

## Variation in Floral Morphology and Seed Production of Buffel and Rhodes Grass

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### ABSTRACT

The use of diversity implies knowing characteristics and traits of interest in genetic resources. In forages, the ability to produce seeds is essential to the persistence of cultivars in livestock systems. To study the floral variability and seed yield, 17 genotypes of *Chloris gayana* Kunth and 14 genotypes of *Cenchrus ciliaris* L. were evaluated. These genotypes were characterized considering floral morphology and total seed yield parameters. A randomized complete block design with four replications was used. In *C. gayana*, accessions 7757, 6631, 981 and 7757 presented the highest ( $P < 0.05$ ) Number of Inflorescences per Plant (NIP, 26.43), number of Spikes per Inflorescence (S/I, 10.73), Weight of Thousand Seeds (WTS, 0.52 g) and Total Seed Production (TSP, 235.69 kg ha<sup>-1</sup>), respectively. In *C. ciliaris*, accessions 15687 (28.67) and 1098 (24.33) presented the highest values ( $P < 0.05$ ) for NIP. Accession 12464 (172.67) had the highest ( $P < 0.05$ ) Number of Seeds by Inflorescences (NSI) and genotype 6652 (0.238 g), 15687 (0.207 g) had the highest ( $P < 0.05$ ) Weight of one Hundred Seeds (WHS). Finally, accessions 6652 (210.93) and 1098 (188.55) had the highest ( $P < 0.05$ ) TSP. The genotypes of *C. gayana* and *C. ciliaris* indicated an important morphology variation. Likewise, higher seed production, which is associated with genetic variability, can be an attribute to be considered during the selection of materials in forage breeding programs, as a complement to traditional evaluation characteristics.

**Keywords:** *Chloris gayana* Kunth, *Cenchrus ciliaris* L., Caryopsis, Genetic variability, Caribbean conditions.

### INTRODUCTION

The offer of new forages adapted to conditions of low water availability is essential in regions negatively affected by climate variability with prolonged and marked periods of drought (Voltaire, 2018; Rajora *et al.*, 2020). However, in these areas, it is not enough to provide new germplasm with high productive potential.

Materials must also have the capacity to produce seed, this being a fundamental attribute for producers to continue with its multiplication, aiming to use them as the main source of bovine feeding. The characterization and evaluation of forage genetic resources available in germplasm banks is essential to conserve diversity and identify attributes and characteristics of the preserved genotypes with the possibility of

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using this information to suggest cultivars to be included in genetic improvement programs.

*Chloris gayana* Kunth. is a C4 grass, originally from Africa, naturalized in the tropics and subtropics. It has tolerance to drought, high temperatures, cold (mainly in diploids), salinity (Loch et al., 2004; Ponsens et al., 2010; Ribotta et al., 2019) and non-prolonged waterlogging (Imaz et al., 2015). It can be propagated by stolons, tillers, and by seeds, facilitating its multiplication (Loch et al., 2004). It is considered to be promising due to its adaptability and forage production, and it is currently used in different regions of the world. Therefore, when evaluating the germplasm of this species, for genotype selection purposes, its ability to produce seed must be known. In this species, the cultivars released are generally diploid or tetraploid, conferring on them differences in habit, seed vigor, ability to produce stolons, tolerance to biotic and abiotic stresses, phenology, and productive potential in terms of seeds and dry matter (Loch et al., 2004). This variability allows selection of genotypes with attributes of interest for different agroclimatic conditions. According to Loch et al. (2004), the inflorescences of *C. gayana* are digitate and have varied number of spikes, in which the spikelets and caryopses are arranged. Seed yield is variable within cultivars and tetraploids generally have a larger inflorescence.

*Cenchrus ciliaris* L. is a C4 species, native to eastern Africa and southern Asia, and is considered a promising species in livestock systems for its adaptation, forage production and good palatability, an aspect of great importance for bovine feeding (Roncallo et al., 2012). It also has good adaptation to conditions of water deficit (Bonney et al., 2017), including desert environments, due to drought tolerance (Bashaw, 1985; Miller et al., 2010; Mansoor et al., 2019), which is favored by the sizeable depth of its roots (Monsoor et al., 2015). It has a good ability to form seeds, through the formation of panicles (3 to 15 cm long and 2.5 to 8 mm

wide) that have different shades due to the color of the fascicle bristles (Hanselka et al., 2004). It has been indicated that this species has a good capacity to produce seed, and its flowering is affected by photoperiod (Hanselka et al., 2004; Beltrán López et al., 2017).

Good seed production capacity is positively correlated with forage production. It has been demonstrated that simultaneous breeding of these parameters can be achieved in other species (Abtahi et al., 2018; Majidi et al., 2017). This has been identified in *Dactylis glomerata* under drought conditions (Saeidnia et al., 2017), constituting a selection trait for this species due to its moderated heritability, thus selection of genotypes for this parameter could be promising (Majidi et al., 2015). On the other hand, seeds represent the most important source of propagation for forage grasses and are of great interest for commercial seed production. Accordingly, *Chloris gayana* Kunth. and *Cenchrus ciliaris* L. genotypes were evaluated to determine their ability to produce seed, as a selection characteristic, for dry Caribbean conditions.

## MATERIALS AND METHODS

### Plant Material

Seventeen accessions of *Chloris gayana* Kunth and fourteen accessions of *Cenchrus ciliaris* L. were characterized in this study. These accessions were obtained from the germplasm bank of the Bioversity alliance-CIAT. The experiment was established in field conditions. Most of the accessions are of African origin (Jorge et al., 2008; Ponsens et al., 2010) (Table 1).

### Location

The research work was developed at the Motilonia Research Center of the Colombian Agricultural Research Corporation

**Table 1.** Genotypes of *Cenchrus ciliaris* and *Chloris gayana*.

Grass	Accession	Origin	Other names or codes
<i>Cenchrus ciliaris</i>	777	Tanzania	CIAT26410, SMT-055F
	1098	Congo	SMZ-010B
	6642	Tanzania	G621 'Lake Manyara'
	6647	Zimbabwe	'Chipinga'
	6652	Kenya	American; A-12a-9
	12464	Antigua	CIAT678
	12825	Kenya	CIAT16643
	13299	Kenya	CIAT16640
	15687	Mauritania	MRT057
	16609	Namibia	MOSS 2072
	16617	Namibia	MOSS 2090
	16660	Namibia	MOSS 2176
	16868	Niger	C-052
	18483		CIAT 18483
<i>Chloris gayana</i>	981	Rwanda	
	1053	Burundi	
	6631		G 638; CPI 118110, PI 307625, Hunter
	6633		N 77265, Callide
	7103	Uganda	N 79134, PI 378042, Mbarara
	7384	Zambia	CPI 13375, 18021, 39156, PI 365980, Katambora
	7757	Ethiopia	
	10097	Ethiopia	CPI 118113
	10225	Ethiopia	CPI 118115
	13053	Kenya	CIAT 16651
	13072	Kenya	CIAT 16652
	13097	Kenya	CIAT 16657
	13103	Kenya	CIAT 16658
	13175	Kenya	CIAT 16662
	13330		Boma
	15570	South Africa	CG 54
	15573		CG 57
	18498	Tanzania	

(AGROSAVIA) located in the municipality of Agustín Codazzi, Cesar department, Colombia, where natural vegetation is classified as tropical dry forest (Phillips *et al.*, 2011). It is located at 10° 00' 09.03" N, 73° 14' 55.88" W with an altitude of 103 masl. The main climatic conditions of the study area are the following: annual precipitation of 1,585 mm; average annual temperature of 27°C; heliophany of 6.9 h d<sup>-1</sup> and average relative humidity of 71% (data obtained from the meteorological station at the Motilonia Research Center). The soils have a loamy-clay texture, neutral pH, and low content of Organic Matter (OM).

### Experimental Design

A randomized complete block design with four replications was used, while each plot had a size of 3×3 m. The accessions were established at 0.5 m between rows and 0.5 m between plants. For the characterization of parameters associated with seed production, 10 plants were selected within each plot, as well as 10 randomized inflorescences for each genotype.



## Response Variables

### *C. gayana*

Numbers of Inflorescences per Plant (NIP), Spikes per Inflorescence (S/I), Seeds per Inflorescence (NSI), Weight of one Thousand Seeds (g) (WTS), and Length of Spikes (cm) (LS) were measured, while the Total Seed Production per area ( $\text{kg ha}^{-1}$ ) (TSP) was estimated.

### *C. ciliaris*

NIP, NSI, Weight of one Hundred Seeds (WHS) (g), Inflorescence Length (cm) (IL), and Inflorescence Diameter (cm) (ID) were measured, while the Total Seed Production per area ( $\text{kg ha}^{-1}$ ) (TSP) was estimated. The number of Caryopses in the First Third of the inflorescence length (CFT), in the Second Third of the inflorescence length (CST) and in the Last Third of the inflorescence length (CLT) from the apex of the inflorescence were also measured. To accurately identify the inflorescence color associated with the genotype, a selected area of RGB images was analyzed using a color measurement plug-in present in Image J (<https://imagej.nih.gov/ij/>), estimating the Red (R), Green (G) and blue (B) channels.

## Data Analysis

Regarding the characteristics of the quantified data in *C. gayana*, the response variables NIP, S/I, WTS, TSP, had a non-parametric Friedman analysis. A mean comparison test was performed using LSD ( $\alpha = 0.05$ ). The response variable LS met the criteria of normal distribution and homoscedasticity through the Shapiro-Wilk and Levene tests, respectively, but it was not statistically different. In the case of NSI, a transformation was performed using log10, being normal and performing a means comparison test using Duncan ( $\alpha = 0.05$ ).

The analyses were performed in SAS 9.4 software.

Considering the characteristics of the quantified data in *C. ciliaris*, the response variables NIP, NSI and TSP had a non-parametric Friedman analysis. A mean comparison test was performed using Fisher's Least Significant Difference (LSD) test ( $\alpha = 0.05$ ). The WHS, IL, ID, RGB parameters fulfilled the assumptions of normality and homogeneity of variances, through the Shapiro-Wilk and Levene tests, respectively; therefore, an ANOVA was performed, and Duncan's multiple range test was used. For the case of variables CFT, CST and CLT, they also met the assumptions to run an ANOVA. A mean comparison using LST was carried out (LSD) ( $\alpha = 0.05$ ). R free software version 4.0.3 (R Foundation for Statistical Computing, Vienna, Austria) was used to perform all analysis.

A hierarchical grouping analysis was also carried out with the parameters of flower morphology and seed production, by means of "hclust", using Ward's agglomeration method to determine the diversity in accessions through the R software.

## RESULTS AND DISCUSSION

### Parameters Associated with Seed Production and Floral Morphology

#### *C. gayana*

The *C. gayana* population was diverse in terms of its floral morphology and parameters related to seed production. It was found that the quantified parameters, NIP ( $P < 0.001$ ), S/I ( $P < 0.0357$ ), NSI ( $P < 0.0001$ ), WTS ( $P < 0.01$ ) and TSP ( $P < 0.0001$ ) presented statistically significant differences between genotypes, while the LS was different considering  $\alpha < 0.1$ .

Accession 7757 presented the highest NIP (26.43) (Table 2). The second group with a high value for this parameter was made up

**Table 2.** Seed production characteristics in genotypes of *C. gayana*.<sup>a</sup>

Genotype	NIP	S/I	NSI	WTS	TSP
981	6.00 d	9.20 abcde	329.58 de	0.52 a	39.40 de
1053	3.00 d	10.57 ab	624.58 bc	0.35 abc	25.52 e
6631	2.83 d	10.73 a	367.83 cde	0.38 abc	14.91 e
6633	21.33 ab	9.93 abcd	411.50 bcde	0.34 abc	112.52 bcd
7384	19.77ab	8.27 bcde	279.96 e	0.32 abc	92.12 bcde
7757	26.43 a	7.33 e	427.08 bcde	0.48 ab	235.69 a
10097	5.85 d	8.30 abcde	593.14 bcde	0.43 abc	60.32 cde
10225	15.35 bc	7.40 de	614.34 bcd	0.27 abc	101.23 bcde
13053	5.90 d	7.93 cde	613.25 bcd	0.30 abc	23.32 e
13072	8.90 cd	7.93 cde	314.83 e	0.19 c	20.14 e
13097	3.23 d	8.40 abcde	351.25 de	0.50 ab	22.62 e
13103	21.73 ab	9.13 abcde	555.00 bcde	0.33 abc	146.13 bc
13175	18.20 b	10.20 abc	966.50 a	0.26 bc	177.03 ab
13330	16.43 b	8.40 abcde	598.67 bcd	0.42 abc	168.36 ab
15570	4.23 d	8.20 bcde	448.83 bcde	0.42 abc	31.41 de
15573	3.17 d	9.87 abcd	660.17 b	0.39 abc	27.43 de
18498	16.33 b	8.27 bcde	619.67 bc	0.36 abc	143.35 bc

<sup>a</sup> NIP= Number of Inflorescences per Plant; S/I = Spikes per Inflorescence; NSI= Number of Seeds per Inflorescence; WTS= Weight one Thousand Seeds (g), TSP= Total Seed Production (kg ha<sup>-1</sup>). Different letters in the same column indicate significant differences (P< 0.05).

of accessions 13103, 6633 and 7384 that had values greater than or close to 20. In contrast, genotypes 981, 10097, 13053, 15570, 13097, 15573, 1053 and 6631 presented less than six flowers at the time of evaluation (Table 2).

For S/I, accession 6631 presented the highest number (10.73); followed by accessions 1053 and 13175 with 10.57 and 10.20 spikes, respectively. The lowest values for this response variable were obtained from accessions 10225 (7.40) and 7757 (7.33). These values are within the range indicated by Loch *et al.* (2004), who mention that some genotypes can have between 3 and 20 spikes. Similarly, in the characterization of a population of *C. gayana*, it was found that the genotypes presented between 8 and 16 spikes per plant (Ponsens *et al.*, 2010), values similar to those found in this research. These morphological variations are important

because they contribute to the phenotypic differentiation of cultivars.

The NSI presented a contrasting variability among the accessions, the largest value was obtained from accession 13175 with 966.50 seeds per inflorescence; while accessions 13072 and 7384 obtained the lowest values with 314.83 and 279.96 seeds per inflorescence, respectively. This value was different and lower than that found in *Chloris virgata* genotypes; however, this variation may be influenced by genotype (Boutsalis *et al.*, 2017).

The accessions 981, 13097 and 7757 presenting higher values in WTS were 0.52, 0.50 and 0.48 g, respectively. By contrast, the lowest values ranged between 0.26 g and 0.19 g corresponding to accessions 13175 and 13072. This seed weight was similar to that found in *Chloris virgata* genotypes with a range between 0.36 and 0.46 g (Boutsalis *et al.*, 2017). Finally, regarding TSP, the best value was obtained by accession 7757



(235.69 kg ha<sup>-1</sup>), being statistically different ( $P < 0.05$ ) from the rest of the accessions. This genotype was followed by accessions 13175 and 13330 that reached yields of 177.03 and 168.36 kg ha<sup>-1</sup> respectively. These values are within the range reported for this species, which can range on average between 100 and 300 kg ha<sup>-1</sup>, although maximum values of up to 850 kg ha<sup>-1</sup> have also been found (Peters *et al.*, 2011), showing the potential of this species to produce seed. The lowest yields were for accessions 13072 and 6631, with values between 20.14 and 14.91 kg ha<sup>-1</sup>, respectively.

The higher TSP obtained in accession 7757 (235.69) was mainly influenced by the higher NIP (26.43). Febles *et al.* (2009) reported a potential production of 175 kg ha<sup>-1</sup> in a registered cultivar of the same species. In this study, the accessions 7757 and 13175, with promising yield, exceeded this value. In the same way, it is evident that they exceed the values of *C. gayana* cv. Callide that produced between 78 and 114 kg ha<sup>-1</sup> (Pérez and Suárez, 2001).

In the cluster analysis, when analyzing the population variability, three groups, namely, A, B, and C were found, of which group A and C had subgroups. The cluster A was made up of two subgroups: in A1 were the accessions 981, 13072, 6631, 13097 and 7384, corresponding to 29.41% of the characterized genotypes and, on average, they presented one of the lowest values for NIP (8.15), and the lowest for TSP (37.84 kg ha<sup>-1</sup>) and NSI (328.69). In A2, the accessions 7757, 6633 and 15570 were grouped, and it was composed of 17.64% of the genotypes. It stood out for having the highest WTS (0.41 g), one of the highest NIP (17.33), and the lowest number of S/I (8.49). In cluster B, only the accession 13175 was grouped. On average this group presented the highest NIP (18.20), S/I (10.20), NSI (966.50), TSP (177.03 kg ha<sup>-1</sup>) and the lowest values for WTS (0.26 g). Regarding cluster C, the subgroup C1 had one (5.88%) of the genotypes belonging to it; and it presented, on average, one of the highest values of NIP (18.16), NSI (591.11) and TSP (152.61 kg

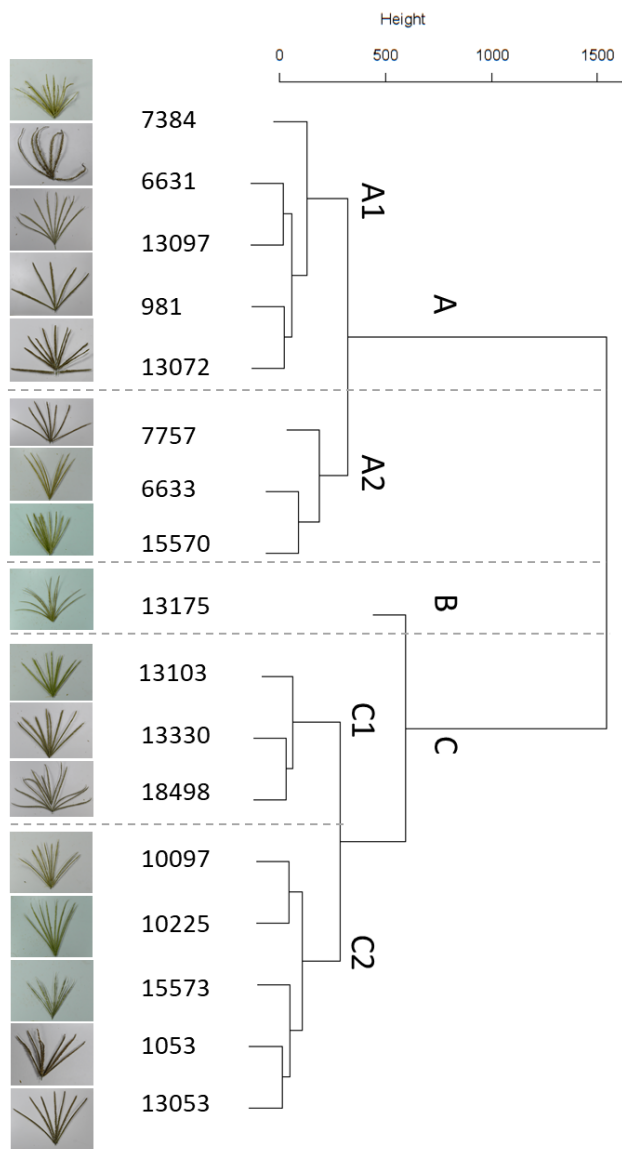
ha<sup>-1</sup>), while an intermediate value for WTS (0.37 g). Finally, in subgroup C2, genotype 10097, 10225, 15573, 1053 and 13053 were present, standing out for having one of the highest values for NSI (621.10), intermediate value for S/I (8.81), and the lowest value for NIP (6.65) (Figure 1).

Regarding the correlation between variables, all the relationships with statistical significance ( $P < 0.05$ ) were direct, except for the correlation between NSI and WTS, which was inverse, indicating that as the NSI increases, the WTS decreases. When analyzing the other correlations, it is evident that increasing the NIP and the NSI, a higher TSP is obtained. Finally, when a higher S/I is found, a high value for NSI is also present (Table 3).

The diversity found in *C. gayana* made it possible to show different responses regarding the capacity to produce seed, which indicates that some materials could be promising due to this parameter. A positive relationship ( $P < 0.05$ ) was also found between most of the morphometric components and seed production.

### *C. ciliaris*

In the characterization of the forage materials it was found that at least one of the accessions of *C. ciliaris* presented statistically significant differences for the response variables NIP ( $P < 0.0001$ ), NSI ( $P < 0.0001$ ), WHS ( $P < 0.0001$ ) and TSP ( $P < 0.0001$ ) (Table 4). Accessions 15687 and 1098 presented the highest values for NIP with 28.67 and 24.33 average units, respectively; while the lowest value was obtained by 12825, 16609, 13299, 18483 and 6642. These values were lower than the value of *C. ciliaris* cv. Formidable, which presented 32 inflorescences per plant. However, the highest values of this research were similar to other commercial cultivars of *C. ciliaris* that had between 2.18 and 32.8 inflorescences, for example, cv. Común (8.96 to 23.56), cv. Formidable (24.96 to 32.83), cv. Nueces (2.18 to 19.10) and



**Figure 1.** Diversity of the population characterized by *Chloris gayana*, regarding floral morphology and ability to produce seeds. The letters indicate groups A (subgroups A1 and A2), B and C (subgroups C1 and C2)

**Table 3.** Pearson's linear correlations for characteristics associated with seed production in *Chloris gayana*.<sup>a</sup>

	S/I	NSI	WTS	TSP	LS
NIP	-	-	-	0.85***	0.45*
S/I		0.22*	-	-	0.42**
NSI			-0.50**	0.33***	-
WTS				-	-
TSP					-

<sup>a</sup> NIP= Number of Inflorescences per Plant; S/I= Spikes per Inflorescence. NSI= Number of Seeds per Inflorescence; WTS= Weight one Thousand Seeds (g); LS= Length of Spikes, TSP= Total Seed Production (kg ha<sup>-1</sup>). \*\*\*: P< 0.0001; \*\*: P< 0.01, \* P< 0.05.



finally, cv T-1754 (4.0 to 21.15) (Conde-Lozano *et al.*, 2011).

For NSI, the values found ranged between 172.67 and 63.33 average units of seeds in the inflorescence, obtained by accessions 12464 and 15687, respectively (Table 4). Although the accessions 777 (151.33) and 6642 (150.67) also had high values. These values exceeded the amount found in commercial Nueces, which had a maximum value of 82 spikes per inflorescence, although this may be due to the edaphoclimatic and agronomic conditions of each evaluation (Conde-Lozano *et al.*, 2011). For the WHS a range between 0.05 and 0.238 g was found (Table 4). Genotypes 6652, 15687 and 16660 were the ones with the higher values, with 0.238, 0.207 and 0.215 g, respectively. In relation to TSP, the values ranged between 21.87 to 210.93 kg ha<sup>-1</sup>, with the best values obtained by 6652 (210.93 kg ha<sup>-1</sup>) and 1098 (188.55 kg ha<sup>-1</sup>), which were different ( $P < 0.05$ ) from the rest of the characterized genotypes (Table 4). These values were within the range 150- 250 kg ha<sup>-1</sup>, reported by Meena and Nagar

(2019); although they were lower than those reported in commercial cultivars (Titan and Regio), in which the seed production is greater than 500 kg ha<sup>-1</sup> (Beltrán López *et al.*, 2017). They were also close to the production (223 kg ha<sup>-1</sup>) of Buffel grass cv Común (Sáenz-Flores *et al.*, 2015) and greatly exceeded the yield between 75.9 and 97.0 kg ha<sup>-1</sup> found by Kumar *et al.* (2005). However, this parameter depended on the conditions in which the genotype is produced (Abtahi *et al.*, 2018).

Regarding the morfometric parameters, it was found that genotypes 16617, 6647, 13299, 6642, 1660, 16609 and 1098 presented the higher IL, ranging between 9.59 cm and 11.58 cm; while genotype 16868 presented the highest ID (2.30 cm). The IL and ID found in this study (Table 5) are within the range described for this species, between 3 and 15 cm and 1 to 2.5 cm, respectively (Hanselka *et al.*, 2004). These values were superior to the length found in cultivars Común, Formidable, Nueces and T-1754, that ranged between 6 and 7 cm (Conde-Lozano *et al.*, 2011). Color

**Table 4.** Parameters related to seed production in *C. ciliaris* genotypes.<sup>a</sup>

Genotype	NIP	NSI	WHS	TSP
777	14.44 cd	151.33 ab	0.127 def	82.74 def
1098	24.33a	136.00 bcd	0.146 d	188.55 a
6642	5.33 g	150.67 ab	0.152 cd	48.05 fgh
6647	8.17 fg	141.00 bcd	0.133 de	68.34 efg
6652	19.45 b	119.33 cd	0.238 a	210.93 a
12464	18.22 bc	172.67 a	0.050 g	60.73 efgh
12825	6.00 g	142.50 abcd	0.070 fg	30.68 gh
13299	5.67 g	119.00 cd	0.083 efg	21.87 h
15687	28.67 a	63.33 e	0.207 abc	127.90 bc
16609	6.00 g	79.33 e	0.152 cd	33.56 gh
16617	14.25 cde	145.00 abc	0.138 de	140.23 b
16660	9.44 efg	138.33 bcd	0.215 ab	110.61 bcd
16868	11.50 def	117.00 cd	0.178 bcd	92.00 cde
18483	5.44 g	115.00 d	0.127 def	24.30 gh

<sup>a</sup> NIP= Number of Inflorescences per Plant; NSI= Number of Seeds per Inflorescence; WHS= Weight one Hundred Seeds (g), TSP= Total Seed Production (kg ha<sup>-1</sup>). Different letters in the same column indicate significant differences ( $P < 0.05$ ).



**Table 5.** Morphometric parameters related with the floral morphology in *C. ciliaris* genotypes.<sup>a</sup>

Genotype	IL	ID	RED	GREEN	BLUE
777	9.30 bc	1.02 f	82.72 cde	79.84 abcd	41.32 ef
1098	9.59 abc	1.16 ef	91.02 abcd	77.14 bcd	46.29 cde
6642	9.73 abc	1.36 bcde	68.52 e	65.92 d	32.47 f
6647	10.94 ab	1.47 bcd	76.04 de	66.88 cd	42.76 def
6652	8.47 cd	1.23 def	92.81 abcd	84.31 abc	71.55 a
12464	9.46 bc	1.03 f	92.74 abcd	84.60 abc	53.56 bcd
12825	8.66 cd	1.23 def	88.91 bcd	80.67 abcd	44.91 cde
13299	10.56 abc	1.32 cde	94.12 abc	84.63 abc	46.14 cde
15687	8.91 bcd	1.46 bcd	87.36 bcd	85.53 ab	52.45 bcde
16609	9.60 abc	1.18 ef	93.57 abcd	94.34 ab	56.15 bc
16617	11.58 a	1.57 b	102.84 ab	87.49 ab	47.40 cde
16660	9.69 abc	1.27 cdef	107.93 a	97.80 a	61.07 b
16868	8.52 cd	2.30 a	94.56 abc	88.46 ab	58.61 b
18483	6.99 d	1.50 bc	100.46 abc	82.64 abcd	50.07 bcde

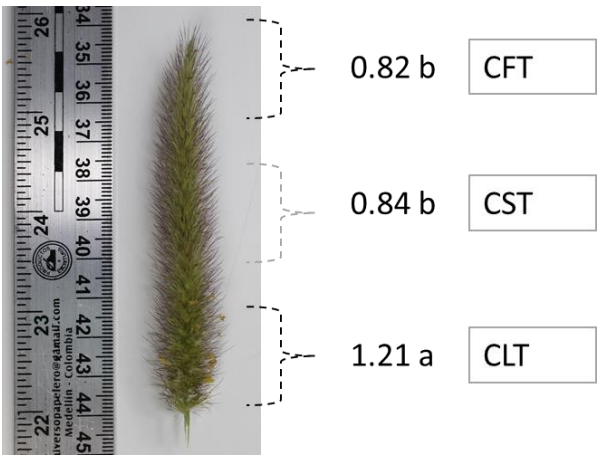
<sup>a</sup> IL= Inflorescence Length (cm); ID= Inflorescence Diameter (cm); RED = Red color channel; GREEN= Green color channel, BLUE= Blue color channel. Different letters in the same column indicate significant differences ( $P < 0.05$ ).

inflorescence showed different channels values (RGB) among the genotypes. In the case of the Red channel (R) the values ranged between 107.93 and 68.52; for Green (G), between 97.80 and 65.92, and for Blue (B) between 71.55 and 34.47 (Table 5). Finally, regarding the amount of caryopses per seed, the lowest value ( $P < 0.01$ ) in the apical (CFT, 0.82) and middle (CST, 0.84) part was found, while in the base (CLT) the highest value (1.21) was observed (Figure 2).

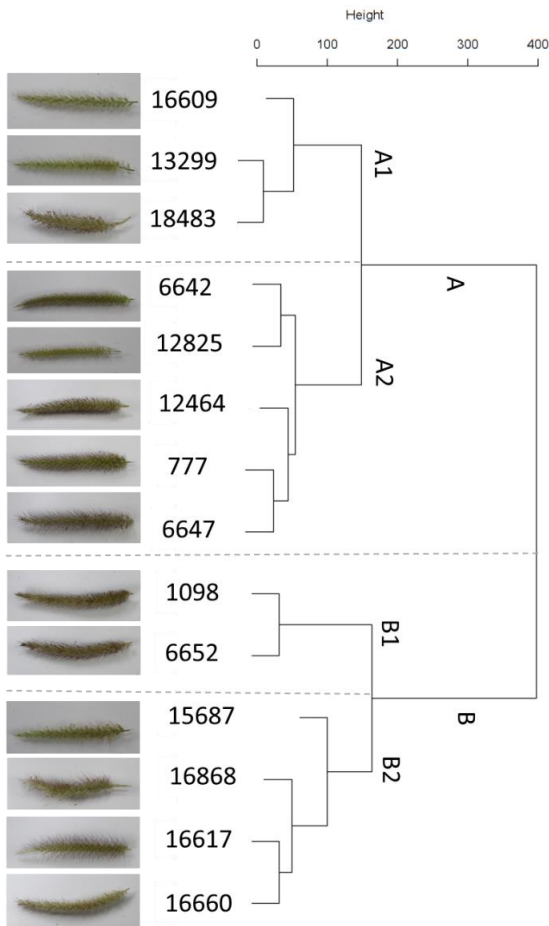
In addition, with Pearson's correlation analysis, a direct and statistically significant correlation, was found between NIP and TSP ( $r = 0.80$ ,  $P < 0.0001$ ), which indicates that when higher NIP was found, a higher TSP was also found. This correlation was also observed between WHS and TSP ( $r = 0.51$ ,  $P < 0.0005$ ). Overall, a greater number of panicles will favor the production of seeds. Additionally, between the WHS and NSI parameters, a statistically significant inverse correlation was present ( $r = -0.55$ ,  $P < 0.03$ ), which indicates that a greater number of seeds in the inflorescence of the *C. ciliaris* plant generated a lower seed weight.

This can be explained by a heterogeneous distribution of photo-assimilates for adequate formation in each one seed, which depends on the species (Shipley and Dion, 1992; Lázaro and Larrinaga, 2018), although it can also be influenced by the presence of some type of abiotic stress during the reproductive cycle of plant (Hanselka *et al.*, 2004). This same correlation was observed in the grass *Trichloris crinita*, indicating a compensatory effect between the weight and number of seeds (Marinoni, 2017).

In the Cluster analysis (Figure 3), two main groups were found. The main group A was composed of subgroups A1 and A2. Subgroup A1 accounted for 21.42% of the genotypes used in this research, accessions 16609, 18483 and 13299, characterized by having the lowest number of NIP (5.70), NSI (104.44), TSP (26.58 kg ha<sup>-1</sup>), IL (8.60) and one of the highest values of ID (1.33), RED (96.05) and GREEN (87.20). Regarding the A2 subgroup (35.71% of the total genotypes), accessions 777, 6647, 6642, 12825, and 12464 were grouped. This subgroup was characterized by an



**Figure 2.** Number of caryopses per seed in the inflorescence length of *C. ciliaris*. Different letters indicate significant differences ( $P < 0.05$ ). Number of Caryopses in the First Third of the inflorescence length (CFT), in the Second Third of the inflorescence length (CST) and in the Last Third of the inflorescence length (CLT).



**Figure 3.** Diversity of the population characterized by *C. ciliaris*, regarding floral morphology and ability to produce seeds. The letters indicate groups A (subgroups A1 and A2) and B (subgroups B1 and B2), confirmed by the cluster analysis

intermediate value of NIP (10.43), the highest values for NSI (151.63) and IL (10.83), and the lowest value for WHS (0.11 g), RED (81.78), GREEN (75.58), and BLUE (43). The second main group, B, also presented two subgroups. Subgroup B1 was composed of only two genotypes, i.e. 6652 and 1098, which stood out for having the highest NIP (21.89), WHS (0.19 g), TSP (199.74 kg ha<sup>-1</sup>) and BLUE (53.36), intermediate values for NSI (127.67), IL (9.58), and RED (91.92), and the lowest value for ID (1.19). On the other hand, B2 was composed of 16868, 16660, 16617, 15687, which accounted for 28.57 % of the total genotypes, presenting intermediate values for NIP (15.96), one of the lowest values of NSI (115.92), one of the highest values for WHS (0.18 g), TSP (117.69 kg ha<sup>-1</sup>), IL (10.34) and BLUE (52.98), and the highest ID (1.63), RED (98.17) and GREEN (89.82) values.

## CONCLUSIONS

The genotypes of *C. gayana* and *C. ciliaris* showed an important variation in characteristics, such as coloration and morphology that differentiated them. The correlations showed a relationship between morphological parameters and seed production, reinforcing the idea that this characteristic might be of interest for the knowledge and use of forage genetic diversity and breeding. Also, genotypes of this species showed higher seed yield, which is an interesting attribute of selection that could favor the adoption of these cultivars by producers. This study might facilitate the multiplication, use and persistence of new commercial forages species for livestock production systems.

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### تنوع در ریخت شناسی گل و تولید بذر دو علف Rhodes و Buffel

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#### چکیده

کاربرد تنوع، به شناخت ویژگی ها و صفات مورد پسند در منابع ژنتیکی نیاز دارد. برای بقا و تداوم کولتیوارهای سامانه‌های دامداری، توانایی تولید دانه در گیاهان علوفه‌ای بسیار ضروری است. به منظور بررسی تنوع در گل و تولید دانه چند علوفه، ۱۷ ژنوتیپ از *Chloris gayana* Kunth و ۱۴ ژنوتیپ از *Cenchrus ciliaris* L. ارزیابی شد. با اجرای آزمایشی با طرح بلوک های کامل تصادفی با ۴ تکرار، ویژگی های این ژنوتیپ ها با در نظر گرفتن ریخت شناسی گل و پارامترهای عملکرد دانه مشخص شد. در مورد *C. gayana*، نمونه های ۷۷۵۷، ۶۶۳۱، ۹۸۱ و ۷۷۵۷ به ترتیب بیشترین ( $p < 0.05$ ) تعداد گل آذین در بوته (NIP, 26.43)، تعداد سنبله در گل آذین (S/I, 10.73)، وزن-هزار دانه (WTS, 0.52 g)، و عملکرد کل دانه ( $TSP, 235.69 \text{ kg ha}^{-1}$ ) را داشتند. در مورد *C. ciliaris* نمونه های 15687 (28.67) و 1098 (24.33) بیشترین ( $p < 0.05$ ) تعداد گل آذین در بوته (NIP) را داشتند. نمونه های 777 (151.33) و 6642 (150.67) بیشترین تعداد دانه در گل آذین (NSI)، و ژنوتیپ های 6652 (0.238 g)، 15687 (0.207 g)، و 16660 (0.215 g) بیشترین ( $p < 0.05$ ) وزن صد دانه (WHS) را داشتند. بالاخره اینکه، بیشترین ( $p < 0.05$ ) عملکرد کل



دانه (TSP) مربوط به نمونه های (210.93) 6652 و (188.55) 1098 بود. ژنوتیپ های *C. ciliaris gayana* تنوع مهمی از ریخت شناسی را نشان دادند. همچنین، صفت تولید دانه بیشتر، که با تغییرات ژنتیکی همراه است، می تواند صفتی باشد که برای تکمیل ارزیابی سنتی و رایج ویژگی های گیاه باید در طی فرایند گزینش و انتخاب مواد برای برنامه بهبود ژنتیکی علوفه در نظر گرفت.