

Agronomic performance and genetic variability of *Panicum maximum* accessions in the Cerrado of Federal District, Brazil

F.D. Fernandes¹, G.B. Martha, Jr¹, F.G. Faleiro¹, A.K.B. Ramos¹, R.P. Andrade¹, C.T. Karia¹, L. Vilela¹ and L. Jank²

¹Embrapa Cerrados, C.P. 08223, 73.310-970, Planaltina-DF, Brazil, Email: duarte@cpac.embrapa.br,

²Embrapa Gado de Corte, C.P. 154, 79.002-970, Campo Grande-MS, Brazil

Keywords: germplasm, selection, tropical forages

Introduction In the last three decades, the Brazilian Savanna (locally called "Cerrado") became the most important beef cattle production region in Brazil. Around 90% of all beef produced in the region comes from pasture-based systems. Intensively-managed and fertilised *Panicum maximum* pastures can be highly productive and economic. As a result, farmers are demanding new *P. maximum* cultivars for using in well-fertilised pastures or in crop-pasture rotation systems. This study aimed to evaluate the agronomic performance and the genetic variability of *P. maximum* accessions in the Brazilian Cerrado.

Material and methods Twenty-four *P. maximum* genotypes, being six cultivars (Mombaça, Tanzânia, Massai, Vencedor, Milênio and Aruana) and 18 previously selected accessions were studied. The experiment was established on 21 Nov. 02 at Embrapa Cerrados (15°35'30" S, 47°42'30" W, altitude 1007 m), on a highly fertilised clayey Dark Red Latosol, in a randomised complete block design with three replicates. Each plot was 12.5 m². Six cuts at a 20-cm stubble height were made in 2003 on 5 Feb., 12 March, 16 April, 25 June, 27 Oct. and 1 Dec. The leaf lamina (LDMY) and stem (SDMY) dry matter yields (kg/ha) in each cut and the crude protein (CP), neutral detergent fibre (NDF) and *in vitro* organic matter digestibility (IVOMD) contents in cuts 1 to 4 were evaluated. Means comparisons were carried out at the $P < 0.05$ significance level. Random Amplified Polymorphic DNA (RAPD) molecular markers were used to estimate the genetic variability.

Results The overall LDMY and SDMY means were 11,266 kg/ha (LSD=3,683 kg/ha) and 3,763 kg/ha (LSD=2,091 kg/ha), respectively (Table 1). The accessions PM31, PM33 and PM34 were the most promising, because of highest leaf production (mean + 1 standard deviation) and lowest stem production (mean - 1 standard deviation). The CP, IVOMD and NDF contents varied similarly throughout the cuts. Crude protein and IVOMD decreased ($P < 0.05$) in the fourth cut while NDF remained fairly constant during the experiment. The genetic distances between the genotypes ranged from 0.054 to 0.415 with the lowest distances occurring between PM39 and PM40 (0.054), PM31 and Massai (0.110), and PM42 and Tanzânia (0.132). Cultivars Mombaça, Milênio, Vencedor and Aruana are genetically distinct and are not related to the remaining collection.

Table 1 Agronomic performance of *Panicum maximum* genotypes in the Brazilian Cerrado

	Accumulated LDMY in six cuts				Accumulated SDMY in six cuts							
Overall mean	11,266				3,763							
Cultivars	10,392				4,158							
Accessions	12,598				3,632							
LSD (0.05)	3,683				2,091							
	CP (g/kg)				IVOMD (g/kg)				NDF (g/kg)			
	1	2	3	4	1	2	3	4	1	2	3	4
Overall mean	178	180	169	102	687	686	703	610	722	746	755	725
Cultivars	183	188	173	105	699	698	704	618	706	745	756	744
Accessions	176	178	168	100	683	682	702	607	727	746	755	719
LSD (0.05)												
genotype (cut)	39				102				76			
cut (genotype)	22				60				54			

Conclusions There were no differences in LDMY and SDMY between the means of cultivars and accessions. However, there were differences among the accessions, thus permitting the identification of promising accessions on the basis of forage production components. Molecular characterisation was an efficient tool to show the variability among the accessions and cultivars.