



Estimation of genetic diversity in *Cenchrus ciliaris* accessions introduced in the Brazilian semi-arid region

Ierla Carla Nunes dos Santos Ribeiro · Tiago Lima do Nascimento ·
Rafaela Priscila Antônio · Nataniel Franklin de Melo

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Abstract The objective of this work was to evaluate the genetic variability of *Cenchrus ciliaris* accessions using morpho-agronomic descriptors for the identification of germplasm with phenotypic divergence that can be used as male parents in breeding programmes for the species. Thirty-eight accessions were characterised using six quantitative and 12 qualitative descriptors. The descriptors that most contributed to the divergence were inflorescence length (22.48%), leaf blade width (19.52%) and leaf blade length (18.35%). Based on the mean grouping test, for the character basal tillering intensity, the accessions were distributed into three groups, of which accessions CPATSA79125 and CPATSA79150 had the most tillers. Thus, there was genetic diversity among the evaluated accessions, with an emphasis on the CPATSA79123 and CPATSA90611 genotypes, as they were the most divergent accessions and thus can

be used in clonal selections and in the prospection of genes of agronomic interest. The different accessions can be selected for the most varied objectives of the improvement programmes for the species.

Keywords Phenotyping · Genetic divergence · Active germplasm bank · Tropical forage

Introduction

Brazil's vast and diverse landscape encompasses a wide range of climatic zones, which greatly influence the distribution of livestock and the importance of forage production. In general, we can divide Brazil into semi-arid zones (Northeast and West Central regions) and humid zones (Amazon, South and Southeast regions) and discuss their significance for livestock and forage production. While humid regions are characterised by a humid tropical or temperate climate with abundant rainfall and well-defined seasons, semi-arid zones of Brazil are characterised by a steppe climate with prolonged dry seasons and irregular and low rainfall. The predominant vegetation includes Caatinga, which consist of drought-resistant shrubs and trees. Livestock, primarily goats and cattle, is raised in this region, and forage production is crucial for their sustenance during dry periods (Sá and Silva 2015).

Research with native and exotic forages for the Brazilian semiarid region is still limited; however, in

I. C. N. dos Santos Ribeiro
Universidade Estadual de Feira de Santana,
Feira de Santana, Brazil
e-mail: ierlacarla@gmail.com

T. L. do Nascimento
Embrapa Semiárido/FACEPE, Petrolina, Brazil
e-mail: tiago_lim.a@hotmail.com

R. P. Antônio · N. F. de Melo (✉)
Embrapa Semiárido, Petrolina, Brazil
e-mail: nataniel.melo@embrapa.br

R. P. Antônio
e-mail: rafaela.antonio@embrapa.br

this region, a promising seed market has been formed mainly by cultivars developed for other regions with different edaphoclimatic conditions (Antônio 2015). Thus, there is a need for initiatives to advance the development of forage cultivars that are more adapted to semi-arid regions. Allied to this, the growth of herds of goats, sheep and cattle in the region is factors that determine the increase in the consumption of forage seeds. According to IBGE (2021), Brazil's goat population stands at 11,923,630 heads, with the state of Pernambuco housing 3,204,448 of them. This figure surpasses all other states in the Northeast region, except for the state of Bahia, which boasts a slightly larger goat herd. Similarly, in terms of cattle, Pernambuco has 2,173,313 heads, which is the highest figure among the states in the Northeast region. In this way, exploring the potential of species, whether native or exotic forage destined for animal feed in the semiarid region, using this information for breeding programmes for these crops is very pertinent. In this sense, the Active Germplasm Bank (BAG) ex situ of Embrapa Semiárida of the genus *Cenchrus* with about 120 accessions exists to keep the genetic variability of the species preserved. These characteristics are positive, especially in regions with a semi-arid climate, since the herds in this region have food available in periods of drought.

Buffelgrass is known for its exceptional drought tolerance, making it well adapted to areas with irregular and low rainfall. It can be used to produce hay and silage due to its high nutritional value, persistence, versatile grazing options and adaptability to a range of soil types; however, there are few commercial genotypes (Voltolini et al. 2019). Therefore, the addition of new accessions is necessary to expand the options for future crossings and, consequently, to obtain new cultivars with desirable characteristics for semi-arid conditions. This need for expansion is due to numerous reasons. For example, in the case of feeding goats that are medium-sized animals, accessions with a more prostrate growth habit facilitate access to food, making it a positive feature to select.

The genetic diversity offered by the BAG is essential for the activities of breeding programmes, enabling the selection of more divergent genitors destined for crosses if this potential is identified (Bonato et al. 2006). In a breeding programme, obligate apomictic plants can only be used as male parents in crosses. The recognition of a good material for incorporation

in breeding programmes is determined by its characterisation or its description, allowing the observation of different patterns and thus the correct identification of each plant material (Nevada 2011). Therefore, we sought to estimate the genetic variability among buffelgrass accessions to identify promising genotypes for incorporation and exploitation in genetic improvement programmes for the species.

Materials and methods

For the evaluated accessions, assessments were carried out at the recommended time for each descriptor/characteristic, using quantitative and qualitative morpho-agronomic descriptors. The experiment was conducted at the Caatinga Experimental Station, which is affiliated with Embrapa Semiárida, situated in Petrolina-PE. The experimental site is located at coordinates S09° 24' 38" and W40° 29' 56". The climate is classified as semi-arid with an altitude of 377 m. The soil in the area is classified as red-yellow dystrophic argisol with a sandy loam texture.

Thirty-eight accessions of the genus *Cenchrus* belonging to the Active Germplasm Bank of Embrapa Semiárida were used (Table 1). The studied accessions were selected because they were the most promising in terms of size for use within the *Cenchrus* genetic improvement program. Seeds of these accessions were sown in trays containing commercial substrates composed of vermiculite. The seedlings were transplanted to the field at a size of about 10 cm. The experiment was carried out in a randomised block design with three replications, where six plants per plot were evaluated.

For the characterisation of accessions, the descriptors and procedures described by MAPA (2019) were used. Twelve qualitative descriptors and six quantitative descriptors were used, as follows: Qualitative descriptors: type of growth—TG (1-erect, 2-semi-erect and 3-prostrate), rhizome shape—RS (1-linear, 2-globose), leaf blade edge—LBE (1-smooth, 2-serrated), leaf blade colour—LBC (1-light green, 2-green, 3-blue green), leaf blade hairiness—LBH (1-absent or 2-present), intensity of the leaf blade hairiness—ILBH (0-no hair, 3-low, 5-medium and 7-high), sheath pilosity—SP (1-absent or 2-present), inflorescence base pilosity—IBP (1-absent or 2-present), inflorescence colouring—IC (1-cream,

Table 1 List with identification and origin of 38 accessions of buffelgrass from *Cenchrus* Germplasm Active Bank of Embrapa Semi-Arid characterised and evaluated in the present work

Accessions	Date of introduction	Origin
CPATSA7757	14/03/1977	Brazil (Matão-SP)
CPATSA78102	27/09/1978	Brazil (Matão-SP)
CPATSA78103	06/07/1979	Brazil (Matão-SP)
CPATSA78122	07/04/1979	Australia (CSIRO)
CPATSA79121	07/04/1979	Australia (CSIRO)
CPATSA79123	07/04/1979	Australia (CSIRO)
CPATSA79125	15/04/1979	USA (USDA)
CPATSA79129	15/04/1979	USA (USDA)
CPATSA79130	15/04/1979	USA (USDA)
CPATSA79134	26/06/1979	USA (USDA)
CPATSA79139	26/06/1979	Brazil (Quissamã-SE)
CPATSA79141	26/06/1979	Brazil (Quissamã-SE)
CPATSA79144	26/06/1979	Brazil (Quissamã-SE)
CPATSA79147	26/06/1979	Brazil (Quissamã-SE)
CPATSA79148	26/06/1979	Brazil (Quissamã-SE)
CPATSA79149	26/06/1979	Brazil (Quissamã-SE)
CPATSA79150	26/06/1979	Brazil (Quissamã-SE)
CPATSA79151	26/06/1979	Brazil (Quissamã-SE)
CPATSA80194	11/05/1980	Tanzania
CPATSA80195	11/05/1980	Tanzania
CPATSA80196	11/05/1980	Tanzania
CPATSA80199	11/05/1980	Tanzania
CPATSA80200	11/05/1980	Tanzania
CPATSA83476	29/09/1983	Brazil (Parafba)
CPATSA90556	10/09/1990	USA (Texas A&M)
CPATSA90558	10/09/1990	USA (Texas A&M)
CPATSA90563	10/09/1990	USA (USDA)
CPATSA90570	10/09/1990	USA (USDA)
CPATSA90572	10/09/1990	USA (USDA)
CPATSA90580	10/09/1990	USA (USDA)
CPATSA90581	10/09/1990	USA (USDA)
CPATSA90591	10/09/1990	USA (USDA)
CPATSA90592	10/09/1990	USA (USDA)
CPATSA90611	10/09/1990	USA (USDA)
CPATSA90613	10/09/1990	USA (USDA)
CPATSA90615	10/09/1990	USA (USDA)
CPATSA7754	14/03/1977	Brazil (Matão-SP)
CPATSA7602	26/02/1976	Brazil (Pernambuco/Agroceres)

2-brown, 3-purple, 4-black, 5-purple with cream, 6-black with cream), spikelet shell shape—SSS (1-bristles together, 2-free bristles), spikelet grouping—SG (1-isolated or 2-grouped) and spikelet anther colour—SAC (1-white, 2-beige, 3-pink, 4-purple, 5-black, 6-yellow, 7-dark yellow, 8-purple); Quantitative descriptors: basal tillering intensity—BTI,

stem diameter—SD, stem internode length—SIL, leaf blade length—LBL, leaf blade width—LBW and inflorescence length—IL.

Qualitative data were presented only in a table of accessions, with the patterns found within the accession considering the large number of classes present within these variables. Data on quantitative

characteristics were subjected to an analysis of variance using the following model:

$$y_{ij} = m + b_j + t_i + e_{ij}$$

where y_{ij} = value observed in the experimental unit that received treatment i , block j ; m = general effect of the mean; b_j = effect of block j ; t_i = effect of treatment i ; e_{ij} = random error (residue).

To estimate the genetic divergence among accessions using data from quantitative morpho-agronomic descriptors, a matrix of genetic distances among accessions was obtained using the generalised distance of Mahalanobis (1936).

The statistical analysis model used for calculating the generalised Mahalanobis distance with quantitative data was as follows:

$$D_{ii'}^2 = \delta' \Psi^{-1} \xi$$

where $D_{ii'}^2$ = Mahalanobis distance between genotypes i and i' ; Ψ^{-1} = the matrix of variance and residual covariances; $\delta' = [d_1, d_2, \dots, d_v]$, where $d_j = y_{ij} - y_{i'j}$; $\xi = y_{ij}$: average of the i -nth genotype in relation to the j -nth variable.

After obtaining the matrix, the accessions were grouped using mean clustering between the groups (UPGMA) to create the dendrogram. The cutline in the dendrogram for the formation of groups was established accord to the method of Mojena (1977), and the consistency of the groups formed by the hierarchical method was verified using the cophenetic correlation coefficient (CCC). In addition, the relative contribution of the descriptors to divergence was

determined using the computational software GENES (Version 2021.1.9) (Cruz 2016). Finally, the average number of accessions for each characteristic was grouped using the Scott and Knott (1974) grouping method.

Results and discussion

There was a significant difference among the accessions for all evaluated traits, which indicates a high level of genotype variation (Table 2). This represents the availability of base materials for exploitation regarding the composition of improved materials. Bruno et al. (2017) evaluated 25 *Cenchrus* accessions with the aim of characterising and identifying genetic diversity and verifying a wide genetic variation among individuals. These results showed that there was variability within the *Cenchrus* BAG of Embrapa Semi-Arid to be explored, which may enable the development of new cultivars, an extremely important factor since there are few cultivars of buffelgrass on the market.

Based on the mean grouping test (Table 3), for the characteristic BTI, the accessions were distributed into three groups. This characteristic defines the ability of the plant to regrow in arid and semi-arid regions, being one of the main characteristics of forage grasses, as it ensures that this plant will regrow after grazing or cutting (Mansoor et al. 2002). The regrowth capacity ensures the perennialism of forage grasses, guaranteeing their survival by enabling the development of a new leaf growth (Costa et al. 2004).

Table 2 Summary of the analysis of variance among 38 accessions of buffelgrass (*Cenchrus ciliaris*) for 6 morpho-agronomic traits

² FV	GL	¹ Traits					
		BTI	SD	SIL	LBL	LBW	IL
Block	2	886.80	0.07	0.12	0.85	0.01	0.11
Accessions	37	7597.18**	0.49**	3.50**	108.03**	0.05**	6.01**
Residue	74	1076.17	0.04	0.42	6.77	0.00	0.38
Average		135.47	2.32	8.12	30.45	0.76	10.25
CV (%)		24.22	8.82	8.55	8.55	7.50	6.05

¹BTI Basal tillering intensity in the stem, SD stem diameter, SIL stem internode length, LBL leaf blade length, LBW leaf blade width, IL inflorescence length

²FV Source of variation, GL degree of freedom

**and *significant at 1 and 5% probability, respectively; ns non-significant, by the F test

Table 3 Mean clustering test of Scott and Knott (1974) among 38 accessions of buffelgrass (*Cenchrus ciliaris*) for 6 morpho-agronomic traits

Accessions	¹ Traits					
	BTI	SD	SIL	LBL	LBW	IL
CPATSA7757	175.61 b	2.46 c	9.28 b	36.50 b	0.92 a	10.56 c
CPATSA78102	158.65 b	2.44 c	6.84 d	30.83 c	0.85 a	9.11 d
CPATSA78103	162.17 b	2.37 c	8.73 b	30.78 c	0.78 b	10.11 d
CPATSA79121	136.17 b	1.83 d	7.60 c	22.69 d	0.58 d	9.81 d
CPATSA78122	160.98 b	3.38 a	6.63 d	52.33 a	0.92 a	10.89 c
CPATSA79123	128.17 b	2.32 c	5.75 d	28.21 c	0.61 d	8.50 e
CPATSA79125	310.83 a	2.80 b	8.18 c	32.53 b	0.86 a	14.61 a
CPATSA79129	128.33 b	1.65 e	7.77 c	24.00 d	0.52 e	7.71 f
CPATSA79130	137.92 b	2.50 c	9.45 b	33.03 b	0.81 b	12.83 b
CPATSA79134	105.00 c	2.42 c	7.63 c	30.20 c	0.80 b	9.11 d
CPATSA79139	151.08 b	2.58 c	7.38 c	30.67 c	0.90 a	9.67 d
CPATSA79141	132.42 b	1.62 e	6.91 d	26.26 d	0.62 d	9.58 d
CPATSA79144	145.00 b	2.68 b	7.63 c	36.19 b	0.79 b	10.55 c
CPATSA79147	107.55 c	1.88 d	7.57 c	29.11 c	0.68 c	10.03 d
CPATSA79148	165.00 b	2.31 c	8.81 b	31.33 c	0.89 a	9.80 d
CPATSA79149	100.42 c	1.82 d	6.75 d	25.31 d	0.62 d	9.08 d
CPATSA79150	267.71 a	2.36 c	9.22 b	37.17 b	0.83 b	11.52 c
CPATSA79151	183.05 b	2.27 c	9.08 b	33.42 b	0.77 b	10.24 d
CPATSA80194	172.17 b	2.53 c	10.44 a	31.30 c	0.79 b	11.00 c
CPATSA80195	146.50 b	2.13 d	6.73 d	26.30 d	0.60 d	9.25 d
CPATSA80196	162.71 b	2.75 b	9.05 b	31.11 c	0.86 a	11.95 b
CPATSA80199	98.22 c	2.00 d	7.83 c	26.25 d	0.84 b	11.03 c
CPATSA80200	169.06 b	2.52 c	7.35 c	36.31 b	0.86 a	9.75 d
CPATSA83476	156.83 b	1.91 d	7.13 d	25.61 d	0.67 c	8.92 d
CPATSA90556	91.72 c	2.93 b	7.98 c	36.44 b	0.92 a	10.97 c
CPATSA90558	123.75 b	2.54 c	8.72 b	36.00 b	0.80 b	12.58 b
CPATSA90563	54.5 c	1.52 e	7.86 c	17.29 e	0.42 f	8.50 e
CPATSA90570	78.25 c	2.42 c	10.08 a	35.86 b	0.80 b	12.25 b
CPATSA90572	56.75 c	2.17 d	9.75 a	27.42 c	0.71 c	11.17 c
CPATSA90580	82.50 c	2.73 b	9.11 b	27.92 c	0.89 a	9.94 d
CPATSA90581	75.00 c	2.45 c	8.02 c	27.31 c	0.86 a	9.75 d
CPATSA90591	148.42 b	2.75 b	7.95 c	30.97 c	0.97 a	10.83 c
CPATSA90592	135.94 b	2.28 c	7.10 d	29.11 c	0.68 c	10.75 c
CPATSA90611	133.58 b	2.07 d	8.18 c	33.64 b	0.82 b	10.42 c
CPATSA90613	117.42 c	2.01 d	7.80 c	23.92 d	0.70 c	7.46 f
CPATSA90615	110.92 c	2.86 b	9.66 a	35.67 b	0.89 a	10.67 c
CPATSA7754	99.92 c	1.98 d	7.63 c	23.58 d	0.55 e	9.50 d
CPATSA7602	77.75 c	1.96 d	9.08 b	24.31 d	0.61 d	9.25 d

Means followed by the same letter in the column do not differ statistically using the Scott and Knott mean clustering test at 5% significance

SD stem diameter, *SIL* stem internode length, *LBL* leaf blade length, *LBW* leaf blade width, *IL* inflorescence length

¹*BTI* basal tillering intensity in the stem

With respect to stem diameter (SD), the accessions were grouped into five groups (a, b, c, d, e). The accessions with the smallest SD were CPATSA 79129, CPATSA 79141 and CPATSA 90563 (Table 3). Accessions with smaller diameters are more palatable, while accessions with larger stem

diameters have a greater capacity for regrowth (Costa et al. 2004).

Some accessions in the present study presented excellent results in the BTI since the raw material destined to feed the animals is the aerial part, allowing greater food production. In this context, accession

CPATSA79125 can be incorporated into breeding for the species, seeking to transfer alleles that confer this pattern to other genotypes. If the accession is apomictic, this gene transfer can be performed via biotechnological methods, such as genetic transformation or gene editing.

Accession CPATSA79125 stands out for its greater leaf blade width (LBW) and inflorescence length (IL), which indicates that this material may present high production of the aerial part that can be used to feed the herds. In addition, this accession is superior to the commercial cultivar Biloela (CPATSA7602), which indicates a certain potential for exploitation within the breeding programmes for the species in the composition of new materials or even in the transfer of these alleles to other genotypes in the final stage of breeding.

Arshad et al. (2007) reported a significant and high correlation between the number of tillers per plant and fresh weight, although the latter trait was not measured in our evaluation. There is evidence that, for this trait, accessions stand out from the rest. The number of tillers per plant is important for ensuring the persistence of buffelgrass pastures, as it shows the capacity for regrowth.

The SIL was another characteristic separated into four groups (a, b, c, d). For the characteristic LBC, four groups were formed (a, b, c, d). LLW and IL were the characteristics with the greatest distribution of accessions, indicative of the dissimilarity between them (a, b, c, d, e, f).

When seeking to obtain a hybrid combination with a greater BTI and LBL, recombination between accessions CPATSA79125 and CPATSA78122 would possibly result in a promising combination in obtaining high productivity materials with greater leaf blade width, with characteristics combined in a potentially vigorous hybrid for biomass production.

IL was the trait that most contributed to estimating genetic diversity (22.48%) (Table 4). When observing the mean clustering test (Table 3), accessions CPATSA 79125, CPATSA79130, CPATSA90558 and CPATSA90570 stood out with lengths ranging from 14.6 to 12.25 cm, which indicates the existence of greater variation in the inflorescence, a behaviour that can be easily explored as it is a characteristic that is easy to see during its evaluation.

In addition, IL, LBW and LBL also stood out with values of 22.48%, 19.52% and 18.35%, respectively

Table 4 Relative contribution of morpho-agronomic traits to estimate the genetic diversity among accessions of buffelgrass (*Cenchrus ciliaris*), according to Singh (1981)

Trait	Contribution (%)
Inflorescence length (IL)	22.48
Leaf blade width (LBW)	19.52
Leaf blade length (LBL)	18.35
Stem diameter (SD)	14.34
Stem internode length (SIL)	13.46
Basal tillering intensity in the stem (BTI)	11.85

(Table 4). These characteristics are related to the aerial part of the grass, one of the main structures, in addition to the stem diameter used for animal feed. In addition to stem diameter, in the present study, the characteristics that most contributed to genetic diversity among accessions were those related to biomass production. In addition, they are characteristics that can be evaluated right away in the initial development of the plant, different from the characteristics related to the inflorescence, for example, which cannot be evaluated until anthesis. Another approach that can be used to facilitate the evaluation of these characteristics is the conversion of quantitative variables into qualitative ones (creating classes from the intervals of quantitative values), seeking to optimise time and effort until reaching the improved genotype.

Based on the qualitative descriptors (Table 5), for the type of growth, 5 accessions were identified as erect, 24 as semi-erect, and 5 as prostrate. The rhizome shape in accessions presented the globose form, and only one had a linear form, which was the commercial cultivar Biloela (CPATSA7602). The rhizomes are a monopolar stem branching system, rich in reserves, as described by Appezzato da Glória (2003). Squires and Myres (1970) highlighted the importance of rhizomes in *Paspalum paniculatum* L. (Poaceae), as they enable greater tolerance to grazing and drought.

All leaves of the evaluated accessions had a smooth leaf blade edge. For leaf blade colouring, 20 accessions were green, and 18 accessions were light green. Hairiness at the base of the inflorescence was absent for 22 accessions and present for 16 accessions. For inflorescence colouration, 25 were cream-coloured, 8 were purple-and-cream, 2 were black, 1 was black-and-cream, 1 was purple and 1 was brown.

Table 5 Qualitative characteristics evaluated in 38 accessions of buffelgrass (*Cenchrus ciliaris*)

Accessions	¹ Traits	TG	RS	LBE	LBC	LBH	ILBH	SP	IBP	IC	SSS	SG	SAC
CPATSA80200	1	2	1	2	1	0	1	1	1	2	1	6	
CPATSA90592	1	2	1	1	2	3	2	1	1	2	1	6	
CPATSA90570	3	2	1	1	1	0	2	1	1	2	1	6	
CPATSA80199	3	2	1	1	1	0	2	1	1	2	1	6	
CPATSA7757	3	2	1	1	1	0	2	1	1	2	1	6	
CPATSA80194	3	2	1	1	1	0	2	2	1	2	1	6	
CPATSA79148	3	2	1	1	1	0	1	2	5	2	1	6	
CPATSA90591	1	2	1	1	1	0	2	1	1	2	1	6	
CPATSA90613	5	2	1	1	2	5	2	1	1	2	1	6	
CPATSA90558	3	2	1	1	1	0	2	1	1	2	1	6	
CPATSA79150	3	2	1	2	2	5	2	1	1	1	1	6	
CPATSA79123	5	2	1	1	2	3	2	1	5	2	1	6	
CPATSA83476	5	2	1	1	2	3	2	1	1	2	1	6	
CPATSA79151	5	2	1	2	2	3	2	1	4	1	1	6	
CPATSA79149	5	2	1	2	2	3	2	1	5	2	1	6	
CPATSA79144	3	2	1	1	2	3	2	1	6	1	1	6	
CPATSA79147	5	2	1	1	1	0	2	1	5	2	1	6	
CPATSA79129	5	2	1	1	2	3	2	1	5	2	1	6	
CPATSA78102	3	2	1	2	1	0	2	1	5	1	1	6	
CPATSA79134	3	2	1	1	1	0	2	1	3	1	1	6	
CPATSA79125	1	2	1	2	1	0	2	1	1	2	1	2	
CPATSA79141	5	2	1	1	1	0	2	1	5	2	1	6	
CPATSA90581	3	2	1	2	1	0	2	1	1	2	1	6	
CPATSA78122	3	2	1	2	1	0	2	1	1	2	1	6	
CPATSA7754	3	2	1	1	1	0	2	1	5	2	1	6	
CPATSA90556	3	2	1	2	1	0	2	1	2	2	1	6	
CPATSA7602	3	1	1	2	1	0	1	1	1	2	1	7	
CPATSA90615	3	2	1	2	2	5	2	1	1	2	1	6	
CPATSA90580	1	2	1	2	2	3	2	1	1	2	1	2	
CPATSA79121	3	2	1	2	2	3	2	1	1	2	1	3	
CPATSA80196	3	2	1	1	2	3	2	1	1	2	1	2	
CPATSA80195	3	2	1	2	2	3	2	1	1	2	1	2	
CPATSA90572	3	2	1	1	1	0	2	1	1	2	1	2	
CPATSA90611	3	2	1	2	1	0	1	1	1	2	1	8	
CPATSA79139	3	2	1	2	2	3	2	1	1	2	1	6	
CPATSA90563	3	2	1	2	2	3	2	1	1	2	1	6	
CPATSA79130	3	2	1	1	1	0	2	1	1	2	1	6	
CPATSA78103	5	2	1	1	1	0	1	1	4	1	1	2	

¹TG type of growth, RS rhizome shape, LBE leaf blade edge, LBC leaf blade colour, LBH leaf blade hairiness, ILBH intensity of leaf blade hairiness, SP sheath pilosity, IBP inflorescence base pilosity, IC inflorescence colouring, SSS spikelet shell shape, SG spikelet grouping, SAC spikelet anther colouring

For the spikelet shape, 32 accessions had free bristles, and 6 accessions had united bristles. There was no variation in the grouping of spikelets, as all were isolated. Spikelet anther colour was as follows: 29 were yellow, 6 were beige, 1 was dark yellow (CPATSA7602), 1 was pink (CPATSA79121), and 1 was purple (CPATSA90611).

IC is a characteristic that is easy to identify and differentiate from other genotypes, as it varies among accessions, as well as the colour of the anthers, which also vary in colour. These qualitative descriptors confirm the dissimilarity among the genotypes, which are of great importance, especially when used together with other traits in the choice of genitors intended for

crosses. Several authors have already attested to the efficiency of characterisation by means of markers or morphological descriptors, such as in elephant grass (Silva et al. 2009) and *Stylosanthes* spp. (Karia et al. 2002). These works were useful in identifying characteristics with great variation in genotypes.

The genetic dissimilarity between the genotypes was estimated according to the Mahalanobis distance (1936), where the distance values among the accessions ranged from 1.98 to 301.11, with emphasis on the accessions CPATSA79147 and CPATSA7754 and CPATSA79123 and CPATSA90611 for being the least and most dissimilar genotypes, respectively (Table 6). This indicates that the recombination between the first two accessions will result in hybrids and segregating populations with a narrow genetic base and, consequently, not very interesting for exploration within the breeding programmes for the species, unlike the second pair of genotypes, which can result in hybrid combinations that complement each other by having different characteristics.

The dendrogram of the graphic representation of the diversity among the accessions, with the cut in the grouping following the method of Mojena (1977), shows the formation of three groups: one composed by accession CPATSA78103, another by accessions CPATSA18621 and CPATSA90611, and the last formed by the other accessions divided into subgroups (Fig. 1). As observed in the dissimilarity measures, the first group presented the most contrasting genotype among the evaluated materials, presenting itself as an excellent genitor for recombination, since this accession “CPATSA78103” has an inflorescence colouration different from the others, black, which identifies it easily for this descriptor. The accessions that also formed a group were CPATSA18621 and CPATSA90611, where they presented pink and purple colouring, respectively, for the descriptor anther colour (spikelet), thus making them easy to identify from these accessions. These results reinforce the existence of genetic divergence among genotypes.

When working with *C. ciliaris*, Bruno et al. (2017), Marshall et al. (2012), Arshad et al. (2007), Jorge et al. (2008), and Mansoor et al. (2002) found genetic divergence among the genotypes they evaluated, which corroborates the results of the present study. Thus, they reinforced the importance of characterising *Cenchrus* germplasm. Based on the

Table 6 Measures of dissimilarity among accessions of buffelgrass (*Cenchrus ciliaris*)

Accessions	Shorter distance	Greater distance
CPATSA7757	4 (2.29)	13 (137.05)
CPATSA78102	3 (4.86)	38 (168.07)
CPATSA78103	4 (56.11)	13 (296.60)
CPATSA79121	11 (17.10)	13 (193.50)
CPATSA78122	22 (3.28)	38 (134.19)
CPATSA79123	15 (16.13)	34 (301.11) **
CPATSA79125	25 (3.28)	38 (149.82)
CPATSA79129	15 (16.99)	34 (219.54)
CPATSA79130	14 (6.03)	13 (119.13)
CPATSA79134	18 (2.49)	38 (171.54)
CPATSA79139	31 (5.97)	34 (113.72)
CPATSA79141	31 (4.59)	13 (121.81)
CPATSA79144	16 (2.49)	38 (169.94)
CPATSA79147	26 (1.98) *	38 (128.17)
CPATSA79148	27 (8.41)	13 (115.24)
CPATSA79149	14 (4.73)	34 (131.91)
CPATSA79150	16 (4.06)	38 (189.50)
CPATSA79151	13 (16.13)	34 (241.79)
CPATSA80194	2 (15.07)	38 (178.44)
CPATSA80195	36 (6.88)	13 (155.27)
CPATSA80196	11 (3.85)	38 (106.83)
CPATSA80199	5 (2.29)	13 (126.26)
CPATSA80200	27 (7.26)	13 (158.41)
CPATSA83476	17 (4.73)	34 (116.70)
CPATSA90556	17 (5.81)	13 (133.41)
CPATSA90558	36 (13.11)	38 (229.26)
CPATSA90563	32 (6.88)	38 (174.67)
CPATSA90570	21 (4.87)	38 (142.30)
CPATSA90572	9 (9.55)	38 (192.24)
CPATSA90580	9 (8.47)	38 (197.76)
CPATSA90581	23 (6.83)	13 (158.15)
CPATSA90591	37 (7.99)	13 (158.25)
CPATSA90592	11 (7.64)	38 (107.76)
CPATSA90611	30 (37.47)	13 (301.11)
CPATSA90613	29 (8.47)	38 (221.07)
CPATSA90615	32 (14.51)	38 (135.59)
CPATSA7754	19 (1.97)	38 (117.58)
CPATSA7602	31 (3.85)	13 (107.33)

*, **Accessions less and more similar, respectively

dendrogram, the CCC presented a value greater than 72%, indicating that the grouping of accessions presents low distortion between the matrix and the dendrogram.

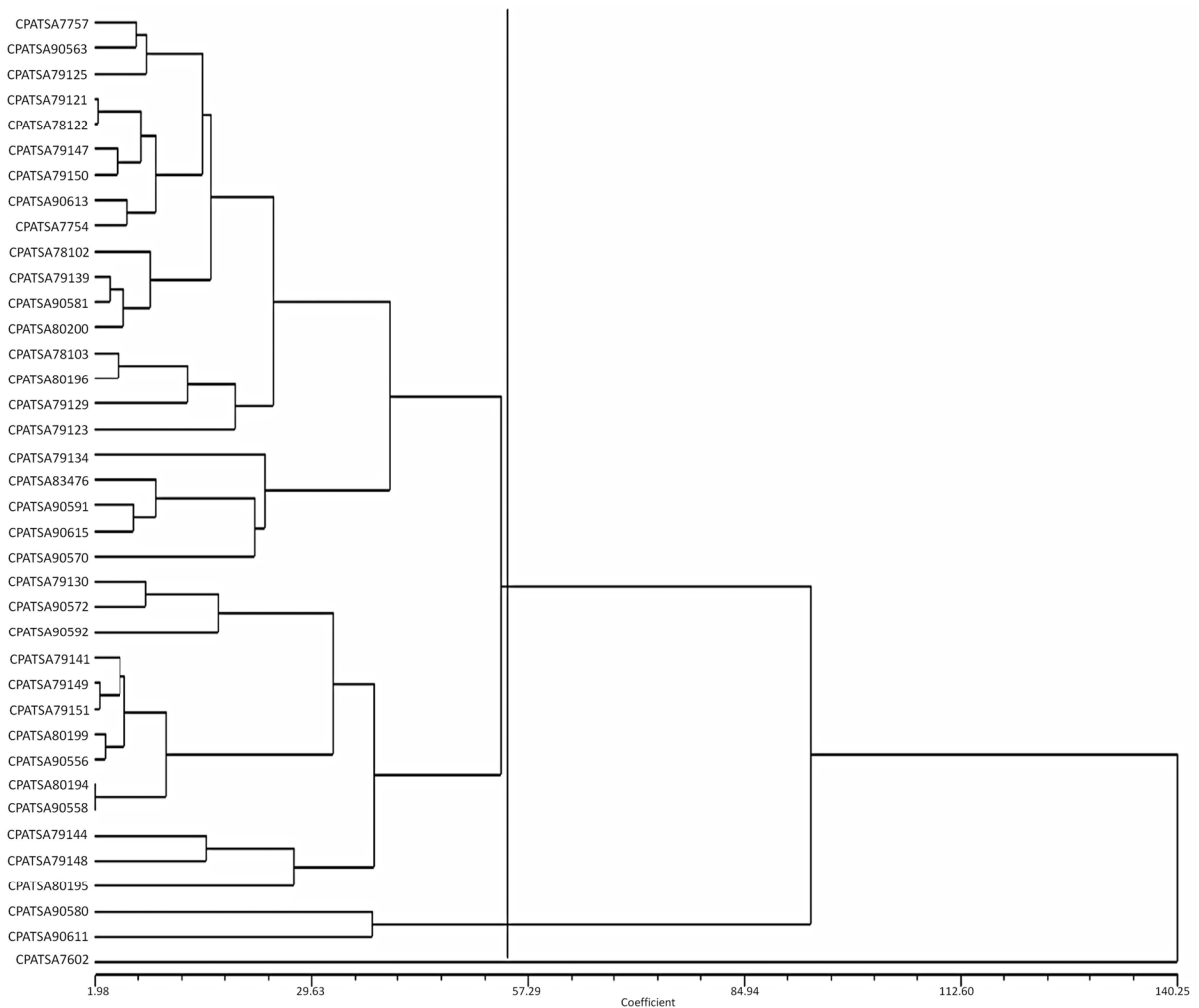


Fig. 1 Dendrogram representative of the genetic diversity among accessions of buffelgrass, using mean linkage clustering between groups (UPGMA), with a cophenetic correlation coefficient of 72%

Conclusion

There was genetic diversity among the evaluated accessions.

Characteristics related to biomass production, such as length and width of the leaf blade and basal tillering intensity, were the most informative in estimating the genetic divergence between accessions.

Accessions CPATSA79123 and CPATSA90611 were the most divergent accessions and thus could be potential male parents in the breeding programme.

Depending on the purpose/objective of the breeding programme, the other accessions could also be

considered for improving the adaptivity and productivity of the species.

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Author contributions ICNSR, RPA and NFM conceived and planned the study and wrote the manuscript. RPA provided the germplasm accessions, which were multiplied by ICNSR for the experiment. ICNSR and RPA carried out the

phenotyping. and ICNSR, NFM and TLN analysed the data. All authors read and approved the final manuscript.

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Declarations

Conflict of interest The authors have not disclosed any competing interests.

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