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ARTICLE

Genetic diversity of common bean accessions in the germplasm bank of the Instituto Agronômico - IAC

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ABSTRACT - *The genetic divergence among 993 accessions of common bean (*Phaseolus vulgaris *L.) in the germplasm bank of the Instituto Agronômico IAC (agronomical Institute in Campinas, state of São Paulo) was evaluated in an analysis using 23 qualitative and quantitative agromorphological/ morphological and agronomic descriptors. Multivariate analyses such as the Euclidean distance, principal component analysis and Tocher's cluster method were used to quantify the divergence among the accessions. The joint use of the analyses allowed the identification of 45 groups of which the first five absorbed 88.28% of all accessions. Among the 23 evaluated descriptors, the principal component analysis allowed the discarding of five that were redundant and/or little variable and the eight first principal components were necessary to explain 70% of the total variation. The multivariate methods proved efficient when used in germplasm collections, optimizing the descriptor set and establishing an orientation for future crossings in the common bean improvement program of the IAC.*

Key words: Common bean, common bean germplasm, multivariate analyses, genetic improvement.

INTRODUCTION

The genetic improvement of common bean involves uncountable processes until the possible recommendation of a cultivar. All of them should be considered equally important, from the choice of the parents to the selection of genotypes in the competition trials. To recommend a common bean cultivar for commercialization, it must bear favorable yield traits, resistance to the main diseases of the crop such as anthracnose and angular leaf spot, and traits of technological qualities such as cooking time,

nutritional qualities and the type of sauce of the black tegument beans. Besides these traits, common beans with carioca and black grain types presenting traits of Mesoamerican origin are preferred by the population in Brazil. Cultivars with traits of Andean origin with their large seeds find little acceptance on the market. These limitations affect the breeder's work, since the reduced number of parents for crossings often hampers the achievement of more productive cultivars (Carbonell et al. 1999).

The progress with improvement for high yielding common bean (*Phaseolus vulgaris* L.) has been somewhat

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modest, around 1.21% per annum (Elias et al. 1999). The use of divergent parents in crossings is an advantageous option, offering favorable genetic combinations through the effects of additivity, pleiotropy and epistasis that stipulate the presence of favorable traits. The establishment of rational and effective criteria for the identification of unrelated parents, aiming at synthesized lines that allow the breeder to meet his objectives has therefore become a burning question in plant improvement.

Dias et al. (2004) explain that there are two ways to attain these objectives. The first is to test the parent types for their combining ability. In this case diallelic crossings systems are conducted to evaluate the general and specific combining ability. The second possibility, which fits better in the common bean improvement, is based on the premise that highly divergent parent genotypes with a high performance mean can create superior lines, i.e., the selection of parents by performance *per se* evades the realization of a large number of crossings.

The characterization of germplasm banks deepens the knowledge about the existing variability, identifies divergent parents and makes the work of the breeder in the elaboration of the crossing blocks easier. The characterization spawns complementary information for the breeder as multiple measurements of the experimental genotypes are obtained. In the simultaneous employment of various descriptors the multivariate techniques (for example the cluster analyses, analysis of principal components and canonic variables) are favorable options for the optimization of germplasm collections and in the prediction of heterotic combinations, where hundreds of undesirable crossings can be avoided.

The principle of the multivariate analysis is to simultaneously consider a set of random variables and their relations among each other. Basically, multivariate techniques for studies of diversity based on measurements of genetic dissimilarity among the genotypes are applied, such as the Euclidean distance, mean Euclidean distance and generalized distance of Mahalanobis. The cluster or grouping analysis deals with the establishment of similar groups of individuals in relation to the observed variables. Among the cluster methods, Tocher's optimization method and the hierarchic methods such as the nearest-neighbor method are noteworthy. These methods have been used by several authors such as Singh et al. (1991), Fonseca and Silva (1999), Ferrão et al. (2002), Machado et al. (2002) and Rodrigues et al. (2002).

The present study had the objective of evaluating common bean accessions by means of botanic agronomical descriptors, aiming at an enhanced conservation and use in the genetic improvement of the crop. Multivariate analyses were used with the objective of quantifying the genetic divergence among the accessions, forming groups of diversity regarding genetic dissimilarity, discarding the redundant descriptors and identifying combinations between the most promising parents for the development of superior lines.

MATERIAL AND METHODS

Altogether, 993 common bean accessions presenting important traits for the genetic improvement of the crop were selected at the IAC and evaluated by means of 23 botanic agronomical descriptors of data of the plant, pod, seeds, and reaction to diseases. The accessions were sown in the years 2002 and 2003 at the Centro Regional Universitário of Espírito Santo do Pinhal - CREUPI, in the county of Espírito Santo do Pinhal, state of São Paulo. The accessions were sown in 3 meter long rows, spaced 0.50 meters apart, without replications for the multiplication of seeds and evaluation of the descriptors. In-between every 10 accessions, a row of cultivar IAC-Carioca Eté was sown as local control.

The assessed post-harvest seed descriptors were the mass of a thousand seeds (SMMS), primary color (SPC), secondary color (SSC), gloss (SG), shape (SSH), number of colors (SNC), color of the halo (SCH), profile (SP), and seed size (SS). The pod descriptors primary colors (PPC), secondary when present (PSC), hue of the secondary color when present (PHSC), length (PL), width (PW), profile (PP) and number of seeds (PNS) were evaluated. The evaluated plant descriptors were the color of the wing in the flower (FLCW), shape of the bracteole (FLFB), plant height (PH) and growth habit (GH). The reaction to diseases was evaluated in laboratories where the 993 accessions with the races 65 (Alfa), 31 (Kappa) and 89 (Sigma) of the anthracnose pathogen *Colletotrichum lindemuthianum* were inoculated under controlled temperature and humidity conditions. All evaluations of the plant, seed, pod, and reaction to diseases were carried out following the national and international (CIAT) norms established for the evaluation of common bean germplasm (Van Schoonhoven and Pastor-Corrales 1987, Vilhordo et al. 1988).

For the quantification of the genetic divergence among the accessions multivariate analyses such as the Euclidean distance, analysis of principal components and of accession clusters by Tocher's algorithm of optimization were used. Cruz (2001) recommends the utilization of the Euclidean distance and principal component analysis to

evaluate accessions of germplasm banks since replications are not always available.

Owing to the different measurement scales the data were standardized before running the analyses. Thus, the original mean X_{ij} obtained in descriptor j of accession i, was divided by the standard error of descriptor j, creating the reduced mean Y_{ij} of unitary variance. Thereafter, the matrix of distance among accessions was created using the Euclidean distance. Considering the observation in the i-th accession of the j-th descriptor, the Euclidean distance between the pair of genotypes i and i' was defined by the following expression:

$$d_{ii'} = \sqrt{\sum_j (Y_{ij} - Y_{i'j})^2}$$

Once the matrix of dissimilarity among accessions was obtained, the clusters were defined according to Tocher's algorithm of optimization as well as the intra and intergroup means. The intergroup distances provide breeders with information on the parents that are to be used in the blocks of crossings. In the following phase, the principal component analysis (PCA), combined with the clusters established by Tocher was run to visualize the divergence in a Cartesian representation. This was possible by the dispersion of the scores of the first principal components, according to the criterion of a minimal absorption of 70% of the total variation in the first components.

Three important procedures were used to discard the descriptors considered redundant or little informative in the analysis. The first was the utilization of principal components to identify redundant descriptors based on the criterion of Jolliffe (1973), complemented by the procedure used by Dias et al. (1997). According to the criterion of Jolliffe (1973) disposable descriptors were those that presented the highest load factors in the eigenvectors of the last principal components. At each disposal, the remaining descriptor set was re-analyzed as Dias et al. (1997) suggested to identify load factors highest value in the last principal component. The reason for this re-analysis process is that discarding a descriptor implies in a modified contribution of the remaining descriptors to the total variance. In the second procedure the coefficients of phenotypic correlation between the descriptors were estimated two by two, by means of the analysis of Pearson's correlation. The significance of these correlations was tested at a level of 5% probability. In the third procedure, the biologic/agronomical importance for the improvement program of the descriptor to be discarded was evaluated. All genetic-statistical analyses were processed by software Genes (Cruz 2001), SAS (SAS Institute Inc. 1989) and Statistica (StatSoft Inc. 1999).

RESULTS AND DISCUSSION

Genetic divergence by cluster analyses

The Tocher method applied the matrix of the Euclidean distances, together with the scores of the principal component analysis discriminated 45 clusters or groups of similarity (Figure 1). The first eight groups were considered the most important for covering 92.30% of all accessions of which group 1 to 8 separately covered 64, 3.63, 12.6, 5.94, 2.11, 1.91, 1, and 1.11%, respectively. The other clusters were marked by quite distinct traits in relation to the total sample.

The analysis of the mean intragroup values characterizes group 1 as containing black tegument accessions with small seeds whose genotypes are mostly susceptible to races 31 and 89 of the anthracnose pathogen. Similarly, group 2 was characterized as a subgroup of group 1, with similar susceptibility traits to anthracnose, differing only in the primary pod color. Recombination between the clusters 1 and 2 is recommended as an important source to obtain lines in the short term, due to the similarity of most of the descriptors. Group 3 held accessions with important descriptors for the improvement program, such as carioca tegument, resistance to three anthracnose pathogen races and a high mass of a thousand seeds. For group 4, the descriptors that differed from the others were primary seed color yellow, growth habit type I and long and full seeds, represented exclusively by accessions of Andean origin.

In group 5 the seeds with white tegument and resistance to race 65 of anthracnose were predominant. As in group 4, group 6 was characterized by accessions of Andean origin with a high mass of a thousand seeds, a triangular bracteole, but with predominantly brown color of the tegument. In groups 7 and 8 the seed teguments were black, and the main traits that differentiated it from groups 1 and 2 were the seed gloss for group 7 and growth habit type III for group 8. The discrimination of the clusters in the first eight groups was influenced by the descriptor tegument color, in agreement with the results obtained by Beebe et al. (1995) and Duarte et al. (1999). These authors also verified that Mesoamerican and Andean cultivar groups tend to be differentiated in function of the tegument color while maintaining similarities regarding other descriptors.
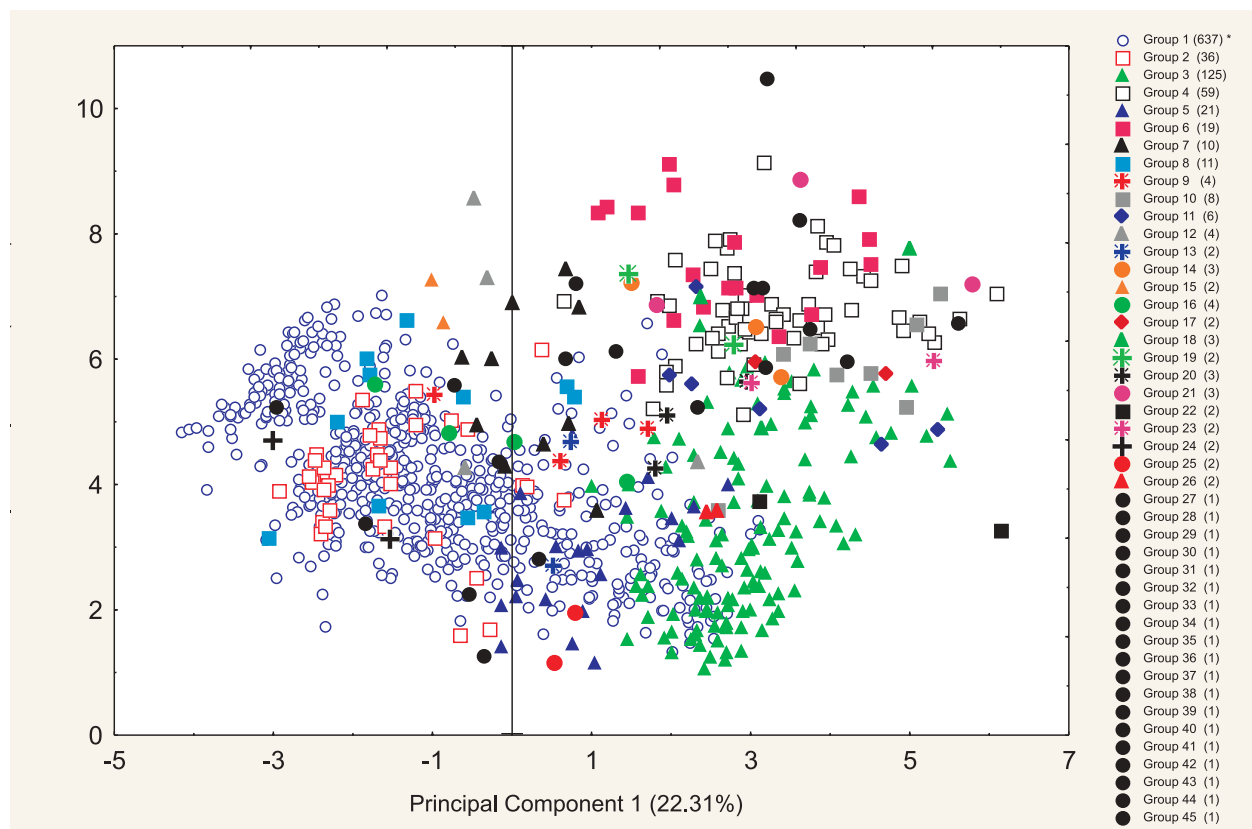
Figure 1. Biplot formed by the first two principal components representing the divergence among 993 common bean accessions in relation to 23 descriptors. *Number of accessions present in each cluster revealed by the algorithm of optimization of Tocher

Dias et al. (1997) emphasized that studies that involve a high number of genotypes should consider groups instead of individual genotypes, and the breeders should therefore base their studies on the intra and intergroup distances. In the comparison the intergroup means of the principal clusters revealed by Tocher (Table 1) were therefore similar up to cluster 27, indicating that the diversity among these groups was similar.

From group 27 on the mean intragroup distances were zero as there was only one accession per group. The maximum intergroup distances were observed between the groups 21 and 43, 37 and 43, and 43 and 45. These groups were the most divergent since their traits were quite distinct from the total sample, principally the seed traits. It is worth remembering that divergence is a necessary condition for the increase of heterosis (Falconer 1989). In common bean improvement programs it is however not sufficient to consider divergence solely as criterion for the orientation of the crossings since the grain represents the main product of the common bean, and the Brazilian population prefers the carioca and black tegument types. Thus, divergent genotypes with exotic traits, mainly size and grain color, provide cultivars of no commercial value. In this context, the indication of crossings between the groups 21 and 43, 37 and 43, and 43 and 45 would indicate broad genetic diversity, but with no commercial value at all.

As a way of meeting the requirements established by the common bean improvement program of the Instituto Agronômico-IAC, recombinations between the groups 3 and 45, 1 and 45, 27 and 45, 2 and 34, and 18 and 45 aiming at the establishment of cultivars with carioca and black teguments are recommended. These groups contain the necessary traits to obtain new cultivars such as presence of genetic dissimilarity, anthracnose-resistance, growth habit type II, high mass of a thousand seeds and principally commercial acceptability. Crossings that should not be discarded are those between the groups 5 and 45, 12 and 45, 4 and 45, and 20 and 21 for the achievement of cultivars with white, pink, jalo, light brown and red teguments, also appreciated in small market niches.

Genetic divergence by principal component analysis

The principal component analysis (PCA) had the objective of demonstrating the existing variability among

Table 1. Estimates of the Euclidean distances intra (bold) and intergroups of the principal groups revealed by the cluster of Tocher, referring to 23 agromorphological descriptors evaluated in 993 common bean accessions

Clusters	1	2	3	4	5	6	7	8	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
1	**5.5**																											
2	7.4	**4.9**																										
3	6.9	8.7	**5.4**																									
4	7.7	9.1	7.0	**5.7**																								
5	6.8	8.5	7.0	7.8	**5.2**																							
6	8.0	9.7	7.3	7.0	8.8	**5.6**																						
7	6.6	8.0	7.3	7.2	7.7	8.0	**5.8**																					
8	6.6	8.4	7.6	8.5	8.0	7.9	7.4	**5.9**																				
26	7.5	9.1	6.4	7.8	7.1	8.0	7.3	8.5	**6.1**																			
27	7.5	9.3	7.3	9.5	7.7	8.1	8.8	7.7	6.7	**0.0**																		
28	7.3	8.5	7.5	6.7	8.2	8.5	6.7	7.8	7.2	9.6	**0.0**																	
29	9.0	10.4	7.6	9.0	9.0	8.5	8.5	9.1	7.7	9.4	10.6	**0.0**																
30	8.3	9.7	7.9	6.4	7.4	7.8	7.5	9.3	7.7	10.2	8.1	8.3	**0.0**															
31	6.6	8.0	7.6	7.6	6.9	8.7	7.4	7.4	7.8	8.0	6.4	9.8	8.9	**0.0**														
32	8.4	9.7	6.9	6.6	9.2	7.3	8.2	9.0	7.9	8.7	7.2	9.4	9.4	7.8	**0.0**													
33	6.6	8.3	7.1	9.3	7.4	9.1	8.5	8.3	8.1	6.9	9.3	10.5	9.8	7.4	9.5	**0.0**												
34	8.2	9.5	7.4	6.9	8.8	7.8	7.7	8.7	8.2	9.4	8.3	8.4	8.0	9.6	8.2	10.1	**0.0**											
35	7.5	9.4	8.5	9.1	7.9	7.9	7.4	7.7	8.3	8.4	9.8	9.1	8.8	9.4	11.2	8.9	8.3	**0.0**										
36	8.5	10.3	7.7	7.7	9.1	6.4	8.3	8.8	8.7	8.8	9.3	10.5	8.0	10.8	8.5	8.8	7.5	7.5	**0.0**									
37	9.6	11.1	8.6	8.2	10.9	7.1	10.0	9.4	8.9	10.0	8.2	10.3	9.7	9.8	7.7	10.5	8.4	10.8	8.0	**0.0**								
38	8.9	6.9	9.1	8.9	9.8	9.6	7.5	8.7	9.0	10.3	7.8	10.0	9.6	8.5	9.5	10.7	8.9	9.3	10.7	11.0	**0.0**							
39	9.3	10.8	7.6	6.6	9.9	7.3	9.4	10.0	9.3	11.0	7.9	9.8	8.4	8.8	6.7	9.5	8.9	11.3	8.5	6.5	10.6	**0.0**						
40	6.4	8.1	8.6	9.2	8.7	8.4	8.4	6.8	9.6	7.5	8.8	11.1	9.4	8.1	10.1	6.4	9.6	8.8	8.7	9.6	10.6	10.4	**0.0**					
41	9.5	10.7	9.2	6.7	9.9	7.1	8.9	9.1	9.7	10.8	7.4	11.3	7.3	9.0	7.7	11.5	8.1	10.5	7.2	6.7	10.1	7.8	9.6	**0.0**				
42	7.1	8.7	8.1	9.0	7.3	9.8	8.6	8.6	9.8	8.4	9.6	10.5	9.8	8.2	9.4	7.3	9.6	9.4	9.5	12.6	11.0	10.9	8.3	11.5	**0.0**			
43	8.9	10.4	9.9	11.2	8.7	10.4	8.9	8.0	9.8	8.5	11.3	9.8	11.1	9.3	12.2	9.9	11.3	7.5	11.4	13.5	9.4	13.2	10.5	12.7	10.0	**0.0**		
44	7.7	8.8	8.3	7.1	9.4	8.1	7.4	8.4	9.9	11.2	7.3	10.4	7.6	8.2	8.0	8.9	9.1	10.5	8.7	8.7	9.5	7.0	7.4	7.3	10.1	12.1	**0.0**	
45	11.1	8.5	10.3	9.5	11.2	10.3	10.6	11.2	11.0	12.0	10.5	11.3	10.5	10.7	10.3	12.6	8.4	11.7	11.1	10.9	7.0	10.4	12.3	10.0	12.4	13.4	11.1	**0.0**

the 993 analyzed accessions graphically. When comparing the methods by the combination of the scores of principal components with the clusters defined by the algorithm of Tocher (Figure 1), a certain concordance of the analyses can be observed, since the discrimination of the groups was similar. Dias (1998) states that when the set of all principal components is used to calculate the Euclidean distance, the two methods produce similar results, at least when the matrix of correlation has an incomplete rank. By the principal component analysis, it is verified that the first two principal components absorbed 32.55% of the entire variation; the first three 40.66% and the first four components 48.09% (Table 2). To obtain 60% of the entire existing variation, the six first components were necessary. Although the absorption of variation seems low in the first two components, it can be considered high when compared to other studies realized by Singh et al. (1991), Rodrigues et al. (2002) and Machado et al. (2002), who analyzed a remarkably smaller quantity of accessions.

Morrison (1976) underlines that a minimum of 75% of the entire variation must be absorbed by the first two principal components. Cruz (2001) argue that when 70 to 80% of the variation in the first two components were not obtained, the graphic dispersion should be realized with

Table 2. Estimates of the eigenvalues associated to the principal components (PC), together with their relative accumulated importances (Root %) and referring to the 23 agromorphological descriptors evaluated in 993 common bean accessions

P C	Root	Root %	Accumulated %
1	5.1323877	0.223147290	22.3147290
2	2.3550974	0.102395540	32.5542830
3	1.8645032	0.081065356	40.6608185
4	1.7089034	0.074300146	48.0908331
5	1.5470334	0.067262322	54.8170653
6	1.1734666	0.051020289	59.9190942
7	1.1464139	0.049844084	64.9035027
8	1.0207306	0.044379591	69.3414617
9	0.9503256	0.041318506	73.4733123
10	0.8997205	0.039118283	77.3851406
11	0.8097989	0.035208649	80.9060054
12	0.7524450	0.032715001	84.1775055
13	0.6222525	0.027054457	86.8829513
14	0.5793158	0.025187642	89.4017155
15	0.5414270	0.023540305	91.7557459
16	0.4971217	0.021613988	93.9171448
17	0.4129096	0.017952592	95.7124040
18	0.3795921	0.016504003	97.3628043
19	0.2704751	0.011759787	98.5387830
20	0.1685948	0.007330208	99.2718038

the necessary components to absorb this percentage. If this criterion were observed, 45 diagrams involving the ten first principal components would be necessary, which is unfeasible.

It must be emphasized that the principal component analysis was used to identify the redundant descriptors and, principally, provide scores for plotting the biplots. Through the scores, the graphs with the principal components 1 and 2, together with the clusters revealed by Tocher agreed in the distinction of the groups. Another point taken into consideration was the quantity of accessions (88.28%) present in the first five groups revealed by the Tocher, which was also evidenced in the principal component analysis, without significant changes when using the other components.

Discarding of the redundant descriptors by principal components

The principal component analysis allowed the identification of the redundant descriptors, i.e., those that influenced the distinction of the accessions little. The hue of the secondary pod color was discarded first. This descriptor was discarded for being redundant, as it was highly correlated (0.99**) with the secondary pod color (Table 3). Secondly, the number of seed colors, which has a high correlation (0.98**) with the secondary seed color was also discarded. Next the primary seed color, which presented a high correlation (0.84%**) with the color of the halo in the seed was discarded. The fourth disposal discarded the seed size for being correlated with the mass of a thousand seeds. The fifth and last descriptor discarded was the pod length, which had a correlation of only moderate magnitude (0.51**) with the seed format. The disposal occurred because in improvement programs the mean number of seeds per pod which in a way involves the pod length is ascribed greater importance.

From the fifth disposal on the methodology used to identify the redundant descriptors became inconsistent. According to the analysis, the next disposal was the color of the seed halo, correlated only with the color of the wing in the flower, without any degree of correlation between the descriptors in botanical terms, since the primary seed color was discarded for being correlated with the color of the halo. In the following, the disposal became more inconsistent since the descriptor mass of a thousand seeds should be discarded, which was correlated with the seed size, discarded in the fourth phase. Thus, the discarding was interrupted in the fifth phase, considering only 18 descriptors of the data set. The quantity of remaining descriptors after the disposal is similar to that obtained by Castineiras (1990) and Rodrigues et al. (2002). These

Table 3. Coefficients of phenotypic correlations between 23 agromorphological descriptors evaluated in 993 common bean accessions

Variables	PPC	PSC	PHSC	PP	PW	PL	PNS	GH	FLCW	FLFB	PH	ANALF	ANSIG	ANKAP	SNC	SPC	SSC	SCH	SS	SSH	SP	SMMS
PSC	0.11*																					
PHSC	-0.11	0.99**																				
PP	-0.04	-0.14	-0.15																			
PW	-0.02	-0.15	-0.15	0.20																		
PL	-0.01	-0.15	-0.15	0.11	0.39																	
PNS	0.00	-0.02	-0.02	0.02	-0.17	0.21																
GH	0.03	0.10	0.10	-0.14	-0.18	-0.02	0.13															
FLCW	0.17	0.21	0.21	-0.15	-0.14	-0.11	0.08	0.09														
FLFB	-0.02	0.05	0.04	-0.11	-0.33	-0.23	0.27	0.12	0.09													
PH	0.04	-0.07	-0.07	-0.11	-0.09	0.10	0.30	0.27	0.02	0.20												
ANALF	-0.02	0.16	0.16	-0.13	-0.21	-0.10	0.05	0.10	0.22	0.09	0.05											
ANSIG	0.04	0.09	0.09	-0.09	-0.19	-0.10	0.06	0.10	0.12	0.11	0.01	0.61										
ANKAP	0.04	0.07	0.07	-0.04	-0.12	-0.03	-0.01	0.04	0.07	-0.02	0.03	0.46	0.46									
SNC	-0.10	-0.17	-0.17	0.13	0.28	0.20	-0.08	-0.06	-0.40	-0.17	0.00	-0.29	-0.23	-0.17								
SPC	0.11	0.29	0.28	-0.17	-0.23	-0.18	0.14	0.13	0.61	0.28	0.10	0.27	0.17	0.10	-0.45							
SSC	-0.09	-0.15	-0.14	0.14	0.29	0.20	-0.10	-0.05	-0.36	-0.21	-0.01	-0.27	-0.23	-0.16	0.98**	-0.45						
SCH	0.10	0.29	0.29	-0.12	-0.20	-0.17	0.05	0.12	0.61	0.14	0.04	0.28	0.17	0.14	-0.47	0.84**	-0.45					
SS	-0.05	-0.08	-0.08	0.11	0.49	0.36	-0.32	-0.09	-0.16	-0.52	-0.12	-0.17	-0.15	-0.03	0.26	-0.31	0.30	-0.24				
SSH	0.00	-0.03	-0.02	0.10	0.13	0.51**	-0.14	-0.14	-0.01	-0.25	-0.15	-0.07	-0.08	0.01	0.08	-0.13	0.08	-0.09	0.38			
SP	-0.04	0.02	0.02	-0.03	-0.13	-0.03	-0.06	-0.04	-0.09	-0.08	-0.02	-0.01	-0.05	0.00	0.04	-0.12	0.04	-0.09	0.08	0.03		
SMMS	-0.08	-0.14	-0.14	0.14	0.49	0.40	-0.24	-0.08	-0.25	-0.47	-0.08	-0.19	-0.17	-0.05	0.36	-0.37	0.37	-0.34	0.82**	0.34	0.08	
SG	0.00	-0.05	-0.05	0.10	0.11	0.10	-0.10	0.02	-0.17	-0.30	-0.14	-0.04	0.00	0.05	0.08	-0.16	0.10	-0.12	0.22	0.10	0.04	0.24

PPC: Pod: primary color; **PSC:** Pod: secondary color; **PHSC:** Pod: hue of the secondary color; **PP:** Pod: profile; **PW:** Pod: width; **PL:** Pod: length; **PNS:** Pod: number of seeds ; **GH:** Growth habit; **FLCW:** Flower: color of the wing; **FLFB:** Flower: format of the bracteole; **PH:** Plant height; **ANALF:** Reaction anthracnose race Alfa (65); **ANSIG:** Reaction anthracnose race Sigma (89); **ANKAP:** Reaction anthracnose race Kappa (31); **SNC:** Seed: number of colors; **SPC:** Seed: primary color; **SSC:** Seed: secondary color; **SCH:** Seed: color of the halo; **SS:** Seed: size ; **SSH:** Seed: shape; **SP:** Seed: profile; **SMMS:** Seeds: mass of thousand seeds; **SG:** Seed: gloss.
*Values in bold are significant at 5% probability.
** Correlated descriptors considered redundant in the analysis.

authors underline that in the characterization studies of common bean germplasm banks 10 to 20 descriptors should be taken into consideration; a quantity exceeding these recommendations would be unnecessary and costly.

After every disposal the data set was re-analyzed to verify possible differences in the clusters. The absorption did not present significant changes in the first two principal components. The Tocher method together with the principal components promoted similar clusters when

applied only to the remaining set of 18 descriptors, indicating that the applied disposal methodology was effective. The conclusion was therefore drawn that the multivariate methods used in germplasm collections optimized the descriptor set and indicate best combinations of crossings between the diversity groups, making the achievement of more productive cultivars for commercialization easier.

Diversidade genética entre acessos de feijoeiro do banco de germoplasma do Instituto Agronômico - IAC

RESUMO - *Avaliou-se a diversidade genética entre 993 acessos de feijoeiro (*Phaseolus vulgaris *L.) do banco de germplasma do Instituto Agronômico - IAC empregando-se 23 descritores agromorfológicos qualitativos e quantitativos. Análises multivariadas como distância euclidiana, componentes principais e agrupamento de Tocher foram processadas para quantificar a divergência. O uso conjunto dessas análise possibilitou a identificação de 45 grupos, com os cinco primeiros retendo 88,28% dos acessos. Componentes principais permitiram o descarte de cinco descritores, dentre os 23 avaliados, por serem redundantes ou pouco variáveis. Foram necessários os oito primeiros componentes principais para reter 70% da variação total. Os métodos multivariados se mostraram eficientes em coleções de germoplasma para otimizar o conjunto de descritores e orientar os futuros cruzamentos no programa de melhoramento do IAC.*

Palavras-chave: feijão, germoplasma, análises multivariadas, melhoramento genético.

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