



EVALUATION OF AGRONOMIC POTENTIAL AND GENETIC PARAMETERS OF COMMON BEAN GENOTYPES IN MOZAMBIQUE

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Abstract: The present research aims to evaluate the agronomic potential, and estimate genetic parameters in common bean characteristics. The experiments were conducted in the experimental area of the Agrarian Station of Sussundenga (ASS), of the Institute of Agricultural Research of Mozambique (IIAM)-Zonal Center (CZC), Manica Province-Mozambique in the three agricultural seasons (2015/16, 2016/17, and 2017/18). The experiments were evaluated using a randomized block design with three replications and 115 entries of common bean genotypes. The agronomic characteristics evaluated were: the number of days to flowering (DF), number of days to maturity (DM), number of pods per plant (NP), plant height (PH), and grain yield (GY). Individual and joint analysis of variance was performed genetic parameters were subsequently estimated for all characteristics. The results showed a significant interaction effect for all characteristics. The highest value of the estimate of the coefficient of genetic variation was observed for GY and NP. High heritability among common bean genotypes was observed. A genotypic correlation was demonstrated for PH, NP, and GY. Finally, it was observed that the genotypes have the potential to compose a breeding program and contribute to increasing grain yield.

Keywords: *Phaseolus vulgaris*, correlation network, genetic gain.

Introduction

Common bean (*Phaseolus vulgaris*, L.) is a source of carbohydrates, essential amino acids, minerals such as iron, zinc, and vitamins, in the diet of the World popula-

tion, and specially for most people in developing countries (Wortman et al., 1998; Broughton et al., 2003; Myer & Kmiecik, 2017). It is a legume that contributes to household income through the sale of surplus collected during agricultural seasons.



In Sub-Saharan African countries, and Mozambique in particular, common bean is produced in intercropping with other crops, such as maize, sorghum, and millet, fixing nitrogen in the soil, improving soil structure, and improving the productivity of the other crops in the field. According to the IAI., (2020), Common bean crop in Mozambique is produced in an area of 123,442 ha, mostly by smallholder farmers with average productivity that is between 0.53 and 0.7ha⁻¹ (Mader., 2021), considered low when compared to the average yield of other countries with a larger production, as is the case of China (1,744.1,t ha⁻¹), United Republic of Tanzania (1,343.7 t ha⁻¹), Myanmar (911,6t ha⁻¹) (Faostat, 2020) and Brazil (1,113 t ha⁻¹), (Conab, 2022). The low yield in Mozambique can be attributed to several factors, such as poor agricultural techniques, abiotic and biotic stresses, and the use of varieties with low genetic potential for yield. This last factor can be increased through genetic improvement (Pedro et al., 2022). The quantification of phenotypic and genetic variability present in a population is of fundamental importance for developing breeding programs, as it allows to know the characteristics of genetic control and the population's potential for selection (Ramalho et al., 2000). The determination of the genetic control of the characteristics that are selection objectives constitutes an initial step that guides the choice of the most appropriate procedures in breeding programs (Santos et al.,1985). The successful development and implementation of improved cultivars depend on the careful evaluation of existing material in germplasm banks and the characteristics to be selected for yield improvement.

However, the breeding program of any species depends on the correct choice of the best individuals used as genitors, thus, the estimation of genetic parameters is essential for the success of this program (Farias Neto et al., 2013). It allows the breeder to know the genetic structure of the populations he intends to evaluate, and the nature of the ac-

tion of the genes involved in the inheritance of the character, in addition to assisting in the choice of methods to be used in the initial and advanced stages of the program (Cockerham, 1956; Fehr, 1987; Cruz and Carneiro, 2014). For the plant breeder, the interest in obtaining great variability to carry out a selective process that effectively results in significant genetic gains, is a fundamental point and important for the development of new cultivars of common bean, after this purpose, there is an urgent need to evaluate the agronomic potential end estimate genetic parameters in common bean characteristics at Institute of Agricultural Research of Mozambique (IIAM) Station, Sussundenga, in Manica province to understand the genetic composition and subsequently select the best ones to be used as potential genetics in breeding programs.

Material and methods

Field experiments to evaluate the agronomic potential and genetic parameters of selected common bean genotypes were conducted at the Institute of Agricultural Research of Mozambique (IIAM) Station, Sussundenga, in Manica province during the 2015/16, 2016/17 and 2017/18 cropping seasons. Geographically, the study site is located in the Revue River basin at latitude 19°32' South, longitude 33°35' East, and 635 m above mean sea level (MAE,2014) (Figure 1). The district presents different soil groupings highlighting red clayey, red sandy red medium-textured, and lithic soils. These soils, except for the lithologic ones in general are, moderately deep to very deep, neither saline nor sodic. The predominantly clay-textured soils have good nutrient and water-holding capacities while the sandy ones are, not very fertile (MAE, 2014). The climate of the region, according to the classification of Köppen (1931), is called Cfb, humid mesothermal with rainy winter and mild summer, with an average temperature between 15°C and 25°C, with an average annual rainfall of 1500 mm.

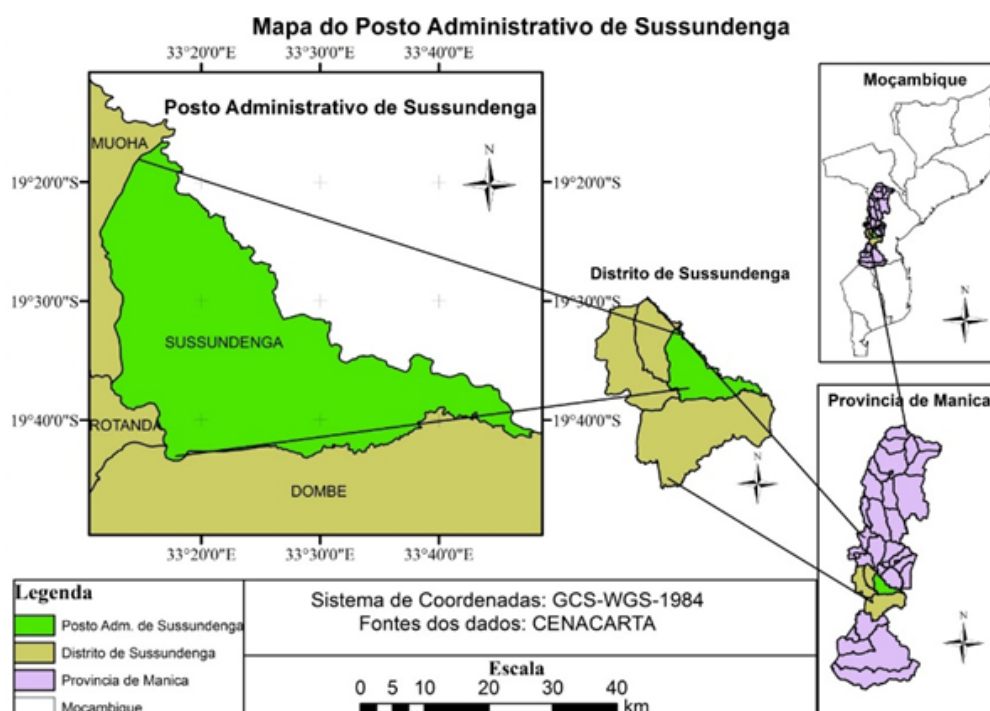


Figure 1. Schematic of the geographical location of the study area

Genetic materials used in the Research

The genetic materials used for this research were 115 common bean genotypes from the legume program of the Instituto de Investigação Agrária de Moçambique-Centro Zonal Centro-Agrarian statio Agraria de Sussundenga (Table 1).

Table 1. One hundred and fifty (115) common bean genotypes from the legume program of the Centro Zonal Center (CZC)-Manica-, Mozambique.

¹ ID	² Gen/Lines	¹ ID	² Gen/Lines	¹ ID	² Gen/Lines	¹ ID	² Gen/Lines	¹ ID	² Gen/Lines	¹ ID	² Gen/Lines
1	A 55	21	BFS 95	41	H9657-27-10	61	PR0806-81	81	Zorro	101	SAP 1
2	A 686	22	BFS 97	42	I9365-31	62	SER 16	82	PR0806-84	102	SB-DT-1
3	ALB 213	23	BK9-2	43	ICA Bunsu	63	SER 48	83	DOR 390	103	SCR 2
4	ALB 74	24	Blush	44	IJR	64	SER 78	84	BFS 101	104	SCR 9
5	ALB 88	25	CAL 143	45	INB 820	65	SIN 526	85	NCB 280	105	SEA 5
6	ALB 91	26	Carioca	46	INB 827	66	SMC 141	86	Pérola	106	SEF 10
7	AP7	27	CELRK	47	INB 834	67	SMC 143	87	PR1146-123	107	SEF 14
8	Badillo	28	Amadeus	48	INB 835	68	SXB 405	88	PR1146-124	108	SEF 15
9	BAT 477	29	CALIMA	49	INB 837	69	SXB 405	89	PR1165-17	109	SEF 16
10	BAT 881	30	Quimbaya	50	INB 841	70	SXB 412	90	PR1165-3	110	SEF 17
11	BFS 10	31	Colorado - 1	51	Jamapa	71	TARS-LFR1	91	PRO633-10	111	SEF 60
12	BFS 112	32	Colorado - 2	52	Matterhorn	72	TARS-MST1	92	PT7-2	112	SEF 71
13	BFS 129	33	Colorado - 3	53	MD 23-24	73	Tepary; Tep 22	93	RCB 593	113	SEN 46
14	BFS 139	34	Colorado - 4	54	Montcalm	74	Tepary; Tep 23	94	Rosetta	114	SER 118
15	BFS 14	35	DICTA 17	55	Morales	75	Tepary; Tep 32	95	SAB 258	115	SER 119
16	BFS 142	36	DOR 364	56	NCB 226	76	USRM-20	96	SAB 560		
17	BFS 29	37	FEB 226	57	SER 125	77	Tio Canela	97	SAB 618		
18	BFS 81	38	G122-Jatu	58	Pijao	78	VAX 1	98	SAB 659		
19	BFS 87	39	G21212	59	PK7-4	79	Verano	99	SAB 686		
20	BFS 94	40	GN9-4	60	PR0737-1	80	XRAV-40-4	100	SAB 691		

¹ID = identification; ²Genotypes/Lines

Experimental design of the research

The trials were conducted in a randomized block design (RBD), with three replications. Each experimental plot consisted of two 5m rows, spaced at 0.5m, and contained approximately 150 plants. Sowing was performed manually in February of each growing season, in rows demarcated with a density of 15 seeds per meter. During planting, N-P-K background fertilizer was applied 150kg ha⁻¹ in the formula 14-28-14. The cultural treatments and phytosanitary control were performed as recommended by the agronomic management literature of common beans (Borém and Carneiro, 2015). However, Macozeby and Cypermitriny were used when necessary to protect the plants from pests and diseases. The following characters were evaluated plant height (PH) 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 (NP): Obtained by counting the number of pods from each plant being taken the average value of six plants within the useful area, number of days to maturity (DM): Period, in days, between sowing and the appearance of the first pod of modified coloration: As for the number of days to flowering (NF), it 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 Grain yield (GY). Estimated by considering the harvested production in the useful area of the plot (m²), extrapolating the value obtained to kg/ha with correction of the mass of the grains to 13% humidity, determined based on the grain production of the two central rows of the plot.

The harvest was performed manually, 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 dried in the sun for four days to allow the pods to dry completely and then followed by tracing, cleaning, weighing, and later extrapolating the quantity corresponding to the unit kg ha⁻¹.

The data obtained at the end of each growing season were submitted to individual analysis of variance to confirm the existence of genetic variability among the genotypes/lineages for all the evaluated characters, and later it was observed that the ratio between the largest and smallest mean square of the residue was less than seven, indicating homogeneity, which allowed the joint analysis of the data. The effect of means and genotypes/lines were considered random and the effects of block error and environment as fixed, as shown in the statistical model below:

$$Y_{ijk} = m + G_i + B/A_{jk} + A_j + GA_{ij} + E_{ijk},$$

where G is random and A is fixed where:

Y_{ijk}: observed value referring to genotypes i in environment j in blocks;

m: general average of the experiment associated with all genotypes;

G_i: effect of genotype i (i = 1, 2, 3, ... ,115);

(B/A)_{ij}: effect of block k within environment j;

A_j: effect of environment j (j = 3);

GA_{ij}: effect of the interaction of genotype i in environment j;

E_{ijk}: random error associated with observation Y_{ijk} ~ NID (0, σ²).

From the individual and joint analysis of variance were estimated the genetic parameters, and their estimators for each character, using the following expressions (CRUZ et al., 2013):

a) Mean genotypic variance:

$$\sigma^2_g = \frac{QMG - QMR}{K}$$

Where: σ²_g, means genetic variance; QMG, refers to the mean square of the genotype, QMR, means the mean square of the residuals.

b) Genetic coefficient of variation:

$$CVg = \sqrt{\frac{\sigma^2_g}{M}} * 100$$

Where: CV_g, means coefficient of genetic variance, σ²_g genetic variance, M- Average.

c) experimental coefficient of variation:

$$CVe = 100 \sqrt{\frac{QME}{M}}$$

Where: CVe- means coefficient of environmental variance, QMR-mean square of waste, M- Mean.

d) Quotientratio:

$$\frac{CVg}{CVe}$$

where: CVg, refers to genetic variance coefficient, and CVe- means environmental variance coefficient.

e) Individual heritability in the broad sense in the block:

$$h^2$$

where: h²- means heritability, σ²g genetic variance, σ²f phenotypic variance.

f) Selection gain: GS =h²*DS

Where: GS means gain by selection, h²- means heritability meaning selection differential.

Results and Discussion

Analysis of variance

The summary of the analysis of individual variances and genetic parameters for the evaluated characters in common bean genotypes in three environments is presented in Table 2. Most of them presented a statistically significant effect between means at a 1% probability level, except for the number of days to flowering (DF) in the environment (E2), which was not significant (Table 2). These results indicate the great possibility of obtaining genetic gains. The experimental coefficients of variation (CVe) for all the characters studied presented low average values, with the exception of grain yield (GY), which had a high experimental coefficient of variation (Table 2), according to the classification proposed by Pimentel-Gomes (2009), in which high values for the coefficient of variation of this characteristics are acceptable under the conditions in which it was evaluated, and for being quantitative and well influenced by the environment. The analysis of the components of genetic variance was higher for the grain yield (GY) character, in all environments with values (Table 2).

Table 2. Summary of individual analysis of variance for the characteristics grain yield (GY) in kg/ha, number of days to flowering (DF), number of pods per plant (NP), plant height (PH) referring to the evaluation of 115 between genotypes of common bean in three environments, Sussundenga-Mozambique.

SV	PH			DF			NP			GY		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
MS	211.8**	141.0**	87.7**	33**	45ns	37**	70.7**	15.9**	30.9**	376050.4**	96335.8**	73605**
AVERAGE	33.5	25.7	25.2	36.9	35.7	36.6	16.9	15.5	12.9	1109.3	1046.9	1071.3
CV(%)	25.4	18.1	25.3	7.2	17.6	5.2	20.8	17.1	9.6	28.8	16.2	11.7
σ ² g	45.51	39.88	15.8	19.4	50.7	12.45	8.41	1.92	11.13	44303.73	22505.34	19303.4
h ²	0.65	0.84	0.54	0.78	0.3	0.9	0.82	0.95	0.96	0.35	0.7	0.87

Environment (E1 to E3) in which the experiments were evaluated, MS = Mean Square of Genotypes; Average of the genotypes in the environments evaluated (AVERAGE); CV(%) = Coefficient of experimental variation; σ²g = genotypic variation, h² = Heritability; PH = plant height expressed in cm, DF = number of days to flowering; NP= number of pods per plant expressed in g and GY = grain yield expressed in kg/ha and **and * significant by F test at 1% probability.

According to Correa et al. (2012) among all the characters studied was the one that showed the greatest variability, being highly promising for the selection process. To have a good selection of genotypes genotypes in breeding work is of fundamental importance the experimental precision, especially in characters such as grain yield, which suffers great envi-

ronmental influence. The highest estimates of heritability were verified for the characters NP in all environments, GY in environments E2 and E3, and DF, in environments E1 and E3, in the three seasons (Table 2). Many authors have found in several works higher magnitude estimates of heritability related to grain yield, as is the case of Coelho et al. (2002); Lobato

et al. (2014), and Paula et al. (2020). The lowest heritability estimates were also found for PH, in environments E1 and E3 and DFin environment E2 (Table 2).

The summary of the joint analysis of variance for the characters grain yield (GY) in kg/ha, number of days to maturity (DM), number of days to flowering (NF), number of pods per plant (NP), plant height (PH) referring to the evaluation of 115 between genotypes of common bean in 3 environments of Sussundenga is presented in table 3. From the data, it was possible to observe the interaction between genotype(G) and environments (E) ($P \geq 0.01$), as well as for other characteristics evaluated were significant at the 1% probability level by the F test, except for the characters (DF) and (NP) that were not significant for the environment (Table 3). Evidence that the genotypes responded differently to environments, for most of the characters studied, with different rankings considering the three environments (years). The existence of genetic variability in a population (germplasm) is a determining factor for any improvement program (Ramalho et al., 2000). For these genotypes under study, they showed, in principle, promise for selection work or with potential for the development of new cultivars. In Table 3, the values of the experimental coefficient of variation (CVe) ranged from 11.22 to 28.8%, being the first value expressing good precision (Pimentel Gomes, 2002).

The genotypic coefficient of variation (CVg%) ranged from 5.18% for (DF),

(8.51%) for (GY), (16.187%) for (PH) and finally (26.4%) for (NP) respectively (Table 3). The estimate of 5.18% for the character (DF) is considered low and indicates among all the characters studied this one that showed less variability, being little promising to perform selection (Mendonça et al., 2018). However, the coefficient of genetic variation (CVg) indicates the genetic variation observed in the field and allows the breeder to have a notion of the relative magnitude of the changes that can be obtained through selection throughout a breeding program. The estimates found are in agreement with Correa et al. (2015) and indicate that among all the characters studied, these were the ones that showed the greatest variability, being highly promising for selection. According to Torres et al. (2015), this set of information is of paramount importance in guiding breeding programs, contributing to the selection of superior genotypes.

The estimated values about heritability in the broad sense for all the characteristics were high for the characters plant height (PH) with a value of 80.6%) and number of pods per plant (NP) with a value of 95%), number of days to flowering (DF) with 65%) and productivity with a value of 44%) respectively. However, in general, the productivity character generally presents low heritability (20-30%), due to its quantitative behavior, because of a large number of loci that control it, since much of the phenotypic variance is due to environmental causes (Hamawaki et al., 2012).

Table 3. Summary of the joint analysis of variance for the characters grain yield (GY) in kg ha⁻¹, number of days to maturity (DM), number of days to flowering (DF), number of pods per plant (NP), plant height (HP) referring to the evaluation of 115 between strains/genotypes of common bean in 3 environments, Sussundenga-Mozambique.

	SV	DF	DF	PH	VP	GY
Mean Square	G	114	48809**	231353**	150759**	171452.81**
	E	2	149.34ns	7462693**	1509.92ns	350382.68**
	GXE	118	32.86**	104679**	58.99**	187268.06**
	R	684	16.71	44.72	7045	95883.73
	Average	1034	36418	28.13	15.12	1075.52
	CV ² (%)		11.22	23.77	17.55	28.79
Genetic Parameter	Cvg (%)		5.187	16.187	26.43	8.51
	Cvg/Cve		0.462	0.680	1.501	0.29
	h ²		65	80.66	95	44.07

SV = Source of Variation; DF = number of days to flowering; PH = plant height (cm); NP = number of pods per plant (gram), GY = dry grain yield (kg ha⁻¹). CV% = coefficient of variation; h² = average heritability; CVg = coefficient of genotypic variation; b = jb quotient = (CVg / CVe); e Significant at 1% probability, respectively, by the F test; ns: not significant.

In addition to the summary of the joint analysis of variance for the evaluated characters, it is important to consider the productive performance of each genotype from a careful analysis of the evaluated characteristics. However, this criterion allows measuring/selecting the best genotypes according to their performance where the best indicated will be used in breeding programs that aim to increase the desired characteristics. In this research the plant height (PH) character, two groups were observed by the Scott and Knott test with greater height in genotypes. Among these groups, group I (one) was composed of genotypes (24, 34, and 60), with higher averages, and the second was composed of genotypes (45, 92, and 107) for the environment (E1). For environment (E2) it was observed the formation of one (1) group composed of genotypes (27, 37, and 68) was. For the environment (E3) it was observed the formation of five (5) groups was, the first composed of genotypes (27 and 37), differing statistically from the other groups found (Table 4). The second composed of (55 and 58), the third composed of (3, 7 and 9), the fourth was composed of (13, 48 and 59) and finally the fifth group was composed of genotypes (5, 25, 44 and 77) respectively (Table 4). The genotypes that have greater heights are considered of great relevance by improvers, due to its ability to facilitate the mechanized harvest, in addition to cultural gains and loss in the mechanized harvest, because it avoid the direct contact of the pods with the soil, thus promoting the better phytosanitary condition of the grains (Salgado et al., 2012).

For the characteristic number of pods per plant (NP), three groups were observed by the Scott and Knott test that showed a higher number of pods. Among these groups it can be highlighted group 1 (one) was composed of genotypes (51, 106, and 107), with higher averages and differed statistically from the others, the second was composed of genotypes (54, 68, and 110) and the third group (3) composed of genotypes (22, 42 and 49), for the environment (E1) respectively. In contrast to environment (E2), the formation of three(3) groups was observed, the first composed of genotypes(44, 51, and 106) with higher averages, the second composed

of genotypes(54, 68, and 110) and finally the third group composed of genotypes(22, 42 and 49) respectively. In the environment (E3) was observed the formation of seven (7) groups, the first composed of only genotype (107), which differed statistically from the others, the second composed of genotype (9), the third composed of genotypes (54, 57 and 74), the fourth composed of genotypes (29, 53 and 106) with higher averages in the group, the fifth composed of genotypes (4, 30 and 56), the sixth group composed of genotypes (18, 71 and 73) and finally the seventh group composed of genotypes (11, 31 and 35) respectively. Most of the results obtained in these environments are superior to the results obtained by Mambrin et al., (2015) evaluating 14 advanced bean lines and by Gonçalves et al., (2016) evaluating 40 traditional bean accessions, thus showing the potential to be selected and compose the improvement program.

Regarding the characteristic number of days to flowering (DF), two groups were observed by the Scott and Knott test in the environment (E1). Among these groups, we can highlight group one (I) composed of genotypes (10, 61, and 65), with higher averages that differed statistically from the others, and the second group (II) composed of genotypes (5, 7, and 58), respectively. For environment (E2) was observed the formation of three (3) groups, being the first (I) composed of genotypes (4, 5, and 80), the second group (II) composed of genotypes (8, 9, and 58) and the third group (III) composed of only genotype (30) respectively. For environment three (E3) four groups (IV) were observed, with the first group (I) composed of genotypes (10, 53, and 55), the second group (II) composed of genotypes (9, 42, and 70), the third group (III) composed of genotypes (29, 46 and 54) and the fourth group(IV) finally composed of genotypes (20, 72 and 34) respectively. Genotypes that have fewer days to flower are desired in many bean breeding programs. Early genotypes are mainly developed to meet renewal areas for other crops (Bizarre 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.

As for the grain yield (GY) characteristic, a single group (I) was formed for the environment (E1) composed of the genotypes (14, 19, and 24), with higher averages that differed statistically from the other groups found (Table 4). In an environment (E2) three distinct groups were observed, being the first group (I) composed of genotypes (14, 20, and 36), the second group (II) composed of genotypes (23, 84, and 111), and the third group (III) composed of genotypes (16, 51 and 82) respectively (Table 4). In the environment (E3) it was observed the formation of three

(3) groups, being the first (I) was composed of genotypes (29, 61, and 36), and the second group (II) was composed of genotypes (26, 49, and 68) and finally, the third group was composed of genotypes (8, 34 and 46) respectively. In general, in all genotypes/lines evaluated the best productivity was observed in the environment (E1). Ribeiro (2007) explains that the variable grain yield (GY), is a characteristic highly influenced by environmental conditions and its various components, the genotypes proved to be quite variable in their behavior in different locations.

Table 4. Averages referring to the comparison of the four (4) morpho-agronomic characters evaluated in 115 common bean genotypes/lines for grain yield (GY) in kg.ha⁻¹, number of days to flowering (DF), number of pods per plant (NP), plant height (HP) in 3 environments, Sussundenga-Mozambique, grouped by the Scott-Knott test (5%) probability, in agricultural seasons 2015/16, 2016/17 and 2017/18.

ID/ CAR	PH			NP			DF			GY		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
1	30b	19a	18.7e	15.7c	10.7g	13.3e	41.7a	36.7a	39b	1763a	1109.3c	987c
2	42a	26a	26d	17.7c	16f	11g	41a	37.7a	38b	912a	945.3c	1179b
3	28b	35a	35c	14.7c	15.7f	15d	35.3b	37.3a	33.7d	1532a	1161.3b	894c
4	30b	26a	25.7d	13.7c	20e	11g	35b	41.7a	34.7c	929a	1044c	1341b
5	28b	21a	21.3e	18c	16.3f	12.7e	37.7b	41.7a	36.3c	1092a	872c	985c
6	33b	27a	27d	16c	14.7f	12.7e	36.3b	37a	36c	1117a	926.7c	1001c
7	37a	37a	37c	18.3c	14.3f	9.7g	37.7b	40.3a	38b	1087a	1041.3c	695c
8	46a	25a	25.3d	14c	16f	8.3h	35.3b	32b	35c	1095a	1006.7c	1105c
9	31b	36a	35.7c	12.7c	35b	10.3g	40.7a	30.3b	40.7b	1133a	1034.7c	1063c
10	26b	23a	23.3d	27.7a	13g	21.7b	45a	37a	44.3a	1127a	920c	1003c
11	39a	23a	22.7d	16.7c	13.7g	15d	37.3b	38.3a	35.7c	989a	905.3c	1189b
12	35b	30a	30c	17.7c	18.7e	9.7g	34b	28.3b	34.7c	1518a	1036c	1241b
13	32b	27a	27d	11.3c	11g	13.3e	34.7b	34.7a	33.7d	1033a	992c	1003c
14	39a	26a	26.3d	13.7c	13.3g	8h	36b	23.7b	36c	3816a	1528a	1252b
15	43a	17a	16.7e	13c	15.3f	14e	36.3b	38.7a	36.3c	1003a	1113.3c	1009c
16	31b	23a	23d	16c	11.7g	12.3f	35.3b	38.3a	34.3c	1181a	1142.7c	835c
17	35b	20a	20e	16c	9.7h	14e	38.3a	40a	35.3c	1037a	1030.7c	1250b
18	32b	20a	20.3e	17c	16.3f	10.3g	35.3b	36a	34.7c	784a	977.3c	1460a
19	34b	21a	20.7e	15.3c	15f	9.7g	36.3b	34a	34.3c	1914a	1025.3c	1208b
20	41a	29a	28.7c	15c	13.3g	12.3f	35.3b	37.7a	34d	1390a	1692a	1183b
21	27b	25a	25.3d	20c	19.7e	11.3f	39.7a	38.3a	41a	1374a	1110.7c	1027c
22	38a	26a	25.7d	19.3c	23.3d	11.7f	37.3b	36.7a	39.7b	927a	968c	1213b
23	34b	26a	26d	15.3c	14f	10g	35.7b	37.3a	34.3c	847a	1324b	1019c
24	57a	23a	23.3d	19c	21.3d	12.7e	41a	30b	42a	1837a	929.3c	1023c
25	32b	21a	21e	25.7a	6.3h	6.7h	33.3b	35.7a	32.7d	987a	777.3c	1063c
26	26b	18a	18.3e	13.3c	11.3g	10.7g	35.7b	27b	36.7c	1599a	908c	1255b
27	41a	49a	49.3a	15c	18e	11.3f	41.7a	38.7a	41.7a	943a	1013.3c	989c
28	24b	25a	24.7d	9.7c	7.3h	8.7h	33b	35.3a	31d	843a	976c	1240b
29	28b	23a	22.7d	28.7a	26d	11.3f	37b	39.7a	37.3c	1316a	1001.3c	1545a
30	30b	17a	25.7d	15.3c	20e	11.7f	41.3a	12c	42.7a	972a	1184b	888c
31	26b	27a	26.7d	17c	13.3g	12.7e	34.3b	38a	34.3c	1063a	1482.7a	1037c
32	28b	18a	18.3e	14.3c	12.7g	10.7g	35b	40.7a	33.3d	1031a	885.3c	1272b
33	45a	37a	36.7c	13c	11.7g	11.3f	35b	38a	34.7c	924a	729.3c	966c

ID/ CAR	PH			NP			DF			GY		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
34	59a	33a	32.7c	14.3c	9.7h	18c	36b	36.3a	35.3c	1421a	1037.3c	1129c
35	41a	30a	30.3c	15.3c	13.7g	7.7h	33.7b	36.3a	33d	920a	997.3c	1057c
36	42a	23a	23d	20.7b	12g	7h	36.7b	37.7a	35.3c	923a	1716a	1475a
37	30b	49a	49.3a	6.3c	27.7c	17.7c	27b	32.3a	41a	581a	977.3c	930c
38	32b	17a	17e	17c	10h	11.3f	41.7a	34.3a	40b	1283a	1046.7c	929c
39	35b	19a	18.7e	15c	8.3h	12.7e	39.3a	29b	35.3c	932a	741.3c	1407a
40	25b	19a	19e	13.3c	8h	8.3h	29.3b	35.7a	28.7d	1541a	925.3c	930c
41	48a	22a	22.3d	17c	12.3g	10.7g	37b	35.7a	36c	948a	930.7c	1037c
42	40a	23a	23.3d	19.7c	10.7g	20.3b	40.3a	36.7a	40.3b	780a	1009.3c	944c
43	45a	28a	28.3c	13c	8.7h	11g	34.7b	22.7b	35c	989a	592c	945c
44	50a	22a	21.7e	29a	13g	9.7g	42.7a	24.7b	42.7a	960a	949.3c	1244b
45	36b	21a	21.3e	20.7b	25d	16.3d	39a	38a	39b	827a	834.7c	1189b
46	32b	20a	20.3e	17.3c	18.7e	17c	36.3b	34.7a	37c	1404a	1166.7b	1114c
47	26b	24a	24.3d	14.7c	15.3f	13e	37b	36.7a	35.7c	1017a	968c	1086c
48	34b	27a	27.3d	15c	15.3f	18c	38a	27.3b	37.3c	999a	925.3c	1060c
49	33b	24a	24.3d	20c	23d	12.7e	35.7b	33.7a	35.7c	817a	1512a	1290b
50	25b	13a	13e	18.3c	14.3f	11.3f	34.3b	36a	33.7d	993a	945.3c	984c
51	28b	19a	19e	30.3a	11g	13.3e	37.3b	36a	40b	1055a	1146.7c	1157b
52	18b	24a	24.3d	15.3c	16f	10.7g	34b	37a	33.3d	904a	896c	1027c
53	31b	18a	18e	19.3c	26.3d	14e	41.3a	34.3a	43.3a	900a	1024c	1040c
54	31b	28a	28.3c	22.3b	28.7c	15d	39.3a	37a	37c	953a	1090.7c	1014c
55	23b	43a	43.3b	16.3c	10h	9.7g	42a	38a	44a	937a	982.7c	1191b
56	30b	26a	26d	10c	20.3e	10.7g	32.7b	35.3a	31.7d	831a	1006.7c	1016c
57	22b	35a	35.3c	14.7c	29.3c	13.3e	41.3a	36a	40.7b	928a	1177.3b	922c
58	39a	40a	40b	27.3a	17.7e	18c	35b	30.7b	34.7c	1695a	1250.7b	1129c
59	48a	28a	27.7d	18.7c	11g	16.3d	33.7b	34.7a	33d	1108a	948c	1035c
60	56a	31a	30.7c	14.3c	9.7h	14.3e	41a	28.7b	43.3a	1041a	893.3c	1021c
61	43a	30a	30c	19c	17f	10.7g	42.3a	38.7a	41.7a	867a	1338.7b	1531a
62	47a	28a	28.3c	15c	12g	13.3e	34.3b	37.3a	33.3d	1170a	1025.3c	1054c
63	47a	31a	31.3c	13.7c	8h	11g	37b	38.3a	37c	1073a	960c	1045c
64	28b	29a	29.3c	26a	27.3c	21b	41a	37.7a	42.7a	1033a	968c	1055c
65	21b	22a	21.7e	12.3c	11.7g	15d	43.3a	35.7a	42.3a	972a	978.7c	1585a
66	21b	15a	15e	13.3c	11.3g	13.7e	36b	39.3a	35.7c	1258a	941.3c	927c
67	24b	17a	16.7e	12c	10h	14.3e	40.7a	40a	39.7b	983a	928c	1019c
68	25b	51a	50.7a	22.7b	10h	13e	33b	39.3a	32.3d	848a	1222.7b	1355b
69	26b	28a	28c	21.7b	20e	13e	41a	30.3b	42.3a	1035a	1002.7c	964c
70	26b	21a	21e	16c	18e	20.3b	38a	38a	40.7b	1264a	994.7c	886c
71	28b	26a	26d	16.3c	12.3g	8.7h	34b	38.3a	33d	1487a	948c	981c
72	38a	22a	22e	13c	13g	14.7d	37b	40.3a	34d	1084a	1061.3c	1034c
73	44a	30a	29.7c	11.3c	17f	11.3f	41.7a	33.3a	40.7b	1228a	930.7c	907c
74	26b	21a	21e	15.7c	30.7c	12.7e	29b	34.3a	29d	845a	1252b	990c
75	26b	32a	32c	18c	21.3d	13e	33.3b	34.3a	32.7d	869a	944c	1023c
76	25b	23a	22.7d	19c	10h	7.3h	33.7b	40a	31.7d	1144a	1069.3c	969c
77	35b	22a	21.7e	15.3c	8.3h	7.3h	33b	34.3a	32.7d	1079a	913.3c	1009c
78	28b	17a	16.7e	7.7c	8h	8h	33.3b	40a	32d	1060a	1108c	1069c
79	24b	17a	17e	15.3c	6h	7.7h	33.3b	37.3a	32d	940a	950.7c	973c
80	31b	37a	37.3c	14.3c	9h	10g	32.7b	41.3a	31.3d	817a	1156b	949c
81	31b	26a	26d	14c	11g	12f	40.7a	36a	41.7a	1157a	1054.7c	1136c
82	38a	21a	21e	14.3c	10h	10.7g	34.7b	36.7a	35c	851a	1140c	1048c
83	23b	31a	31c	14.7c	14.3f	13e	35.3b	37.7a	36c	1063a	940c	880c
84	38a	19a	19.3e	15.3c	7h	12.3f	38a	37.7a	37.3c	985a	1394.7b	1099c
85	44a	31a	31.3c	14.7c	14.3f	10.3g	35.3b	35a	35.3c	947a	1041.3c	1097c
86	32b	26a	26d	14c	12g	13.3e	34b	36.7a	33d	1017a	865.3c	1053c

ID/ CAR	PH			NP			DF			GY		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
87	41a	33a	33.3c	12.3c	11.3g	10.7g	34b	33.7a	34d	840a	968c	1083c
88	25b	16a	16e	11.3c	10h	11g	34.7b	39a	35c	1063a	1416a	1002c
89	25b	21a	21.3e	16.3c	11.3g	12f	37b	35.3a	36c	1111a	944c	891c
90	25b	25a	25d	13c	15.3f	10g	33.7b	41a	33d	870a	1006.7c	1033c
91	29b	30a	30c	15.3c	14.7f	16d	38.3a	28.7b	37.3c	1101a	876c	1020c
92	36b	34a	34.3c	18c	16f	17c	37b	34.7a	38b	1296a	892c	941c
93	30b	30a	29.7c	14c	18.3e	17c	34.3b	37a	33.7d	1688a	1210.7b	1483a
94	20b	26a	25.7d	11.3c	13.3g	10g	39.7a	29.3b	39.7b	827a	850.7c	898c
95	28b	25a	25.3d	17c	10.7g	9h	35.7b	37.7a	35c	1108a	949.3c	963c
96	39a	21a	20.7e	14c	12g	13e	35.3b	35a	34d	1711a	1001.3c	1029c
97	33b	21a	20.7e	21b	18e	18c	36.3b	35.3a	33.3d	961a	1296b	1041c
98	33b	24a	24d	14.7c	11g	12.7e	36.3b	37.7a	35.3c	1053a	1140c	911c
99	40a	24a	23.7d	16c	22d	17.3c	36.3b	36.7a	35.7c	1065a	1000c	1036c
100	23b	21a	21.3e	18c	11.7g	14.7d	34.3b	37.3a	32.7d	828a	982c	889c
101	43a	30a	30.3c	13.3c	11g	9h	40.3a	39.3a	39b	1668a	1000c	1093c
102	46a	31a	31c	14c	19.3e	14e	41.7a	36.7a	40.7b	921a	1014.7c	1076c
103	45a	29a	29.3c	16c	16.3f	8.7h	39.3a	33.3a	37.3c	1061a	961.3c	973c
104	36a	23a	22.7d	17c	16.3f	10.7g	41.3a	36.3a	41.7a	932a	962.7c	937c
105	34b	19a	18.7e	18.3c	12.3g	17c	40.3a	40.3a	36.7c	967a	941.3c	1153b
106	27b	27a	27.3d	32.3a	25.3d	19c	39.7a	35.7a	40b	1023a	1226.7b	1063c
107	30b	25a	25d	32a	64.3a	26a	34b	36.7a	34d	1126a	1136c	890c
108	23b	22a	21.7e	25.7a	18.7e	24a	34b	40.3a	33.3d	1131a	1005.3c	932c
109	37a	20a	20.3e	26a	19.3e	17.7c	35b	37.3a	34d	1008a	1208b	1113c
110	38a	24a	23.7d	23.3b	20e	14e	41.3a	34.7a	38b	1297a	1016c	1123c
111	28b	20a	20e	21.3b	16f	11.7f	36.3b	34a	36.3c	971a	1369.3b	1022c
112	50a	31a	31.3c	16.7c	11.3g	15.3d	37b	29.3b	37.7b	952a	934.7c	993c
113	30b	23a	23.3d	28a	14f	11g	42.3a	36.7a	41.7a	1131a	958.7c	944c
114	27b	19a	19e	16.7c	10.7g	17c	39.3a	37.3a	38.7b	1031a	1298.7b	1190b
115	27b	29a	29.3c	15.3c	22.3d	15d	41.3a	34.3a	41.7a	949a	1298.7b	1115c
Average	33.4	25	25.2	16.9	15.5	12.9	37	35.7	36.6	1109	1045	1071
CV (%)	25.4	18	24.3	20.8	17.1	9.7	7.2	17.6	5.2	28.8	16.2	11.7

Environment= year of experiment evaluation, ID=identification of genotypes/lineages; plant height (PH) expressed in (cm); the number of pods per plant (Nthe P); the number of days to flowering (DF), and pod productivity (GY) in kg ha-1. Averages followed with the same letter do not differ statistically by Scott and Knott test at a 5% probability level.

Positive and significant genotypic correlations were observed between the characteristics of (DM, NP, and DF). Likewise, a positive and non-significant correlation between (DM) and (DF). This means that practicing plant selection using several days to maturity, implies the selection of genotypes with fewer days to flowering, which probably implies the selection of genotypes with a higher number of pods respectively.

These results are similar to those obtained by Pedro et al. (2022) and Silva et al., (2014) who refer that one of the most important components of seed production is the number of pods per plant. Positive and non-significant genotypic correlations were observed among the characters (DF, PH, and

GY). (Figure 2). On the contrary, a negative and non-significant correlation was observed between the section (PH, NP, and DM) for the environment (E1) respectively. Similar results were reported by AlBallat and Al-Araby (2019) having observed positive and significant correlations between (PH and DM). Basavaraja et al. (2021) observed positive and significant correlations of (PH). Sharma et al. (2019) observed positive and significant correlations between (PH and DM) and non-significant negative correlations with (SM).

Highly positive and significant genotypic correlations were observed among the characters (DF, DM, GY, and PH). Positive and non-significant correlations were observed

between the characteristics (PH, GY, and DM), as well as a positive and non-significant correlation between the characteristics (NP, MD) with (PH) respectively. A negative and non-significant correlation was observed between the character (DF) (NP, DF, and PH). This means that practicing plant selection using several days to flowering variable implies the selection of genotypes with shorter days to maturity, post selection of genotypes with higher plant height and grain yield, which are less susceptible to pathogen attack and facilitate mechanized harvesting (Figure 2 respectively. Pedro et al (2022) also observed a non-significant positive correlation between (PH and BP) and Basavaraja et al, (2021) observed a non-significant positive correlation between (PH and DF).

Highly positive and significant correlations were observed between the character (DF) with the (NP). Additionally, a statistically positive and non-significant correlation was observed between the (DM, DF, NP, and GY) trait (Figure 2). This indicates that making selection use of the character number of days to maturity may contribute to a higher number of pods on plants, fewer days to maturity reduces days to flowering of the plant, probably does not affect several pods per plant, but increases plant productivity. A negative and non-significant correlation was observed

between the section (PH, GY, DM, and DF) and the section (GY with NP). This implies that making selection uses of the plant height character may likely reduce productivity, still may imply obtaining genotypes with late maturation, however, late emergence contributes to a higher number of pods in plants, and consequently increases productivity, which was what was observed in this research in the environment (E3) respectively. Sharma et al. (2019) observed a negative and non-significant correlation between BP and DF. Different results were observed by Basavaraja et al. (2021), having found non-significant positive correlations between the characters (DF and DM). However, these results show the differential behavior of the genotype against the variations of the environment, so the best individuals in one environment were not better in other environments, thus becoming a complicating factor in the selection, if not considered properly (Resende et al., 2014). For the character number of pods per plant (NP), plant height (PH) should be preferred, for presenting a greater magnitude of correlation with grain yield in all three environments(E). The network of genotypic correlation allows visualization of the main groups of genotypes correlated with each other and with productivity as the main character of the study.

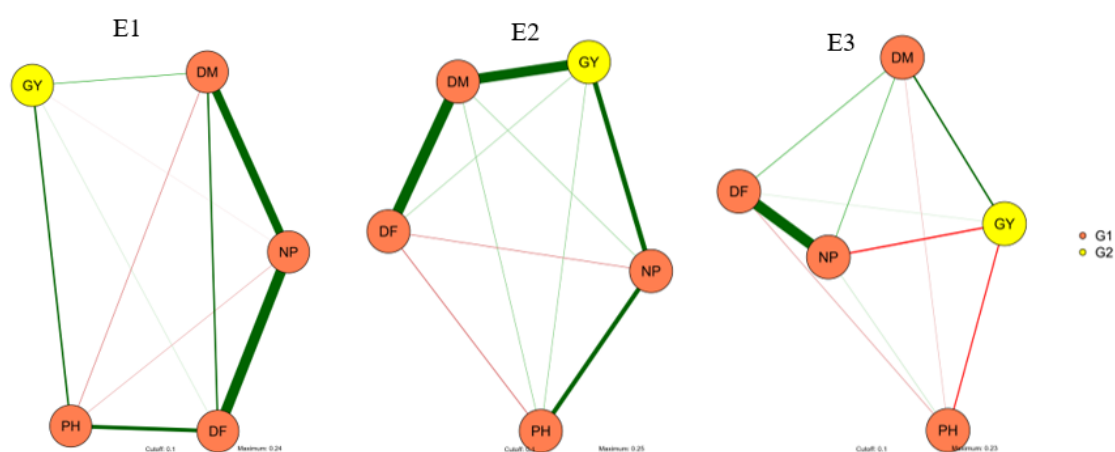


Figure 2. Similarity network based on genetic correlation between characters that contributed to productivity (brown colored circles, DM, NP, DF, and PH respectively) and Productivity (yellow colored circle GY) regarding the evaluation of 115 among common bean lines/genotypes in 3 environments, Manica-Mozambique. Green color link vectors indicate a positive correlation and red color vectors indicate a negative correlation. The higher thickness of vectors indicates a higher correlation and lower thickness indicates a lower correlation. DM= days to maturity, NP = Number of pods per plant, DF=Days to flowering, PH = Plant height, and GY= Grain yield

Figure 3 graphically presents the results of gain by selection (SG) performed on 115 common bean genotypes for grain yield (GY) in kg ha⁻¹ in 3 environments, Sussundenga-Mozambique, grouped by the Scott-Knott test (5%) (Table 4). Fifteen genotypes were selected in each environment (E), which presented the highest averages respectively. In all environments evaluated the productivity character had a greater gain (positive), and only the character number of days to flowering (DF) had a negative gain, in general, these results meet the purpose of this research since it reduces the crop cycle. Genotypes with fewer days to flower are desired in several bean breeding programs because they allow a harvest in a given period and reduce the period of culture in the field, besides being used to meet the situa-

tion of climate change that has plagued the world (Bizari et al., 2014). However, the selection of superior genotypes is a very laborious task, because the characters of importance, usually quantitative, present complex behavior because they are influenced by the environment and are interrelated, so that the selection of one, causes a series of changes in others (Cruz et al., 2012). The results of these authors collaborate with those found in this research. The use of the selection index theory is considered a good alternative since it facilitates the improver in observing that the performance of a genotype for a particular characteristic compensates some other, and can be considered more flexible when compared to independent levels of elimination (Bernardo, 2002).

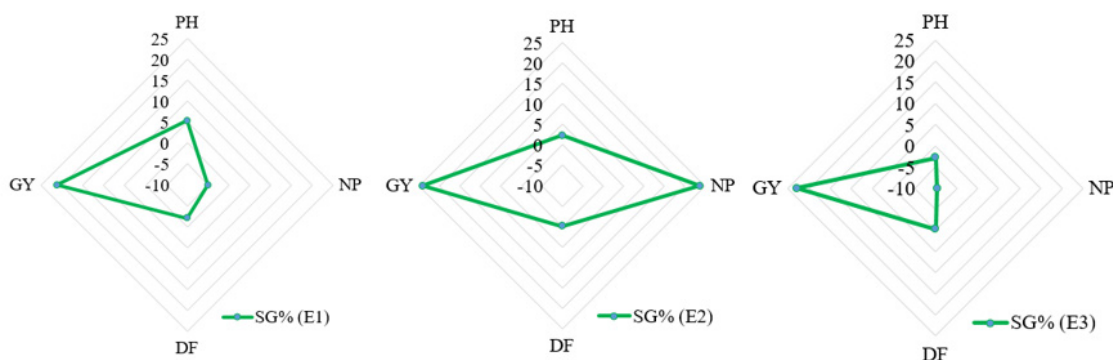


Figure 3. Graphical representation of the performance of the genotypes/ with the best grain averages, using the graphical method evaluated in three environments Sussundenga-Mozambique. These are the following characteristics DM= days to maturity, NP = Number of pods per plant, DF= Days to flowering, PH = Plant height, and GY= Grain yield.

Conclusion

For all environments, the agronomic characteristics number of pods per plant (NP) and plant height (PH), showed higher heritability, high positive correlation genotypic can be used as parameters for the selection of common bean for the development of varieties that have high yield. The genotypes selected in this research showed genetic variability, and high genetic gain for the productivity character. Therefore they are considered promising and can be used as genitors in future breeding programs.

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