




Potential of forage and grain yield of maize genotypes in the Brazilian semiarid region¹

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ABSTRACT

Maize is importance in the semiarid region due to its forage potential. However, the large number of hybrids on the market hampers the selection of the hybrid by the producer. Given the above, the objective of this paper is to identify genotypes with productive potential for forage and grain production according to the characteristics of the semiarid region of Brazil. Twenty genotypes with different genotypic classes were evaluated in two years (2018 and 2019) in the municipality of Gracho Cardoso, state of Sergipe. The experiments were carried out in a randomized complete block design (RCBD), with two replicates. Genotype characteristics, grain yield, and forage mass were evaluated and the results were estimated using mixed models and GT Biplots. The genotypic classes consisting of topcrosses and intervarietal hybrids showed high average grain yield and the three classes produced equally on average for forage mass. It was observed that the HI, HTC, and V genotypic classes were the most responsive for grain yield, forage mass, and dry matter content, respectively. Therefore, it is concluded that the genetically broad-based hybrids (HTC and HI) were the most promising for the semiarid of region of Sergipe, while interspecific hybrids were the most productive and stable.

Keywords: hybrids; *GT Biplot*; *Zea Mays L.*; multivariate analysis.

INTRODUCTION

Maize crops are of great importance in human and animal nutrition for presenting high yield, easy management, high nutritional value, and superior bromatological quality. Maize cultivation is growing for both grain and silage production due to its properties as animal feed (Silva *et al.*, 2018). In cattle production systems, the main forage used as animal feed is maize silage. Thus, making good quality silage requires proper fermentation, a large amount of grains, and high dry matter contents (Neumann *et al.*, 2017).

Maize silage is important in the Brazilian Northeast for dairy cattle production, which is one of the main activities of the agricultural sector in the region. The most productive microregions in the Brazilian Northeast, producing a total volume of 996.7 million liters of milk, are the Vale do Ipanema and Garanhuns, in the state of

Pernambuco; Batalha, Palmeira do Índios, Arapiraca, and Traipu, in the state of Alagoas; and Sertão de São Francisco, in the state of Sergipe (Zoccal, 2019).

However, maize grain yield in the semiarid region is still low mainly due to the climatic conditions of the region, such as high temperatures and water deficit, which limit maize cultivation (Artuzo *et al.*, 2019). The semiarid region is also characterized by low rainfall (Tinôco *et al.*, 2019). During drought periods, animal feed is maintained mainly through ensiled forage, which can be properly conserved under drought conditions (Giachini *et al.*, 2020). Thus, the evaluation and selection of new genotypes that produce good-quality forage is extremely important for the supply of animal feed during drought (Simões *et al.*, 2017).

The selection of maize hybrids is essential for good quality forage. However, given the large number of hybrids on the market, it is necessary to obtain information on

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their performance when subjected to the environmental conditions of the region of interest. For maize cultivation in environments with limitations, it is necessary to obtain productive genotypes that adapt to these conditions (Macedo Junior *et al.*, 2018). Maize cultivation is indicated in the state of Sergipe in accordance with the Agricultural Climate Risk Zoning, which is an instrument built by Embrapa that indicates the planting dates, type of cultivars, and soils suitable for cultivation. In the municipality of Gracho Cardoso, sowing is indicated between April 1st and June 20th, although these dates vary according to the soil type and cultivar indicated. Therefore, the objective of this study was to identify genotypes with productive potential for forage and grain production according to the characteristics of the semiarid region of Brazil.

MATERIAL AND METHODS

We tested 20 maize genotypes from different genotypic classes and with different breeding steps (Table 1). The genotypes were evaluated according to their genotypic class and their behavior in the semiarid. The experiments were performed in the agricultural years 2018 and 2019 in the farm of Embrapa Semiarid, located in the municipality of Gracho Cardoso, state of Sergipe, Brazil (10°13'36"S latitude, 37°11'54"W longitude, mean altitude of 242 m).

Table 1: List of genotypes evaluated at the farm area of Embrapa Semiarid in Gracho Cardoso, state of Sergipe, Brazil, in the agricultural years 2018 and 2019

Type	Phase	Origin
V-1	Experimental	UFV
V-2	Commercial	Embrapa
V-6	Commercial	EMPARN
V-13	Experimental	IAPAR
V-14	Experimental	IAPAR
V-15	Experimental	IAPAR
V-4	Experimental	Embrapa
V-5	Experimental	Embrapa
V-19	Commercial	CATI
V-3	Experimental	UFV
HTC-7	Experimental	Embrapa
HTC-8	Experimental	Embrapa
HTC-9	Experimental	Embrapa
HTC-10	Experimental	Embrapa
HTC-11	Experimental	Embrapa
HTC-17	Experimental	Embrapa
HTC-18	Experimental	Embrapa
HI-12	Experimental	Embrapa
HI-16	Experimental	Embrapa
HI-20	Experimental	Embrapa

V = Variety; HTC = topcross hybrid; HI = Interspecific hybrid. Commercial genotypes: V-2 (Potiguar-G13); V-6 (BR5037-Cruzeta-G19); and V-19 (AL AVARÉ)

During 2018, the accumulated rainfall in the study region was 378.8 mm, planting was carried out in 05/24/2018, and harvesting was carried out in 09/08/2018. In 2019, the accumulated rainfall in the study region was 747.6 mm, planting was carried out in 01/06/2019, and harvesting was carried out in 08/09/2019 (Figure 1). The experimental area was not irrigated in these years.

Regarding the destructive procedures to evaluate forage, evaluations of forage and grain yield potential were performed for each agricultural year separately. Forage (kg ha⁻¹) and grain yield (kg ha⁻¹) were evaluated in the agricultural years 2018 and 2019, respectively.

The experiments followed the randomized complete block design, with two replicates. The plots consisted of two meter long rows spaced 20 cm between each plant and 80 cm between each row. Grain yield data was adjusted to 13% moisture per plot using covariance and was then converted to kilograms per hectare. Forage mass was calculated using equation 1. For all experiments, the soil was prepared by conventional procedures. The fertilizer was applied according to the soil analysis conducted in the two agricultural years (Table 2). For base fertilization, 20 Kg/ha N, 120 Kg/ha P₂O₅, and 60 Kg/ha K₂O were applied, while 100 Kg/ha N was applied as topdressing fertilization.

$$FM = \frac{WFM(g) * DM}{plot\ area} * 10 \quad \text{Equation 1}$$

Where: FM – Forage mass; WFM – weight of fresh matter harvested in the plot, DM – dry matter content, calculated using equation 2.

$$DM = DMS/FMS \quad \text{Equation 2}$$

Where: DM – dry matter content; DMS - dry matter; FMS – fresh matter.

The variable DMS was obtained through two fresh matter samples, which were weighted, maintained in a laboratory drying oven during three days, and weighted after removal.

Analyses using a mixed model approach were analyzed using the SAS Studio software (SAS Institute, 2009). The following model was used (Equation 3):

$$y = Xb + Zg + e \quad \text{Equation 3}$$

where 'y', 'b', 'g', and 'e' correspond to the vectors of observed data, block effects (assumed to be fixed), effect of genitors involved in the cross vector (assumed to be random), and random error, respectively. 'X' and 'Z', respectively, are the incidence matrices for this effect. The significance of the effects of the model was calculated using the likelihood ratio chi-square test at 1% probability, according to Resende (2000).

The GT Biplot method was based on the following model by Yan (2001) (Equation 4):

$$Y_{ij} - \bar{y}_j = y_1 \epsilon_{i1} p_{j1} + y_2 \epsilon_{i2} p_{j2} + \epsilon_{ij} \quad \text{Equation 4}$$

where Y_{ij} represents the average yield of the i -th genotype on the j -th variable, \bar{y}_j is the general mean of the genotypes for the variable j , $y_1 \epsilon_{i1} \bar{\eta}_{j1}$ is the first principal component (PC1), $y_2 \epsilon_{i2} \bar{\eta}_{j2}$ is the second principal component (PC2), y_1 and y_2 are the eigenvalues associated with PC1 and PC2, respectively, ϵ_1 and ϵ_2 are the scores of the first and second principal components, respectively, of the i -th genotype, $\bar{\eta}_{j1}$ and $\bar{\eta}_{j2}$ are the scores of the first and second principal components, respectively, for the j -th variable, and ϵ_{ij} is the model error associated with the i -th genotype and j -th variable.

Using the means of each variable, the GT biplots were made in the R software (R Foundation, 2014) using the 'GGEbiplotGUI' package (Frutos *et al.*, 2014).

RESULTS AND DISCUSSION

The genotypic classes consisting of topcross hybrids, interspecific hybrids, and varieties were significant for grain yield, showing that at least one of the classes was superior to the others. The classes were not significant for forage mass and could be indicated as an excellent forage option in the Sergipe semiarid area (Table 3).

The coefficients of variation (CV) were within the acceptable limits for maize crops, below 20%, demonstrating the reliability of the estimates of averages of the experiment (Fritsche-Neto *et al.*, 2012).

The presence of superior genotypes is important for plant breeding programs aiming at increasing yield. The genotypic classes showed a relatively high average (2741.05 kg/ha) for the environmental conditions subjected. According to the national grain yield estimate of IBGE/SIDRA, the third 2018/19 maize crop season presented yields of 3.189 Kg/ha (2018) and 4.838 Kg/ha (2019) in Sergipe; 1.924 Kg/ha (2018) and 2.473 Kg/ha (2019) in Alagoas, and 1.236Kg/ha (2018) and 2.487 Kg/ha (2019) in northeastern Bahia. However, compared to the average yield of the first and second crop seasons in Brazil, 5.108Kg/ha (2018) and 5.773 kg/ha (2019), this region produced less due to adverse environmental conditions, showing the importance of selecting more productive genotypes adapted to these conditions, specially to water deficit (IBGE, 2021).

Table 3: Deviance analysis of grain yield (GY, kg/ha) and forage mass (FM, kg/ha) in the genotypic classes of maize

Effect	Deviance			
	GY	RLT	FM	RLT
Class	363.5	6.1**	370.6	0.5 ^{ns}
Complete model	369.6		370.1	
Blocks	Fixed effect			
	GY	FM		
Mean	2,741.05	1,112.50		
VC (%)	14.37	14.42		

LRT – Likelihood Ratio Test

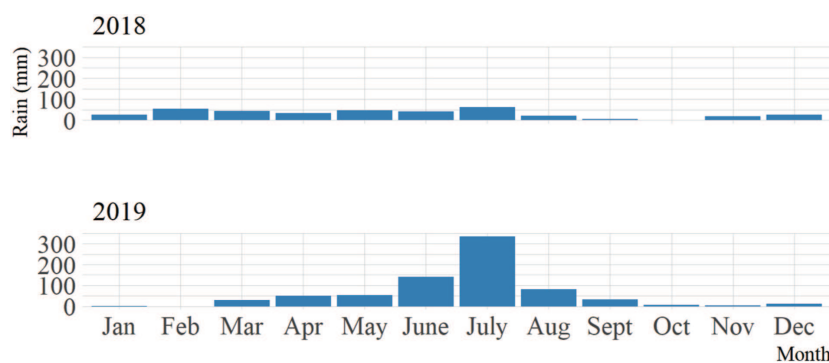


Figure 1: Climatic data recorded by the National Institute of Meteorology (INMET, acronym in Portuguese) in 2018 and 2019.

Table 2: Soil chemical analysis, carried out in the soil testing laboratory of Embrapa Coastal Tablelands

O.M.	pH in H ₂ O	Ca	Mg	H+Al	Al	P	K	Na
(g kg ⁻¹)		(mmol _c dm ⁻³)					(mg dm ⁻³)	
2018								
22.54	5.83	19.63	18.99	48.02	0.39	1.84	134.91	23.55
2019								
23.35	5.23	15.07	8.61	56.18	6.40	10.91	66.00	30.34

O.M. – Organic matter.

Among the genotypic classes studied, topcross hybrids showed on average higher grain yield (GY) (Table 4). It is worth mentioning that open-pollinated varieties showed on average the lowest yields. However, they are an economical alternative of cultivation for small farmers, as on average their grain yield is similar to that of interspecific hybrids. When forage mass (FM) was evaluated, all genotypic classes produced similarly (Table 4). Drought during the rainy season contributed to this result, as it was necessary to harvest the forage in advance in the field, when they showed 30 to 35% DM.

The best gains with selection were shown by topcross and interspecific hybrids. In the variety class, gains with selection were not observed under the conditions of this study (Table 5).

Based on the individual means of the genotypes, the best genotypes for grain yield (GY) were V-3, HI-12, HTC-10, HTC-8, and V-4. For the forage mass (FM) variable, the best genotypes were HTC-11, HTC-10, HI-20, V-6, and V-15 (Table 6). Thus, we can select genotypes for the variables individually, although it is still necessary to select genotypes for both variables simultaneously.

The results indicate that genetically broad-based genotypes are the most promising when selecting productive materials for grain production under the conditions of this study. Topcross hybrids stood out as they increased averages, being formed by crossing several strains with a common tester genotype (Possatto–Junior *et al.*, 2017). The common tester can be a genetically broad- or narrow-based genotype. In this case, it is better to use a genetically broad-based tester. Broad-based testers are also used to observe strains with a high general combining ability (GCA) (Rodvalho *et al.*, 2012).

Topcross hybrids have the advantage of simplifying the breeding process, reducing costs and experimental

Table 4: Tukey test in different maize genotypic classes for grain yield (GY) and forage mass (FM)

Class	GY	FM
Topcross Hybrid	4,138.9 a	1,092.2 a
Interspecific hybrid	3,262.1ab	1,183.3 a
Variety	2,006.1 b	1,104.4 a

Table 5: BLUPs with standard error and t test, genotypic values with standard error and confidence limits, gains, and averages for grain yield (GY) in different genotypic classes

GEN	g	u+g	Gain	New average
HTC	807.08	3073.08	807.08	3880.32
HI	124.04	3197.12	465.56	3538.80
V	-931.13	3073.08	-0.000	3073.23

g=BLUP; u+g=Genotypic value + General average (phenotypic value); HTC: Topcross Hybrid ; HI: Interspecific hybrid; V: Variety.

analysis. These hybrids have the advantage of enabling the crossing of a high-yielding strain with a population or single, double, or triple hybrids. Thus, it is possible to obtain highly productive hybrids of lower cost with these crossings. In addition, increased heterozygosity in these hybrids allows better adaptation to environmental adversities that may occur during cultivation (Menkir *et al.*, 2016).

The effects of the variables analyzed in the genotypic classes and within classes were studied using the GT biplot analysis (Yan, 2001). It was observed that the first two principal components (PCs) explained 100% of the variability of the observed data, showing reliability in the graphs (Yan, 2001).

Performance is observed from the arrow and the concentric circle in Figure 2A, which represents a genotypic class with ideal production. Phenotypic stability is represented from the projection that a genotypic class shows in face of the ordinate axis. Genotypic classes are considered of low yield when being after the ordinance axis (Yan & Tinker, 2006). In figure 2A, it is possible to observe that the genotypic class H1 was the most productive and stable for the variables grain yield (GY), dry matter content (DM), and forage mass (FM), unlike HTC and V.

In Figure 2B, formed by polygons, the vertices show genotypes responsive to the characteristics under study (Yan & Tinker, 2006). It was observed that each genotypic class formed a single group with responsive characteristics to grain production, forage mass, and dry matter

Table 6: Genotype means for the GY (grain yield) variables evaluated in 2019 and for forage mass (FM) in 2018

TRAT	GY	FM
V-1	2,569.136	29.32
V-2	1,768.164	28.79
V-6	1,321.715	34.83
V-13	1,501.315	32.80
V-14	774.336	32.69
V-15	3,693.764	34.17
V-4	4,055.666	30.31
V-5	3,735.636	29.59
V-19	1,321.266	27.59
V-3	5,841.564	29.76
HTC-7	3,812.136	29.93
HTC-8	4,216.636	30.48
HTC-9	1,554.250	27.00
HTC-10	4,626.264	36.17
HTC-11	3,329.564	40.18
HTC-17	3,223.775	30.67
HTC-18	3,462.866	29.40
HI-12	4,891.914	30.34
HI-16	1,180.386	29.84
HI-20	1,150.436	35.30

content (HI, HTC, and V, respectively). These results indicate that it is possible to select superior genotypes for grain production and forage mass. Moreover, it is possible to maintain breed programs and explore the genotypes of each class, in order to obtain strains responsive to the study variables (Kumar *et al.*, 2020).

The variables that most discriminate and represent the genotypic classes can be observed in Figure 2C. The longest vectors after concentric circles have discriminatory effects. Circled arrows show representativeness. Variables that are closer to the line form smaller angles, being the most representative (Yan & Tinker, 2006). Thus, all variables were discriminatory. However, for being the most representative variable, we could only use grain yield in terms of genotype selection.

The best genotype is selected according to its proximity to the arrow in the center of the concentric circle from the abscissa (Yan & Tinker, 2006) (Figure 2D). Interspecific hybrids were the genotypic class with the best performance for the variables GY, FM, and DM. The formation of these hybrids occurs through the crossing of two varieties, providing genetically broad-based hybrids with high capacity to adapt to adverse environmental conditions. These hybrids are important for requiring less technology in their cultivation, being also relevant in breeding programs to maintain genetic variability in populations and enable new crosses (Carpentieri-Pípulo *et al.*, 2010).

Besides characterization based on genotypic classes, genotypes were also classified in relation to the

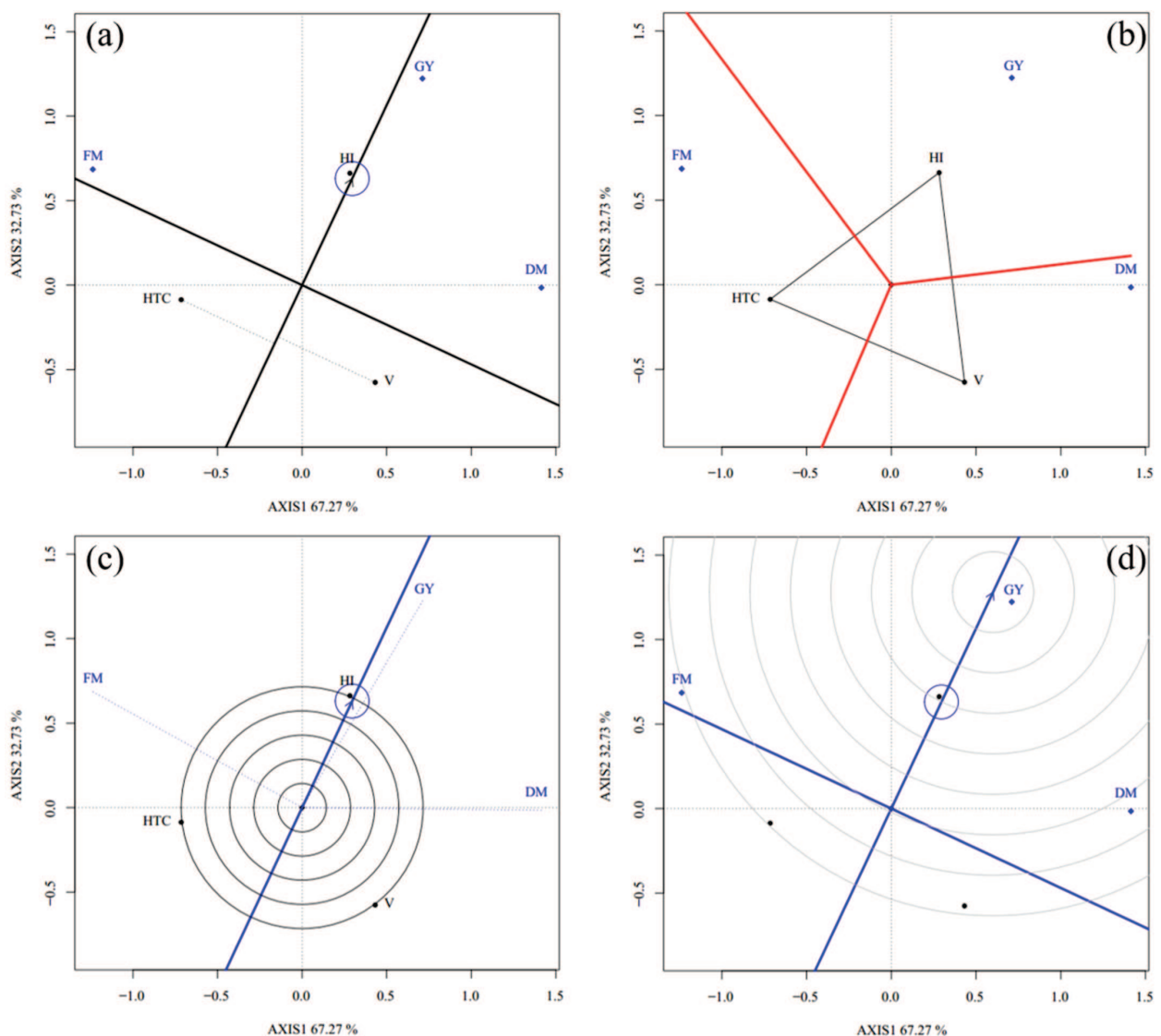


Figure 2: GT biplots representing the 'phenotypic stability and yield' (A), 'which-won-where' (B), 'discrimination-and-representativeness' (C), and 'best performance' (D), representing the characterization of different genotypic classes (V - variety; HTC - topcross hybrid; HI - intervarietal hybrid) of maize regarding grain yield (GY), dry matter content (DM), and forage mass (FM) analyzed in the Brazilian semiarid.

variables (Figure 3). The PCs of these graphs explained 71.64% of the total variation, showing reliability of information (Yan, 2001).

When all variables are observed (GY, FM, and DM), the varieties V-15, V-6, and V-14 showed the highest yields. Genotypes V-19, HI-16, HI-12, HTC-11, HTC-8, HTC-10, and HI-20 showed average yields, and genotypes V-5, V-13, HTC-9, V-2, HTC-17, V-3, V-1, V-4, HTC-7, and HTC-18 showed low yields. V-6, V-14, and V-19 were the genotypes that showed the highest stability (Figure 3A).

V-6 and V-14 stood out from the other genotypes for obtaining high performance and high stability, possibly being the genotypes more adapted to the conditions submitted in this study. However, when the genotypic class of varieties was evaluated, they did not exhibit

significant superiority, since open-pollinated populations have lower yields compared to hybrids. Corroborating this fact, V-5, V-13, V-2, V-3, V-1, and V-4 were the genotypes that presented the lowest performance in this study, decreasing the average of the genotypic class.

V-15 was the most productive and stable variety for the variable dry matter content (DM). The genotypes HI-20, V-14, V-3, V-6, V-4, V-19, and V-5 showed average yield and low stability (Figure 3B). The DM variable (dry matter content) allows observing forage quality, silage conservation, and the amount of forage to be consumed of a given genotype, with the ideal values being from 30 to 35% DM (Rezende *et al.*, 2008).

For grain yield (GY), the most productive genotypes were HTC-10, HI-12, V-6, HTC-8, and HTC-11. V-14, HTC-

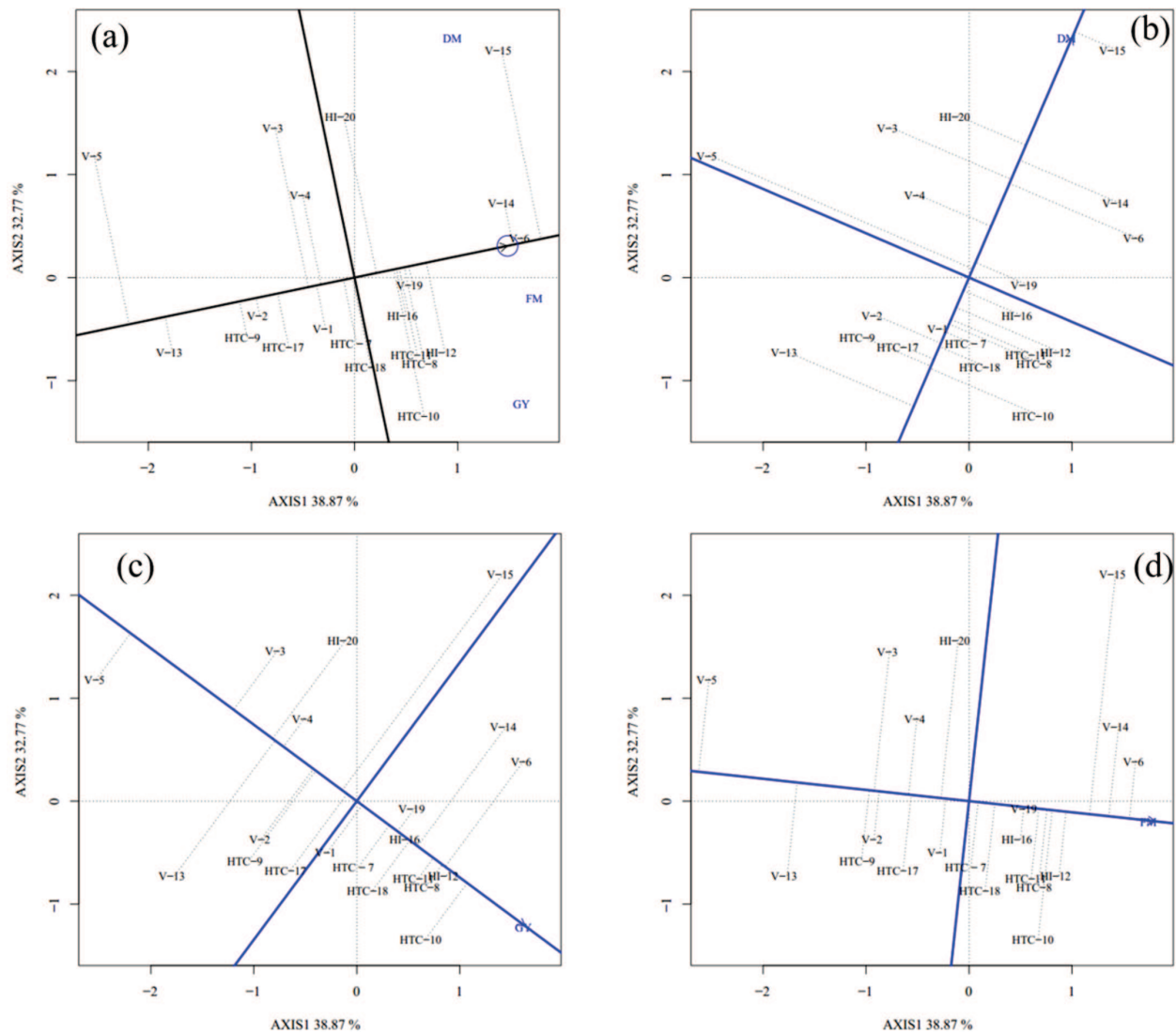


Figure 3: GT biplot representing 'phenotypic stability and yield' (A) considering an ideal variable and 'Phenotypic stability and yield' considering the variables dry matter index (B), grain yield (C), and forage mass (D) and representing the characterization of individual genotypes of different genotypic classes of maize regarding grain yield (GY), dry matter content (DM), and forage mass (FM) analyzed in the Brazilian semiarid.

18, HI-16, V-19, HTC-7, and V-1 showed average yields. The most stable genotypes were HI-16, HI-12, and HTC-8 (Figure 3C). It is possible to observe that some topcross hybrids were present in the classification of superior genotypes, corroborating BLUP data and demonstrating the importance of broad-based hybrids.

For the variable forage mass (FM), the most productive genotypes were V-6, V-14, and V-15. HI-12, HTC-10, HTC-8, HTC-11, V-19, and HI-16 showed average yields. The most stable genotypes were V-19 and HI-16 (Figure 3D). Forage mass is important when the purpose is using maize as food for animals during drought. Thus, highly productive genotypes are the most appropriate for indication to producers in this region.

Interspecific hybrids showed the highest average yield and stability, also showing increased genetic variability in the class, being the most adaptable for these regions. However, when the genotypes under study were removed from the groupings of genotypic classes, it was observed that the varieties V-6, V-14, and V-15 showed the best genotypic performance for the variables studied.

The adaptability and stability of maize genotypes in the Brazilian northeast has been studied by Carvalho *et al.* (2011); Embrapa (2017); Oliveira *et al.* (2019); and Oliveira *et al.* (2020), who they observed that hybrids adapt better, and materials differ regarding adaptability. Therefore, more experiments can be developed evaluating forage and grain production in two different years and/or environments, in order to indicate the ideal cultivar and increase yield, as these environments tend to show limiting climatic conditions.

CONCLUSIONS

In the semiarid region of the state of Sergipe, Brazil, it is ideal to prioritize genetically broad-based hybrids. Thus, both topcross and interspecific hybrids were promising for this region.

In a possible breeding program study, interspecific hybrids may contain more alleles favorable to grain yield, while topcross hybrids may contain more alleles favorable to forage mass. In general, interspecific hybrids were the most productive and stable.

The genotypes with the best forage and grain yield potential were V-6 (BR5037-Cruzeta-G19), V-14 (IPR164), V-15 (PC0905), V-19 (ALAVARÉ), HTC-8 (HTC717), HTC-10 (HTC781), HTC-11 (HSmsxHTMV1), HI-12 (HI771xHTMV1), and HI-16 (HI707xHTMV1).

In order to indicate the variable to be prioritized and increase yield, it is necessary to carry out more experiments evaluating forage production and grain yield in different environments.

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