Allohexaploid pearl millet x elephantgrass population potential for a recurrent selection program

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Abstract – The objective of this work was to evaluate the potential of allohexaploid pearl millet x elephantgrass (HGL) population for a recurrent selection program through open-pollinated progenies. Seventy-eight progenies, one representative sample of the population, and two commercial cultivars, Pioneiro and Paraíso, were evaluated in a 9x9 triple lattice design, in two sites. Plant height and dry matter yield were evaluated in three and four cuts, respectively. For plant height, the 17 best progenies were similar to both commercial controls, while for dry matter yield they were higher than 'Paraíso' and lower than 'Pioneiro'. The correlation between progenies and cuts indicated that the fourth cut represents the mean of all cuts, and the possibility of using early selection. Heritability estimates considering cuts and sites were 56.9% for plant height and 58.8% for dry matter yield, and the expected response to selection was 23.4% for dry matter yield and 18.1% for plant height. These results demonstrate the promising HGL population potential for a recurrent selection program.

Index terms: *Pennisetum*, heritability, response to selection, split-plot lattice design.

Potencial da população alohexaplóide de milheto x capim-elefante para um programa de seleção recorrente

Resumo – O objetivo deste trabalho foi avaliar o potencial para programa de seleção recorrente, em uma população alohexaplóide de milheto x capim-elefante (HGL), por meio de progênies de polinização aberta. Setenta e oito progênies, uma testemunha representativa da população e duas cultivares comerciais, a Pioneiro e a Paraíso, foram avaliadas no delineamento látice triplo 9x9, em dois locais. Os caracteres altura de plantas e produtividade de matéria seca foram avaliados por três e quatro cortes, respectivamente. Quanto à altura de plantas, a média das 17 melhores progênies foi similar às das testemunhas comerciais e, quanto à produtividade de matéria seca, foi maior do que a da 'Paraíso' e menor do que a da 'Pioneiro'. A correlação entre progênies e colheitas mostrou que a quarta colheita representa a média de todas as colheitas e a possibilidade de seleção precoce. As estimativas de herdabilidade na média das colheitas e locais foram de 56,9% para altura de plantas e de 58,8% para produtividade de matéria seca, e a reposta esperada com a seleção foi de 23,4% para produtividade de matéria seca e 18,1% para altura de plantas. Esses resultados demonstram o potencial promissor da população HGL para programa de seleção recorrente.

Termos para indexação: *Pennisetum*, herdabilidade, resposta à seleção, látice de parcelas subdividas.

Introduction

Elephantgrass (*Pennisetum purpureum* Schum.) is one of the most widespread tropical fodder grasses in Brazil. It is also one of the forage species of highest dry matter yield with good nutritive quality. The need for vegetative propagation and lack of cultivars adapted to diverse edaphoclimatic conditions are considerable constraints on an expansion of areas cultivated with this forage (Pereira et al., 2001).

The ease of crossing elephantgrass with pearl millet [*P. glaucum* (L.) R.Br.] suggests the excellent possibility of establishing new seed-propagated cultivars (Jauhar & Hanna, 1998). The F_1 hybrids are sterile triploids, but fertility can be restored by chromosome duplication (Hanna, 1981; Abreu et al., 2006). These amphiploids (allohexaploids) have meiosis with typical diploid behavior, and have a high degree of regular meiosis, pollen fertility, and seed viability. Studies with pearl millet x elephantgrass allohexaploid hybrids indicate high yield

potential and possible usefulness, because these hybrids are more easily propagated through seeds than allotetraploid elephantgrass (Schank, 1999).

Improved populations derived from a recurrent selection program can be used to develop new high-yielding and seed-propagated cultivars, adapted to the different regions where this forage is important. To have success with a recurrent selection program, the population must present the highest possible yield means, as well as genetic variability for traits under selection (Souza Júnior, 2005).

This research aimed to evaluate the potential of allohexaploid pearl millet x elephantgrass (HGL) population for a recurrent selection program through open-pollinated (OP) progenies.

Materials and Methods

The experiments were conducted at the Embrapa Gado de Leite research stations, in Coronel Pacheco, Minas Gerais State (21°35'S, 45°15'W and 414 m) in a Typic Haplustox soil, and in Valença, Rio de Janeiro State (22°21'S, 43°42'W and 363 m) in a Typic Humaquept soil. The former area was cultivated over six years with elephantgrass experiments, and the other was previously a pasture composed by *Brachiaria* and *Cynodon*. Both areas presented average soil fertility.

The study involved 78 OP allohexaploid pearl millet x elephantgrass progenies selected from a composite population, synthesized from eight base populations of the University of Florida, which were randomly mated in two cycles. A sample of HGL population, and two commercial cultivars, Paraíso (allohexaploid) and Pioneiro (allotetraploid), were used as control.

The treatments were evaluated in a 9x9 triple lattice design with single-row plots (6 plants in a 3 m row) spaced 1 m from each other, and plants were spaced 0.5 m apart. To establish seedlings, seeds of each progeny were germinated in styrofoam. In the case of the commercial cultivars, plants were obtained from stem cuttings. Seedlings were transplanted about 45 days after sowing, in late October 2003 in Valença, and late November 2003 in Coronel Pacheco. A level cutting was performed ninety days after planting, followed by cuts every 60 days in the rainy season and every 90 days in the dry season. At planting, 300 kg ha^{-1} of the compound fertilizer N–P$_2$O$_5$–K$_2$O (8–28–16) were applied as topdressing, and 100 kg ha^{-1} of the same fertilizer (20–5–20) were applied as topdressing after each harvest (Monteiro, 1997).

The following traits were evaluated: plant height (PH), from the ground level to the highest completely unrolled leaf; and dry matter yield (DMY).

The split-plot model in time was applied for the analyses of repeated cuts at each site (Steel et al., 1997). The underlying statistical model for the analyses at each site was the following:

$$Y_{ijkm} = \mu + R_j + B_{k(j)} + P_i + (PB)_{ik(j)} + C_m + (CB)_{mk(j)} + (PC)_{im} + e_{(ijkm)},$$

in which: Y_{ijkm} is the observed value of the ith progeny in the kth block, within jth replication j of the mth cut; μ is the overall mean of the experiment; R_j is the effect of the jth replication (j = 1, 2,…, r); $B_{k(j)}$ is the effect of the kth block (k = 1, 2, 3...,9), within the jth replication; P_i is the effect of the ith OP progeny (i = 1, 2, 3, ..., 78); $(PB)_{ik(j)}$ is the interaction effect of the ith progeny with the kth block, within the jth replication; C_m is the effect of the mth cut (m = 1, 2, …, c); $(CB)_{mk(j)}$ is the interaction effect of the mth cut with the kth block, within the jth replication; $(PC)_{im}$ is the interaction effect of the ith progeny with the mth cut; $e_{(ijkm)}$ is the experimental error associated to observation Y_{ijkm}.

Joint analysis of sites was performed. All analysis were performed through SAS procedure general linear model (PROC GLM). Since the adjusted means could not be estimated by PROC GLM, the procedure mixed linear models (PROC MIXED) was used, which allowed the prediction of genotypic deviations of each treatment. These deviations were, then, added to the overall mean, in order to obtain the genotypic values of each treatment ($g_{i's} = \mu + BLUP's$).

The genetic parameters for the OP progenies were estimated considering the effects progenies and error as random, and cuts and sites as fixed. A detailed description of the estimates was given by Reis (2005).

The expected responses to selection (RS), in the means of the OP progenies, were estimated through the following expression (Resende, 2002):

$$RS = i \cdot \frac{\hat{\sigma}_G^2}{\hat{\sigma}_P^2},$$

in which: i is the differential of selection standard, considering a selection intensity of 20.99%; $\hat{\sigma}_G^2$ is the estimate of the genetic variance in OP progenies; and $\hat{\sigma}_P^2$ is the estimate of the phenotypic variance in OP progeny means.

The pairwise genetic correlations between the cuts were estimated according to Vencovsky & Barriga (1992). It was, therefore, necessary to perform individual and joint pairwise analyses taking both sites into consideration.

Results and Discussion

All sources of variation presented significant differences (p<0.01) for both evaluated traits (PH and DMY) in joint analysis, with exception for the progenies x cuts x sites interaction, for plant height. These results suggest the existence of variability in evaluated progenies, and that progenies performance were not consistent across sites and cuts, due to the significance of the double interaction for traits and the triple interaction for DMY.

The coefficients of determination were superior to 0.91, indicating that the model explained the observed variation (Table 1). The experimental coefficient of variation estimated for DMY was high according to Clemente & Muniz (2002), who suggest low, medium, high, and very high ranges for experimental coefficient of variation. However, this classification is based on experiments, which, in most cases, involve clones. In this study, OP progenies, where the variation is usually larger, were used. Thus the experimental coefficient of variation estimate should be consequently higher.

Another important aspect, when estimates of genetic parameters are considered, is whether the number of progenies represents the population under study. Since 78 progenies were evaluated in this study, the sample was presumably representative. To corroborate this observation, a sample population was included in the experiment as control. This control mean was very similar to the overall mean of the 78 progenies, which indicates that it was sufficient to represent the population under study (Table 1). In the case of half-sib progenies in maize, for the trait grain yield, evaluation of 50 progenies at least is recommended (Souza Júnior, 2001).

The DMY mean of OP progenies was similar to the one obtained by Souza Sobrinho et al. (2005) for pearl millet x elephantgrass triploid hybrids. The mean performance of the 17 best progenies for DMY was superior to 'Paraíso' and slightly lower than 'Pioneiro', although this latter cultivar had been developed under conditions similar to those in this study (Table 1). These results confirm the yield potential of the HGL population.

Progenies x cuts interaction is fundamental for decisions about early selection, and was significant in individual and joint analyses. Nevertheless, the estimates of genetic correlations between mean progeny performance in different cuts were high (Table 2). Even when data of the first and fourth cuts were compared, where the correlation was smaller, six of the best ten progenies were coincident. The nine best progenies in fourth cut were among the ten best ones in the cuts mean, suggesting that the fourth cut was representative for the others, and that the responses to selection obtained among progenies, regarding only this cut, was similar to the others. These results suggest that early selection could be feasible, but more information concerning this subject is necessary.

The amplitude of variation among progenies means for DMY was approximately 6.8 t DM ha^{-1} per cut, equivalent to 105.8% of the overall mean. For PH, the amplitude was smaller (0.4 m or 38.5% of the mean). The estimates of genetic variance and heritability also

Table 1. Mean predicted genotypic values, coefficient of variation (CV) and coefficient of determination (R^2), in per site and joint analyses for plant height (PH, m) and dry matter yield (DMY, t ha^{-1} per cut) of allohexaploid pearl millet x elephantgrass (HGL) population open-pollinated progenies[1].

Progenies	Valença		Coronel Pacheco		Joint analysis	
	PH	DMY	PH	DMY	PH	DMY
78 progenies	0.96	5.98	1.10	6.79	1.03	6.38
	(1.15–0.86)	(9.84–4.67)	(1.47–0.92)	(12.4–4.55)	(1.30–0.93)	(11.59–4.80)
Selected progenies	1.03	7.16	1.25	8.66	1.12	7.81
	(1.15–1.00)	(9.84–6.27)	(1.47–1.17)	(12.4–7.38)	(1.30–1.08)	(11.59–6.74)
'Pioneiro'	1.12	8.87	1.31	8.71	1.22	9.12
'Paraíso'	0.95	5.19	1.27	8.99	1.10	6.97
HGL pop.[2]	0.95	5.66	1.05	6.06	1.00	5.82
Overall mean	0.97	6.00	1.11	6.84	1.04	6.42
CV (%)	13.93	45.24	13.25	25.25	13.58	35.43
R^2	0.97	0.86	0.95	0.95	0.97	0.91

[1]Values in brackets were upper and lower limits of mean predicted genotypic values. [2]HGL population sample.

illustrate this variability. The heritability (h^2) estimates were higher than 45%, and the estimate of lower limit with 95% confidence interval was always positive for both traits, indicating that it differs from zero (Table 3). The only report found in the literature showed heritability estimates obtained from S_1 progenies of allohexaploid pearl millet x elephantgrass, for plant height, were 7.6 times lower than those observed here (Diz & Schank, 1995). Daher et al. (2004) reported contrasting results, obtained from intra-specifics hybrids of elephantgrass, higher for PH (84.34%) and lower for DMY (33.49%). In maize, very similar estimates for silage DMY were also described (Ramalho, 1999).

The expected responses to selection were estimated using the mean performance in four cuts for DMY, and in three cuts for PH, considering per site and joint analyses (Table 4). In all cases, the expected responses to selection were greater for DMY, which can be explained by the higher variation in this trait, since the heritability estimates were similar and the precision in the PH evaluation was greater.

The estimates of the expected response to selection of 23.41% for DMY and 18.12% for plant height suggest

Table 2. Estimates of pairwise genetic correlations between the cuts in allohexaploid pearl millet x elephantgrass population open-pollinated progenies, considering two sites for dry matter yield.

	2nd cut	3rd cut	4th cut
1st cut	1.00 (7)[1]	0.60 (8)	0.53 (6)
2nd cut	-	0.89 (8)	0.93 (7)
3rd cut	-	-	1.03 (9)

[1]Number of progenies that were coincident among ten best progenies in each cut.

Table 3. Estimates of the genetic variance ($\hat{\sigma}_G^2$), phenotypic variance ($\hat{\sigma}_P^2$), mean broad-sense heritability (h^2_m%) and respective lower (LL) and upper (UL) limits, with 95% interval of confidence, and coefficient of genetic variation (CVg) for plant height and dry matter yield (DMY), of allohexaploid pearl millet x elephantgrass population open-pollinated progenies.

Parameter	Valença		Coronel Pacheco		Joint analysis	
	Height	DMY	Height	DMY	Height	DMY
$\hat{\sigma}_G^2$	0.0058	1.6416	0.0175	3.4881	0.0082	2.0326
$\hat{\sigma}_P^2$	0.0126	3.6176	0.0258	5.5793	0.0144	3.4583
h^2_m%	46.03	45.38	67.83	62.52	56.94	58.77
LL%	19.41	19.31	51.96	44.86	34.28	37.31
UL%	62.83	62.03	77.99	73.79	71.49	72.56
CVg	7.87	21.35	11.95	27.30	8.73	22.21

Table 4. Estimates of the expected responses to selection (RSe), in units of phenotypic standard deviation and in percentage (%), for plant height (PH, m) and for dry matter yield (DMY, t ha⁻¹ per cut), of the HGL population, considering per site and joint analysis.

Variable	Valença		Coronel Pacheco		Joint analysis	
	PH	DMY	PH	DMY	PH	DMY
RSe	0.07	1.19	0.15	2.03	0.19	1.50
RSe (%)	7.34	19.78	13.56	29.69	18.12	23.41

the potential of HGL population for a recurrent selection program (Table 4). In fact, these estimates of genetic progress were overestimated, because part of the genetic variance in OP and half-sib progenies of polyploids was due to the variance of dominance (σ_D^2). In autotetraploids, this component is $1/36 \, \sigma_D^2$ (Wricke & Weber, 1986). No report about components of genetic variance in allohexaploid progenies was found. However, this proportion is small, indicating that the estimates obtained would not be very different. Moreover, if selection within progenies was performed, the expected responses to selection should be higher. It was, therefore, inferred that HGL population has an excellent potential for recurrent selection, in view of the genetic variability available and of the elevated means observed.

Since the mean performance of the 17 selected progenies was superior to that of 'Paraíso', which is also allohexaploid and seed-propagated, a new cultivar could possibly be recommended after few cycles of selection.

Conclusion

The allohexaploid pearl millet x elephantgrass population of Embrapa Gado de Leite is promising for a recurrent selection program, since it combines high mean and enough variability for successful selection.

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