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Genetics/ Original Article

Variability and genetic associations of pigeon pea yield traits in Mozambique

Abstract – The objective of this work was to evaluate the genetic variability and associations of yield traits of pigeon pea, for indication of this crop for the breeding program in Mozambique. Eleven pigeon pea traits were evaluated in a experimental design with three randomized complete blocks, in the environments of Namapa (I) and Montepuez (II), in 2017/2018. To evaluate the traits, analyses of variance, genetic parameters, correlations, correlation network, and path analysis were used. In both environments, there is a high genetic and phenotypic variability for primary branches, secondary branches, pods per plant, number of seed per pod, pod width, pod length, and yield, as well as a high heritability for all traits except for plant height. The primary and secondary branches have a high correlation with yield and a positive direct effect on it. However, plant height and pods per plant show a high phenotypic variability and a positive correlation with yield in environment I. Pods per plant, weight of 100 seed, and primary branches show high direct positive effects in environment I, and secondary branches and number of seed per pod, in environment II. The primary and secondary branches show high variability and associations with yield in both environments and are indicated for the pigeon pea breeding program in Mozambique.

Index terms: *Cajanus cajan*, correlation, genetic parameters, path analysis.

Variabilidade e associações genéticas das características de produção de feijão-bóer em Moçambique

Resumo – O objetivo deste trabalho foi avaliar a variabilidade genética e as associações de características produtivas do feijão-bóer, para indicação dessa cultura ao programa de melhoramento em Moçambique. Foram avaliadas 11 características do feijão-bóer, em delineamento de três blocos ao acaso, nos ambientes de Namapa (I) e Montepuez (II), em 2017/2018. Para avaliação das características, utilizaram-se análises de variância, parâmetros genéticos, correlações, rede de correlação e análise de trilha. Em ambos os ambientes, há alta variabilidade genética e fenotípica para ramos primários, ramos secundários, vagens por planta, número de sementes por vagem, largura e comprimento da vagem e produtividade, bem como alta herdabilidade para todas as características, exceto para altura da planta. Os ramos primários e secundários apresentam alta correlação com a produtividade e efeito direto positivo sobre ela. No entanto, altura de planta e vagens por planta apresentam alta variabilidade fenotípica e correlação positiva com a produtividade no ambiente I. Vagens por planta, peso de 100 sementes e ramos primários apresentam altos efeitos positivos diretos no ambiente I, e ramos secundários e número de sementes por vagem, no ambiente II. Os ramos primários e secundários apresentam alta variabilidade e associações com a produtividade em ambos os ambientes e são indicados para o programa de melhoramento do feijão-bóer em Moçambique.

Termos para indexação: *Cajanus cajan*, correlação, parâmetros genéticos, análise de trilha.

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Introduction

Pigeon pea [*Cajanus cajan* (L.) Millspaugh] is an important multipurpose legume crop grown in semiarid regions of Asia, Africa, Latin America, and Caribbean (Kaoneka et al., 2016; Nagesh Kumar et al., 2021). As food, it is a rich source of proteins (20–22%), and as component of production systems, it contributes to the improvement of soil fertility through biological nitrogen fixation (Thanga Hemavathy et al., 2019; Bopape et al., 2021). This legume is considered to have originated in India (Saxena et al., 2014) and it is cultivated in many parts of the world, including Southern Africa, particularly the region spanning Kenya, Malawi, Mozambique, and Tanzania (Kaoneka et al., 2016). In Mozambique, it plays a great role as food for poor families, and its fresh and dry grains are sold to generate income for small farmers (Donça et al., 2021). The increase of the number of households and the area per household justify the increase of pigeon pea production, indicating that yield was not identified as a cause (Walker et al., 2015). The main concern of the pigeon pea breeding program in Mozambique is to increase grain yield; however, the yield achieved at the smallholder level varies between 300–400 kg ha^{-1} (Walker et al., 2015), which is considered low in relation to the following production results: world average yield (822.2 kg ha^{-1}); India (776.3 kg ha^{-1}); Africa (1,233.9 kg ha^{-1}); neighboring countries such as Malawi (1,657.7 kg ha^{-1}) and Tanzania (1,059.4 kg ha^{-1}); and countries such as Burundi (1,202.9), Kenya (925.9) and Congo (592.8) from the African continent (FAO, 2020a, 2020b). Yield is a polygenic trait affected by the environment, usually it shows low heritability and is the result of the direct or indirect association of several component traits (Pal et al., 2018). Therefore, the knowledge of the associations between these traits through studies of genetic parameters, correlation, and path analysis are of great importance for breeding work, especially if the selection of one of them presents difficulties, due to low heritability, and/or if it shows measurement and identification problems (Cruz et al., 2014). Similar studies aiming to select traits to improve the grain yield of pigeon pea were carried out by Meena et al. (2017), Thanga Hemavathy et al. (2019), Gaur et al. (2020), Sharma et al. (2021), and others, on different genetic materials and in environmental conditions. Correlation network studies on pigeon peas are scarce, but some of them have been carried out on passion fruit (Rosado et al., 2017), coffee (Barbosa et al., 2019), and eucalyptus (Ferraz et al., 2020), among other crops, which makes it interesting to apply this technique to increase the efficiency in the trait selection process.

The objective of this work was to evaluate the genetic variability and associations of yield traits of pigeon pea, for the indication of this crop for the breeding program in Mozambique.

Materials and Methods

The trials were carried out in the experimental areas of the Instituto de Investigação Agrária de Moçambique, Centro Zonal Nordeste (IIAM), in two locations: Namapa (13º43'34"S, 39º46'14"W) and Montepuez (13º12'56"S, 38º52'50"W), in the 2017/2018 agricultural year. Namapa is a district from the Nampula province, and Montepuez is a district from the Cabo Delgado province, both located in Northern Mozambique, East of the African continent.

The soils of the experimental areas belong to the class of Latossolo Vermelho aluminoférrico according to Santos et al. (2018), i.e., Lixisol. The climate by the Köppen-Geiger's classification is tropical savannah (Aw) in both areas. The annual means for temperature and rainfall are respectively 23.9°C and 959 mm, in Namapa, and 25.6°C and 1,142 mm, in Montepuez.

An experimental design was carried out in three randomized blocks and six pigeon pea genotypes (ICP 8863, ICPL 85063, ICEAP 00557, LRG41, ICPL 87119, BSMR 736) of medium maturity and indeterminate growth habit from ICRISAT (International Crops Research Institute for the Semi-Arid Tropics), Kenya. The plot size was 5.0x1.8 m, with two lines. Sowing was carried out at 0.9 m spacing between rows, with four seed per linear meter. In the experimental management, two weedings were carried out along the crop cycle. From flowering to pod drying, pest control was carried out with the insecticides cypermethrin 10% EC and acetamiprid 40 g L^{-1}, every 15 days. Harvesting was carried out manually, on the entire plot, when 90% of the pods were dry. Drying was performed in the sun, and the pods were threshed manually. Eleven traits were evaluated, as follows: plant height, primary branches, secondary branches, days to flowering, days to maturity, pod length, pod width, number of seed per pod, pods per plant, weight of 100 seed, and yield.

Before the analysis of variance, the Shapiro-Wilk´s normality tests were performed, at 5% probability. To verify the existence of variability in the traits, the analysis of variance was performed based on the statistical model

$$Y_{ij} = \mu + g_i + b_j + \varepsilon_{ij}$$

where: Y_{ij} is the phenotypic value of the observation referring to the ith genotype, in the jth block; μ is the overall g mean; g_i is the random effect of the ith genotype (i = 1, 2, 3, ..., g; g = 6); b_j is the effect of the jth block (j = 1, 2, ..., r; r = 3); ε_{ij} is the effect of the experimental error, and $\varepsilon_{ij} \sim$ NID (0, σ^2).

The mathematical hopes of the mean square were established to obtain estimates of the components of phenotypic variance ($\hat{\sigma}^2_p$), genotypic variance ($\hat{\sigma}^2_g$), environmental variance ($\hat{\sigma}^2_I$), and heritability (h^2) in the broad sense, between mean plots in each environment.

Subsequently, the coefficients of experimental variation, phenotypic variation, genotypic variation and the ratio between the coefficient of genotypic and experimental variation), in each environment, were estimated.

The existence of associations between the traits was estimated by the phenotypic correlation coefficient, which is a function of genotypic coefficient and environmental correlation between traits in each environment. Afterward, to evaluate the cause and effect relationships between traits, a path analysis was performed, developed by Wright (1921), considering a casual model of a chain, after the diagnosis of multicollinearity in the matrix of phenotypic correlations, by the method of Montgomery et al. (2012). Finally, the relationships between the traits were shown in the correlation network structures (similarity), to identify the groups of correlated traits. For better visualization and interpretation, the traits were partitioned into groups of primary and secondary components, considering their relationship with the main trait (yield). The negative correlations were represented by red lines, the positive correlations were represented by green lines, and the line thickness was considered proportional to the correlation magnitude. The lines showed a correlation in module greater than 0.3 (Cutoff: 0.3). The statistical analysis procedures were performed in the Genes software (Cruz, 2016).

Results and Discussion

The errors associated with the collected data followed the normal distribution, by the Shapiro-Wilk's test, for all traits (Table 1). The variance analysis indicated, except for plant height, the existence of genetic variance in the traits primary branches, secondary branches, pod length, pod width, number of seed per pod, pods per plant, weight of 100 seed, and grain yield, in both environments; besides, it also showed genetic variance for days to flowering and days to maturity in environment II. Similar results have been reported by Pal et al. (2018), Satapathy et al. (2019), Gaur et al. (2020), and Pandey et al. (2021). The precision of the experiments was evaluated by the coefficient of variation, which is considered low, medium and high, based on the evaluation criteria by Pimentel-Gomes (2009), who considers the values of coefficient of variation as low, when they are less than 10%, medium, when they are between 10 and 20%, and high, when they are between 20 and 30%.

The estimates of genetic parameters that make it possible to infer the feasibility of using selective practices, as well as their effectiveness, were determined for all traits (except for plant height and grain yield) exhibiting high heritability (above 75%), indicating an association between phenotypic and genotypic values in both environments (Table 2). Similar results were reported by Pandey et al. (2021) and Sharma et al. (2021), who observed high heritability for primary branches, secondary branches, days to flowering, days to maturity, pod length, pod width, number of seed per pod, pods per plant, and weight of 100 seed. Pal et al. (2018) observed high heritability for days to flowering, days to maturity and weight of 100 seed. Gaur et al. (2020) observed high heritability for days to flowering, days to maturity, weight of 100 seed, pods per plant and pod length. Pandey et al. (2021) observed high heritability for primary branches, days to flowering, days to maturity, weight of 100 seed, pods per plant and pod length.

Cruz et al. (2014) report that the success of the genetic improvement of any trait requires that it is inheritable and that there is variation in the population in which the selection is practiced. Thus, phenotypic variation (PCV) estimates were higher in pods per plant and grain yield in the environment I; and pods per plant and secondary branches, in the environment II, indicating higher phenotypic variability in these traits. For the genotypic variation (GCV), the highest estimates were observed in pods per plant and grain yield in the environment I, and in secondary branches in environment II, which allows of inferring the magnitude of the genetic variability present in the population in these traits, and serves as an indicator of genetic gain, according to Resende (1991). In general, PCV estimates were higher than GCV estimates in both environments, indicating a greater influence of the environmental effect. Similar results were reported by Pal et al. (2018), who observed

Table 1. Analysis of variance for plant height (PH), primary branches (PB), secondary branches (SB), days to flowering (DF), days to maturity (DM), pod length (PL), pod width (PW), number of seed per pod (SP), pods per plant (PP), weight of 100 seed (WS), and yield (Y), in six pigeon pea (*Cajanus cajan*) genotypes cultivated in Namapa (environment I) and Montepuez (envronment II), Mozambique.

Trait	Environment	Block	Genotype	Error	Coefficient of variation (%)	Shapiro-Wilk's test ($p \leq 0.05$)	
		DF^{+}				Wilk	p-value
		2	5	10			
		Mean square					
Plant height (PH, cm)	I	4,268.805	2,230.22	1,498.596	26.41	0.923	0.147
	II	117.927	54.309	48.324	5.41	0.974	0.871
Primary branches (PB)	I	0.672	5.037*	1.228	16.25	0.941	0.2972
	II	2.727	2.912*	0.599	9.67	0.956	0.528
Secondary branches (SB)	I	17.374	10.087*	2.445	16.25	0.978	0.9268
	II	3.1667	87.833**	2.1	22.29	0.963	0.659
Pod length (PL, cm)	I	0.103	2.478**	0.276	9.06	0.92	0.13
	II	0.03	3.325**	0.175	6.97	0.93	0.192
Pod width (PW, cm)	I	0.005	0.042**	0.002	6.06	0.979	0.939
	II	0.0012	0.044**	0.002	6.03	0.957	0.549
Number of seed per pod (SP)	I	0.272	1.16*	0.242	14.05	0.959	0.58
	II	0.0139	0.446*	0.086	7.66	0.959	0.585
Pods per plant (PP)	I	1,341.721	1,453.871**	159.127	19.01	0.929	0.185
	II	1,913.556	2,095.022**	349.556	14.48	0.977	0.909
Weight of 100 seed (WS, g)	I	2.002	1.931*	0.348	4.85	0.981	0.963
	II	0.314	6.304*	1.224	10.49	0.955	0.507
Yield (kg ha^{-1})	I	218,883.1	150,707.55*	39,744.69	27.75	0.95	0.417
	II	114,198.2	119,293.467*	34,601.03	15.83	0.971	0.822
Days to flowering (DF)	II	15.056	161.022**	13.256	4.09	0.957	0.537
Days to maturity (DM)	II	32.667	171.567**	16.933	3.35	0.973	0.847

**, *Significant at 1% and 5% probability, respectively. DF+, degree of freedom.

Table 2. Genetic parameters of plant height (PH), primary branches (PB), secondary branches (SB), days to flowering (DF), days to maturity (DM), pod length (PL), pod width (PW), number of seed per pod (SP), pods per plant (PP), weight of 100 seed (WS) and yield (Y), in six pigeon pea (*Cajanus cajan*) genotypes cultivated in Namapa (environment I) and Montepuez (envronment II), Mozambique.

Parameter(1)	Environment	PH (cm)	PB	SB	PL (cm)	PW (cm)	SP	PP	WS (g)	Y (kg ha^{-1})	DF	DM
h^2 (%)	I	32.810	75.630	75.760	88.850	94.950	79.240	89.050	81.990	73.630	-(2)	-
	II	11.020	79.440	97.610	94.730	95.480	80.740	83.310	80.580	71.000	91.770	90.130
PCV (%)	I	18.602	18.990	19.061	15.670	15.624	17.797	33.174	6.603	31.194	-	-
	II	3.309	12.320	83.245	17.520	16.384	10.065	20.468	13.753	16.971	8.222	6.418
GCV (%)	I	10.650	16.530	16.580	14.770	15.180	15.840	31.300	5.980	26.770	-	-
	II	1.100	10.980	82.240	17.060	15.990	9.050	18.680	12.340	14.300	7.880	5.845
GCV/CV	I	0.400	1.020	1.020	1.630	2.500	1.130	1.6500	1.230	0.960	-	-
	II	0.200	1.130	3.690	2.450	2.650	1.180	1.2900	1.180	0.900	1.930	1.745

(1)Heritability (h^2); phenotypic (PCV) and genotypic variation (GCV) coefficient of variability; coefficient of variation (CV). (2)Unmeasured traits.

moderate to high PCV and GCV for primary branches, secondary branches, pods per plant, and yield. Sharma et al. (2021) observed high GCV for primary branches, secondary branches, pods per plant, and yield; moderate for weight of 100 seed, and low number of seed per pod. Pandey et al. (2021) observed high PCV and GCV for secondary branches and pods per plant; and moderate for primary branches, pod length, pod width, number of seed per pod, weight of 100 seed, and yield. Gaur et al. (2020) low PCV and GCV for days to flowering, days to maturity and weight of 100 seed; and moderate to high for primary branches, secondary branches, pod length, pod width, number of seed per pod, pods per plant, and yield. Satapathy et al. (2019) observed moderate to high for plant height, primary branches, pod length, pod width, seeds per pod, pods per plant, weight of 100 seeds, and yield.

The estimates for the ratio between the coefficient of genotypic and experimental variation (GCV/CV) were relatively higher in the environment II. The GCV/CV ratio ≥ 1.0 observed in both environments − for primary branches, secondary branches, pod length, pod width, number of seed per pod, weight of 100 seed, days to flowering, and days to maturity − confirms a favorable situation for the practice of the selection process.

The correlation results were significant at 1% and 5% probability by the t-test (Figure 1). However, attention should be paid to the significance observed in high magnitude values, due to the small sample of the evaluated data. High magnitude correlation coefficients between traits are needed, when dealing with small samples, according to Sari et al. (2017) and Toebe et al. (2019). From a practical point of view, although the value of the linear correlation coefficient is not statistically significant, depending on the magnitude, it may have biological significance in the increase or decrease of the means of the traits. In the present work, values with moderate magnitude (3.0 ≤ r < 6.0), according to the classification by Callegari & Jacques (2003), together with the values that were statistically significant, were considered of biological significance.

Thus, in the environment I (Figure 1), the plant height showed a correlation greater than 3.0, which was nonsignificant and positive with the weight of 100

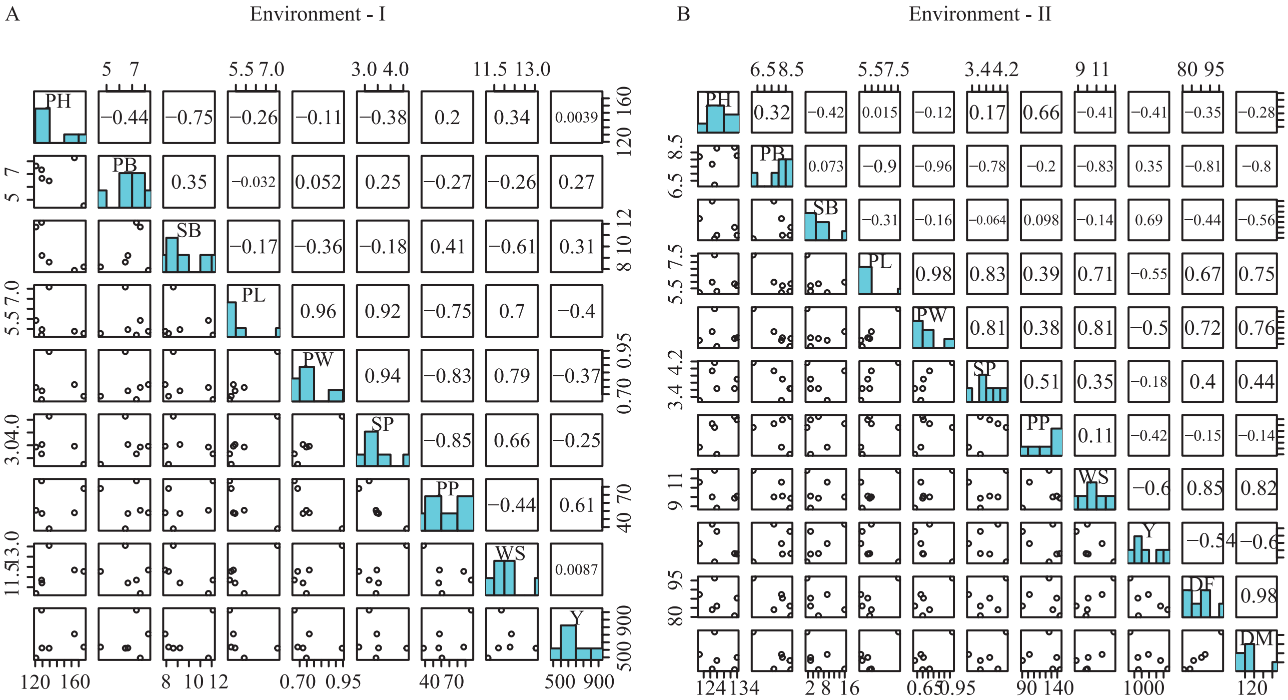

Figure 1. The upper part of the main diagonal of the figure shows the values of trait correlations. At the bottom of the main diagonal are the dispersions and trend lines between the traits. On the main diagonal are the traits [plant height (PH), primary branches (PB), secondary branches (SB), days to flowering (DF), days to maturity (DM), pod length (PL), pod width (PW), number of seed per pod (SP), pods per plant (PP), weight of 100 seed (WS), and yield (Y)], in six pigeon pea (*Cajanus cajan*) genotypes, for environments I (Namapa) and II (Montepuez), Mozambique.

seed, and negative with secondary branches, primary branches and number of seed per pod; besides, it showed nonsignificant correlations smaller than 3.0 that were positive and negative with the other traits.

The primary branches showed a nonsignificant correlation greater than 3.0 that was positive with the secondary branches; and nonsignificant correlations smaller than 3.0 that were positive and negative with the other traits.

The secondary branches showed a nonsignificant correlation that was positive with pods per plant and yield, and negative with the weight of 100 seed and pod width; as well as a nonsignificant negative correlation with the other traits. Similar results have been reported by Gaur et al. (2020), who observed a nonsignificant correlation of secondary branches with pods per plant. Sharma et al. (2021) observed a significant positive correlation between secondary branches and pods per plant, and between these traits and yield.

The pod length showed a significant positive correlation with pod width and number of seed per pod; a nonsignificant correlation greater than 3.0 with weight of 100 seed; and a nonsignificant and negative correlation greater than 3.0 with pods per plant and yield. Similar results were reported by Satapathy et al. (2019), who observed a positive correlation between seed per pod and pod length.

The pod width showed the following results: a significant positive correlation with the number of seed per pod; a nonsignificant correlation greater than 3.0 with the weight of 100 seed; a significant negative correlation with pods per plant; and a nonsignificant correlation greater than 3.0 with yield.

The number of seed per pod showed a nonsignificant, positive correlation greater than 3.0 with the weight of 100 seed; a significant negative correlation with pods per plant; and a nonsignificant negative correlation less than 3.0 with yield.

The trait pods per plant showed a nonsignificant positive correlation greater than 3.0 with yield; and a nonsignificant negative correlation greater than 3.0 with the weight of 100 seed. Similar results have been reported by Gaur et al. (2020) and Sharma et al. (2021), who observed a significant positive correlation between pods per plant and yield.

The weight of 100 seed was not correlated with yield. Contrary results were presented by Sharma et al. (2021), who observed a positive correlation between the weight of 100 seed and yield. To improve yield in this environment, it is recommended to select the largest number of pods per plants and secondary branches which also showed high heritability.

In the environment II (Figure 1), the plant height showed a nonsignificant positive correlation greater than 3.0 with pods per plant and primary branches; besides, it showed a nonsignificant negative correlation greater than 3.0 with secondary branches, weight of 100 seed, yield, and days to flowering; as well as nonsignificant positive and negative correlations smaller than 3.0 with the other traits.

The primary branches showed a nonsignificant positive correlation greater than 3.0 with yield; a nonsignificant and negative correlation greater than 3.0 with days to maturity and number of seed per pod; besides significant negative correlations with pod width, pod length, weight of 100 seed, and days to flowering; and nonsignificant positive and negative correlations smaller than 3.0 with the other traits. Similar results have been reported by Gaur et al. (2020), who observed a significant negative correlation of the primary branches with days to flowering and days to maturity.

The secondary branches showed a nonsignificant positive correlation with yield; and nonsignificant negative correlations greater than 3.0 with days to maturity, days to flowering, and pod length; besides nonsignificant positive and negative correlations smaller than 3.0 with the other traits. Similar results have been reported by Gaur et al. (2020) and Sharma et al. (2021), who observed a significant positive correlation of the secondary branches with yield.

Pod length showed a significant positive correlation with pod width and number of seed per pod; and nonsignificant positive correlation with weight of 100 seed; besides a nonsignificant negative correlation with yield, which was positive and greater than 3.0 with pods per plant, days to flowering, and days to maturity. Satapathy et al. (2019) also observed a positive correlation between the number of seed per pod and pod length.

The pod width showed significant positive correlations with the number of seed per pod and weight of 100 seed; nonsignificant positive correlations greater than 3.0 with days to maturity, days to flowering, and pods per plant; and a nonsignificant negative correlation greater than 3.0 with yield.

The number of seed per pod showed nonsignificant positive correlations greater than 3.0 with pods per plant, days to maturity, days to flowering, and weight of 100 seed; and a nonsignificant, negative correlation greater than 3.0 with yield.

The pods per plant showed a nonsignificant negative correlation greater than 3.0 with yield; and nonsignificant positive and negative correlations with the other traits.

The weight of 100 seed showed significant positive correlations with days to flowering and days to maturity; and a nonsignificant negative correlation greater than 3.0 with yield.

The days to flowering showed a significant positive correlation with the days to maturity; and both traits showed a nonsignificant negative correlation greater than 3.0 with yield. Similar results have been reported by Gaur et al. (2020), who observed a negative correlation between the weight of 100 seed and yield, and a significant positive correlation between days to flowering and days to maturity.

In the environment II, it is recommended to practice the selection by the largest number of secondary branches and primary branches to improve yield.

Subsequently, a path analysis was performed using the crest regression method, as recommended by Carvalho & Cruz (1996) (Table 3). Except for plant height in the environment I and primary branches in environment II, the direct effects had the same sign as the correlations. The coefficients of determination were greater than the residual effects in both environments, with a higher coefficient of determination and low residual effect in the environment II, indicating that the set of variables included in the model satisfactorily explains the variations in the main variable, and that few important traits can play a critical role in the genetic improvement of the studied material.

In the environment I, pods per plant, weight of 100 seed, and primary branches showed the greatest positive direct effects on yield. For this environment, the selection of these traits is suggested with emphasis on pods per plant that showed a direct effect of greater magnitude. Similar results have been reported by Thanga Hemavathy et al. (2019), who observed a greater direct effect of pods per plant and primary branches. The greatest positive indirect effects were exerted by the pod width, pod length, and number of seed per pod, through the weight of 100 seed. The greatest negative indirect effects on yield were exerted by the number of

Table 3. Estimates of the direct and indirect effects of plant height (PH), primary branches (PB), secondary branches (SB), days to flowering (DF), days to maturity (DM), pod length (PL), pod width (PW), number of seed per pod (SP), pods per plant (PP), weight of 100 seed (WS), and yield (Y), in six pigeon pea (*Cajanus cajan*) genotypes cultivated in Namapa (environment I) and Montepuez (envronment II), Mozambique, obtained by the crest regression analysis method.

Environment	Trait	Direct effect on	Indirect effect through									
		yield (kg ha^{-1})	PH (cm)	PB	SB	PL (cm)	PW (cm)	SP	PP	WS (g)	DF	DM
I	PH (cm)	-0.070		-0.173	-0.096	0.074	0.016	-0.051	0.119	0.199	-(1)	-
II		-0.288		-0.034	-0.150	-0.002	0.012	0.062	-0.229	0.172	0.036	0.044
I	PB	0.395	0.030		0.045	0.009	-0.007	0.033	-0.162	-0.153	-	-
II		-0.104	-0.090		0.026	0.102	0.091	-0.291	0.069	0.350	0.082	0.127
I	SB	0.128	0.052	0.138		0.048	0.052	-0.024	0.243	-0.354	-	-
II		0.356	0.121	-0.008		0.035	0.015	-0.024	-0.034	0.059	0.045	0.088
I	PL (cm)	-0.280	0.018	-0.012	-0.022		-0.138	0.124	-0.444	0.408	-	-
II		-0.114	-0.000	0.093	-0.111		-0.093	0.310	-0.135	-0.301	-0.068	-0.118
I	PW (cm)	-0.143	0.008	0.021	-0.046	-0.270		0.128	-0.494	0.458	-	-
II		-0.095	0.035	0.099	-0.058	-0.111		0.303	-0.133	-0.342	-0.073	-0.120
I	SP	0.135	0.026	0.098	-0.023	-0.258	-0.135		-0.504	0.380	-	-
II		0.373	-0.050	0.081	-0.023	-0.094	-0.077		-0.177	-0.147	-0.041	-0.069
I	PP	0.596	-0.010	-0.107	0.052	0.209	0.118	-0.114		-0.253	-	-
II		-0.347	-0.190	0.020	0.035	-0.044	-0.036	0.190		-0.048	0.015	0.022
I	WS (g)	0.58	-0.02	-0.104	-0.078	-0.197	-0.113	0.088	-0.26		-	-
II		-0.423	0.117	0.086	-0.049	-0.081	-0.077	0.129	-0.04		-0.086	-0.13
II	DF	-0.101	0.101	0.084	-0.158	-0.076	-0.068	0.15	0.05	-0.36		-0.154
II	DM	-0.158	0.08	0.083	-0.198	-0.085	-0.072	0.163	-0.349	-0.349	-0.099	

(1)Unmeasured traits. Determination coefficient (R^2) = 0.644 for the environment I, and 0.917 for the environment II. Effect of residual variable (ε) = 0.597 for the environment I, and 0.289 for the environment II. Coefficient of the regression method of the crest (k) = 0.20 for the environment I, and 0.10 for environment II. Determinant of the correlation matrix between explanatory variables =1.758 for the environment I, and 2.906 for the environment II.

seed per pod, pod width, and pod length through pods per plant, and by days to flowering and secondary branches through the weight of 100 seed.

In the environment II, the secondary branches and the number of seed per pod showed a greater positive direct effect on yield, suggesting that, in this environment, the selection for the largest number of secondary branches improves yield. Similar results have been reported by Thanga Hemavathy et al. (2019), who observed greater positive direct effects of seed per pod and secondary branches on yield. The greatest negative direct effects were exerted by the weight of 100 seed, pods per plant, and plant height; and the smallest negative direct effects were exerted by pod length, pod width, and days to flowering. Contrary results have been reported by Thanga Hemavathy et al. (2019) and Sharma et al. (2021), who observed a positive direct effect of the plant height, weight of 100 seed, and pods per plant. Days to maturity, pod length, primary branches, days to flowering, and pod width showed a less negative direct effect on yield. Similar results have been reported by Meena et al. (2017), who observed negative direct effects of days to flowering, days to maturity, and primary branches. The major positive indirect effects were exerted by the primary branches through the weight of 100 seed, and by pod length through the number of seed per pod. The negative indirect effects were exerted by pod width, pod length, and days to maturity through the weight of 100 seed.

Correlation network structures for the environments I and t II (Figure 2) showed that the traits pod length,

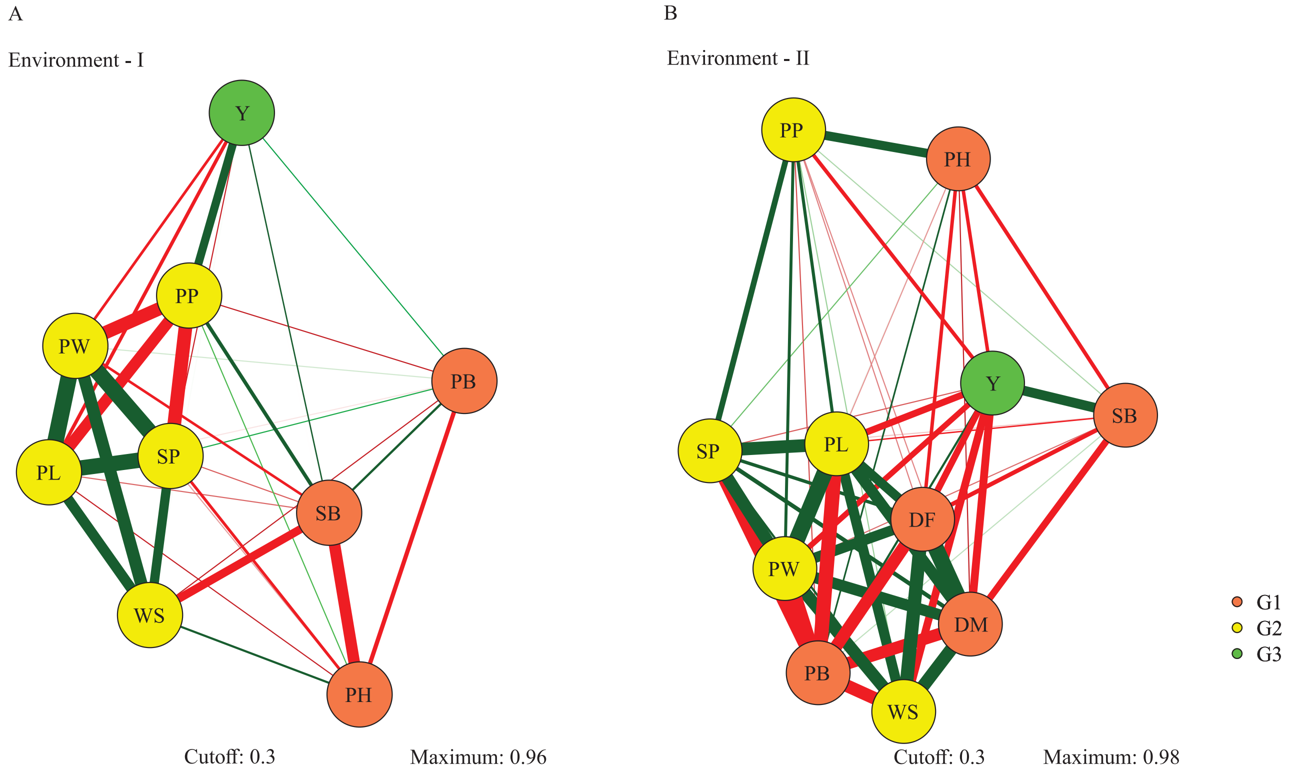

Figure 2. Phenotypic correlation network between traits of six pigeon pea (*Cajanus cajan*) genotypes for the environments I (Namapa) and II (Montepuez), Mozambique. Secondary components (G1), primary components (G2), and yield (G3). The red and green lines represent negative and positive correlations, respectively. The width of the line is proportional to the intensity of the correlation. The thickness of the lines was controlled by applying a cutoff value of 0.3, where only |rij| ≥ 0.3 had their line thickness increased proportionally based on the intensity of the correlation. The fine lines represent correlations lower than 0.3 and are not highlighted. Primary components: pod length (PL), pod width (PW), number of seed per pod (SP), pods per plant (PP), weight of 100 seed (WS). Secondary components: days to flowering (DF), days to maturity (DM), plant height (PH), primary branches (PB), secondary branches (SB).

pod width, number of seed per pod, and weight of 100 seed, in both environments, and the days to flowering and days to maturity, in environment II, form a group of traits positively correlated with each other in greater magnitude. However, this group correlated negatively with yield, secondary branches, and primary branches, in the environment II, except for number of seed per pod that showed a positive correlation with primary branches in the environment I. This fact suggests that the selection for one of these traits may represent the other correlated ones, and that it may cause changes in a favorable direction to improve one of these traits in both environments; it may also cause changes in an unfavorable direction to improve yield, pods per plant, secondary branches, and primary branches.

The results of the associations between traits, observed in environments I and II, show differences for direction, magnitude, and significance. This fact can be explained by the variability effect of the conditions in which the traits were evaluated. This way, the selection strategy for the improvement of pigeon pea should be practiced under the environmental conditions in which the experiment was conducted.

Conclusions

1. In the environments of Namapa and Montepuez, there is high genetic and phenotypic variability for the traits primary branches, secondary branches, pods per plant, number of seed per pod, pod width, pod length and yield, and high heritability for all traits, except for plant height.
2. The primary and secondary branches show high variability and positive direct effect with yield in both environments of Namapa and Montepuez, Mozambique.

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