

# **AUTOTETRAPLOID** Urochloa ruziziensis BREEDING

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#### Introduction

The forage grass Urochloa ruziziensis autotetraploid and with sexual mode of

**Objectives** 

The objectives of this study were to (1) assess the genetic variation and

reproduction is an important component of the *Urochloa spp.* breeding programs. The intrapopulation breeding objectives are to increase biomass and seed yield, and nutritional forage quality aiming to cross-pollinate with apomictic species. As with other tropical forage grass species, the association between flowering and seed yield components, the mode of inheritance and the effects of population structure on phenotypic breeding are scarce.

## Methods

Twenty-one characteristics evaluated in fifty-nine half-sib progenies of seven subpopulations were analyzed using a mixed model methodology. the experiment included 20 replications and one plant per plot (1.5 m x 1.5 m spacing), in a randomized block design. The experiment was performed at Embrapa Gado de Corte in Campo Grande, Mato Grosso do Sul State, Brazil, 20°28' latitude south, 55°39' longitude west, altitude 530 m. The field soil is classified as Haplic Ferralsol (Rhodic) (FAO 2006). According to the Köppen climate classification, the region has a type Aw. The statistical analysis was performed using the Selegen - REML/BLUP software (Resende 2002, Simeão et al. 2016), which provides statistical estimates of genetic parameters and breeding value prediction.

heritability of traits related to seed yield, (2) determine the genetic correlations and commonality between seed yield and its components, (3) determine the association between the phenological behavior of flowering and seed yield, and (4) estimate the population differentiation and its effect on *Urochloa ruziziensis* breeding.

### **Results and Discussion**

The characteristics index of flowering, number of panicles, seed weight, *seed-set* and all those associated with the production of biomass, excluding regrowth in the dry season, showed additive genetic variation statistically significant between and within populations. The genetic variability available in experimental breeding populations is derived from the structuring of subpopulations and progeny and from Mendelian segregation effects within progeny. All three pieces of information can and should be capitalized on genetic improvement programes based on phenotyping. The null commonality evidenced between the filled seed production and biomass production is advantageous for the selection and genetic gain in both characteristics, i.e., there is not causal relationship between them which is useful for selection and breeder decision-making.

#### Genetic parameters in Urochloa ruziziensis.

 $h_{a}^{2a} h_{a}^{2b}$ 

LRT<sup>d</sup>

Mean

#### **Characteristics**



	a	pop	88		
Reproductive					
Flowering synchrony index	0.21	0.04	0.80	0.80	**/**
Seed synchrony index	0.06	0.01	0.47	0.40	ns/ns
Total number of panicles	0.22	0.16	0.78	89.30	**/**
Total seed yield (g)	0.07	0.02	0.59	28.10	ns/ns
Filled seed yield (g)	0.11	0.10	0.69	9.60	*/*
Number of days to flowering	0.23	0.01	0.71	68.00	**/ns
Seed-set	0.12	0.15	0.81	0.31	*/**
Nutritional quality					
Neutral detergent fiber (g kg <sup>-1</sup> )	0.01	0.01	0.56	653.60	ns/ns
Acid detergent fiber (g kg <sup>-1</sup> )	0.09	0.03	0.64	332.90	ns/ns
Cellulose (g kg <sup>-1</sup> )	0.18	0.01	0.73	193.80	**/ns
Lignin P (g kg <sup>-1</sup> )	0.20	0.02	0.75	97.60	**/ns
Crude protein (g kg <sup>-1</sup> )	0.11	0.02	0.64	164.10	ns/ns
DIVMO <sup>e</sup> (%)	0.02	0.01	0.37	56.90	ns/ns
Agronomic: wet season					
Green matter yield (kg plant <sup>-1</sup> )	0.28	0.13	0.85	0.50	**/**
Dry matter yield (kg plant <sup>-1</sup> )	0.30	0.15	0.86	0.10	**/**
Regrowth	0.23	0.14	0.84	3.10	**/**
Leaf dry matter yield (kg plant-1)	0.30	0.07	0.88	0.09	**/**
Stem dry matter yield (kg plant <sup>-1</sup> )	80.0	0.03	0.66	0.03	ns/ns
Agronomic: dry season					

### Conclusion

The fitting of population structure effects in a model of genetic evaluation is straightforward and can be done routinely. This will increase selection efficiency by fitting the structure between groups (or cluster or subpopulation) simultaneously to within group effects.



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Green matter yield (kg plant <sup>-1</sup> )	0.29	0.22	0.87	0.20	**/**
Dry matter yield (kg plant <sup>-1</sup> )	0.26	0.21	0.87	0.07	**/**
Regrowth	0.17	0.15	0.83	2.90	**/**

\*, \*\**P* < 0.01, 0.005; ns: not significant; anarrow sense heritability; bamong population heritability; caccuracy; <sup>d</sup>likelihood ratio test for among progeny genetic variation/among population genetic variation; DIVMO – *in vitro* digestibility of dry matter.



FAO, 2006: World reference base for soil resources 2006 ftp://ftp.fao.org/agl/agll/docs/wsrr103e.pdf.

Resende, M. D. V., 2002: Software Selegen – REML/BLUP. Embrapa Florestas, Colombo.

Simeão, R., A. Silva, C. Valle, M. D. Resende, and S. Medeiros, 2016: Genetic evaluation and selection index in tetraploid *Brachiaria ruziziensis*. Plant Breeding **135**, 246-253.