Vol 3 No 4 December 2022 Pages 27-33 e-ISSN 2708-5694

Journal of Agriculture, Food and Environment (JAFE)
Journal Homepage: http://journal.safebd.org/index.php/jafe
https://doi.org/10.47440/JAFE.2022.3405

Original Article

Genetic Divergence and Selection of Common Bean Genotypes with High Agronomic Performance in Mozambique

Dique JEL[1,4*], Pedro C[2], Fernando CJJ[1], Silota G[1], Savanguane LC[1], Bungala LTDC[1], Manhoca PF[1], Charimba AM[2], Miguel MA[3], Quinhentos MDL[1], Dias D[1], Carneiro VQ[4]

[1]Instituto de Investigação Agrária de Moçambique-Centro Zonal Centro (CZC), Leguminosas, Estrada Nacional no 6, C. P. 42, Contact +258 866427666 - Manica, Mozambique
[2]Instituto de Investigação Agrária de Moçambique-Centro Zonal Nordeste (CZnd), Leguminosas, Av. FPLM. Estrada de Corrane, Km 7, C.P.622. Nampula, Moçambique.
[3]Universidade Zambezi-Departamento de Agronómia e Engenharia Florestal (FAEF), Campos de Nacogolone- contacto- +2588468814580-Mocuba, Moçambique.
[4]Univesridade Federal de Lavras, Departamento da Biologia, Instituto de Ciênciaas Naturais-Contact +553187169844-Brasil

Article History

Received: 01 November 2022

Revised: 21 December 2022

Accepted: 28 December 2022

Published online: 31 December 2022

***Corresponding Author**

Dique JEL, E-mail: diquejosedique4@gmail.com

Keywords

Phaseolus vulgaris L. UPGMA, generalized Mahalanobis distance.

How to cite: Dique JEL, Pedro C, Fernando CJJ, Silota G, Savanguane LC, Bungala LTDC, Manhoca PF, Charimba AM, Miguel MA, Quinhentos MDL, Dias D, Carneiro VQ (2022). Genetic Divergence and Selection of Common Bean Genotypes with High Agronomic Performance in Mozambique. J. Agric. Food Environ. 3(4): 27-33.

ABSTRACT

The deep knowledge of genetic diversity in access, in the breeding program, and the contribution of genetic factors as well as the phenotypic expression is of extreme importance for the development of new cultivars and maintenance of the program. This research aimed to study the genetic diversity and selection of the best common bean genotypes with high agronomic performance in the Agrarian Station of Sussundenga-Mozambique. Twenty-two common bean genotypes were evaluated in a randomized block design with three repetitions in the 2021/2022 agricultural season. The agronomic characteristics evaluated were: the number of days to flowering, plant height, plant architecture, number of pods per plant, the weight of 100 seeds, and grain yield. The data obtained were submitted to individual variance analysis, followed by the Scott-Knott grouping test. For the effect of genetic divergence between the genotypes, multivariate analysis was used based on the generalized Mahalanobis distance and Tocher optimization method, UPGMA, and canonical variables for the projection of distance in the 2D plane. It was also verified by the Cophenetic Correlation Coefficient. The Singh criterion (1981) was used, indicating the characteristics Number of pods per plant (42.81%), the weight of 100 seeds (19.59%), and Plant height (16.08%) as the most important for the genetic divergence of bean genotypes.

Introduction

The common bean (Phaseolus vulgaris L., $2n = 2x = 22$) is one of the main crops in the World. It is also one of the agricultural products of greatest socio-economic importance, due to the large volume of labor employed during the crop cycle (Vieira *et al.*, 2006). For Africa, this legume, plays a key role, since they provide quality protein, vitamins, and dietary fiber (Mercat *et al.*, 2013), is the third most important source of calories after corn (Zea mays L.) and cassava (Manihot esculenta Crantz), covering the needs of millions of low-income families, mainly in rural areas (Alemu h, 2017). The global production of this crop is about 12 million tons per year. However, the East and Southern Africa regions produce about 2.5 million tons per year (Party *et al.*, 2015). Approximately 40 percent of Africa's production is marketed and generates about 450 million US dollars (Wortmann *et al.*, 1998 in David *et al.*, 2000), and small Producers account for most of the production.

The average yield of common bean in Southern Africa, particularly Mozambique is very low (ranging from 500 to 700 kg ha^{-1}) compared to the global average of 2000 kg ha^{-1} (Kimani P *et al.*, 2005; Margaret N *Et Al.*, 2014; bitocchi *et al.*, 2012; Alemu H, 2017 and Fao, 2019). The low productivity of common bean is attributed to several biotic and abiotic constraints, as is the case of low availability of production medium, a poor Storage system (infrastructures to adequate), use of unimproved seed for a long time, as much as the use of seeds with doubtful origin. Therefore, there is a need to develop high-yielding, stress-tolerant cultivars to improve production. The successful development and implementation of improved cultivars depend on the genetic diversity available in the program, the implementation strategies as well as the solidification of existing breeding programs.

Genetic diversity studies have been of great importance in breeding programs, by providing information on characteristics to identify genitors that allow great heterotic effect and greater segregation in recombinants, increasing the probability of the appearance of superior genotypes in the progenies (Silva *et al.*, 2008). Furthermore, it allows the identification of duplicates, thus reducing considerable expenses in the maintenance of germplasm banks (Rodrigues *et al.*, 2002). The existence of genetic variability is essential for the success of improvement programs for practically all characteristics of economic importance (Costa *et al.*, 2004).

The breeding programs of the common bean are based almost exclusively on the hybridization of cultivars and obtaining superior lines from segregating populations (Blair MW *et al.*, 2009; Tsutsumi *et al.*, 2015). The choice of genitors to compose the hybridization block is a crucial step, and should be carried out thoroughly and carefully since the success of the subsequent stages of the breeding program depends on it (Sicard d *et al.*, 2005; VALE *et al.*, 2015).

Among the methods used for choosing genitors, predictive models based on genetic distance have been widely used by several researchers (Gonçalves *et al.*, 2016; Sebim *et al.*, 2016; Maziero *et al.*, 2017; Sulbacher *et al.*, 2017; Vidyakar *et al.*, 2017). This model dispenses with the prior procurement of hybrid combinations, as it considers the agronomic, morphological, physiological, and/or molecular differences exhibited by the genitors in determining genetic variability (Cruz *et al.*, 2014). This genetic variability is under a constant selection process in the environments where they are cultivated, and the intensive cultivation with the employment of few cultivars constitutes a market requirement of modern agriculture (Tsutsumi *et al.*, 2015), contributing to the reduction of genetic variability.

The knowledge of genetic diversity between local cultivars and improved ones is important to subsidize plant breeding programs, making it possible to explore the existing variability and already adapted to the climatic conditions of specific regions (Franco *et al*, 2001), with this purpose, there is an urgent need to evaluate the genetic divergence and selection of best common bean genotypes with the high agronomic performance of the Agricultural Research Institute of Mozambique (IIAM) to understand the genetic composition and differentiation of genetic loci in common bean for the development of cultivars (Kwak m *et al.*, 2009), and continue to expand the variety release program.

Material and Methods

Description of the study area and genetic material

The experiment was conducted at the Agricultural Research Institute of Mozambique (IIAM), specifically at the Centro Zonal Centro (CZC), in the Experimental Station of Sussundenga, Manica Province - Mozambique. Geographically, the study site is located in the Revue River basin, at latitude 19°32′ South, longitude 33°35′ East, and at 635 m above mean sea level (Mae, 2014) (Fig. 1).

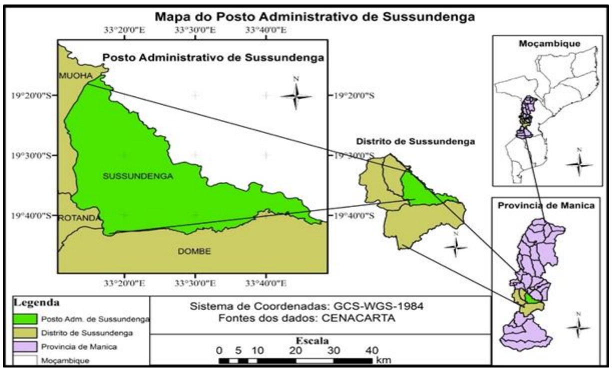

Figure 1. Schematic of the geographical location of the study area.

The genetic material used in the Research

The genetic material used in this study consisted of 22 genotypes from the Legume Program of the Sussundenga Agricultural Station, among Andean and Mesoamerican beans (Table 1).

Table 1. 22 Genotypes from the Legume Program of the Sussundenga Agricultural Station.

N°	Genotypes	Origins	Type of grain	Cycle (days)	Growth habit
1	BONUS ANDINO	IIAM/CIAT	Especial	70-85	Determined
2	NUA 45 ANDINO	IIAM/CIAT	Especial	70-85	Determined
3	PRO 0731 ANDINO	IIAM/CIAT	Especial	70-85	Determined
4	AP 20 ANDINO	IIAM/Macknight	Especial	70-85	Determined
5	SUGAR131 ANDINO	IIAM/CIAT	Especial	70-85	Determined
6	BFS 81 MESO	CRIB/IIAM	Mesoamericana	70-90	Determined
7	SER 9 MESO	CRIB/IIAM	Mesoamericana	70-90	Determined
8	BFS 29 MESO	CRIB/IIAM	Mesoamericana	70-90	Determined
9	KUFUNA ANDINO	IIAM/Macknight	Especial	70-85	Determined
10	DOR 364	IIAM/Macknight	Mesoamericana	70-85	Determined
11	MATINA ANDINO	IIAM/Macknight	Especial	70-85	Determined
12	TIO CANELA MESO	CRIB/IIAM	Mesoamericana	70-90	Determined
13	BFS 142 MESO	CRIB/IIAM	Mesoamericana	70-90	Determined
14	PRO737-1 ANDINO	IIAM/Macknight	Especial	70-85	Determined
15	ANDINO X	IIAM/Macknight	Especial	70-85	Determined
16	ICAPIJAO MESO	CRIB/IIAM	Mesoamericana	70-90	Determined
17	YIELD ANDINO	IIAM/Macknight	Especial	70-85	Determined
18	MANTEIGA	IIAM/CIAT	Especial	70-85	Determined
19	SEF 16 MESO	IIAM/Macknight	Especial	70-85	Determined
20	AP 48 ANDINO	IIAM/Macknight	Especial	70-85	Determined
21	AP 3 ANDIN	CRIB/IIAM	Mesoamericana	70-90	Determined
22	BFS 14 MESO	CRIB/IIAM	Mesoamericana	70-90	Determined

Temperature, precipitation, and humidity

The range of air temperature ideal for the development of common bean culture is between 15 and 27 °C, and the ideal average temperature is 21 ºC; being suitable for cultivation, in regions that have values of 15 to 29 ºC (Embrapa, 2014). In the occurrence of high temperatures, between 30 and 40 ºC, practically no pods are set, and in low-temperature conditions, the cycle is considerably increased (Fancelli & Dourado Neto, 2000; Embrapa, 2014). The availability of water is certainly one of the most important factors in the cultivation of plant species, its presence is essential for good development in its phenological phase. Low humidity can severely reduce crop production. The water deficit hurts productivity, by reducing the percentage of setting, production of "shocked" pods in the pod-filling phase, and the reduction of the number of seeds per pod (Diniz, 2006). The average annual precipitation is about 1,171 mm, while the average annual potential evapotranspiration is around 1,271 mm, respectively (Mae, 2014).

Figure 2 below shows the daily temperature variation from January to July 2022 at the experimental site.

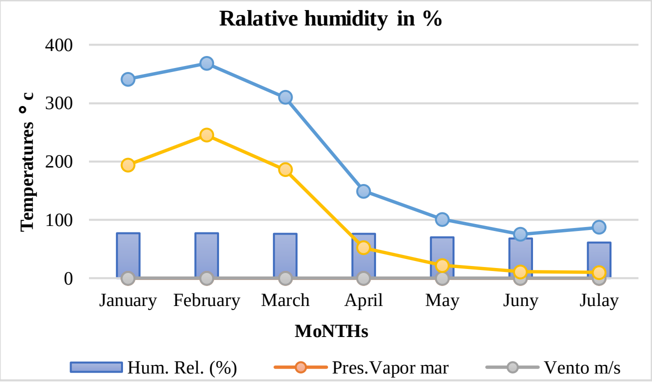

Figure 2. Daily temperature, precipitation, and humidity from January to July.

Experimental design of the research

The trial was conducted in a randomized block design with three replications. Each experimental plot consisted of two rows 5 m long, spaced 0.5 m apart, and contained approximately 150 plants. Sowing was performed manually in February 2022, dry in demarcated rows with a sowing density of 15 seeds per meter. During planting, N-P-K background fertilizer was applied 150kg/ha in the formula 14-28-14 The cultural treatments and phytosanitary control were performed as recommended by the bean agronomic management literature, besides the use of Macozeby and the Cypermethrin (Borém and Carneiro, 2015). The following characteristics were collected: Height of plants (HP) obtained by measuring, in centimeters (cm), from the neck of the plant to the apex of the main stem, through the average of six plants taken at random within the useful area, number of pods per plant (NPP), obtained by counting the number of pods from each plant being taken the average value of six plants within the useful area, the weight of 100 seeds (P100S), randomly counted followed by weighing using a precision scale, the plant architecture (PARC) was evaluated using a scale with grades from 1 to 5, where the closer to 1 the more erect the plants in the plot, and the closer to 5 the more prostrate the plants (Collicchio, 1995), the number of days to flowering (NDF), which was obtained from the counts of six plants to the case within the useful area from planting until 50% of its flowering, and finally was the record of the Grain yield (YIELD) that was determined based on the grain production of the two central rows of the plot, converted to kg ha^{-1}.

The harvest was performed at the physiological maturity stage of the crop, that is when the plants presented above 90% of dry pods and all yellowish leaves, separately and coded. The grains were sun-dried for four days, followed by tracing, cleaning, weighing, and later extrapolating the quantity corresponding to kg ha-^{1}.

The recorded data were submitted to individual analysis of variance, according to the statistical model (1):

$Yik = \mu + gi + bk + eik$ (1)

Where: $Yiik$ is the observation referring to the genotype (strain) in the k the block; μ is the overall mean; gi is the fixed effect of genotype i; bk is the random effect of block k; eik is the random error associated with the observation. It is emphasized that for the plant architecture in which the evaluation was performed by grading scale, the coefficient of experimental variation (CV%) was estimated according to an unbiased estimator proposed by dos Anjos *et al.* (2019), presented below:

$CV\ (\%) = 100(\sqrt{QMR} / |\bar{X} - u|)$ (2)

Where QMR is the mean square of the residual; $\bar{X}$ is the mean of the genotypes (strains) and u is the score assigned to the undesirable phenotype relative to the characteristic under analysis. Likewise, the results were analyzed by the Scott and Knott grouping test of means at 5% probability. For the analysis of genetic divergence among cultivars/lines, multivariate analysis was employed based on the generalized Mahalanobis distance, subsequently performing the agglomerative methods of Tocher optimization, hierarchical UPGM, and distance projection in the 2D plane. The degree of preservation of genetic distances in the dendrogram was verified from the Coefficient of Cophenetic Correlation (CCC). Singh's (1981) criterion was also used to quantify the relative contribution of traits to genetic divergence. All analyses were performed using the computational resources of the GENES portal (Cruz, 2014).

Results and Discussion

The summary of the individual analyses of the variance of the experiment is shown in Table 2. However, the results show that there was a statistically significant difference, in the characteristics of plant height (PH), number of pods per plant (NPP), hundred-grain weight (100w), and Plant Architecture (PARC). These results were also verified by Lima *et al.* (2012), who observed variability for the characteristic mass of 100 grains in 100 bean genotypes. While a characteristic number of days to flowering (DF), and grain yield (YIELD), showed no statistically significant difference in this study. The non-significance occurred due to the great environmental influence that can be proven by the high coefficient of variation verified for the characteristics, and also because it is still segregating material.

Table 2. Summary of analysis of variance of the characteristics evaluated in the experiment on common bean genotypes, in the season year 2021/2022 in the agrarian station of Sussundenga. Plant height (HP), number of pods per plant (NPP), the weight of 100 seeds (P100S) in grams, number of days to flowering (DF), plant architecture (PARC), and grain yield (YIELD).

[1]SV	DF	Mean Square					
		PH	NPP	100w	PARC	DF	YIELD
Blocks	2	1.31	3.37	20.74	0.22	62.46	932174.13
Genotypes	21	13.78**	283.35**	253.67**	1.63**	23.10ns	943225.76ns
Residue	42	4.49	29.41	49.49	0.43	28.64	995806.96
Average		14.93	20.80	34.12	1.71	40.17	1203.41
[2]CV%		14.19	26.06	20.62	20.31	13.32	24.92

[1]Source of variation; [2]coefficient of variation. **Significant by F test at 1% probability.

Table 3 shows the comparison values of the means of the six agronomic characteristics evaluated in 22 common bean genotypes, grouped by the Scott-Knott test (5%). For the characteristic of plant height, values of 10.8 (genotype 21) to 18.6 (genotype 3) were found, and the genotypes AP20, TIO CANELA, and AP3 showed the lowest value for this characteristic (Table 3). In bean culture, the taller the plant, the greater the susceptibility to lodging. However, Simone *et al.* (1992) revealed that the ideal bean plant for mechanized harvesting needs a height of more than 50 cm. From another point of view, it is observed that plants with greater height, contributed a lot to the increase in grain numbers. The varieties that have greater heights are considered of great relevance by improvers, since it facilitates mechanized harvesting, in addition to cultural gains and loss in mechanized harvesting, because it avoids the direct contact of the pods with the soil, thus promoting the better phytosanitary condition of the grains (Salgado *et al.*, 2012).
Regarding the number of pods per plant, the values found ranged from 8.0 to 41.3, with AP3, MANTEIGA, and Bonus showing lower values for these characteristics. These results are similar to the results obtained by Mambrin *et al.* (2015) evaluating 14 advanced bean lineages and by Gonçalves *et al.* (2016) evaluating 40 traditional bean accessions.
For the characteristic of 100-seed weight, the values ranged from 20.6 to 46 respectively, and the lowest values were presented by genotypes BFS 14, BFS 29, and BFS 81. These results are an indication that the genotypes used to belong to the Andean as well as Mesoamerican gene group, since, as pointed out by Gepts and Bliss (1986) and Coelho *et al.* (2007) 100-seed weight lower than 25 g indicates bean belonging to the Mesoamerican center. For the plant architecture characteristic, the values varied *from* 1 to 2.7, with the lowest values observed in the genotypes MATINA, PRO 731, and PRO 737-1. The genotypes that presented architecture scores equal to or lower than 2 are considered promising for use in crossbreeding to obtain new strains of erect growth, adapted to mechanical harvesting. Regarding the number of days to flowering, it was found that the genotypes presented averages between 34.6 and 44.6 days (Table 3). Cultivars with fewer days to flower are desired in several bean breeding programs. Early genotypes are developed, mainly, to meet areas of sugarcane plantation renewal (Bizari *et al.*, 2014). They are also used to meet the situation of climate change that has plagued the world since it allows a harvest in a certain period. For the grain yield characteristic (Table 4), the genotypes presented values from 867.3 to 3696.9 kg ha^{-1}, with the lowest values found in the following genotypes MANTEIGA, BONUS, and BFS 142 respectively. Regarding grain yield, Ribeiro (2007) explains that these variables are highly influenced by environmental conditions and their various components, and the genotypes have shown to be quite variable in their behavior.

Table 3. Comparison of means of the six agronomic characteristics evaluated in 22 common bean genotypes, grouped by the Scott-Knott test (5%), the season year 2021/2022.

ID	PH	ID	NPP	ID	100w	ID	PARC	ID	DF	ID	YIELD
3	18.6 a	12	41.3 a	20	46.0a	16	2.7 a	2	44.6a	15	3696.9a
12	18.6 a	2	37.6 a	6	46.0a	13	2.6 a	14	43a	12	1218.0a
1	18.3 a	17	36.6 a	19	45.6a	15	2.0 a	20	42.6a	22	1189.7a
4	18.0 a	5	33.3 a	3	43.6a	5	1.8 a	19	42.3a	18	1134.0a
5	17.7 a	18	29.0 b	14	43.0a	2	1.6 a	8	42.3a	8	1064.2a
11	16.3 a	13	27.6 b	1	41.0a	21	1.6 a	7	42.3a	20	1056.1a
6	15.0 b	19	23.6 b	9	40.6a	18	1.6 a	4	42.3a	21	1048.4a
8	15.0 b	15	22.6 b	10	40.3a	17	1.4 b	15	41.6a	19	1036.5a
19	14.8 b	16	22.0 b	21	39.0a	12	1.3 b	3	41.6a	4	1028.1a
14	14.7 b	4	21.6 b	7	38.6a	4	1.3 b	1	41.6a	2	1028a
16	14.8 b	21	13.0 c	8	38.0a	3	1.3 b	13	41.3a	13	1018.6a
22	14.6 b	22	12.6 c	11	37.0a	1	11.3 b	5	41.3a	3	1013.3a
17	14.5 b	11	12.6 c	22	36.6a	22	10.6 b	16	40.3a	1	1002.6a
15	14.0 b	8	12.3 c	13	26.3b	8	1.0 b	11	40.3	9	9782.1a
18	13.8 b	3	12.3 c	4	25.3b	20	1.0 b	17	39.3a	6	974.0 a
9	13.6 b	1	12.3 c	2	25.0b	19	1.0 b	9	38.6a	5	9078.1a
10	13.3 b	9	11.6 c	12	24.6b	14	1.0 b	10	38a	7	896.0 a
7	13.2 b	7	11.6 c	5	24.6b	11	1.0 b	18	37.3a	16	879.7a
13	13.0 b	6	11.6 c	17	24.0b	10	1.0 b	6	36.6	11	879.7a
20	12.8 b	14	11.0 c	15	23.0b	9	1.0 b	22	36a	17	878.0a
2	12.6 b	10	10.6 c	16	21.0b	7	1.0 b	12	35.3a	14	875.9a
21	10.8 b	20	8.0 c	18	20.6b	6	1.0 b	21	34.6a	10	867.3a
Means	**14.93**		**20.80**		**34.12**		**1.71**		**40.17**		**1203.41**

*Means followed by the same letter do not differ statistically at 5% probability by the Scott-Knott test. ID: Genotype identification number; PH: plant height NPP: number of pods per plant: 100w: 100 seeds weight, PARC: plant architecture; PDF: number of days to flowering and Yield.

The characteristics with the highest relative contributions were the number of pods per plant (42.81%), followed by the weight of 100 seeds (19.56%), plant height (16.08%), and plant architecture (12.09%) respectively. Similar results were demonstrated by Coelho *et al* (2007). Elias *et al* (2007) observed that the characteristic 100 seed weight had the greatest contribution to the separation of bean accessions. The yield, despite being an important commercial characteristic, had low discriminating power among the accessions, which can be explained by the low productive heterogeneity observed among accessions, as also observed by Coelho *et al.* (2007). The characteristics that contributed less to differentiate the accessions were the number of days to flowering (4.74%), and yield (4.72%) respectively. Cruz and Carneiro (2006) reported that the characteristics of less importance for estimating diversity among individuals are those that have less variability or are represented by others. In a research work conducted by Grigolo *et al.* (2018), evaluating 20 accessions of common beans found similar results. However, these authors, suggest that this characteristic should be prioritized in studies of the genetic divergence of common beans. However, the characteristic number of days to flowering (DF), had a very low contribution to obtaining the genetic variability in the present research, suggesting that it should be discarded.

The correlation coefficient (CCC) is a measure of agreement between the original values of dissimilarity and those represented by the dendrogram, the higher the CCC the lower the distortion of the grouping (Cruz; Carneiro, 2006). The CCC obtained was 0.71 and significant at 5% probability by the t-test, which represents a high fit between the cophenetic matrix and the dissimilarity matrix based on the generalized Mahalanobis distance, demonstrating high clustering reliability. Bertan *et al.* (2006) reported the high accuracy of UPGMA clustering by the dissimilarity obtained by the generalized Mahalanobis distance about other dissimilarity measures. Using the generalized Mahalanobis distance for the 22 genotypes, they were similarly grouped into six groups by the Tocher optimization method (Table 5) and the UPGMA method (Figure 3), but the 2D projection showed four groups (Figure 4). This equivalence in the grouping of the genotypes by the first two methods is a clarity of the consistency in the results, although the 2D projection reduced the number of groups formed by one genotype.

Table 4. The relative contribution of the ten agronomic characteristics to the genetic divergence between 22 common bean genotypes was evaluated in the 2021/2022 crop year in the Agrarian Station of Sussundenga Mozambique.

Characteristics	S.J	Relative importance (%)
NPP	1407.42	42.81
100w	642.98	19.56.
PH	528.63	16.08
PARC	397.45	12.09
PDF	155.97	4.73
YIELD	155.45	4.72

NPP = number of pods per plant; 100w = 100 seed weight; PH= plant height; PARC = plant architecture; DF = the number of days to flowering and yield.

The cluster analysis by Tocher's method, based on the Mahalanobis matrix, formed the 22 genotypes into six groups (Table 5). However, of the groups formed, four (4) were constituted by only one genotype, one group by six, and one group by twelve genotypes respectively. The formation of six groups in this research indicates the existence of variability among the genotypes evaluated. According to Kwak and Gepts (2009), beans were domesticated in the Americas in two main centers of origin, one comprising the region of Mexico and Central America, and the genotypes from this center are called Mesoamerican, and the other in the region of Peru, called Andean. Coelho *et al.* (2007) reported that the bean genotypes with a 100-seed weight below 25.00 g possibly belong to the Mesoamerican center and those with a weight above 33.00 g, to the Andean center. For this research, they were similar to what has been reported, since the experiment consisted of genetic material from both Mesoamerican and Andean grains. In the group formation, a small influence was verified, in that the formation of the groups was done mostly by the origin of the genotypes.

Thus, the clustering was able to separate the accessions according to the center of origin. Similar results were reported by Coelho *et al.* (2007) and Barelli *et al.* (2009). Cabral *et al.* (2011) evaluated the diversity of bean genotypes through microsatellite (SSR) molecular markers, and observed clustering according to the centers of origin.

Table 5. Group of bean genotypes with similar patterns, established by the Tocher method, using the Generalized Mahalanobis Distance as a measure of disparity evaluated in the 2021/2022 season year in the Agricultural Station of Sussundenga-Mozambique.

Groups	Genotypes	(%)
I	Matina, Mantega, Pro 0731, Bonus, Nua 45, Pro 737-1, Andino X, Kufuna, AP3, Tiyela, AP20 e Sugar 131	68.73
II	Tio Canela, BFS142, SEF16, BFS14, DOR364 e BFS29	27.33
III	Ser9	1
IV	Icapijão	1
V	BFS81	1
VI	AP48	1

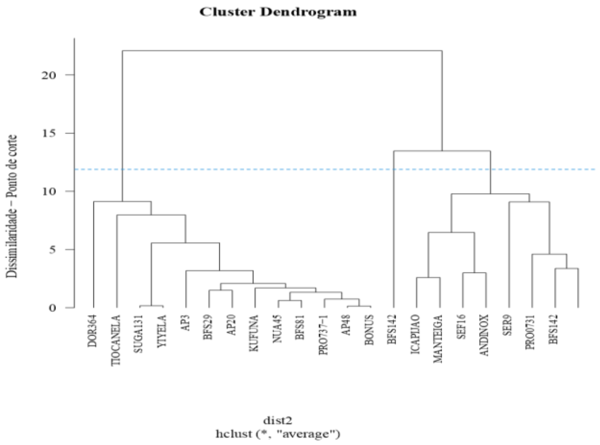

Figure 3. Dendrogram of the genetic divergence among 22 common bean genotypes, obtained by the average linkage method (UPGMA) using the generalized Mahalanobis distance as a measure of dissimilarity, evaluated in the 2021/2022 season year in the Agricultural Station of Sussundenga.

The first two variables explained 88.52% of the total variation, 72.7% for the first, and 15.82% for the second (Figure 4). Krause *et al.* (2009) observed that the first two canonical variables explained approximately 80% of the total variation. Machado *et al.* (2002) evaluating the genetic diversity among bean genotypes through canonical variables observed that the first three variables explained 99% of the total variation. Cruz and Carneiro (2006) emphasize that the analysis by canonical variables should only be used when, in two or three canonical variables, more than 80% of the total variation is explained.

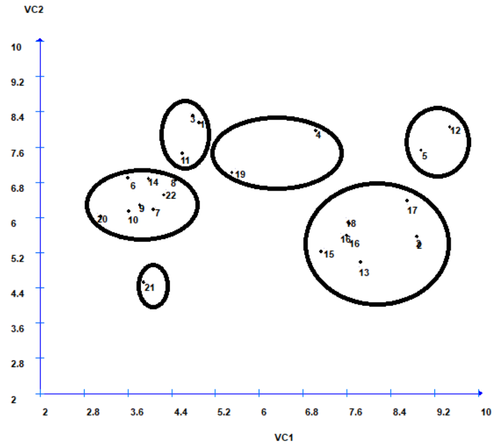

Figure 4. Graphical scatter of the 22 common bean genotypes on the first two canonical variables, established by the linear combination of six agronomic traits evaluated in the year 2021/2022 in the Agricultural Station of Sussundenga.

Note that 6 groups were formed, since each group has a color that differs from the other, as shown in Figure 4, respectively.

In figure 4, the formation of different groups was indicated, however, these groups formed clearly show the existence of genetic divergence, showing positive aspects within the material used (genotypes), both from the economic and agronomic point of view, since in breeding programs the efficiency of acquiring good material in a short period is needed. Then, the genotypes of different groups can be indicated because they show greater genetic distance (Rotili *et al*., 2012; Vidyakar *et al*., 2017). However, it should be noted that for the choice of genitors in addition to genetic contrast it is necessary to the presence of desirable agronomic characteristics according to the breeding program.

Conclusions

The genotypes evaluated in this experiment showed genetic variability and diversity. Most of them are promising and can be used as genitors in breeding programs.

The variables that contributed to genetic divergence among genotypes were plant height, 100-seed weight, and the number of pods per plant.

Acknowledgment

As IIAM researchers, our thanks go to all who have collaborated directly and indirectly to make this research a success. All the authors put a lot of effort into all the activities, from field preparation to data collection, digitization, and the interpretation of the results. A special thanks also go to Bheard, the funder of the master's scholarship. Other special thanks go to the National Council for Scientific and Technological Development (CNPQ), for its support in funding the Ph.D. fellowship.

Conflicts of interest

For this research entitled Genetic Divergence and Selection of Common bean Genotypes with high Agronomic performance, we declare no disagreements between the authors.

References

Carneiro JES, Ferreira LR, Ferreira FA & Silva JF (2015). Culture. In (Eds.). Beans from planting to harvest. 1. ed. Viçosa, MG: UFV, p. 207-238.

Alemu H (2017). Review paper on breeding common bean (Phaseolus vulgaris L.) genotypes for acidic soil tolerance. International Journal of Advanced research and publications.; 1(3):39-46.

Anjos RSR, Marçal TS, Carneiro PCS, Carneiro JES (2019). New proposals to estimate unbiased selection gain and coefficient of variation in traits evaluated using score scales. Crop Science, v. 59, n. 3, p. 937-944, 2019.

Barelli MAA 2009. Genetic divergence in common bean landrace cultivars from Mato Grosso do Sul State. Seminar: Agricultural Sciences, v. 30, p. 1061-1072.

Bertan I 2006. Comparison of clustering methods in representing morphological distance among wheat genotypes Brazilian Journal of Agroscience, v. 12, n. 03, p. 279-286.

Bitocchi E, Nanni L, Bellucci E, Rossi M, Giardini A, Zeuli PS (2012). The mesoamerican origin of the common bean (Phaseolus vulgaris L.) is revealed by sequence data. Proceedings of the National Academy of Sciences.

Bizari EH (2014). Genetic diversity in early-maturing soybean genotypes based on biometric and molecular parameters. Journal of Food, Agriculture & Environment, v. 12, n. 1, p. 259-265.

Blair MW, Diaz LM, Buendia HF, Duque MC (2009). Genetic diversity, seed size associations, and population structure of a core collection of common beans (Phaseolus vulgaris L.). Theoretical and Applied Genetics.

Borém A, Carneiro JES, Carneiro EJ, Júnior TJP, Borém A (2015). Beans: from planting to harvest. Viçosa: Editor UFV, p. 1-15.

Cabral PDS (2011). Analysis of trailing of bean (Phaseolus vulgaris L.) grain yield and its components. Journal Science Agronomics, Fortaleza, v. 42, n. 1, p. 132-138, Jan/Mar.

Coelho CMM, Coimbra JL, Souza CA, Bogo A, Guidolin AF (2007). Genetic divergence in bean (Phaseolus vulgaris L.) accessions. Rural Science, Santa Maria, v. 37, n. 5, p.1241-1247.

Collicchio E (1995). Association between bean plant size and grain size. 1995. Dissertation (Master in Genetics and Plant Improvement) - Federal University of Lavras, MG, 98 p.

Costa MM (2004). Genetic gain by different selection criteria in segregating populations of soybean. Brazilian Agricultural Research, v. 39, n. 11, p. 1095-1102.

Cruz CD, Carneiro PCS (2006). Biometric models applied to genetic improvement. 2. ed. Viçosa: UFV, v2, p. 585.

Cruz CD, Carneiro PCS, Regazzi AJ (2014) Biometric models applied to genetic improvement. v. 2, 3. ed. Viçosa, MG: Editors UFV, A668 p.

David, S., R. Kirkby and S. Kasozi, (2000). Assessing the Impact of Bush Bean Varieties on Poverty Reduction in sub-Saharan Africa: Evidence from Uganda. Network on Bean Research in Africa, Occasional Publication series N0.31, CIAT, Kampala, Uganda.

Diniz, Belísia Lúcia Moreira T (2006). common bean culture. Santa Catarina: UFSC

Elias HT (2007). Genetic variability in traditional black bean germplasm in Santa Catarina. Brazilian Agricultural Research, v. 42, n. 10, p. 1443-1449.

Embrapa (2014). Brazilian Agricultural Research Corporation. Embrapa Rice and Beans. Common Bean Cultivation. Systems of Production. Electronic version. 2003. Available at: Accessed on: May 16.

Fancelli, A Dourado Neto DL (2000). Bean production. Guaíba: Agriculture, 385 p.

Food and Agriculture Organization of The United Nations Accra, (2019). Promoting regional trade in pulses in the Horn of Africa.

Franco MC (2001). Characterization of genetic diversity in beans by means of RAPD marker. Brazilian Agricultural Research. 36, p. 381-385.

Gepts P, Bliss FA (1986). Phaseolin variability among wild and cultivated common bean (Phaseolus vulgaris L.) from Colombia. Economic Botany, New York, v. 40, n. 4, p.469- 478.

Gonçalves DL, Barelli MAA, Santos PRJ, Oliveira TC, Silva CR, Neves LG, Poletine JP, Luz PB (2016). Genetic variability of traditional germplasm of common bean in the region of Caceres-MT. Rural Science, Santa Maria, v. 46, n. 1, p.100-107.

Grigolo S, Fioreze AC, Denardi DL, Vacari SJ (2018). Implications of univariate and multivariate analysis on the dissimilarity of common bean accessions. Journal of Agroveterinary Sciences, Lages, v. 17, n. 3, p.351-360.

Kimani P, Buruchara R, Ampofo K, Pyndji M, Chirwa R, Kirkby R (2005). Smallholder bean farming in eastern, central, and southern Africa: constraints, achievements, and potential. In: Kirkby R, editor. PABRA Millennium Workshop; September.

Krause W (2009). Genetic divergence in snap beans based on agronomic traits and resistance to bacterial wilt. Crop Breeding and Applied Biotechnology, v. 09, p. 246-252.

Kwak M, Gepts P (2009). Structure of genetic diversity in the two major genetic groups of common beans (Phaseolus vulgaris L., Fabaceae). Theoretical and Applied Genetics, v. 118, p. 979-992.

Lima MS (2012). Characterization of genetic variability among common bean genotypes by morphological descriptors. Crop breeding and applied biotechnology 12: 76-84.

Machado CdeF (2002). Genetic divergence among bean genotypes using multivariate techniques. Rural Science, v. 32, n. 02, p. 251-258.

Mambrin RB, Ribeiro ND, Storck L, Domingues LL, Barkert KA (2015). Selection of bean lines based on morphological, phenological, and yield characteristics. Journal of Agriculture, Piracicaba, v. 90, n. 2, p.141-155.

Margaret N, Tenywa JS, Otabbong E, Mubiru DN, Ali T (2014). Development of Common Bean (Phaseolus Vulgaris L.) Production Under Low Soil Phosphorus and Drought in Sub-Saharan Africa: A. Journal of Sustainable Development.

Mazieiro SM, Ribeiro ND, Casagrande CR (2017) Genetic dissimilarity of common bean lines for agronomic and biofortification traits. Genetic and Molecular Research, [s. n.], v. 16, n. 3, p.1-13.

Mercati F, Leone M, Lupini A, Sorgona A, Bacchi M, Abenavoli MR (2013). Genetic diversity and population structure of a common bean (*Phaseolus vulgaris L.*) collection from Calabria (Italy). Genetic resources and crop evolution.

Ministry of State Administration (2014) Profile of Sussundenga District, Manica Province, Mozambique.

Petry N, Boy E, Wirth J, Hurrell R (2015). The potential of the common bean (Phaseolus vulgaris L) as a vehicle for iron biofortification. Nutrients.

Rodrigues LS (2002). Genetic divergence between local and improved bean cultivars. Research on Brazilian Agriculture and Livestock, v. 37, n. 09, p. 1275-1284, 2002.

Rotili EA, Cancellier LL, Dotto MA, Peluzio JM, Carvalho EV (2012) Genetic divergence in corn genotypes in Tocantins State. Agronomic Science Magazine, v. 43, n. 3, p.516-521.

Salgado FHM (2012). Effect of nitrogen on beans grown in uplands in the south of the state of Tocantins. Environment, Guarapuava.

Sebim DE, Oliveira PH, Brusamarello AP, Baretta DR, Brum B (2016). Genetic diversity among Creole bean populations through multivariate analysis of morphoagronomic characters. Espacios, Caracas, v. 37, n. 16, p.19-31.

Sicard D, Nanni L, Porfiri O, Bulfon D, Papa R. Genetic diversity of Phaseolus vulgaris L. and P. Coccineus L (2005). landraces in central Italy. Plant Breeding.

Silva God (2008). Importance of characters in the dissimilarity of potato progenies in early generations of selection. Bragantia, v. 67, n. 01, p. 141-144, 2008.

Simone Mde, Failde V, Garcia S, Panadero PC (1992). Adaptation of varieties and lines of dry beans (Phaseolus vulgaris L.) to direct mechanical harvesting. Salta: INTA, 1992. 5p.

Singh D (1981). The relative importance of characters affecting genetic divergence. The Indian Journal of Genetics & Plant Breeding, New Delhi, v. 41, p.237-245.

Sulzbacher LJ, Silva VP, Zago BW, Corrêa CL, Duarte AVM, Barelli MAA (2017). Analysis of genetic divergence through agronomic characters in common bean genotypes. Espaces, Caracas, v. 38, n. 23, p.26-39.

Tsutsumi CY, Bulegon LG, Piano JT (2015). Genetic improvement of the bean: advances, perspectives, and new studies, nationally. Native, Sinop, v. 3, n. 3, p.217-223.

Vale NM, Barili LD, OLIVEIRA HM, CARNEIRO JES, Carneiro PCS, Silva FL (2015). Selection of genitors for precocity and productivity of carioca beans. Research on Brazilian agricultural production, Brasília, v. 50, n. 2, p.141-148.

Vidyakar V, Lal GM, Singh MK, Kumar A (2017). Study on genetic diversity in French bean (Phaseolus vulgaris L.). Journal of Pharmacognosy and Phytochemistry, New Delhi, v. 6, n. 6, p.184-187, 2017.

Vieira, C. Bean culture. 2. ed. Viçosa, MG: UFV, 146 p, 2006. Potassium and Phosphate Research, 1988.

Wortmann, C.S, R. A. Kirby, C.A. Eledu and D.J. Allen (1998). Atlas of common bean production in Africa, CIAT publication No. 297.

Ribeiro-Costa CS, Pereira PRV da S, Zukovski L (2007). Development of Zabrotessubfasciatus (Boh.) (Coleoptera: Chrysomelidae, Bruchinaos) on Phaseolus vulgaris L. (Fabaceae) genotypes grown in Paraná state and containing arcelin. Neotropical Entomology, v. 36, p.560-564, 2007.