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CORRELATION AND PATH ANALYSIS AMONG QUANTITATIVE TRAITS OF FORAGE SORGHUM GROWN IN THE SEMIARID REGION

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Abstract – Forage sorghum (*Sorghum bicolor* L.) has been grown in diverse climate variations, in warm and dry regions, or in regions with short drought periods. Thus, there is a need to select sorghum genotypes adapted to production systems under drought or rainy irregularities. This study evaluated the direct and indirect correlations among morphophysiological and productive characters of forage sorghum genotypes with Pearson's correlation and path analysis. The experiment was designed under complete randomized blocks, with 25 treatments (genotypes) and three replicates. Analyzes of phenotypic correlation and the path analysis were done for plant height, panicle length, stem diameter, plant stand, green matter and dry matter yields, stem weight, plant weight, panicle weight, dry matter content, and forage mass. Plant weight presented the most significant direct effect on the forage mass (target variable), contributing to the increase in forage sorghum production. Therefore, heavier plants are more suitable to select forage sorghum genotypes indirectly, aiming to increase forage mass.

Keywords: Association among variables, *Sorghum bicolor* L., Sorghum for feed.

CORRELAÇÃO E ANÁLISE DE TRILHA ENTRE CARACTERES QUANTITATIVOS DE SORGO FORRAGEIRO CULTIVADO EM REGIÃO SEMIÁRIDA

Resumo – O sorgo forrageiro vem sendo cultivado em uma ampla faixa climática, regiões muito quentes, secas ou onde ocorrem veranicos. Com isso há a necessidade de realizar estudos que conduzam a seleção de genótipos adequados ao sistema de produção e adaptados a regiões com escassez e/ou irregularidade hídrica. O presente estudo objetivou avaliar por meio da análise de correlação de Pearson e análise de trilha as relações diretas e indiretas existentes entre os caracteres morfofisiológicos e produtivos de sorgo forrageiro. O delineamento utilizado foi em blocos casualizados, constituído por 25 tratamentos (genótipos) e três repetições. Foram realizadas análises de correlação fenotípica e análise de trilha para as variáveis, altura da planta, comprimento da panícula, diâmetro do colmo, estande final, matéria verde, matéria seca, peso do colmo, peso da planta, peso da panícula, peso da folha, percentagem de matéria seca e massa de forragem. A variável peso da planta foi a que apresentou o maior efeito direto favorável sobre a variável massa de forragem, contribuindo para o aumento da massa de forragem, sendo assim plantas com maiores pesos são as mais indicadas para a seleção indireta para o aumento da massa de forragem.

Palavras-chaves: Associação entre variáveis; *Sorghum bicolor* L; Forragem.

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Forage sorghum (*Sorghum bicolor* L.) has been grown in a considerable climate variation, in warm and dry regions, or regions with short drought periods due to its morphological characteristics (Ribas, 2000). Considering the enormous adaptability of sorghum (Silva et al., 2022), this crop is suitable for development and expansion in regions with irregular rainfall, besides the successions of summer crops.

For the success of a breeding program of forage sorghum, it is crucial to know the correlations among variables to plan strategies for increasing genetic gains through the selection of many characters simultaneously (Souza et al., 2014). Thereby, in the initial phases of a breeding program, the indirect selection of characters with low heritability, correlated to others with great heritability, is indicated to obtain more significant genetic gains and efficiency in the breeding program (Rios et al., 2012).

In this sense, Pearson's correlation shows the magnitude and direction of the linear association between two characters (Entringer et al., 2014; Crispim Filho, 2018). The nature of this correlation may be phenotypic, genotypic, or environmental, although the genotypic correlation instigates a greater interest in the breeders because of its hereditary nature (Salla et al., 2015). Nevertheless, only the study of correlations does not allow conclusions about cause-effect ratios; that is, the correlation is only a simple measurement of linear association (Souza et al., 2014).

Aiming to overcome this limitation, the method of path analysis allows the breakdown of correlation coefficients into direct and indirect effects, estimated by a regression equation of the characters on a target variable, guarantying more excellent reliability on the choice of characters for selection (Rios et al., 2012; Faria et al., 2015). Based on this context, the study aimed to evaluate the association among quantitative characters of forage sorghum grown in a semiarid region.

Material and Methods

The experiment was carried out at the Experimental Farm from Embrapa Semiárido, located in Graccho Cardoso, SE, Brazil (10º13'06" S, 37º25'13" W, 291 m). According to Köppen's classification, the climate is BSsh, hot climate, Steppe type, and the rainy season occurs in the winter. The experiment was carried out from June 25 to December 9 in the agricultural year of 2019. Climate data were recorded from the meteorological station of Embrapa Semiárido (Figure 1).

Twenty-five forage sorghum genotypes were assessed, within commercial and experimental ones (Table 1), under a randomized complete block design with 25 treatments and three replications, totalizing 75 experimental plots. Each plot was composed of two rows with five meters, spaced by 0.10 m between plants and 0.50 m between rows, totalizing 50 plants per row, besides a complete stand of 200,000 plants per hectare. The seeding was made manually after the opening of furrows and the distribution of one sorghum seed for each 0.10-m distance. In addition, two seeds were added at the beginning and the end of each row, aiming to avoid bias regarding the border effect.

Initially, the conventional tillage of soil was made with a disc-plow, used at 0.3-m depth. Moreover, the row markings for the seeding were made using a 3-rod furrower. Then, the furrower regulation was made, aiming that the rods stayed at a 0.5-m distance and 0.05-m depth, approximately. After that, the experimental units (plots) demarcation was made with ropes, the plots were identified, the

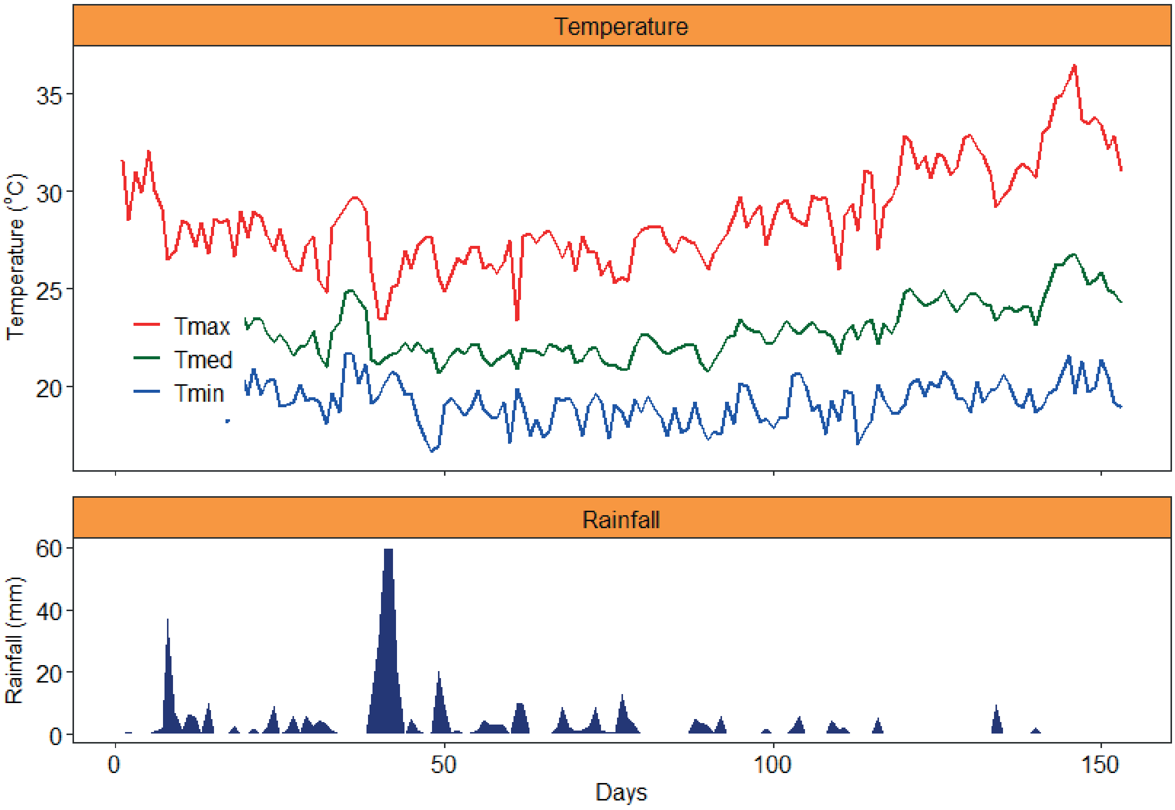

Figure 1: Climate data recorded from the meteorological station of Embrapa Semiárido during the period from 06/01/19 to 10/31/19.

seeds were distributed, and the forming fertilization was made.

Forming fertilization was made simultaneously with the seeding, according to the chemical soil properties (Table 2). First, commercial fertilizer was distributed into the furrows with a formulation of 8-28-16 (nitrogen-phosphorous-potassium) applied by 300 kg/ha. Then, after 40 days from the seeding, 60-g urea was manually applied to each plot row as a nitrogen source for the cover fertilization. Cultural practices were done according to the recommendations and requirements of sorghum cropping management (Ribas, 2000).

At the time of evaluations, the plots were tagged correctly to identify the genotypes and provide a good precision regarding the following variables: Average plant height (PH, m): average height of five plants, randomly selected and assessed with the aid of a graduated ruler; Average panicle length (PL, cm): average of panicle length of five plants, which were representative of the plot, measured from the basis to the apices with the aid of a graduated ruler; Stem diameter (SD, cm): average of stem diameter obtained from five plants, measured with a manual pachymeter; Plant stand (ST, plants/plot): counting of the number of live plants for each plot; Green matter yield (GMY, g): the plants of each treatment were chopped into a stationary forage machine, and thereafter, two samples were collected, put on paper bags and weighted on a digital balance; Dry matter

Table 1: Collection of the 25 forage sorghum genotypes (22 experimental hybrids and 3 commercial cultivars) that were assessed in the experiment, carried out at the experimental farm from Embrapa Semiárido, located at Graccho Cardoso municipality, Sergipe state.

Nº	Genotypes	Phase	Origin
1	G1	Experimental	Embrapa Milho e Sorgo
2	G2	Experimental	Embrapa Milho e Sorgo
3	G3	Experimental	Embrapa Milho e Sorgo
4	G4	Experimental	Embrapa Milho e Sorgo
5	G5	Experimental	Embrapa Milho e Sorgo
6	G6	Experimental	Embrapa Milho e Sorgo
7	G7	Experimental	Embrapa Milho e Sorgo
8	G8	Experimental	Embrapa Milho e Sorgo
9	G9	Experimental	Embrapa Milho e Sorgo
10	G10	Experimental	Embrapa Milho e Sorgo
11	G11	Experimental	Embrapa Milho e Sorgo
12	G12	Experimental	Embrapa Milho e Sorgo
13	G13	Experimental	Embrapa Milho e Sorgo
14	G14	Experimental	Embrapa Milho e Sorgo
15	G15	Experimental	Embrapa Milho e Sorgo
16	G16	Experimental	Embrapa Milho e Sorgo
17	G17	Experimental	Embrapa Milho e Sorgo
18	G18	Experimental	Embrapa Milho e Sorgo
19	G19	Experimental	Embrapa Milho e Sorgo
20	G20	Experimental	Embrapa Milho e Sorgo
21	G21	Experimental	Embrapa Milho e Sorgo
22	G22	Experimental	Embrapa Milho e Sorgo
23	G23	Commercial	Embrapa Milho e Sorgo
24	G24	Commercial	Embrapa Milho e Sorgo
25	G25	Commercial	Monsanto/Agroceres

Table 2: Soil chemical analyzes made in the Soil laboratory from Embrapa Tabuleiros Costeiros.

OM	pH (H_2O)	Ca	Mg	H+Al	Al	P	K	Na
------- ($g\ kg^{-1}$) -------		--------- ($mmol_c\ dm^{-3}$) ---------				--------- ($mg\ dm^{-3}$) ---------		
12.29	5.17	16.74	10.71	31.05	3.01	1.46	67.92	32.88

OM – organic matter; Ca – Calcium; Mg – Magnesium; H+Al – Hydrogen added to aluminum; Al – aluminum; P – phosphorous, K – Potassium and Na - Sodium.

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yield (DMY, g): two samples of the GMY were dried at 65 °C for 72 hours, with the aid of a forced-air ventilation oven, and thereafter, these samples were weighted again; Stem weight (SW, kg): average weight of stems from five plants, which were representative of the plot, weighed on a digital balance; Plant weight (PW, kg): obtained from the weight of all plants for each plot, weighed on a digital balance; Panicle weight (PNW, g): obtained from the weight of all panicle from five plants, weighed on a digital balance; Leaf weight (LW, kg): obtained from the weight of all leaves collected from five plants, weighed on a digital balance; Dry matter content (DM , %): obtained by the following equation:

$$DM = \left(\frac{DMY}{GMY}\right) * 100 \quad \text{Equation 1}$$

Where:

DM: dry matter content; DMY: dry matter yield; GMY: green matter yield.

Forage mass – FM (kg ha^{-1}): obtained by the following equation:

$$FM = \left(\left(\frac{PW}{ST}\right) * ST\ p/ha\right) * \left(\frac{DMY}{100}\right) \quad \text{Equation 2}$$

Where:

FM: forage mass; PP: Plant weight for each plot; ST: stand of plants for each plot; ST p/ha: stand of plants per hectare, obtained by the equation: $\left(\frac{ST}{10}\right) * 20000$; DMY: Dry matter yield.

Analyzes of the production variables were made through the average values from each plot. Then, data from each variable were submitted for analysis of variance (ANOVA). After that, the genetic parameters were analyzed by the methodology of Vencovsky and Barriga (1992).

Estimation of phenotypic, genotypic, and environmental correlation coefficients was obtained from the original data using Pearson’s linear correlation results. The correlation coefficients were broken down into direct and indirect effects on the F.M. (target variable) through the path analysis, considering the characters with agronomic importance for the forage sorghum (independent variables of the regression model). For that, it was indispensable that the matrix X’X was well-conditioned.

Multicollinearity diagnosis was made to identify the nature of linear dependence among variables based on this number of conditions (IN) defined by Montgomery et al. (2012). The multicollinearity was classified from moderate to strong ($100 \leq NC < 1000$). The variables that showed greater auto-vectors associated with lower auto-values were those that more contributed to this appearing. Because of that, variables such as stem weight, panicle length, and dry matter yield were eliminated from this analysis. After the path analysis, the constant K (0.23) was added to the diagonal matrix to attenuate data reliability. All statistical analyses were made using GENES software (Cruz, 2013).

Results and Discussion

A significant difference among genotypes for all traits was observed for PL and DMY (Table 3). A significant part of phenotypic variance occurred due to the genotypic one for LW, SW, PW, GMY, ST, PH, PNW, and DMY variables. Therefore, these characteristics could be attributed to genetic expression (Table 4).

Table 3: Mean squares of the analysis of variance and the coefficient of environmental variation (CV%) from plant's height (PH), stem diameter (SD, cm); panicle length (PL, cm); plant stand (ST, plant/plot); green matter yield (GMY, g); dry matter yield (DMY, g); stem weight (SW, g); plants' weight (PW, kg); panicle weight (PNW, g); leaves weight (LW, kg); dry matter content (DM, %); and forage mass (FM, kg ha^{-1}) from populations of forage sorghum genotypes, within commercial and experimental ones. Graccho Cardoso – SE, 2019.

		Mean squares											
SV	DF	PH	SD	PL	ST	GMY	DMY	SW	PW	PNW	LW	DM	FM
Treatment	24	1813.03**	0.07**	23.45	1566.88**	4602.10**	258.47	30.60**	38.66**	62.67**	0.59**	143.12**	17513228**
Block	2	2008.49	0.21	54.44	784.41	516.72	41.44	13.70	32.26	31.37	0.87	127.26	21746836,4
Residue	48	183.76	0.01	13.49	214.21	1635.81	227.85	2.84	4.85	8.56	0.07	29.32	4105373,6
CV (%)		6.34	11.15	14.21	17.35	26.62	20.94	28.46	25.31	17.35	30.16	10.91	24.64
Mean		213.66	1.04	25.83	84.33	151.89	72.07	5.92	8.70	16.86	0.89	49.60	8221.33

(DF) = degrees of freedom; SV = source of variation; ** Significant at 1% probability error by the F test, respectively. Measurement units were estimated for each plot.

Table 4: General means (M), phenotypic variance (σ^2_p), genotypic variance (σ^2_g), environmental variance (σ^2_e), broad-sense heritability (h^2), genetic coefficient of variation (CV_g) besides the ratio between genetic and experimental coefficients of variation (CV_g/CV_e) for the twelve variables of forage sorghum, Graccho Cardoso – SE, 2019.

Genetic parameters	SD	LW	PW	SW	GMY	DMY	ST	PH	PNW	PL	DM	FM
M	1.04	0.89	8.70	5.92	151.89	72.07	84.33	213.66	16.86	25.83	49.60	8932.30
σ^2_f	0.02	0.19	12.88	10.20	1534.03	86.15	522.29	606.28	20.89	7.82	47.71	17171508.77
σ^2_g	0.01	0.17	11.27	9.25	988.76	10.20	450.89	544.18	18.03	3.26	37.93	2175197.35
σ^2_e	0.00	0.02	1.61	0.94	545.27	75.95	71.40	62.09	2.85	4.56	9.77	14996311.41
h^2 (%)	80.87	87.61	87.44	90.69	64.45	11.84	86.32	89.75	86.32	41.71	79.51	12.66
CV_g (%)	13.24	46.31	38.56	51.30	20.70	4.43	25.17	10.91	25.17	6.99	12.41	16.51
CV_g/CV_e	1.18	1.53	1.52	1.80	0.77	0.21	1.45	1.72	1.45	0.49	1.13	0.21

SD = stem diameter (cm); LW = leaf weight (kg); PW = plants weight (kg); SW = stem weight (kg); GMY = green matter yield (g); DMY = dry matter yield (g); ST = plant stand; PH = plant height (m); PNW = panicle weight (g), PL = panicle length (cm); DM = dry matter content (%) and FM = forage mass (kg ha^{-1}).

The measurement units were estimated for each plot

Thereby, it was possible to observe a very high heritability magnitude for the following variables: SW (90.69 %); PH (89.75 %); LW (87.61 %); PW (87.44 %); ST (86.32 %); PNW (86.32 %); SD (80.87 %) and DM (79.51 %). Conversely, low magnitude values were observed for the variables: DMY (11.84 %); FM (12.66 %); PL (41.71 %) and GMY (64.45 %). Santosh et al. (2020) found a very high heritability for plant height when assessing yield characteristics on forage sorghum genotypes. High heritability values are often related to lower environmental influence (Araújo et al., 2014). According to Tabosa et al. (2016), the heritability values over 70 % indicate the possibility of success in selecting promisor genotypes since the results of the relative heritability estimate provide the necessary knowledge on the relative magnitude of genetic and environmental variations.

The coefficient of genetic variation (CVg) and the CVg/CVe ratio are parameters used to quantify the available genetic variability of a population when the intention is to estimate its potential aiming for genetic improvement, where the CVg indicates the proportion of gain regarding the average, in case of selection. Additionally, the CVg/CVe ratio suggests a favorable scenario for the selection (Araújo et al., 2014).

Thus, SW (51.30 %), LW (46.31 %), PW (38.56 %), ST (25.17 %), PNW (25.17 %), and GMY (20.70 %) showed better results, indicating that they are more suitable for immediate genetic gain due to their greater variability. Conversely, FM (16.51 %), SD (13.24 %), DM (12.41 %), PH (10.91 %), PL (6.99 %) and DMY (4.43 %) presented lower genetic values of coefficient of variation. Low values of CVg did not indicate that these variables would not have genetic gains but suggest that their gains likely will take more time, precisely for the low variability (Araújo et al., 2014).

According to Yokomizo et al. (2016), the methodology developed by Vencovsky & Barriga (1992) points out that CVg/CVe ratio greater than one (1), or near to this, is favorable to obtain immediate genetic gains, but only if the genetic variation overcome the environmental variable. Given that 96 % of all the studied variables presented coefficient values of genetic variation more significant than those of the experimental variation. This data made the genetic variation suitable for obtaining genetic gains.

Regarding the values of the CVg/CVe ratio, the results of SW (1.80), PH (1.72), PW (1.52), ST (1.45), PNW (1.45), SD (1.18) and DM (1.13) showed indexes over one (1), in concordance with the greater values of heritability. According to Souza et al. (2013), results greater than one indicate good perspectives for genetic gain through the selection of characters.

Phenotypic, genotypic, and environmental correlation coefficients were estimated from the analysis of covariance, combining the data from all variables (12).

Concerning the coefficients of phenotypic (*r*P) and genotypic (*r*G) correlations, the dissimilarity between some variable pairs was present considering the sign and the magnitude (Table 5). Because of this dissimilarity, phenotypic correlations were analyzed in detail.

In 96.9 % of total variable pairs, the phenotypic correlations were equal to or higher than genotypic ones. Likewise, 96.9 % of the results were more significant than the environmental correlations. In addition, it was verified that in 66 possible combinations for 12 analyzed variables, no environmental correlations were more remarkable

Table 5: Estimation of phenotypic (*r*P), genotypic (*r*G) and environmental (*r*E) correlation coefficients among twelve variables assessed on forage sorghum genotypes. Graccho Cardoso – SE, 2019.

Variables	*r*	LW	PW	SW	GMY	DMY	ST	PH	PNW	PL	DM	FM
	P	0.32	0.39*	0.44*	0.27	0.13	0.55**	0.56*	0.55**	0.77**	-0.31	0.36
SD	G	0.19	0.18	0.19	0.20	0.18	0.19	0.19	0.19	-0.46	0.19	0.19
	E	0.07	-0.06	-0.06	-0.08	-0.06	-0.07	-0.06	-0.07	-0.04	-0.07	-0.07
	P		0.90**	0.90**	0.63**	0.34	0.06	0.51	0.06	0.39	0.69**	0.79**
LW	G		0.18	0.19	0.20	0.18	0.19	0.19	0.19	-0.46	0.19	0.19
	E		-0.06	-0.06	-0.08	-0.06	-0.07	-0.06	-0.07	-0.04	-0.07	-0.07
	P			0.98**	0.67**	0.41*	0.05	0.64	0.05	0.36	0.74**	0.93**
PW	G			0.18	0.19	0.17	0.18	0.18	0.18	-0.47	0.18	0.18
	E			-0.06	-0.08	-0.05	-0.06	-0.06	-0.06	-0.00	-0.06	-0.06
	P				0.69**	0.41*	-0.03	0.72**	-0.03	0.39	0.76**	0.88**
SW	G				0.20	0.18	0.19	0.19	0.19	-0.46	0.19	0.19
	E				-0.08	-0.06	-0.07	-0.06	-0.06	-0.04	-0.06	-0.06
	P					0.87**	-0.23	0.50	-0.23	0.18	0.93**	0.44*
GMY	G					0.18	0.20	0.19	0.20	-0.45	0.20	0.20
	E					-0.07	-0.08	-0.08	-0.08	-0.02	-0.08	-0.08
	P						-0.10	0.31	-0.10	-0.05	0.68**	0.26
DMY	G						0.18	0.17	0.18	-0.45	0.18	0.18
	E						-0.06	-0.05	-0.06	-0.03	-0.06	-0.06

...to be continued

...Continuation

Table 5: Estimation of phenotypic (*r*P), genotypic (*r*G) and environmental (*r*E) correlation coefficients among twelve variables assessed on forage sorghum genotypes. Graccho Cardoso – SE, 2019.

Variables	*r*	LW	PW	SW	GMY	DMY	ST	PH	PNW	PL	DM	FM
	P							-0.25	0.98**	0.54**	0.30*	0.22
ST	G							0.19	0.20	-0.46	0.19	0.19
	E							-0.06	-0.07	-0.04	-0.07	-0.07
	P								-0.25	0.36*	-0.57	0.55
PH	G								0.19	-0.46	0.19	0.19
	E								-0.06	-0.05	-0.06	-0.06
	P									-0.54*	0.30	0.22
PNW	G									-0.46	0.19	0.19
	E									-0.05	-0.07	-0.07
	P										-0.32	0.30
PL	G										-0.46	-0.46
	E										-0.05	-0.05
	P											-0.50*
DM	G											0.19
	E											-0.07

** and * significant at 1 % and 5 % of probability by T test. SD = stem diameter; LW = leaf weight; PW = plants’ weight; SW = stem weight; GMY = green matter yield; DMY = dry matter yield; ST = stand; PH = plant’s height; PNW = panicle weight, PL = panicle length; DM = dry matter content and FM = forage mass.

than genotypic variables.

Regarding the environmental correlation, 11 variable pairs showed values lower than 0.5. When variable pairs present correlation coefficients lower than 0.5, there is a contribution of genetic factors regarding the environmental ones (Santosh et al., 2020). However, variable pairs with an environmental correlation over 0.5 are more influenced by the environment.

Coefficients of Pearson's correlation were classified as weak (*r* from 0.10 to 0.30), moderate (*r* from 0.40 to 0.60), or strong (*r* from 0.70 to 1) (Oliveira et al., 2021).

The SD showed a strong and positive phenotypic correlation with PL. That is, plants with greater stem diameter are favorable to present greater panicles. The LW presented a strong and positive phenotypic correlation with PW (0.90), PL (0.90), and FM (0.79). Thereby, plants with heavier leaves produce heavier stems and have a greater forage mass.

The PW presented a strong positive phenotypic correlation with the SW (0.98). Consequently, heavier plants present heavier stems. Conversely, the PW presented a negative genotypic correlation with the DM (-0.74). According to Guimarães (2014), genotypes with a lower dry matter content indicate that these plants have mechanisms to reduce water losses, which are characteristics associated with the capacity of forage sorghum for tolerance regarding longer dry seasons.

The SW presented a strong and positive phenotypic correlation with the PH (0.72) and the FM (0.88). However, as the PW, SW presented a considerable negative correlation with the DM (-0.76); thus, genotypes with heavier stems tend to be taller, more productive, and have lower dry matter content. These results suggest that plants with heavier stems tend to have a greater moisture content, influencing silage fermentation (Basso et al., 2012).

The GMY presented a strong and positive phenotypic correlation with the DMY (0.87) and a negative correlation with the DM (-0.93). Regarding the GMY, the negative correlation with DM was already expected because it is necessary to remove all moisture content to obtain the dry matter content.

The ST presented a strong and positive phenotypic correlation with PNW (0.98). Thus, the greater the stand formation, the heavier the panicles. The SD presented a positive but weak correlation with GMY (0.27) and DMY (0.13). Thus, these variables are not strongly influenced by the stem diameter.

The GMY presented a weak and positive correlation with the PL (0.18). Likewise, its correlation with ST and PNW, both valued at -0.23. Contrary, the DMY presented a weak and positive correlation with FM (0.26) and showed weak and negative correlations with ST and PNW (-0.10). Based on these results, the green and dry matter yields are slightly influenced by the panicle length and forage mass, respectively.

The PH presented a weak and negative correlation with the PNW (-0.25). Thus, how heavier the plant, how heavier the panicle will be. According to Araújo et al. (2014), the reduction of panicle size occurs due to the water deficit, mainly in the plants' flowering and maturity stages.

The ST presented a weak and positive correlation with DM (0.30) and FM (0.22), besides a negative correlation with the PH (-0.25). Thus, the stand of plants has a low influence on the dry matter yield of the forage mass. Moreover, how greater the stand formation, the shorter the plants will be due to the great competition among plants for nutrients and water.

The PL and PNW variables showed weak

and positive correlations with FM (0.30), DM (0.30), and FM (0.22), respectively. PL and PNW present little influence on the forage quality and production due to their low correlations with FM and DM. The panicle proportion in the silage composition modifies the final quality (Behling Neto et al., 2017; Paziani et al., 2019).

Regarding the path analysis, when the path coefficient (direct effect) from an explicative variable is lower than the effect of a residual variable, but the correlation coefficient (total effect) is more significant than this residual effect (in the module); this explicative variable influences the primary variable only indirectly. Thus, its importance occurs only in-group. Contrary, if the path coefficient is greater than the residual variable (in the module), there is a direct effect of the explicative variable on the primary one (Souza, 2013).

Determination coefficients for the path analysis models presented greater values, suggesting that the assessed variables explain 80% of phenotypic variation on the F.M. (Table 6).

According to the path analysis, the P.W. was the component with the most significant direct effect on FM (0.54) and showed the most remarkable total positive correlation (0.93). Therefore, the plants' weight must be indicated for the indirect selection of forage sorghum genotypes with great F.M. due to the difficulty of measuring F.M. because this variable depends on others.

The second and the third components, which had more significant total effects on the FM, were LW (0.79) and PH (0.55), respectively. Thus, taller genotypes with heavier leaves consequently will be

Table 6: Estimation of direct (in black and diagonal) and indirect effects of the explain variables on the forage mass, from 25 genotypes of forage sorghum. Graccho Cardoso – SE, 2019.

Variables	Direct and indirect effects							
	SD	**LW**	**PW**	**GMY**	**DMY**	**ST**	**PH**	**PNW**
SD	**0.15**	0.05	0.06	0.04	0.02	-0.08	0.08	-0.08
LW	0.05	**0.17**	0.15	0.11	0.06	0.01	0.09	0.01
PW	0.21	0.49	**0.54**	0.36	0.22	0.02	0.34	0.02
GMY	-0.01	-0.02	-0.03	**-0.04**	-0.04	0.01	-0.02	0.01
DMY	-0.00	-0.00	-0.00	-0.00	**-0.00**	0.00	-0.00	0.00
ST	-0.07	0.00	0.00	-0.03	-0.01	**0.13**	-0.03	0.13
PH	0.05	0.05	0.06	0.05	0.03	-0.02	**0.10**	-0.02
PNW	-0.07	0.00	0.00	-0.03	-0.01	0.13	-0.03	**0.13**
Total	0.36	0.79	0.93	0.44	0.26	0.22	0.55	0.22
Determination coefficient								0.80
Constant K								0.23
Residual effect								0.44

more productive, with greater forage mass.

The moderate correlation between GMY and FM only could be observed when the GMY was grouped with other variables because its direct effect on the FM was negative (-0.04). Other components had very slight phenotypic direct effects, most of which were near zero.

Conclusions

The variables SW, PH, LW, PW, ST, PNW, SD, and DM presented good perspectives regarding the genetic gain for selection.

The PW was the component with the most remarkable and favorable direct effect on forage mass. Moreover, it had the most outstanding contribution to increasing this target variable. Therefore, heavier plants are more suitable for indirect selection for forage mass increase.

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