Single- and multiple-trait BLUP in genetic selection of parents and hybrids of grain sorghum

BLUP mono y múltiple característica en la selección genética de parentales e híbridos de sorgo

Nadson Oliveira de Souza [1*], Rodrigo Silva Alves [1], Paulo Eduardo Teodoro [2], Lidiane Aparecida Silva [1], Flávio Dessaune Tardin [3], Aisy Baldoni Tardin [3], Marcos Deon Vilela de Resende [4], Leonardo Lopes Bhering [1]

ABSTRACT

To increase yield, breeding programs must search for innovative and efficient methodologies for the development and selection of superior genotypes. Therefore, this study aimed to compare the single- and multiple-trait best linear unbiased prediction (BLUP) in genetic selection of parents and hybrids of grain sorghum. For this, an experiment conducted in alpha-lattice design with two replications was used. Flowering time (FT), plant height (PH), and grain yield (GY) were evaluated in 502 grain sorghum hybrids obtained by the cross of ten restorer lines and 54 male-sterile lines. Variance components were estimated via restricted maximum likelihood (REML). Significant effects of restorer lines, of male-sterile lines, and of specific combining ability were detected by the likelihood ratio test (LRT). The estimates of variance components, genetic parameters, and correlations were similar when obtained via single- and multiple trait-BLUP. Considering hybrids, the multiple-trait BLUP resulted in slightly higher predicted selection gain for the three evaluated traits and, therefore, can be efficiently applied in the genetic selection of grain sorghum.

Keywords
plant breeding • partial diallel • mixed model methodology • genetic correlation • heterosis

1   Universidad Federal de Viçosa. Departamento de Biología General. Viçosa. Minas Gerais. Brasil. * nadson.zootecnia@gmail.com
2   Universidad Estatal de Mato Grosso do Sul. Departamento de Ciencia de las Plantas. Chapadão do Sul. Mato Grosso do Sul. Brasil
3   Embrapa Maize and Sorghum. Sinop. Mato Grosso. Brasil
4   Universidad Federal de Viçosa. Departamento de Estadística. Viçosa. Minas Gerais. Brasil

Resumen

Para incrementar el rendimiento, los programas de mejoramiento deben buscar metodologías innovadoras y eficientes para el desarrollo y la selección de genotipos superiores. De esta forma, este estudio tuvo como objetivo comparar la mejor predicción lineal no viciada (BLUP) mono y múltiple característica, en la selección genética de parentales e híbridos de sorgo granelero. Para esto, fue usado un experimento con diseño alfa latice con dos repeticiones. Se evaluó el tiempo de floración (FT), la altura de planta (AP) y el rendimiento de granos (GY) en 502 híbridos de sorgo, obtenidos por el cruzamiento entre diez líneas restauradoras y 54 líneas macho estériles. Los componentes de varianza se estimaron mediante el método de máxima verosimilitud restringida (REML). Observamos que varias veces el BLUP múltiple característica da como resultado estimaciones de correlación genética más precisas. En este trabajo, se encontraron mayores correlaciones entre FT y GY a través de BLUP múltiple característica. Estos resultados llevaron a mayores ganancias genéticas para la selección de híbridos en comparación con BLUP mono característica.

Palabras clave
fitomejoramiento • dialelo parcial • modelos mixtos • correlación genética • heterosis

Introduction

Grain sorghum (*Sorghum bicolor* L. Moench) is among the five most widely cultivated species in the world. This crop stands out for its several uses, such as biomass, ethanol production, grains, fertilizers, and fiber (19). The high efficiency in solar energy conversion and water use are factors that favored the expansion of sorghum cultivation (16), enabling it develop in environments with low rainfall and high temperatures, such as the semiarid regions.

Aiming at increasing yield, grain sorghum has undergone modifications related to the genetic architecture, which has resulted in the development of early cultivars with high grain yield (4), and ideal plant height for harvest. Despite being less effective in autogamous than in allogamous species, the heterosis effect is widely explored in grain sorghum breeding programs. Thus, studies that address heterosis in sorghum have been reported in the literature, especially for traits related to grain yield (14, 24). Moreover, plant height and flowering time are target traits in grain sorghum breeding programs for they allow the early selection of more promising lines and with ideal height for mechanized harvesting. According to Silva *et al.* (2009), genotypes that present shorter height, associated with greater stem resistance, had less susceptibility to lodging or plant breakage. For grain sorghum, plant height should be between 100 and 150 cm (3), since sorghum harvesting uses adaptations of machines normally used for corn or soybeans, which operate in this height range. Improvement grain yield is associated with undesired increase in plant height and late flowering time (10).

Furthermore, in an effort to develop a suitable method for genetic evaluation,

Henderson (1975) proposed the best linear unbiased prediction (BLUP) to predict random effects, by adjusting the data to fixed effects. The empirical BLUP assumes that the values of the variance components estimated by the restricted maximum likelihood (REML) are true. Thus, the REML/BLUP is the standard procedure used to estimate variance components and to predict genetic values in plant breeding (21).

Currently, the single-trait BLUP has been widely used in genetic selection of grain sorghum. However, when the traits present genetic and residual correlations, the multiple-trait BLUP can be more accurate, as demonstrated by Viana *et al.* (2010). Therefore, the genetic evaluation via multiple-trait BLUP is considered as more efficient when traits are correlated, resulting in a lower mean bias than that of the single-trait BLUP (17, 18). This methodology is commonly used in animal breeding (9) and has been successfully applied to plant breeding (18, 29). Therefore, this study aimed to compare the single- and multiple-trait BLUP in genetic selection of parents and hybrids of grain sorghum.

Material and methods

Experimental data

The experiment consisted of a performance evaluation of 502 grain sorghum hybrids in the 2011/2012 season at Embrapa Agrosilvopastoral (lat. 55°36' W, long. 11°51' S,

alt. 307 m a. s. l.), in Sinop/MT, Brazil. The hybrids were obtained by the cross of ten restorer lines and 53 male-sterile lines from the breeding program of Embrapa Maize and Sorghum. Due to the low pollen production of some restorer lines, there was imbalance in crosses, with loss of 38 hybrids (*).

Due to the large number of hybrids to be evaluated, the experimental design adopted was alpha-lattice design 42x12 with two replications. That is, each of the two replication of lattice were composed of 42 replicates and in each replicate 12 hybrids were evaluated, totalizing 504 plots in each of the two lattices. As their efficiency was low (<2%) for all traits, each lattice repetition was considered to a complete block (includes all treatments), and the usual model was used for analysis of complete randomized blocks, based in recommendations of Cochran and Cox (1957). Each plot consisted of two five-meter rows, spaced at of 0.50 m between rows. Planting fertilization and topdressing were carried out according to soil analyses. Cultural and phytosanitary treatments were performed based on the crop needs.

The evaluated traits were: flowering time (FT) (number of days from the emergence to when 50% of the plants in the plot reached the flowering stage); plant height (PH) (mean height of two plants of the useful area of the plot, measured from the soil surface to the apex of the panicle, at harvest time); and grain yield (GY) (corrected to 13% moisture and extrapolated to kg ha^{-1}).

---

* Identification of the two selected restorer lines (RL), of the eight selected male-sterile lines (ML), and the 25 hybrids selected for the traits flowering (FL), plant height (PH), and grain yield (GY), evaluated in 502 grain sorghum hybrids via single- and multiple-trait BLUP.

* Identificación de las dos líneas restauradoras selecionadas (RL), de las ocho líneas macho estériles (ML) seleccionadas y de los 25 híbridos seleccionados, para las características floración: (FL), altura de planta (PH) y rendimiento de grano (GY), evaluadas en 502 híbridos de sorgo vía BLUP mono y múltiple característica.

Statistical analyses

The REML/BLUP procedure was performed to estimate the variance components and to predict the genetic values, according to Resende *et al.* (2014). The statistical model associated with the evaluation of hybrids, obtained by partial diallel crosses, in a randomized block design, with one observation per plot, is given by:

$$y = Xr + Zm + Wf + T + e. \qquad (1)$$

where:

y = the observation vector

r = the vector of replication effects (assumed as fixed) summed to the general mean

m = the vector of the effects of the restorer lines (assumed as random)

f = the vector of the effects of male-sterile lines (assumed as random)

c = the vector of the effects of specific combining ability of restorer lines with the male-sterile lines (random)

e = the vector of residues (random)

X, Z, W, and T = the incidence matrices for the referred effects.

For the random effects of the model, significance for the likelihood ratio test (LRT) was tested using Chi-square statistics with one degree of freedom according to Resende (2014).

Accuracies were estimated using the single- and multiple-trait BLUP, based on the expression:

$$r_{\hat{a}a}^2 = \sqrt{(\sigma_a^2 - PEV) / \sigma_a^2} \qquad (2)$$

where:

σ_a^2 = estimator of the additive genetic variance

PEV = prediction error variance.

To estimate the genetic covariance via single-trait BLUP, individual analyses and the analysis of the sum of the values of traits were performed pair-to-pair so that the covariances were estimated based on the equation:

$$(3)$$

$$\sigma_{g(trait_i+trait_j)} = \frac{\sigma_{g(trait_i+trait_j)}^2 + \sigma_{g(trait_i)-\sigma_{g(trait_i)}^2}^2}{2}$$

where:

$\sigma_{g(trait_i+trait_j)}$ = estimate of the genetic covariance between trait *i* and trait *j*

$\sigma_{g(trait_i)}^2$ = estimator of the genetic variance to trait *i* and trait *j*, respectively.

The genetic correlation coefficients (ρ) between the traits FT, PH, and GY for restorer lines, male-sterile lines, and hybrids, via single- and multiple-trait BLUP, were obtained based on the expression:

$$\rho = \frac{\sigma_{g(trait_i,trait_j)}}{\sqrt{\sigma_{g(trait_i)}^2 \sigma_{g(trait_j)}^2}} \qquad (4)$$

Selection gains (*SG*), considering each methodology, were predicted for the restorer lines, male-sterile lines, and hybrid, following the equation:

$$SG = \frac{\sum_{i=1}^{n} PGV_i}{n} \qquad (5)$$

where:

PGV_i = predicted genetic value

n = quantity selected in function of the selection intensity of 2 (20%), 8 (15%), and 25 (5%) for restorer lines, male-sterile lines, and hybrids, respectively. These intensities of selection were established for purposes of comparison between single- and multiple-trait BLUP.

The selection coincidence between the individuals selected by single- and multiple-trait BLUP was verified for two restorer lines, eight male-sterile lines, and 25 hybrids. Statistical analyses were carried out in the software Selegen REML/BLUP (22), ASReml 4.1 (7) and R (27).

RESULTS

Analysis of deviance
Significant effects of restorer lines ($g1$), of male-sterile lines ($g2$), and of specific combining ability of restorer lines with the male-sterile lines (*SCA*) (P < 0.01) were detected in the LRT for the traits FT, PH, and GY (table 1). Thus, according to the LRT, the full model was the most suitable to estimate the genetic parameters and to predict the genetic values. Consequently, the respective variance components are significantly different from zero, and so are the respective coefficients of determination.

Variance components
The estimates of genetic variance between restorer lines crossed with the male-sterile lines (σ^2_{g1}); male-sterile lines crossed with restorer lines (σ^2_{g2}); mean additive genetic variance (σ^2_a); residual variance (σ^2_e) and specific combining ability between two parents (σ^2_{sca}), via single and multiple-trait BLUP, for the traits FT, PH, and GY were similar (table 2, page 6).

Consequently, heritability values, mean accuracy of the restorer lines (Acc_{g1}), mean accuracy of the male-sterile lines (Acc_{g2}) and mean accuracy of hybrids (Acc_{hyb}) were also similar between the two models for all analyzed traits (table 2, page 6).

Genetic correlation
Table 3 (page 7) shows the genetic correlations between FT, PH, and GY estimated via single- and multiple-trait BLUP. The genetic correlations between the evaluated traits had similar results when comparing the two models, with no signal inversion and with low magnitude estimates.

Selection of parents
Selection coincidences and predicted selection gains of the male-sterile and restorer lines for FT, PH, and GY via single- and multiple-trait BLUP are presented in table 4 (page 7).

Table 1. Deviance and likelihood ratio test (LRT) for the traits: flowering time (FT), plant height (PH), and grain yield (GY), evaluated in 502 grain sorghum hybrids.

Tabla 1. Análisis de deviación y prueba de razón de verosimilitud (LRT) para los caracteres: tiempo de floración (FT), altura de planta (PH) y rendimiento de grano (GY), evaluados en 502 híbridos de sorgo.

Effect	FT				GY	
	Deviance	LRT	Deviance	LRT	Deviance	LRT
g1	3034.14	145.27**	-2644.27	185.97**	1224.23	334.30**
g2	3205.67	316.80**	-2607.62	222.62**	1007.38	117.45**
SCA	2987.82	98.95**	-2774.9	55.34**	930.87	40.94**
Full model	2888.87	-	-2830.24	-	889.93	-

g1: restorer lines; g2: male-sterile lines; SCA: specific combining ability; and **: significant at the 0.01 probability level according to the Chi-square test.

g1: líneas restauradoras; g2: líneas macho estériles; SCA: capacidad de combinación específica; y **: significativo en el nivel de probabilidad de 0,01 de acuerdo con la prueba de Chi-cuadrado.

Table 2. Estimates of variance components and genetic and non-genetic parameters for the traits: flowering time (FT), plant height (PH), and grain yield (GY), evaluated in 502 grain sorghum hybrids, via single- and multiple-trait BLUP.

Tabla 2. Estimación de componentes de varianza, parámetros genéticos y no genéticos para los caracteres: tiempo de floración (FT), altura de planta (PH) y rendimiento de grano (GY), evaluados en 502 híbridos de sorgo, a través de BLUP mono y múltiple característica.

Component	Single-trait BLUP			Multiple-trait BLUP		
	FT	PH	GY	FT	PH	GY
σ_{g1}^2	2.2067	0.0078	0.7065	2.2086	0.0078	0.7058
σ_{g2}^2	6.6537	0.0131	0.3031	6.6506	0.0131	0.3034
σ_a^2	8.8603	0.0209	1.0096	8.8591	0.0209	1.0092
σ_{sca}^2	2.6215	0.0065	0.2443	2.6217	0.0065	0.2465
σ_e^2	3.4353	0.0130	0.5774	3.4353	0.0130	0.5759
σ_f^2	14.9171	0.0404	1.8314	14.9161	0.0404	1.8317
h_{a1}^2	0.2959	0.3857	0.7716	0.2961	0.3867	0.7707
h_{a2}^2	0.8921	0.6503	0.3310	0.8917	0.6495	0.3313
c_{sca}^2	0.1757	0.1600	0.1334	0.1758	0.1599	0.1346
h_{dom}^2	0.1757	0.1600	0.1334	0.1758	0.1599	0.1346
h_a^2	0.5940	0.5180	0.5513	0.5939	0.5181	0.5510
h_g^2	0.7697	0.6779	0.6847	0.7697	0.6781	0.6856
Acc_{g1}	0.9303	0.9331	0.9414	0.9303	0.9334	0.9414
Acc_{g2}	0.9572	0.9413	0.9065	0.9573	0.9417	0.9069
Acc_{hyb}	0.9283	0.9095	0.9248	0.9284	0.9111	0.9262

σ_{g1}^2: genetic variance between restorer lines crossed with male-sterile lines; σ_{g2}^2: genetic variance between male-sterile lines crossed with restorer lines; σ_a^2: mean additive genetic variance; σ_{sca}^2: variance of specific combining ability between two parents; σ_e^2: residual variance; σ_f^2: individual phenotypic variance; h_{a1}^2: narrow-sense individual heritability in restorer lines; h_{a2}^2: narrow-sense individual heritability in male-sterile lines; c_{sca}^2: coefficient of determination of the effects of specific combining ability; h_{dom}^2: individual heritability of dominance effects; h_a^2: narrow-sense individual interpopulational heritability, mean for the two populations; h_g^2: broad-sense individual interpopulational heritability (total genotypic effects); Acc_{g1}: mean accuracy of restorer lines; Acc_{g2}: mean accuracy of male-sterile lines; and Acc_{hyb}: mean accuracy of hybrids.

σ_{g1}^2: varianza genética entre líneas restauradoras cruzadas con líneas macho estériles; σ_{g2}^2: varianza genética entre líneas macho estériles cruzadas con líneas restauradoras; σ_a^2: varianza genética aditiva media; σ_{sca}^2: varianza de la capacidad de combinación específica entre dos padres; σ_e^2: varianza residual; σ_f^2: varianza fenotípica individual; h_{a1}^2: heredabilidad individual de sentido estrecho en líneas restauradoras; h_{a2}^2: heredabilidad individual de sentido estrecho en líneas macho estériles; c_{sca}^2: coeficiente de determinación de los efectos de la capacidad de combinación específica; h_{dom}^2: heredabilidad individual de los efectos de dominio; h_a^2: heredabilidad interpoblacional individual en sentido estrecho, media para las dos poblaciones; h_g^2: heredabilidad interpoblacional individual de sentido amplio (efectos genotípicos totales); Acc_{g1}: precisión media de las líneas restauradoras; Acc_{g2}: precisión media de líneas macho estériles; y Acc_{hyb}: precisión media de los híbridos.

Table 3. Genetic correlations between flowering time (FT), plant height (PH), and grain yield (GY), evaluated in 502 grain sorghum hybrids, via single- (above diagonal) and multiple-trait BLUP (below diagonal).

Tabla 3. Correlaciones genéticas entre tiempo de floración (FT), altura de planta (PH) y rendimiento de grano (GY), evaluados en 502 híbridos de sorgo, a través de BLUP para mono (arriba de diagonal) y múltiples características (debajo de diagonal).

Traits	FT	PH	GY
FT	-	0.03[a] | -0.01[b] | 0.00[c]	0.28[a] | 0.04[b] | 0.08[c]
PH	0.04[a] | -0.03[b] | 0.00[c]	-	0.06[a] | 0.00[b] | 0.03[c]
GY	0.46[a] | 0.10[b] | 0.13[c]	0.05[a] | 0.00[b] | 0.02[c]	-

[a]: restorer lines; [b]: male-sterile lines; and [c]: hybrids.

[a]: líneas restauradoras; [b]: líneas macho estériles; [c]: híbridos

Table 4. Selection coincidence and predicted selection gain for male-sterile and restorer lines for the traits: flowering time (FT), plant height (PH), and grain yield (GY), evaluated in 502 grain sorghum hybrids, via single- and multiple-trait BLUP.

Tabla 4. Coincidencia de selección y ganancia de selección predicha para líneas macho estériles y restauradoras, en las características: tiempo de floración (FT), altura de planta (PH) y rendimiento de grano (GY), evaluados en 502 híbridos de sorgo, por medio BLUP mono y múltiple característica.

Traits	Selection coincidence (%)	Predicted selection gain	
		Single-trait BLUP	Multiple-trait BLUP
FT	100[d] | 100[e]	-2.1479[d] | -4.3482[e]	-2.1479[d] | -4.3482[e]
PH	100[d] | 100[e]	-0.0789[d] | -0.1497[e]	-0.0789[d] | -0.1497[e]
GY	100[d] | 100[e]	1.2636[d] | 0.8578[e]	1.2636[d] | 0.8578[e]

[d]: restorer lines and [e]: male-sterile lines.

[d]: líneas restauradoras y [e]: líneas macho estériles.

For the evaluated traits, the predicted selection gains for restorer and male-sterile lines via single- and multiple-trait procedures showed no differences in values. Regardless of the trait evaluated, the models revealed selection coincidence of 100%, that is, the individuals selected by the single-trait model were the same as those selected by the multiple-trait model (table 4).

Selection of hybrids

Table 5 (page 8), presents the selection coincidences and predicted selection gains of hybrids for the traits FT, PH, and GY, via single- and multiple-trait BLUP. The multiple-trait BLUP resulted in slightly higher predicted selection gain for the three evaluated traits. Selection coincidences varied between traits (96% for FT, 88% for PH, and 84% for PY) and confirms the small difference between the hybrids selected by each methodology.

Table 5. Selection coincidence and predicted selection gain of hybrids for the traits flowering time (FT), plant height (PH), and grain yield (GY), evaluated in 502 grain sorghum hybrids, via single- and multiple-trait BLUP.

Tabla 5. Coincidencia de selección y ganancia de selección predicha para híbridos, en las características: tiempo de floración (FT), altura de planta (PH) y rendimiento de grano (GY), evaluados en 502 híbridos de sorgo, mediante BLUP mono y múltiple característica.

Traits	Selection coincidence (%)	Predicted selection gain	
		Single-trait BLUP	Multiple-trait BLUP
FT	96	-2.2273	-2.2280
PH	88	-0.1226	-0.1227
GY	84	0.6881	0.6921

DISCUSSION

Variance components

Variance components is of great importance in plant breeding, since the population and the breeding method to be used depend on information that can be obtained from these components. The estimates of variance components, the prediction of genetic values, and the accuracies are crucial factors to a plant breeding program. A greater set of candidate genotypes must be used in selection for the development of new cultivars and the recommendation of newly-released varieties. The BLUP methodology is widely used to predict genetic values due to several benefits, such as unbiased prediction, and reduction of variances and errors when compared with other methods (31).

In this study, the estimates for variance components and genetic and non-genetic parameters obtained for the restorer and male-sterile lines and hybrids were the same for the traits analyzed for both single- and multiple-trait BLUP. This fact can be explained by the similarity in the deviations value between the estimation of the genetic and residual variance components considering the two procedures (29). Based on Schaeffer (23), when the heritability values of the traits are similar, and the genetic correlations between the traits are low, the use of the multiple-trait model may not increase the accuracy for the prediction of genetic values.

The estimates of the individual heritability of dominance effects and the narrow-sense individual interpopulational heritability mean for the two populations, indicate that most of the broad-sense individual interpopulational heritability is due additive effects. According to Viana (2005), regardless of the selection unit or type of epistasis, the bias in the estimate of the additive variance when assuming the additive-dominant model is considerable. This implies overestimation of the heritabilities at half sib family mean, plant within family, and plant levels; and underestimation if the selection units are full sib progenies. Thus, the predicted gains have a bias proportional to that of the heritability.

Genetic correlation

In plant breeding programs, the selection of superior genotypes based on several traits of agronomic interest is appropriate. However, when considering the existence of a correlation between traits, these correlations must be analyzed together to avoid selection bias (20). Viana *et al.* (2010) emphasized that the advantage of using the multiple-trait BLUP model is mainly dependent on heritability values and genetic correlations between the evaluated traits.

Piepho *et al.* (2008) stated that the multiple-trait model is more appropriate for highly correlated traits. However, when including information of traits of low magnitude correlation (as evaluated in this study) in multiple-trait BLUP analysis, no improvements in the estimate of genetic correlation were observed in relation to the single-trait BLUP (table 3, page 7).

Conversely, when considering the most correlated traits (GY and FT), multiple-trait BLUP correlations estimates were always higher. Persson and Andersson (2004) compared the genetic values predicted via single- and multiple-trait BLUP in *Pinus sylvestris* L. and reported that the multiple-trait model had a lower mean bias than the single-trait model. Moreover, the authors stated that the genetic correlations between traits by the single-trait BLUP were underestimated. Kadarmideen *et al.* (2003) observed that predicted genetic values and animal ranking were significantly different between single- and multiple-trait analyses in milk cattle. The same authors also reported that the single-trait analysis was shown to be biased, and thus recommended the use of multiple-trait BLUP. Kadarmideen *et al.* (2003), working with simulated low- and high-heritability trait

data, found that the multiple-trait genomic model resulted in more accurate genomic predictions when compared with genomic single-trait model, especially for low heritability traits.

Parents selection

Grain sorghum genetic improvement must be performed individually in each group of lines (restorer or male-sterile). The improvement of male-sterile lines must be carried out in isogenic lines and, subsequently, introduced to cytoplasmic male sterility. Therefore, the identification of parents of each group that donate alleles with desirable effects is a promising strategy for the development of future hybrids with broad adaptability for these traits.

This work identified lines of each group that contribute to the desirable phenotype in the respective hybrids generated. The favorable alleles for each trait are found in different parents (* page 3). Finally, the two procedures evaluated led to the selection of the same parents from each line and, consequently, to the same estimates of selection gain (table 4, page 7).

The selection of relatives via single- and multiple-trait BLUP for annual crops such as sorghum is still scarce in the literature. The coincidence in the selection between the procedures is proportional to the absolute difference between the genetic and environmental correlations of the traits and the sample size (26). Thus, although there were small differences between the procedures for the genetic correlations of restorer lines and male-sterile lines (table 3, page 7), sample size did not allow detecting differences in selection coincidence and predicted selection gain for male-sterile and restorer lines (table 4, page 7).

In the breeding of perennial plants, the multiple-trait BLUP is a consolidated strategy. Several authors have detected superiority of this procedure in the selection of parents due to the great imbalance in the data that influences the residual correlation between the traits and consequently their heritability and genetic values. Imai *et al.* (2016), Costa *et al.* (2002), Kerr (1998), Alves *et al.* (2019) and Alves *et al.* (2018) applied multiple-trait BLUP in parent selection of perennial crops demonstrated the usefulness of the method in parent selection when the information of kinship among genotypes is known and in the presence of unbalanced data.

Hybrid selection

Currently, grain sorghum breeding programs seek to develop hybrids with high earliness, low plant height, and high grain yield (15). Thus, the selection of hybrids with the highest genetic value (* page 3) is fundamental to breeding programs. The differences in selection coincidence and predicted selection of hybrids for the traits can be explained mainly by the magnitude of the correlation obtained between GY and FL by single- (0.08) and multiple-trait BLUP (0.13), in addition to the larger sample size (504 hybrids).

In general, the gains obtained with the multiple-trait BLUP were slightly higher than the single-trait BLUP for all traits. Recently, Volpato *et al.* (2019) observed that multiple-trait BLUP is a suitable procedure for genetic selection of segregating soybean progeny. These results are important because they report the first application of this procedure for selection of hybrids in annual crops.

Conclusions

Significant effects of restorer lines, of male-sterile lines, and of specific combining ability were detected. The estimates of variance components, genetic parameters, and correlations were similar when obtained via single- and multiple trait-BLUP. Considering hybrids, the multiple-trait BLUP resulted in slightly higher predicted selection gain for the three evaluated traits and, therefore, can be efficiently applied in the genetic selection of grain sorghum.

References

1. Alves, R. S.; Rocha, J. R. A. S. C.; Teodoro, P. E.; Resende, M. D. V.; Henriques, E. P.; Silva, L. A.; Carneiro, P. C. S.; Bhering, L. L. 2018. Multiple-trait BLUP: a suitable strategy for genetic selection of Eucalyptus. Tree Genet. Genomes. 14: 77.
2. Alves, R. S.; Teodoro, P. E.; Peixoto, L. A.; Rocha, J. R. A. S.C.; Silva, L. A.; Laviola, B. G.; Resende, M. D. V.; Bhering, L. L. 2019. Multiple-trait BLUP in longitudinal data analysis on *Jatropha curcas* breeding for bioenergy. Ind. Crop Prod. 130: 558-561.
3. Batista, P. S. C.; Carvalho, A. J.; Portugal, A. F.; Bastos, E. A., Cardoso, M. J.; Torres, L. G.; Mingote Júlio, M. P.; Menezes, C. B. 2018. Selection of sorghum for drought tolerance in a semiarid environment. Genetics and Molecular Research 18: (1). Available in: http://dx.doi.org/10.4238/gmr18194
4. Cisneros-López, M. E.; Valencia-Botín, A. J.; Estrada-Girón, Y. 2017. Sorghum (*Sorghum bicolor*) pollen availability and seed set under different proportion male:female plants in Mexican highlands. Revista de la Facultad de Ciencias Agrarias. Universidad Nacional de Cuyo. Mendoza. Argentina. 49(2): 51-66.

5. Cochran, W. G.; Cox G. M. 1957. 2° ed. Experimental designs. New York. J Wiley. 611 p.
6. Costa, R. B.; Resende, M. D. V.; Gonçalves, P. D. S.; Silva, M. A. 2002. Individual multivariate REML/ BLUP in the presence of genotype x environment interaction in rubber tree (*Hevea*) breeding. Crop Breeding and Applied Biotechnology 2.
7. Gilmour, A. R.; Gogel, B. J.; Cullis, B. R.; Welham, S. J.; Thompson, R. 2015. ASReml user guide release 4.1 structural specification. Hemel Hempstead: VSN International Ltd.
8. Henderson, C. R. 1975. Best linear unbiased estimation and prediction under a selection model. Biometrics: 423-447. 10.2307/2529430
9. Henderson, C. R.; Quaas, R. L. 1976. Multiple trait evaluation using relatives' records. Journal of Animal Science 43: 1188-1197. Available in: https://doi.org/10.2527/jas1976.4361188x
10. Igaruta, E.; Gracia, M. P.; Lasa, J. M. 1996. Selection for increased yield under limited irrigation in four grain sorghum random mating populations. Maydica. 41: 149-154.
11. Imai, A.; Kuniga, T.; Yoshioka, T.; Nonaka, K.; Mitani, N.; Fukamachi, H.; Hiehata, N.; Yamamoto, M.; Hayashi, T. 2016. Evaluation of the best linear unbiased prediction method for breeding values of fruit-quality traits in citrus. Tree Genet. Genomes. 12: 119.
12. Kadarmideen, H. N.; Thompson, R.; Coffey, M. P.; Kossaibati, M. A. 2003. Genetic parameters and evaluations from single-and multiple-trait analysis of dairy cow fertility and milk production. Livestock Production Science 81: 183-195. Available in: https://doi.org/10.1016/S0301-6226(02)00274-9
13. Kerr, R. J. 1998. Asymptotic rates of response from forest tree breeding strategies using best linear unbiased prediction. Theor. Appl. Genet. 96: 484-493.
14. Kumar, A. A.; Reddy, B. V. S.; Ramaiah, B.; Sahrawat, K. L.; Pfeiffer, W. H. 2013. Gene effects and heterosis for grain iron and zinc concentration in sorghum [Sorghum bicolor (L.) Moench]. Field Crops Research 146: 86-95. Available in: https://doi.org/10.1016/j.fcr.2013.03.001
15. Menezes, C. B.; Carvalho Júnior, G. A.; Silva, L. A.; Bernardino, K. C.; Souza, V. F.; Tardin, F. D.; Schaffert, R. E. 2014. Combining ability of grain sorghum lines selected for aluminum tolerance. Crop Breeding and Applied Biotechnology. 14: 42-48. Available in: http://dx.doi.org/10.1590/S1984-70332014000100007
16. Morris, G. P.; Ramu, P.; Deshpande, S. P.; Hash, C. T.; Shah, T.; Upadhyaya, H. D.; Riera-Lizarazu, O.; Brown, P. J.; Acharya, C. B.; Mitchell, S. E.; Harriman, J.; Glaubitz, J. C.; Buckler, E. S.; Kresovich, S. 2013. Population genomic and genome-wide association studies of agroclimatic traits in sorghum. Proceedings of the National Academy of Sciences. 110: 453-458. Available in: https://doi.org/10.1073/pnas.1215985110
17. Mrode, R. A. 2000. Linear models for the prediction of animal breeding values. CAB International, New York. 10.1079/9781780643915.0000
18. Persson, T.; Andersson, B. 2004. Accuracy of Single-and Multiple-Trait REML Evaluation of Data Including Non-Random Missing Records. Silvae Genetica. 53: 135-138. Available in: https://doi.org/10.1515/sg-2004-0024
19. Piepho, H. P.; Möhring, J.; Melchinger, A. E.; Büchse, A. 2008. BLUP for phenotypic selection in plant breeding and variety testing. Euphytica. 161: 209-228.
20. Pollak, E. J.; Van der, Werf J.; Quaas, R. L. 1984. Selection bias and multiple trait evaluation. Journal of Dairy Science. 67: 1590-1595. Available in: https://doi.org/10.3168/jds.S0022-0302(84)81481-2
21. Resende, M. D. V. 2016. Software Selegen-REML/BLUP: a useful tool for plant breeding. Crop Breeding and Applied Biotechnology. 16: 330-339. Available in: http://dx.doi.org/10.1590/1984-70332016v16n4a49
22. Resende, M. D. V.; Silva, F. F.; Azevedo, C. F. 2014. Estatística matemática, biométrica e computacional. Suprema. Visconde do Rio Branco. MG. Brasil.
23. Schaeffer, L. R. 1984. Sire and cow evaluation under multiple trait models. Journal of Dairy Science. 67: 1567-1580. Available in: https://doi.org/10.3168/jds.S0022-0302(84)81479-4

24. Senthil, N.; Ramasamy, P.; Khan, F. 1998. Fertility restoration and heterosis involving different cytoplasms in sorghum (*Sorghum bicolor* (L) Moench) hybrids. Journal of Genetics & Breeding (Italy).

25. Silva, A. G.; Barros, A. S.; Silva, L. H. C. P.; Moraes, E. B.; Pires, R.; Rosa Teixeira, I. 2009. Avaliação de cultivares de sorgo granífero na safrinha no sudoeste do estado de Goiás. Pesqui. Agrop. Trop. 39: 168-174.

26. Tari, I.; Laskay, G.; Takács, Z.; Poór, P. 2012. Response of sorghum to abiotic stresses: a review. Journal of Agronomy and Crop Science. 199: 264-274. Available in: https://doi.org/10.1111/jac.12017

27. Team, R. C. 2015. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

28. Viana, J. M. S. 2005. Dominance, epistasis, heritabilities and expected genetic gains. Genet. Mol. Biol. 28 (1): 67-74.

29. Viana, J. M. S.; Sobreira, F. M.; De Resende, M. D. V.; Faria, V. R. 2010. Multi-trait BLUP in half-sib selection of annual crops. Plant Breeding. 129: 599-604. Available in: https://doi.org/10.1111/j.1439-0523.2009.01745.x.

30. Volpato, L.; Alves, R. S.; Teodoro, P. E.; de Resende, M. D. V.; Nascimento, M.; Nascimento, A. C. C.; Ludke, W. H.; Silva, F. L.; Borém, A. 2019. Multi-trait multi-environment models in the genetic selection of segregating soybean progeny. PLOS ONE. 14(4): e0215315.

31. White, T. L.; Hodge, G. R. 2013. Predicting breeding values with applications in forest tree improvement: Springer Science & Business Media.