Revista Ciência Agronômica, v. 48, n. 4, p. 663-673, out-dez, 2017
Centro de Ciências Agrárias - Universidade Federal do Ceará, Fortaleza, CE
www.ccarevista.ufc.br

Artigo Científico
ISSN 1806-6690

Concordance between botanical groups and genetic diversity in peanut[1]

Concordância entre grupos botânicos e diversidade genética em amendoim

Ingrid Pinheiro Machado[2], Fernanda Helena Oliveira da Silva[2], Renata Fernandes de Matos[2], Tamiris Pereira da Silva[2] and Júlio César DoVale[2]*

ABSTRACT - The aims of this study were to characterize peanut accessions of germplasm collection of the CCA/UFC and check consistency between the pre-existing botanical groups to estimates of genetic diversity. For this were conducted a trial with 43 accessions of peanut in a randomized block design with three replications. To characterization were used 21 morphological descriptors, where revealed large genetic variation. The mass hundred grains trait showed the main discriminating factors, with relative percentage of 22.1%. The cluster obtained with the linkage complete method, it was possible to view the dendrogram the formation of seven groups based on the Mahalanobis distance. By principal components analysis was identified phenotypic diversity among genotypes. The first three components explained 81% of the total variation. Subsequently, built a three-dimensional scatter chart for access of visualization, eight groups being formed. There was medium magnitude of agreement between the botanical groups and genetic diversity, both by the dendrogram and graphic dispersion proving the dissimilarity between genotypes of different botanic groups. Therefore, crossings between group access botanical Spanish or Valencia with those belonging to the Virginia group should generate segregating populations with high genetic potential.

Key words: *Arachis hipogaea* L.. Morphological descriptors. Genetics Resources. Conservation.

RESUMO - Objetivou-se com esse estudo caracterizar acessos de amendoim da coleção de germoplasma do CCA/UFC e verificar concordância entre os grupos botânicos preexistentes com as estimativas de diversidade genética. Para isso, foi conduzido um ensaio com 43 acessos de amendoim no delineamento em blocos casualizados com três repetições. Para caracterização dos acessos foram utilizados 21 descritores morfoagronômicos, os quais revelaram grande variação genética. O caráter massa de cem grãos se mostrou o principal fator discriminante, com porcentagem relativa de discriminação de 22,1%. Pelo agrupamento obtido com o método de ligação completa, foi possível visualizar no dendrograma a formação de sete grupos com base na distância generalizada de Mahalanobis. Pela análise dos componentes principais também foi constatada grande diversidade fenotípica entre os acessos da coleção. Os três primeiros componentes explicaram 81% da variação total. Posteriormente, foi construído um gráfico tridimensional para visualização da dispersão dos acessos, na qual se verificou a formação de oito grupos. Constatou-se concordância de média magnitude entre os grupos botânicos e diversidade genética, tanto pela classificação observada no dendrograma quanto pela dispersão gráfica, comprovando a dissimilaridade entre acessos de grupos botânicos distintos. Assim, cruzamentos entre acessos do grupo botânico Spanish ou Valência com aqueles pertencentes ao Virginia devem gerar populações-base com elevado potencial genético.

Palavras-chave: *Arachis hipogaea* L.. Descritores morfoagronômicos. Recursos genéticos. Conservação.

DOI: 10.5935/1806-6690.20170077
*Autor para correspondência
Recebido para publicação em 16/09/2015; aprovado em 02/02/2017
[1] Parte da Monografia da primeira autora apresentada à Universidade Federal do Ceará/UFC
[2] Departamento de Fitotecnia, Centro de Ciências Agrárias, Universidade Federal do Ceará/UFC, Fortaleza-CE, Brasil, ingridpin03@hotmail.com, fernandahelena_ufc@hotmail.com, renatafmatos@hotmail.com, tamirisjua@gmail.com, juliodovale@ufc.br

INTRODUCTION

All over the world, germplasm banks have been established for the purpose of conserving plant genetic resources (which are invaluable, both presently and in the future), either by conventional methods of genetic improvement or by recent genetic engineering techniques. In this way, plant genetic resources are considered a reservoir in which solutions can be found for various environmental changes, serving as raw material for agricultural development (NASS, 2001).

Active germplasm banks are conservative units of genetic materials with potential for both immediate and future use. They are considered active because are close to the researcher, who performs the exchange of germplasm and frequent plantings for characterization, as well as providing conservation in the short and medium term. However, an active collection of germplasm, to be efficiently used, should have its accessions characterized and evaluated in order to identify the diversity within and between accessions, with all the information available in a computerized system to facilitate the search for users (FREITAS *et al.*, 2011).

Peanut is a rich source of protein and vegetable oil, being consumed worldwide in the most varied forms. The grains of this crop contain approximately 20-25% of high quality protein and 45% of oil (SILVEIRA *et al*., 2011). About 60% of the world’s production is destined for oil extraction, thereby generating industrial by-products used in animal feed while the rest is destined for human consumption in the natural form (SANTOS *et al*., 2010).

The expansion of the commercial peanut farm in Brazil depends on its technological level and competitiveness, where the availability of productive, profitable and adapted cultivars for the different regions, production systems and market standards is of primary importance (SANTOS, 2010). In this sense, the conservation of collections of accessions, such as the Agricultural Sciences Center of the Federal University of Ceará (CCA / UFC), can support the research on genetic improvement in the search for greater development and adaptation of the culture. This collection was started in 1983 from collections in the state of Ceará, inputs were received from other Brazilian and foreign institutions, mainly from the Senegalese Agricultural Research Institute (ISRA), in Senegal, Africa. Among the Brazilian institutions, the greatest contributions were obtained from the Agronomic Institute of Campinas (IAC), the extinct Agricultural Research Company of Ceará (EPACE) and the National Center for Cotton Research linked to EMBRAPA. The collection has approximately 90 peanut accessions, but little is known about their characterization.

Currently, three botanical groups have been explored in the peanut crop: 1) Spanish, 2) Valencia and 3) Virginia. Genotypes belonging to each of these groups present very striking characteristics that help to differentiate them. However, that does not mean that they are genetically dissimilar. This information is crucial for breeding programs, since the crossbreeding in a breeding program and derived segregant populations are directed to the search for progenies that present gene complementation (MARIM *et al.*, 2009; SUDRÉ *et al.*, 2005). Thus, once the agreement between botanical groups and genetic diversity is established, time can be gained in the breeding process, since there will no longer be a need to make complex evaluations and analyses to identify divergent genotypes.

There are few papers in the literature which address the genetic diversity of peanuts. Also, of the few papers in existence, the vast majority aimed only to evaluate genetic variability, as in the work conducted by Borges, Xavier e Rumjanek (2007), in which were used 29 accessions of peanuts. Others aimed to test different methodologies, in order to group divergent genotypes, as in the work conducted by Ramos *et al.* (2015), in which 77 accessions of peanuts were evaluated, based on the different methods of grouping. Therefore, no study was identified as linking the botanical groups currently explored with the group formation proposed by diversity analyses.

In this context, the aim of this study was to characterize peanut accessions from the CCA / UFC germplasm collection and to verify the agreement between pre-existing botanical groups and the formation of groups based on estimates of genetic diversity.

MATERIALS AND METHODS

This experiment was conducted at the Federal University of Ceará (UFC), Campus of Pici, in Fortaleza, Ceará, located at 03°47’25” S latitude and 38°30’30” W longitude and an altitude of 21 m. For this, was used a randomized block design with three replications. The treatments consisted of 43 peanut accessions from the CCA / UFC collection (Table 1). Was used a spacing of 0.60 x 0.20 m. Each plot had a total area of 1.8 m^2, consisting of a row of 3 m. All the cultural treatments from sowing to harvesting were carried out according to the recommendations of peanut cultivation in the region (BOLONHEZI; GODOY; SANTOS, 2013).

The check (control) used was the cultivar BR-1, obtained through selection among segregating populations derived from crosses involving parents of the Valencia group, adapted to the conditions of Northeast Brazil.

Table 1 - Botanical group, genotype, origin and order of registration of the 43 accessions of peanut used in the present study and belonging to the CCA/UFC

Botanical group	Genotype	Origin	Registration in the CCA / UFC collection
Valencia	CE 6811	Ceará	EAC-002
	TATU	Ceará	EAC-003
	DWARF (M-1)	Índia	EAC-008
	V-4	-	EAC-010
	GDM	Índia	EAC-011
	A-8	Ceará	EAC-015
	A-25	Ceará	EAC-018
	B-8	Ceará	EAC-020
	B-9	Ceará	EAC-021
	B-28	Ceará	EAC-022
	B-34	Ceará	EAC-024
	Tatu-aéreo	Ceará	EAC-025
	GDM(M1)	Ceará	EAC-026
	HP-2V3mM	Índia	EAC-027
	494	UPL/EPACE	EAC-030
	1028	UPL/EPACE	EAC-034
	1066	UPL/EPACE	EAC-035
	BR-1	Paraíba	EAC-105
Spanish	496	UPL/EPACE	EAC-038
	GEORGIA	USA	EAC-039
	PI 269.689	USA	EAC-040
	DIXIE-SPANISH	USA	EAC-041
	IAL-18	Bahia	EAC-042
	PI 165-317	USA	EAC-043
	TATUÍ	IAC/SP	EAC-044
	J-11	Ceará	EAC-045
	JH-113	Ceará	EAC-046
	SPANISH IMPRO	USA	EAC-048
	55-4-37	Senegal	EAC-050
	MH-1R33/1	Ceará	EAC-052
	CHICO	Senegal	EAC-088
	GC 337	Senegal	EAC-089
	841.111	IAC/SP	EAC-106
Virginia	TMVZNLM	Índia	EAC-056
	MK374	Nigéria	EAC-057
	SHULAMAH	USA	EAC-061
	GMLM	Índia	EAC-062
	HP-65	-	EAC-068
	HP-77	-	EAC-070
	DWARF	UPL/EPACE	EAC-076
	(MI)BELTVILLE	UPL/EPACE	EAC-077
	73-33	Senegal	EAC-085
	57422	Senegal	EAC-086

This cultivar presents tolerance to water stress and to cercosporiosis. Moreover, it reaches maturity around eighty days, which makes it one of the most recommended cultivars for the various growing environments in the region.

During the execution of the test, were used the main descriptors of peanut for characterization of the 43 accessions. This information is used, *a posteriori*, to avoid the conservation of duplicate accessions, as well as to subsidize new breeding programs.

In the vegetative phase, from the 30 days after planting, the following morphological descriptors were evaluated in five plants of the useful area: botanical group; branching type; growth habit; presence of flowers on the main axis; gynophore color; seed color; leaflet color; leaflet format (structure) and leaflet length.

The agronomic characterization was based on the descriptors linked to the crop production components. Data collection were obtained considering the total production of pods of each accession in their respective areas of use. Were measured the other components based on the five plants collected at random. Were adopted the descriptors: cycle; number of days for the appearance of the first flower; number of days to 50% of flowering; plant height; seed / fruit ratio; pod length; number of fruits per plant; percentage of immature fruits; production per plant; mass hundred grains and productivity.

Was performed analysis of variance for each trait and multicollinearity utilized for the identification of possible problems in the residual correlation matrices. Were eliminated the traits that showed multicollinearity at moderate to severe levels. Afterwards, the relative importance of each character for genetic divergence was determined using the methodology of Singh (1981) and the methodology proposed by Garcia (1998) to discard the least important traits.

In the multivariate analyses, the generalized distance of Mahalanobis was used as a measure of dissimilarity and, for the formation of the groups. Were used the complete bonding method and the Tocher optimization method. Were performed all analyses by computational application in Genetics and Statistics GENES (CRUZ, 2013).

Was used the Jaccard coefficient (1901) as the basis for calculating the coincidence index between botanical groups and groups formed by genetic diversity methods (dendrogram and graphic dispersion), determined by equation:

$$CI = \frac{a}{a + b + c} \tag{1}$$

where: CI = coincidence index; a = value that quantifies the number of coincidence; b = value that quantifies the number of discordance of type 1-0; c = value that quantifies the discordance number of type 0-1.

By adjusting this method, the discordance b and c would be quantified in the same way, thus resulting in a simplified equation:

$$CI_{adj} = \frac{NC}{NC + NCC} \tag{2}$$

where: CI_{adj} = coincidence index adjusted; NC = Number of coincidence between botanical groups and dissimilarity groups; NNC = number of non-coincidence.

RESULTS AND DISCUSSION

Regarding the morphological descriptors, there was a great variation in the behavior of the CCA/UFC accessions in the peanut collection (Table 2). Approximately 77% of the accessions presented sequential branching, while the others showed branching of the alternate type. This behavior is similar for the presence of flowers on the main axis, with all accessions belonging to either of the botanical groups Valencia or Spanish. The same accessions which had the sequential type of branching, also presented flowers in the main axis, while those with alternating type of branching did not show flowers in the main axis. However, all accessions that expressed this last phenotype are from the Virginia botanical group. According to Alvarez *et al.* (2005), the sequential branching behavior is typical of the groups Valencia and Spanish, as well as the alternating type that is characteristic of the group Virgínia.

On the other hand, approximately 60% of the accessions had a decumbent growth habit-3, and 33% presented a growth habit of the erect type, the other 7% were divided between procumbent and decumbent-1. All accessions were classified as precocious or semi precocious, since they closed the cycle between 90 and 110 days.

Precocity (early maturation) and erect/upright stance are highlighted as desirable characteristics for a peanut cultivar to be recommended for the Northeast conditions, since they present important agronomic implications such as greater use of rainfall in short-cycle materials (SANTOS *et al.*, 2013). In this way, the plants spend less time in the field, thus reducing the risk of production losses caused by drought. In addition, cultivars of erect size allow greater densification in the field, in spite of the fact that there is less production per plant, there is a compensatory effect when considering the production area (DUARTE; MELO FILHO; SANTOS, 2013).

Table 2 - Characterization of the 43 accessions of peanut by means of morphoagronomic descriptors

Registration in the CCA/UFC	Type of branching	Growth habit	Presence of flowers on the main axis	Gynophore color	Seed color
EAC-002	Sequential	Erect	Yes	Purple	Light brown
EAC-003	Sequential	Erect	Yes	Purple	Red
EAC-008	Sequential	Erect	Yes	Purple	Dark red
EAC-010	Sequential	Erect	Yes	Purple	Dark red
EAC-011	Sequential	Decumbent-3	Yes	Purple	Dark red
EAC-015	Sequential	Decumbent-3	Yes	Purple	Red
EAC-018	Sequential	Decumbent-3	Yes	Purple	Red
EAC-020	Sequential	Decumbent-3	Yes	Purple	Light brown
EAC-021	Sequential	Decumbent-3	Yes	Purple	Red
EAC-022	Sequential	Decumbent-3	Yes	Purple	Creme
EAC-024	Sequential	Decumbent-3	Yes	Purple	Red
EAC-025	Sequential	Decumbent-3	Yes	Purple	Red
EAC-026	Sequential	Erect	Yes	Purple	Dark red
EAC-027	Sequential	Decumbent-3	Yes	Purple	Cream
EAC-030	Sequential	Erect	Yes	Purple	Light brown
EAC-034	Sequential	Decumbent-3	Yes	Purple	Cream
EAC-035	Sequential	Decumbent-3	Yes	Purple	Rosy
EAC-038	Sequential	Decumbent-3	Yes	Purple	Cream
EAC-039	Sequential	Erect	Yes	Purple	Light brown
EAC-040	Sequential	Decumbent-3	Yes	Purple	Light brown
EAC-041	Sequential	Erect	Yes	Purple	Light brown
EAC-042	Sequential	Decumbent-3	Yes	Purple	Light brown
EAC-043	Sequential	Erect	Yes	Purple	Light brown
EAC-044	Sequential	Decumbent-3	Yes	Purple	Light brown
EAC-045	Sequential	Decumbent-3	Yes	Purple	Cream
EAC-046	Sequential	Decumbent-3	Yes	Purple	Cream
EAC-048	Sequential	Decumbent-3	Yes	Purple	Cream
EAC-050	Sequential	Decumbent-3	Yes	Purple	Light brown
EAC-052	Sequential	Decumbent-3	Yes	Purple	Cream
EAC-056	Alternating	Decumbent-3	No	Purple	Spotted rosy
EAC-057	Alternating	Erect	No	Green	Spotted rosy
EAC-061	Alternating	Procumbent	No	Purple	Spotted rosy
EAC-062	Alternating	Decumbent-1	No	Purple	Spotted rosy
EAC-068	Alternating	Decumbent-3	No	Purple	Light brown
EAC-070	Alternating	Decumbent-3	No	Purple	Spotted rosy
EAC-076	Alternating	Erect	No	Purple	Spotted rosy
EAC-077	Alternating	Procumbent	No	Purple	Spotted rosy
EAC-085	Alternating	Decumbent-3	No	Purple	Spotted rosy
EAC-086	Alternating	Decumbent-3	No	Purple	Rosy
EAC-088	Sequential	Erect	Yes	Purple	Light brown
EAC-089	Sequential	Decumbent-3	Yes	Purple	Light brown
EAC-106	Sequential	Erect	Yes	Purple	Light brown
BR-1 (Check)	Sequential	Erect	Yes	Purple	Red

The vegetative structure of low-ground peanut accessions (procumbent, decumbent-1 and decumbent-2), which are generally allocated to the Virginia botanical group, allows greater contact of the gynophore with the soil (LUZ *et al.*, 2010; SANTOS; CUSTÓDIO; SANTOS, 2000), a fact also observed in the present study. According to the same authors, upright and semi-erect (decumbent-3) plants have their floriferous buds more distant from the soil, which does not contribute to the reproductive efficiency of the culture.

Most of the morphoagronomic descriptors present qualitative inheritance, i.e., controlled by one or a few genes, with little influence of the environment (ALLARD, 1971). In this sense, since there is variability for these traits, the selection practiced by the breeder may be at the individual level, and should always seek to meet market requirements.

Of all the descriptors, the coloration of the gynophore was the least varied. Only two accessions (EAC-038 and EAC-057) presented the green color of the gynophore, while the others exhibited a purple coloration. However, for the coloring of the seed, there was a variation between light brown, red, dark red, rosy and spotted rosy colors.

In relation to the traits involving the leaflet, there was a predominance of light green coloration, elliptical shape and mean length (Table 3). Was identified a large variation for the number of secondary branches, from an average of 3.4 branches for EAC-042 accessions to 7.1 branches for EAC-057 accessions. The variation was also evident for the number of tertiary branches, with lower mean for EAC-046 accessions and higher for EAC-062. According to Silveira (2010), the increase in the number of secondary and total branches per plant, promotes an increase in the number of gynophores, and these correlate with seed production.

The distinction between botanical groups and their most divergent characteristics is remarkable. For example, Virginia seed has mainly the spotted rosy color, seeds of the Spanish cultivar have the light brown color while that of Valencia has a dark red color. However, in general the analyzed traits also show a positive relationship between the Spanish and Valencia groups, such as growth habit, cycle, and type of branching and presence of flowers on the main stem.

Among the quantitative traits studied, the mass hundred grains was the main discriminant factor among the accessions, with a relative percentage of 22.1% (Table 4). In addition, three other characters presented a great contribution to distinguish between the accessions, including the number of days for the appearance of the first flower, number of days for 50% of the stand to reach flowering, and the percentage of immature fruits, of which the four characters together accounted for 63.9% of the contribution to the divergence.

From the grouping obtained with the complete binding method, were formed eight groups based on the generalized Mahalanobis distance (Figure 1). Group I consisted of accessions EAC-056, EAC-057, EAC-061, EAC-062, EAC-070, EAC-077, EAC-085 and EAC-086. In this, 100% of the accessions are from the Virginia botanical group (Table 1). Group II was formed by only EAC-035, since this accession presented more than 50% level of dissimilarity in relation to group I. Group III was formed by accessions EAC-024, EAC-046, EAC-076, which belong to the groups Valencia, Spanish and Virginia, respectively. Group IV was formed by two accessions, these being EAC-038 and EAC-045, both belonging to the Spanish group.

Were formed groups V, VII and VIII only by accessions of the groups Valencia and Spanish. The following accessions EAC-015, EAC-018, EAC-021, EAC-025, EAC-027, EAC-034, EAC-048 and EAC-052 are present in group V, while group VIII consisted of only one accession, EAC-022, of the botanical group Valencia. Group VI consisted of the other accessions evaluated in the present study and not classified in the aforementioned groups. It is noteworthy that in the latter, there are accessions of the three botanical groups, with 50% belonging to Spanish and 44.44% to Valencia.

According to Sudré *et al.* (2006), multivariate analysis allows us to make inference about the genetic diversity of genotypes based on several characters simultaneously. Thus, traits that contribute very little to the computation of genetic dissimilarity between genetic materials, should be eliminated from subsequent analyses. The productivity trait, one of the most important, regardless of the culture, contributed least in this sense. Therefore, in order to discriminate efficiently between the accessions of the CCA/UFC collection, the traits related to precocity (early maturation), the number of days for the appearance of the first flower and number of days for 50% of the booth to reach flowering should be considered. This includes traits associated with yield, percentage of immature fruits and mass hundred grains.

Were formed the botanical groups from agronomic classifications based on vegetative and reproductive characteristics that distinguish between subspecies. Thus, genotypes of the Virginia group present the morphological characteristics of representatives of the subspecies *hypogaea*, var. *hypogaea*. On the other hand, the groups Valencia and Spanish are denominations of the morphological groups associated with the subspecies *fastigiata* (*fastigiata* and *vulgaris* varieties, respectively).

Table 3 - Characterization of the 43 accessions of peanuts by means of morphoagronomic descriptors

Registration in CCA/UFC	Leaflet color	Leaflet format (structure)	Leaflet length	Number of secondary branches	Number of tertiary branches	Cycle
EAC-002	Light green	Elliptical	Mean	4.6	1.0	90
EAC-003	Light green	Elliptical	Large	4.6	1.0	90
EAC-008	Light green	Elliptical	Mean	4.8	-	90
EAC-010	Green	Elliptical	Mean	4.4	1.3	90
EAC-011	Green	Elliptical	Mean	5.4	2.0	90
EAC-015	Green	Cuneate	Mean	4.2	0.5	90
EAC-018	Dark green	Elliptical	Mean	4.0	0.7	90
EAC-020	Light green	Elliptical	Mean	4.1	-	90
EAC-021	Green	Elliptical	Mean	4.5	0.8	90
EAC-022	Green	Elliptical	Mean	4.2	0.5	90
EAC-024	Dark green	Elliptical	Mean	4.7	1.5	90
EAC-025	Green	Elliptical	Mean	4.5	0.8	90
EAC-026	Dark green	Elliptical	Mean	3.4	-	90
EAC-027	Green	Elliptical	Mean	4.9	1.6	90
EAC-030	Light green	Elliptical	Large	4.8	-	90
EAC-034	Dark green	Elliptical	Mean	5.7	1.4	90
EAC-035	Green	Elliptical	Mean	5.4	2.8	90
EAC-038	Green	Elliptical	Little	6.9	4.9	90
EAC-039	Green	Elliptical	Mean	4.1	-	90
EAC-040	Light green	Elliptical	Mean	4.8	-	90
EAC-041	Light green	Elliptical	Mean	5.4	-	90
EAC-042	Light green	Elliptical	Mean	3.4	1.3	90
EAC-043	Light green	Elliptical	Mean	5.5	-	90
EAC-044	Green	Elliptical	Mean	4.4	-	90
EAC-045	Green	Elliptical	Mean	5.9	3.8	90
EAC-046	Green	Elliptical	Mean	5.8	0.3	90
EAC-048	Green	Elliptical	Mean	4.0	0.5	90
EAC-050	Light green	Elliptical	Mean	4.6	1.0	90
EAC-052	Green	Elliptical	Mean	3.5	0.7	90
EAC-056	Dark green	Lanceolate	Little	5.7	11.0	110
EAC-057	Dark green	Obovate	Little	7.1	7.0	110
EAC-061	Green	Elliptical	Mean	5.3	10.9	110
EAC-062	Dark green	Lanceolate	Mean	5.9	11.2	110
EAC-068	Green	Elliptical	Mean	4.2	-	110
EAC-070	Green	Elliptical	Little	6.2	9.9	110
EAC-076	Green	Elliptical	Mean	5.6	7.0	110
EAC-077	Dark green	Elliptical	Little	5.9	9.2	110
EAC-085	Green	Elliptical	Mean	6.0	5.1	110
EAC-086	Green	Elliptical	Mean	5.5	5.0	110
EAC-088	Light green	Elliptical	Mean	4.0	-	90
EAC-089	Light green	Elliptical	Mean	4.1	-	90
EAC-106	Light green	Obovate	Mean	4.9	1.3	90
BR-1 (Check)	Light green	Elliptical	Mean	4.5	-	90

A consequence of this may be the formation of groups V, VI and VII, in which the presence of only or mainly the Spanish and Valencia groups were observed. Probably, the subspecies determined the similarity in the characteristics of the studied accessions. In addition, it was observed that group I formed only by accessions of the Virginia group.

He and Prakash (2001) verified the formation of two main groups among different peanut cultivars, in which an association with the botanical classification was not characterized. In this study, the two groups formed even with the presence of Virginia, Valencia and Spanish as a whole, showed the prevalence of one of the three botanical groups in general. It was observed in the first group that 64.28% of the cultivars belong to the Virginia group while 55.17% belong to the second group (Valencia).

In order to simplify the data set, were obtained the main components in relation to the seven quantitative characters evaluated in peanut accessions. From the estimation of eigenvalues and eigenvectors obtained from the covariance matrix between the standardized values, 71% of the retained variation was observed in the first two components, which somehow justifies the use of a two-dimensional graph (Table 5). However, the three-dimensional graphic dispersion (Figure 2) was chosen to have a notion of "depth", being considered simultaneously as the scores of the first three main components. These results refer to a cumulative variation of 81% with the first three components, since according to Cruz and Carneiro (2006), accumulated variations that add more than 80% in the first main components make possible an analysis through dispersion graphs.

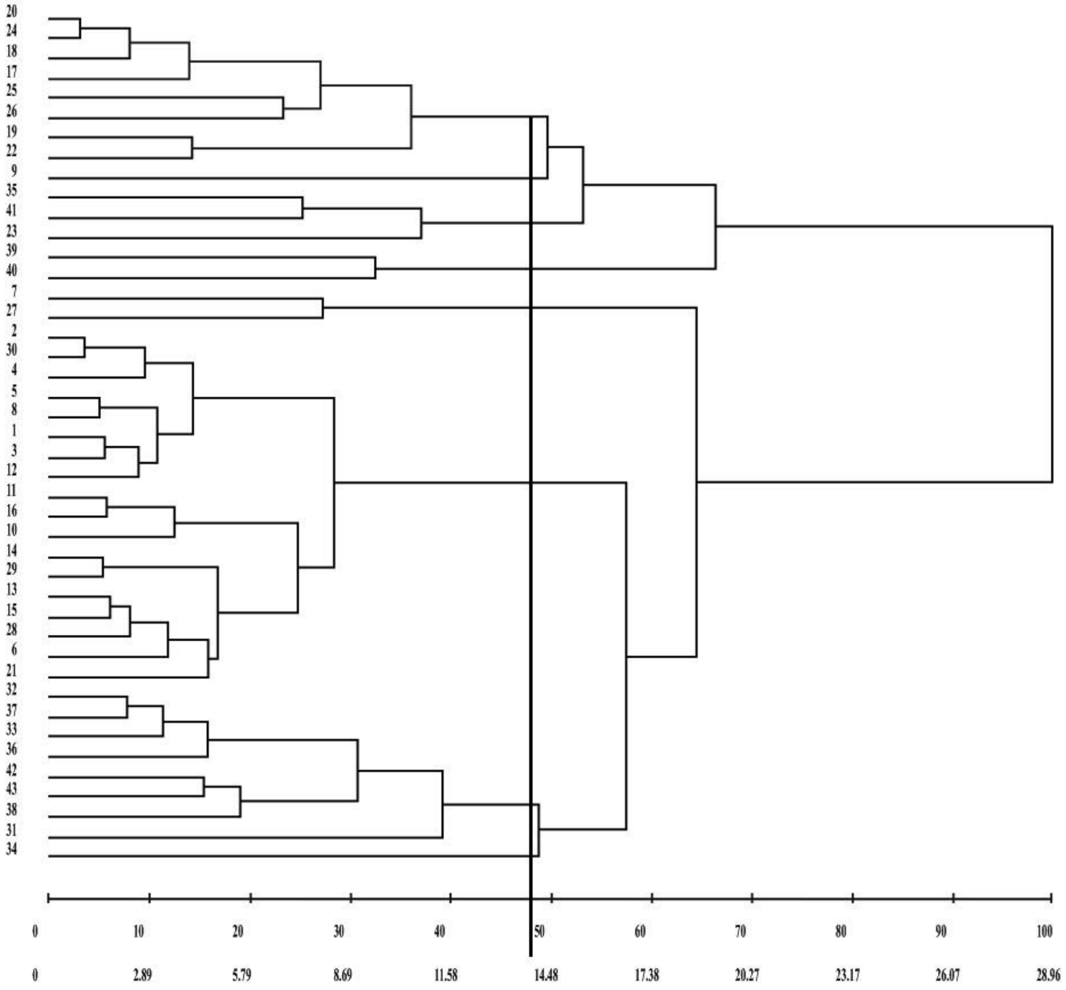
An inspection of the scores on the chart allowed us to subjectively divide the 43 accessions into eight groups. Group 1: EAC-088, belonging to the Spanish botanical group. Group 2: EAC-026, EAC-039, EAC-040 and EAC-050; in this group, 75% of the accessions belong to the Spanish botanical group while only 25% belong to the Valencia group. Group 3: (EAC-02, EAC-003, EAC-008, EAC-010, EAC-011, EAC-020, EAC-024, EAC-030, EAC-041, EAC-042, EAC-043, EAC-044, EAC-068, EAC-076, EAC-089, EAC-105 and EAC-106). In this group, there are accessions belonging to the three botanical groups, being 52.94% of the accessions of the botanical group Valencia and 35.29% of the Spanish group. Group 4: EAC-025 of the botanical group Valencia. Group 5: EAC-015, EAC-018, EAC-021, EAC-022, EAC-027, EAC-034, EAC-035, EAC-046, EAC-048, EAC-052, EAC-056, EAC-057, EAC-061, EAC-062, EAC-070, EAC-077 and EAC-085. In this group, similar to the third, there are accessions belonging to the three botanical groups, of which the groups Valencia and Virginia have 41.17% each. Group 6: EAC-045 of the Spanish botanical group. Group 7: EAC-038 of the Spanish botanical group, and group 8 with accession EAC-086 of the botanical group Virginia.

For the great majority of accessions, there was coincidence in the formation of the groups by both procedures. The coincidence index adjusted was of medium magnitude when considering both the dendrogram and the graphical dispersion (Table 6). However, the division of groups by the dendrogram presented the most conservative to established botanical groups. This shows that there is an association between botanical groups and those formed by estimates of genetic diversity, that is, accessions belonging to distinct botanical classes tend to be more dissimilar than accessions belonging to the same group. This is due to the different characteristics of each botanical group already established.

Table 4 - Relative contribution of quantitative traits to genetic diversity according to the methodology proposed by Singh (1981) based on the generalized distance of Mahalanobis, obtained from 43 accessions of peanuts

Traits	Relative contribution	
	S.j	%
Number of days for the appearance of the first flower	7608.7	16.2
Number of days for 50% of the booth to reach flowering	5983.1	12.7
Plant height	3803.4	8.1
Seed / fruit ratio	3905.3	8.3
Pod length	4313.3	9.2
Number of fruits per plant	2004.0	4.3
Percentage of immature fruits	6039.3	12.8
Production per plant	2353.5	5.00
Mass hundred grains	10395.9	22.1
Productivity	618.3	1.3

Figure 1 - Dendrogram among 43 accessions of peanut, obtained by the full link method - more distant neighbor, based on the seven most important quantitative traits for genetic dissimilarity



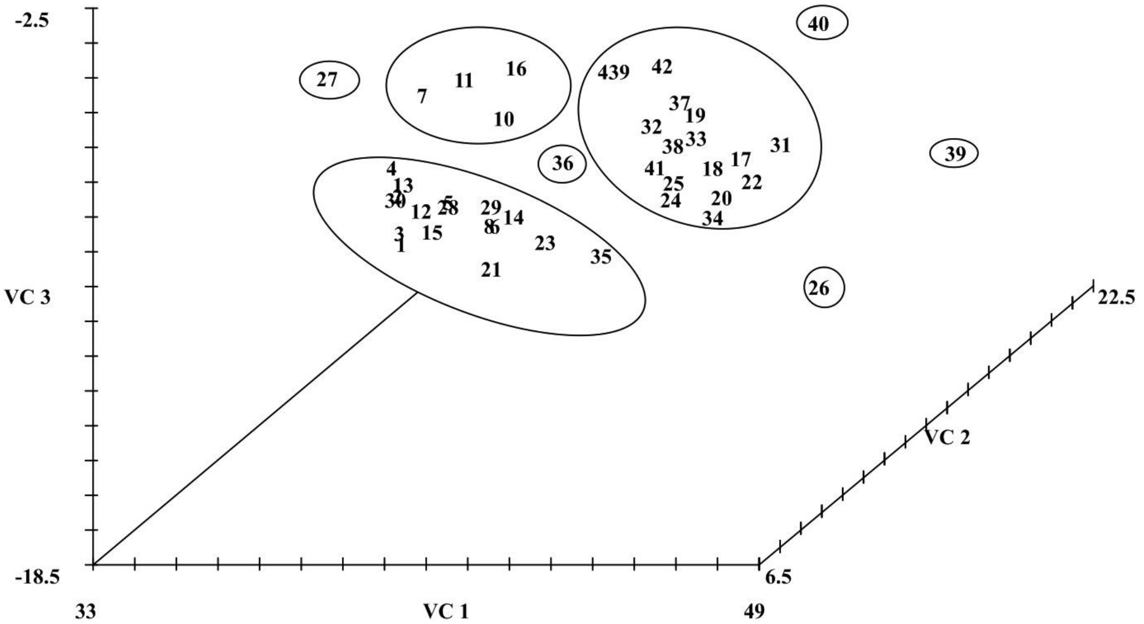
Accesses: (1) = EAC-002; (2) = EAC-003; (3) = EAC-008; (4) = EAC-010; (5) = EAC-011; (6) = EAC-020; (7) = EAC-026; (8) = EAC-030; (9) = EAC-035; (10) = EAC-039; (11) = EAC-040; (12) = EAC-041; (13) = EAC-042; (14) = EAC-043; (15) = EAC-044; (16) = EAC-050; (17) = EAC-056; (18) = EAC-057; (19) = EAC-061; (20) = EAC-062; (21) = EAC-068; (22) = EAC-070; (23) = EAC-076; (24) = EAC-077; (25) = EAC-085; (26) = EAC-086; (27) = EAC-088; (28) = EAC-089; (29) = EAC-106; (30) = EAC-105; (31) = EAC-015; (32) = EAC-018; (33) = EAC-021; (34) = EAC-022; (35) = EAC-024; (36) = EAC-025; (37) = EAC-027; (38) = EAC-034; (39) = EAC-038; (40) = EAC-045; (41) = EAC-046; (42) = EAC-048; (43) = EAC-052

Table 5 - Estimates of the variances (eigenvalues) associated with the main components of the seven quantitative traits most important for genetic diversity $^{(1)}$, evaluated in 43 peanut accessions

Eigenvalue	Eigenvalue (%)	% accumulated
11.154	49.82	49.82
4.876	21.78	71.61
2.118	9.46	81.07
1.892	8.45	89.52
1.159	5.18	94.69
0.957	4.28	98.97
0.231	1.03	100.00

(1): Mass hundred grains; Number of days for the appearance of the first flower; Percentage of immature fruits; Number of days for 50% of the booth to reach flowering; Pod length; Seed / fruit ratio; Plant height

Figure 2 - Graphical dispersion of the scores in relation to the representative axes of the canonical variables (VC1, VC2 and VC3) of 43 peanut accessions



Accesses: (1) = EAC-002; (2) = EAC-003; (3) = EAC-008; (4) = EAC-010; (5) = EAC-011; (6) = EAC-020; (7) = EAC-026; (8) = EAC-030; (9) = EAC-035; (10) = EAC-039; (11) = EAC-040; (12) = EAC-041; (13) = EAC-042; (14) = EAC-043; (15) = EAC-044; (16) = EAC-050; (17) = EAC-056; (18) = EAC-057; (19) = EAC-061; (20) = EAC-062; (21) = EAC-068; (22) = EAC-070; (23) = EAC-076; (24) = EAC-077; (25) = EAC-085; (26) = EAC-086; (27) = EAC-088; (28) = EAC-089; (29) = EAC-106; (30) = EAC-105; (31) = EAC-015; (32) = EAC-018; (33) = EAC-021; (34) = EAC-022; (35) = EAC-024; (36) = EAC-025; (37) = EAC-027; (38) = EAC-034; (39) = EAC-038; (40) = EAC-045; (41) = EAC-046; (42) = EAC-048; (43) = EAC-052

Table 6 - Coincidence index adjusted between the formation of botanical groups and groups formed by dendrogram procedures and graphic dispersion considering seven quantitative traits evaluated in 43 peanut accessions belonging to the CCA/UFC germplasm collection

	Dendrogram	Graphical dispersion
Coincidence index adjusted	0.628	0.558

According to Souza, Queiróz e Dias (2005), this information can be very useful to breeding programs, since in hybridization activities is evaluated not only the agronomic performance but also the genetic complementarity for the formation of segregating populations. In addition, such information may provide more accurate assessments and analyses in defining the parents for use in breeding programs.

In view of the variability for the various morphological or agronomic traits it was verified a great potential of the accessions pertaining to the collection of the peanut germplasm of the CCA/UFC. This potential refers to the performance of studies aimed at the inheritance or the genetic control of traits and the obtaining of cultivars that may be recommended for the Ceará State in the future. Either way, the breeder must be alert to the requirements of peanut farmers in the state. For this, it is advisable to insert in future crosses, parents who present precocity, upright posture, satisfactory yield per plant, low percentage of immature pods, and adequate productivity (DUARTE; MELO FILHO; SANTOS, 2013).

CONCLUSIONS

1. The peanut accessions obtained from the CCA/UFC germplasm collection are genetically dissimilar;
2. The methods of multivariate analysis, generalized distance of Mahalanobis, complete binding and optimization of Tocher, used in this study were efficient to separate the accessions with greater genetic dissimilarity;
3. There is an agreement of 0.558 for the graphical dispersion and of 0.628 for the dendrogram, between the botanical groups and those generated by the estimates of genetic diversity;
4. Crossings between accessions of the botanical group Spanish or Valencia with those belonging to the Virginia

group should generate segregating populations with high genetic potential;

5. For the formation of base populations, may be combined alleles of accessions EAC-057 and EAC-062 (Virginia group) with alleles of accessions EAC-025 (Valencia group) or EAC-038 (Spanish group).

REFERENCES

ALLARD, R. W. **Princípios do melhoramento genético de plantas**. São Paulo: Edgard Blucher, 1971. 381 p.

ALVAREZ, R. D. C. F. *et al.* Análise de crescimento de duas cultivares de amendoim (*Arachis hypogaea L.*). **Acta Scientiarum. Agronomy**, v. 27, n. 4, p. 611-616, 2005.

BOLONHEZI, D.; GODOY, I. J.; SANTOS, R. C. Manejo cultural do amendoim. *In*: SANTOS, R. C. dos; FREIRE, R. M. M.; LIMA, L. M. **O agronegócio do amendoim no Brasil**. Campina Grande: Embrapa Algodão, 2013. p. 185-237.

BORGES, W. L; XAVIER, G. R., RUMJANEK, N. G. Variabilidade genética entre acessos de amendoim. **Pesquisa Agropecuária Brasileira**, v. 42, n. 8, p. 1151-1157, 2007.

CRUZ, C. D. Genes: a software package for analysis in experimental statistics and quantitative genetics. **Acta Scientiarum Agronomy**, v. 35, p. 271-276, 2013.

CRUZ, C. D.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. 2. ed. rev. Viçosa, MG: UFV, 2006. 585 p.

DUARTE, E. A. A.; MELO FILHO, P. A.; SANTOS, R. C. Características agronômicas e índice de colheita de diferentes genótipos de amendoim submetidos a estresse hídrico. **Revista Brasileira de Engenharia Agrícola e Ambiental**, v. 17, p. 843-847, 2013.

FREITAS, J. P. X *et al.* Avaliação de recursos genéticos de maracujazeiro-amarelo. **Pesquisa Agropecuária Brasileira**, v. 46, n. 9, p. 1013-1020, 2011.

GARCIA, S. L. R. **Importância de características de crescimento, de qualidade da madeira e da polpa na diversidade genética de clones de eucalipto**. 1998. 103 f. Dissertação (Mestrado em Genética e Melhoramento) - Universidade Federal de Viçosa, Viçosa, MG, 1998.

HE, G.; PRAKASH, C. S. Evaluation of genetic relationship among botanical varieties of cultivated peanut (*Arachishypogaea* L.) using AFLP markers. **Genetic Resources and Crop Evolution**, v. 48, n. 4, p. 347-352, 2001.

JACCARD, P. Étude comparative de la distribution florale dans une portion des Alpes et des Jura. **Bulletin de la Société Vaudoise des Sciences Naturelles**, v. 37, n. 142, p. 5 47-579, 1901.

LUZ, L. N. da. Estimativas de parâmetros genéticos em linhagens de amendoim baseadas em descritores associados ao ginóforo. **Revista Ciência Agronômica**, v. 41, n. 1, p. 132-138, 2010.

MARIM, B. G. *et al.* Variabilidade genética e importância relativa de caracteres em acessos de germoplasma de tomateiro. **Pesquisa Agropecuária Brasileira**, v. 44, p. 1283-1290, 2009.

NASS, L. L. Utilização de recursos genéticos vegetais no melhoramento. *In*: NASS, L. L. *et al.* (Ed.). **Recursos genéticos e melhoramento**: plantas. Rondonópolis: Fundação MT, 2001. p. 30-55.

RAMOS, J. P. C. *et al.* Clustering fastigiata peanut accessions for selection of early-mature types suitable for the food Market. **Australian Journal of Crop Science**, v. 9, p. 1089-1094, 2015.

SANTOS, R. C. *et al.* Variabilidade de progênies F2 de amendoim geradas por meio de seleção de genitores ISSR-divergentes. **Revista Ciência Agronômica**, v. 44, n. 3, p. 578-586, 2013.

SANTOS, R. C.; CUSTODIO, R. J. M.; SANTOS, V. F. Eficiência reprodutiva em genótipos de amendoim e correlação fenotípica entre caracteres ligados ao ginóforo. **Ciência e Agrotecnologia**, v. 24, p. 617-622, 2000.

SANTOS, R. F. **Desenvolvimento de ferramentas genéticas e genômicas para introgressão de genes silvestres no amendoim cultivado**. 2010. 55 f. Dissertação (Mestrado em Agronomia) - Universidade Federal de Brasília, Brasília, 2010.

SANTOS, T. S. *et al.* Respostas de sementes de amendoim a diferentes doses de radiação gama (60Co)1. **Revista Brasileira de Engenharia Agrícola e Ambiental**, v. 14, n. 10, p. 1074-1078, 2010.

SILVEIRA, P. S. da *et al.* Teor de proteínas e óleo de amendoim em diferentes épocas de semeadura e densidade de plantas. **Revista da FZVA**, v. 18, n. 1, p. 34-45, 2011.

SILVEIRA, P. S. da. **Época de semeadura e densidade de plantas em cultivares de amendoim no Recôncavo Sul Baiano**. 2010. 95 f. Dissertação (Mestrado em Ciências Agrárias) – Centro de Ciências Agrárias, Ambientais e Biológicas, Universidade Federal do Recôncavo da Bahia, Cruz das Almas, 2010.

SINGH, D. The relative importance of characters affecting genetic divergence. **The Indian Journal of Genetic and Plant Breeding**, v. 41, n. 2, p. 237-245, 1981.

SOUZA, F. F.; QUEIRÓZ, M. A.; DIAS, R. C. S. Divergência genética entre linhagens de melancia. **Horticultura Brasileira**, v. 23, n. 2, p. 179-183, 2005.

SUDRÉ, C. P. *et al*. Divergência genética entre acessos de pimenta e pimentão utilizando técnicas multivariadas. **Horticultura Brasileira**, v. 23, n. 1, p. 22-27, 2005.

SUDRÉ, C. P. *et al.* Variáveis multicategóricas na determinação da divergência genética entre acessos de pimenta e pimentão. **Horticultura Brasileira**, v. 24, n. 01, p. 88-93, 2006.