grasses

MDPI

Article

Genetic Variability, Heritability, and Expected Gains for Yield and Forage Quality in Gamba Grass (*Andropogon gayanus*) Populations

Carlos Eduardo Lazarini da Fonseca *, Marcelo Ayres Carvalho *, Marco Pessoa-Filho, Allan Kardec Braga Ramos, Cláudio Takao Karia, Gustavo José Braga, Natália Bortoleto Athayde Maciel and Suelen Nogueira Dessaune Tameirão

Embrapa Cerrados, BR 020, km 18, Planaltina/DF 73310-970, Brazil; marco.pessoa@embrapa.br (M.P.-F.); allan.ramos@embrapa.br (A.K.B.R.); claudio.karia@embrapa.br (C.T.K.); gustavo.braga@embrapa.br (G.J.B.); natalia.athayde@embrapa.br (N.B.A.M.); suelen.dessaune@embrapa.br (S.N.D.T.)
* Correspondence: carlos.lazarini@embrapa.br (C.E.L.d.F.); marcelo.ayres@embrapa.br (M.A.C.)

Abstract

Gamba grass (*Andropogon gayanus* Kunth) is a promising forage alternative for Brazil's Cerrado regions, attracting increasing research interest due to its potential to complement or replace widely planted species such as *Urochloa* and *Megathyrsus*. Despite the release of three cultivars, significant improvements in dry matter (DM) yield and forage quality are needed to fully realize its agronomic potential. This study aimed to evaluate genetic variability, estimate narrow sense heritability, and predict expected genetic gains for DM yield and key forage quality traits in two gamba grass populations derived from the cultivars BRS Sarandi and Planaltina. Trials were established in spring 2017 in Planaltina, DF, and evaluated during February–March 2018 and January–March 2019. Crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), cellulose (CEL), and hemicellulose (HEMIC) were quantified alongside DM yield. BRS Sarandi exhibited higher CP (12.3% vs. 9.8%) and lower NDF (57.1% vs. 63.4%), ADF (36.2% vs. 41.5%), CEL (20.8% vs. 23.7%), and HEMIC (20.9% vs. 21.9%) compared to Planaltina, while DM yield did not differ significantly between populations (4.57 t·ha^{-1} vs. 4.50 t·ha^{-1} per harvest, $p > 0.05$). Heritability estimates for individual harvests ranged from 0.31 to 0.68 for DM yield and 0.28 to 0.62 for quality traits, whereas multi-harvest models across years yielded lower estimates (0.07–0.27). Expected annual genetic gains were modest, with the highest predicted increase for CP (0.45% per year) and the largest decrease for NDF (−0.78% per year), reflecting the quantitative nature of trait inheritance and strong environmental influence. This study provides novel insights by simultaneously comparing two populations for multiple harvests and quantifying both yield and detailed forage quality traits, offering practical guidance for gamba grass breeding strategies. Results indicate that breeding programs should prioritize multiple selection cycles, precise phenotyping, genotypic and potentially genomic selection to accelerate improvement in both DM yield and forage quality, overcoming the constraints of low heritability and multi-trait selection.

Keywords: tropical grass; breeding; heritability; half-sib families; forage quality traits; Cerrado

check for updates

Academic Editor: Fabio Gresta

Received: 11 August 2025
Revised: 2 October 2025
Accepted: 21 October 2025
Published: 3 November 2025

Citation: da Fonseca, C.E.L.; Carvalho, M.A.; Pessoa-Filho, M.; Ramos, A.K.B.; Karia, C.T.; Braga, G.J.; Maciel, N.B.A.; Tameirão, S.N.D. Genetic Variability, Heritability, and Expected Gains for Yield and Forage Quality in Gamba Grass (*Andropogon gayanus*) Populations. *Grasses* **2025**, *4*, 44. https://doi.org/10.3390/grasses4040044

Copyright: © 2025 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).

1. Introduction

Gamba grass (*Andropogon gayanus* Kunth) is a cross-pollinated forage species native to Africa, well adapted to tropical savannas across a range of altitudes, climates, and soils [1]. Since the early 1980s, it has been used in livestock production systems in Brazil's Cerrado ecoregion due to its natural resistance to spittlebug, ability to grow on acidic and low-fertility soils, and rapid regrowth at the end of the dry season following the first rains. Gamba grass is obligatorily allogamous, anemophilous, and self-incompatible [2]. The species is tetraploid (2n = 4x = 40), with a basic chromosome number of n = 10, and belongs to the bisquamulatus botanical group [3,4], a classification supported by recent molecular studies [5].

As obligate allogamous plants, populations are highly heterozygous and phenotypically heterogeneous, and their improvement requires strategies and methods that differ from those used in the improvement of autogamous and apomictic plants.

In Brazil, most cultivated pastures consist of species from the genera *Urochloa* (syn. *Brachiaria*) and *Megathyrsus* (syn. *Panicum*), which are largely apomictic. Their low genetic variability, due to clonal seed propagation, covers extensive areas and introduces risks to livestock production systems [6]. The development of new cultivars from diverse grass species is therefore strategic for diversification and sustainable intensification. Gamba grass represents a promising alternative for increasing pasture diversity in the Brazilian savannas, given its adaptation to and reported variability for several traits, suggesting potential gains through selective breeding [7].

Although dry matter (DM) yield remains the main focus of breeding programs, quality traits, such as higher digestibility and lower content of certain fibers, are becoming increasingly important targets for forage grass improvement [8]. Other characteristics linked to the environment and global climate change, such as GHG emissions, are being discussed and incorporated as important focuses for the genetic improvement of forage crops [9].

In perennial grasses, which are cross-pollinated and can be cloned, breeding is usually performed through mass selection or the production of synthetic varieties via parental lines or clones [10]. Mass selection is the simplest and, historically, the most widely used method of population improvement. It is the most frequently used phenotypic method because it is simple, fast, and less costly when compared to genotypic methods. However, its success depends on high heritability for the traits to be selected [10]. Therefore, increasing the frequency of favorable alleles in a population can be efficiently achieved through this method.

The development of synthetic varieties is based on progeny tests from open-pollinated seeds from the initial population, the selection of parents with good overall combinatorial ability, and their isolation in polycross blocks at each selection cycle. This method can be successfully used in the production of synthetic varieties of *Andropogon* with high dry matter production. The result of the synthetic variety development process is a population that usually has to be rebuilt from parental lines or clones through open pollination for one or two generations, thus moving away from the original synthetic variety. The number of parents or clones that are crossed to compose a synthetic variety varies from 3 to 15, with an average between 5 and 10 [10].

However, there is a notable gap in the literature regarding the quantitative metrics, like heritability, genetic variance, and coefficient of genotypic variation, that measure the genetic control and potential for improvement for a specific trait. These parameters help breeders understand existing genetic variability, predict the expected genetic progress from selection, determine the efficiency of breeding methods, and inform decisions on selecting superior genotypes for developing new cultivars. This lack of information hinders the

development of effective breeding strategies aimed at enhancing both dry matter (DM) yield and forage quality.

Simultaneous selection for yield and quality is a common goal in other forage breeding programs, including alfalfa [11,12], bermudagrass [13] and forage peanuts [14]. Achieving genetic gains depends on both the existing variability in populations and an understanding of the gene action governing trait inheritance. Currently, knowledge of genetic variability, gene action, and potential genetic gains in gamba grass populations grown in Brazilian savannas is limited.

The objective of this study was to estimate dry matter (DM) yield and forage quality trait heritability, as well as expected genetic gains, using half-sib (HS) family tests of two gamba grass populations. These data are essential to assess the genetic potential of DM yield and quality traits and to inform strategies for selecting superior germplasm and releasing improved gamba grass cultivars.

2. Material and Methods

Two genetically broad-based gamba grass populations, cv. Planaltina and cv. BRS Sarandi, from the Embrapa Cerrados forage breeding program, were used. Planaltina was the first gamba grass cultivar released in 1981 in Brazil and was a direct introduction of CIAT 621 collected in Africa [15]. Cultivar BRS Sarandi was derived from Planaltina and developed primarily through phenotypic recurrent selection for higher leaf to stem ratio and more homogenous population. BRS Sarandi was registered and protected in 2019 and has a higher frequency of plants with a semi-erect growth habit, higher number of tillers, and increased leaf to stem ratio, when compared to Planaltina and Baeti [16].

A total of 120 seeds from the Planaltina and BRS Sarandi cultivars, randomly selected, were used to establish isolated crossing blocks that produced open-pollinated seeds, which were harvested individually from each plant. These seeds gave rise to half-sibling families, which were evaluated in this study. The 120 parental plants from which these populations originated were maintained in the field. On 22 September 2017, HS families were sown in plastic trays and, on 22 November, 2-month-old seedlings were manually transplanted from the greenhouse to the field. Each experiment was laid out in a four replicate randomized complete block design with 10 seedlings planted in single family-row plot in each replicate, spaced 0.3 m apart within and 1.0 m across rows (Figure 1). The experiments were conducted in Planaltina, Federal District, Brazil (15°35′ S, 47°42′ W; 993 m a.s.l.), from September 2017 to April 2019. The climate at the experimental site is tropical savannah, according to the Köppen–Geiger classification [17], with a seasonal rain distribution and a very well-defined dry season between May and September.

The experiments were planted in a clay soil (Rhodic Haplustox Oxisol) with pH(H_2O) 5.3, OM concentration of 27 g·kg^{-1}, K concentration of 48 mg·kg^{-1}, Al concentration of 24 mg·kg^{-1}, and P concentration of 2.0 mg·kg^{-1} (Mehlich-I) at 0–0.2 m soil depth. The experimental area was uniformly fertilized with a commercial granular fertilizer surface applied at rates of 100 kg N ha^{-1}, 40 kg P_2O_5 ha^{-1}, and 60 kg K_2O ha^{-1}.

Half-sibs were sampled only during the wet season, two times in 2018 in February and March (January harvest was discarded as usual for the first one), and three times in 2019, January, February, and March, at 5 wk. intervals. Each sample weighed about 400 g fresh and was composed of randomly selected above ground material harvested with a hedge trimmer with a 66 cm long shaft, at a stubble height of 20 cm, from all plants in each HS row. All plant material from each plot was weighed with a field scale and the weights were further converted to DM yield per hectare, based on the dry weights of the samples collected during the harvest. All samples were dried for 72 h in a forced-air oven at 55 °C,

ground through a 1 mm screen in a Wiley mill (A.H. Thomas Co., Philadelphia, PA, USA), and stored in 200 mL plastic containers for laboratory analyses.



Figure 1. Aerial view of the gamba grass populations from the Embrapa Cerrados forage breeding program.

Near infrared reflectance spectroscopy (NIRS) calibrations were used to predict the conventional quality traits. The models were specifically developed for gamba grass and 10% of the samples from all harvests of the above experiments were used in the calibration process, as described by Fonseca et al. [18]. Spectral data were collected for 4640 samples of the above-described experiments using a NIRS FOSS 5000 System II type 461006 (FOSS Analytical SA, Hilleroed, Denmark) with the ISIScan software v.2.85.3 (ISI Software, FOSS Analytical AB, Höganãs, Sweden). About 2 g homogenized samples were placed in 3.8 cm inner diameter ring cup cells, with a quartz window, and closed with foam cardboard rings for the spectral readings. Scans were collected over a wavelength range of 1100 to 2498 nm with 2 nm resolution and 32 scans averaged for each sample. The spectral absorbance was recorded as the logarithm of the inverse of the reflectance ($A = 1/R$) and was used to predict crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), in vitro dry matter digestibility (IVDMD), cellulose (CEL), and hemicellulose (HEMIC) concentrations of all ground samples from both field experiments.

Linear mixed models were fitted to the data using the restricted maximum likelihood method (REML) to estimate the variance components. All statistical analyses were carried out using RStudio v.2022.07.1 Build 554 and R version 4.2.1 (2022-06-23 ucrt) with lme4 package v.1.1-34. The analyses for each trait were performed with data (i) from each individual harvest, (ii) averaged across harvests within each year, (iii) across years model, and (iv) averaged across populations. Narrow sense heritability estimates and associated standard errors on a HS progeny means basis were computed for all traits. Harvest was considered a fixed effect while years, replicated blocks, and HS families were random.

To compare both trials, population and harvests were considered fixed effects and block nested within trial was random:

(i) $Y_{bf} = \mu + B_b + F_f + \varepsilon_{bf}$, model for individual data harvest, all effects random;
(ii) $Y_{bhf} = \mu + B_b + H_h + BH_{bh} + F_f + FB_{fb} + FH_{fh} + \varepsilon_{bhf}$, model across harvests, all effects random but harvest;
(iii) $Y_{yhbf} = \mu + Y_y + H_h + YH_{yh} + B_b + BY_{by} + BH_{bh} + F_f + FY_{fy} + FB_{fb} + FH_{fh} + FYH_{fyh} + \varepsilon_{yhbf}$, model across years and harvests, all effects random but harvest; and
(iv) $Y_{ph} = \mu + P_p + H_h + B(P)_{bp}$, model across populations, all effects fixed but blocks nested within population.

Here, Y is the observations on the traits of interest; μ is the overall mean; B_b is the random effect of the 'b^h' replicated block; F_f is the random additive genetic effect of the 'fth' HS family; H_h is the fixed effect of the 'hth' harvest; Y_y is the random effect of the 'yth' year; P_p is the fixed effect of the pth population; BH_{bh} is the random effect interaction between block 'b' and harvest 'h'; FB_{fb} is the random effect interaction between HS family 'f' and block 'b'; FH_{fh} is the random effect interaction between HS family 'f' and harvest 'h'; YH_{yh} is the random effect interaction between year 'y' and harvest 'h'; BY_{by} is the random effect interaction between block 'b' and year 'y'; FY_{fy} is the random effect interaction between HS family 'f' and year 'y'; $B(P)_{bp}$ is the random effect block 'b' nested within population 'p'; FYH_{fyh} is the random effect interaction among HS family 'f', year 'y', and harvest 'h'; and ε_{yhbf} is the residual random error.

Narrow sense heritability on a HS progeny means basis (h^2), associated standard errors (SE), and expected gains (ΔG) were computed for all traits for each population, within, across, and over harvests and years according to Nguyen and Sleper [19] and Hallauer, Carena and Miranda [20]. The following equations were used to estimate heritability for each above model:

$$h^2 = \frac{\hat{\sigma}^2_F}{\hat{\sigma}^2_F + \frac{\hat{\sigma}^2_e}{b}} \pm \frac{SE(\hat{\sigma}^2_F)}{\frac{\hat{\sigma}^2_e + b\hat{\sigma}^2_F}{b}}$$

$$\text{and } SE\left(\hat{\sigma}^2_F\right) = \sqrt{Var\left(\hat{\sigma}^2_F\right)} = \sqrt{\frac{2}{b^2}\left[\frac{\left(\hat{\sigma}^2_e + b\hat{\sigma}^2_F\right)^2}{df_F + 2} + \frac{\left(\hat{\sigma}^2_e\right)^2}{df_e + 2}\right]}$$

$$h^2 = \frac{\hat{\sigma}^2_F}{\hat{\sigma}^2_F + \frac{\hat{\sigma}^2_{FH}}{h} + \frac{\hat{\sigma}^2_{FB}}{b} + \frac{\hat{\sigma}^2_e}{bh}} \pm \frac{SE(\hat{\sigma}^2_F)}{\frac{\hat{\sigma}^2_e + h\hat{\sigma}^2_{FB} + hb\hat{\sigma}^2_F}{bh}}$$

$$\text{and } SE\left(\hat{\sigma}^2_F\right) = \sqrt{\frac{2}{b^2h^2}\left[\frac{\left(\hat{\sigma}^2_e + h\hat{\sigma}^2_{FB} + hb\hat{\sigma}^2_F\right)^2}{df_F + 2} + \frac{\left(\hat{\sigma}^2_e + h\hat{\sigma}^2_{FB}\right)^2}{df_{FB} + 2}\right]}$$

$$h^2 = \frac{\hat{\sigma}^2_F}{\hat{\sigma}^2_F + \frac{\hat{\sigma}^2_{FY}}{y} + \frac{\hat{\sigma}^2_{FH}}{h} + \frac{\hat{\sigma}^2_{FB}}{b} + \frac{\hat{\sigma}^2_{FYB}}{yb} + \frac{\hat{\sigma}^2_e}{byh}} \pm \frac{SE(\hat{\sigma}^2_F)}{\frac{\hat{\sigma}^2_e + hy\hat{\sigma}^2_{FB} + bh\sigma^2_{FY} + bhy\hat{\sigma}^2_F}{byh}}$$

$$\text{and } SE\left(\hat{\sigma}^2_F\right) = \sqrt{\frac{2}{b^2h^2y^2}\left[\frac{\left(\hat{\sigma}^2_e + bh\hat{\sigma}^2_{FY}\right)^2}{df_{FY} + 2} + \frac{\left(\hat{\sigma}^2_e + b\left(\frac{h}{h-1}\right)\hat{\sigma}^2_{FYH}\right)^2}{df_{FYH} + 2} + \frac{\left(\hat{\sigma}^2_e\right)^2}{df_e + 2}\right]}$$

Expected gains per cycle of direct selection were computed for each trait using the formula $\Delta G = kch^2\hat{\sigma}_P$, where k is the standardized selection differential which equals to 1.75 for 10% selection pressure, c is the parental control factor which equals to 2 for crossing among only selected parentals, h^2 is the narrow sense heritability estimate, and $\hat{\sigma}_P$ is the phenotypic standard deviation [19,20].

3. Results

In Table 1, a summary of trait measurements and associated statistics for two populations of gamba grass, Planaltina and BRS Sarandi, are presented. These traits are related to forage yield and nutritional composition and reflect the built-in variations between the two populations. Planaltina DM yield averaged 4.57 t·ha^{-1}·harvest^{-1}, ranging from 0.37 to 12.01 t·ha^{-1}, and BRS Sarandi averaged 4.71 t·ha^{-1}·harvest^{-1}, varying across a wider range, from 0.29 to 21.18 t·ha^{-1}. No significant difference was found for DM yield between the two populations.

Table 1. Mean, associated standard error (SE), and range for DM yield in t·ha^{-1}·harvest^{-1} and forage quality traits in g·kg^{-1} of DM, of two gamba grass populations, cv. Planaltina and cv. Sarandi, and the overall population statistics with mean, range, mean square (MS), and significance level from ANOVA.

Trait	Planaltina (Mean ± SE, Range)	BRS Sarandi (Mean ± SE, Range)	Overall (Mean ± SE, Range)	Pop. MS
DM Yield (t·ha^{-1}·harvest^{-1})	4.57 ± 0.06 (0.37–12.01)	4.83 ± 0.06 (0.29–21.18)	4.71 ± 0.05 (0.29–21.18)	6.800 ns
CP (g·kg^{-1} DM)	104.94 ± 0.23 (72.0–135.4)	110.67 ± 0.24 (56.8–148.0)	107.92 ± 0.20 (56.8–148.0)	9.834 **
IVDMD (g·kg^{-1} DM)	537.11 ± 0.98 (359.0–648.6)	537.91 ± 0.77 (379.0–653.8)	537.59 ± 0.77 (359.0–653.8)	47.100 ns
NDF (g·kg^{-1} DM)	689.34 ± 0.70 (631.9–796.9)	668.67 ± 0.57 (609.6–753.1)	678.78 ± 0.56 (609.6–796.9)	106.88 **
ADF (g·kg^{-1} DM)	399.63 ± 0.66 (347.5–516.5)	389.90 ± 0.44 (325.4–461.7)	394.40 ± 0.40 (325.4–516.5)	52.960 **
ADL (g·kg^{-1} DM)	35.61 ± 0.12 (25.2–52.0)	37.20 ± 0.14 (22.4–69.9)	36.44 ± 0.10 (22.4–69.9)	0.606 ns
CEL (g·kg^{-1} DM)	364.03 ± 0.59 (310.4–471.5)	352.70 ± 0.43 (270.1–424.4)	358.14 ± 0.37 (270.1–471.5)	133.23 **
HEMIC (g·kg^{-1} DM)	289.71 ± 0.22 (258.1–323.2)	278.62 ± 0.26 (160.4–319.5)	283.64 ± 0.20 (160.4–323.2)	77.70 **

ns—nonsignificant differences between populations. **—significant differences between populations at alfa level 0.01.

Planaltina had a CP content of 104.94 g·kg^{-1}, varying between 72.0 and 135.4 g·kg^{-1}, and BRS Sarandi had a statistically significant higher mean of 110.67 g·kg^{-1}, varying across a broader range, from 56.8 to 148 g·kg^{-1}. Planaltina showed an IVDMD mean of 537.11 g·kg^{-1}, close to the BRS Sarandi mean of 543.65 g·kg^{-1}, and no significant difference. Planaltina showed a higher mean NDF content of 689.34 g·kg^{-1}, with a range of 631.9 to 796.9 g·kg^{-1}, while BRS Sarandi presented a relatively lower mean of 668.67 g·kg^{-1}, statistically significant, and a broader range extending from 499.6 to 753.1 g·kg^{-1}. Similarly to NDF, Planaltina had a higher mean ADF content (399.63 g·kg^{-1}) while BRS Sarandi had a lower mean of 389.9 g·kg^{-1}, statistically different. Similarly to NDF and ADF, Planaltina had significantly higher CEL and HEMIC contents compared to BRS Sarandi. ADL content was 36.44 g·kg^{-1} on average with means not statistically different between the two populations.

BRS Sarandi data revealed wider ranges of variation, with magnitudes of 20.89 t·ha^{-1}·harvest^{-1} for DM yield, 9.12 g·kg^{-1} for CP, and 23.35 g·kg^{-1} for NDF, when compared to those from Planaltina with magnitudes of 11.64 t·ha^{-1}·harvest^{-1} for DM yield, 6.34 g·kg^{-1} for CP and 16.5 g·kg^{-1} for NDF. Also, the lower and upper bounds of the ranges for DM yield and PB from BRS Sarandi outgrew those from Planaltina (Table 1).

In Tables 2 and 3, information on the mean ± SE, range, and HS components of variance for dry matter (DM) yield and all forage quality traits from 115 HS Planaltina families, and from 117 HS BRS Sarandi families, with data collected from two harvests in February and March 2018 and three harvests in January, February, and March 2019, is presented.

Table 2. Mean and associated SE range and HS components of variance (σ_{HS}^2) for DM yield and forage quality traits from 115 half-sib Planaltina families estimated from two harvests in 2018 and three harvests in 2019.

Trait	Statistics	2018			2019				2018–19	2018–19
		2	**3**	**2, 3** †	**1**	**2**	**3**	**1, 2, 3** †	**2, 3 and 2, 3** ‡	**1, 2, 3, 4, 5** †
DM Yield (t/ha)	Mean ± SE	6.07 ± 0.06	7.09 ± 0.08	6.58 ± 0.05	3.86 ± 0.05	2.30 ± 0.03	2.80 ± 0.04	2.99 ± 0.03	4.56 ± 0.06	4.42 ± 0.05
	Range	2.80–10.61	0.37–12.01	0.37–12.01	0.41–9.59	1.18–5.40	1.20–7.74	0.41–9.59	0.37–12.01	0.37–12.01
	σ_{HS}^2	0.581	0.594	0.125	0.059	0.032	0.056	0.023	0.057	0.069
CP ($g \cdot kg^{-1}$)	Mean ± SE	102.50 ± 0.51	107.67 ± 0.39	105.10 ± 0.33	89.51 ± 0.47	103.81 ± 0.45	105.76 ± 0.41	99.69 ± 0.32	104.93 ± 0.23	101.85 ± 0.24
	Range	72.0–135.4	79.5–133.2	72.0–135.4	60.7–130.3	81.7–128.4	75.2–133.4	60.7–133.4	72.0–135.4	60.7–135.4
	σ_{HS}^2	0.077	0.080	0.071	0.085	0.042	0.074	0.045	0.025	0.036
IVDMD ($g \cdot kg^{-1}$)	Mean ± SE	494.50 ± 1.80	536.69 ± 1.58	515.59 ± 1.39	487.1 ± 1.44	551.48 ± 1.40	565.73 ± 1.1	534.77 ± 1.20	537.10 ± 0.97	527.10 ± 0.93
	Range	359.0–587.5	428.5–648.6	359.0–648.6	389.2–581.9	629.0–436.6	423.1–618.6	389.2–629.0	359.0–648.6	359.0–648.6
	σ_{HS}^2	1.451	0.650	0.383	0.517	0.070	0.759	0.222	0.440	0.315
NDF ($g \cdot kg^{-1}$)	Mean ± SE	727.29 ± 1.04	695.84 ± 0.79	711.57 ± 0.83	674.66 ± 0.61	669.19 ± 0.63	665.01 ± 0.55	669.62 ± 0.36	689.33 ± 0.70	686.40 ± 0.58
	Range	668.1–796.9	648.4–731.6	648.4–796.9	639.1–742.5	713.5–634.9	631.9–709.8	631.9–742.5	631.9–796.9	631.9–796.9
	σ_{HS}^2	0.534	0.153	0.048	0.186	0.135	0.169	0.152	0.128	0.114
ADF ($g \cdot kg^{-1}$)	Mean ± SE	436.60 ± 1.11	401.20 ± 0.65	418.90 ± 0.87	413.23 ± 0.62	380.03 ± 0.58	380.66 ± 0.47	391.31 ± 0.53	399.62 ± 0.65	402.35 ± 0.55
	Range	372.1–516.5	360.7–442.5	360.7–516.5	378.4–469.9	422.6–347.5	353.6–429.8	347.5–469.9	347.5–516.5	347.5–516.5
	σ_{HS}^2	0.574	0.137	0.029	0.254	0.167	0.198	0.163	0.099	0.110
ADL ($g \cdot kg^{-1}$)	Mean ± SE	39.03 ± 0.18	38.22 ± 0.25	38.63 ± 0.15	32.58 ± 0.17	33.75 ± 0.16	31.41 ± 0.11	32.58 ± 0.09	35.60 ± 0.12	35.00 ± 0.10
	Range	28.8–51.6	25.2–52.0	25.2–52.0	22.6–43.4	49.8–26.8	26.0–46.2	22.6–49.8	25.2–52.0	22.6–52.0
	σ_{HS}^2	0.019	0.010	0.006	0.000	0.001	0.002	0.000	0.004	0.002
CEL ($g \cdot kg^{-1}$)	Mean ± SE	397.57 ± 1.01	362.97 ± 0.58	380.27 ± 0.82	380.65 ± 0.61	346.28 ± 0.54	349.26 ± 0.46	358.73 ± 0.52	364.02 ± 0.58	367.35 ± 0.5
	Range	330.6–471.5	329.4–397.2	329.4–471.5	345.9–429.5	387.6–310.4	324.4–383.6	310.4–429.5	310.4–471.5	310.4–471.5
	σ_{HS}^2	0.448	0.131	0.048	0.227	0.163	0.210	0.163	0.099	0.110
HEMIC ($g \cdot kg^{-1}$)	Mean ± SE	290.69 ± 0.33	294.63 ± 0.48	292.66 ± 0.30	261.42 ± 0.47	289.16 ± 0.40	284.35 ± 0.35	278.31 ± 0.40	289.71 ± 0.21	284.05 ± 0.31
	Range	271.2–309.9	258.1–323.2	258.1–323.2	230.2–290.6	313.2–263.5	263.6–308.5	230.2–313.2	258.1–323.2	230.2–323.2
	σ_{HS}^2	0.039	0.022	0.026	0.057	0.019	0.066	0.041	0.036	0.040

† Data combined across harvests. ‡ Data combined across years.

Table 3. Mean DM yield and associated SE range and HS components of variance (σ_{HS}^2) for DM yield and forage quality traits from 117 half-sib BRS Sarandi families estimated from two harvests in 2018 and three harvests in 2019.

Trait	Statistics	2018			2019				2018–19	2018–19
		2	**3**	**2, 3** †	**1**	**2**	**3**	**1, 2, 3** †	**2, 3 and 2, 3** ‡	**1, 2, 3, 4, 5** †
DM Yield (t/ha)	Mean ± SE	5.43 ± 0.07	8.38 ± 0.10	6.9 ± 0.08	3.43 ± 0.04	2.58 ± 0.03	2.78 ± 0.03	2.93 ± 0.02	4.79 ± 0.06	4.52 ± 0.05
	Range	1.6–13.3	3.3–21.2	1.6–21.2	0.3–9.8	1.1–6.6	0.3–6.2	0.3–9.8	0.3–21.2	0.3–21.2
	σ_{HS}^2	0.393	0.430	0.186	0.133	0.067	0.040	0.068	0.077	0.069
CP (g·kg^{-1})	Mean ± SE	118.43 ± 0.43	93.42 ± 0.49	105.92 ± 0.52	117.28 ± 0.45	111.09 ± 0.39	121.13 ± 0.4	116.5 ± 0.26	111.01 ± 0.33	112.27 ± 0.28
	Range	93.2–145.3	56.8–128.6	56.8–145.3	82–148	143.3–84.6	95.8–144.9	82.0–148.0	56.8–145.3	56.8–148
	σ_{HS}^2	0.115	0.051	0.047	0.164	0.166	0.099	0.125	0.069	0.036
IVDMD (g·kg^{-1})	Mean ± SE	569.36 ± 1.34	466.13 ± 1.32	517.74 ± 1.93	563.37 ± 1.33	560.64 ± 1.13	605.05 ± 0.96	576.35 ± 0.86	550.29 ± 1.33	552.91 ± 1.1
	Range	488.5–644.1	379.2–559	379.2–644.1	497.2–645.9	616.5–478.3	501.4–685.3	478.3–685.3	379.2–685.3	379.2–685.3
	σ_{HS}^2	0.647	0.268	0.318	1.466	0.643	0.833	0.840	0.430	0.315
NDF (g·kg^{-1})	Mean ± SE	686.86 ± 1.00	650.37 ± 1.47	668.62 ± 1.07	673.51 ± 0.57	667.97 ± 0.72	654.26 ± 0.72	665.25 ± 0.45	664.87 ± 0.61	666.6 ± 0.51
	Range	561.8–753.1	499.6–705.1	499.6–753.1	634.9–706.6	721.9–625.2	606.4–699.4	606.4–721.9	499.6–753.1	499.6–753.1
	σ_{HS}^2	0.105	0.336	0.071	0.205	0.183	0.121	0.130	0.055	0.114
ADF (g·kg^{-1})	Mean ± SE	398.63 ± 0.7	406.44 ± 0.8	402.54 ± 0.55	384.47 ± 0.58	374.85 ± 0.63	367.87 ± 0.48	375.73 ± 0.37	386.95 ± 0.5	386.45 ± 0.41
	Range	343.4–446	325.4–461.7	325.4–461.7	347.3–424	420.2–333.9	331.9–403.8	331.9–424	325.4–461.7	325.4–461.7
	σ_{HS}^2	0.105	0.135	0.123	0.200	0.129	0.043	0.063	0.060	0.110
ADL (g·kg^{-1})	Mean ± SE	41.15 ± 0.32	37.16 ± 0.33	39.15 ± 0.24	37.52 ± 0.17	34.96 ± 0.14	32.91 ± 0.25	35.13 ± 0.12	36.54 ± 0.15	36.74 ± 0.13
	Range	26.3–69.9	22.4–69.3	22.4–69.9	27.8–51.7	43.6–28.1	22.7–43.9	22.7–51.7	22.4–69.9	22.4–69.9
	σ_{HS}^2	0.030	0.015	0.006	0.005	0.008	0.006	0.006	0.003	0.002
CEL (g·kg^{-1})	Mean ± SE	357.48 ± 0.64	369.29 ± 0.98	363.39 ± 0.61	346.95 ± 0.56	339.89 ± 0.62	334.96 ± 0.52	340.60 ± 0.35	350.41 ± 0.48	349.72 ± 0.4
	Range	293.7–393.9	270.1–424.4	270.1–424.4	308.7–386.8	386.2–298.1	295.6–370	295.6–386.8	270.1–424.4	270.1–424.4
	σ_{HS}^2	0.136	0.239	0.096	0.189	0.115	0.040	0.071	0.064	0.110
HEMIC (g·kg^{-1})	Mean ± SE	288.23 ± 0.77	243.92 ± 1.02	266.08 ± 0.97	289.04 ± 0.45	293.12 ± 0.4	286.40 ± 0.56	289.52 ± 0.28	277.92 ± 0.58	280.14 ± 0.48
	Range	212–315.7	160.4–279.9	160.4–315.7	259.7–313.9	319.5–266.3	249.8–311.7	249.8–319.5	160.4–319.5	160.4–319.5
	σ_{HS}^2	0.155	0.082	0.024	0.020	0.102	0.049	0.052	0.037	0.040

† Data combined across harvests. ‡ Data combined across years.

The mean DM yield and the HS component of variance for both populations, Planaltina and BRS Sarandi, were consistently higher within and across harvests in 2018 than in 2019. The overall mean for DM yield across harvests and years, as well as across harvests 1 to 5 independent of year, had similar magnitudes for both populations (Tables 2 and 3). Most of the quality traits estimates were similar in magnitude across harvests within each year for both populations. Fiber components NDF, ADF, ADL, and CEL estimates were lower in 2019 than in 2018. Yet, CP and IVDMD were higher in 2019. Variations for all other traits were similar in magnitude across harvests and years, as well as across harvests 1 to 5 independent of year, for both populations (Tables 2 and 3).

Narrow sense heritability estimates on a half-sib family mean basis (h^2) were very low to moderate in magnitude for DM yield and all quality traits. Their associated standard errors ranged from low to high. All h^2 estimates for DM yield were significantly greater than zero, except for 2018's first harvest and across harvests for Planaltina, and 2019's third harvest for BRS Sarandi. DM yield ranged from 0.07 to 0.68 for the Planaltina population (Table 4) and from 0.07 to 0.53 for the BRS Sarandi population (Table 5).

Table 4. Half-sib family narrow sense heritability estimates and associated standard errors (SE) for dry matter yield (DM yield) and forage quality traits in gamba grass cultivar Planaltina.

Year	Harvest	DM Yield	CP	IVDMD	NDF	ADF	ADL	CEL	HEMIC
2018	2	0.68 ± 0.14	0.25 ± 0.15	0.46 ± 0.14	0.37 ± 0.14	0.37 ± 0.15	0.50 ± 0.14	0.34 ± 0.15	0.29 ± 0.15
	3	0.54 ± 0.14	0.35 ± 0.15	0.20 ± 0.15	0.23 ± 0.15	0.24 ± 0.15	0.21 ± 0.15	0.30 ± 0.15	0.15 ± 0.15
	2, 3 †	0.13 ± 0.07	0.16 ± 0.07	0.07 ± 0.07	0.02 ± 0.07	0.01 ± 0.07	0.08 ± 0.07	0.03 ± 0.07	0.10 ± 0.08
2019	1	0.29 ± 0.15	0.27 ± 0.15	0.23 ± 0.15	0.35 ± 0.15	0.43 ± 0.14	0.00 ± 0.16	0.42 ± 0.14	0.22 ± 0.15
	2	0.35 ± 0.15	0.23 ± 0.15	0.04 ± 0.16	0.28 ± 0.15	0.35 ± 0.15	0.04 ± 0.16	0.37 ± 0.14	0.12 ± 0.15
	3	0.31 ± 0.15	0.36 ± 0.15	0.43 ± 0.14	0.40 ± 0.14	0.50 ± 0.14	0.14 ± 0.15	0.53 ± 0.14	0.38 ± 0.14
	1, 2, 3 †	0.11 ± 0.05	0.10 ± 0.05	0.05 ± 0.05	0.15 ± 0.05	0.17 ± 0.05	0.01 ± 0.06	0.18 ± 0.05	0.08 ± 0.05
2018–19	2, 3 and 2, 3 ‡	0.07 ± 0.01	0.04 ± 0.02	0.05 ± 0.02	0.06 ± 0.02	0.05 ± 0.02	0.04 ± 0.02	0.06 ± 0.02	0.07 ± 0.02

† Data combined across harvests. ‡ Data combined across years; all heritability estimates greater than 2 SE are significant.

Table 5. Half-sib family heritability estimates and associated standard errors (SE) for dry matter yield (DM yield) and forage quality traits in gamba grass cultivar BRS Sarandi.

Year	Harvest	DM Yield	CP	IVDMD	NDF	ADF	ADL	CEL	HEMIC
2018	2	0.53 ± 0.14	0.51 ± 0.14	0.34 ± 0.14	0.09 ± 0.15	0.21 ± 0.15	0.36 ± 0.14	0.26 ± 0.15	0.21 ± 0.15
	3	0.32 ± 0.15	0.18 ± 0.15	0.13 ± 0.15	0.16 ± 0.15	0.19 ± 0.15	0.16 ± 0.15	0.24 ± 0.15	0.08 ± 0.15
	2, 3 †	0.15 ± 0.07	0.13 ± 0.07	0.09 ± 0.07	0.02 ± 0.08	0.11 ± 0.08	0.03 ± 0.08	0.07 ± 0.08	0.01 ± 0.08
2019	1	0.43 ± 0.14	0.47 ± 0.14	0.56 ± 0.14	0.46 ± 0.14	0.39 ± 0.14	0.22 ± 0.15	0.39 ± 0.14	0.09 ± 0.15
	2	0.42 ± 0.14	0.55 ± 0.14	0.39 ± 0.14	0.27 ± 0.15	0.24 ± 0.15	0.33 ± 0.14	0.22 ± 0.15	0.39 ± 0.14
	3	0.25 ± 0.15	0.43 ± 0.14	0.49 ± 0.14	0.27 ± 0.15	0.15 ± 0.15	0.23 ± 0.15	0.14 ± 0.15	0.23 ± 0.15
	1, 2, 3 †	0.27 ± 0.05	0.24 ± 0.05	0.24 ± 0.05	0.12 ± 0.05	0.07 ± 0.05	0.11 ± 0.05	0.08 ± 0.05	0.09 ± 0.05
2018–19	2, 3 and 2, 3 ‡	0.07 ± 0.01	0.11 ± 0.01	0.08 ± 0.01	0.02 ± 0.02	0.04 ± 0.02	0.02 ± 0.02	0.04 ± 0.02	0.02 ± 0.02

† Data combined across harvests; ‡ Data combined across years; all heritability estimates greater than 2 SE are significant.

For CP, only three of the eight h^2 estimates were greater than zero for Planaltina and six for BRS Sarandi (2018 harvest 3 and across harvests, and 2019 harvest 3). CP h^2 ranged from 0.16 to 0.36 and from 0.11 to 0.55 for Planaltina and BRS Sarandi, respectively.

IVDMD had three out of eight h^2 estimates greater than zero (2018 harvest 2, 2019 harvest 3, and across years) for Planaltina, and five (2018 harvest 2, 2019 harvests 1, 2, 3, across harvests, and across years) for BRS Sarandi. IVDMD h^2 ranged from 0.05 to 0.46 and from 0.08 to 0.56 for Planaltina and BRS Sarandi, respectively (Tables 4 and 5). The fiber components NDF, ADF, and CEL were more consistent for Planaltina with five of eight h^2

estimates significantly greater than zero. BRS Sarandi had only two significant h^2 estimates for NDF and one significant h^2 estimate for each of ADF, CEL, and HEMIC.

In general, significant heritability estimates across harvests and across years were lower when compared to those from individual harvests. For DM yield, they ranged from 0.07 to 0.15 and 0.07 to 0.13, while for individual harvests they ranged from 0.25 to 0.53 for Planaltina and from 0.29 to 0.60 for BRS Sarandi (Tables 4 and 5). Similar performances related to heritability estimates across harvests and across years versus individual harvests were observed for all quality traits as well.

The expected gains estimated across harvests and across years were also lower when compared to those from individual harvests. For DM yield, expected gains per cycle ranged from 0.17 to 0.22 t·ha^{-1} and 0.24 to 0.58 t·ha^{-1} across harvests and across years, while for individual harvests they ranged from 0.37 to 2.19 and from 0.58 to 1.58 t·ha^{-1} for Planaltina and BRS Sarandi populations, respectively (Tables 6 and 7). As the h^2 estimates were low in magnitude, similar lower expected gains estimates per cycle of selection were observed for all quality traits as well.

Table 6. Expected gains per cycle of selection based on half-sib family means for dry matter yield (DM yield) and forage quality traits in gamba grass cultivar Planaltina, estimated only for heritability greater than 2 SE.

Year	Harvest	DM Yield (t/ha)	CP (g·kg^{-1})	IVDMD (g·kg^{-1})	NDF (g·kg^{-1})	ADF (g·kg^{-1})	ADL (g·kg^{-1})	CEL (g·kg^{-1})	HEMIC (g·kg^{-1})
2018	2	2.19	-	284.48	156.46	159.39	33.94	135.34	36.90
	3	1.97	57.90	-	-	-	-	68.60	-
	2, 3 †	-	37.14	-	-	-	-	-	-
2019	1	-	-	-	88.90	116.62	-	107.48	-
	2	0.37	-	-	68.18	85.01	-	87.01	-
	3	0.46	57.11	198.08	90.06	109.63	-	116.50	55.26
	1, 2, 3 †	0.17	22.41	-	52.12	57.57	-	58.97	-
2018–19	2, 3 and 2, 3 ‡	0.22	-	51.19	30.16	23.28	4.18	25.21	16.51

† Data combined across harvests; ‡ Data combined across years.

Table 7. Expected gains per cycle of selection based on half-sib family means for dry matter yield (DM yield) and forage quality traits in gamba grass cultivar Sarandi, estimated only for heritability greater than 2 SE.

Year	Harvest	DM Yield (t/ha)	CP (g·kg^{-1})	IVDMD (g·kg^{-1})	NDF (g·kg^{-1})	ADF (g·kg^{-1})	ADL (g·kg^{-1})	CEL (g·kg^{-1})	HEMIC (g·kg^{-1})
2018	2	1.58	84.40	163.92	35.30	50.87	35.77	64.84	62.31
	3	1.29	-	-	-	-	-	-	-
	2, 3 †	0.58	-	-	-	-	-	-	-
2019	1	0.83	97.07	317.02	106.69	98.84	11.98	94.03	14.75
	2	0.58	105.57	177.41	-	-	17.76	56.67	70.25
	3	-	71.90	222.67	-	-	-	-	-
	1, 2, 3 †	0.47	59.83	154.57	43.12	-	9.11	-	-
2018–19	2, 3 and 2, 3 ‡	0.24	29.40	64.13	-	-	-	-	-

† Data combined across harvests; ‡ Data combined across years.

All expected gains estimates from now on are reported only for traits with h^2 estimates significantly different from zero. Also, all sequentially reported data below are for Planaltina and BRS Sarandi, respectively: the CP expected gains per cycle of selection ranged from 22.41 to 57.90 g·kg^{-1} and 29.40 to 105.57 g·kg^{-1}; IVDMD ranged from 51.19 to 284.48 g·kg^{-1} and 64.13 to 317.02 g·kg^{-1}; NDF ranged from 30.16 to 156.46 g·kg^{-1} and 43.12

to 106.69 g·kg^{-1}; ADF ranged from 23.28 to 159.39 and 50.87 to 98.84 g·kg^{-1}; ADL ranged from 4.18 to 33.94 g·kg^{-1} and 9.11 to 35.77 g·kg^{-1}; CEL ranged from 25.21 to 135.34 g·kg^{-1} and 56.67 to 94.03 g·kg^{-1}; and HEMIC from 16.51 to 55.26 g·kg^{-1} and 14.75 to 70.25 g·kg^{-1} (Tables 6 and 7).

4. Discussion

4.1. Genetic Variation and Trait Expression in Andropogon gayanus

The results highlighted significant variations between the Planaltina and BRS Sarandi populations for the forage quality traits of CP, NDF, ADF, CEL, and HEMIC contents. Cultivar BRS Sarandi had better forage quality characteristics than did cv. Planaltina due to higher CP and lower NDF, ADF, CEL, and HEMIC contents. This may be explained by the breeding strategy during BRS Sarandi development. Five phenotypic recurrent selection generations were carried out from cv. Planaltina germplasm to select semi-erect growth habit genotypes, with higher number of tillers, and higher leaf to stem ratio [16]. The BRS Sarandi had higher frequency of individuals with higher leaf to stem ratio which, indirectly, resulted in higher CP content and lower non-digestible fibers content of the resulting population. It is widely known that CP content is higher in leaves than in stems of forage species. The significant differences found between both gamba grass populations for most quality traits confirm that the newly developed population, BRS Sarandi, had significantly better forage quality properties when compared to its parental population, Planaltina. Similar trends were observed in newly developed populations of alfalfa and red clover, which are reported to have significantly better forage quality properties in relation to parent cultivars [21].

The fact that the two populations did not differ for DM yield may be explained by the following: (i) there was no direct selection for DM yield in the development of BRS Sarandi; and (ii) simultaneous selection for semi-erect growth habit, higher number of tillers, and higher leaf to stem ratio, in the development of BRS Sarandi, may not be genetically correlated to DM yield. Indeed, previous studies reported a negative association between tiller number and DM yield in *Panicum maximum* (Jacq.) L. [22], whereas only weak correlations were observed between canopy traits and sweetgrass (*Panicum virgatum* L.) yield [23].

Wider ranges of DM yield, and CP and NDF contents within a population may lead to a better effectiveness of forage breeding selection programs. Wider ranges indicate a potential higher genetic diversity within the population, which is essential for providing a broader pool of genetic material to select from.

The observed partitioning of variation in the two *A. gayanus* populations, significant within-population variability for quality traits, and moderate to low additive variance for most traits when data are pooled across harvests and years, are consistent with expectations for an obligate outcrossing perennial grass with a tetraploid cytology. In outcrossing grasses, substantial within-population variance and transgressive segregation after recombination are common and provide the raw material for selection [24,25]. The pattern seen here is a clearer signal of additive variance at the single-harvest level, but reduced h^2 across environments mirrors results from other perennial forage species where environment and G × E inflate the phenotypic variance when multiple seasons/sites are combined (e.g., perennial ryegrass and other temperate grasses).

Comparative studies in tropical forages show similar magnitudes and interpretation. For example, heritability and genetic variance studies in Urochloa and Panicum have reported moderate heritabilities for some quality or morphological traits at single sites or single harvests, but much lower realized additive variance when multi-environment datasets are analyzed, a pattern attributed to strong environment and G × E effects in

tropical systems [26,27]. These parallels support the conclusion that the genetic architecture inferred for A. gayanus is typical for perennial forage species and that the low across-environment h^2 does not necessarily indicate an absence of useful genetic variation but rather a predominance of non-repeatable environmental variance.

4.2. Heritability Patterns, Genotype × Environment, and Implications for Selection Timing

Narrow sense heritability (h^2) is the ratio of the additive genetic variation to the total phenotypic variation among families or plants. In other words, it is the proportion of trait variation within a population that can be attributed to genetic causes. In practice, h^2 is routinely used by breeders to estimate gain from selection in breeding programs. In this study, although most of the h^2 estimates were significantly greater than zero, they were predominantly low to moderate in magnitude, which suggested that both additive and non-additive gene effects played an important role in the genetic regulation of most traits.

The contrast between higher heritabilities estimated for individual harvests and lower estimates when pooling harvests/year highlights two methodological points: (i) single-harvest estimates can overestimate the proportion of variance that is additive and stable across environments, and (ii) pooling across environments better reflects the breeder's long-term target (stable performance). This is a recurrent observation across the forage breeding literature—single-environment h^2 are useful for within-season selection but are optimistic if the breeding objective includes across-season stability (G × E). Several recent studies of genotype × environment interactions in forage species advocate explicitly quantifying stability and using multi-environment trials to identify families or genotypes with favorable average performance and low sensitivity to environmental fluctuation. Approaches such as stability indices, AMMI/GGE analyses, or random regression can be used to rank families by both mean performance and stability.

The DM yield estimates within and across harvests decreased from 2018 to 2019 in both populations (Tables 2 and 3). These changes in forage DM yield between the two harvest years may be due to unfavorable environmental conditions, such as weather patterns (Figure 2). In the 2019 period, it rained 134.5 mm, 34. 2% of the total rainfall from the same period in 2018, which was 393.6 mm, and 39.5% of the average rainfall from the last 20 years prior to 2017 [28]. Lower rainfall in 2019 resulted in higher forage quality, for both populations.

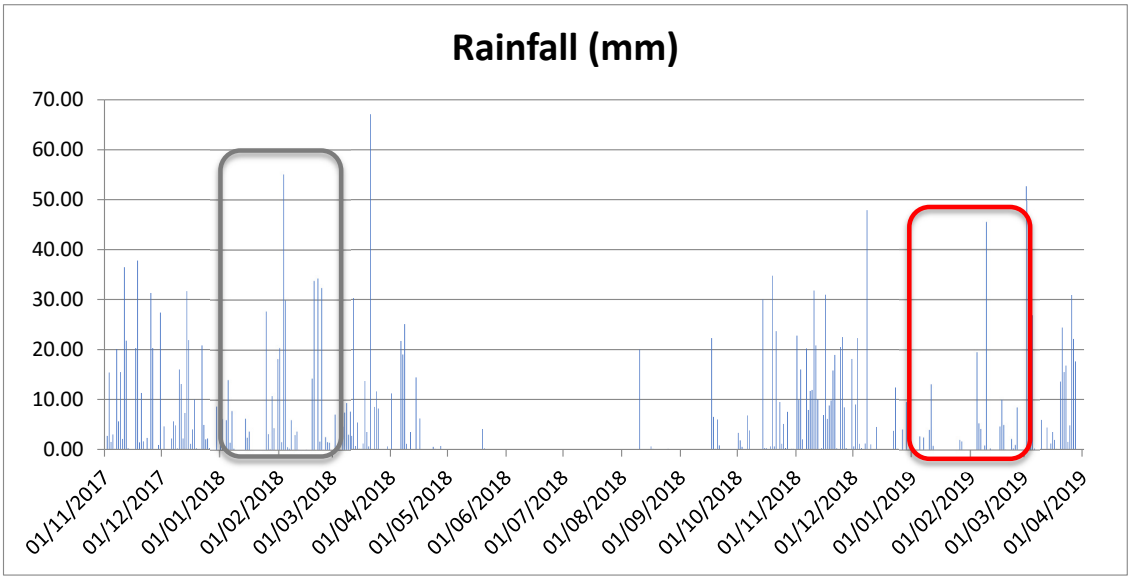


Figure 2. Daily rainfall (mm) from the main Embrapa Cerrados' weather station from November 2017 to March 2019.

The rainfall-related changes observed, which resulted in lower total biomass but improved forage quality during the drier year, reflect well-documented physiological responses: water stress reduces structural biomass deposition and can concentrate protein and alter fiber composition, improving digestibility in some cases [29–31]. Water stress has been reported to reduce seed and forage yield of smooth bromegrass genotypes by 38 and 14%, respectively, and has a higher impact on reproductive growth than on vegetative growth [32]. For breeders, this means selection strategies should explicitly consider seasonal timing of evaluation (e.g., selecting in both "favorable" and "stress" seasons) or use trial designs and selection indices that weight stability and mean performance according to the production target.

Annual expected gains for DM yield from direct selection across harvests and years ranged from 0.09 to 0.11 t·ha^{-1} yr^{-1} for cv. Planaltina, and 0.12 to 0.29 t·ha^{-1} yr^{-1} for BRS Sarandi. The potential genetic gains are from 0.39% to 0.48% yr^{-1} for Planaltina, and about the same magnitude from 0.50% to 1.20% yr^{-1} for BRS Sarandi. Those estimates are consistent with the expected gains for forage crops elsewhere in the literature. Gains in forage yield from breeding forage crops have been reported as low or nonexistent [33]. The genetic gain in annual DM yield of perennial ryegrass has been estimated to be about 4 to 5% decade^{-1} in Europe and New Zealand and less than 1% in the USA [34]. Some studies reported that DM yield can be increased by selection at rates above 4.0 to 5.0% per decade, such as orchard grass, with an average gain in DM yield of 1.3% yr^{-1} [35], and perennial ryegrass, with DM yield gains of 1.1% yr^{-1} [36]. Selection for DM yield in upland switchgrass resulted in gains of 0.71 t·ha^{-1} cycle^{-1} or 4% yr^{-1}, while selection in lowland switchgrass resulted in gains of 0.89 t·ha^{-1} cycle^{-1} or 1% yr^{-1} [37].

4.3. Expected Selection Gains

One of the main goals in forage breeding for quality is increasing protein content and fiber digestibility [21]. Expected gains for CP across harvests and years ranged from 11.2 to 18.6 g·kg^{-1} yr^{-1} for Planaltina and were lower than those for BRS Sarandi, which ranged from 14.7 to 29.9 g·kg^{-1} yr^{-1}. Gains from selection for CP may be effective for both populations and may be more effective for the latter. Expected gains for IVDMD across harvests/years was 25.5 g·kg^{-1} yr^{-1} for Planaltina and were lower than those for BRS Sarandi, which ranged from 32.1 to 77.5 g·kg^{-1} yr^{-1}. As for CP, gains from selection for IVDMD may be effective for both populations. Again, gains from cv. BRS Sarandi may be more effective. CP and IVDMD contents are the most important traits in forage quality and genetic improvement in IVDMD has been reported to improve animal daily gains at a rate of 3.2% increase for each 1% increase in IVDMD [38]. Also, concomitant selection for increased forage DM yield and IVDMD was reported as successful in the development of improved cultivars of switchgrass [39]. Improved rates of ruminant live weight gain due to increased IVDMD have been responsible for rapid adoption rates of new cultivars for grazing and hay production [40].

Certain forage breeding programs emphasize reducing fiber fractions, largely composed of non-digestible carbohydrates, to improve forage quality. Casler [40], Cardinal et al. [41], and Tucak et al. [21] described how lower NDF, acid detergent ADF, and lignin levels improve digestibility and nutritional value. Nonetheless, such reductions may adversely affect biomass yield and other key agronomic traits. Casler [40] notes that improvements in forage quality can sometimes come at the expense of yield or disease resistance, particularly when reducing lignification. The expected genetic gains for fiber components revealed contrasting patterns between the two cultivars. In cv. Planaltina, positive gains were estimated for all traits, with the largest values observed for ADF (up to 28.78 g·kg^{-1} yr^{-1}) and cellulose (up to 29.48 g·kg^{-1} yr^{-1}). These results indi-

cated the presence of exploitable genetic variability for cell wall components, although increases in ADF and lignin may negatively affect forage digestibility. Moderate gains for NDF (15.8–21.1 $g \cdot kg^{-1}$ yr^{-1}) and hemicellulose (8.26 $g \cdot kg^{-1}$ yr^{-1}) further suggested balanced opportunities for selection. By contrast, BRS Sarandi exhibited gains only for NDF (21.6 $g \cdot kg^{-1}$ yr^{-1}) and lignin (4.6 $g \cdot kg^{-1}$ yr^{-1}), with no improvement in ADF, cellulose, or hemicellulose, reflecting limited additive variance or unfavorable genetic correlations. The increase in lignin is of particular concern, as it is generally associated with reduced digestibility. Collectively, these results demonstrate greater breeding potential in cv. Planaltina for modifying fiber fractions, but emphasize the need to balance structural improvements with the maintenance of nutritive value.

There were no expected gains estimates for the fiber components ADF, CEL, and HEMIC for BRS Sarandi due to the non-significance of h^2. Lower NDF and ADF contents, which are structural components rich in non-digestible cellulose and lignin, have the potential to increase the feeding value of the forage by improving voluntary intake and fiber digestibility, respectively.

4.4. Trait Relationships, Indirect Selection, and Breeding Targets

Our finding that selection for architectural traits (leaf:stem ratio, tiller number) in BRS Sarandi produced measurable improvements in quality without a concomitant yield penalty is important and echoes results from other programs. In many forage programs, indirect selection for architecture has been an effective path to improved nutritive value because leaf tissue is richer in protein and more digestible than stem tissue; similar indirect responses have been harnessed in Megathyrsus and Urochloa breeding programs [13,26]. Empirical correlations between yield and quality are species and environment dependent. In some contexts, improvements in leafiness have been achieved at the expense of bulk yield, whereas in other breeding programs, simultaneous gains in both traits have been obtained through the use of selection indices and recurrent selection schemes [21,38]. This implies that a selection index incorporating direct measures of IVDMD or CP together with yield (or reliable proxies) is likely to be more effective than relying solely on architectural traits.

NDF has been reported to be positively correlated with forage yield of smooth bromegrass [42] and with plant vigor of alfalfa populations [43]. NDF has been negatively correlated with a high digestible carbohydrate, pectin, the predominant component of neutral detergent-soluble fiber (NDSF) in alfalfa [43,44] and CP. Improvements in timothy (*Phleum pretense* L.) digestibility can only be achieved by reducing the proportion of the structural components, and increments in forage yield reduced its nutritive value [45]. Cultivar Planaltina shows a better potential to be selected for low fiber contents.

Furthermore, the broader phenotypic ranges in BRS Sarandi suggest that recurrent selection expanded the segregating variance available for breeders, a desirable outcome for continued selection and crossing. Similar observations have been made in switchgrass and alfalfa where breeding populations derived from recurrent selection contained increased variance and thus greater opportunities for genetic gain in subsequent cycles. This underlines the potential of BRS Sarandi as both a cultivar and a breeding population.

4.5. Comparisons with the Literature on Temperate Forage Breeding: Lessons and Methods Transferable to A. gayanus

Temperate forage breeding has developed mature methodological tools—including selection indices, multi-environment trials, REML/BLUP frameworks, and genomic prediction—that may be directly applicable to tropical perennial breeding programs. For example, genomic selection (GS) has been applied with success in switchgrass [27] and alfalfa (recent accuracy studies), demonstrating that GS can shorten cycle length and increase genetic gain per unit time even in outcrossing, polyploid systems when prediction

models are carefully calibrated. The forage genomics literature recommends coupling GS with optimized phenotyping (high-throughput NIRS for quality traits) and smart training-population design to capture G × E patterns, strategies directly applicable to *A. gayanus*.

Given the low across-environment h^2 observed, genomic selection may enhance breeding efficiency by extracting additive signals from noisy phenotypes and enabling earlier selection prior to completion of multi-year evaluations.

Phenotypic data on forage productivity and quality from the half-sib families evaluated in this study, together with forthcoming genotypic data, may be used to calibrate genomic prediction models. Within the best-performing families, individual plants may then be selected as parents for a new breeding cycle, guided by the prediction models.

Temperate studies also highlight the value of using derivative or correlated traits (e.g., spectral indices, rapid field proxies) to increase accuracy and throughput of selection. NIRS calibrations for quality traits could be integrated to spectral signatures or simple morphological proxies into genomic or phenotypic prediction models.

4.6. Evidence from Tropical Grass Genomics and Diversity Studies

Recent genomic and population genetic studies in tropical forages (Urochloa and Cynodon) show high levels of genetic diversity and complex population structure that breeders can exploit [46–48]. These studies demonstrate that (i) reference panels and training populations can be assembled from existing cultivar and germplasm collections, and (ii) that molecular markers can reveal a subpopulation structure that matters for prediction accuracy and crossing strategy. The breeding system of *A. gayanus*, a tetraploid and obligate outcrossing species, is well suited to approaches that integrate pedigree information, molecular markers, and multi-environment phenotyping to estimate breeding values and optimize cross design.

5. Conclusions

This study was the first to provide a comprehensive assessment of heritability and genetic gain for both yield and forage quality traits in *Andropogon gayanus* populations. By addressing the study objectives, we demonstrated that although heritability values across harvests and years were generally low to moderate, there is exploitable genetic variation for dry matter yield, crude protein, and digestibility, particularly within the BRS Sarandi population. These findings confirm our initial hypothesis that both populations harbor sufficient variability to support genetic progress, while also highlighting the challenges posed by strong environmental influence on trait expression.

The novel contribution of this work lies in quantifying realistic expected gains from selection in a tropical grass where such estimates were previously lacking. The results show that incremental but cumulative improvements are feasible and that breeding strategies must integrate family-based selection, multi-environment evaluation, and possibly genomic selection to overcome the limitations of low heritability and lengthy cycles. The evidence that BRS Sarandi combines superior forage quality with broader trait variability indicates its value as a base population for future cultivar development.

This study advances understanding of the genetic architecture of *A. gayanus* and establishes a foundation for targeted breeding strategies that translate incremental genetic gains into tangible benefits for tropical livestock systems. The integration of genomics-assisted breeding may offer a powerful pathway to accelerate progress and deliver cultivars that simultaneously enhance productivity and sustainability.

From a practical standpoint, even modest genetic gains in digestibility and protein content can yield substantial improvements in animal performance, reduce land-use pressure, and lower greenhouse gas emissions per unit of beef or milk produced. For grassland

management, our findings support diversification beyond apomictic Urochloa pastures, providing producers with better options adapted to acidic and low-fertility soils. In the context of climate adaptation, the identification of families with more stable performance across variable rainfall regimes provides a pathway for developing cultivars capable of maintaining productivity under increasing climatic uncertainty.

Author Contributions: All authors contributed to the study conception, design, evaluation, data and lab analysis, and writing. C.E.L.d.F., M.A.C., M.P.-F. and C.T.K. were effective in the experimental planning, seedlings production, experiments set up and conduction, data collection, writing—review and manuscript editing. M.A.C. and C.T.K. were responsible for funding acquisition. A.K.B.R. for all genetic material preparation, field and glass house logistics, as well as the manuscript review. C.E.L.d.F. and M.P.-F. performed all statistics and quantitative analysis. G.J.B. was responsible for countless scientific discussions, editing, and for several manuscript reviews. N.B.A.M. and S.N.D.T. performed all wet lab and NIRS analysis with respective interpretation and discussion. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded jointly by Embrapa—Brazilian Agricultural Research Corporation (Grant number SEG 20.19.01.014.00.00 and SEG 20.23.01.006.00.00 and UNIPASTO—Association for the Promotion of Forage Breeding Research (Grant number SAIC 10200.14/0096-4).

Data Availability Statement: The raw data supporting the conclusions of this article will be made available by the authors on request.

Conflicts of Interest: All authors are Embrapa's employees with no involvement with UNIPASO or any other organization or entity with any financial interest or non-financial interest in the subject matter or materials discussed in this manuscript.

Abbreviations

ADF, acid detergent fiber; ADL, acid detergent lignin; CP, crude protein; CE, cellulose; DM, dry matter; HEMIC, hemicellulose; h^2, narrow sense heritability; HS, half-sib; IVDMD, in vitro dry matter digestibility; N, nitrogen; NDF, neutral detergent fiber; NIRS, near-infrared reflectance spectroscopy; OM, organic matter; REML, restricted maximum likelihood; SE, standard error of the mean.

References

1. Grof, B.; Thomas, D. The agronomy of *Andropogon gayanus*. In *Andropogon gayanus Kunth—A Grass for Tropical Acid Soils*; Toledo, J.M., Vera, R., Lascano, C., Lenné, J.M., Eds.; CIAT: Cali, Colombia, 1990; pp. 157–177.
2. Foster, W.H. Investigations preliminary to the production of cultivars of *Andropogon gayanus*. *Euphytica* **1962**, *11*, 47–52. [CrossRef]
3. Okoli, B.E.; Olorode, O. Cytogenetic studies in the *Andropogon gayanus–A. tectorum* complex (Gramineae). *Bot. J. Linn. Soc.* **1983**, *87*, 263–271. [CrossRef]
4. Nagahama, N.; Norrmann, G. Review of the genus Andropogon (Poaceae: Andropogoneae) in America based on cytogenetic studies. *J. Bot.* **2012**, *2012*, 632547. [CrossRef]
5. Pessoa Filho, M.A.C.P.; Azevedo, A.L.S.; Ramos, A.K.B.; Carvalho, M.A.; Fonseca, C.E.L. *Estimativa do Tamanho do Genoma em Cultivares de Capim-Andropogon (Andropogon gayanus Kunth)*; Boletim de Pesquisa e Desenvolvimento 372; Embrapa Cerrados: Planaltina, DF, Brazil, 2021; 13p. Available online: https://ainfo.cnptia.embrapa.br/digital/bitstream/item/224864/1/Estimativa-do-tamanho-do-genoma-Boletim-372.pdf (accessed on 2 October 2025).
6. Jank, L.; Barrios, S.C.; do Valle, C.B.; Simeão, R.M.; Alves, G.F. The value of improved pastures to Brazilian beef production. *Crop Pasture Sci.* **2014**, *65*, 1132–1137. [CrossRef]
7. Miles, J.W.; Grof, B. Genetics and plant breeding of *Andropogon gayanus*. In *Andropogon gayanus Kunth: A Grass for Tropical Acid Soils*; Toledo, J.M., Vera, R., Lascano, C., Lenné, J.M., Eds.; CIAT: Cali, Colombia, 1990; pp. 19–35.
8. Kingston-Smith, A.H.; Marshall, A.H.; Moorby, J.M. Breeding for genetic improvement of forage plants in relation to increasing animal production with reduced environmental footprint. *Animal* **2013**, *7* (Suppl. 1), 79–88. [CrossRef]
9. Wróbel, B.; Zielewicz, W.; Paszkiewicz-Jasińska, A. Improving Forage Quality from Permanent Grasslands to Enhance Ruminant Productivity. *Agriculture* **2025**, *15*, 1438. [CrossRef]
10. Simmonds, N.W.; Smartt, J. *Principles of Crop Improvememnt*, 2nd ed.; Blackwell Science: Berlim, Germany, 1999.

11. Béguier, V.; Guillemot, E.; Julier, B. Alfalfa forage quality breeding in France: 30 years of common efforts from seed industry, dehydration industry and public research. In Proceedings of the Second World Alfalfa Congress, Córdoba, Argentina, 11–14 November 2018; Instituto Nacional de Tecnología Agropecuaria (INTA): Buenos Aires, Argentina, 2018. Available online: https://worldalfalfacongress.ucdavis.edu/sites/g/files/dgvnsk8841/files/media/documents/Alfalfa%20forage%20quality%20breeding%20in%20France%3B%2030%20years%20of%20common%20efforts%20from%20seed%20industry%2C%20dehydratation%20industry%20and%20public%20research..pdf (accessed on 2 October 2025).
12. Santos, I.G.D.; Cruz, C.D.; Nascimento, M.; Rosado, R.D.S.; Ferreira, R.D.P. Direct, indirect and simultaneous selection as strategies for alfalfa breeding on forage yield and nutritive value. *Pesqui. Agropecu. Trop.* **2018**, *48*, 178–189. Available online: http://www.alice.cnptia.embrapa.br/alice/handle/doc/1096305 (accessed on 2 October 2025). [CrossRef]
13. Souza, C.D.; Lopez, Y.; Munoz, P.; Anderson, W.; Dall'Agnol, M.; Wallau, M.; Rios, E. Natural genetic diversity of nutritive value traits in the genus *Cynodon*. *Agronomy* **2020**, *10*, 1729. [CrossRef]
14. Simeão, R.M.; Assis, G.M.L.; Montagner, D.B.; Ferreira, R.C.U. Forage peanut (*Arachis* spp.) genetic evaluation and selection. *Grass Forage Sci.* **2017**, *72*, 322–332. [CrossRef]
15. Thomas, D.; Andrade, R.P.; Couto, W.; Rocha, C.M.C.; Moore, P. *Andropogon gayanus* var. bisquamulatus cv. Planaltina: Principais características forrageiras. *Pesqui. Agropecu. Bras.* **1981**, *16*, 347–355. Available online: https://seer.sct.embrapa.br/index.php/pab/article/view/16890 (accessed on 2 October 2025).
16. Carvalho, M.A.; Fonseca, C.E.L.; Ramos, A.K.B.; Braga, G.J.; Fernandes, F.D.; Pessoa Filho, M.A.C.P. BRS Sarandi: A new *Andropogon gayanus* cultivar for tropical pastures. In Proceedings of the XXV International Grassland Congress (IGC) "Grasslands for Animal, Soil and Human Health", Covington, KT, USA, 14–19 May 2023. [CrossRef]
17. Peel, M.C.; Finlayson, B.L.; McMahon, T.A. Updated world map of the Köppen–Geiger climate classification. *Hydrol. Earth Syst. Sci.* **2007**, *11*, 1633–1644. [CrossRef]
18. Fonseca, C.E.L.; Pessoa Filho, M.; Braga, G.J.; Ramos, A.K.B.; Carvalho, M.A.; Fernandes, F.D.; Karia, C.T.; Maciel, G.A.; Athayde, N.B.; Dessaune, S.N.; et al. Near-infrared reflectance spectroscopy as a tool for breeding *Andropogon gayanus* Kunth for forage quality. *IOSR J. Agric. Vet. Sci.* **2020**, *13*, 57–66. Available online: http://www.iosrjournals.org/iosr-javs/papers/Vol13-issue6/Series-1/H1306015766.pdf (accessed on 2 October 2025).
19. Nguyen, H.T.; Sleper, D.A. Theory and application of half-sib matings in forage grass breeding. *Theor. Appl. Genet.* **1983**, *64*, 187–196. [CrossRef] [PubMed]
20. Hallauer, A.R.; Carena, M.J.; Miranda, J.B. *Quantitative Genetics in Maize Breeding*, 2nd ed.; Iowa State University Press: Ames, IA, USA, 1988. [CrossRef]
21. Tucak, M.; Ravlić, M.; Horvat, D.; Čupić, T. Improvement of forage nutritive quality of alfalfa and red clover through plant breeding. *Agronomy* **2021**, *11*, 2176. [CrossRef]
22. Singh, D.K.; Singh, V.; Sale, P.W. Effect of cutting management on yield and quality of different selections of Guinea grass [*Panicum maximum* (Jacq.) L.] in a humid subtropical environment. *Trop. Agric.* **1995**, *72*, 181–187. Available online: https://journals.sta.uwi.edu/ojs/index.php/ta/article/view/2458 (accessed on 2 October 2025).
23. Redfearn, D.D.; Moore, K.J.; Vogel, K.P.; Waller, S.S.; Mitchell, R.B. Canopy Architecture and Morphology of Switchgrass Populations Differing in Forage Yield. *Agron. J.* **1997**, *89*, 262–269. [CrossRef]
24. Mackay, I.J.; Cockram, J.; Howell, P.; Powell, W. Understanding the classics: The unifying concepts of transgressive segregation, inbreeding depression and heterosis and their central relevance for crop breeding. *Plant Biotechnol. J.* **2020**, *19*, 1873–1875. [CrossRef] [PubMed]
25. Ferreira, R.C.U.; Costa Lima Moraes, A.D.; Chiari, L.; Simeão, R.M.; Vigna, B.B.Z.; de Souza, A.P. An overview of the genetics and genomics of the *Urochloa* species most commonly used in pastures. *Front. Plant Sci.* **2021**, *12*, 770461. [CrossRef]
26. Jank, L.; Valle, C.B.; Resende, R.M.S. Breeding tropical forages. *Crop Breed. Appl. Biotechnol.* **2011**, *11*, 27–34. [CrossRef]
27. Ramstein, G.P.; Evans, J.; Kaeppler, S.M.; Mitchell, R.B.; Vogel, K.P.; Buell, C.R.; Casler, M.D. Accuracy of genomic prediction in switchgrass (*Panicum virgatum* L.) improved by accounting for linkage disequilibrium. *G3* **2016**, *6*, 1049–1062. [CrossRef]
28. Alves, M.E.B.; Muller, A.G.; de Oliveira, A.D.; da Silva, F.A.M. *Boletim Agrometeorológico do ano 2021 para Planaltina, DF*; Documentos/Embrapa Cerrados, 402; Embrapa Cerrados: Planaltina, DF, Brazil, 2023; p. 49, ISSN 1517-5111, e-ISSN 2176-5081.
29. Peterson, P.R.; Sheaffer, C.C.; Hall, M.H. Drought Effects on Perennial Forage Legume Yield and Quality. *Agron. J.* **1992**, *84*, 774–779. [CrossRef]
30. Sheaffer, C.C.; Peterson, P.R.; Hall, M.H.; Stordahl, J.B. Drought effects on yield and quality of perennial grasses in the North Central United States. *J. Prod. Agric.* **1992**, *5*, 556–561. [CrossRef]
31. Bittman, S.; Simpson, G.M.; Mir, Z. Leaf senescence and seasonal decline in nutritional quality of three temperate forage grasses as influenced by drought. *Crop Sci.* **1988**, *28*, 546–552. [CrossRef]
32. Saeidnia, F.; Majidi, M.M.; Mirlohi, A.; Soltan, S. Physiological and tolerance indices useful for drought tolerance selection in smooth bromegrass. *Crop Sci.* **2017**, *57*, 282–289. [CrossRef]

33. Casler, M.D.; Brummer, E.C. Theoretical expected genetic gains for among- and within-family selection methods in perennial forage crops. *Crop Sci.* **2008**, *48*, 890–902. [CrossRef]
34. Stewart, A.; Hayes, R. Ryegrass breeding—Balancing trait priorities. *Ir. J. Agric. Food Res.* **2011**, *50*, 31–46. Available online: https://www.jstor.org/stable/41348154 (accessed on 2 October 2025).
35. Casler, M.D.; Fales, S.L.; McElroy, A.R.; Hall, M.H.; Hoffman, L.D.; Undersander, D.J.; Leath, K.T. Half-sib family selection for forage yield in orchardgrass. *Plant Breed.* **2002**, *121*, 43–48. [CrossRef]
36. Wilkins, P.W.; Humphreys, M.O. Progress in breeding perennial forage grasses for temperate agriculture. *J. Agric. Sci.* **2003**, *140*, 129–150. [CrossRef]
37. Casler, M.D.; Vogel, K.P. Selection for biomass yield in upland, lowland, and hybrid switchgrass. *Crop Sci.* **2014**, *54*, 626–636. [CrossRef]
38. Casler, M.D.; Vogel, K.P. Accomplishments and impact from breeding for increased forage nutritional value. *Crop Sci.* **1999**, *39*, 12–20. [CrossRef]
39. Vogel, K.P. Comparison of two perennial grass breeding systems in switchgrass. *Crop Sci.* **2013**, *53*, 863–870. [CrossRef]
40. Casler, M.D. Session 17-Forage Quality BREEDING FOR IMPROVED FORAGE QUALITY: POTENTIALS AND PROBLEMS. Agricultural and Food Sciences. Available online: https://www.semanticscholar.org/paper/Session-17-Forage-Quality-BREEDING-FOR-IMPROVED-%3A-Casler/0430c2216f4d60db1218581b6f5d7e5c15a62176 (accessed on 2 October 2025).
41. Cardinal, A.J.; Lee, M.; Moore, K.M. Genetic mapping and analysis of quantitative trait loci affecting fiber and lignin content in maize. *Theor. Appl. Genet.* **2003**, *106*, 866–874. [CrossRef] [PubMed]
42. Casler, M.D. Agricultural fitness of smooth bromegrass populations selected for divergent fiber concentration. *Crop Sci.* **2005**, *45*, 36–43. [CrossRef]
43. Fonseca, C.E.L.; Viands, D.R.; Hansen, J.; Pell, A. Associations among forage quality traits, vigor, and disease resistance in alfalfa. *Crop Sci.* **1999**, *39*, 1271–1276. [CrossRef]
44. Tecle, I.Y.; Viands, D.R.; Hansen, J.L.; Pell, A.N. Response from selection for pectin concentration and indirect response in digestibility of alfalfa. *Crop Sci.* **2006**, *46*, 1081–1087. [CrossRef]
45. Bélanger, G.; Michaud, R.; Jefferson, P.G.; Tremblay, G.F.; Brégard, A. Improving the nutritive value of timothy through management and breeding. *Can. J. Plant Sci.* **2001**, *81*, 577–585. [CrossRef]
46. Higgins, J.; Tomaszewska, P.; Pellny, T.K.; Castiblanco, V.; Arango, J.; Tohme, J.; Schwarzacher, T.; Mitchell, R.A.; Heslop-Harrison, J.S.; De Vega, J.J. Diverged subpopulations in tropical *Urochloa* (*Brachiaria*) forage species indicate a role for facultative apomixis and varying ploidy in their population structure and evolution. *Annals of Botany* **2022**, *130*, 657–669. [CrossRef]
47. Mushagalusa, P.B.; Kimwemwe, P.K.; Katunga, D.M.; Mondo, J.M.; Cirezi, N.C.; Ayagirwe, R.B.; Bacigale, S.B.; Mutai, C.; Muktar, M.S.; Kimani, W.; et al. Population structure and genetic diversity of Brachiaria grass (*Urochloa* spp.) accessions from the Democratic Republic of Congo using DArTseq single nucleotide polymorphism markers. *Crop Sci.* **2025**, *65*, e70102. [CrossRef]
48. Singh, L.; Wu, Y.; McCurdy, J.D.; Stewart, B.R.; Warburton, M.L.; Baldwin, B.S.; Dong, H. Genetic diversity and population structure of bermudagrass (*Cynodon* spp.) revealed by genotyping-by-sequencing. *Front. Plant Sci.* **2023**, *14*, 1155721. [CrossRef]

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.