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Genetic divergence in sesame based on morphological and agronomic traits

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ABSTRACT - *The evaluation of diversity in germplasm collections is important for both plant breeders and germplasm curators to optimize the use of the variability available. Diversity can be estimated by different genetic markers. The purpose of this study was to estimate the genetic divergence of 30 morphological and agronomic traits in 108 sesame genotypes by multivariate analysis. The Cole-Rodgers index was used to establish the dissimilarity matrices. The principal component analysis identified the traits that contributed most to the divergence and the genotypes were clustered by Tocher's optimization. Despite the narrow genetic basis, the markers were efficient to characterize the genotypes and identify the most similar groups or duplicate and divergent genotypes. Greatest variation was found for the traits number of capsules per plant and grain yield.*

Key words: multivariate analysis, genetic diversity, germplasm, *Sesamum indicum* L.

INTRODUCTION

Germplasm banks, as pools of the genetic variability available, are fundamental for the development of species. This variability must be characterized by genetic and phenotypic parameters for the identification of duplicates and the organization of core collections and as a support in the choice of parents for breeding programs.

Traditionally, studies of genetic characterization and divergence are based on morphological markers and quantitative traits (Cruz et al. 2004). For sesame, the characterization of the diversity in Brazil is still in the early stages (Arriel et al. 2000). As a general rule, breeding programs have evaluated large quantities of traits owing to the lack of reliable information on the performance of the main morphological and agronomic descriptors. In particular cases traits are used before it is known how much they contribute to the variability. Dispensable traits in studies of genetic diversity are relatively invariant ones, highly influenced by the environment or redundant for being correlated to other traits. In other words, those that contribute most to the divergence must be weakly correlated. In a study, these traits are expected to contribute with exclusive information and their joint action to be complementary to the description of the study genotypes (Bedigian et al. 1986, Cruz and Regazzi 1997).

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Multivariate procedures that allow the simultaneous evaluation of diverse trait types (Chiorato et al. 2005), as for example grouping (hierarchization and optimization) and ranking (principal components and principal coordinates) have been used in the studies of characterization. It is worth pointing out that the traits related to morphological aspects and plant structure can represent more than one category (ordinal variables and quantitative variables), which makes the evaluation of dissimilarity difficult when data of different nature are involved. In this case, the use of traditional measures is not appropriate, since plants of the pair of most discrepant values are not necessarily more distant than plants of another pair with closer values (Cruz and Carneiro 2003). Cole-Rodgers et al. (1997) proposed simple statistics to estimate this dissimilarity for a set of multi- category variables, where the similarity index can be established in function of concordance and discordance, thus allowing joint analysis involving all study traits, the qualitative and quantitative.

This study had the purpose of characterizing the genetic diversity in sesame genotypes, based on morphological and agronomic traits, to classify accessions according to their similarity.

MATERIAL AND METHODS

Sesame accessions from the Embrapa Cotton germplasm bank were evaluated (Table 1), planted in an experimental area of the Department of Plant Production of the UNESP, Campus de Jaboticabal, São Paulo. The experiment was arranged in an incomplete block design with an intermediate control every ten accessions, in 5 m long rows without replication, in a spacing of 1.00 m between plots, leaving 10 plants per meter after thinning.

The 108 accessions were characterized by 30 descriptors according to the methodology described by Veiga et al. (1985) and IPGRI and NBPGR (2004). The following data were recorded in 10 plants per plot: 1-flowering; 2-plant height; 3-insertion height of first capsule; 4-number of capsules/plant ; 5- capsule length; 6-number of branches; 7-stand; 8-grain yield; 9-cycle; 10-weight of 1000 seeds; 11-number of capsules/axil; 12-growth; 13-capsule insertion; 14-angular leaf spot; 15- black rot; 16-pests; 17-stem shape; 18-stem pilosity; 19-branch color; 20-branch; 21-leaf color; 22-leaf pilosity; 23- leaf position; 24- leaf shape; 25-leaf size; 26-basal leaf shape; 27-V-shaped flower pigmentation; 28- flower color; 29-capsule dehiscence; 30-seed color.

The methodology proposed by Cole-Rodgers et al. (1997) was adopted to make the joint analysis possible. The variables of different nature related to morphological aspects and plant structure, such as shape and fruit color, flowers, branches, etc, represent more than one category: ordinal variables and quantitative variables. All traits were transformed into binary variables, thus, in spite of losing information (sensitivity) the diversity was estimated related to the function of the total number of variables evaluated (Bussab et al 1990, Cruz and Carneiro 2003).

Next, the dissimilarity was estimated by the arithmetic complement of the Cole-Rodgers similarity index. With this index, a determined value expresses the percentage of coincidence of similarity considering the different study traits for each characteristic, including information of concordance and discordance. This allows for a joint analysis involving all qualitative and quantitative traits considered. The program Genes (Cruz 2001) was used for this procedure based on the following expression:

$$d_{ii'} = \frac{D_1}{C_1 + D_1} + \frac{D_2}{C_2 + D_2} + \ldots + \frac{D_v}{C_v + D_v} = \sum_{j=1}^{v} \frac{D_j}{C_j + D_j}$$

where:

$d_{ii'}$: percentage of dissimilarity considering the coincident values of multi-category variables for each pair of accessions;

C_j: number of concordances of categories for the j^{th} multi-category variable;

D_j: number of discordances of categories for the j^{th} multi-category variable.

The Tocher optimization technique was used with the underlying distances, and the graphic of the grouping represented in a tridimensional plan, by the projection of the new scores, obtained in the principal component analysis to identify the formation of the most similar groups and the most important traits for characterization of the germplasm under study, using Genes (Cruz 2001) software.

RESULTS AND DISCUSSION

In general, the accessions had lateral branches and a quadrangular stem with sparse pilosity. At maturity the branches turned green-yellowish; the leaves of the mid-plant part were also sparsely pilose, medium-sized and alternately distributed on the branches. It was observed that 58% of the leaves were

Table 1. Identification of the evaluated 108 sesame accessions

Identification	Accession code	Denomination	Identification	Accession code	Denomination	Identification	Accession code	Denomination
Genotype 1	-	Cultivar Guatemala	Genotype 40	BRA-003361	Sample 4/196	Genotype 79	BRA-003280	Amosta 1/188
Genotype 2	-	Cultivar Seridó	Genotype 41	BRA-003379	Patos PB 02	Genotype 80	BRA-003298	Sample 4/189
Genotype 3	-	Cultivar Nicarágua	Genotype 42	BRA-003468	Sample 6/206	Genotype 81	BRA-003301	Sample 3/190
Genotype 4	-	Cultivar Venezuela	Genotype 43	BRA-003557	Sample 6/215	Genotype 82	BRA-003310	Sample 4/191
Genotype 5	-	Cultivar Paquistão	Genotype 44	BRA-003484	Picos 06	Genotype 83	BRA-003328	Sample 1/192
Genotype 6	-	Cultivar Mexicana	Genotype 45	BRA-003531	Sample 4/213	Genotype 84	BRA-003620	Sample 2/222
Genotype 7	-	Cultivar CNPA G2	Genotype 46	BRA-003573	Sample 6/217	Genotype 85	BRA-003450	Sample 1/205
Genotype 8	-	Cultivar CNPA G3	Genotype 47	BRA-003409	Campina Grande 03	Genotype 86	BRA-003476	Sample 2/207
Genotype 9	-	Cultivar CNPA G4	Genotype 48	BRA-003484	Sample 1/208	Genotype 87	BRA-003506	Sample 1/210
Genotype 10	BRA-001767	FAO Nº52593	Genotype 49	BRA-003590	Sample 1/219	Genotype 88	BRA-003514	Campina Grande 04
Genotype 11	BRA-002381	Arawaca 02	Genotype 50	BRA-003603	Sample 1/220	Genotype 89	BRA-003522	Sample 2/212
Genotype 12	BRA-002402	Arawaca 04	Genotype 51	BRA-003611	Sample 5/221	Genotype 90	BRA-003549	Sample 1/214
Genotype 13	BRA-002691	IAPAR 320	Genotype 52	BRA-003620	Sample 2/222	Genotype 91	BRA-003247	Campina Grande 05
Genotype 14	BRA-002712	IAPAR 322	Genotype 53	BRA-003638	Sample 5/223	Genotype 92	BRA-003735	Sample 1/233
Genotype 15	BRA-002810	Valls et all 7834	Genotype 54	BRA-003646	Sample 5/224	Genotype 93	BRA-003743	Patos 05
Genotype 16	BRA-002828	Valls et all 7835	Genotype 55	BRA-003654	Sample 2/225	Genotype 94	BRA-003751	Sample 2/235
Genotype 17	BRA-003026	SB IMPROVED BACO	Genotype 56	BRA-003671	Patos 06	Genotype 95	BRA-003417	Sample 6/201
Genotype 18	BRA-003051	SB-S-9-LP-85	Genotype 57	BRA-003697	Sample 7/229	Genotype 96	BRA-003760	Fazenda Viola/236
Genotype 19	BRA-003123	TMV5	Genotype 58	BRA-003701	Sample 3/230	Genotype 97	BRA-003778	Cruzeta 01
Genotype 20	BRA-003131	TMV6	Genotype 59	BRA-003719	Sample 4/231	Genotype 98	BRA-003786	Sample 1/238
Genotype 21	BRA-003212	Campina Grande/181	Genotype 60	BRA-003727	Sample 3/232	Genotype 99	BRA-003816	Sample 1/241
Genotype 22	BRA-003221	Campina Grande/182	Genotype 61	BRA-003689	Sample 4/228	Genotype 100	BRA-003841	Serido/244
Genotype 23	BRA-003239	Campina Grande/183	Genotype 62	BRA-003794	Sample 2/239	Genotype 101	BRA-003859	Turem-CE
Genotype 24	BRA-003387	Picos 05	Genotype 63	BRA-003824	Patos 03	Genotype 102	BRA-003981	VCR-2-RA-21-CE
Genotype 25	BRA-003425	Fazenda Viola/202	Genotype 64	BRA-003832	Sample 1/243	Genotype 103	BRA-003999	Itaira-CE
Genotype 26	BRA-003433	Sample 3/203	Genotype 65	BRA-003841	Seridó /244	Genotype 104	BRA-003344	Currais Novos-RN05
Genotype 27	BRA-003441	Sample 5/204	Genotype 66	BRA-003867	Sample 3/246	Genotype 105	BRA-004014	Sample 3-BA
Genotype 28	BRA-003662	Currais Novos 06	Genotype 67	BRA-003875	Juazeiro 01	Genotype 106	BRA-004146	CNPA 220
Genotype 29	BRA-003808	Jericó 01	Genotype 68	BRA-003883	Sample 2/248	Genotype 107	BRA-004154	CNPA G2
Genotype 30	BRA-004022	VCR-101	Genotype 69	BRA-003891	Currais Novos 03	Genotype 108	BRA-004162	Venezuela1
Genotype 31	BRA-004073	GP 3314	Genotype 70	BRA-003905	Sample 1/250			
Genotype 32	BRA-000132	Branched purple stem	Genotype 71	BRA-004006	Regional MAN			
Genotype 33	BRA-022853	Indehiscent	Genotype 72	BRA-004031	Mármore Capistrano-CE			
Genotype 34	BRA-002879	Indehiscent	Genotype 73	BRA-004049	Bom Jesus Acara-CE			
Genotype 35	BRA-022861	Indehiscent	Genotype 74	BRA-004057	Piritu			
Genotype 36	BRA-003395	Sample 5/199	Genotype 75	BRA-000906	X 17-M(3)-6-3-M(3)			
Genotype 37	BRA-002496	A.R.Miranda 672	Genotype 76	BRA-003018	SB-S-BLOCK			
Genotype 38	BRA-003255	Boqueirão-CE	Genotype 77	BRA-003158	Seridó/175			
Genotype 39	BRA-003263	Iguatu 01	Genotype 78	BRA-003271	Sample 1/187			

broad and 42% narrow, while the leaves of the basal plant part were mostly lobate (dented). The flower color differed in the accessions, varying from white (30%), pink (1%) to lilac (69%); the pigmentation of 65% of the genotypes was V-shaped. The capsule opened (dehiscence) in 97% of the genotypes. Of all accessions, 76% had cream-colored seed and the others brown, black and white seeds. Some were difficult to classify, and were described as mixed-color seed (3%). For the yield-related traits, 90% of the genotypes had tall growth with mean insertion height of the first capsule at not more than 80 cm from the plant base. With respect to diseases and pests the genotypes presented different levels of susceptibility to angular leaf spot caused by the fungus *Cylindrosporium sesami*, to stem black rot (*Macrophomina phaseolina*) and to infestation caused by aphids (*Aphis* sp) and silverleaf whitefly (*Bemisia argentifolii*).

For the quantitative traits the period of beginning of flowering varied from 30 to 48 days, allowing the identification of genotypes with early to medium maturity cycle (between 97 and 115 days). The first capsules were inserted at 25 cm to 161.3 cm, closely related with mean plant height, which varied from 149.0 to 310.67 cm; this growth exceeded the crop mean in commercial cultivation conditions. The number of branches also varied considerably (2 to 20 branches/plant). In some accessions branches were observed growing from the basal part of the branches and producing numerous secondary branches, in other types, the branches appeared inserted in the terminal part of the main branch, without producing lateral branches. The seed production and number of capsules per plant also varied greatly (14 to 901.80 g per plot and 6 to 205 capsules per plant). The genotypes with lowest yields were characterized by the trait of indehiscent capsules, i.e., capsules that do not open at the end of plant maturity, which is controlled by a pair of recessive alleles. Pleiotropic effects of the genes of this trait have been detected that affect the leaves, flowers, fruits, cycle and yield, aside from the modifier genes that influence fruit fertility and dehiscence. However, Yermanos (1980) revealed that for some undesirable traits related to fruit indehiscence, it is not yet known whether there are pleiotropic effects or if the traits are controlled by different loci with strong linkage. Delgado et al. (1994) did not observe significant correlations between adnate leaves, leaf appendices and capsule opening and stated that the percentage of capsule opening was not correlated with the fruit yield of the indehiscent genotypes.

The multivariate analysis of the qualitative traits based on the dissimilarity estimated by the Cole-Rodgers index identified the most similar plants as genotypes 92 x 94 and 96 x 93. The most divergent genotypes on the other hand corresponded to the plants 10 x 15. The grouping of the 108 accessions by the Tocher optimization criterion (Table 2) formed seven conglomerates; one group comprised 87% of the genotypes, two groups contained four plants, one group the genotypes 30, 108 and 18, while the genotypes 4, 95 and 10 formed separate groups. A common trait in the group of genotypes 32, 33, 34 and 35 was capsule indehiscence. The second group consisted of cultivars CNPA G3, CNPA G4 and CNPA G2, and genotype 36, which represents a sample collected in a cultivation area in the northeastern region; the main traits of this latter and 95 were resistance to angular leaf spot and stem black rot as well as black seeds. Genotype 4 (Cultivar Venezuela), isolated from the others, had been evaluated earlier in initial studies of genetic breeding to develop varieties for the northeastern region, but, in spite of being early and uniform, the cultivar was not adaptable or tolerant to the drought stress of the region. Genotypes 30 (VCR-101), 108 (Venezuela 1), 18 (SB-S-9-LP-85) and 10 (FAO Nº 52593) are introductions from other countries. The main distinguishing traits of genotype 10 were three fruits/leaf axil, disease and pest tolerance and leaf position on the branches.

Aside from the selection pressure of the breeding studies influencing the genetic divergence of the genotypes, the geographic origin can be considered a synonym of dissimilarity. Nevertheless, group I with the majority of the evaluated accessions consisted of genotypes from different origins. The lack of relation between the similarity pattern and the geographic origin of varieties was discussed elsewhere (Patil and Sheriff 1994).

For the quantitative traits, 11 most similar genotype pairs were identified by dissimilarity, while the most divergent pairs were formed by the genotypes 32, 33, 34 and 35, associated to genotype 10. The main variables that differentiated genotype 10 from the others were probably the performance regarding the traits number of capsules per plant (205) together with capsule length (3.25cm), number of branches (16) and

Table 2. Grouping of the 108 sesame accessions by the Tocher optimization criterion, considering the evaluated qualitative traits

Groups	Accessions*
I	92 94 96 93 97 88 85 86 98 103 91 87 104 105 90 89 84 82 79 83 80 81 3 66 56 46 45 49 51 39 63 52 64 65 67 28 72 54 55 62 26 69 59 29 43 58 50 57 48 68 44 73 61 42 53 27 40 31 22 101 5 74 70 21 15 102 23 41 77 78 47 25 38 17 6 99 100 2 76 107 106 1 16 20 11 71 60 14 13 37 75 19 12 24
II	33 34 35 32
III	8 9 7 36
IV	30 108 18
V	4
VI	95
VII	10

* identification of the accessions in Table 1.

weight of 1000 seeds (3.50g). The yield further revealed the greatest divergence in the group of genotypes 32, 33, 34 and 35, which presented lowest seed yields.

The Tocher method based on the quantitative traits is shown in Table 3. In spite of the difference in the composition of the groups formed by the underlying qualitative traits (Table 2), some accessions maintained their position, e.g., genotypes 4, 7, 9, 10, 18, and 36. Of the quantitative traits, 94% were clustered in one large group.

By the principal component analysis it is possible to determine the relative contribution of each trait to the total variation in accessions and to identify the most informative to represent the variability of the germplasm available. The importance of the component is evaluated by means of the percentage of the total variation it explains. The first component is defined as the most important, since it accounts for the greatest part of the total variation found in the original data. If the first components accumulate a relatively high percentage of the total variation, generally determined as over 80%, they satisfactorily explain the variability expressed in the evaluated plants (Cruz and Carneiro 2003).

The variances (eigenvalues), the percentage and accumulated variances of each component are shown in Table 4. It was verified that the first two principal components explain only 28.49% of the variation and only from 13 eigenvalues onwards it is possible to represent 81% of the total variation in the genotypes. These results indicate that the existing variability is diluted in these components.

Other authors conducted similar studies, e.g., Bedigian et al. (1986) evaluated 300 sesame accessions and stated that the information of five components was necessary to explain 90% of the variance, since the two first concentrated only 53% of the variation in 32 evaluated traits. Arriel et al. (2000) observed that the total variation in 58 sesame accessions, evaluated based on six quantitative traits, was distributed in the first four principal components. These values are specific to the genotypes in the conditions they were conducted and evaluated, which hampers the comparative analysis, since the differences found can be understood by the fact that the concentration of the variance in the first components was associated to the nature and number of the descriptors.

The graphic representation of the scores of the principal components based on the traits evaluated is presented in Figure 1. Three conglomerates were formed where the greater divergence of the genotypes 10, 32, 33,

Table 3. Grouping of the 108 sesame accessions by the Tocher optimization criterion, considering the quantitative traits evaluated

Groups	Accessions
I	33 34 32 35 95 3 83 6 72 3 7 64 29 23 22 93 88 86 66 84 63 97 81 41 79 96 56 39 5 52 46 85 65 100 92 58 103 67 68 98 2 94 82 69 78 61 90 62 77 59 40 38 25 48 51 91 54 87 50 26 21 104 15 2 7 80 101 73 57 43 28 89 102 105 44 45 74 108 53 75 17 1 30 24 14 42 20 99 13 31 60 16 70 47 11 19 106 71 12 107 8
II	9 18 36 7
III	4
IV	10

* identification of the accessions shown in Table 1.

Table 4. Accumulated variances and variance percentage associated to the principal components for the 30 morphological and agronomic traits, evaluated in 108 sesame accessions

Principal component	Variance	Variance (%)	Accumulated variance (%)	Principal component	Variance	Variance (%)	Accumulated variance (%)
1	5.030	16.780	16.770	16	0.630	2.090	88.040
2	3.510	11.720	28.490	17	0.480	1.610	89.660
3	2.430	8.100	36.600	18	0.420	1.390	91.060
4	2.130	7.110	43.720	19	0.360	1.210	92.270
5	1.710	5.720	49.440	20	0.350	1.190	93.470
6	1.670	5.570	55.010	21	0.350	1.080	94.550
7	1.440	4.820	59.840	22	0.280	0.960	95.510
8	1.400	4.670	64.520	23	0.260	0.880	96.400
9	1.200	4.030	68.550	24	0.250	0.830	97.230
10	1.180	3.940	72.490	25	0.200	0.680	97.910
11	1.060	3.540	76.040	26	0.170	0.590	98.500
12	0.810	2.720	78.760	27	0.160	0.540	99.050
13	0.780	2.600	81.360	28	0.130	0.420	99.480
14	0.690	2.300	83.670	29	0.090	0.310	99.800
15	0.680	2.270	85.940	30	0.060	0.200	100.000

34 and 35 in relation to the others was confirmed. Moreover, the occurrence of superposition and /or close proximity between many genotypes evidenced the narrow genetic base in most sesame accessions from which the cultivars developed in selection studies were derived.

In germplasm collections it is common to find similar accessions with different registration. Likewise, it is possible that, in accessions of distinct origin, genotypes with the same name can be found, however phenotypically different, since the same genotype cultivated in different regions can undergo variations by the differential gene action due to the climate conditions. The first situation was true for the accessions 77 and 100 which, according to the denomination (Table 1), would be samples of cultivar Seridó.

The results of the two multivariate procedures (optimization and ranking), show that, in spite of the nature of the scales and disregarding the criterion of group composition, there was a certain consistence in the classification of the genotypes by the different methodologies, probably due to the low correlation between the majority of the variables evaluated determining their independence (Cruz and Regazzi 1997).

The importance of a trait is given by its discriminating power in the accessions and its stability of expression. In the analyses those are kept by that represent the fundamental structure of the biologic system under study (Cruz and Regazzi 1997). The

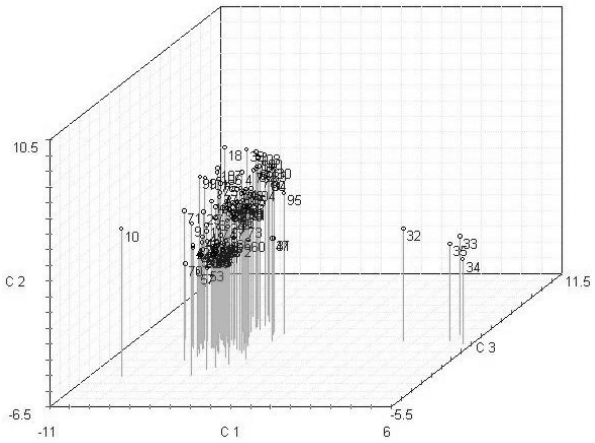

Figure 1. Tridimensional representation of the results of the principal component analysis of 108 sesame accessions based on scores of 30 morpho-agronomic traits

participation of each one, in the total variation for genetic divergence, was expressed by the highest coefficients, in absolute values associated to the last principal components (Table 5). Therefore, those that contributed least to the genetic divergence were: plant growth, insertion of first capsule, leaf shape, number of branches, capsule dehiscence, capsule length, stem shape and tolerance to angular leaf spot. The highest contributions were represented by the number of capsules per plant, grain yield, maturity cycle, branch color, pilosity of the branch, leaf position and basal leaf size.

Table 5. Weighting coefficients associated to the 30 morpho-agronomic traits (*) to obtain the principal components (CP) based on the analysis of 108 sesame accessions

CP	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	1.00	-0.15	-0.09	-0.04	-0.10	0.00	-0.13	-0.10	0.27	-0.01	-0.04	-0.10	0.00	-0.04	0.01	-0.24	-0.02	-0.02	0.01	-0.02	-0.06	-0.10	-0.10	0.08	0.07	-0.15	-0.02	-0.19	-0.09	0.16
2		1.00	0.39	0.15	-0.14	0.60	0.36	-0.02	-0.44	-0.03	-0.19	0.56	0.43	-0.21	0.03	0.22	0.11	0.04	-0.10	0.05	0.04	0.05	0.10	-0.09	-0.06	0.32	0.32	-0.10	0.48	-0.19
3			1.00	0.05	-0.23	0.52	0.21	-0.09	-0.36	0.04	0.10	0.35	0.77	-0.23	-0.05	0.24	0.00	-0.20	0.02	0.00	-0.05	-0.08	0.07	-0.33	-0.20	0.24	0.25	0.19	0.31	0.06
4				1.00	0.23	0.27	0.24	0.53	-0.38	0.20	0.29	0.35	-0.03	0.17	0.05	-0.01	-0.07	-0.16	-0.13	-0.03	-0.06	-0.11	-0.02	0.23	0.08	0.06	-0.08	0.11	0.33	0.12
5					1.00	-0.26	0.10	0.42	-0.01	-0.02	0.21	-0.03	-0.14	0.15	-0.08	0.15	-0.06	-0.03	-0.10	-0.04	-0.14	-0.06	-0.10	0.42	0.25	-0.11	-0.40	-0.27	-0.01	-0.18
6						1.00	0.20	-0.17	-0.32	0.01	-0.11	0.42	0.49	-0.31	-0.14	0.06	0.11	-0.14	-0.04	0.12	0.19	-0.09	0.10	-0.07	0.00	0.31	0.17	-0.07	0.36	-0.02
7							1.00	0.17	-0.52	0.04	0.13	0.58	0.17	0.16	0.19	0.13	0.05	-0.14	-0.13	0.00	-0.04	-0.05	-0.03	0.23	-0.01	0.33	0.17	0.06	0.50	-0.03
8								1.00	-0.23	0.09	0.34	0.16	-0.25	0.30	-0.07	0.07	0.02	0.03	-0.18	0.01	-0.22	0.05	0.00	0.05	0.10	-0.17	-0.14	0.17	0.14	-0.05
9									1.00	-0.05	-0.10	-0.87	-0.31	-0.18	-0.04	-0.29	-0.05	0.00	0.27	-0.04	0.10	-0.10	0.06	-0.19	0.00	-0.50	-0.06	0.03	-0.75	-0.11
10										1.00	0.14	0.00	0.01	0.19	-0.14	-0.24	-0.01	-0.37	0.07	-0.03	0.07	-0.08	0.08	0.04	0.01	-0.08	-0.02	0.10	0.01	0.07
11											1.00	0.05	-0.09	0.24	-0.02	-0.05	-0.04	0.11	-0.09	-0.02	-0.16	0.04	0.05	0.13	-0.08	-0.14	-0.22	0.20	0.05	0.10
12												1.00	0.31	0.11	0.01	0.22	0.02	0.03	-0.30	0.01	-0.09	0.05	-0.08	0.18	-0.01	0.58	0.14	-0.13	0.86	0.13
13													1.00	-0.24	0.02	0.33	0.03	-0.18	-0.07	0.02	0.01	-0.11	-0.02	-0.13	-0.13	0.21	0.11	-0.08	0.27	0.00
14														1.00	0.16	-0.05	-0.08	-0.03	-0.04	-0.05	-0.22	0.33	-0.42	0.24	0.01	0.02	-0.08	0.10	0.10	-0.04
15															1.00	0.00	-0.01	-0.01	0.02	0.00	-0.20	-0.02	-0.12	0.10	0.00	0.02	0.13	0.06	0.01	-0.03
16																1.00	-0.15	0.17	-0.12	-0.10	0.00	0.13	0.02	-0.09	0.09	0.13	-0.02	0.05	0.19	-0.12
17																	1.00	-0.02	-0.13	0.70	0.06	-0.03	-0.05	0.00	0.00	0.03	0.04	-0.05	0.02	-0.04
18																		1.00	-0.30	-0.01	-0.14	0.45	-0.18	-0.06	0.09	0.00	-0.10	-0.13	0.03	-0.13
19																			1.00	-0.21	0.00	-0.10	0.39	-0.20	-0.07	-0.22	0.10	0.21	-0.33	-0.08
20																				1.00	0.04	-0.02	-0.12	0.10	0.00	0.02	-0.07	-0.14	0.01	-0.03
21																					1.00	-0.06	0.21	-0.14	0.02	0.26	0.03	0.08	-0.07	0.09
22																						1.00	-0.21	-0.05	0.07	0.07	0.10	0.02	0.04	-0.31
23																							1.00	-0.31	0.06	-0.22	0.12	0.20	-0.07	0.07
24																								1.00	0.14	0.13	-0.46	-0.57	0.15	0.03
25																									1.00	0.05	0.04	-0.01	-0.01	0.06
26																										1.00	0.13	-0.18	0.50	0.13
27																											1.00	0.24	0.12	-0.03
28																												1.00	-0.11	0.14
29																													1.00	0.13
30																														1.00

*1-Flowering; 2- plant height; 3- insertion height of the 1st capsule; 4- no. of capsules/plant ; 5- capsule length; 6-no. of branches; 7-stand; 8-grain yield; 9-cycle; 10-weight of 1000 seeds; 11- no. of capsules/axil; 12-plant growth; 13- capsule insertion; 14- angular leaf spot; 15- black rot; 16-pests; 17-stem shape; 18-stem pilosity; 19-branch color; 20-branch; 21-leaf color; 22-leaf pilosity; 23- leaf position; 24- leaf shape; 25-leaf size; 26- basal leaf shape; 27- V- pigmentation of the flower; 28- flower color; 29- capsule dehiscence; 30-seed color.

In an evaluation of 13 quantitative traits using 40 sesame genotypes, Swain and Dikshit (1997) observed the greatest contribution to genetic divergence in the traits weight of 1000 seeds, capsule length, number of days until flowering and oil content. In our study, capsule length and flowering represented a secondary contribution. In a preliminary characterization study involving 58 sesame accessions, Arriel et al. (2000) stated that number of fruits/axil and grain yield contributed most, while cycle, flowering, stand and black rot incidence were considered less important.

The contribution of a trait to the total variability is relative, since its identification is based on the principle that it can be discarded if it is little discriminating in the evaluated accessions. As an example, resistance to stem black rot and plant growth, which were both practically invariant, would be dispensable. However, for the sesame breeding program, resistance sources to the fungus *Cylindrosporium sesami* are of extreme importance for the development of cultivars. For plant growth, the first variable to be discarded was highly correlated with grain yield and number of capsules per plant. These traits were determinant in the identification of diversity in the studied genotypes, and, despite the low total variability, these traits made genetic gains in the crop possible, as reported earlier by Arriel et al. (1999).

In spite of the narrow genetic base, the characterization based on the combination of the information derived from morphological and agronomic traits is useful in the maximization of the genetic potential of the germplasm under study, since it allowed the discrimination of the accessions, with the identification of very similar duplicate groups and divergent genotypes. This makes the identification of the germplasm of the research program of Embrapa Cotton more reliable, to meet the needs of different segments.

It is emphasized that for the germplasm under study, the characterization and distinction of the accessions must be based on the qualitative selection of few important agronomic parameters, since in morphological terms the variation is minimal and contributes little to the discrimination of the evaluated accessions. Therefore, the variability found in the traits number of capsules per plant and grain yield must be exploited in breeding programs, while the possibility of introduction or collection of resistance sources against main diseases to establish new cultivars is also fundamental.

Divergência genética em gergelim a partir de caracteres morfológicos e agronômicos

RESUMO - *A caracterização da diversidade em uma coleção de germoplasma é importante tanto para curadores como para melhoristas de plantas, pois permite maximizar o uso da variabilidade disponível. Essa diversidade pode ser estimada a partir de diferentes marcadores genéticos. Assim, o objetivo deste trabalho foi estimar a divergência genética entre 108 genótipos de gergelim mediante a análise multivariada de 30 caracteres morfo-agronômicos, utilizando-se o índice de Cole-Rodgers para obtenção das matrizes de dissimilaridades. Empregaram-se as análises de componentes principais para identificação dos caracteres que mais contribuem para a divergência e o agrupamento dos genótipos foi realizado pelo critério de otimização de Tocher. Constatou-se que apesar da estreita base genética, os marcadores foram eficientes na caracterização dos genótipos, identificando-se grupos mais similares, duplicatas e genótipos divergentes. Os caracteres número de cápsulas/planta e rendimento de grãos responderam pela maior parte da variação existente.*

Palavras-chave: análise multivariada, diversidade genética, germoplasma, *Sesamum indicum* L.

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