

# Selecting new *Brachiaria humidicola* hybrids for Western Brazilian Amazon

Giselle Mariano L de Assis, Cacilda Borges do Valle, Carlos Mauricio S de Andrade and Judson F Valentim

Brazilian Agricultural Research Corporation, Embrapa [www.embrapa.br](http://www.embrapa.br)  
Contact email: [giselle.assis@embrapa.br](mailto:giselle.assis@embrapa.br)

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## Introduction

*Brachiaria humidicola* is a perennial and stoloniferous forage grass, with excellent adaptation to infertile soils and waterlogging. Producers in northern Brazil have become interested in this species, especially after the degradation of large areas of lowly permeable soils sown with *B. brizantha* cv. Marandu, which is highly intolerant of soil waterlogging (Andrade and Valentim 2006). However, since only 3 cultivars of *B. humidicola* are registered in Brazil (Mapa 2013), there is a need to develop new cultivars adapted to the range of environmental conditions experienced. Recently, Embrapa Beef Cattle obtained intraspecific hybrids of *B. humidicola* that need to be evaluated agronomically, aiming at subsequent grazing trials and future releases. The objective of this study was to evaluate and select apomictic and sexual hybrids of *B. humidicola* in the environmental conditions of the state of Acre, in western Brazilian Amazon.

## Methods

The research was conducted at the Experimental Station of Embrapa Acre in western Brazilian Amazon. Fourteen sexual and apomictic hybrids of *B. humidicola* and cv. Tully were evaluated, in a randomised block design with 6 replications in plots of 3 m<sup>2</sup>. These hybrids were previously evaluated and selected from a small plot experiment with 50 hybrids at Campo Grande, MS, Brazil (Figueiredo *et al.* 2012).

The hybrids were planted by stolon pieces in December

2008 and, after establishment, plots were standardised with cuts in April and July 2009. The experimental period was November 2009-June 2011, with 8 harvests, 2 in the dry season and 6 in the rainy season. The agronomic traits evaluated were: total dry matter (DM) yield and leaf DM yield, obtained after determining the percentage of leaves in the samples. Additionally, crude protein (CP), neutral detergent fibre (NDF), acid detergent fibre (ADF) and lignin concentrations were obtained from July 2009 and July 2010 harvests (dry season) and January, March and November 2010 harvests (rainy season).

The data were processed using a mixed model methodology, in that variances were estimated by restricted maximum likelihood and genotypic values were predicted by the best linear unbiased prediction methods. Initially, one analysis per harvest was run to verify the existence or not of heterogeneity of residual variances. Afterwards, analysis of the data including all harvests was conducted simultaneously. Phenotypic data were multiplied by  $h_i/h_g$ , as proposed by Resende *et al.* (2008), where  $h_i$  is the square root of heritability in harvest  $i$  and  $h_g$  is the square root of the mean of the heritabilities in all harvests. The significance of variances was verified by analysis of deviance (Resende *et al.* 2008). Genotypes were ranked on a selection index, in which the predicted genotypic values were standardised and traits received different weightings: total DM yield was weighted by 0.4; leaf DM yield by 0.4; NDF by 0.1 and ADF by 0.1. The other traits were not included in the selection index owing to lack of genetic variability.

**Table 1. Estimates of general mean (m), genotypic variance (V<sub>g</sub>), variance of the genotype x harvests interaction (V<sub>gh</sub>), mean genotype heritability (h<sup>2</sup><sub>m</sub>), genotypic correlations between harvests (r<sub>gh</sub>), individual repeatability (r) and accuracy (Acc) for agronomic and nutritional traits of *Brachiaria humidicola* genotypes.**

Trait <sup>1</sup>	m	V <sub>g</sub>	V <sub>gh</sub>	h <sup>2</sup> <sub>m</sub>	r <sub>gh</sub>	r	Acc (%)
TDM (kg/ha/harvest)	3038.8	119550.4**	353175.5**	62.7**	0.2529	0.4394	79.15
LDM (kg/ha/harvest)	1576.4	63624.6**	78528.1**	76.6**	0.4476	0.5019	87.55
CP (%)	5.52	0.0034 ns	0.1114**	7.4 ns	0.0298	0.3712	27.33
NDF (%)	70.24	0.2980**	0.5300**	58.1**	0.3599	0.2085	76.22
ADF (%)	36.65	0.0754**	0.2303**	37.1**	0.2468	0.1624	60.89
LIG (%)	4.01	0.0026 ns	0.2706**	2.8 ns	0.0097	0.2209	16.68

<sup>1</sup>TDM: total dry matter yield; LDM: leaf dry matter yield; CP: crude protein; NDF: neutral detergent fibre; ADF: acid detergent fibre; LIG: lignin.  
\*\* Significant by the  $\chi^2$  test, at  $P < 0.01$ .

**Table 2. Ranking of *Brachiaria humidicola* hybrids and cv. Tully, based on the selection index obtained from predicted genotypic values by the method of best linear unbiased prediction.**

Rank	Genotype	Rank	Genotype	Rank	Genotype
1	216 (S)	6	297 (S)	11	138 (S)
2	289 (S)	7	350 (S)	12	111 (A)
3	193 (A)	8	146 (A)	13	29 (A)
4	242 (A)	9	185 (S)	14	3 (A)
5	88 (A)	10	Tully (A)	15	64 (S)

(S): sexual hybrid; (A): apomictic hybrid.

## Results and Discussion

There was genetic variability for total DM yield, leaf DM yield, NDF and ADF (Table 1). The lack of genetic variability for CP and lignin concentrations prevented selection of hybrids based on these traits. The ranking of genotypes was influenced by harvest, since the variance of genotype x harvest interaction was significant for all traits. Estimates of heritability in the genotype mean were moderate to high for total DM yield, leaf DM yield and NDF, but low to moderate for ADF. The remaining estimates were not significantly different from zero. The genotypic correlations between harvests were low to medium for total DM yield, leaf DM yield, NDF and ADF, indicating no high coincidence of the best genotypes in all harvests, which reinforces the importance of including the effect of genotype x harvest in the model (Table 1). According to individual repeatabilities, 5, 4, 7, 15, 21 and 14 harvests would be required to achieve a determination coefficient of 80% in the plot evaluation of permanent phenotypic value for total DM yield, leaf DM yield, and CP, NDF, ADF and lignin concentrations, respectively. The experiment conducted has high accuracy for total DM yield, leaf DM yield and NDF; moderate for ADF; and low accuracy for CP and lignin (Table 1).

Classification of hybrids based on the selection index (Table 2) showed 9 genotypes superior to cv. Tully. Among these, there are 4 apomictic and 5 sexual hybrids. Sexual hybrids may be recombined in the recurrent selection program while apomictic hybrids can advance to evaluation trials with animals, being candidates for release as new cultivars for western Brazilian Amazon.

## Conclusion

The variability and genetic superiority among the hybrids

allows selection of apomictic genotypes for further evaluation with animals, with the ultimate release of new cultivars adapted to the environmental conditions of western Brazilian Amazon. The superior sexual hybrids identified will allow recombination of these genotypes, enabling new cycles of evaluation and selection in the breeding program of *B. humidicola*. While the experimental precision for selection of hybrids is high for agronomic traits, precision of the nutritional traits is much lower and must be improved in order to minimise environmental influences.

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