

# Evaluation of common bean accesses with multi-category variables

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**ABSTRACT.** The morphologic traits of the common bean genotype (*Phaseolus vulgaris* L.) in Cáceres MT, Brazil, are evaluated to optimize genotypes for future improvement breeding cultures. Sixteen genotypes were evaluated through 33 morphological characters. The experiment was carried out in randomized blocks with four replicates at the Mato Grosso Company for Research and Extension (EMPAER) in Cáceres, Mato Grosso State. A dendrogram was produced by Unweighted Pair Group Method with Arithmetic Mean (UPGMA) and Plan projection. Results showed the occurrence of genetic variability among the genotypes and the dendrogram revealed the formation of two main groups, one comprised genotypes of the black group and the other comprised genotypes of the Cores and Carioca group, placed side by side. This fact may also be observed by a projection on a bi-dimension plane. The most divergent materials were LP 98-122 and Jalo Precoce, whereas the most similar genotypes were IPR Chopin and BRS Grafite, IPR Chopin and Graúna, IPR Chopin and LP 98-122. Genotypes in the experiment have a possible genetic variability of being used in genetic breeding programs.

**Keywords:** *Phaseolus vulgaris*, morphological description, UPGMA, genetic divergence.

**RESUMO. Avaliação de acessos de feijoeiro com uso de variáveis multicategóricas.** O presente estudo teve por objetivo avaliar caracteres morfológicos dos genótipos de feijão presentes no município de Cáceres, Estado do Mato Grosso, visando otimizar a utilização de genótipos para futuros programas de melhoramento com a cultura. Foram avaliados 16 genótipos, utilizando-se 32 caracteres morfológicos. O experimento foi conduzido em blocos ao acaso, com quatro repetições na Empresa Matogrossense de Pesquisa e Extensão no município de Cáceres, Estado do Mato Grosso. Foi gerado um dendrograma empregando-se o Método de Agrupamento Médio Entre Grupos (UPGMA). Os resultados obtidos demonstraram ocorrência de variabilidade genética entre os genótipos avaliados. O dendrograma mostrou a formação de dois grupos principais, sendo um constituído por genótipos do grupo preto, e outro por genótipos do grupo Cores e Carioca, alocados juntos, o qual também pôde ser observado através de uma projeção em um plano bidimensional. Os materiais mais divergentes foram LP 98-122 e Jalo Precoce e os genótipos mais similares foram IPR Chopin e BRS Grafite, IPR Chopin e Graúna e IPR Chopin e LP 98-122, e os genótipos utilizados no experimento possuem variabilidade genética possível de utilizar em programas de melhoramento.

**Palavras-chave:** *Phaseolus vulgaris*, descritores morfológicos, UPGMA, divergência genética.

## Introduction

Common beans are an important protein source in human diet in developing countries of tropical and subtropical regions. In Brazil, the common bean is one of the basic components of the population's diet, especially for the economically disadvantaged section of society (WANDER, 2005). Due to their nutritional and therapeutic properties, the common bean is a highly desirable component of diets since it combats hunger and malnutrition (AIDAR; YOKOYAMA, 2003).

According to Silva and Costa (2003), common bean species are distributed worldwide and have

been cultivated in tropical and temperate zones of the northern and southern hemispheres.

Vieira (1988) reports that common bean culture is very widespread across Brazil, especially in homesteads. This is due to diverse preferences of consumers and farmers, but mainly because of the environmental conditions in which they exploit the culture. According to the same author, the enormous genetic variability existing in the national germplasm is beyond the innumerable introductions that are being carried through. The availability of ample variability is essential for successful improvement programs practically across all the relevant economic characteristics.

The genetic diversity of plants is fundamental for survival and at the same time allows the development of different varieties with their distinct levels of adaptation within the available environment necessary for culture (FUKUDA, 1996).

The genetic variability in the common bean germplasm used in family agriculture is essential as a survival strategy for small farmers. In fact, they employ suitable materials within their economic and agricultural-ecologic conditions. The efficiency of conservation and the exploration of this variability increases when this is duly characterized (RODRIGUES et al., 2002).

The genetic variability of the common bean has been preserved, evaluated, organized and made available to the scientific community. This fact brings about high genetic profits for culture and for Brazilian agriculture. The knowledge and exploration of this variability favors continued research on the culture and guarantees the support of the competitive and productive Brazilian agricultural system (FONSECA; SILVA, 2005).

The determination of existing genetic divergence in the germplasm bank facilitates the characterization and identification of duplicates. This also opens up the possibility of identifying genitors of interest in the attainment of hybrids with bigger potential heterotic effects. The later will be used in improvement programs (SUDRÉ et al., 2006).

Querol (1993) reported that the botanical characterization of germplasm identified and differentiated the phenotypes of the varieties, preventing the duplication of accesses within the collection. They thus used descriptions with high heritability, easy identification and expressions in all environments. The agronomical describers were of low heritability, even desirable to the producer. They had to visualize adaptation of the material and its productive potential, placing in evidence promising genotypes and their use in improvement programs.

Morphological describers include all characteristics that easily identify and differentiate them among the accesses of culture in the field. They generally have high heritability and they are expressed in all environments. The convergence of the morphological describers with the descriptions of molecular biochemists constitutes a valuable tool for the identification of duplicate accesses in the collection (FUKUDA; GUEVARA, 1998).

Cruz and Carneiro (2003) report that multi-categorical characteristics are commonly used in vegetal genetic improvement, especially those

related to morphology and plant structure. Moreover, they are of great interest to the commercialized product quality. The value of the multi-categorical characteristics, when organized on an established scale, may be analyzed as a quantitative, changeable and discrete variable.

The above authors have, consequently, attributed numerical values to each category. Thus, the use of traditional measures for dissimilation was not appropriate, which was also the case in the Euclidean distance, as it was not yet possible to affirm that the individuals of a pair had close values (CRUZ; CARNEIRO, 2003).

In the case of multi-categorical variables the similarity index is used, in which a determined value is expressed in a percentage of coincidences, taking into consideration some analyzed characteristics. Thus, obtaining the dissimilarity from these indexes for posterior use is an accomplishment of the grouping analyses (CRUZ; CARNEIRO, 2003).

According to Cruz and Carneiro (2003), the prior analysis of dissimilarity grouping and multi-categorical data are presented as a viable alternative to evaluate the divergence among genotypes.

Daros et al. (2002) used multi-categorical variables in the morphological characterization of 14 sweet potato accesses of the germplasm collection from the Universidade Estadual do Norte Fluminense (UENF), state of Rio de Janeiro, Brazil. Trial was undertaken with 20 characteristics of the aerial part and roots, and mainly evidenced the occurrence of variability among the accesses proportionate to the pubescence characteristics of the apex rames, the inferior ribbing pigmentation leaves and roots.

Bertan et al. (2006) used changeable multi-categorical experiments with wheat until the blooming period. They demonstrated the existence of dissimilarity among the genotypes of the studied characteristics.

Sudré et al. (2006) reported that the accomplishment of the collection of multi-categorical data was a practical alternative because it was economical and faster to compare with quantitative or molecular data. However, each type of data has its singular importance and becomes interesting in the wider study of the collection of germplasm, providing greater support to researches and to data bank collection.

Current research evaluated suitable morphologic characteristics to cultivate the common bean adapted to Mato Grosso's conditions and furthermore to estimate the genetic divergence, through multi-

categorical data, propitiating the identification of genitors which will be able to produce hybrids in programs of local improvement.

### Material and methods

Research was carried in an experimental area belonging to the Mato Grosso Company for Research and Extension (EMPAER) in Cáceres, Mato Grosso State, Brazil (16°09'20.03" S and 57°37'49.15" N; altitude 118 meters), during the crop season in July 2008.

Table 1 show the sixteen common bean accesses used. They were obtained from the collection of the Agronomic Institute of Paraná (IAPAR), Agronomic Institute of Campinas (IAC), and the National Center of Researches in Rice and Common Bean (CNPaf/EMBRAPA).

Treatments were set out in completely randomized blocks, with four replications, in which the experimental parcels were made up of 5 rows of 5 meters in length, with 50 cm spacing between the rows and 35 cm between plants. The cultural treatments used during the experiment had been necessary for culture and manual harvest. They were made when 90% of the string beans were dried, separating the plants of each parcel and each block and labeling them.

**Table 1.** Genotypes of beans during harvest 2007/08, commercial group, and institution origin.

Order	Genotypes	Group	Origin
1	IAC Jabola	Colors	IAC
2	Mouro	Black	IAC
3	BRS Valente	Black	EMBRAPA
4	BRS Horizonte	Carioca	EMBRAPA
5	BRS Grafite	Black	EMBRAPA
6	Uirapuru	Black	IAPAR
7	Carioca magnífico	Carioca	IAC
8	Goiano Precoce	Colors	IAC
9	Jalo Precoce	Colors	IAC
10	Carioca Silmar	Carioca	IAC
11	IPR Chopin	Black	IAPAR
12	Juruti	Carioca	IAPAR
13	Graúna	Black	IAPAR
14	LP 98-122	Black	IAPAR
15	Diamante Negro	Black	IAPAR
16	Unknown	Colors	IAC

The evaluated characteristics had been affected through morphological describers for *Phaseolus vulgaris* L., standardized according to International Plant Genetic Resources Institute (IPGRI, 2001). The following characteristics were used: bracteole form, vegetation habit, standard color, wings color, string bean color, string bean transversal section, string bean bending, string bean suture, string bean color at the physiological maturation,

wall of the string bean staple fibers, string bean standard tegument, seeds tegument darker color, seeds brightness, seeds form, hypocotyls pigmentation, emergent cotyledon color, color tonality from the chlorophyll leaf, anthocyanin in the leaf, leaf form, leaves persistence, lodging, floral size, bracteoles button size, bracteole/chalice length relation, chalice/bracteole color, wings opening, stiletto/keel relation, string bean position in the plant, string bean apex position and dry string bean color and seeds ribbing.

Data were analyzed following the methodology of multi-categorical variables, according to Cruz and Carneiro (2003), using the formula below:

$$d_{ii'} = \frac{D}{C + D}$$

in which:

$d_{ii'}$ : dissimilarity, taking into consideration a set of multi-categorical variables;

D: category agreement;

C: category discord.

To avoid possible problems caused by indetermination in conditions where the coefficient is zero, the inverse of the similarity coefficient was increased by a unit (CRUZ; CARNEIRO, 2003).

UPGMA was the method for average grouping among groups. A dendrogram was therefore constructed from the genetic distances among the evaluated materials. The measures of genetic dissimilarity had also been projected in a bi-dimensional plan to allow the best visualization of the relative position accesses (CRUZ; CARNEIRO, 2003).

The statistical analyses had been carried through with genes software, version 2007 (CRUZ, 2006).

### Results and discussion

An analysis of Table 2 and Figure 1 together shows that the most divergent genotypes were Jalo Precoce and LP 98-122, with 21 different characteristics. They had the lowest distance, with 29 characteristics in common ( $d_{ii'} = 52.8\%$ ) and 3 not common characteristics, or rather, BRS Graphite, IPR Chopin and Graúna (bracteoles different forms, leaves persistence and seed forms) and IPR Chopin and LP 98-122 (different for the floral button size, bracteolas form and leaves persistence).

**Table 2.** Measures of genetic dissimilarity between the genotypes of beans, in relation to 32 characteristics with the multi-categorical variables used as bases.

Genotypes <sup>1</sup>	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	0.50	0.70	0.71	0.65	0.68	0.65	0.63	0.68	0.68	0.70	0.66	0.64	0.70	0.68	0.68	0.67
2		0.50	0.65	0.61	0.60	0.56	0.59	0.66	0.65	0.67	0.59	0.64	0.59	0.59	0.62	0.70
3			0.50	0.75	0.58	0.62	0.70	0.70	0.73	0.75	0.59	0.68	0.59	0.58	0.58	0.71
4				0.50	0.65	0.63	0.55	0.65	0.63	0.58	0.63	0.59	0.66	0.65	0.68	0.67
5					0.50	0.53	0.63	0.75	0.77	0.66	0.52	0.65	0.53	0.56	0.56	0.65
6						0.50	0.60	0.70	0.70	0.68	0.54	0.62	0.53	0.57	0.57	0.65
7							0.50	0.62	0.63	0.64	0.62	0.60	0.66	0.66	0.66	0.63
8								0.50	0.57	0.68	0.75	0.66	0.75	0.75	0.73	0.70
9									0.50	0.62	0.75	0.63	0.77	0.80	0.71	0.65
10										0.50	0.65	0.61	0.68	0.66	0.70	0.65
11											0.50	0.62	0.52	0.52	0.54	0.68
12												0.50	0.65	0.63	0.66	0.69
13													0.50	0.53	0.54	0.70
14														0.50	0.56	0.73
15															0.50	0.63
16																0.50

<sup>1</sup>1 = IAC Jabola, 2 = Mouro, 3 = BRS Valente, 4 = BRS Horizonte, 5 = BRS Grafite, 6 = Uirapuru, 7 = Carioca Magnífico, 8 = Goiano Precoce, 9 = Jalo Precoce, 10 = Carioca Silmar, 11 = IPR Chopin, 12 = Juruti, 13 = Graúna, 14 = LP 98 122, 15 = Diamante Negro, 16 = Unknown.

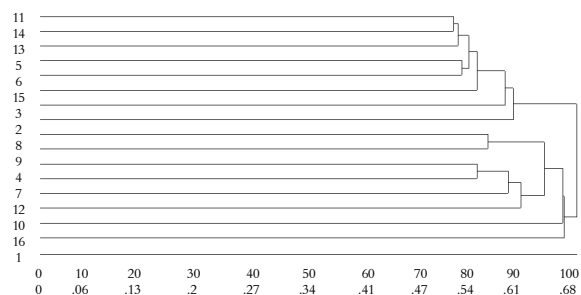
The 3 combinations presented the genotypes IRP Chopin in common. Within the combinations, the genotypes BRS Graphite, IRP Graúna and LP 98-122 produced low values of dissimilarity (5 and 13 = 0.54; 5 and 14 = 0.56), which indicated kinship between them or common genitors during the new cultivation process. Even the most similar characteristics had some genetic diversity; sometimes they did not have the minimum distance value, or rather, 52.83% and not 50%.

According to Maluf and Ferreira (1983), the measures of genetic dissimilarity were used as the predictive hybrid values for initiating the genetic improvement program. This is a useful tool because instead of choosing randomly the genitors for the hybrids, they may be chosen by a study on genetic diversity, carrying through and limiting the crossings only with the most promising combinations. The process turns out to be more efficient.

The dendrogram used in the UPGMA method (Figure 1) is taken as a measurement of dissimilarity in the distance based on multi-categorical variables, where the divergence inside each group is restricted. When carrying out this type of genetic distance analysis, the accesses with lesser distances had been grouped into 2 main groups.

The first group was subdivided into 3 sub-groups: subgroup Ia, containing genotypes IRP Chopin, Graúna and LP 98-122; subgroup Ib, with BRS Graphite, Uirapuru and Diamante Negro genotypes; subgroup Ic containing the Mouro and BRS genotypes. The second group also was divided into 3 sub-groups: subgroup IIa contained the genotypes Goiano Precoce and Jalo Precoce; the subgroup IIb contained the genotypes BRS Horizonte, Carioca Magnífico, Carioca Silmar and

Juruti, and the subgroup IIc that contained genotypes IAC Jabola and Unknown.



**Figure 1.** Representative dendrogram of genetic divergence among 32 bean genotypes (*Phaseolus vulgaris* L.), obtained by the method of grouping Media Liaison between groups (UPGMA), using  $d_{ii}$ , as a measure of dissimilarity.

Genotypes: 1 = IAC Jabola, 2 = Mouro, 3 = BRS Valente, 4 = BRS Horizonte, 5 = BRS Grafite, 6 = Uirapuru, 7 = Carioca Magnífico, 8 = Goiano Precoce, 9 = Jalo Precoce, 10 = Carioca Silmar, 11 = IPR Chopin, 12 = Juruti, 13 = Graúna, 14 = LP 98 122, 15 = Diamante Negro, 16 = Unknown.

The formatted material group belonging to the Black commercial group was isolated from group II because it contained materials pertaining to the commercial groups Color and Carioca.

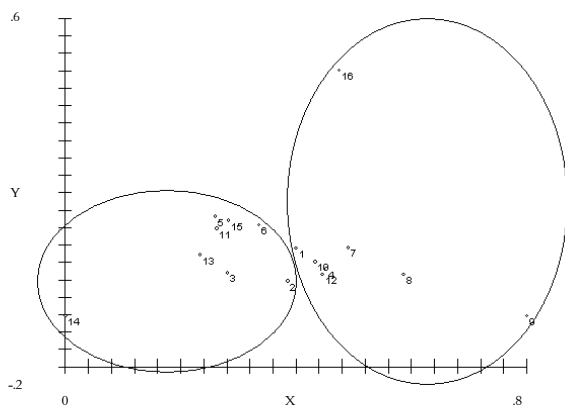
Results by the multi-categorical variable analysis of the bean accesses of the experiment demonstrate the existence of genetic variability between the cultivars. In the case of the 32 evaluated characteristics, only anthocyanin in the leaf, relation stiletto/keel, the string suture bean, staple fibers wall in the string bean, seeds ribbing tonality and the chlorophyll color in the leaf did not have any detected variability. All the evaluated accesses had the same value for the mentioned characteristics.

A considerable genetic similarity between BRS Graphite of the subgroup and IPR Chopin of the subgroup Ia could be verified between the subgroup Ia and Ib. Within the subgroup Ia, all the materials (IPR Chopin, LP 98-122 and Graúna) were

genetically very similar, as also occurred with regard to the functions of the characteristics under analysis.

When groups I and II were compared, the differences in morphological characteristics among the genotypes were highlighted, determining that the two groups had hypocotyls pigmentation, emergent cotyledon, standard color, wings color, string bean color, and darker seeds color.

When analyzing the projection of the distance in the plan (Figure 2), the genotypes partition into two distinct groups in which the Jalo Precoce genotype of group I and LP98-122 of group II are most dissimilar, confirms the results evidenced by the dendrogram.



**Figure 2.** Projection of the distance in the plan, considering the 16 genotypes of *Phaseolus vulgaris* L.

Morphological diversity is an important tool to identify the studied genotypes, to differentiate them from the ones that contain some similar characteristics and to identify the possible duplicates in germplasm banks or in situ, where there might be equal genotypes with different names or different accesses that received the same name. Moreover, it precociously allows the election of ancestors for the improvement of future programs, as registered by Bertan et al. (2006).

Sudré et al. (2006) report that the use of multicategorical data is a practical, economic and fast alternative when compared to quantitative and molecular data. However, each has a singular importance. It is, moreover, preferable that a germplasm collection was widely studied to improve ample supported researches and the formation of databases. The collection of the multi-categorical characterization and the divergence study based on quantitative data are a viable alternative to start the study of germplasm banks with few financial resources and a little man power.

The gauging of the genetic divergence between the genotypes used in the experiment is practical and economically faster to demonstrate which ones have

the most and the least similar materials. It may be used to initiate an improvement program using the materials with greater genetic diversity. It is thus possible to obtain materials with the desired characteristics.

When materials that present greater dissimilarity are used, the farmer gains time and maximizes efforts. In fact, such combinations are highly promising. When genetically similar materials are used, they generate lineages with a low genetic diversity, reducing the possibility for genetic profits when these combinations are made. Since information on genetic dissimilarity among materials is an excellent tool, it may be an asset in improvement programs coupled to a higher efficiency in germplasm banks in the conservation of materials. Consequently, the number of duplicate samples is reduced.

## Conclusion

Results show that the morphological characteristics evaluated enabled the identification of genotypes Jalo Precoce and LP 98-122 as the most divergent; identified three combinations as the most similar, IPR Chopin, making links between the genotypes BRS Grafite, and Graúna and LP 98-122; the commercial group Black was isolated by groups of commercial Color and Carioca; the access IPR Chopin, Graúna and LP 98-122 were less divergent.

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