

ARTICLE

Phenotypic variability and correlations of seed yield and seed quality traits in *Urochloa ruziziensis* (R. Germ. & Evrard) Crins genotypes

Érika Moreira dos Santos^{1,2} , Ricardo Carmona¹ , Cláudio Takao Karia² , Carlos Eduardo Lazarini da Fonseca² , Allan Kardec Braga Ramos² , Marco Pessoa-Filho^{2,3*} 

¹Universidade de Brasília, Faculdade de Agronomia e Medicina Veterinária, Programa de Pós-Graduação em Agronomia, Campus Darcy Ribeiro, 70910-900, Brasília-DF, Brasil.

²Embrapa Cerrados, Caixa Postal 08223, 73310-970, Brasília-DF, Brasil.

³Embrapa Recursos Genéticos e Biotecnologia, Caixa Postal 02372, 70770-917, Brasília-DF, Brasil.

ABSTRACT: Tropical forage seed production is strategically important to Brazil, and integrated crop-livestock-forest systems create a continuous demand for superior *Urochloa ruziziensis* cultivars. Optimizing commercial seed yield and quality is challenging, due to the inherent complexity of reproductive traits, seed dormancy, and highly variable seed filling. This study aimed to assess the phenotypic variability and correlations among 24 *U. ruziziensis* genotypes previously selected for high forage yield. Plants were evaluated for key flowering traits, filled seed mass, seed filling percentage, seed viability, germination rates, and seed dormancy. The results confirmed the existence of broad and significant phenotypic variability among the tested genotypes across all components of yield, quality, and dormancy, showing substantial potential for genetic improvement. Crucially, strong positive correlations were established between essential flowering components, such as the number of inflorescences per plant, and subsequent filled seed mass and seed viability. This study successfully identified elite genotypes exhibiting superior combined yield and quality, as well as specific genotypes with notably low dormancy. The identified genetic diversity and trait correlations provide criteria for guiding selection efforts in similar environments for *U. ruziziensis* breeding programs.

Index terms: brachiaria, breeding, forage, *Urochloa*.

RESUMO: A produção de sementes forrageiras é estratégica para o Brasil. Entretanto, a melhoria da produtividade e da qualidade de sementes é um desafio devido à complexidade dos caracteres reprodutivos, à dormência de sementes e à alta variabilidade na produção de sementes cheias. Este estudo teve como objetivo avaliar a variabilidade fenotípica e as correlações entre 24 genótipos de capim-ruziziensis selecionados para alta produção de forragem. As plantas foram avaliadas quanto a caracteres de florescimento, massa de sementes cheias, percentual de enchimento das sementes, viabilidade das sementes, taxas de germinação e dormência. Os resultados confirmaram a existência de ampla variabilidade fenotípica entre os genótipos testados em todos os componentes de rendimento, qualidade e dormência, demonstrando considerável potencial para melhoramento genético. Foram identificadas fortes correlações positivas entre componentes essenciais do florescimento, como o número de inflorescências por planta, e a massa de sementes cheias e a viabilidade das sementes. Este trabalho identificou genótipos elite com produtividade e qualidade superiores, bem como genótipos específicos com baixa dormência de sementes. A diversidade genética e as correlações identificadas fornecem critérios para orientar os esforços de seleção em programas de melhoramento de capim-ruziziensis em ambientes similares.

Termos para indexação: braquiária, melhoramento, forrageira, *Urochloa*.

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Corresponding author
marco.pessoa@embrapa.br

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INTRODUCTION

Brazil has been the largest producer, consumer, and exporter of tropical forage seeds worldwide for at least two decades. In 2006, the country marketed about 100,000 tons of tropical forage seeds per year, generating revenues of 250 million dollars, with 10% of that being exported to more than 20 countries (Pariz et al., 2010). Recent estimates indicate a production of around 500,000 tons of tropical forage seeds in 2023/2024 (Brasil, 2025a), with revenues exceeding 700 million dollars (Roveri-José, 2025). Advancements in the implementation of integrated crop-livestock-forest systems have driven increased demand for species with higher forage productivity, nutritional value, and seed yield.

Urochloa ruziziensis (R. Germ. & Evrard) Crins is native to the Ruzizi plain in Burundi and the Democratic Republic of the Congo. It spread to tropical-humid and sub-humid regions in Africa as a forage species. It was also introduced into Puerto Rico and Australia (Renard and Capelle, 1976). Its first introduction in Brazil probably occurred in the 1960s (Pessoa-Filho et al., 2015). *U. ruziziensis* has gained prominence in Brazilian agriculture because of its high seed yield (the highest among cultivated *Urochloa*), lower seed production costs, deep root systems, and traits that facilitate its management as both a cover crop and a forage. In the last four years, planting *U. ruziziensis* for seed production accounted for 51% of the area of all fields established with *Urochloa* in Brazil, with about 61% of the total volume (kg pure seed/hectare) for the genus (Roveri-José, 2025). In addition to its use as a cover crop in integrated production systems in Brazil, reports indicate its importance in India (Antony et al., 2017), Thailand (Juntasin et al., 2022b), and Africa (Clémence-Aggy et al., 2021).

Seed yield is a complex trait that involves several components, including the number of reproductive tillers and spikelets per tiller, seed set and seed weight, and the number of spikelets that produce marketable seeds. In grasses, factors such as genetic, cytological, physiological, sexual, and environmental conditions can affect filled seed yield (Simeão et al., 2017). Successful forage seed production depends on factors such as planting site, climate, irrigation, soil fertility, crop management strategies, and harvest methods (Antony et al., 2017; Juntasin et al., 2022a, b; Imura et al., 2024). Seed quality refers to attributes such as genetic and physical purity, viability, vigor, and health (Pariz et al., 2010). The quality of seeds is also shaped by optimizing production system components such as cultivation, agricultural management, storage, and shipping (Juntasin et al., 2022b). Genetic factors include vigor, longevity, and heterosis. Environmental conditions affect physiological traits during production, harvest, and storage. Sanitary factors involve the negative impact of microorganisms and insects on seeds, which can reduce yield and physiological quality, ultimately affecting sales and planting (Pariz et al., 2010).

Characterizing seed yield and quality is essential for selecting genotypes that can reproduce successfully and produce enough seeds to meet market demands (Simeão et al., 2017). Selection for forage yield and forage quality may adversely affect seed production in the improved population if there is antagonism between vegetative growth and reproductive effort. The complex and inverse correlation between forage yield and seed production is evidenced in forage grasses such as ryegrass (*Lolium multiflorum*), typical of temperate climates (Müller et al., 2012). Previous reports in *U. ruziziensis*, however, indicate that selection for seed yield would not impact biomass yield (Simeão et al., 2017).

In this context, this study aims to evaluate the phenotypic variability for seed yield, quality, and dormancy, as well as the correlations between traits, in diploid *U. ruziziensis* genotypes selected for high forage yield (Santos et al., 2024).

MATERIAL AND METHODS

The study was conducted at Embrapa Cerrados in Brasília, DF, Brazil (15°35' S, 47°42' W, altitude 1007 m) on a clayey Oxisol (*Latossolo Vermelho Distrófico*). The genotypes evaluated in this work were obtained by random recombination of plants from 13 accessions of Embrapa's Base Collection, along with commercially available seeds and collections from long-established pastures, as previously described (Santos et al., 2024). From this base population, a total of 240 randomly selected *U. ruziziensis* plants were transplanted to the field in November 2019 to establish an open-cross

plot for random pollination, with a spacing of 1.5 m x 1.5 m, one plant per plot, and no replications. Management practices included manual weeding, annual uniformity cuts at the start of the rainy season, and yearly fertilization with 500 kg.ha⁻¹ of 10-10-10 NPK, along with topdressing of 50 kg N.ha⁻¹ (urea). Within the 240 genotypes, 24 top genotypes (10%) were selected based on their general combining ability, estimated from the performance of their half-sib progenies, which were phenotyped for forage yield and nutritional quality traits, as previously described (Santos et al., 2024). These 24 plants were evaluated for seed yield, seed yield components, and seed physiological quality.

Custom-made seed collectors, built with shading screen cloth and PVC pipes, were assembled in the field. The shading screen cloths measured 120 cm by 75 cm and were sewn onto 250 mm PVC pipes, which were held in place by stakes to cover all inflorescences of each plant. The collectors were installed in January 2023, before anthesis, and remained in the field until the end of seed shattering. For each plant, the number of inflorescences (PI) was counted, and five inflorescences were randomly collected to determine the number of racemes per inflorescence (NRI), the number of seeds in the median raceme (NSMR), and the average raceme length (RL). In May 2023, all spikelets—both filled and empty seeds—were collected from each plant, manually pre-cleaned with sieves of 2.0 mm and 1.5 mm mesh sizes, then homogenized and weighed. Filled seeds (caryopses) were separated from empty seeds using a Motoyama Engineering Works seed blower, model 17350, set to the 2 cm ventilation opening. The filled seed mass (FSM) and its percentage (FSM%) relative to the total seeds collected from each plant were calculated. Additionally, five replicates of 100 pre-cleaned seeds were evaluated to determine seed filling percentage (SF%). The mass of 1,000 pure, filled seeds (MPFS₁₀₀₀) was estimated exclusively from the filled seed fraction.

The number of inflorescences per plant (PI), filled seed mass (FSM), and filled seed percentage by weight (FSM%) were obtained from the absolute measurements per plant, which is why they were not replicated and did not undergo analysis of variance. Only descriptive statistics for those traits were reported for the set of 24 selected plants.

The viability of the filled seeds was assessed by the tetrazolium test, as outlined by the Brazilian Ministry of Agriculture and Livestock (Brasil, 2025b). For this purpose, four replicates of 25 seeds each were soaked in distilled water for 16 hours at 30 °C, then cut lengthwise (endosperm and embryo) so that the glumes enclosed the two halves of the seeds. The seeds were subsequently immersed in a 0.5% w/v solution of 2,3,5-triphenyl tetrazolium chloride for 3 hours at 30 °C in the dark. Using a stereoscopic magnifying glass and based on the distribution and intensity of embryo staining, the seeds were classified as viable or non-viable.

The germination of filled seeds was tested under two conditions in germination chambers: at 30 °C in the dark with distilled water (constant-temperature germination, CTG); and at 20-30 °C, 12 hours with light, in 0.2% w/v potassium nitrate solution (alternating-temperature germination, ATG) (Brasil, 2025b). For each test, four replicates of 100 seeds were used in germination boxes lined with two sheets of blotting paper soaked with 2.5 times their weight of water or potassium nitrate solution, according to the test condition (Brasil, 2025b). Normal seedlings were counted seven days after the experiment was set up. The experiment lasted 21 days, after which the number of normal seedlings was counted again, along with ungerminated seeds, abnormal seedlings and dead seeds (Brasil, 2025b). The mean germination under the two conditions (MG) was calculated. Seed dormancy (SD) was estimated as the difference between mean germination and seed viability, as determined by the tetrazolium test.

Analysis of variance was undertaken on the seed production components (mass of 1,000 filled seeds, number of seeds in the median raceme, average raceme length, number of racemes per inflorescence, and seed filling percentage), as well as on seed viability and germination. If significant differences were detected, the means were grouped using the Scott-Knott test ($p \leq 0.05$). Simple linear correlations (Pearson) were calculated using R v.4.1.2 (R Core Team, 2025).

RESULTS AND DISCUSSION

The average number of inflorescences per plant (PI) observed in diploid *U. ruziziensis* genotypes was 544, with a range of 96-904 (Table 1). Previous reports for this trait in tetraploid *U. ruziziensis* half-sib progenies evaluated in

Campo Grande, Brazil, ranged between 3 and 430, with a mean of 89 (Simeão et al., 2016, 2017). More recently, the mean value for an open-pollinated tetraploid *U. ruziziensis* cultivar released and evaluated in Thailand (OKI-1) was 140 (Imura et al., 2024). The initiation of inflorescence development is strongly affected by environmental conditions, such as photoperiod and temperature; therefore, comparisons with results from experiments carried out in other locations have limited significance. However, the total number of panicles was genetically correlated with biomass production in tetraploid *U. ruziziensis* (Simeão et al., 2017). Since the genotypes evaluated in this study were selected based on the total dry matter yield of their progenies, this may, to some degree, explain the high number of inflorescences per plant reported here.

Table 1. Flowering traits and seed yield components of 24 superior genotypes of *U. ruziziensis*. Means followed by the same letter in the columns do not differ by the Scott-Knott mean clustering test ($p>0.05$).

Sample	PI	NRI	RL (cm)	FSM (g)	FSM%	SF%	MPFS ₁₀₀₀ (g)	NSMR
48	869	4 a	6 a	354	82	50 a	8.7 c	38 a
120	766	3 a	5 b	265	79	44 b	8.5 c	36 a
197	648	3 a	5 b	186	84	63 a	10.2 a	28 b
46	633	4 a	6 a	185	80	30 c	8.6 c	41 a
54	547	4 a	6 a	176	77	15 d	8.0 d	35 a
204	481	4 a	5 b	156	83	39 b	6.9 e	33 a
187	532	6 a	5 b	152	80	57 a	9.3 b	31 a
65	858	4 a	5 b	133	65	12 d	8.4 c	30 b
5	904	5 a	5 b	132	71	30 c	7.6 d	32 a
43	795	4 a	6 a	130	67	29 c	8.6 c	37 a
40	603	4 a	4 b	101	81	43 b	8.4 c	25 b
92	475	4 a	5 b	97	73	28 c	9.5 b	30 b
167	556	4 a	5 b	97	71	22 c	9.0 c	33 a
180	359	5 a	4 b	93	72	33 c	8.4 c	29 b
101	538	4 a	5 b	87	71	13 d	8.5 c	30 b
170	455	4 a	4 b	84	72	35 c	8.7 c	33 a
45	541	5 a	5 b	80	69	34 c	9.5 b	38 a
56	570	5 a	4 b	63	75	27 c	9.0 c	23 b
34	526	4 a	4 b	54	46	4 d	8.3 c	33 a
195	511	3 a	4 b	53	68	17 d	9.0 c	25 b
157	293	5 a	5 b	35	68	47 b	7.9 d	33 a
133	283	4 a	4 b	30	61	16 d	8.3 c	23 b
203	96	3 a	4 b	24	89	52 a	7.3 e	33 a
181	207	4 a	4 b	16	56	26 c	7.3 e	28 b
Mean	544	4	5	116	73	32	8.5	32
Std Dev	205	1	1	79	10	17	0,1	89
CV	37	28	25	68	13	53	10	25
Range	96-904	3-6	4-6	16-354	46-89	4-63	6.9-10.2	23-41

PI, number of inflorescences per plant; NRI, number of racemes per inflorescence; RL, raceme length (cm); FSM, filled seed mass (g); FSM%, filled seed mass in percentage (% w/w); SF%, seed filling percentage; MPFS₁₀₀₀, mass of one thousand pure, filled seeds (g); NSMR, number of seeds in the median raceme; Std Dev: standard deviation; CV: coefficient of variation.

The number of racemes per inflorescence (NRI) varied significantly among the tested genotypes (Table 2). However, the Scott-Knott test grouped all genotypes into a single cluster, indicating that no partitions were found that would maximize differences between groups (Table 1). The average for the 24 genotypes was 4 ± 1 racemes per inflorescence, ranging from 1 to 6, similar to the *U. ruziziensis* cultivars 'Kennedy' and 'BRS Integra' (Souza-Sobrinho et al., 2022). Previous studies on this trait showed values of 1-8 (Wongsuwan et al., 1997), with a higher frequency of 2-3 racemes per inflorescence (Antony et al., 2017). A positive correlation between the number of racemes per inflorescence and total seed yield, as well as total filled seed yield, has been reported for *U. ruziziensis* in India (Antony et al., 2017).

The mean raceme length (RL) was 5 cm, with a range of 4 to 6 cm (Table 1). According to the Scott-Knott test, these means formed two groups: one with six genotypes and another with 18 genotypes. The group averages were 6.0 cm and 4.5 cm, respectively. It was previously reported that the number of florets per raceme had more influence on seed yield than the number of racemes per inflorescence (Wongsuwan et al., 1997). However, it is unclear whether there is a positive correlation between raceme length and the number of spikelets per raceme. Such a positive correlation might suggest that selection for longer racemes would increase seed yield. The length of the basal raceme was proposed as one of the traits for genotype discrimination in *U. ruziziensis* (Rezende et al., 2016).

The mean filled seed mass (FSM) per plant was 116 g, with a range from 16 g to 354 g, while the mean filled seed mass percentage (FSM%) was 73%, ranging from 46% to 89% (Table 1). The 22-fold difference in FSM between the lowest and the highest values among the genotypes (genotypes 48 and 181) indicates considerable variability in this trait, likely due to the species' allogamous reproduction and to the fact that genotypes are a sample of a broad representation of the available genetic diversity for *U. ruziziensis* in germplasm collections in Brazil (Pessoa-Filho et al., 2015). Previously, an evaluation of filled seed mass in tetraploid *U. ruziziensis* used as parent plants for half-sib progenies showed a mean of 154 g per plant. The average seed filling percentage varied considerably among the genotypes tested, ranging from 4% to 63%, with an overall average of 32%. The Scott-Knott mean clustering identified four groups: the first, with four genotypes and an average of 55.5% of SF%, the second, with four genotypes and an average of 43%, the third, with 10 genotypes and an average of 29%, and the last group, with six genotypes and an average of 13%. High spikelet sterility indexes are a common phenomenon in several grasses (Carmona et al., 1999) and can significantly reduce their seed production potential. These results indicate that variability exists that could be exploited for selecting genotypes with lower spikelet sterility in *U. ruziziensis* breeding programs. Seed set for open-pollinated progenies from parent plants of tetraploid *U. ruziziensis* progenies ranged between 13 and 46% (Simeão et al., 2012). Seed sets of the tetraploid *U. ruziziensis* cultivar 'OKI-1' ranged between 18.8% and 34% (Juntasin et al., 2022b) in an experiment testing different plant densities; values varied between 32.3% and 39.4% for the same cultivar depending on the harvest method (Imura et al., 2024). Early assessments of seed set in diploid *U. ruziziensis* reported values of 30% and 20% (Ferguson and Crowder, 1974; Wongsuwan et al., 1997). However, a more recent study showed values ranging from 5.25 to 76% for cultivar 'Kennedy', depending on how long the seed was collected after harvest, with an observation that seed filling percentage in *U. ruziziensis* depended on the location of racemes and of spikelets in the racemes (Antony et al., 2017).

Table 2. Summary of the analysis of variance for seed yield components of 24 superior genotypes of *U. ruziziensis*.

Trait ¹	Average	CV(%)	d.f.	SS	F-value	Significance
MPFS ₁₀₀₀	8.5	10.1	23	0.6685	13.377	***
NSMR	32	25.1	23	2670.7	2.309	**
RL	5	24.6	23	77.3	4.039	***
NRI	4	28.1	23	55.9	2.163	**
SF%	32	52.9	23	26896.8	16.045	***

** Significant at 1% probability level. ***Significant at 0.1% probability level. MPFS₁₀₀₀, mass of one thousand pure, filled seeds (g); NSMR, number of seeds in the median raceme; RL, raceme length (cm); NRI, number of racemes per inflorescence; SF%, seed filling percentage. CV(%), coefficient of variation; d.f., degrees of freedom; SS, sum of squares.

The average number of seeds in the median raceme (NSMR) was 32, with a range of 23 to 41 seeds. The 24 genotypes were divided into two groups for this trait: one with an average of 35 seeds (14 plants) and the other with an average of 27 seeds (10 plants). As mentioned above, a previous study indicated that the number of florets per raceme had a positive influence on seed yield in *U. ruziziensis* (Wongsuwan et al., 1997), and the species had an average of 33 florets per raceme in *U. ruziziensis* (Wongsuwan et al., 1997). Another study reported that the number of spikelets per raceme decreased as the number of racemes per plant increased in *U. ruziziensis* (Antony et al., 2017). Still, in these cases, the total number of spikelets also increased (Antony et al., 2017). The 'OKI-1' tetraploid *U. ruziziensis* cultivar had mean values of spikelet number per raceme ranging between 35.48 and 37.74 in an experiment evaluating the effect of plant spacings on seed yield in Thailand (Juntasin et al., 2022b), and 32.54 and 36.62 in a second experiment evaluating harvest methods (Imura et al., 2024).

The average mass of 1,000 seeds (FSM_{1000}) was 8.5 grams, ranging from 6.9 to 10.2 grams. In this case, the genotypes were distributed in five groups, the first composed only of genotype 197, with an average of 10.2 g, the second with three genotypes and an average of 9.4 g, the third with 14 genotypes and an average of 8.6 g, the fourth group with three genotypes and an average of 7.8 g and the fifth group also with three genotypes and an average of 7.2 g. Antony et al. (2017) reported a weight of 1,000 *U. ruziziensis* seeds of 7.82 g.

Seed viability estimated by the tetrazolium test varied between 55% and 97%, with an average of 80% (Table 4) and the test of averages resulted in two groups, containing 12 genotypes each, with averages of 89 and 70%, highlighting genotypes 120 and 197, which, in addition to exhibiting high viability (97% and 92%, respectively), also had high values for filled seed mass (265 g and 186 g, respectively). A previous report on seed viability for *U. ruziziensis* showed a value of 70% (Pariz et al., 2010). Depending on the period after harvest that seeds were collected, viability ranged between 25 and 73% in a rainfed treatment without fertilization, and from 30 to 86% under irrigation and fertilization (Antony et al., 2017). Additionally, six-month-old seeds showed 80% viability (Antony et al., 2017). The viability of *U. ruziziensis* seeds changes as they mature after anthesis, from as low as 15% at 10 days after anthesis, reaching 36% at 20 days after anthesis (Wongsuwan et al., 1997).

Germination at constant temperature varied significantly among the tested genotypes (Table 3), ranging from 14% to 55% and an overall average of 37% (Table 4). Due to the absence of light, the seedlings exhibited etiolation. The genotypes were grouped into three clusters containing 13, nine, and two genotypes, with mean germination of 43%, 32%, and 16%, respectively. Germination at alternating temperatures also showed significant variation among genotypes, ranging from 15% to 66%, with an overall average of 31%. Under this condition, seedlings appeared vigorous and exhibited intense green coloration due to light exposure. Here, the genotypes were divided into two groups: one with five and the other with 19 genotypes, with mean germination rates of 55% and 25%, respectively. The mean germination in both tests (MG) was 34%. The 24 genotypes were divided into two groups: one with eight genotypes and a mean germination of 45%, and the other with 16 genotypes and an average of 28%.

Table 3. Summary of the analysis of variance for the viability, germination, and dormancy of seeds of 24 superior genotypes of *U. ruziziensis*.

Trait	Average	CV(%)	d.f.	SS	F-value	Significance
TZ	80	21.4	23	10904	2.069	*
CTG	37	32.2	23	7411.3	4.081	***
ATG	31	60.9	23	18448	3.629	***
MG	34	34.5	23	7837.6	4.850	***
SD	46	43.5	23	16492	2.448	**

*Significant at 5% probability level; **Significant at 1% probability level; ***Significant at 0.1% probability level. TZ, tetrazolium viability; CTG, constant-temperature germination; ATG, alternating-temperature germination; MG, mean germination (ATG and CTG); SD, seed dormancy; CV(%), coefficient of variation; d.f., degrees of freedom; SS, sum of squares.

Table 4. Viability, germination, and dormancy of seeds from 24 genotypes of *U. ruziziensis*. Means followed by the same letter in the columns did not differ by the Scott-Knott mean clustering test ($p \leq 0.05$).

Sample	TZ	CTG	ATG	MG	SD	HS% _{CTG}	FS% _{ATG}
48	87 a	28 b	17 b	22 b	65 a	4	6
120	97 a	55 a	32 b	43 a	54 a	3	2
197	92 a	41 a	19 b	30 b	62 a	6	1
46	87 a	35 b	17 b	26 b	61 a	5	3
54	85 a	32 b	51 a	41 a	44 b	3	3
204	89 a	35 b	15 b	25 b	64 a	8	7
187	70 b	40 a	32 b	36 b	35 b	7	2
65	73 b	42 a	46 a	44 a	29 b	6	3
5	89 a	34 b	17 b	25 b	64 a	3	6
43	94 a	43 a	25 b	34 a	60 a	8	3
40	73 b	44 a	59 a	52 a	22 b	8	2
92	68 b	34 b	26 b	30 b	39 b	2	4
167	68 b	34 b	19 b	26 b	42 b	8	3
180	76 b	48 a	52 a	50 a	26 b	8	3
101	68 b	40 a	24 b	32 b	36 b	1	7
170	72 b	42 a	19 b	30 b	42 b	7	5
45	88 a	38 a	29 b	33 b	55 a	0	2
56	55 b	14 c	33 b	24 b	31 b	12	2
34	91 a	37 a	66 a	51 a	40 b	5	2
195	90 a	39 a	34 b	36 b	54 a	6	2
157	71 b	30 b	23 b	26 b	45 b	5	7
133	74 b	47 a	37 b	42 a	32 b	6	4
203	80 a	18 c	26 b	22 b	58 a	15	0
181	71 b	29 b	35 b	32 b	39 b	8	2
Mean	80	37	31	34	46	6	3
Std Dev	16.9	11.7	19	11.7	19.9	6.9	4.1
CV	21.4	32.2	60.9	34.5	43.5	118.3	133.5
Range	55-97	14-55	15-66	22-51	22-65	0-15	0-7

TZ, tetrazolium viability (%); CTG, constant-temperature germination (%); ATG, alternating-temperature germination (%); MG, average of the germination rates for the two experimental conditions; FS%_{CTG}, percentage of filled seeds at constant-temperature germination; FS%_{ATG}, percentage of filled seeds at alternating-temperature germination; SD: seed dormancy, estimated by the difference between TZ and MG. Std Dev: standard deviation; CV, coefficient of variation.

The germination rates reported in this study are consistent with those previously reported. Early seed germination data for *U. ruziziensis* showed rates ranging from 10.8% to 40%, with a positive impact of acid scarification (McLean and Grof, 1968), and seedling emergence reaching 50% for open-pollinated populations (Ferguson and Crowder, 1974). Removing seed hulls increased germination from 20% to 93% in six-month-old seeds, and from 17% to 88% in 10-month-old seeds (Renard and Capelle, 1976). More recent findings reported rates of 28.5% and 51% after 7 and 21 days after the establishment of the germination test, respectively (Pariz et al., 2010).

Considering that the average tetrazolium viability was 80%, about 46% of viable seeds failed to germinate under the test conditions, likely due to the species' characteristic seed dormancy (McLean and Grof, 1968). The overall

average seed dormancy (SD) of 46% was spread across two groups: 10 genotypes with 60% dormancy and 14 with 36% dormancy. According to Normative Instruction No. 30 of the Brazilian Ministry of Agriculture, Livestock, and Supply (2008), the minimum germination rate for the sale of *Urochloa ruziziensis* seeds is 60%. However, seeds of the species can also be commercialized based on tetrazolium viability results (Brasil, 2010), considering that not all viable seeds germinate immediately. Of the 24 tested genotypes, only genotype 34 met the minimum germination requirement, achieving 66% under alternating temperatures, while the others had mean germination below the MAPA limit. The viability results, on the other hand, show that only one genotype was below the set limit.

There was no significant difference in the number of filled seeds among genotypes under either germination condition, with overall averages across the two tests of 6% and 3%. These values are lower than the 29% of filled seeds observed in a study assessing the physiological quality of seeds from four *Urochloa* species after simulated chewing (Bolzan et al., 2019).

The number of inflorescences per plant showed a strong, highly significant positive correlation with filled seed mass (0.71) and viability (0.93), and a moderate, highly significant positive correlation with raceme length (0.57) and seed dormancy (0.54) (Table 5). Filled seed mass exhibited a highly significant moderate to high correlation with raceme length (0.69), viability (0.66), and the number of seeds in the median raceme (0.52). Because PI, FSM, and FSM% were measured once per genotype, correlations involving these variables are exploratory and may reflect microenvironmental effects. Raceme length showed a strong, highly significant positive correlation with the number of seeds in the median raceme (0.72). Viability in tetrazolium showed a strong positive correlation with seed dormancy (0.73), a moderate correlation with raceme length (0.57), and no correlation with filled seed percentage and alternating-temperature germination. Constant-temperature germination showed a moderate, highly significant positive correlation with mean germination (0.66). Seed dormancy had a moderate negative correlation with alternating-temperature germination (-0.66) and mean germination (-0.60). The seed filling percentage showed a strong positive correlation with the mass of filled seed as a percentage (0.72). The correlations between constant-temperature germination (CTG) and mean germination (MG), and between seed dormancy and number of inflorescences per plant (PI), seed viability (TZ), mean germination (MG), and alternating-temperature germination (ATG) are cited but are not relevant because SD was

Table 5. Simple linear correlation coefficients (Pearson) between components of seed yield and quality for *U. ruziziensis* genotypes.

	PI	FSM	FSM%	SF%	FSM ₁₀₀₀	NSMR	RL	NRI	TZ	CTG	ATG	MG	SD
PI	1.00	0.71***	0.11	-0.03	0.30	0.31	0.57**	0.02	0.93***	0.49*	0.10	0.30	0.54**
FSM		1.00	0.50*	0.37	0.20	0.52**	0.69***	-0.12	0.66***	0.30	-0.07	0.08	0.47*
FSM%			1.00	0.72***	0.09	0.19**	0.31***	-0.14	0.15***	-0.21	-0.31	-0.34	0.35
SF%				1.00	0.16	0.16	0.12	0.05	-0.01	-0.15	-0.34	-0.34	0.22
FSM ₁₀₀₀					1.00	-0.07	0.13	0.04	0.30	-0.13	-0.06	-0.11	0.32
NSMR						1.00	0.72***	0.00	0.26	-0.07	0.14	0.08	0.15
RL							1.00	0.05	0.57**	0.18	0.08	0.14	0.36
NRI								1.00	0.02	0.24	-0.08	0.05	-0.01
TZ									1.00	0.36	-0.07	0.11	0.73***
CTG										1.00	0.23	0.66***	-0.16
ATG											1.00	0.88***	-0.66***
MG												1.00	-0.60**
SD													1.00

Significant at 5% probability level (*), 1% probability level (**) and 0.1% probability level (***). PI, number of inflorescences per plant; FSM, filled seed mass; FSM%, filled seed percentage by weight; FSM₁₀₀₀, mass of 1,000 filled seeds; NSMR, number of seeds in the median raceme; RL, raceme length; NRI, number of racemes/inflorescence; SF%, seed filling percentage; TZ, seed viability from tetrazolium test; CTG, constant-temperature germination; ATG, alternating-temperature germination; MG, mean germination; SD, seed dormancy.

estimated as the difference between MG and TZ, and MG was calculated as the mean of the two germination conditions.

In forage grasses, reproductive characteristics linked to seed yield can help make breeding programs more efficient (Simeão et al., 2017). In this study, the correlations observed among seed production traits and physiological quality suggest that secondary traits may be valuable for identifying superior *U. ruziziensis* genotypes. In particular, the positive associations between the number of inflorescences per plant and filled seed mass, seed viability, and raceme length indicate that simple reproductive measurements could be useful in the early stages of selection within this environment. However, we are aware that these are single-environment phenotypic correlations and that multi-environment/year validation is needed before inferring the reliability of indirect selection for these traits for breeding. Similarly, the positive relationship between raceme length and the number of seeds per raceme suggests that selecting plants with longer racemes may indirectly favor greater seed production. This is especially important because direct assessment of seed yield is laborious, time-consuming, and highly variable due to environmental conditions. On the other hand, the negative association between seed dormancy and germination underscores the need to simultaneously select for high viability and lower dormancy to improve commercial seed quality and crop establishment. Taken together, these correlations provide a useful basis for developing selection indices and refining breeding strategies to combine high seed yield with suitable physiological seed quality in *U. ruziziensis*.

Genotypes 197, 187, 48, and 203 combine a high filled seed percentage with key traits for vigor and establishment. They consistently appeared in the top Scott-Knott group for traits associated with seedling emergence and seed quality, indicating both high physiological quality and early growth. These genotypes represent a good balance between seed filling and seedling vigor. A focus on selecting for low seed dormancy would target genotypes 40, 180, and 65, without compromising seed quality and vigor.

CONCLUSIONS

The assessment of 24 superior *Urochloa ruziziensis* genotypes revealed extensive and significant phenotypic variability in traits related to seed yield, quality, and dormancy. The analysis of phenotypic correlations identified key traits—such as the number of inflorescences per plant and raceme length—that could serve as effective criteria for indirect selection within the evaluated environment. The genetic diversity and strong correlations among yield components, viability, and dormancy demonstrate the high potential for using these traits directly in breeding programs to develop *U. ruziziensis* cultivars that offer both high forage yield and seed production.

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AUTHORS' CONTRIBUTION

Érika Moreira dos Santos contributed with: Data collection, Experiment set up, Formal analysis, Writing – original draft; Ricardo Carmona contributed with: Conceptualization, Methodology, Experiment design, Data curation, Writing – review & editing; Cláudio Takao Karia contributed with: Conceptualization, Funding acquisition; Methodology, Data curation, Data analysis, Writing – review & editing; Carlos Eduardo Lazarini da Fonseca contributed with: Funding acquisition, Data curation, Data analysis, Writing – review & editing; Allan Kardec Braga Ramos contributed with: Funding Acquisition, Conceptualization, Methodology, Data curation, Writing – review & editing; Marco Pessoa-Filho contributed with: Conceptualization, Funding acquisition, Visualization, Data curation, Project supervision, Writing – original draft, review & editing.

DATA AVAILABILITY

Additional data will be made available by the authors upon reasonable request.

REFERENCES

- ANTONY, E.; SRIDHAR, K.; KUMAR, V. Effect of chemical sprays and management practices on *Brachiaria ruziziensis* seed production. *Field Crops Research*, v.211, p.19-26, 2017. <http://dx.doi.org/10.1016/j.fcr.2017.06.009>
- BOLZAN, F.; DEMINICIS, B.; VALENTE, T.; LIMA, E. Qualidade fisiológica de sementes de *Brachiaris* spp. após mastigação simulada, digestão ácido enzimática e fermentação in vitro. *Agrotrópica*, v.31, n.2, p.131-140, 2019. <https://repositorio-dspace.agricultura.gov.br/handle/1/1976>
- BRASIL. *Instrução Normativa nº 30, de 21 de maio de 2008*. <https://www.gov.br/agricultura/pt-br/assuntos/insumos-agropecuarios/insumos-agricolas/sementes-e-mudas/publicacoes-sementes-e-mudas/INN30de21demaiode2008.pdf>
- BRASIL. *Instrução Normativa nº 30, de 26 de outubro de 2010*. <https://www.gov.br/agricultura/pt-br/assuntos/insumos-agropecuarios/insumos-agricolas/sementes-e-mudas/publicacoes-sementes-e-mudas/INN30de26deoutubrode2010.pdf>
- BRASIL. Ministério da Agricultura e Pecuária. *SIGEF - controle da produção de sementes e mudas*. Brasília: MAPA 2025a. <https://mapa-indicadores.agricultura.gov.br/publico/extensions/SIGEF/SIGEF.html>
- BRASIL. Ministério da Agricultura, Pecuária e Abastecimento. *Regras para Análise de Sementes*. Brasília: MAPA, 2025b. https://wikisda.agricultura.gov.br/pt-br/Laborat%C3%B3rios/Metodologia/Sementes/RAS_2025/Amostragem
- CARMONA, R.; MARTINS, C.R.; FÁVERO, A.P. Características de sementes de gramíneas nativas do Cerrado. *Pesquisa Agropecuária Brasileira*, v.34, p.1066-1074, 1999. <https://www.scielo.br/j/pab/a/9vQvWqp8Mnh3nh6NdKq8Hmc/?format=pdf&lang=pt>
- CLÉMENTE-AGGY, N.; FIDÈLE, N.; RAPHAEL, K.J.; AGBOR, E.K.; GHIMIRE, S.R. Quality assessment of *Urochloa* (syn. *Brachiaria*) seeds produced in Cameroon. *Scientific Reports*, v.11, n.1, p.15053, 2021. <https://pubmed.ncbi.nlm.nih.gov/34301980>
- FERGUSON, J.E.; CROWDER, L.V. Cytology and breeding behavior of *Brachiaria ruziziensis* Germain et Evrard. *Crop Science*, v.14, n.6, p.893-895, 1974. <https://doi.org/10.2135/cropsci1974.0011183x001400060036x>
- IMURA, Y.; NAKAMURA, I.; JUNTASIN, W.; HOSSAIN, M.A.; THAIKUA, S.; POUNGKAEW, R.; KAWAMOTO, Y. Effects of harvesting method on seed yield and seed quality in *Urochloa ruziziensis* (cv. 'OKI-1' and cv. 'BR-203'). *Agronomy*, v.14, n.3, p.509, 2024. <http://dx.doi.org/10.3390/agronomy14030509>
- JUNTASIN, W.; IMURA, Y.; NAKAMURA, I.; HOSSAIN, M.A.; THAIKUA, S.; POUNGKAEW, R.; KAWAMOTO, Y. Effects of closing cut date and nitrogen fertilization on seed yield and seed quality in two novel cultivars of *Urochloa* spp. *Agronomy*, v.12, n.2, p.513, 2022a. <https://doi.org/10.3390/agronomy12020513>
- JUNTASIN, W.; IMURA, Y.; THAIKUA, S.; POUNGKAEW, R.; KAWAMOTO, Y. Effects of plant spacing on seed yield and seed quality in new *Urochloa* cultivars. *Grassland Science*, v.68, n.1, p.88-98, 2022b. <http://dx.doi.org/10.1111/grs.12352>
- MCLEAN, D.; GROF, B. Effect of seed treatments on *Brachiaria mutica* and *B. ruziziensis*. *Queensland Journal of Agricultural and Animal Sciences*, v.25, p.81-83, 1968.
- MÜLLER, L.; MANFRON, P.A.; MEDEIROS, S.L.P.; RIGÃO, M.H.; BANDEIRA, A.H.; TONETTO, C.J.; DOURADO-NETO, D. Correlações de Pearson e canônica entre componentes da matéria seca da forragem e sementes de azevém. *Revista Brasileira de Sementes*, v.34, p.86-93, 2012. <https://www.scielo.br/j/rbs/a/3dybVpM4XVVBzJRQR8B6VM/?format=pdf&lang=pt>
- PARIZ, C.M.; FERREIRA, R.L.; SÁ, M.E.; ANDREOTTI, M.; CHIODEROLI, C.A.; RIBEIRO, A.P. Qualidade fisiológica de sementes de *Brachiaria* e avaliação da produtividade de massa seca, em diferentes sistemas de integração lavoura-pecuária sob irrigação. *Pesquisa Agropecuária Tropical*, v.40, n.3, p.6, 2010. <https://doi.org/10.5216/pat.v40i3.6590>
- PESSOA-FILHO, M.; AZEVEDO, A.L.S.; SOUZA-SOBRINHO, F.; GOUVEA, E.G.; MARTINS, A.M.; FERREIRA, M.E. Genetic diversity and structure of ruzigrass germplasm collected in Africa and Brazil. *Crop Science*, v.55, n.6, p.2736-2745, 2015. <http://dx.doi.org/10.2135/cropsci2015.02.0096>

R Core Team. *R: A language and environment for statistical computing*. Vienna, Austria, 2025. <https://www.R-project.org>

RENARD, C.; CAPELLE, P. Seed germination in ruzizi grass (*Brachiaria ruziziensis* Germain & Evrard). *Australian Journal of Botany*, v.24, p.437-446, 1976.

REZENDE, B.A.; RIBEIRO, C.B.; TEIXEIRA, D.H.L.; GONÇALVES, F.M.A.; SOUZA SOBRINHO, F. Phenotypic characteristics for discrimination between advanced genotypes of *Brachiaria ruziziensis*. *Genetics and Molecular Research*, v.15, n.1, p.2016.

ROVERI-JOSÉ, M. Sementes de forrageiras: transformações no mercado diante das demandas de sustentabilidade e inovações da agropecuária. *Anuário ABRASEM 2025*, p.63-66, 2025. https://www.abrasem.com.br/wp-content/uploads/2025/09/Anuario-Abrasem-2025-com-capa_compactado.pdf

SANTOS, É.M.D.; FONSECA, C.E.L.; KARIA, C.T.; RAMOS, A.; CARMONA, R.; PESSOA-FILHO, M. Genetic parameters and correlations of forage yield and nutritional quality in ruzigrass (*Urochloa ruziziensis*) half-sib families. *Crop Breeding and Applied Biotechnology*, v.24, n.4, e486124411, 2024. <https://doi.org/10.1590/1984-70332024v24n4a48>

SIMEÃO, R.M.; VALLE, C.B.; ALVES, G.F.; MOREIRA, D.A.L.; SILVA, D.R.; ARAÚJO, D.D.F.; FERREIRA, R.C.U.; BARRIOS, S.C.L.; JANK, L.; CARAMALAC, G.R.; NAKA, I.M.; CALIXTO, S.; CARVALHO, J. Melhoramento de *Brachiaria ruziziensis* tetraploide sexual na Embrapa: Métodos e avanços. *Documentos Embrapa Gado de Corte*, v.194, p.28, 2012.

SIMEÃO, R.M.; VALLE, C.B.; RESENDE, M.D. V. Unravelling the inheritance, Qst and reproductive phenology attributes of the tetraploid tropical grass *Brachiaria ruziziensis* (Germain et Evrard). *Plant Breeding*, v.136, n.1, p.101-110, 2017. <http://dx.doi.org/10.1111/pbr.12429>

SIMEÃO, R.M.; SILVA, A.S.; VALLE, C.B.D. Flowering traits in tetraploid *Brachiaria ruziziensis* breeding. *Crop Breeding and Applied Biotechnology*, v.16, n.2, p.95-101, 2016. <http://dx.doi.org/10.1590/1984-70332016v16n2a15>

SOUZA-SOBRINHO, F.; AUAD, A.M.; SANTOS, A.M.B.; GOMIDE, C.A.M.; MARTINS, C.E.; CASTRO, C.R.T.; PACIULLO, D.S.C.; BENITES, F.R.G.; ROCHA, W.S.D. BRS Integra: Nova cultivar de *Urochloa ruziziensis* para a ILPF. *Comunicado Técnico*, v.93, p.1-19, 2022. <https://www.infoteca.cnptia.embrapa.br/infoteca/handle/doc/1140781>

WONGSUWAN, N.; HILL, M.J.; HAMPTON, J.G. Reproductive morphological changes in ruzi grass (*Brachiaria ruziziensis* Germain and Everard). *Journal of Applied Seed Production*, v.15, p.71-74, 1997.

