^a	4.0 ^b	50.3 ^a
HLA 05-62	3142.0 ^b	54.6 ^a	23.2 ^c	18.3 ^a	203.8 ^a	4.3 ^b	49.4 ^b
HLA 44-63	2367.0 ^d	51.4 ^a	22.8 ^c	21.8 ^a	193.0 ^a	4.3 ^b	47.4 ^b
HLA 11-26	3193.0 ^b	57.3 ^a	23.9 ^c	17.5 ^a	189.0 ^a	4.3 ^b	49.0 ^b
V 60415	2144.0 ^d	63.5 ^a	24.9 ^b	22.3 ^a	216.3 ^a	4.0 ^b	47.5 ^b
V 70153	2144.0 ^d	52.6 ^a	29.5 ^a	20.8 ^a	216.0 ^a	4.5 ^a	53.5 ^a
QC 6730	3009.0 ^b	53.4 ^a	26.4 ^b	24.3 ^a	224.5 ^a	4.8 ^a	50.4 ^a
SULFOSOL	1813.0 ^e	52.6 ^a	21.6 ^c	23.5 ^a	195.0 ^a	3.5 ^b	51.5 ^a
SYN 034 A	1925.0 ^e	55.8 ^a	20.5 ^c	22.0 ^a	202.5 ^a	4.3 ^b	48.5 ^b
SYN 039 A	3362.0 ^b	47.6 ^a	24.6 ^b	29.0 ^a	200.5 ^a	4.0 ^a	50.3 ^a
SYN 042	2101.0 ^d	54.5 ^a	22.7 ^c	27.3 ^a	198.3 ^a	4.8 ^a	51.8 ^a
SYN 045	4180.0 ^a	58.5 ^a	21.1 ^c	26.3 ^a	207.3 ^a	5.0 ^a	46.3 ^b

GRAIN = Grain yield; WTA = Weight of 1000 achene's; CS = chapter size; STD = final stande; PH = plant height; CC = chapter curvature; OIL = oil content (%).

Hierarchical Method "UPGMA" with genotypes clustered by a process that repeats for several levels until it is established the dendrogram, where demarcations may be established by a visual examination of this tree in which occurs the assessment of points with high change level, taking them as delimiters of genotypes number in order to determine a group (Cruz and Regazzi, 1994). Both variance analysis and multivariate analysis were performed by using Gene's computational program (Cruz, 2006).

RESULTS AND DISCUSSION

By variance analysis (Table 2) there were found significant differences (1% probability level), for GRAIN, TC and CC characteristics. STD and OIL (%) showed significant differences at 5% probability level, by F test, demonstrating the existence of variability among genotypes and suggesting that evaluated characters are important in characterizing genetic divergence, with the

exception for WTA and PH parameters, that showed no significant differences. Variant coefficient ranged from 5.67 to 19.70%, revealing appropriate experimental precision, close to the ones found by Amorim et al. (2007) and Vogt et al. (2010).

Table 3 shows mean values for the seven evaluated characteristics, with Scott and Knott clustering at 5% probability level. For GRAIN parameter (grain yield per hectare), it was observed the constitution of five distinct groups, with mean yield around 2632.94 kg ha⁻¹, with SYN 045 hybrid the most productive, followed by the second group, that contemplated M 734 (T), HLA 05-62, HLA 11-26, QC 6730 and SYN 039A hybrids. Balbinot Jr. et al. (2009), in genotypes evaluation experiment in 2007/2008 agricultural year, for the same seeded period, in Santa Catarina State, obtained mean yield inferior to this study, as much as cultivars and hybrids. This happened because of water deficiency during grain filling,

showing in chapter size, achenes with reduced mass. It is worth mentioning that during the grain filling period (December to January) in this present study, accumulated rainfall exceeds 240 mm, what contributed to higher grain yield. Matter et al. (2009), in South region of Brazil, also found maximum grain yield around 2485 kg ha⁻¹, studying similar genotypes.

Observing the results obtained by Embrapa (2011), it is possible to verify that SYN 045 hybrid, also presented high grain yield in Coxilha and Rio Pardo Counties, Rio Grande do Sul State and Londrina County, Parana State. For the characteristics weight of 1000 achene's, final stand and plants height, it was observed the formation of only one group, by the statistical method used, indicating that there is no genetic variability for 16 sunflower hybrids, in relation to these parameters. Vogt et al. (2010), in sunflower cultivars competition experiments at North region of Santa Catarina State, observed similar results to this present study, for mean values of chapter size, chapter curvature and weight of 1000 achene's. To WTA characteristic, hybrids showed mean of 55.15 g, less than the values obtained by Backes et al. (2008) and Balbinot Jr. et al. (2009), but higher than the results from Amorim et al. (2008).

Plants height ranged from 174.8 cm (Helium 358 (T) hybrid) and 224.5 cm (QC 6730 hybrid), corroborating the extent of results obtained by Castiglioni et al. (1994) and Embrapa (2011), but lower than data published by Amorim et al. (2008). The mean chapter size reached 23.86 cm, agreeing with Castro et al. (1996) and Rossi (1998) who cited that this characteristic ranges from 6 to 50 cm depending on the genotype, with higher values achieved by hybrid genotypes and confirming the results obtained by Amorim et al. (2008).

Chapter curvature showed mean value around 4.31, with evaluations conducted according to Knowles (1978) methodology, closer to the means obtained by Amorim et al. (2007) and Vogt et al. (2010).

Coimbra et al. (2009), studying sunflower hybrids, genetically similar to the ones of this present study, in Palmas County, Tocantins State, observed mean values for plants height (115.77 cm), grain yield (1280.8 and 1280,8 kg ha⁻¹), weight of 1000 achene's (48.5 g), chapter size (14 cm) and oil content (47.8%), lower than those obtained for Umuarama County, in this analysis. It should be noted that in the experiment conducted in Tocantins State, sowing occurred in February, in a place with higher temperature and means rainfalls throughout the cycle around 290 mm, with lower water demand of the experiment in this study area, what may cause decrease in grain yield and oil content (Acosta, 2009).

When the evaluation refers to oil content, Scott-Knott test separated genotypes in two groups, with mean oil content around 50.3%, considered ideal for the crop, agreeing with the results obtained by Coimbra et al. (2009), whose study revealed mean levels around 47.8%. According to Embrapa (2011), considering the results

obtained in counties of Parana and Rio Grande do Sul States, using the same genotypes of this present study, it was possible to observe oil levels of 44% in Campo Mourão, 43.4% in Londrina (Parana State Counties) and 46.3% in Pelotas, 41% in Rio Pardo and 45.7% in Coxilha, Rio Grande do Sul, State, Brazil. In all environments from Parana and Rio Grande do Sul States, stands out HLA 05-62 hybrid, with oil content ranging from 44 to 53.4%, agreeing with the obtained values in Piauí State (49.2%), according to Ribeiro and Carvalho (2011).

SYN 042, SYN 045, SYN 034A and SYN 039A genotypes also presented high oil content in this study. According to the obtaining company, SYN 042 and SYN 045 are considered conventional, while SYN 034A and SYN 039A are high oleic mutants, which grain products a kind of oil with modified fatty acid profile that, due to its characteristics (lipidic profile), does not oxidize easily avoiding the partial hydrogenation process and for consequence, does not generating "Trans" fat.

Based on Mahalanobis Generalized Distance (D^2_{ij}), the measures of genetic dissimilarity were established (Table 4), where SULFOSOL and SYN 045 genotypes were the most dissimilar with D^2_{ij} of 134.54%, while HLA 05-62 and HLA 11-26 hybrids were the most similar showing D^2_{ij} of 2.03%.

Due to the found results in relation to the formation of dissimilar pairs, the combinations for hybrid constitution most promising are those involving genotypes with higher values of D^2_{ij} or crosses between SYN 045 x SULFOSOL, SYN 045 x HLA 44-49, SYN 045 x SYN 034A, SYN 045 x V70153 and SYN 045 x PARAÍSO 65 genotypes, which would express the greatest heterotical potential and better use in crop breeding programs.

When calculating the relation of distance between a genotype in the presence of the others, it was observed that SYN 045 genotype composed five combinations with high dissimilarity values with magnitude of D^2_{ij} around 134.54; 131.61; 111.40; 108.03 and 100.48% to the combinations between SYN 045 x SULFOSOL, SYN 045 x HLA 44-49, SYN 045 x SYN 034A, SYN 045 x V70153 and SYN 045 x PARAÍSO 65 genotypes, respectively. The most similar combinations were obtained between HLA 44-49 x SULFOSOL, HLA 05-62 x HLA 11-26, M 734 (T) x HLA 11-26 and HLA 44-63 x V60415 genotypes, with the respective magnitudes of D^2_{ij} around 2.03; 4.32; 4.33 e 4.64%. HLA 11-26 genotype had participation in more than one combination.

Clustering by Tocher Method (Table 5), by using D^2_{ij} as dissimilarity measure, divided the hybrids in two groups, with restricted genetic divergence. In Group I were allocated 15 evaluated genotypes, where the highest dissimilarity was observed between HLA 44-49 and HLA 11-26 (D^2_{ij} 41.85) genotypes and the highest similarity between HLA 05-62 and HLA 11-26 genotypes (D^2_{ij} 2,03) inside the same group. Genotype 16 (SYN 045) was isolated by the clustering methodology used, constituting

Table 4. Dissimilarity matrix – measures of dissimilarity among 16 sunflower genotypes, in relation to seven characteristics, based on Mahalanobis Generalized Distance () (Umuarama – PR, 2011).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	0.00	6.12	9.98	23.13	42.30	6.60	19.42	4.33	29.36	35.18	13.73	43.97	37.48	9.23	24.87	34.04
2		0.00	13.24	16.23	24.52	10.86	11.38	11.28	21.50	25.22	14.06	32.72	24.12	16.41	10.13	53.95
3			0.00	11.31	30.33	5.70	10.54	5.73	13.62	13.89	6.88	33.88	29.82	10.45	20.44	56.22
4				0.00	8.27	13.80	6.50	21.03	5.75	13.31	22.86	8.67	8.65	32.17	8.46	100.48
5					0.00	31.72	10.19	41.85	11.36	23.88	40.33	4.64	6.45	47.31	7.01	131.64
6						0.00	8.21	2.03	14.88	27.27	10.26	30.68	22.31	11.79	20.43	43.22
7							0.00	14.24	4.32	17.08	14.16	14.32	7.72	20.08	6.55	74.86
8								0.00	23.12	33.14	11.57	43.08	34.29	9.43	28.39	33.16
9									0.00	16.64	19.07	12.79	7.10	30.25	8.64	91.55
10										0.00	14.51	34.52	31.63	32.38	16.17	108.03
11											0.00	48.28	36.57	8.69	20.28	45.05
12												0.00	5.13	51.92	14.08	134.54
13													0.00	46.82	8.23	111.40
14														0.00	30.63	32.55
15															0.00	94.00
16																0.00

Table 5. Representation of clustering generated by Tocher Optimization Method based on Mahalanobis Generalized Distance (), estimated from seven agronomic characteristics, evaluated in 16 sunflowers genotypes (Umuarama – PR, 2011).

Group	Individuals
I	HLA 05-62, HLA 11-26, M 734 (T), HN 5218, SYN 039 A, QC 6730, HELIO 358 (T), HLA 44-63, PARAÍSO 65, V60415, SYN 042, V70153, SYN 034 A, HLA 44-49 e SULFOSOL
II	SYN 045
Total	16

Group II genotype is characterized by higher grain yield, lower size chapter, higher chapter curvature and lower oil content.

Results obtained by Tocher clustering correspond with the ones from Mahalanobis Generalized Distance (D_{ii}^2), since SULFOSOL and SYN 045 genotypes were the most dissimilar ($D_{ii}^2=134,54$), being allocated in Groups I and II, respectively. Crosses more similar revealed by Mahalanobis Generalized Distance were obtained between HLA 44-49 x SULFOSOL, HLA 05-62 x HLA 11-26, M 734 (T) x HLA 11-26 and HLA 44-63 x V60415 genotypes, belonging to the same group (I) by Tocher clustering, concurring with Mahalanobis methodology. The dendrogram (Figure 1) generated by Unweighted Pair Group Method with Arithmetic Mean (UPGMA) was constituted by three groups.

Group I was composed by HLA 05-62 (6), HLA 11-26 (8), M 734 (T) (1), HELIO 358 (T) (2), HN 5218 (3), QC 6730 (11) and SYN 039 A (14) genotypes. Group II was subdivided in two groups, with subgroup IIa constituted by HLA 44-49(5), SULFOSOL (12), SYN 034 A (13), HLA 44-63 (7), V60415 (9), PARAÍSO 65 (4) and SYN 042 (15) genotypes. Subgroup IIb allocated only V70153 (10)

genotype and Group III was composed only by SYN 045(16) genotype, being this one the most dissimilar among the evaluated hybrids.

It is important to highlight that methodologies used for genetic divergence analysis (Tocher Optimization and Hierarchical Method "UPGMA") are based on the same Dissimilarity Matrix (Table 4). However, the calculation used for genotypes grouping is originated from different analysis, considering UPGMA method as more discerning, showing the formation of subgroups (Figure 1). Thus, it is common in studies of genetic divergence, the presentation of both methodologies (Cruz, 1990; Amorim et al., 2007; Vogt et al., 2010), with comparative purposes. This way, it was possible to observe that, being characterized as more detailed, genetic divergence obtained through Hierarchical method "UPGMA" pointed to the formation of subgroups, agreeing with Tocher Optimization Method, positioning SYN 045 genotype (16) disconnected. This situation was already expected because of its character highly productive, confirmed in Table 3 (agronomic characteristics analysis) and by canonic variables through scores of graphical dispersion (Figure 2).

Cofenetic correlation coefficient (CCC), applied to

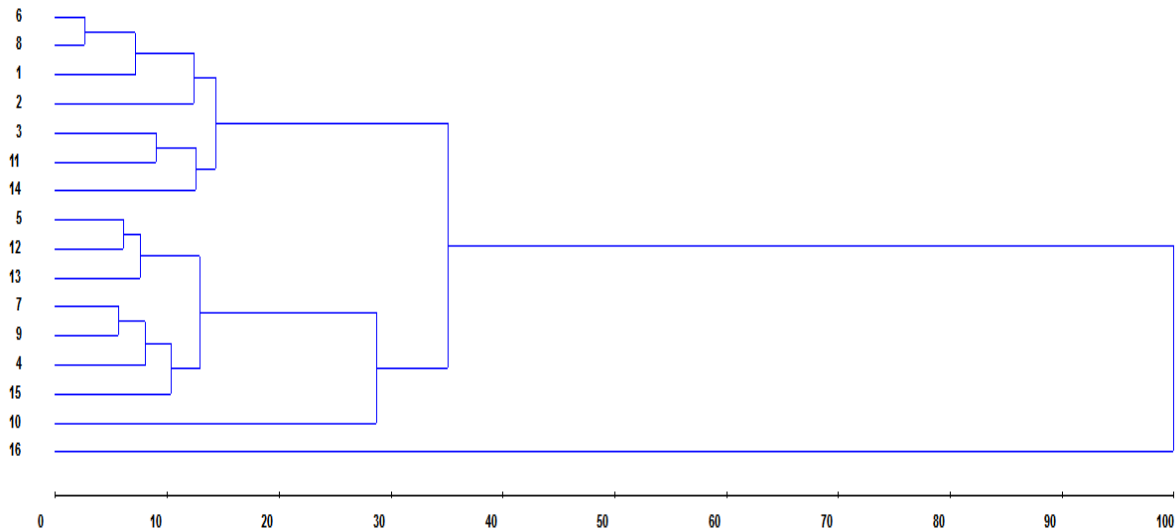


Figure 1. Representative dendrogram of genetic divergence among 16 sunflowers genotypes, obtained by Unweighted Pair Group Method with Arithmetic Mean (UPGMA), used as dissimilarity measure (Umuarama – PR, 2011).

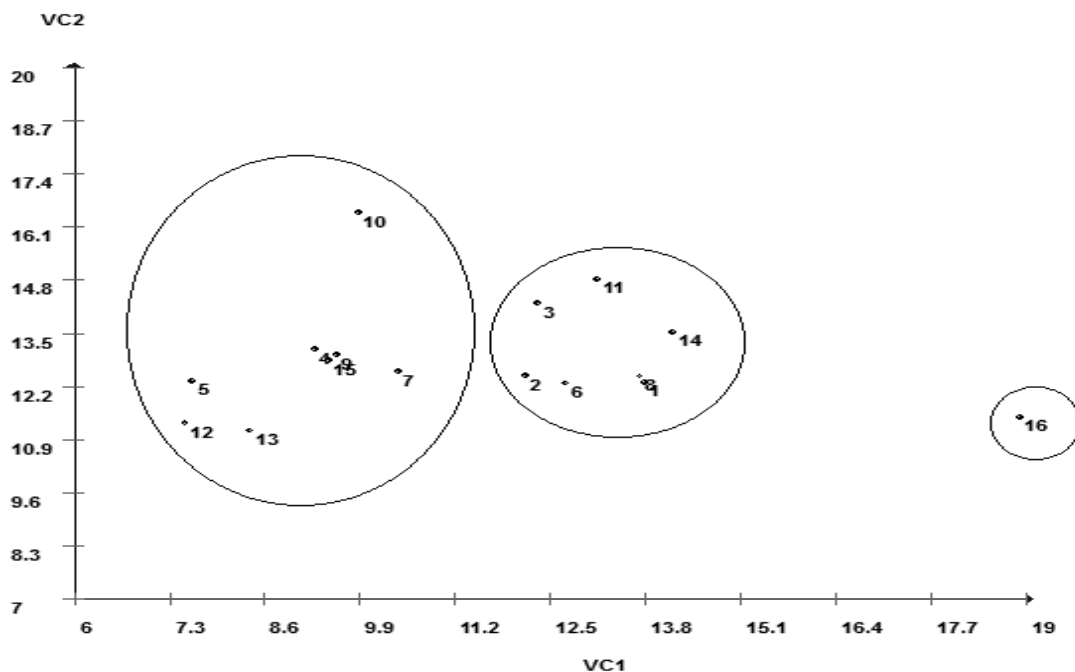


Figure 2. Scores of graphical dispersion, in relation to two axes representing the first two Canonical Variables (CV1 and CV2), obtained from seven characteristics evaluated in 16 sunflowers cultivars (Umuarama – PR, 2011).

UPGMA clustering method, demonstrated significance at 1% probability level ($P < 0.01$) in relation to the reliability of the relation between the matrix and the dendrogram, showing value of 0.81**, demonstrating satisfactory adjustment between the graphical representation of distances and its original matrix, enabling the achievement of inferences through visual assessment. Analyzing

the genetic divergence based on Canonical Variables (Table 6) it is possible to verify that the first two variables explained 82.07% of total variation (68.03% for first and 14.04% for the second one), enabling the transposition of genetic divergence of p-dimensional space ($p = 7$, in this case) to the bi-dimensional with negligible degree of distortion, caused by the distances between the genotypes.

Table 6. Eigenvalues (λ_i) corresponding to the variations percentages, explained by Canonical Variables (CV_i) and consideration coefficient (eigenvalues) from seven characteristics, evaluated in 16 sunflowers genotypes (Umuarama – PR, 2011).

CV _i	Eigen values		Consideration coefficient associated to characteristics ^{1/}						
	λ_i	% Acumulated	GRAIN	WTA	CS	STD	PH	OIL	CC
VC ₁	68.03	68.03	0.006	0.013	-0.008	-0.005	0.006	-0.090	0.779
VC ₂	14.04	82.07	-0.004	-0.059	0.578	0.034	0.001	-0.025	0.785
VC ₃	6.69	88.77	-0.006	-0.004	0.026	0.145	-0.027	0.109	1.496
VC ₄	5.54	94.31	0.009	0.013	-0.034	-0.096	-0.026	0.283	-0.769
VC ₅	3.42	97.74	0.005	-0.049	0.085	0.140	-0.010	-0.036	-1.306
VC ₆	1.32	99.07	0.002	0.054	-0.136	0.045	0.030	0.195	-0.417
VC ₇	0.92	100.00	-0.001	0.097	0.137	0.093	-0.024	-0.071	-0.144

^{1/} GRAIN = Grain yield; WTA = Weight of 1000 achene's; CS = chapter size; STD = final stande; PH = plant height; CC = chapter curvature; OIL = oil content (%).

Table 7. Relative contribution of seven agronomic characters evaluated for genetic divergence in 16 sunflower genotypes, according to Singh (1981) criterion and associated parameters (Umuarama – PR, 2011).

Characteristics ^{1/}	S.j	S.j (%)	Heritability (%)	CV _g	CV _g /CV _e
GRAIN	1990.40	62.73	96.65	24.96	2.68
WTA	59.82	1.88	0.00	0.00	0.00
CS	427.56	13.47	82.70	9.15	1.09
STD	138.18	4.35	55.70	11.04	0.56
PH	112.80	3.55	46.18	4.56	0.46
% OIL	157.75	4.97	58.14	3.34	0.59
CC	285.98	9.01	71.95	8.13	0.80

Graphical analysis, in comparison studies of similarity between cultivars must be considered when it is possible to summarize in a few variables more than 80% of the total available variation. For Bock (1975), if the first canonical variables accumulate 70% or more of total available variation between individuals assessed, the descriptors may be substituted for them. The results obtained in this study allow to demonstrate with trust the graphical dispersion, in relation to the first two canonical variables in bi-dimensional space (Figure 2), where it is possible to observe total agreement of graphical dispersion with UPGMA clustering method, and partially agreeing with the methodology proposed by Tocher.

Knowledge of relative importance of the characteristics for genetic divergence allows discarding characteristics with little contribution, thereby reducing manpower, time and costs spent on experimentation (Cruz, 1990). The criterion proposed by Singh (1981), based on Mahalanobis Generalized Distance (D_{ii}^2) evidenced that GRAIN and SC characteristics (Table 7) were the ones that most contributed to divergence characterization, with 62.73 and 13.47%, respectively. CC (9.01%), OIL (4.97%), STD (4.35%), PH (3.55%) and WTA (1.88%) characteristics, showed minor contribution being WTA the suggested variable for disposition. Through the ratio of

of CV_g and CV_e greater than unity, it is possible to use with ease the variables GRAIN and CS in selection, since also presented high heritability values.

Results obtained by Amorim et al. (2007), aiming to estimate the relative contribution of each characteristic to the expression of genetic divergence, indicated that flowering initial (13.10%), flowering days (37.10%), height of chapter insertion (18.55%) and number of leaves (9.10%) characteristics were the ones that most contributed to total divergence among 15 sunflower genotypes (78.05%). The authors still commented that Alvarez et al. (1996) verified that flowering initial and number of leaves were also important in discriminating genetic divergence among sunflowers populations. Such characters were not evaluated in this work, but due to its importance, it will be subject to further studies.

It is observed through the ratio between Genetic Variation Coefficient (CV_g) and Experimental Variation Coefficient (CV_e), value greater than the unit for GRAIN and CS characteristics, inferring by the ease on selection for such characters. Besides it, the high heritabilities (96.65%) and (82.70%) respectively, also contribute to selection procedures. According to Amorim and Souza (2005), the lines obtaining from hybrids is a viable alternative, since the behavior of the genotypes has been studied in distinct environments and it is still possible to

find satisfactory ratio of favourable locos already fixed.

Conclusion

Although restricted, there is genetic variability among 16 sunflower hybrids for the evaluated agronomic characteristics, except for weight of 1000 achene's and plant height. Grain yield and chapter size characteristics contributed significantly in genetic divergence observed among hybrids. It is possible to identify divergent genetic materials for obtaining lines and/or formation of new populations, aiming biodiesel production, in conditions of Parana State North western region.

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