Nutritive Value in the USDA-NPGS *Cynodon* Germplasm Collection

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Introduction

Bermudagrass (*Cynodon* spp. L.) is an important warm-season perennial grass grown for forage (Kohmann et al. 2017; Silva et al. 2015). A world collection of *Cynodon* species is available at the USDA National Plant Germplasm System (USDA-NPGS) and a forage core collection was developed by Anderson et al (2009). Improvements in forage nutritive value (NV) would lead to higher animal performance; however, no efforts have been placed in this area recently. Screening bermudagrass plant introductions (PI's) would reveal the genetic diversity present in these germplasm for future use in breeding. The objectives of this study were: i) estimate genetic parameters and genotypic performance for nutritive value in the USDA-NPGS Collection, and ii) estimate nutritive value across harvests in selected PI's.
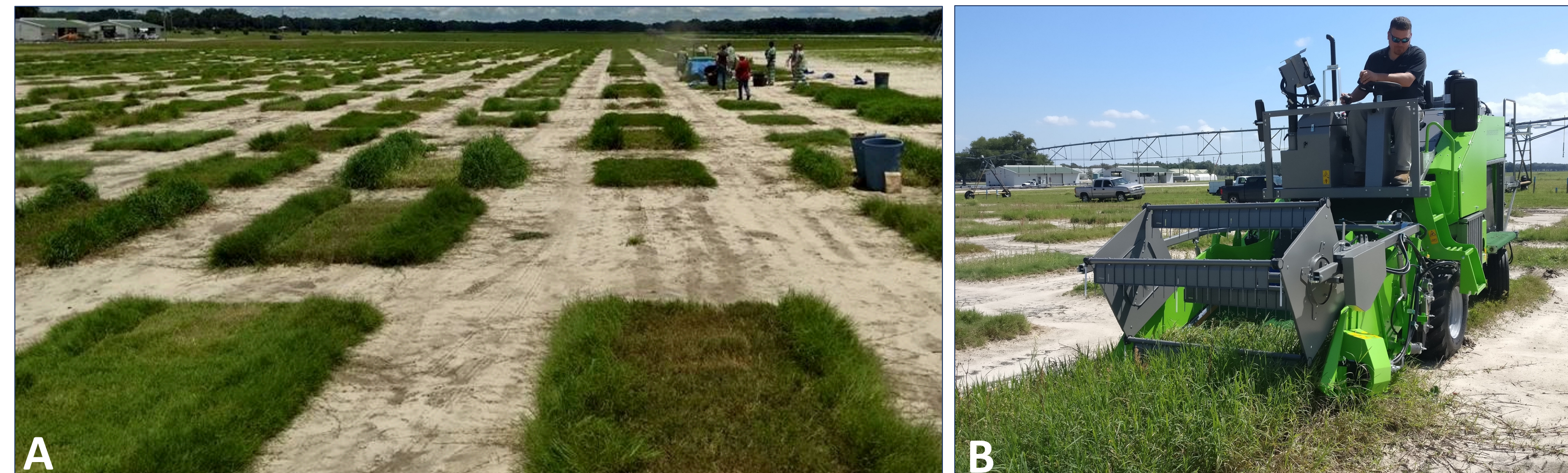

Fig 1. Row-column experimental design in Citra, FL (A); and forage harvesting (B).

Results

Low to medium H^2 were observed for dry matter yield and nutritive value (Table 1). Low r_{gb} was observed for dry matter yield (DMY), while high r_{gb} values were observed for nutritive value traits (Table 1). High negative genetic correlations were found between NDF and CP, P, IVOMD; while, CP positively correlated with P and it had a weak negative correlation with DM. IVOMD had a medium correlation with DMY, CP and P. Large genetic diversity exist among PI's for all traits (Fig 2). Tifton 85 had the highest DMY and IVOMD among cultivars (Fig 2).

For the subset of 15 genotypes and 11 harvests, significant genotype and harvest main effects were observed for all traits ($P<0.001$), while their interaction was not statistically significant for any trait (Table 3). PI's with improved NV have been identified (Table 4). Different PI's were placed at the top of the ranking for each NV trait (Table 4). Except for CP and IVOMD, some PI's showed statistically significant improved performance compared to Tifton 85.

Table 1. Repeatability ($H^2 \pm$ SE) and genotype by harvest correlation (r_{gb}) for dry matter yield and nutritive value.

TRAIT	$H^2 \pm$ SE	r_{gb}
DMY	0.21 ± 0.04	0.40
CP	0.23 ± 0.04	0.76
P	0.49 ± 0.03	0.99
IVOMD	0.38 ± 0.04	0.78
NDF	0.49 ± 0.03	0.99

Table 2. Pearson genetic correlations among dry matter yield and nutritive value traits

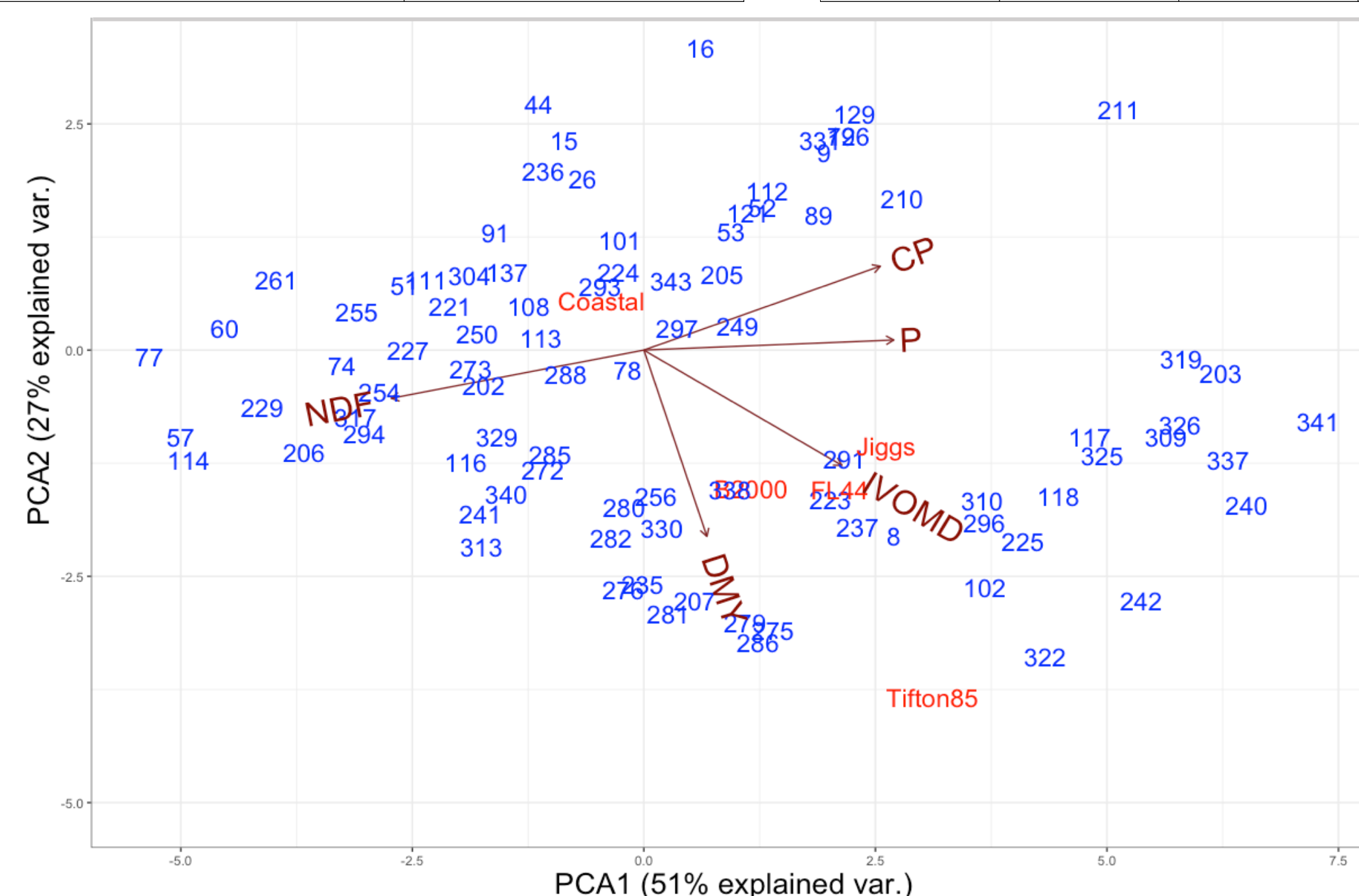|	CP	P	IVOMD	NDF
DMY	-0.12	0.13	0.46	-0.01
CP		0.60	0.29	-0.69
P			0.45	-0.62
IVOMD				-0.41

Fig 2. Principal Component Analysis (PCA) for five traits using genotypic values (BLUPS) for two harvests.

Materials and Methods

The experiment was conducted in Citra, FL, from July 2014 (planting) to November 2016. A row-column experimental design was established with two replicates (Fig 1 A). The population was composed of 286 genotypes: i) 137 PI's from NPGS; ii) 146 PI's from the bermudagrass core collection, and iii) commercial cultivars: "Tifton 85", "Coastal", and "Jiggs". The entire population was harvested twice (Jun 2nd and Aug 12th 2015), while 15 genotypes were sampled nine more times (2015: Jul 7th, Aug 11th, Sep 22th, Nov 3rd, and 2016: Apr 14th, May 19th, Jun 23th, Jul 28th, Sep 13th and Nov 1st). Plots were cut at 10 cm stubble height and fertilized with 90 kg N ha^{-1} and 45 kg K_2O ha^{-1} after each harvest (Fig 1 B). Nutritive value traits were determined by wet chemistry: crude protein (CP), phosphorus (P), in-vitro dry organic matter digestibility (IVOMD) and neutral detergent fiber (NDF). Linear mixed models with repeated measures were implemented in ASReml (Gilmour et al., 2009) to estimate variance components and calculate repeatability (H^2), genetic correlations and genotype by harvest correlation (r_{gb}). Genotypic values were used to perform a Principal Component Analysis (PCA) in R. Linear mixed models were implemented in R to estimate NV traits across harvests.

Table 3. Analysis of variance showing sources of variation, degrees of freedom (DF) and mean square values for each nutritive value trait.

Source of Variation	DF	Mean Square Values			
		CP	P	IVOMD	NDF
Block	1	0.15	0.00019	1.2	44.47***
Genotype	14	16.66***	0.05361***	284.2***	98.38***
Harvest	10	91.29***	0.02211***	511.4***	85.93***
Harvest by Genotype	140	2.46	0.00178	14.0	2.51
Error	170	3.64	0.0017	14.3	3.78

$P < 0.001$ ***

Table 4. Average nutritive value for plant introductions and two cultivars across eleven harvests.

Genotypes	CP g.kg^{-1}		P g.kg^{-1}		IVOMD g.kg^{-1}		NDF g.kg^{-1}	
PI 308193	**145.2**	a	3.16	bc	467.4	fg	678.2	cd
PI 316510	138.8	ab	3.24	bc	**556.5**	a	662.0	de
PI 316536	138.5	abc	3.11	bcd	529.0	abcd	669.7	de
PI 364484	133.8	abcd	3.42	b	503.3	cdef	**656.3**	e
Breeding line 240	133.1	abcd	**3.95**	a	550.9	ab	653.5	e
Breeding line 8	132.5	abcd	2.54	ef	542.6	abc	690.5	bc
PI 292143	127.3	abcd	3.20	bc	515.5	bcde	679.2	cd
PI 294467	124.7	abcd	2.59	ef	488.3	efg	708.0	ab
PI 255456	123.7	bcd	3.36	b	498.7	defg	669.4	de
PI 255450	121.8	bcd	3.89	a	**564.0**	a	679.5	cd
PI 290813	118.9	cd	2.41	f	482.8	efg	708.3	ab
PI 290664	115.2	d	2.52	ef	479.2	efg	715.9	a
PI 295114	114.5	d	2.43	f	463.1	fg	719.3	a
Florida 44	127.4	abcd	2.89	cde	460.6	g	666.6	de
Tifton 85	132.5	abcd	2.75	def	540.9	abc	692.7	bc
C.V. (%)	19.47		22.25		12.39		4.57	

*Mean values with same letter do not differ statistically (P≤0.05) by Tukey Test

Conclusions

Genetic variability exists for forage NV traits in the bermudagrass germplasm collection, and selective breeding for increased forage NV could be an attainable goal in the collection.

Besides, the high r_{gb} for NV traits indicates that selection for those traits could be performed with less evaluations, as opposed to DMY.

Indirect selection for those traits could be achieved in this population, especially for those traits exhibiting higher H^2 estimates.

Phenotyping perennial forage species should be performed across several harvests and years. Our results showed that selection for NV traits could be done with less evaluations, evidence by the lack of interaction effect between 15 diverse genotypes and 11 harvests.

These results will guide plant breeders in the selection of parents at the time of developing breeding/genetic populations.

References

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