Agricultural Zoning and Recommendation of Pigeon Pea Cultivars in Mozambique

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Abstract: Pigeon pea is one of the important legumes for export and domestic consumption in Mozambique. The objective was to evaluate the performance of the genotypes and to stratify environments for agricultural zoning and subsequent recommendation. The experiments were conducted in the northern region of Mozambique, to evaluate grain yield, in randomized blocks, with three replications and 20 long-maturing genotypes, in the 2016/2017 season in four environments. The results were obtained through the joint analysis and the complementarity of information from the biometric methodologies of Eberhart and Russell, Centroid and GGE-biplot aiming at better use of the significant GXE interaction. A mega-environment (Nampula and Namapa) was observed, of which Namapa district was the most discriminating and representative. The genotypes suggested for a recommendation as cultivars showed average performance. The ICEAP01490 genotype was of specific adaptability to favorable environments (Nametil and Namapa district) and high stability, is recommended for medium to high technology environments and the ICEAP01498 genotype was of specific adaptability to unfavorable environments (Nampula and Montepuez district), is recommended for low technology environments. The ICEAP01409 genotype can be indicated for a general recommendation. The ideal genotype with high mean, general adaptability and high stability was not observed, suggesting evaluations in more environments.

Key words: *Cajan cajan*, environment, adaptability, stability

1. Introduction

Pigeonpea (*Cajanus cajan* (L). Millspaugh) is an important crop in tropical and subtropical semi-arid areas, for export and domestic consumption in Mozambique. It is a rich source of protein (20-23%), in addition to fixing atmospheric nitrogen with benefits for fertility and reduced soil erosion [1]. India is the native home of pigeonpea [2]. Pigeonpea is grown in many parts of the world including southern Africa particularly the region encompassing Kenya, Mozambique, Malawi and southern of Tanzania [3]. In Mozambique, more households cultivating pigeon pea

has been the dominant force driving increasing pigeon pea production. Increasing area per growing household is a secondary driver. Rising productivity has not figured prominently in the expansion of production [4]. The productivity achieved at the level of small farmers varies from 300-400 kg.ha^{-1} [4] which is relatively low, which can be attributed to the lack of genetically superior varieties adapted to different environments. The pigeonpea breeding program in Mozambique covers Agroecological Zones R7, R8 and R9, where it is planned the experimental network for final evaluation of elite strains.

The selection of productive genotypes is the main challenge, however, when evaluated in a series of environments, genetic and environmental effects are detected, an additional effect provided by their

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interaction [5]. In this case, there is a possibility that the best genotype in one environment is not in another. This fact influences the selection gain and makes it difficult to recommend cultivars. However, it is up to the breeder to assess its magnitude and significance, quantify its effects on breeding techniques, technology diffusion strategies and provide subsidies that enable the adoption of procedures for its minimization and, or, its use.

Thus, the definition of homogeneous agricultural sub-regions and productive genotypes, with general, specific adaptability and high stability are extremely important, aiming to reduce risks in agriculture and to guide the farmer on the best cultivars for his environment. To the breeder, to identify key locations for the efficient conduct of his breeding program. Thus, the objective was to evaluate the performance of genotypes and stratify environments for agricultural zoning and recommendation of cultivars of this crop.

2. Material and Methods

The experiments were carried out at the Agricultural Research Institute of Mozambique, Northeast Zonal Center, in four environments in the agroecological zones R7 and R8 (Fig. 1), in the 2016/2017 season, under rainfed conditions, in random blocks with three repetitions and 20 genotypes of pigeo npea (Table 3) with long maturation and indeterminate growth habit, from ICRISAT-Keny. Sowing was carried out in spacing of two meters between rows, in plots of two rows of five meters in length each, placing four seeds per linear meter. Two weeding were carried out throughout the crop cycle. Pest control was performed using synthetic insecticides (Cypermetrina and Zakanaca) every 15 days from flowering to physiological pod maturation. Harvesting was carried out on the entire plot manually, when about 90% of the pods were dry and brown. It was followed by sun drying, manual threshing to obtain the production per plot and subsequent determination of grain yield in kg.ha^{-1}. Simple analysis
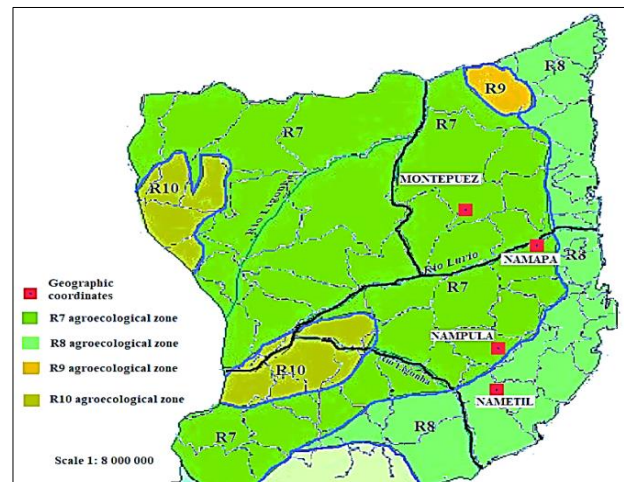

Fig. 1   Environments evaluated in the Agroecological Zone R7 (Nampula:-15.147796,39.309723 Montepuez:-13.216220, 38.884738, Namapa:-13.725419,39.772064) and R8 (Nametil:- 15.734794, 39.283867).

of variance were carried out and, subsequently, the combined analysis, after verifying the homogeneity of the residual variances. Clustering of averages was performed using the Scott Knott test [6] at 5% probability. In sequence, adaptability, phenotypic stability and environment stratification were studied using the biometric methodologies of Eberhart & Russell [7], which have as a statistical principle the simple linear regression analysis, modified centroid method [8] which consists on the addition of three new ideotypes (centroid) aiming to provide greater biological sense and the GGE-Biblot method [10] that does not separate the effects of the genotype and the G × E interaction, keeping them together in two multiplicative terms. The latter are based on multivariate analysis using the principal components. The analyzes were performed with the aid of the Genes software [11].

3. Results and Discussion

3.1 Simple and Combined Analysis of Variance

The results of the simple analysis of variance indicated the existence of statistical differences between the averages of genotypes of pigeon pea at the level of 1% probability. The ratio between the largest and the smallest average square of the residue was less

than seven, indicating the homogeneity of variances (Table 1), which enabled the combined analysis of the data. The effect of the environment and interaction G x E were significant at the level of 1% probability by the F test, showing the existence of environmental variations and differentiated performance of the genotypes compared to the observed variations (Table 2). Similar results were obtained by U. Chand et al. (2014) and N. Pagi (2017) [12, 13] who observed the significant interaction between genotypes and environments. In combined analysis, the significant effect of the genotypes was not observed due to the suppression of the genotypic variance based on the average of the environments [14].

Table 1   Summary of the simple analysis of variance for grain yield from the 20 genotypes in four environments.

		A1	A2	A3	A4
S	DF		MS		
B	2	525.65	15078.12	24509.15	27570.35
G	19	58884.33**	147397.83**	217254.78**	103298.01**
R	38	3418.16	12931.03	11480.20	5078.32
Average		504.15	916.28	639.05	472.45
CV%		11.60	12.41	16.77	15.08
Relação maior (QMR)/menor (QMR) = 3.78					

**Significant at 0.001 probability level, by F.test. S = Source, B = Blocks, G = Genotypes, R = Residual, E = Environments, A1 = Nampula, A2 = Nametil, A3 = Namapa, A4 = Montepuez. CV = Coefficient of Variation, DF = Degrees of Freedom, SQ = Sum of Squares, MS = Mean Square.

Table 2   Summary of the combined analysis of variance for grain yield from the 20 genotypes, in four environments.

S	DF	SS	MS	F.test
G	19	2265564.93	119240.26	0.88
E	3	7359880.40	2453293.47	144.99**
GXE	57	7744299.27	135864.90	16.52**
R	152	1250492.80	8226.93	
Total	239	18755603.90		
Average	632.98			
CV (%)	14.33			

**Significant at 0.001 probability level, by the F.test. S = source, G = Genotypes, R = Residual. E = Environment, GxE = genotype by environment interaction, CV = Coefficient of Variation, DF = Degrees of Freedom, SS = Sum of Square, MS = Mean Square.

The presence of interaction between a determined genotype and an environment, makes it difficult to recommend cultivars. To minimize and take advantage of the effects of the interaction, based on detailed studies using the methodologies of Eberhart & Russell [7], Centroide [8] modified by Nascimento [9] and GGE-Biplot [10], it was possible to identify genotypes of predictable performance and responsive to environmental variations, under specific or general conditions.

3.2 Selection of Cultivars by the Eberhart and Russell Method

According to the methodology of Eberhart and Russell [7], a genotype with a regression coefficient greater than 1.0 has a consistently better performance in favorable environments, when less than 1.0 is considered to performance relatively better in unfavorable environments, and when is equal to 1.0 for general adaptability. The magnitude and significance of the regression deviations gives an estimate of the predictability of genetic material. The results

illustrated in Table 3, showed that the genotypes G14 and G17 formed first cluster while the genotypes G4, G16, G11, G9 and G3 formed the second cluster with high averages of grain productivity. According to S. A. Eberhart and W. A. Russell (1996) [7], as ß0 represents the general average of the genotype for all environments, it should not be the main factor for selection. Thus, the genotype that has a high average, will not always be the best for all environments.

Table 3 Mean, adaptability and stability parameters of the Eberhart and Russell method (7) for grain yield (Kg.ha^{-1}) in 20 pigeon pea genotypes, evaluated in four environments.

Identification	Genotypes	Mean (ß$_0$)	ß1	t (ß1 = 1)	P (%)	S²d	P (%)	R² (%)
G1	ICEAP01420	460.08^e	0.54	-3.10	0.25	4765.47	6.79	70.22
G2	ICEAP01476	620.25^c	0.87	-0.89	37.60	22422.38	.017**	64.65
G3	ICEAP01479	683.83^b	1.21	1.42	15.34	-1743.72	100.0	98.90
G4	ICEAP01187	754.08^b	1.12	0.78	44.49	179867.40	.0**	29.49
G5	ICEAP01416	512.67^e	0.98	-0.15	87.53	27563.84	.003**	65.91
G6	ICEAP01423	571.42^d	1.15	1.03	30.32	38763.08	.0**	66.33
G7	ICEAP01392	643.33^c	0.84	-1.09	27.59	55862.94	.0**	42.28
G8	ICEAP01417	498.67^e	0.29	-4.73	0.00	12556.68	.46**	25.59
G9	ICEAP01482	684.25^b	1.63	4.24	0.01	94515.50	.0**	62.74
G10	ICEAP01523	611.83^c	0.15	-5.72	0.00	5496.61	5.25	13.60
G11	ICEAP01490	694.25^b	2.80	12.01	0.00	11881.11	.58**	97.04
G12	ICEAP01513	651.67^c	0.72	-1.86	6.15	76850.59	.0**	28.65
G13	ICEAP01534	570.17^d	0.80	-1.37	16.94	24930.80	.007**	58.37
G14	ICEAP01498	859.42^a	0.26	-4.95	0.00	95877.23	.0**	4.05
G15	ICEAP01413	624.50^c	1.67	4.50	0.00	-2727.64	100.0	99.99
G16	ICEAP01409	708.17^b	1.26	1.72	8.43	2228.60	16.67	95.12
G17	ICEAP01507	787.50^a	0.39	-4.11	0.01	137215.60	.0**	6.13
G18	ICEAP01511	546.83^d	1.41	2.71	0.74	-1029.95	100.0	98.61
G19	ICEAP00040	559.42^d	0.97	-0.23	81.55	4286.97	8.04	89.06
G20	ICEAP00053	617.33^c	0.97	-0.22	82.05	21499.32	.023**	70.29

The mean (ß0) followed by the same letters do not differ at 0.05 probability level, using the Scott Knott cluster test.
** Significant at 1% probability level.

Thus, for the recommendation of selected genotypes in the favorable (positive index) and unfavorable (negative index) environments, the predictability of the performance was considered (Fig. 2), which uses the coefficient of determination of the linear regression R² above 80%, as an auxiliary measure in assessing the stability of genotypes, when the regression deviations are statistically different from zero [5]. Thus, the G11 genotype can be recommended for favorable environments (A2 and A3), as it has a regression coefficient higher than the unit and a high determination coefficient that indicates greater predictability of increasing productivity with the improvement of environments. The G16 and G3 genotypes, while with superior performance in favorable environments, can also be recommended for unfavorable environments because they have a regression coefficient statistically equal to the unit, non-significant regression deviation and high determination coefficient as an indicator of greater predictability of productivity of genotypes. Genotypes G14 and G17 are adaptable to unfavorable environments, but showed significant regression deviations and a low coefficient of determination, with unstable or unpredictable productivity in environments. The G4 and G9 genotypes showed a regression

coefficient equal and higher than the unit, respectively, being of general and specific adaptability to favorable environments, however they are unstable due to the significant regression deviation and low determination coefficient. Similar results were observed by U. Chand et al. (2014) and N. Pagi (2017) [12, 13].

3.3 Selection of Cultivars by the Centroid Method

After the orthogonal decomposition of the environmental vectors, the first two principal components were maintained, which were sufficient to explain 73.7% of the total variation (Table 4), which is considered reasonable for the representation of the data in the two-dimensional space [5]. From the scores, 20

genotypes were plotted on a two-dimensional graph with the addition of seven centroids (Fig. 3), created based on experimental data [8]. On this method, the most important criterion for the quantitative inference of adaptability through an adequate visual inspection is the proximity of the genotype to one of the seven centroids [8, 9]. Thus, according to the centroid methodology [8] modified by [9], genotypes are classified as having maximum general adaptability-I, maximum specific adaptability to favorable environments-II, maximum specific adaptability to unfavorable environments-III and average specific adaptability to VI-favorable environments were not observed.
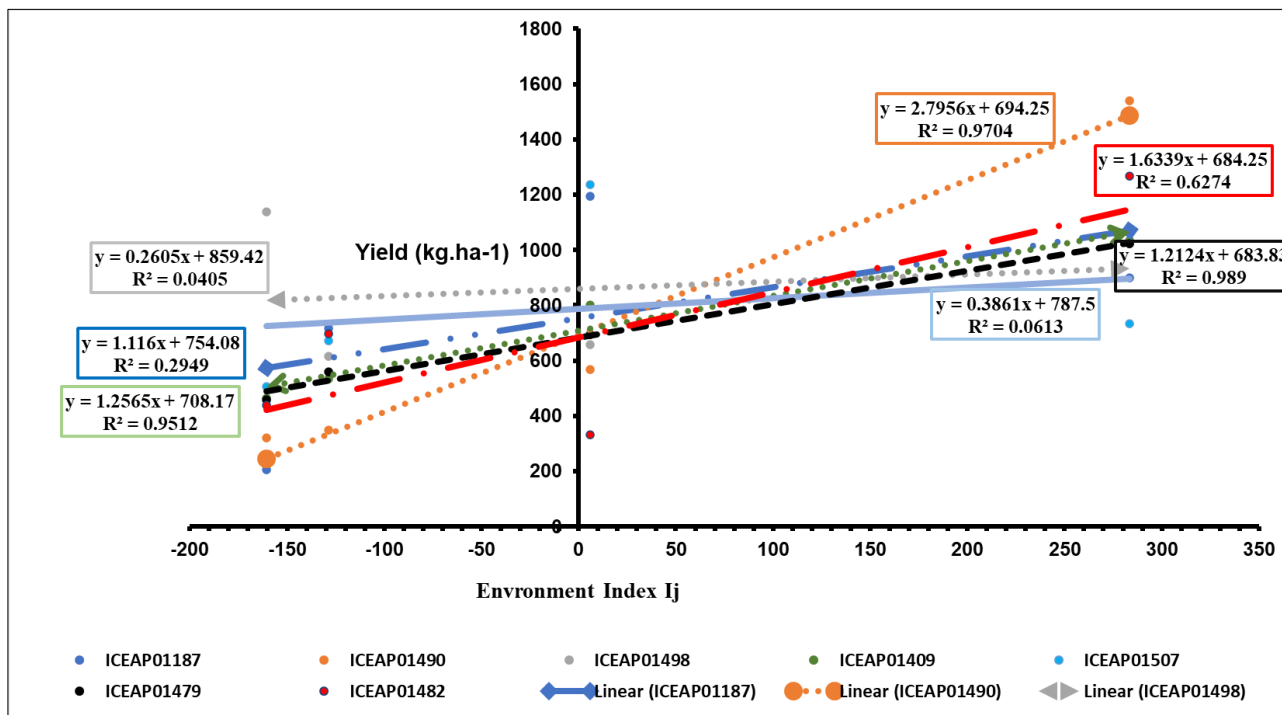

Fig. 2 Performance of genotype grain yield in unfavorable and favorable environments in an Eberhart and Russell environmental index graph [7]. On the left unfavorable environments (A1-Nampula and A4-Montepuez), on the right favorable environments (A2-Nametil and A3-Namapa).

Table 4 Eigenvalues and cumulative fraction of variance.

PC	PC (%)	% Accumulated
1.52	37.95	37.95
1.43	35.76	73.71
0.62	15.46	89.17
0.43	10.83	100.00

Genotypes G1, G5 and G8 were classified as being of minimal adaptability-IV, genotypes G2, G3, G4, G6, G7, G9, G10, G11, G12, G13, G15, G16, G20, G18, G19, G17 as of general adaptability-V, and G14 genotype was classified as medium specific adaptability to unfavorable environments-VII. Thus considering the average performance, the genotypes
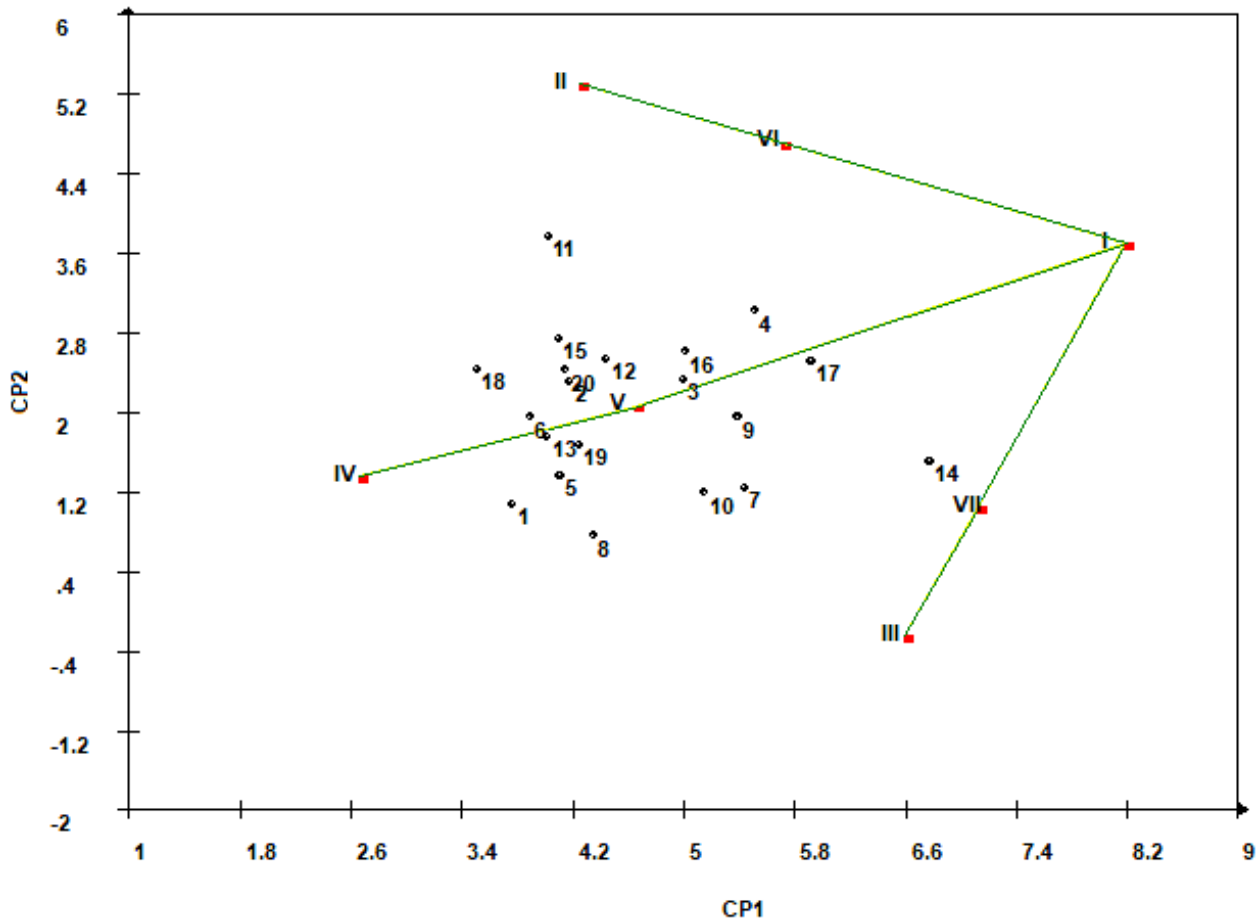
Fig. 3   Graphic dispersion of the first two principal components in 20 genotypes of pigeonpea, for grain productivity in four environments. PC1, principal component 1; PC2, principal component 2.

G3, G4, G9, G11, G17, G16 can be recommended for average general adaptability-V and G14 for average specific adaptability to unfavorable environments-VII.

3.4 Selection of Cultivars by the GGE Biplot Method

Based on GGE Biplot methodology (Fig. 4), the first two components explained 72.95% of the total variation for grain yield, which allows for good reliability of the biplot analysis [15]. By thegraphic criterion "which-won-where" (Fig. 4a) it was possible to observe (in red lines) the formation of seven sectors and indicated existence of a mega-environment grouping Nampula and Namapa district. Similar results were observed by N. Pagi (2017) [13]. A mega-environment can be defined as a group of positively correlated environments or sub-regions, in which a genotype or a group of genotypes are

specifically adapted and achieve better performance [10]. At the vertices of the polygon (Fig. 4a), the genotypes most distant from the origin of the biplot are those that present the best performance in one or more environments [16]. The G4 and G17 genotypes showed better average performance in the mega-environment (Nampula and Namapa), G9 and G11 better average performance in Nametil district and the G5, G8 and G10 with better average performance in Montepuez district.

On graphic criterion "Mean vs. Stability" (Fig. 4b), the continuous green line with a single arrow, called "average-environment axis" (AEA) is defined by the average coordinate of all test environments in biplot. The genotypes G14, G17, G4, G16, G11, G9, G3, G12, G7, G15, G2 and G20 are located above the average, that is, with higher average productive performance
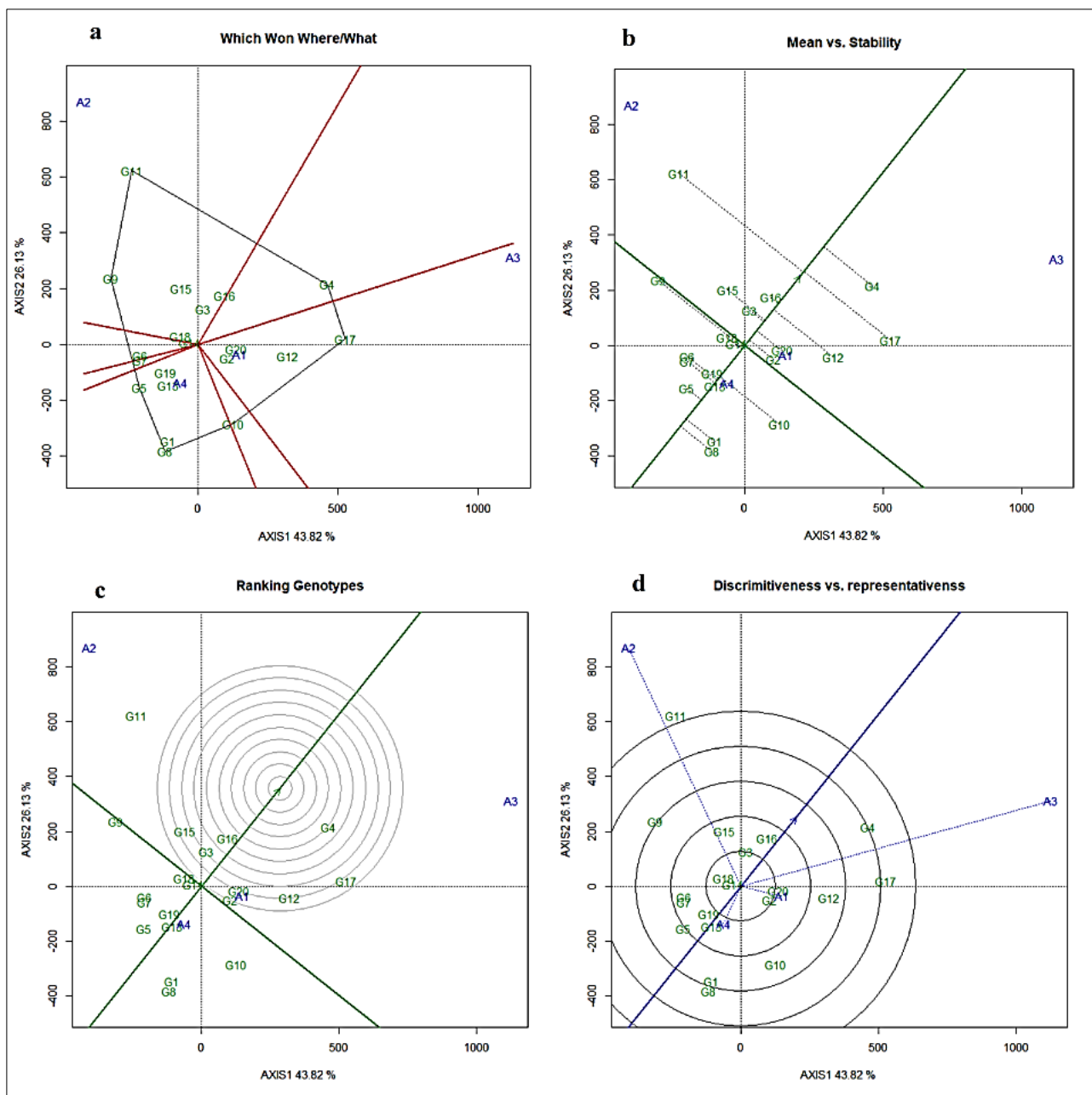
Fig. 4   (a) "which-won-where", (b) "Mean vs. Stability", (c) "Ranking Genotypes", (d) "Discrmimitiveness vs. Representativenss". A1-Nampula, A2-Nametil, A3-Namapa, A4-Montepuez.

between environments. The genotypes located below the average were those with the lowest performance. The second continuous green line (Fig. 4b), perpendicular to the AEA, points to greater stability, so that the greater the length of the dotted green line, the more unstable is the genotype [17]. The genotype must have both high productive performance and high stability [10]. Based on this criterion, the G16 and G3

genotypes are indicated for having, simultaneously, high average production and stability. Similar results were observed by U. Chand et al. (2014) and N. Pagi et al. (2017) [12, 13]. The graphic criterion "Ranking Genotypes" (Fig. 4c) indicates that the genotypes that are closest to the center of concentric circles are the most desirable. Therefore, the G16 and G4 genotypes are the ones that come closest to an ideal hypothetical

genotype. Similar results were observed by U. Chand et al. (2014) and R. K. Srivastava et al. (2012) [12, 18]. By the criterion "Discrmitiveness vs. Representativenss" (Fig. 4d) [19], the environments with the longest vectors are the most discriminative and those with the shortest vectors are the least discriminating, providing little or no information about the genotypez and can be discarded as a test environment. The most representative environments are those that form a smaller angle between its vector (blue dotted line) and AEA (continuous blue line) [17]. Thus, the A3 and A2 environments were the most discriminating and the A4 and A3 environments were the most representative for the genotypes (Fig. 4d). The ideal test environments for identifying and selecting superior genotypes should be both discriminative and representative. The A3 environment is the closest to the ideal, since it presents, simultaneously, high discrimination and representativeness. Similar results were observed by U. Chand et al. (2014) and N. Pagi et al. (2017) [12, 13]. Analyzing the results of the three methods, there are slight differences in the classification of genotypes, as well as much similarity, however, the study does not intend to compare them, but rather, to complement the information provided by each method to select genotypes with desired characteristics for a reliable recommendation in environments.

4. Conclusion

The ICEAP01490 genotype can be recommended for favorable environments (Nametil and Namapa district) and ICEAP01498 genotype can be recommended for unfavorable environments (Nampula and Montepuez district).

ICEAP01409 and ICEAP01479 genotypes, can be recommended for favorable and unfavorable environments.

The environments Nampula and Namapa district, formed a mega-environment and Namapa was the most discriminating and representative.

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