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Genetic diversity based on morphological data in *Panicum maximum* hybrids

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ABSTRACT - The objective of this experiment was to evaluate the genetic divergence between hybrids obtained from 10 sexual genitors of the *Panicum maximum* breeding program at Embrapa Beef Cattle. For this, the following morphological descriptors were used: plant height, growth habit, leaf aspect, leaf waxiness, hair density on the sheath (DePB) and blade (DePL), degree of hardiness of the hairs on the leaf sheath (DuPB) and blade (DuPL) and length of hairs on the sheath and blade. The characteristics growth habit and waxiness were not included in the analysis for being invariant. The phenotypic correlations were low and, therefore, not used to eliminate variables. By the principal component analysis, an 84.3% accumulation of the variation was observed until the fourth component. The last four principal components presented an estimate lower than 0.7 and allowed the identification of the variables DePB, DuPB and DuPL as the least important for diversity studies. The morphological characters used were not efficient to distinguish the progenies, but allowed the formation of morphological groups that converged with the graphic analysis of the principal components. An apparent error rate of 17.04% was observed in the classification of the individuals in the groups and 55.5% in the classification of the individuals in the progenies. The individuals in the *P. maximum* half-sib progenies are genetically divergent, but may not be grouped with only the descriptors used in this experiment. The pubescence characteristics were the least important in the discrimination of the genotypes.

Key Words: discriminating analysis, optimization method, principal components, relative importance of the characteristics, Tocher

Introduction

It is estimated that Brazil has approximately 172 million hectares of pastures, which represent around 22% of its territory. However, a major portion of this area is established with exotic cultivars of clonal reproduction, which represents a serious risk to the overall pasture-based systems (Valle et al., 2009).

Forage monoculture have brought many serious problems to the country, such as spittlebug incidence on *Brachiaria decumbens* pastures, sudden death on Marandu pastures (*B. brizantha*) and the leaf fungus *Bipolaris maydis* on Tanzaniagrass (*Panicum maximum*), and contributed to pasture degradation in Brazil.

In fact, it is necessary to increase the availability of forage grasses adapted to the different edaphic and climatic Brazilian conditions as well as to the requirements of the farmers in the different regions of the country. In this sense, genetic improvement and the release of new cultivars of *P. maximum* arise as a strategy of diversification.

Recent research has allowed crosses between sexual and apomictic plants and, thus to obtain hybrids with high release potential (Resende et al., 2008). Also, due to the segregation of the sexual character in forages, these crosses also result in potential sexual genitors.

It is known that plants of asexual reproduction, vegetative or apomictic, present high degree of heterozigosity (Borém & Miranda, 2009) and that apomictic forages are polyploid, factors that contribute to the great segregation in crosses. In this sense, studies of genetic diversity may allow the identification of discrepant genitors with greater chance of obtaining heterosis or genetic variability in the progeny, an essential condition for selection.

Genetic diversity among accessions may be studied by various measures as molecular markers and biochemical, agronomic and morphological characters. The use of morphological descriptors in the study of genetic diversity is important, because it allows the identification of the most discrepant genitors (Carvalho et al., 2003).

In view of what has been presented, the objectives of this research were to evaluate the genetic diversity among individuals of half-sib hybrid progenies from the open-pollination of 10 genitors of the germplasm bank of Embrapa Beef Cattle using morphological characteristics.

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Material and Methods

The experiment was conducted at Embrapa Beef Cattle in Campo Grande, Mato Grosso do Sul, Brazil, at 20°27' latitude and 54°57' longitude. The climate, according to the classification of Köppen, is of the rainy tropical savanna type, subtype Aw, characterized by an irregular annual distribution of the precipitation and by the occurrence of a well-defined dry period during the cold months and a rainy period in the summer.

The 250 accessions of the *Panicum maximum* germplasm bank were conserved in the field in 4 × 4 m² plots 2 m apart from each other. Ten plots of sexual plants (tetraploid) whose chromosome numbers had been previously doubled by colchicine were randomly distributed among the apomictic (tetraploid) accessions. At flowering (March to May), sexual plants were naturally pollinated by the neighboring plants, so that their seeds would generate half-sib families. Hybrid seeds of ten sexual plants were harvested in May and June 2004 and germinated in October in Styrofoam trays with vermiculite:sand at 1:1. After two months, 30 seedlings of each sexual progenitor were transplanted to plastic bags with soil and maintained until adequate conditions for transplanting in the field.

In December 2005, the seedlings of each progeny were transplanted to the experimental area in a randomized block design, with five plants per plot and six replications, in a total of 30 plants per family. Spacing between plots and between plants in plots was of 1 m and between replications, 2 m. The soil of the experimental area, a dark red latosol (oxisol), presented the following characteristics: pH $CaCl_2$ = 4.53; P = 1.29 mg/dm^3; K = 48.6 mg/dm^3; Ca^{2+} = 1.64 cmol/dm^3; Mg^{2+} = 0.93 cmol/dm^3; H + Al = 8.31 cmol/dm^3).

In the beginning of November 2005, dolomitic lime was applied (3 t/ha) and incorporated. Phosphate and potassium fertilization consisted of 100 kg of P_2O_5/ha (simple superphosphate) and 100 kg K_2O/ha (potassium chloride), respectively. A micronutrient mixture FTE BR16 (50 kg/ha) and nitrogen fertilizer (100 kg N/ha as urea) at transplant were also applied. Fertilization was again applied on December 2005, as above, with the exception of 50 kg FTE BR16/ha.

Plots were managed through cuts with a coastal mower with the objective of simulating a rotational stocking.

The hybrids were morphologically characterized for their vegetative, reproductive and pubescence characteristics, with the descriptors proposed by Jank et al. (1997) in the Catalogue of Characterization and Evaluation of the *P. maximum* germplasm. The following vegetative characteristics were evaluated: height - height of the plant (m), measured from the soil to the highest point disregarding the inflorescences; growth habit - 0 (stoloniferous – growth parallel to the soil), 1 (cespitose stoloniferous – growth in bunches, with the presence of stolons), 2 (cespitose – growth in bunches); leaf aspect - 0 (decumbent – leaves bent down), 1 (brittle – leaves reaching a point then abruptly bending at the tips), 2 (erect – leaves with a defined vertical growth); leaf waxiness (presence of wax on the stems and blades) - 0 (absent), 1 (present).

The following reproductive characteristics were evaluated: inflorescence shape - 0 (panicle), 1 (type C – intermediate type between panicle and raceme), 2 (raceme); primary ramification - 0 (short – shorter than half the length of the rachis), 1 (long – longer than half the length of the rachis); secondary ramification (visual observation of the length of the secondary ramifications) - 0 (absent), 1 (short), 2 (long); height of the secondary ramification (visual observation of the site of occurrence of the secondary ramification in relation to the primary ramification) - 0 (absent), 1 (concentrated at the base), 2 (throughout the ramification); distribution of the spikelets - 0 (dispersed throughout the inflorescences), 1 (uniformly distributed along the ramifications); spots on the spikelets (quantity evaluated visually) - 0 (absent), 1 (few), 2 (medium), 3 (many); color of the spots - 0 (absent), 1 (light brown), 2 (brown), 3 (purplish).

Pubescence characteristics were also evaluated: density or comparative quantity of hairs on the blades (visual evaluation of the classes): 0 (absent, glabrous), 1 (low), 2 (medium), 3 (high); length of hairs on the blades (visual evaluation of the classes) - 0 (absent, glabrous), 1 (short), 2 (long); degree of hardness of the hairs on the blades - 0 (absent or glabrous), 1 (hard), 2 (soft); density (comparative quantity of hairs on the sheath) - 0 (absent), 1 (low quantity), 2 (medium), 3 (high); length of hairs on the sheath - 0 (absent, glabrous), 1 (short), 2 (long); degree of hardness of hairs on the sheath - 0 (absent, glabrous), 1 (hard), 2 (soft).

The characteristics growth habit and waxiness were not used in the divergence analysis for being invariable among the evaluated genotypes. The reproductive characteristics were also not included in the analysis because some of the evaluated genotypes did not flower thus were not able to be evaluated.

Pearson's correlation was used for identifying redundant variables, which were eliminated when they shared a correlation greater than 0.8.

The data were subjected to principal component analysis to study the relative importance of the morphological descriptors for the discrimination of genetic diversity among evaluated hybrids and progenitors. In this case, the variables that presented the highest weights in the last associated eigenvectors represent redundant variables and do not contribute to the evaluation of the dispersion of the genotypes.

The study of the genetic diversity was done based on measures of the mean Euclidian distance between pairs of genotypes based on their phenotypic values, which allowed to obtain a dissimilarity matrix required for their clustering. The genotypes were clustered according to the optimization method of Tocher to determine the number of existing groups (Cruz & Carneiro, 2006).

Standardized variables were used both in the principal components analysis and in the clustering.

For the evaluation of the clustering efficiency, the discriminate analysis of Anderson (Cruz & Carneiro, 2006) was used with the results of the clustering, and also based on the progeny to evaluate if the methodology was able to discriminate the genotypes according to their origin.

Results and Discussion

In the dataset, variables with a correlation coefficient greater than 0.8 were not identified, which would justify their removal prior to the principal components analysis (Table 1). According to Resende (2007), variables that have very high genetic correlations may be discarded for not implying a better discrimination of the genotypes, which also applies to the phenotypic correlation. Moreover, van de Wouw et al. (2008) and Jorge et al. (2008) based their research on correlations above 0.7 for discarding redundant variables in the study of genetic diversity.

The highest correlation coefficients were recorded between the variables DePB and CoPB, DuPL and DePL, CoPL and DuPL and DuPB and DePB, which were 0.73; 0.69; 0.69 and 0.64, respectively (Table 1). The high correlation coefficients observed between these variables are probably due to the narrow difference in the evaluation manner. The variables least correlated with the other variables were plant height and leaf aspect, which indicates that these favorable attributes come together to assess the genetic variability.

In a similar study on genetic variability of the *Brachiaria* germplasm bank, Assis et al. (2003) found high correlations between the pubescence characters. These authors observed coefficients of 0.98; 0.93; 0.96; and 0.90 between the variables leaf hair density and sheath hair density; leaf hair density and sheath hair length; and leaf hair length and sheath hair length, respectively. In the present research, pubescence characteristics in the sheath showed low correlation with characteristics of pubescence on the blade (correlation < 0.40).

In an experiment involving the characterization of accessions of the germplasm bank of the genus *Panicum* of the *International Livestock Research Institute*, van de Wouw et al. (2008) observed correlations of 0.71 to 0.93 between the variables hair density in the stems, leaf, sheath, and used only the density of the hairs in the abaxial region of the leaf in the multivariate analysis. According to these authors, the characters hardness and length of hairs were highly correlated and, therefore, hardness was discarded for being a more subjective variable.

The relative importance of the characters for the study of genetic diversity is evaluated by observing the characteristics with more weight in the eigenvectors associated to the eigenvalues with an estimate smaller than 0.7. In this study, the last four eigenvalues were estimated at less than 0.7 (Table 2). The characteristics of greater weight in the last four associated eigenvalues were, in decreasing order, sheath hair density, leaf hair hardness, leaf hair density and sheath hair hardness (Table 2). According to Cruz & Carneiro (2006), the characters of greater weight in the last eigenvalues are said to be redundant characters,

Table 1 - Pearson correlation coefficient between the phenotypic values of relative importance characters in *Panicum maximum* hybrids

	Plant height	Leaf aspect	Sheath hair density	Sheath hair hardness	Sheath hair length	Leaf hair density	Leaf hair hardness	Leaf hair length
Plant height	1.00	0.08	0.11	-0.01	0.16**	0.05	0.16**	0.11
Leaf aspect		1.00	0.15**	0.09	0.17**	0.24**	0.15**	0.32**
Sheath hair density			1.00	0.64**	0.73**	0.40**	0.19**	0.18**
Sheath hair hardness				1.00	0.59**	0.29**	0.25**	0.12*
Sheath hair length					1.00	0.31**	0.13*	0.27**
Leaf hair density						1.00	0.69**	0.69**
Leaf hair hardness							1.00	0.65**
Leaf hair length								1.00

**, *: significant by the t test at 1 and 5%, respectively.

which may also be confirmed through the observation of the phenotypic correlation matrix (Table 1), where they presented high correlation coefficients with the other descriptors evaluated in the study.

Shimoya et al. (2002), evaluating the diversity in the elephantgrass germplasm bank based on 17 morphological descriptors, observed that the last five canonic variables presented a variance lower than 0.7 and that the characteristics of greatest weight were, in decreasing order, stem diameter, leaf width in the middle of the adult mean leaf, leaf width in the base of the adult mean leaf, awn length and spikelet length. Assis et al. (2002) identified the pubescence variables as those less efficient in the discrimination of *Brachiaria* accessions. According to these authors, in the classification of the accessions according to the species, the pubescence characteristics resulted in a larger apparent error rate when compared with reproductive and vegetative characteristics.

According to Cruz (2008), characters liable of discard in genetic diversity studies are those invariant or redundant, but criteria as their stability, ease of measure and cost, among others, may be considered. From the identification of the least important variables to discriminate genotypes, the recommendation to remove these variables in future evaluations may be made.

Cluster analysis based on the mean Euclidian distance provided the formation of 15 groups. Of the 270 individuals evaluated, 93 could be clustered in the first and largest group and five were allocated to individual groups. The groups with the highest number of individuals were groups 1, 2 and 3, with 93, 65 and 62 hybrids, respectively. Groups 4, 5, 6, 7, 8, 9 and 10 assembled 15, 6, 11, 6, 3, 2 and 2 individuals, respectively. Of the 270 individuals evaluated, five could not be grouped due to the high dissimilarity index observed between these and the other groups. In this sense, these individuals remained in individual groups.

Groups 1, 2 and 3 covered 34.44; 24.07; and 22.96% of the individuals of the population. Shimoya et al. (2002), in a study on the genetic diversity among genotypes of the germplasm bank of elephantgrass, observed the formation of 18 groups according to the Tocher methodology, based on the matrix of generalized distances of Mahalanobis and the inclusion of 44% of the genotypes of the first group. Nevertheless, according to Mohammadi & Prasanna (2003), the Euclidian distance is the statistics most often used to estimate the genetic distance between individuals based on morphological data.

The greatest distance between groups was estimated between groups 7 and 15 (2.4232). The groups that presented the lowest distance values were 11 and 13 (1.1115) (Table 4). Although these groups presented greater and lower distance values, groups 11, 13 and 15 are comprised of only one individual. In this sense, considering those groups with more than one individual, we have 2.1165 as maximum distance between groups 3 and 10 and 1.1890 as the minimum distance between groups 2 and 8. The mean distance between groups was estimated as 1.6143.

The maximum distance between individuals was observed between individuals 33 and 246, which belong to group 1 and the progenies 7 and 10, respectively.

The identification of individuals or the most discrepant groups, in addition to the performance of the genotype, is also important in the choice of those which will be recombined. It is known that individuals 188 and 238, despite presenting high dissimilarity, also present good performance (Martuscello, 2007) and may be recommended as progenitors for obtaining the recombination population. Individuals 1 and 107, 1 and 134, and 134 and 204 are also high-performance individuals and present above-average dissimilarity values. Although there are superior and discrepant individuals, the hybrids identified by Martuscello (2007), as having good performance

Table 2 - Estimates of eigenvalues (λj), percentage of accumulated variation (λ%) and eigenvectors associated to the principal components in *Panicum maximum* hybrids

Principal components	λj	λ (%)	Associated eigenvectors							
			Plant height	Leaf aspect	Sheath hair density	Sheath hair hardness	Sheath hair length	Leaf hair density	Leaf hair hardness	Leaf hair length
1	3.1799	39.75	0.112	0.209	0.404	0.359	0.391	0.447	0.381	0.393
2	1.6294	20.37	-0.035	-0.148	0.428	0.421	0.424	-0.292	-0.408	-0.430
3	1.0185	12.73	0.920	0.258	0.001	-0.186	0.101	-0.183	-0.090	-0.035
4	0.9201	11.50	-0.316	0.890	-0.010	-0.071	0.051	-0.096	-0.298	0.038
5	0.4822	6.03	0.106	0.247	-0.161	0.626	-0.443	-0.126	0.400	-0.372
6	0.3432	4.29	-0.032	-0.075	-0.531	0.319	0.364	-0.498	0.033	0.478
7	0.2341	2.93	-0.168	0.072	0.234	-0.396	0.253	-0.476	0.649	-0.209
8	0.1926	2.41	-0.010	0.055	-0.539	-0.068	0.512	0.426	0.096	-0.498

Total = 60.513

according to the selection index in the rainy season, were clustered primarily in groups 1, 3 and 4, which showed, in general, dissimilarity index below 1.6143, except for the combination of groups 3 and 4 (Table 3).

The identification of discrepant pairs of genotypes with good performance is important so that they can eventually be used in the future in forage breeding programs aiming to exploit the hybrid vigor of the cross.

The principal component analysis based on morphological characters of the half-sib progenies of *P. maximum* only presented more than 80% of the accumulated variation when up to the fourth principal component was considered, where they accumulated 84.3% of the total variation (Table 2). According to Cruz & Carneiro (2006), the principal component analysis should accumulate 80% of the variation up to the second principal component to be considered efficient, which would summarize all the variation in only two axes.

Assis (2001), in a genetic diversity study based on 24 morphological characters of *Brachiaria* species, observed an accumulation of 85.4% of the total variation on the third eigenvalue associated, when the 24 morphological characters were simultaneously evaluated. Shimoya et al. (2002), evaluating 17 morphological characters in accessions of elephantgrass, observed 81.8% of accumulation in the seventh principal component.

The accumulation of 84.3% of the variation up to the fourth principal component allowed the evaluation of the dispersion of the hybrids in four axes (Figure 1). It can be observed that the limit between the progenies was not well defined (Figure 1A, 1B and 1C). On the other hand, when the points were plotted as a function of groups formed by

Table 3 - Distance between groups (above the diagonal) and mean distance between the individuals in the group (in the diagonal) formed by the optimization method based on morphological characteristics of half-sib progenies of *Panicum maximum*

	Groups														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	0.7263	1.6514	1.3075	1.3261	1.4746	2.0492	1.6114	1.8380	1.9826	1.8009	1.4281	2.2622	1.4030	1.7498	2.2801
2		0.9499	1.3250	1.4895	1.2196	1.3009	1.3694	1.1890	1.3358	1.6998	1.8170	1.6773	1.2797	1.2117	1.6273
3			0.7973	1.7475	1.5142	1.7561	1.4415	1.6970	1.8689	2.1165	1.8438	2.0845	1.1545	1.7430	2.0797
4				0.9115	1.3580	1.7396	1.5972	1.4343	1.7278	1.3720	1.4367	1.9860	1.5284	1.4044	2.0131
5					0.8722	1.5256	1.2267	1.7008	1.2904	1.5824	1.7290	1.6668	1.5498	1.2991	2.1180
6						0.9179	1.4852	1.4957	1.2191	1.4296	1.6679	1.1147	1.1825	1.7219	1.5312
7							0.9377	1.9218	1.6745	1.6109	1.9030	1.3296	1.4389	1.8545	2.4232
8								0.7574	1.5602	1.7400	1.7955	2.0698	1.4218	1.2580	1.2057
9									0.9730	1.4625	1.5573	1.4865	1.4470	1.4369	1.5543
10										0.9737	1.1938	1.3224	1.4947	1.8213	1.8907
11											0.0000	1.9421	1.1115	1.8835	1.7864
12												0.0000	1.5297	2.2798	2.2139
13													0.0000	1.8281	1.5691
14														0.0000	1.5921
15															0.0000

Table 4 - Correct classification (in the diagonal) and misclassification (outside the diagonal) of the individuals of half-sib progenies of *Panicum maximum* grouped according to the optimization method of the discriminate analysis of Anderson, considering eight morphological characters

	Groups														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	84.95	0	12.9	0	0	0	2.15	0	0	0	0	0	0	0	0
2	0	66.15	4.62	1.54	12.31	0	3.08	7.69	1.54	0	0	0	0	3.08	0
3	0	0	95.16	0	0	0	4.84	0	0	0	0	0	0	0	0
4	6.67	0	0	80	6.67	0	6.67	0	0	0	0	0	0	0	0
5	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	9.09	63.64	9.09	0	9.09	0	0	9.09	0	0	0
7	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0
10	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0
11	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100

the optimization method, the limit of the groups in the four axes may be more clearly defined (Figure 1D, 1E and 1F).

The first and second principal components represented 60.3% of the variation and allowed the identification of a reasonable part of the morphological groups based on the optimization methodology. In this sense, groups 1, 2, 3 and 4 were the most easily identifiable (Figure 1D). Nevertheless, group 2 did not show well-defined limits when compared with the others, when only two axes were considered. By observing axes 1 and 3, the limit between group 2 and groups 5, 6, 7 and 15 may be more easily observed. With the inclusion of the fourth axis, the limits of groups 2, 8 and 10 may be verified.

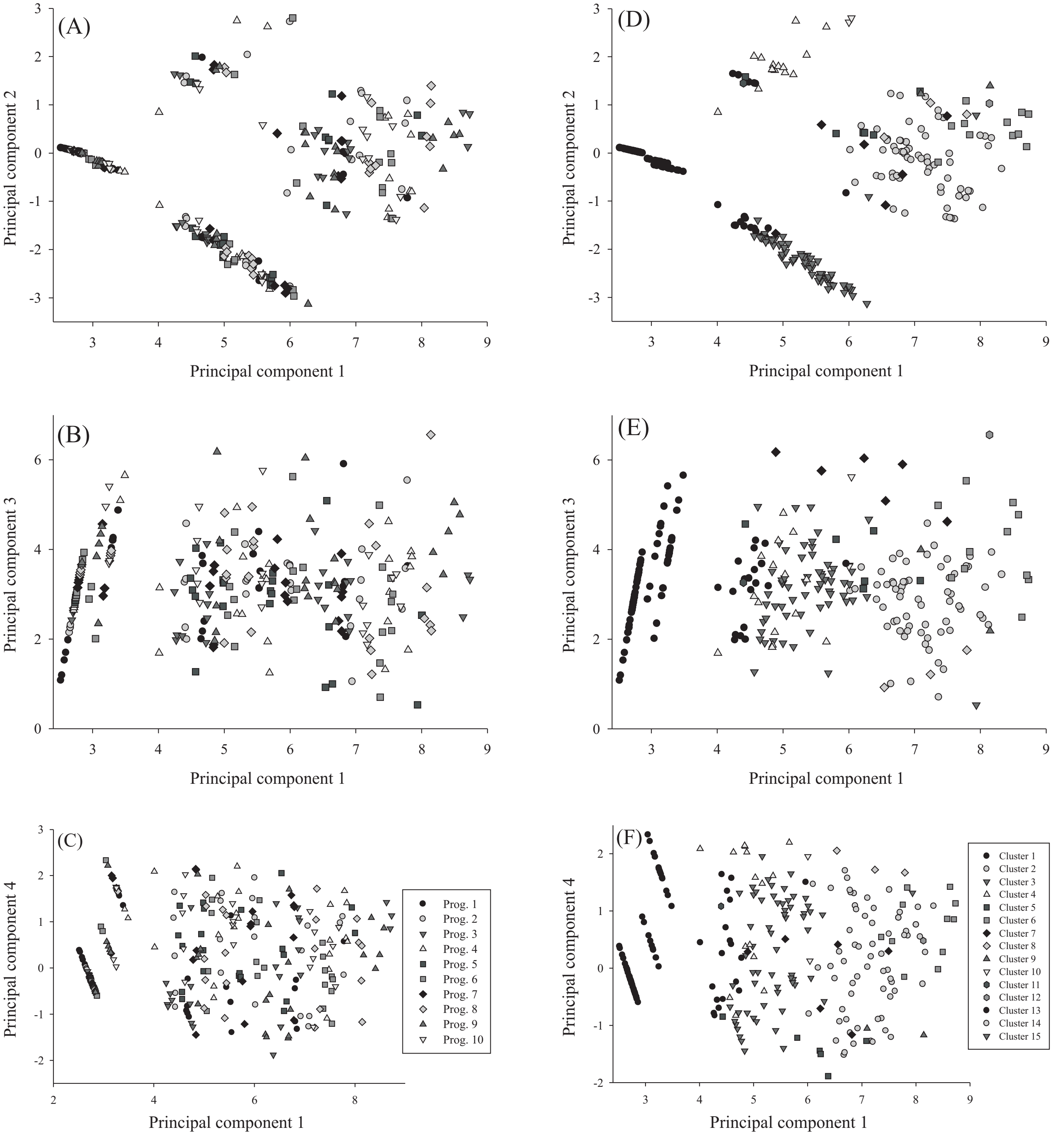

Figure 1 - Dispersion of 270 hybrids of half-sib progenies (Prog.) of *Panicum maximum*, considering the principal components (CP) 1 and 2 (A), 1 and 3 (B) and 1 and 4 (C).

Groups 11, 12, 13 and 14, formed by a single individual, could not be discerned in the dispersion. Nevertheless, it was expected that they would be easily identifiable due to their more discrepant morphological nature.

The discriminate analysis of Anderson indicated an apparent rate of discordance of 17.04%, in which 46 of the 270 individuals clustered by the optimization method were incorrectly classified, but when the discriminate analysis was performed using as basis the progeny, there was an increase in the misclassification rate, which was 55.5%. The increase in the apparent error rate indicates that the characteristics assessed were not sufficient to promote differentiation by the discriminate analysis of the progenies, or that there is a strong genetic recombination in the hybrids involving multiple genitors due to the process of open pollination.

Groups 2 and 6 presented more misclassified individuals, with only 66.15 and 63.64% of correct classifications, respectively (Table 4). Group 2 had 4.62; 1.54; 12.31; 3.08; 7.69; 1.64; and 3.08% of the individuals classified in the groups 3, 4, 5, 7, 8, 9, 14, respectively. Group 6 had 9.09% of the individuals classified in each of the groups 5, 7, 9 and 12.

It can be observed that the eight characteristics were only able to completely discriminate the hybrids of groups 5, 7, 8, 9, 10, 11, 12, 13, 14 and 15. It is noteworthy that the groups constituted by a few individuals normally present divergent characteristics from the others, mainly when they are constituted by a single individual.

The morphological characteristics assessed were not able to completely discriminate any of the evaluated progenies (Table 5). Probably, the high discordance rate was due to the low number of variables and also to the genetic similarity between individuals of the progenies, since they are half-sib progenies and the population is the common pollen donor. On the other hand, van de Wouw et al. (2008) discriminated well the species *P. antidotale*, *P. phragmites* and *P. turgidum* from the other species based on 32 morphological and agronomic characters in both the principal component analysis and the nearest neighbor method; however, the group formed by *P. maximum*, *P. coloratum* and *P. infestum* was extremely variable, and these three species were not discriminated.

Although Group 1 contained individuals of all the progenies, it was formed primarily by the progenies 1, 3, 4, 5, 7 and 10 (Table 6). Group 2 had a higher frequency

Table 5 - Correct classification (in the diagonal) and misclassification (outside the diagonal) of the individuals of half-sib progenies of *Panicum maximum* grouped according to the discriminate analysis of Anderson, considering eight morphological characters

	Progenies									
	1	2	3	4	5	6	7	8	9	10
1	16.67	12.5	20.8	4.17	12.5	13.0	8.33	0	0	12.5
2	0	51.85	7.41	3.7	11.1	3.7	3.7	0	3.7	14.81
3	0	7.14	32.1	7.14	10.7	3.6	10.7	3.57	3.57	21.43
4	7.41	7.41	14.8	33.3	7.41	0	0	3.7	3.7	22.22
5	0	0	0	7.14	50.0	7.1	7.14	3.57	14.3	10.71
6	0	10.34	0	6.9	6.9	59.0	13.8	3.45	0	0
7	4.0	4.0	28.0	4.0	12.0	4.0	28.0	12.0	4.0	0
8	0	6.67	10.0	3.33	0	3.3	3.33	63.3	10.0	0
9	0	3.45	6.9	0	10.3	3.5	0	24.1	44.8	6.9
10	0	4.35	0	17.4	8.7	0	0	0	8.7	60.87

Table 6 - Frequency of progenies in the groups (g) resulting from the optimization clustering of *Panicum maximum* hybrids

Progeny	Frequency of progenies in the groups														
	g1	g2	g3	g4	g5	g6	g7	g8	g9	g10	g11	g12	g13	g14	g15
1	10	8	2	1	0	1	0	0	0	0	0	0	1	1	0
2	6	11	3	2	0	0	0	3	0	1	0	0	0	0	1
3	15	1	4	6	0	0	1	0	0	1	0	0	0	0	0
4	11	8	5	2	0	0	0	0	1	0	0	0	0	0	0
5	16	1	7	0	1	3	0	0	0	0	0	0	0	0	0
6	2	14	3	0	3	1	5	0	1	0	0	0	0	0	0
7	9	1	6	3	2	3	0	0	0	0	0	1	0	0	0
8	4	11	14	0	0	1	0	0	0	0	0	0	0	0	0
9	4	9	14	0	0	2	0	0	0	0	0	0	0	0	0
10	16	1	4	1	0	0	0	0	0	0	1	0	0	0	0

of individuals of progenies 1, 2, 4, 6, 8 and 9. Group 3 also contained individuals of all the progenies in similar frequencies, except for progenies 8 and 9, which were less frequent. In Group 4, a higher frequency of progeny 3 was observed, and in group 5, there was higher frequency of the progenies 6 and 7. Group 6 included primarily the progenies 5, 7 and 9 and group 8 was comprised of plants of progeny 2 alone.

Conclusions

Individuals of half-sib progenies of *Panicum maximum* are genetically divergent. The characteristics used were not able to differentiate the individuals according to their progeny; however, distinct morphological groups could be established according to the methodology of Tocher. The pubescence characteristics were the least important in the discrimination of the genotypes.

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