



Genetic divergence in snap-bean (*Phaseolus vulgaris* L.) evaluated by different methodologies

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ABSTRACT - Fourteen snap-bean accessions of the Germplasm Bank of the Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) were analyzed for their morphoagronomical diversity in genotype-environment (sowing season) interaction, by multivariate analyses. The experiment was conducted in a randomized block design with four replications, in two sowing seasons (April to August - autumn/winter and October to December - summer), in 2001. The clustering grouping methods were in more agreement with autumn/winter data than with the summer data. There was a reduced similarity in the clusters among environments (sowing season). Crossings between UENF 1469 and UENF 1488 and between UENF 1469 and UENF 1486 were indicated, as well as their F_1 hybrid in combination with UENF 1488 for providing segregant generations. Accessions UENF 1486, UENF 1487, UENF 1488, UENF 1483, and UENF 1579 are also indicated for summer planting, in an experimental level.

Key words: snap-bean, multivariate analysis, genetic divergence, genotype-environment interaction.

INTRODUCTION

In the search for superior cultivars, the use of the genetic variability in crosses from groups genetically divergent represents an important strategy to obtain selection gains. The use of multivariate techniques is a feasible option for this purpose, since they allow combinations of multiple information within the experimental unit, through genotype discrimination based on a variable complex (Cruz and Regazzi 2001).

The importance of genetic diversity for improvement lies in the fact that crosses which involve parents genetically divergent are the most suitable to bring forth high heterotic effects and, also, a greater genetic variability in segregating generations (Rao et al. 1981, Cruz 1990).

In relation to breeding programs, Falconer (1981) emphasizes that when the genotypes are evaluated in more than one environment, with the objective of quantifying the diversity

found in the interaction, the differences in performance can be due to different groups, when compared to groups in each environment. Since the accessions are developed in dynamic systems, there is, generally, a differentiated behavior of the latter regarding to the response to the environmental variations.

The interaction genotype x environment is a constant challenge for breeders, due to the complications that it causes at selecting accessions evaluated in different environments. The greater the diversity among genotypes and environments, mainly in those with considerable variations in temperature and precipitation, the greater is the importance of the interaction (Borém 2001).

Consequently, the evaluation of genetic diversity in more than one environment could bring forth more clarifying results on the behavior of genotypes, with a subsequent influence on the performance of these in future breeding programs.

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In spite of their importance, studies with heterotic snap-bean groups conducted with multivariate techniques are scarcely (Maluf and Ferreira 1983, Rodrigues et al. 1998, Abreu 2001), especially with genotypes evaluated in different environments. Such research could work out recommendations for crosses in future breeding programs with the crop. In this context, this study aimed to quantify the genetic diversity of 14 snap-bean accessions in two environments (sowing season), to identify genotypes that could be recommended for crossings or even, on an experimental level, for producers in the Northern Fluminense Region.

MATERIAL AND METHODS

The experiments were conducted between 24/04/2001 and 01/08/2001 (autumn/winter) and between 03/10/2001 and 12/12/2001 (summer), at the Research Support Unit of the Center for Science and Technologies of Agriculture and Animal Husbandry, of the State University Darcy Ribeiro of the Northern Fluminense Region (UENF), Campos dos Goytacazes, in the Northern Fluminense Region, Rio de Janeiro State, Brazil.

The experimental design was the randomized blocks with 14 treatments and four replications. Each plot contained 30 plants in 6.0 m long rows (rows spaced 1 m apart and plants 0.40 m); ten plants per plot were used for morphoagronomical characterization.

Based on the International Board for Plant Genetic Resources (1982), currently IPGRI, the following descriptors were evaluated for a quantification of the genetic diversity: DF - days to flowering, expressing the number of days to flowering when at least 50% of the plants per plot presented recently opened flowers; PH - plant height, expressing the distance from the colon to the end of the main stem, as soon as the plants developed the inflorescence at the apex of the main stem, in mm; IFP - insertion height of the first pod, expressing the distance from the colon to the insertion of the first pod, in mm; TPW - total pod weight, obtained by the quantification of the weight of all pods per plot, expressed in grams; TNP - total number of pods, expressed by the total number of pods per plot; MW - mean pod weight per plant, obtained by the ratio between the total weight and number of plants per plot, expressed in grams; MN - mean number of pods per plant, given by the ratio between the total number of pods and the number of plants per plot. Samples of ten pods per plant were evaluated for: PL - pod length, expressed in mm, obtained by the longitudinal measure of the harvested pods; PD - pod diameter, expressed in mm, considered as the transversal section of the pod for consumption; NS - number of seeds per pod, obtained by the count of immature seeds harvested per pod; FIB - fiber content of the pod, in samples of 10 g of pods *in natura*, according to the procedure described by Frank et al. (1961), modified by Rodrigues (1997).

Initially, an individual analysis of variance was carried out for each sowing season, and thereafter a joint analysis of variance for each trait, considering the mixed model with fixed environmental effect (Vencovsky and Barriga 1992, Cruz and

Regazzi 2001). The clustering test of means, as proposed by Scott-Knott (1974), was applied at the 5% probability level, to compare access means. The multivariate analysis evaluated the genetic divergence among accessions by the methods nearest neighbor clustering, Tocher's algorithm, based on the Mahalanobis' generalized distance, and canonical variables (Cruz and Regazzi 2001). All analyses were performed with the GENES software (Cruz 2001).

RESULTS AND DISCUSSION

All traits presented significant differences in the analysis of variance, for both sowing seasons - an essential feature for the establishment of breeding programs. This fact indicates the possibility of selecting snap-bean superior accessions to those of the Germplasm Bank of the UENF for the Northern Fluminense Region.

All traits presented a significant difference for the interaction genotypes x environment, except the pod diameter (PD) and insertion height of the first pod (IFP). This confirms a differential response of the genotypes to environmental changes, a fact that could be explained by the climatic difference between the two studied sowing seasons. This argument is based on the fact that the first crop (autumn/winter season) was grown under ideal cultivation conditions [according to Castellane et al. (1988) and Viana (1993) in a temperature range between 18 and 24 °C], and the second crop (summer season), however, under high temperatures and high precipitation. These factors, according to Castellane et al. (1988), cause a decrease of 40 to 65% in the flowers number. High temperature periods and humidity in excess, which favor the appearance of anthracnose (*Colletotrichum lindemuthianum*) and common bacterial blight (*Xanthomonas campestris* pv. *phaseoli*), common mosaic (*Potyvirus* sp.) and white mold (*Sclerotinia sclerotiorum*) must be avoided in *Phaseolus vulgaris* crop.

It must be pointed out that in the joint analysis of variance, the traits days to flowering (DF), pod length (PL), pod diameter (PD), and the number of seeds per pod (NS) presented high values of experimental variation coefficient, which might stand in direct connection with the climatic difference between the two sowing seasons.

The nearest neighbor clustering (Figure 1), based on seasonal data (autumn/winter), revealed four groups: I - accessions UENF 1453, UENF 1480, UENF 1469, and UENF 1466; II - UENF 1483, UENF 1579, UENF 1487, UENF 1481, UENF 1488, UENF 1485, UENF 1486, and UENF 1484; III - UENF 1467; and IV - UENF 1482.

Figure 2 shows accessions of *Phaseolus vulgaris* in the summer sowing season crop. Similarly to the clustering of autumn/winter crop (Figure 1), four groups were formed, however with the different composition: I - accessions UENF 1486, UENF 1488, UENF 1487, UENF 1483, and UENF 1579; II - UENF 1466 and UENF 1467; III -

UENF 1482, UENF 1453, UENF 1480, UENF 1484, UENF 1485, and UENF 1481; IV - UENF 1469.

A reduced similarity in group compositions between autumn/winter and summer was observed, attributed to the significance found for genotype x environment (sowing season) interaction due to the inconsistent accessions behavior in reaction to environmental variations. Consequently, the intended recommendation of genetic materials for producers of the Northern Fluminense Region, even if on an experimental level, should not be excepted from a more profound analysis of the genotypic behavior in different planting seasons and, if possible, at different sites.

Five groups were formed for the autumn/winter sowing season by the Tocher's algorithm (Table 1), with 71.43% of the accessions in group I. This clustering algorithm agrees

partially with those obtained by the nearest neighbor clustering (Figure 1); only few similarities are observed. The existence of contrasting results between these two methods was also verified by Amaral Júnior (1996), who evaluated the genetic divergence among accessions of pumpkin (*Cucurbita maxima*).

The result of the Tocher's clustering for autumn/winter (Table 1) shows that accessions 1 (UENF 1467), 6 (UENF 1486), 10 (UENF 1482), and 11 (UENF 1484) include discrepant traits that hinder their participation in the same group. Thus, these accessions are very divergent, so they can be employed in crosses to exploit the heterotic effect.

For the summer season, the Tocher's algorithm gave rise to the formation of four groups (Table 2). Tocher's group I agreed with groups I and II of the nearest neighbor clustering dendrogram (Figure 2). In both methods, group IV contained

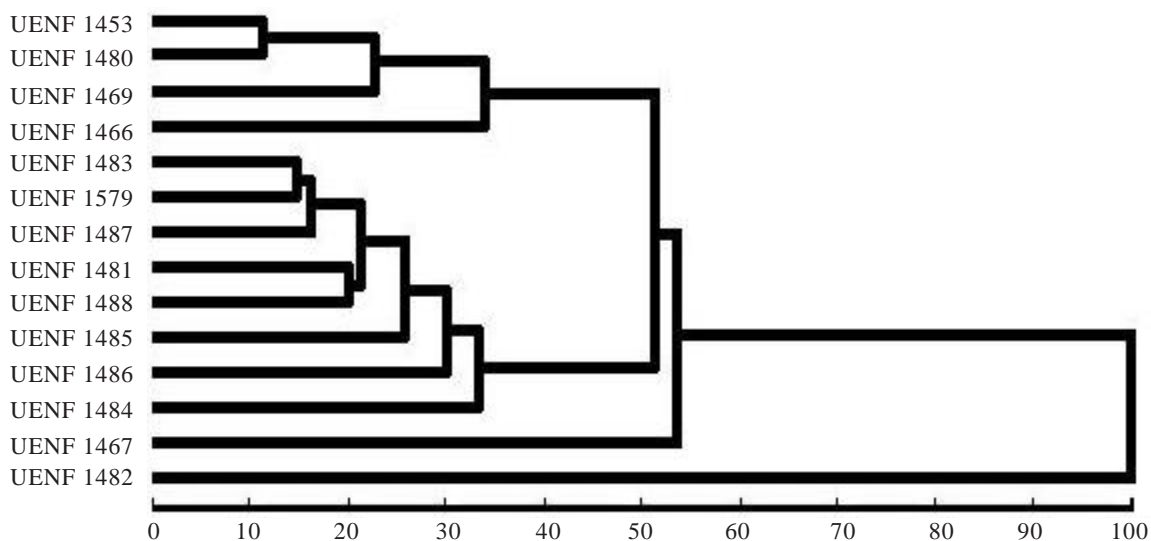


Figure 1. Nearest neighbor clustering dendrogram of genetic dissimilarities among 14 accessions of snap-bean, based on 11 traits evaluated in the autumn/winter crop.

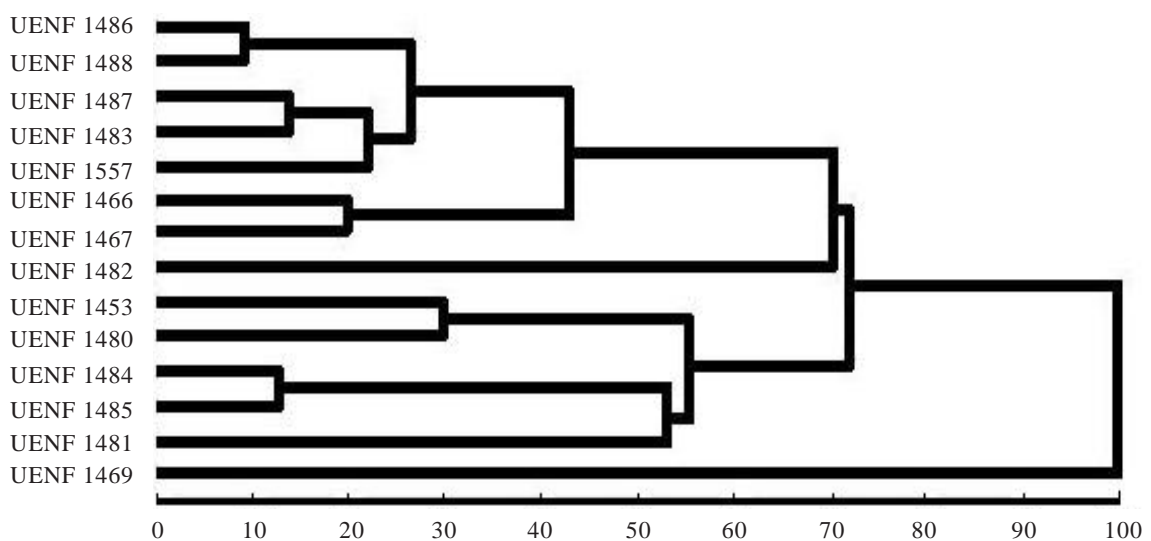


Figure 2. Nearest neighbor clustering dendrogram of genetic dissimilarities among 14 accessions of snap-bean, based on 11 traits evaluated in the summer crop.

Table 1. Tocher algorithm of clustering for 14 snap-bean accessions in relation to 11 traits evaluated in the autumn/winter crop

Groups	Accessions ¹
I	1, 5, 4, 2, 7, 9, 14, 12, 8, 13
II	6
III	11
IV	3
V	10

¹ 1 = UENF 1453; 2 = UENF 1466; 3 = UENF 1467; 4 = UENF 1469; 5 = UENF 1480; 6 = UENF 1486; 7 = UENF 1481; 8 = UENF 1487; 9 = UENF 1488; 10 = UENF 1482; 11 = UENF 1484; 12 = UENF 1483; 13 = UENF 1485; and 14 = UENF 1579.

Table 2. Tocher algorithm of clustering for 14 snap-bean accessions in relation to 11 traits evaluated in the summer crop

Groups	Accessions ¹
I	6, 9, 12, 14, 8, 2, 3
II	11, 13, 5, 1, 7
III	10
IV	40

¹ coded as in Table 1.

only accession 4 (UENF 1469), outstanding as one of the most divergent of the summer season. There was no concordance among the other groups.

When applying canonical variables, the first two variables explained 74.20% of the total variation and their scores were used to build a plot (Figure 3). An analysis of Figure 3 reveals four groups of accessions. Accessions 2 (UENF 1466) and 10 (UENF 1482) were the most genetically distant, each one forming a group of its own. The other groups consisted of two large divergent groups, of special interest to orientate crosses in future breeding programs. To a certain extent, these results agree with the Tocher’s algorithm (Table 1), and are therefore trustworthy for the identification of highly divergent parents.

The two first canonical variables for the summer season explained nearly 88.44% of the total variation, which allows a description of the genetic divergence of the accessions in a plot (Figure 4). Five groups can be observed in a visual analysis of the plot. Accession 4 (UENF 1469) was outstanding for its divergence, confirmed by the other analyzed group methods. In analogy, access 10 (UENF 1482) formed a group in agreement with the Tocher’s algorithm (Table 2), demonstrating a somewhat divergent material. The spatially formed groups, for the summer season (Figure 4), also differed from the graphically composed groups for autumn/winter (Figure 3), with exception of accession 10 (UENF 1482), which stood out with expressive divergence in both seasons, manifesting the influence of the environment on dissimilarity among genotypes.

Despite the discordance in the group formation of autumn/winter and summer (Figures 3 and 4), there are some similarities, in the sense of recommending crosses for future breeding programs. For instance, conclusion can be drawn that crosses among access 4 (UENF 1469), with the group formed by accessions 6 (UENF 1486), 8 (UENF 1487), 9 (UENF 1488), 12 (UENF 1483), and 14 (UENF 1579); besides the group with accession 10 (UENF 1482) are promising for an exploitation of the genetic distance.

When the traits of interest for breeding are considered (mean pod weight per plot, total number of pods per plot, mean number of pods per plot, fiber content, days to flowering, plant height, pod length, pod diameter, number of seeds per pod, and insertion height of the first pod), the conclusion is drawn that accessions 4 (UENF 1469), 6 (UENF 1486) and 9 (UENF 1488) are attractive, since they present good performance for yield and its components (Tables 3 and 4). Crosses between the accessions 4 (UENF 1469) and 6 (UENF 1486), and between the accessions 4 (UENF 1469) and 9 (UENF 1488) are recommended. Furthermore, the strategy of crossing accessions 4 (UENF 1469) with 6 (UENF 1486), and, thereafter, using F₁ in combination with accession 9 (UENF 1488), might allow a greater genetic recombination, with an increased opportunity to obtain superior segregates in advanced generations. It should be emphasize that accessions 6 (UENF 1486) and 9 (UENF 1488) are the cultivars ‘Alessa’ and ‘Cota’, developed earlier for the producing regions Baixada and Serrana, in the State of Rio de Janeiro, although they also presented good performance when grown on other sites of the Southerastern Region of Brazil (Leal 1990, Leal and Bliss 1990).

Accessions 8 (UENF 1487), cultivar ‘Andra’; 12 (UENF 1483), cultivar ‘Isla’; and 14 (UENF 1579), with ‘Noodle’ pods type are well accepted in other localities of the Southerastern Region, and have already gained some share on the Fluminense market; thus, they could be recommended to supply fresh fruit markets, since during the year, the Northern Fluminense Region presents high temperatures. Based on the summer season results accessions 6 (UENF 1486), ‘Alessa’; 8 (UENF 1487), ‘Andra’; 9 (UENF 1488), ‘Cota’; 12

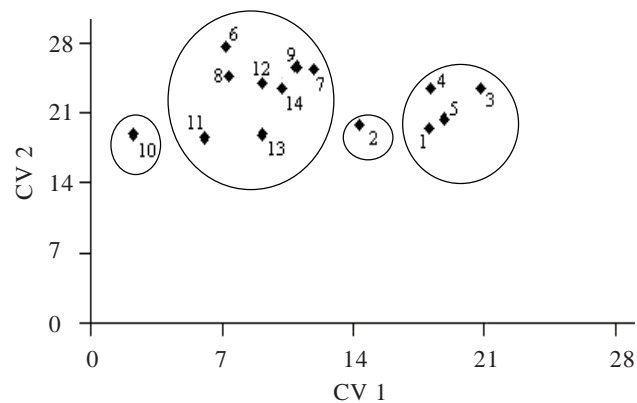


Figure 3. Plot of scores of the first two canonical variables (CV1 and CV2) for 14 accessions of snap-bean in the autumn/winter season. Accessions coded as in Table 1.

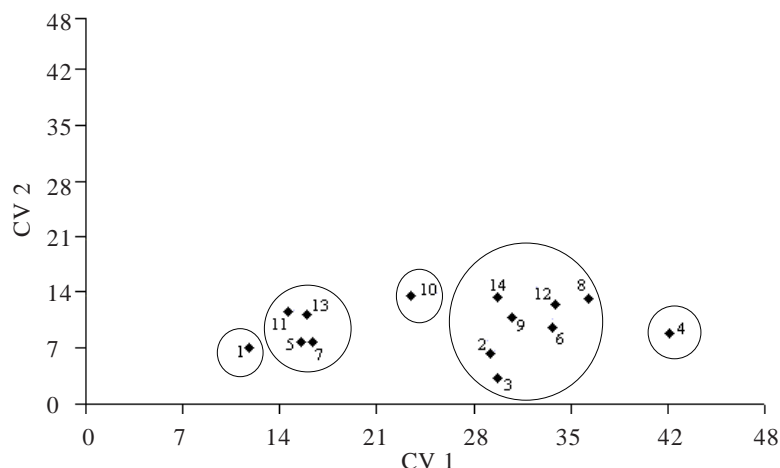


Figure 4. Plot of scores of the first two canonical variables (CV1 and CV2) for 14 accessions of snap-bean in the summer crop. Accessions coded as in Table 1.

Table 3. Means¹ of the snap-bean accessions in relation to the 11 evaluated traits in the autumn/winter crop

Accessions ²	Traits										
	TPW	MW	TNP	MN	FIB	DF	PH	PL	PD	NS	IFP
1	1711.89 a	171.19 a	835.25 a	83.53 a	0.40 b	46.75 b	446.51 c	80.02 d	9.42 b	6.78 a	88.44 a
2	1577.02 a	161.05 a	742.36 a	75.43 a	0.50 b	41.00 c	389.74 c	96.75 c	9.60 b	6.34 a	89.16 a
3	1675.91 a	167.59 a	621.25 b	62.13 b	0.39 b	42.50 c	708.05 a	84.67 d	10.21 a	5.58 b	74.23 b
4	1617.36 a	161.74 a	537.25 b	53.73 b	0.32 c	41.25 c	566.23 b	96.05 c	10.29 a	6.83 a	106.63 a
5	1661.10 a	166.11 a	837.25 a	83.73 a	0.40 b	44.50 b	563.10 b	82.74 d	9.68 b	6.90 a	106.60 a
6	2265.91 a	226.59 a	400.75 c	40.08 c	0.20 d	39.50 c	343.13 d	150.02 a	10.86 a	6.41 a	86.58 a
7	1735.85 a	173.59 a	353.50 c	35.35 c	0.31 c	38.25 c	309.93 d	116.24 b	10.52 a	5.86 b	75.80 b
8	1650.64 a	165.07 a	257.25 c	25.73 c	0.30 c	47.50 b	296.20 d	128.12 b	8.77 c	6.24 b	98.41 a
9	1559.78 a	155.98 a	327.53 c	32.75 c	0.13 d	46.00 b	290.19 d	122.54 b	10.08 a	5.97 b	77.74 b
10	1232.23 a	132.41 a	251.00 c	27.25 c	0.67 a	45.75 b	300.24 d	125.28 b	7.20 d	6.60 a	95.74 a
11	2259.65 a	225.97 a	614.00 b	61.40 b	0.35 c	46.00 b	284.34 d	121.89 b	6.99 d	6.84 a	70.95 b
12	1460.92 a	146.09 a	272.88 c	27.29 c	0.16 d	49.00 b	276.18 d	117.70 b	8.05 c	5.72 b	76.26 b
13	1030.22 a	103.77 a	271.79 c	27.18 c	0.23 d	54.00 a	263.00 d	101.39 c	6.88 d	6.63 a	66.03 b
14	1777.51 a	177.75 a	345.00 c	34.50 c	0.21 d	45.75 b	343.68 d	117.61 b	8.46 c	6.73 a	95.43 a

¹ Values followed by the same letter in each column belong to the same group, according to the Scott-Knott test, at the 5% level. ² Accessions coded as in Table 1.

Table 4. Means¹ of the snap-bean accessions in relation to the 11 evaluated traits in the summer crop

Accessions ²	Traits										
	TPW	MW	TNP	MN	FIB	DF	PH	PL	PD	NS	IFP
1	320.57 b	47.83 a	173.00 a	25.33 b	0.58 b	46.75 b	536.63 a	74.95 b	9.03 c	5.46 a	126.66 a
2	584.26 b	54.84 a	210.75 a	38.75 a	0.75 a	50.50 a	370.44 b	85.24 b	9.44 c	4.82 b	99.38 a
3	535.15 b	43.79 a	222.00 a	39.44 a	0.92 a	53.25 a	593.13 a	104.96 a	10.21 b	4.58 b	87.34 a
4	722.48 a	35.60 a	234.00 a	40.59 a	1.05 a	53.00 a	463.91 b	92.46 b	9.91 b	5.72 a	126.09 a
5	426.96 b	49.92 a	217.00 a	31.63 b	0.70 a	45.50 b	526.88 a	73.85 b	8.48 c	5.72 a	140.16 a
6	792.03 a	61.18 a	167.50 a	29.56 b	0.56 b	41.75 c	421.56 b	118.80 a	10.71 b	5.55 a	95.78 a
7	351.44 b	73.03 a	90.54 b	26.34 b	0.39 b	37.00 d	328.13 b	100.03 b	13.88 a	4.28 b	289.06 a
8	929.85 a	69.90 a	147.50 b	26.25 b	0.52 b	36.00 d	409.53 b	119.46 a	7.89 c	5.97 a	97.72 a
9	844.35 a	70.67 a	161.00 a	27.41 b	0.54 b	36.00 d	436.09 b	126.35 a	11.01 b	5.68 a	94.44 a
10	592.30 b	67.39 a	142.50 b	27.03 b	0.54 b	36.00 d	358.13 b	111.68 a	7.05 c	5.97 a	85.16 a
11	251.89 b	66.89 a	102.56 b	27.75 b	0.78 a	37.00 d	361.56 b	93.83 b	7.00 c	5.32 a	100.70 a
12	941.30 a	66.24 a	171.00 a	25.88 b	0.65 b	40.75 c	427.03 b	110.13 a	8.43 b	5.59 a	110.47 a
13	326.92 b	67.96 a	91.25 b	24.88 b	0.57 b	41.75 c	352.97 b	94.33 b	7.38 c	5.02 b	72.73 a
14	983.93 a	91.93 a	179.00 a	29.82 b	0.28 b	42.75 c	426.44 b	116.89 a	8.78 b	6.24 a	107.50 a

¹ Values followed by the same letter in each column belong to the same group, according to the Scott-Knott test, at the 5% level. ² Accessions coded as in Table 1.

(UENF 1483), 'Isla'; and 14 (UENF 1579) could be, on an experimental scale, indicated for regional producers, as a new option of crop rotation in summer. As shown in the Tables 3 and 4, these accessions could, even under high temperatures, maintain a good performance of yield and related traits.

CONCLUSIONS

1. The clustering methods, from the morphoagronomical traits, presented more similar results in the autumn/winter than the summer season.

2. Owing to the inconsistent behavior of the accessions in reaction to the genotype-season interaction, the similarity in the group composition of the environments was reduced.

3. Crosses between accessions 4 (UENF 1469) and 9 (UENF 1488) and accessions 4 (UENF 1469) and 6

(UENF 1486); as well as the use of their F_1 in combination with access 9 (UENF 1488), are recommended to obtain superior segregates in advanced generations.

4. Accessions 6 (UENF 1486 - 'Alessa'), 8 (UENF 1487 - 'Andra'), 9 (UENF 1488 - 'Cota'), 12 (UENF 1483 - 'Isla'), and 14 (UENF 1579) are indicated for the use by regional producers, in an experimental state, as a new option for crop rotation.

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Divergência genética em feijão-de-vagem (*Phaseolus vulgaris* L.) avaliada por diferentes metodologias

RESUMO - Quatorze acessos de feijão-de-vagem do Banco de Germoplasma da UENF foram avaliados quanto à diversidade morfoagronômica, em interação com épocas de semeadura, por técnicas multivariadas. Utilizaram-se blocos ao acaso com quatro repetições, em duas épocas (abril a agosto - outono/inverno e outubro a dezembro - verão) de 2001. A coincidência dos métodos de agrupamento foi maior no outono/inverno do que no verão. Houve reduzida semelhança na composição dos grupos entre épocas, decorrente da interação genótipos x épocas. Recomenda-se o cruzamento entre os acessos (UENF 1469) e (UENF 1488) e entre os acessos (UENF 1469) e (UENF 1486); bem como utilizar o F_1 destes últimos em combinação com o acesso (UENF 1488), para obtenção de segregantes superiores em gerações avançadas. Os acessos (UENF 1486), (UENF 1487), (UENF 1488), (UENF 1483) e (UENF 1579) são indicados para plantio de verão, em caráter experimental.

Palavras-chave: feijão-vagem, análises multivariadas, divergência genética, interação genótipos por épocas.

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