

## Genetic parameters and selection for multiple traits in sorghum for forage purposes

José Maurílio Moreira de Figueiredo Júnior<sup>1</sup>, Rafael Augusto da Costa Parrella<sup>2</sup> and Jose Airton Rodrigues Nunes<sup>1\*</sup>

Crop Breeding and Applied Biotechnology  
24(2): e48122429, 2024  
Brazilian Society of Plant Breeding.  
Printed in Brazil  
<http://dx.doi.org/10.1590/1984-70332024v24n2a22>

**Abstract:** We aimed to estimate genetic parameters and select sorghum lines for forage purposes based on agronomic and chemical traits. A total of 100 inbred lines, comprising the biomass/bmr, biomass, dual purpose (sweet/forage), and forage types, were evaluated in the 2020/2021 and 2021/2022 crop years. We analyzed the data using a linear mixed model approach. Genetic variance, line mean-based heritability, selection accuracy, genetic correlation between traits and crops and the coefficient of experimental variation were estimated. The breeding values of the lines were predicted, and the factor analysis and genotype-ideotype distance index based on BLUP (FAI-BLUP) were applied for multi-trait selection. Biomass production and cell wall composition traits were measured. There was genetic variation among the lines, with moderate to high heritability. The lines selected by the FAI-BLUP index resulted in significant genetic gains expected with selection for all traits.

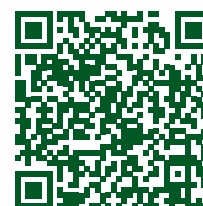
**Keywords:** Sorghum bicolor (L.) Moench, brown midrib, variance components, correlated response, selection gain

### INTRODUCTION

Brazil has the largest commercial cattle herd in the world, with approximately 190 million head, and is the leader in meat exports (ABIEC 2021). This scenario results in a significant demand for forage to supply the meat production chain throughout the year, as well as the need to store forage. Currently, corn (*Zea mays* L.) is a crop widely used in silage production. However, alternative crops adapted to different environmental conditions are needed (Rossi et al. 2015).


Compared with corn, forage sorghum (*Sorghum bicolor* (L.) Moench) has favorable agronomic and chemical traits for adequate ensiling, such as high fresh and dry mass yields and a high concentration of soluble carbohydrates that confer adequate fermentation quality and result in silage with high nutritional value, yielding high animal production gains (Rosa et al. 2022). Additionally, sorghum has well-defined phytotechnical management practices, such as fully mechanized cultivation, seed planting and high resistance to major pests and diseases and has adapted to different regions and climatic conditions (Oliveira et al. 2019, Rosa et al. 2022).

The use of sorghum to increase the forage supply depends on certain factors, including the development of cultivars by breeding programs. During the breeding process, it is important to determine the potential of the genotypes



\*Corresponding author:

E-mail: [jarnunes@ufla.br](mailto:jarnunes@ufla.br)

 ORCID: 0000-0002-6260-7890

Received: 12 January 2024

Accepted: 07 March 2024

Published: 15 March 2024

<sup>1</sup> Universidade Federal de Lavras, Trevo Rotatório Professor Edmir Sá Santos, 37203-202, Lavras, MG, Brazil

<sup>2</sup> Embrapa Milho e Sorgo, Rodovia MG 424, km 45, Zona Rural, 35701-970, Sete Lagoas, MG, Brazil

that could be used as parents or even released on the market (Gomes et al. 2020). Furthermore, it is especially important to estimate the genetic parameters that guide breeders' decisions regarding the main target traits of breeding, such as heritability, correlation, and selection accuracy (Resende and Alves 2020).

The target traits of sorghum breeding for forage purposes are related to biomass production and forage quality (Cunha and Lima 2010, Von Pinho et al. 2022). The selection of genotypes based on these multiple agronomic (e.g., biomass production) and chemical (e.g., cell wall components, such as cellulose, hemicellulose and lignin contents) traits should account for the existing correlations. This allows for the prediction of the impact and applicability of indirect selection, as well as possible challenging aspects of the process of selecting superior genotypes based on multiple traits (Ramalho et al. 2012).

The selection index is a strategy often employed in the simultaneous selection of traits. Several selection indices have been used in sorghum breeding (Oliveira et al. 2019, Botelho et al. 2021). The factor analysis and genotype-ideotype distance index based on BLUP (FAI-BLUP) has several advantages, such as considering the interrelationship of traits, addressing multicollinearity, and delimiting selection based on ideotypes (Rocha et al. 2017). Thus, we aimed to estimate genetic parameters and select sorghum lines for forage purposes based on multiple agronomic and chemical traits.

## **MATERIAL AND METHODS**

### **Experimental sites**

The experiments were conducted in 2020/2021 and 2021/2022 crop years at the Embrapa Maize and Sorghum experimental area (lat 19° 27' 57" S, long 44° 14' 49" W, alt 767 m asl) in Sete Lagoas, Minas Gerais State, Brazil. The mean annual temperature is approximately 23 °C, and the mean annual rainfall is 1,400 mm. The climate is classified as highland tropical (Cwa) on the Köppen scale. The soil type is Red Oxisol.

Daily climatic data, including precipitation and minimum, average and maximum temperature, during the experimental period (from sowing to harvest) in both crop years were obtained from the INMET meteorological station and are presented in Figure 1.

### **Lines evaluated**

A total of 100 sorghum lines of different types were evaluated: 12 biomass/bmr (brown-midrib) type lines (coded from 1 to 12), 40 biomass type lines (coded from 13 to 52), 1 sweet/forage dual purpose type line (coded 63), and the remaining 47 forage type lines. These lines are potential parents for obtaining hybrids or cultivars for forage purposes in the sorghum breeding program at Embrapa Maize and Sorghum.

### **Planning and management of experiments**

The experiments were conducted in an area under no-tillage. At presowing, the area preparation consisted of desiccating the weeds with the 2-4-D NORTOX® and Round Up® herbicides and mowing. Furrowing, sowing, and planting fertilization were performed using a seeder. The experimental design was a 10 × 10 square lattice with three replicates. The plot consisted of two 5.0-m rows spaced 0.70 m apart. A total of 420 kg ha<sup>-1</sup> of 8:28:16 formulated NPK fertilizer was applied. Twenty days after plant emergence, manual thinning was performed to adjust the initial ideal population to 140,000 plants ha<sup>-1</sup>, with 10 plants per linear meter. Topdressing fertilization with 250 kg ha<sup>-1</sup> urea was applied 30 days after sowing. Weeds were controlled by applying an Atrazine®-based herbicide at a dose of 3.0 kg ha<sup>-1</sup> of the active ingredient.

In 2020/2021 crop year, the experiment was sown on December 9, 2020, and harvested on April 23, 2021, while in 2021/2022, it was sown on December 10, 2021, and harvested on April 7, 2022. In both crop years the harvest was carried out using a Wintersteiger Cibus S® harvester, which grinds, weighs and homogenizes all the plants in each plot.

### **Agronomic and chemical trait measurements**

The following agronomic traits were measured in both crop years: fresh mass yield (FMY, t ha<sup>-1</sup>) – the plants in each plot were harvested, crushed, and weighed using a mechanical harvester; dry mass percentage (DM, %) – a sample of

approximately 500 g of ground forage was taken, and the initial mass (IM) was recorded. This sample was predried in a forced ventilation oven at 65°C for 72 hours and kept at room temperature for two hours, after which the final mass of the oven-dried sample (FM) was recorded. DM was calculated by the following expression:  $DM = \left[ \frac{(IM - FM)}{IM} \right] \times 100$ . The dry mass yield (DMY, t ha<sup>-1</sup>) was estimated according to the expression  $DMY = FMY \times \frac{DM}{100}$ .

The chemical traits were measured in both crop years at the Laboratory of Chemical Analysis of Plants of Embrapa Maize and Sorghum using near infrared spectrometry (NIR) equipment (Guimaraes et al. 2014). The following chemical traits related to cell wall composition (expressed as percentages) were measured: neutral detergent fiber (NDF), acid detergent fiber (ADF), cellulose (CEL), hemicellulose (HMC) and lignin (LIG).

### Statistical analyses

We analyzed the data using a linear mixed model approach (Henderson 1984). The variance components were estimated by the residual maximum likelihood method, and significance was assessed by the likelihood ratio test at 5% probability. BLUE (best linear unbiased estimator) estimates of the fixed effects and BLUP (best linear unbiased predictor) predictions of the random effects were also obtained.

Analyses were performed individually per crop year using the lme4 R package (Bates et al. 2015) in R software (R Core Team 2022) according to the following statistical model:  $y = 1\mu + X_r\beta_r + Z_bu_b + Z_gu_g + e$ , where  $y$  is the  $n \times 1$  vector of phenotypic data for each crop year;  $\mu$  is the intercept;  $\beta_r$  is the  $r \times 1$  vector of the fixed effects of replicates; and  $u_b$  is the  $b \times 1$  vector of the random effects of blocks within the replicates, with  $u_b \sim N(0, I_b\sigma_b^2)$ .  $I_b$  is an identity matrix of order  $b$ ,  $\sigma_b^2$  is the variance component of the blocks within replicates, and  $u_g$  is the  $g \times 1$  vector of the random effects of lines, with  $u_g \sim N(0, I_g\sigma_g^2)$ .  $I_g$  is an identity matrix of order  $g$ , where  $g$  is the number of lines,  $\sigma_g^2$  is the variance component of the lines, and  $e$  is the  $n \times 1$  vector of errors, with  $e \sim N(0, I_n\sigma_e^2)$ .  $I_m$  is an identity matrix of order  $n$ ,  $\sigma_e^2$  is the variance component of the errors,  $1$  is the  $n \times 1$  vector of 1's,  $X_r$  is the  $n \times r$  design matrix associated with  $\beta_r$ ,  $Z_b$  is the  $n \times b$  design matrix associated with  $u_b$ , and  $Z_g$  is the  $n \times g$  design matrix associated with  $u_g$ .

The joint analysis of the crop years was performed using the Sommer R package (Covarrubias-Pazaran 2016, 2018) according to the following statistical model:  $y = 1\mu + X_s\beta_s + X_r\beta_r + Z_bu_b + Z_gu_g + e$ , where  $y$  is the  $N \times 1$  vector of phenotypic data across crop years;  $\mu$  is the intercept;  $\beta_s$  is the  $s \times 1$  vector of fixed crop year effects;  $\beta_r$  is the  $r \times 1$  vector of the fixed effects of replicates within crop years; and  $u_b$  is the  $b \times 1$  vector of the random effects of blocks within the replicates in the crop years, with  $u_b \sim N(0, I_b\sigma_b^2)$ .  $I_b$  is an identity matrix of order  $b$ ,  $\sigma_b^2$  is the variance component associated with the effect of blocks within replicates in the crop years, and  $u_g$  is the  $g \times 1$  vector of the random effects of lines within each crop year, with  $u_g \sim N(0, \Sigma_s \otimes I_g)$ .  $\Sigma_s$  is an unstructured variance-covariance matrix among lines across crop years;  $I_g$  is an identity matrix of order  $g$ ;  $\otimes$  is the Kronecker product; and  $e$  is the  $N \times 1$  vector of errors, with  $e \sim N(0, D_e)$ .  $D_e$  is a diagonal matrix expressing the heterogeneity of the error variances in the two crop years given by  $D_e = \bigoplus_{i=1}^2 \sigma_{e_i}^2$ , where  $\bigoplus$  is the direct sum of the matrices and  $\sigma_{e_i}^2$  is the error variance in each crop year  $i$ .  $1$  is the  $N \times 1$  vector of 1's;  $X_s$  is the  $N \times s$  design matrix associated with  $\beta_s$ ;  $X_r$  is the  $N \times r$  design matrix associated with  $\beta_r$ ;  $Z_b$  is the  $N \times b$  design matrix associated with  $u_b$ ; and  $Z_g$  is the  $N \times g$  design matrix associated with  $u_g$ .

From the individual and joint analyses, the following parameters were additionally estimated: selection accuracy on the line-mean basis ( $r_{gg}$ ) per crop year, based on an estimator (Henderson 1984):  $r_{gg} = \sqrt{1 - \frac{PEV}{\hat{\sigma}_g^2}}$ , where  $PEV$  is the average of the prediction error variance associated with the BLUP of the line effect. The experimental coefficient of variation ( $CV_e$ ) per crop year was based on the following estimator (Pimentel-Gomes 2000):  $CV_e = \frac{\sqrt{\hat{\sigma}_e^2}}{\bar{y}}$ , where  $\bar{y}$  is the overall mean of the experiment in each crop year. The generalized heritability ( $h_L^2$ ) of Cullis et al. (2006) on a line-mean basis per crop year was obtained using the following estimator:  $h_L^2 = 1 - \left[ \frac{v_{BLUP}}{2 \times \hat{\sigma}_g^2} \right]$ , where  $v_{BLUP}$  is the average of the prediction error variance of the difference between the BLUPs of two lines. The genetic correlation between crop years ( $r_B$ ) was estimated by  $r_B = \frac{\sigma_{g_{12}}}{\sqrt{\sigma_{g_1}^2 \times \sigma_{g_2}^2}}$ , where  $\sigma_{g_1}^2$ ,  $\sigma_{g_2}^2$  are the genetic variances of lines in crop year 1 (2020/2021) and crop year 2 (2021/2022), respectively, and  $\sigma_{g_{12}}$  is the genetic covariance of lines between crop years 1 and 2. The genetic

correlations between traits  $t$  and  $t'$  ( $r_{g(t,t')}$ ) were estimated from the crop year mean-based BLUP predictions of the lines, and their significances were verified using nonparametric bootstrapping with the boot package in R software (Cathy and Ripley 2019).

The noncrossover and crossover parts related to the variance of the line  $\times$  crop year interaction were estimated ( $\hat{\sigma}_{g_c}^2$ ) according to the following expression by Robertson (1959):  $\hat{\sigma}_{g_1}^2 = \frac{1}{2}(\hat{\sigma}_{g_1}^2 - \hat{\sigma}_{g_2}^2)^2 + (1 - r_g)\hat{\sigma}_{g_1}^2\hat{\sigma}_{g_2}^2$ , where  $\frac{1}{2}(\hat{\sigma}_{g_1}^2 - \hat{\sigma}_{g_2}^2)^2$  is the noncrossover part of the line  $\times$  crop year interaction and  $(1 - r_g)\hat{\sigma}_{g_1}^2\hat{\sigma}_{g_2}^2$  is the crossover part.

From the BLUP predictions of the lines on the crop year-mean basis for all the measured traits, principal component analysis was performed using the prcomp function of the R package (R Core Team 2022). Additionally, a biplot was generated using the factoextra R package (Kassambara and Mundt 2017). The selection of the 15% best lines for forage purposes based on multiple agronomic and chemical traits was performed using the factor analysis and genotype-ideotype distance index based on BLUP (FAI-BLUP), as proposed by Rocha et al. (2017). This index-based approach was computed from the BLUPs of the lines on a crop year-mean basis using the metan R package (Olivoto and Lúcio 2020). The favorable ideotype was defined as that with increasing FMY, DM, and DMY and decreasing NDF, ADF, CEL, HMC and LIG. In contrast, the unfavorable ideotype was defined in the opposite direction, that is, as decreasing FMY, DM, and DMY and increasing the levels of the cell wall components NDF, ADF, CEL, HMC, and LIG.

The expected genetic gain with selection by the FAI-BLUP index,  $GS(\%)$ , was estimated based on the BLUPs of the top 15% of the selected lines by the following expression:

$GS(\%) = \frac{\overline{BLUP}_{s_t}}{\bar{y}_t} \times 100$ , in which  $\overline{BLUP}_{s_t}$  is the mean of the BLUPs of the lines selected by the FAI-BLUP index according to the 15% selection fraction for trait  $t$ ;  $\bar{y}_t$  is the general mean of trait  $t$ .

## RESULTS AND DISCUSSION

The traits related to biomass quality had lower Cve than biomass yield traits (Table 1). This is due to the greater influence of environmental factors on the expression of yield traits. The values of  $r_{gg}$  were very high for all traits in both crop years ( $\geq 0.9$ ), except for HMC in the 2021/2022 crop year (0.74). The values of  $r_{gg}$  indicated a favorable scenario for selection (Resende and Duarte 2007), as the genetic variances were significant (Table 1) and corroborated those reported by Oliveira et al. (2019).

The genetic variances ( $\sigma_g^2$ ) were significant ( $P < 0.05$ ) for all traits in both crop years (Table 1). The existence of genetic variation has also been reported in the evaluation of genotypes of different sorghum types, such as forage sorghum (Cunha and Lima 2010), sweet sorghum (Botelho et al. 2021, Pereira et al. 2022) and biomass sorghum (Oliveira et al. 2019).

The reliability of selection is directly related to heritability. In the 2020/2021 crop year, the heritability on a line-mean basis ( $h_g^2$ ) ranged between 81% (CEL) and 91% (DM), while in the 2021/2022 crop year, it ranged between 55% (HMC) and 96% (FMY) (Table 1). For HMC,  $h_g^2$  significantly varied from the 2020/2021 crop year (83%) to the 2021/2022 crop year (55%), which may have been caused by the line  $\times$  crop year interaction.

The crop year effect was significant for all traits except NDF (Table 1). In general, the climatic variables air temperature and precipitation presented similar variation patterns in both crop years when we considered the sorghum crop development stages (Figure 1). The greater means of the FMY, DM, DMY, ADF, LIG and CEL traits in the 2020/2021 crop year than in the 2021/2022 crop year may be more strongly associated with harvest time, as the 2020/2021 harvest was performed later (135 days) than the 2021/2022 harvest (117 days). Some of the tested lines are sensitive to photoperiod, especially those of the biomass type, and therefore, when performing the late harvest, they had greater biomass accumulation due to the longer vegetative period. In contrast, the tested photoperiod-insensitive lines had greater dry matter contents due to the early senescence process and moisture reduction.

There was a predominance of the noncrossover type of the line  $\times$  crop year interaction for the FMY, DM and DMY traits (Table 1). The genetic correlation between the crop years ( $r_b$ ) was close to 1.0 for these traits, indicating that there was no significant change in the ranking of the lines across crop years. However, for NDF, ADF, CEL, HMC and LIG, the percentage of the crossover type exceeded 78%, suggesting a significant change in the ranking of the lines across crop years (Table 1).

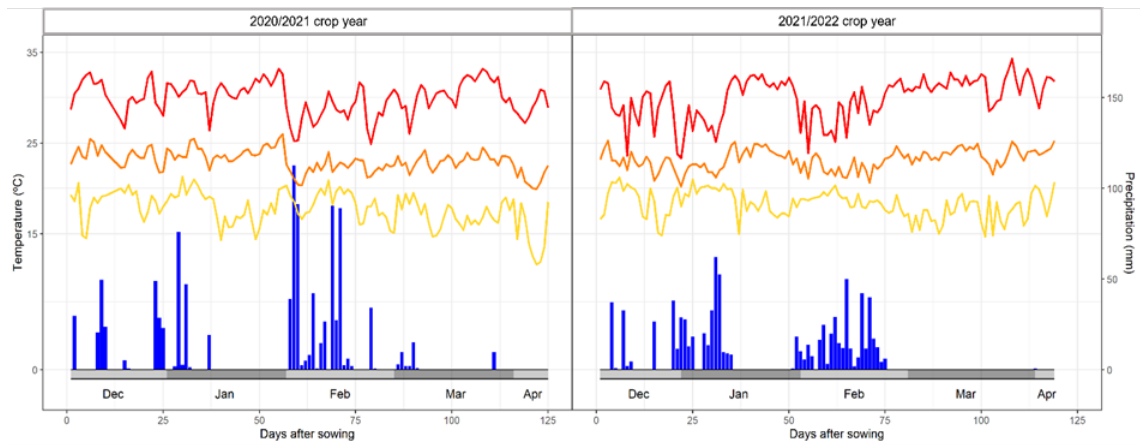
**Table 1.** Estimates of genetic and environmental parameters (parms) for the fresh mass yield (FMY, t ha<sup>-1</sup>), dry matter percentage (DM), dry matter yield (DMY, t ha<sup>-1</sup>), neutral detergent fiber (NDF, %), acid detergent fiber (ADF, %) cellulose (CEL, %), hemicellulose (HMC, %) and lignin (LIG, %) traits for the evaluation of sorghum lines in the 2020/2021 and 2021/2022 crop years

Parms	FMY	DM	DMY	NDF	ADF	CEL	HMC	LIG
<b>2020/2021 Crop Year</b>								
$\sigma_{g1}^2$	1098.44*	47.84*	86.74*	9.49*	4.67*	2.32*	1.20*	0.60*
$\sigma_{e1}^2$	366.34	13.42	36.68	5.04	2.60	1.55	0.73	0.27
$h_g^2$ (%)	90	91	87	84	84	81	83	86
$r_{gg}$	0.94	0.95	0.93	0.91	0.91	0.89	0.90	0.92
Mean	77	32	23	67	42	36	25	6
$CV_e$ (%)	25	11	26	3	4	4	3	8
<b>2021/2022 Crop Year</b>								
$\sigma_{g2}^2$	672.95*	13.84*	43.09*	7.49*	9.31*	6.61*	0.64*	0.38*
$\sigma_{e2}^2$	77.96	7.67	9.88	3.65	3.14	2.33	1.44	0.19
$h_g^2$ (%)	96	83	92	85	89	89	55	84
$r_{gg}$	0.97	0.91	0.96	0.92	0.94	0.94	0.74	0.91
Mean	71	28	20	67	34	30	32	5
$CV_e$ (%)	12	10	16	3	5	5	4	9
<b>Joint</b>								
$\sigma_{g1}^2$	1126.68*	47.56*	88.68*	9.34*	4.65*	2.35*	1.2*	0.59*
$\sigma_{g12}$	869.08*	22.77*	61.96*	6.73*	4.07*	2.01*	0.12	0.43*
$\sigma_{g2}^2$	672.62*	13.84*	43.24*	7.67*	9.38*	6.6*	0.67*	0.39*
$\sigma_{e1}^2$	358.75	13.48	35.95	5.04	2.61	1.58	0.72	0.28
$\sigma_{e2}^2$	77.91	7.85	9.90	3.71	3.18	2.30	1.47	0.20
$r_b$	1.00*	0.89*	1.00*	0.80*	0.62*	0.51*	0.14	0.90*
$\sigma_{sc}^2$	2593	7.94	3.78	1.75	2.90	2.47	0.80	0.06
% noncrossover	100	64	100	3	14	22	5	20
% crossover	0	36	0	97	86	78	95	80
<b>Mean (Minimum; Maximum)</b>								
Biomass	101 (98;103)	29.3 (28.8;30.0)	29.4 (28.4;30.3)	67.9 (67.5;68.3)	39.6 (39.3;39.9)	33.8 (33.6;34.1)	28.5 (28.4;28.6)	5.8 (5.7;5.9)
Biomass/bmr	62 (54;71)	28.6 (27.0;29.9)	18.0 (15.5;20.5)	66.2 (64.9;67.5)	37.4 (36.4;38.4)	32.5 (31.7;33.3)	28.8 (28.5;29.2)	4.9 (4.6;5.1)
Forage	57 (50;65)	31.0 (29;32.9)	16.3 (14.7;18.0)	66.23 (65.3;67.2)	37.3 (36.6;38.0)	31.8 (31.3;32.3)	28.8 (25.6;29.0)	5.5 (5.3;5.8)
Sweet/Forage	66	29.1	18.9	64.5	35.7	30.4	28.7	5.3
GS	15	-4	1	-5	-4	-3	-1	-1
GS (%)	20	-14	5	-7	-11	-9	-3	-20

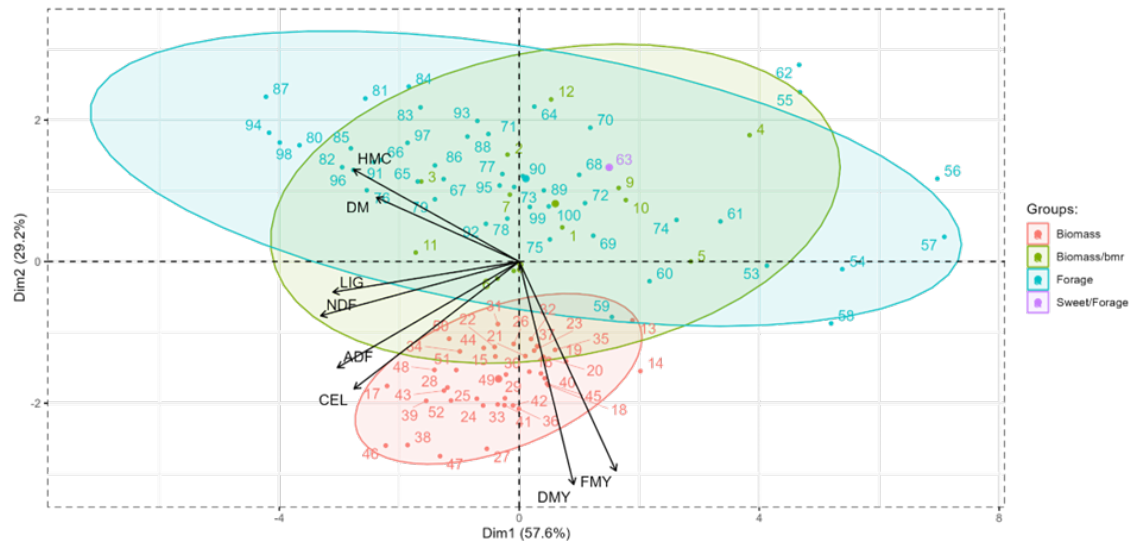
\* Significant at 5% probability according to the likelihood ratio test;  $\sigma_{g1}^2, \sigma_{g2}^2$ : genetic variance of lines in crop years 1 (2020/2021) and 2 (2021/2022);  $\sigma_{e1}^2, \sigma_{e2}^2$ : residual variance in crop years 1 (2020/2021) and 2 (2021/2022);  $\sigma_{g12}$ : genetic covariance between crop years;  $\sigma_{g1}^2$ : variance of the line  $\times$  crop year interaction;  $r_b$ : genetic correlation between crop years;  $h_g^2$ : generalized heritability of Cullis et al. (2006) on the line-mean basis per crop year;  $r_{gg}$ : selection accuracy;  $CV_e$ : coefficient of experimental variation; % noncrossover: percentage of the noncrossover type of line  $\times$  crop year interaction; % crossover: percentage of the crossover type of line  $\times$  crop year interaction; GS: expected genetic gain with the selection of the 15% best lines.

The genotype  $\times$  environment interaction is frequently reported in sorghum, such as in sweet sorghum (Pereira et al. 2022) and biomass sorghum (Oliveira et al. 2020, Castro et al. 2022). Oliveira et al. (2020) evaluated biomass sorghum hybrids over five crop years (2013/2014 to 2017/2018) and observed nonnull and high genetic correlations of genotypes across crop years for DMY. According to these authors, 65% of the correlation values were above 0.6, indicating a predominance of the noncrossover type of the genotype  $\times$  environment interaction.

For the selection of superior sorghum lines, breeders should account for agronomic traits related to biomass yield and chemical traits related to cell wall composition. Thus, an understanding of the correlation between traits is necessary, as it may impact gains from selection. According to the classification by Resende and Alves (2020), significant correlations can be considered high ( $r > 0.66$ ), intermediate ( $0.34 < r < 0.66$ ) and low ( $r < 0.34$ ).



**Figure 1.** Daily rainfall data and minimum, average and maximum temperatures during the growing period of the sorghum line evaluation experiments in the 2020/2021 and 2021/2022 crop years.



**Figure 2.** Biplot of the principal component analysis for the fresh mass yield (FMY,  $t\ ha^{-1}$ ), dry matter percentage (DM), dry matter yield (DMY,  $t\ ha^{-1}$ ), neutral detergent fiber (NDF, %), acid detergent fiber (ADF, %) cellulose (CEL, %), hemicellulose (HMC, %) and lignin (LIG, %) traits for the evaluation of sorghum lines in the 2020/2021 and 2021/2022 crop years.

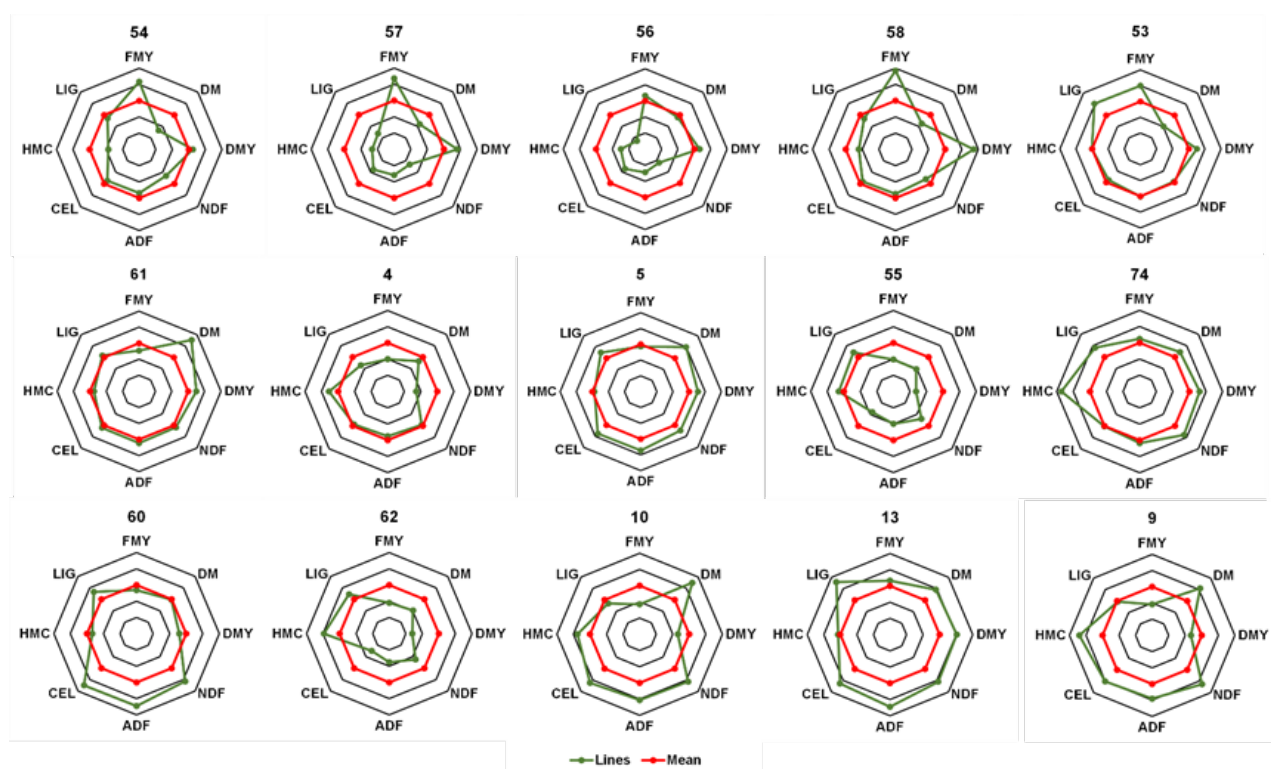
The genetic correlation between FMY and DMY was positive and of high magnitude (0.95). This result has also been reported in studies with forage sorghum (Cunha and Lima 2010) and biomass sorghum (Castro et al. 2015, Oliveira et al. 2020). From a practical point of view, there is, therefore, the possibility of performing indirect selection for DMY based on the FMY, providing flexibility in the selection with savings of resources and time.

There was a negative intermediate correlation between FMY and DM (-0.52), indicating that, in general, with the increase in FMY, there was a reduction in DM. This result was expected because the harvest was not performed when the DM was within the ideal harvest range. Under these harvesting conditions, the lines insensitive to photoperiod had greater DM, while the lines sensitive to photoperiod had greater fresh biomass accumulation and lower DM.

Regarding FMY and the chemical traits related to the cell wall composition, a negative and significant correlation was observed, classified as intermediate for HMC (-0.66) and low for LIG (-0.30) and NDF (-0.27), and for ADF and CEL, there was no correlation. These results show, in principle, that HMC was most negatively associated with FMY, i.e., that the proportion of HMC decreased with increasing FMY. In general, the cell wall constituents are little affected by the fresh mass yield. Rosa et al. (2022) and Rossi et al. (2015) noted that the NDF and ADF levels in forage sorghum stabilize or may decrease starting at the milky grain stage and are dependent on the amount of grains in the total weight and the leaf/stem ratio. The patterns of correlations between DMY and the other traits were similar to those observed for FMY.

The correlations between DM and chemical traits were generally positive and intermediate. The correlations between the cell wall components were positive and of intermediate to high magnitudes. NDF, ADF and CEL presented correlations above 0.9. The lignin content also showed high correlations (above 0.65) with the other components of the cell wall. High fibrous plant fractions are undesirable because they are negatively correlated with dry matter digestibility (Rossi et al. 2015, Magalhães et al. 2010). Furthermore, according to Paziani et al. (2019), when the proportion of grains in the total dry mass increases, the NDF and ADF contents are diluted, increasing the dry matter digestibility due to the greater participation of starch. Importantly, lines with high FMY and DMY tend to have a lower total mass/panicle ratio, interfering with dry matter digestibility in ruminants. In this sense, it is important to select lines with high levels of FMY and DMY and that have high grain participation, which can indirectly be selected for lower NDF and ADF values.

The first two axes of the principal component analysis based on the average BLUPs of the lines explained 86.8% of the variation in all the agronomic and chemical traits measured (Figure 2). The line by trait biplot confirms the correlations between the traits based on the cosines of the angles formed between the vectors, in which lower magnitude acute angles depict positive and high correlations, while angles close to 90° depict independent traits, and obtuse angles depict



**Figure 3.** Radar charts of the performance of the top 15% of the selected lines according to the FAI-BLUP index for the fresh mass yield (FMY,  $t\ ha^{-1}$ ), dry matter percentage (DM), dry matter yield (DMY,  $t\ ha^{-1}$ ), neutral detergent fiber (NDF, %), acid detergent fiber (ADF, %) cellulose (NEL, %), hemicellulose (HMC, %) and lignin (LIG, %) traits for the evaluation of sorghum lines in the 2020/2021 and 2021/2022 crop years.

negative and high correlations. In addition, Figure 2 shows the different profiles of the tested sorghum lines. Clusters were observed in the biplot, with an emphasis on the biomass sorghum lines that combined high FMY and DMY values and low DM and HMC levels, while the other biomass/bmr, forage and sweet/forage lines, in general, were characterized by high DM and HMC contents. Forage-type lines with a profile for high biomass production and low levels of cell wall components were also observed.

The FAI-BLUP index was used to select the 15% best lines. Lines with high biomass production and low levels of chemical traits were selected as the ideotype. According to the index, the lines selected in order were 54, 57, 56, 58, 53, 61, 4, 5, 55, 74, 60, 62, 10, 13 and 9, with line 13 being the biomass type; lines 4, 5, 9 and 10 being the biomass/bmr type; and the others being the forage type (Figure 3). Line 13 of the biomass type was characterized by high dry biomass production and cell wall component levels above the average of the selected lines. The biomass/bmr lines presented distinct profiles, with line 5 having a similar profile to that of the biomass line, while lines 4, 9 and 10 presented FMY and DMY values below average. Notably, lines 9 and 10 presented above average DM, NDF, ADF, CEL and HMC levels. Among the forage lines, 54, 56, 57 and 58 exhibited high FMY and DMY values and below average DM and cell wall component contents.

The expected genetic gains resulting from the selection of the 15% best lines were in the order of 20% for FMY, 5% for DMY and -14% for DM. The estimates of genetic gains for the cell wall components were negative, ranging from 3% (HMC) to 20% (LIG) (Table 1). Thus, targeting the desired ideotype resulted in positive effects on the agronomic traits of biomass yield and a reduction in DM and cell wall components. These results corroborate the advantages reported by Rocha et al. (2017) regarding the FAI-BLUP index, which include enabling selection for multiple traits based on ideotypes, mitigating the influence of multicollinearity, and leading to gains in the desired directions for all traits.

## ACKNOWLEDGMENTS

The authors thank FAPEMIG, CAPES and BNDES for the financial support; CNPq for the master's degree scholarship for the first author in the Graduate Program in Genetics and Plant Breeding at UFLA; a CNPq research grant 315748/2021 to the corresponding author; and Embrapa Maize and Sorghum for the infrastructure and support of the field and laboratory teams.

## REFERENCES

- ABIEC - Associação Brasileira das Indústrias Exportadoras de Carnes (2021) Beef report: perfil da pecuária no Brasil. Available at <<https://www.abiec.com.br/publicacoes/beef-report-2021/>>. Accessed on October 22, 2022.
- Bates D, Maechler M, Bolker B and Walker S (2015) Fitting linear mixed-effects models using lme4. *Journal of Statistical Software* **67**: 1-48.
- Botelho TT, Leite PSS, Parrella, RAC and Nunes JAR (2021) Strategies for multi-trait selection of sweet sorghum progenies Strategies for multi-trait selection of sweet sorghum progenies. *Crop Breeding and Applied Biotechnology* **21**: e388221410.
- Castro FMR, Bruzi AT, Nunes JAR, Parrella RAC, Lombardi GMR, Albuquerque CJB and Lopes M (2015) Agronomic and energetic potential of biomass sorghum genotypes. *American Journal of Plant Sciences* **6**: 1862-1873.
- Castro FMR, Lombardi GMR, Nunes JAR, Parrella RAC and Bruzi AT (2022) Accumulation of biomass and lignocellulosic compounds in photoperiod-sensitive biomass sorghum genotypes. *Biomass and Bioenergy* **158**: 106344.
- Cathy A and Ripley B (2019) **Boot: Bootstrap R (S-Plus) functions**. R package version 1.3-22.
- Covarrubias-Pazaran G (2016) Genome assisted prediction of quantitative traits using the R package sommer. *PLoS One* **11**: 1-15.
- Covarrubias-Pazaran G (2018) Software update: moving the R package sommer to multivariate mixed models for genome-assisted prediction. *BioRxiv* **1**: 1-14.
- Cullis BR, Smith AB and Coombes NE (2006) On the design of early generation variety trials with correlated data. *Journal of Agricultural, Biological and Environmental Statistics* **11**: 381-393.
- Cunha EE and Lima JMP (2010) Caracterização de genótipos e estimativa de parâmetros genéticos de características produtivas de sorgo forrageiro. *Revista Brasileira de Zootecnia* **39**: 701-706.
- Gomes LRDR, Menezes CB, Simon GA, Silva AG and Braz AJBP (2020) Combining ability of grain sorghum inbred lines grown during off-season. *Revista Caatinga* **33**: 888-897.
- Guimarães CC, MLF Simeone, RAC Parrella and MM Sena (2014) Use of NIRS to predict composition and bioethanol yield from cell wall structural components of sweet sorghum biomass. *Microchemical Journal* **117**: 194-201.
- Henderson CR (1984) **Applications of linear models in animal breeding**. University of Guelph, Guelph, 462p.



## Genetic parameters and selection for multiple traits in sorghum for forage purposes

- Kassambara A and Mundt F (2017) **factoextra: Extract and visualize the results of multivariate data analyses** (R package version 1.0.7). Available at <<https://CRAN.R-project.org/package=factoextra>>. Accessed on December 08, 2022.
- Magalhães RT, Gonçalves LC, Borges I, Rodrigues JAS and Fonseca JF (2010) Produção e composição bromatológica de vinte e cinco genótipos de sorgo (*Sorghum bicolor* (L.) Moench). **Arquivo Brasileiro de Medicina Veterinária e Zootecnia** **62**: 747-751.
- Oliveira I M, Guilhen JHS, Ribeiro PCO, Gezan SA, Schaffert RE, Simeone MLF, Damasceno CMB, Carneiro JES, Carneiro PCS, Parrella RAC and Pastina MM (2020) Genotype-by-environment interaction and yield stability analysis of biomass sorghum hybrids using factor analytic models and environmental covariates. **Field Crops Research** **257**: 107929.
- Oliveira ICM, Marçal TS, Bernardino KDC, Ribeiro PCO, Parrella RAC, Carneiro PCS, Schaffert RE and Carneiro JES (2019) Combining ability of biomass sorghum lines for agroindustrial characters and multitrait selection of photosensitive hybrids for energy cogeneration. **Crop Science** **59**: 1554-1566.
- Olivoto T and Lúcio ADC (2020) metan: An R package for multi-environment trial analysis. **Methods in Ecology and Evolution** **11**: 783-789.
- Paziani SDF, Duarte AP, Nussio LG, Freitas RS, Gallo PB and Mateus GP (2019) Correlações entre variáveis quantitativas e qualitativas de milho e de sorgo para silagem. **Revista Brasileira de Milho e Sorgo** **18**: 408-416.
- Pereira DA, Parrella RAC, Oliveira CRS and Nunes JAR (2022) Agroindustrial performance and heterosis in sweet sorghum using male-sterile lines with high stem sugar content. **Crop Breeding and Applied Biotechnology** **22**: e42342235.
- Pimentel-Gomes F (2000) **Curso de estatística experimental** **1**. Livraria Nobel, Piracicaba, 451p.
- R Core Team (2022) **R: A language and environment for statistical computing**. R Foundation for Statistical Computing. Available at <<https://www.r-project.org/>>. Accessed on December 08, 2022.
- Ramalho MAP, Abreu AFB, Santos JB and Nunes JAR (2012) **Aplicações da genética quantitativa no melhoramento de plantas autógamas**. UFLA, Lavras, 522p.
- Resende MDV and Alves RS (2020) Linear, generalized, hierarchical, Bayesian and random regression mixed models in genetics/genomics in plant breeding. **Functional Plant Breeding Journal** **3**: 121-152.
- Resende MDV and Duarte JB (2007) Precisão e controle de qualidade em experimentos de avaliação de cultivares. **Pesquisa Agropecuária Tropical** **37**: 182-194.
- Robertson A (1959) **Experimental design on the measurement of heritabilities and genetic correlation**. Biometrical genetics. Pergamon Press, New York, 186p.
- Rocha JRASC, Machado JC and Carneiro PCS (2017) Multitrait index based on factor analysis and ideotype-design: proposal and application on elephant grass breeding for bioenergy. **GCB Bioenergy** **10**: 52-60.
- Rosa MAB, Tardin FD, Souza JMS, Santos JAP, Macedo TF, Santos J, Freitas, MH, Todescato F, Parrella RAC, Figueiredo JEF, Behling Neto A and Pereira DH (2022) Characterization of forage, sweet and biomass sorghum for agronomic performance and ensilability. **Revista Brasileira de Milho e Sorgo** **21**: e1239.
- Rossi ES, Carletto R, Possatto Junior O, Neumann M and Faria MV (2015) Genetic improvement and quality parameters of sorghum silage (*Sorghum bicolor* L. Moench) in relation to maize silage (*Zea mays* L.). **Revista Brasileira de Tecnologia Aplicada nas Ciências Agrárias** **8**: 89-98.
- Von Pinho RG, Silva EVV, Oliveira TL, Souza VF and Menezes CB (2022) Breeding sorghum for grain, forage and bioenergy in Brazil. **Revista Brasileira de Milho e Sorgo** **22**: e1275.