Breeding *Urochloa* and *Megathyrsus* forage grasses for low methane livestock systems

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Introduction

- Global ruminant populations exceed one billion head, predominantly supported by ~100 million hectares of *Urochloa* (syn. *Brachiaria*) and *Megathyrsus* (syn. *Panicum*) forages in tropical regions. They represent over 16% of all anthropogenic methane (CH_4) emissions (Mwendia et al., 2021).
- At CIAT, the Breeding Program focuses on three forage grass species: *Megathyrsus maximus* (guinea grass) *Urochloa humidicola*, and interspecific *Urochloa* (*U. ruziziensis* × *U. brizantha* × *U. decumbens*).
- In the Low-Methane Forages (LMF) project, elite breeding lines are being evaluated for their potential to reduce methane emissions, having been primarily selected for their tolerance to acidic, low-fertility soils, resistance to spittlebugs (Homoptera: Cercopidae), high biomass yield, and resilience to abiotic stress.

Objectives

Find promising genotypes from the *Urochloa* and *Megathyrsus* breeding programs to mitigate greenhouse gas emissions from livestock with high True Digested Dry Matter (TDDM), lower CH_4 intensity (ml/g TDDM), and high biomass yield.

Introduce traits (CH_4 intensity and TDDM) that will reduce enteric CH_4 production into widely used forage-grass cultivars through conventional breeding methods.

Methodology

- A total of 294 interspecific *Urochloa* hybrids, 147 *U. humidicola*, and 138 *M. maximus* genotypes were sown in a randomized alpha-lattice design.
- 10 interspecific *Urochloa* hybrids, 10 *U. humidicola* and 35 *M. maximus* were collected at the optimal phenological stage for grazing and/or cut and carry for each species and sampled and tested *in vitro* for CH_4 intensity, TDDM, crude protein (CP) and nutritional quality traits (Figure 1).
- Data was analyzed using a linear mixed-effects and pairwise comparisons were conducted using Tukey's HSD test (α = 0.05).

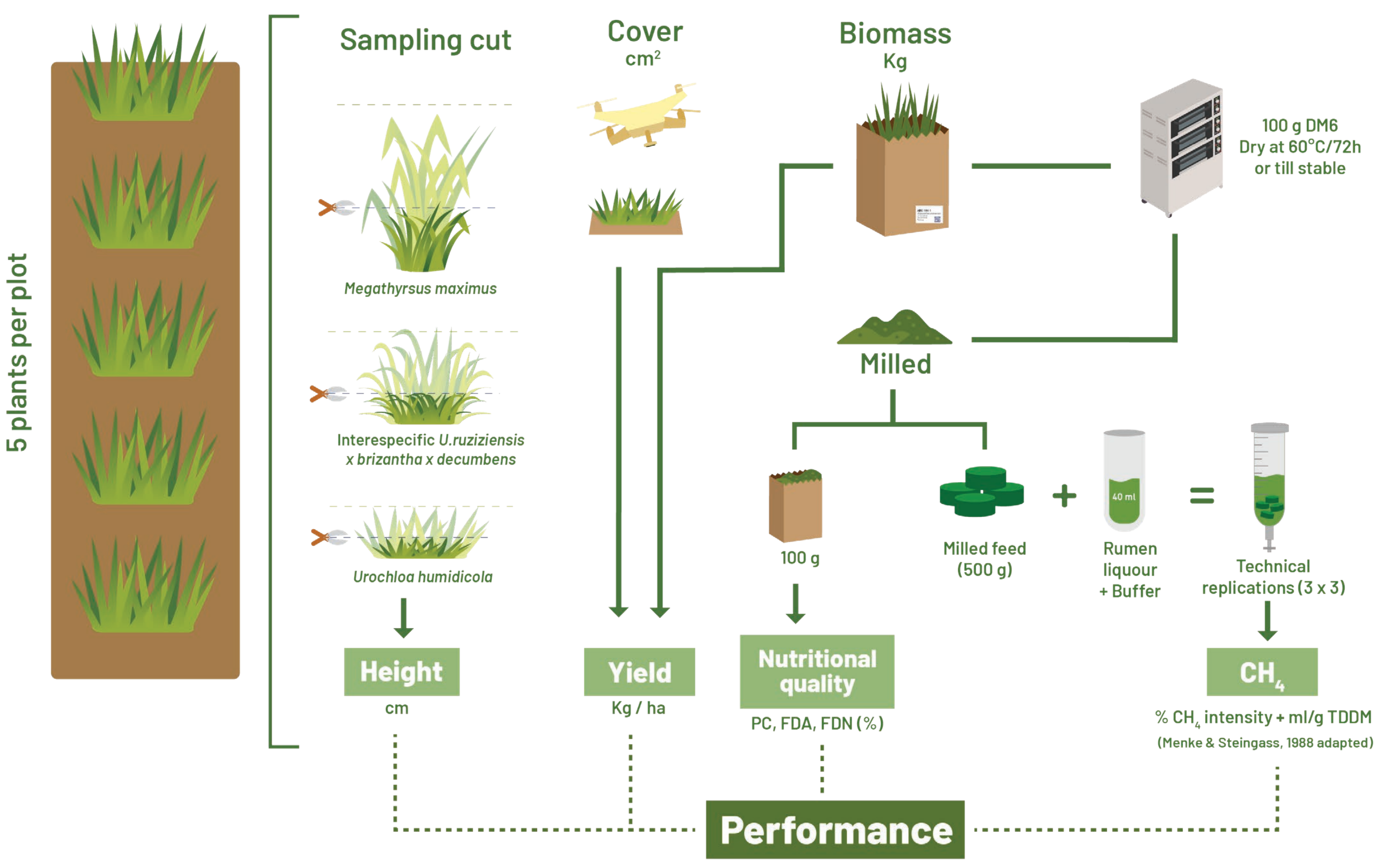

Figure 1. Illustrative methodology for forage performance, nutritional quality, and methane reduction potential evaluation.

Results

- Initial results showed significant differences between species in CH_4 intensity (Fig. 1a) and crude protein content (Fig. 1b).
- Within species, genotypes showed significant differences for TDDM and methane emission intensity (CH_4 ml/g TDDM) (Fig 2 a,b,c).
- Reference lines based on the mean of each variable allowed the classification of genotypes into four categories (I, II, III, IV), identifying those with high TDDM and low methane intensity as the most promising (quadrant IV).

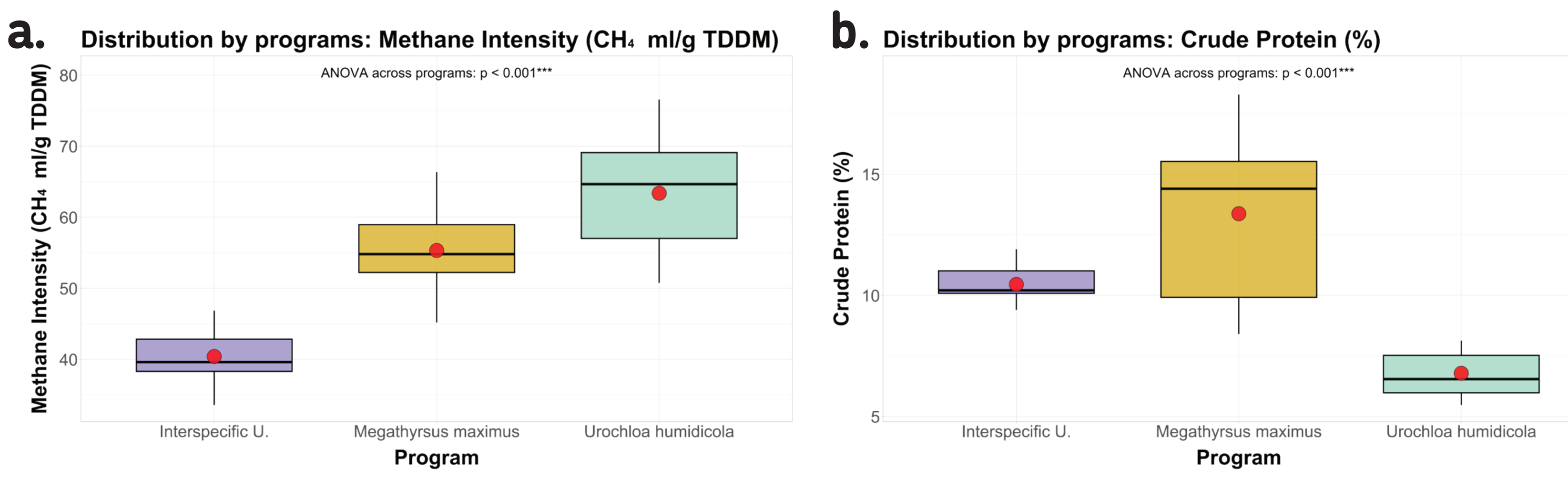

Figure 2. Box plot distributions for *U. interspecific*, *M. maximus* and *U. humidicola* genotypes. a. CH_4 ml/g TDDM; b. % Crude Protein.

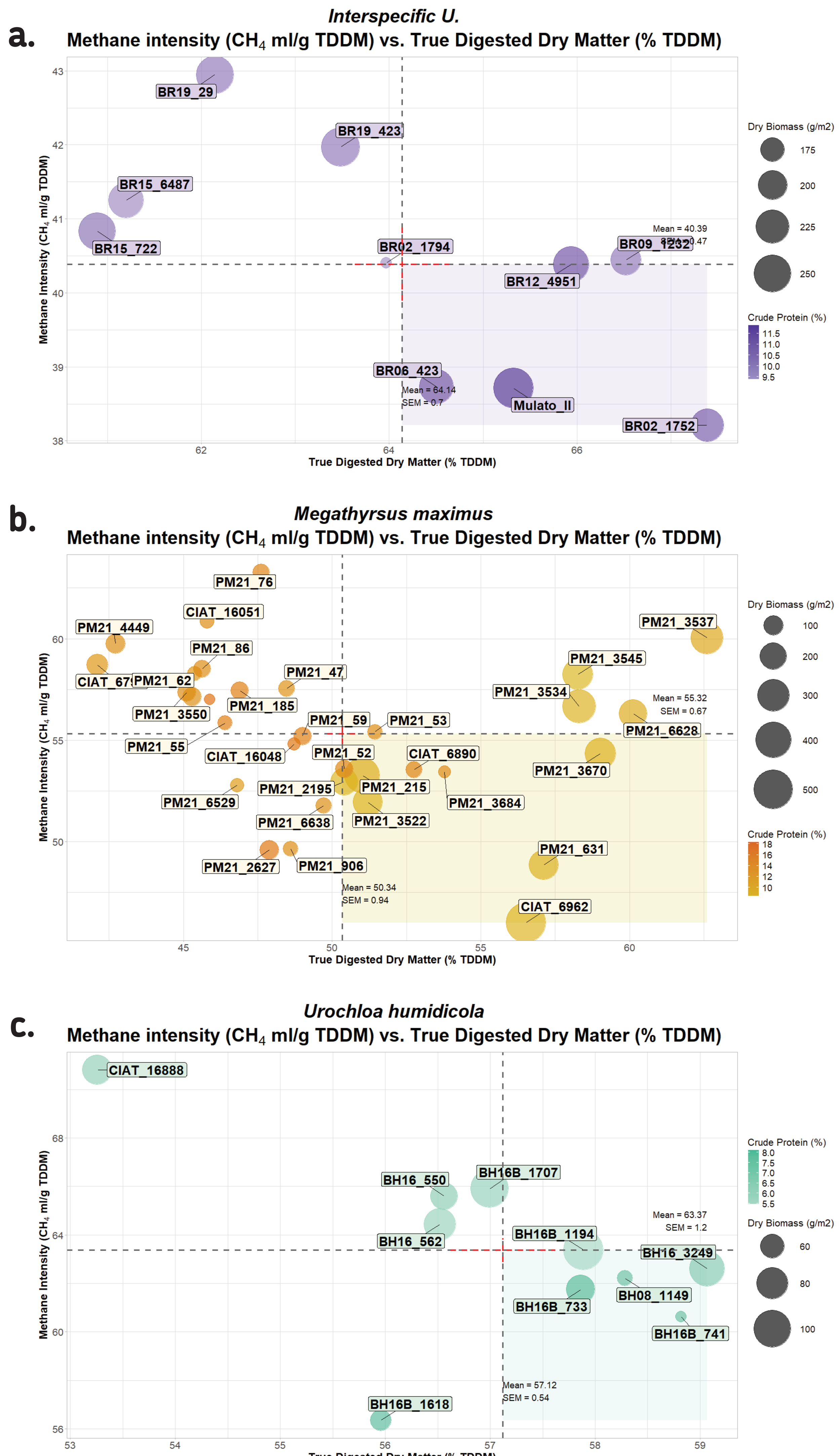

Figure 3. Relationship between methane intensity (CH_4 ml/g TDDM) and true digested dry matter (% TDDM). In addition Bubble size indicates dry biomass yield per genotype (g) and color intensity indicates variation in CP%: a. Interspecific *Urochloa*; b. *Megathyrsus maximus* and c. *U. humidicola*.

Conclusions

- Promising genotypes with low CH_4 intensity (ml/g TDDM) and high TDDM were identified in interespecific *Urochloa*, *U. humidicola* and *M. maximus* showing the potential to be scaled as low methane forages (LMFs), and to introduce these traits as objectives in the improvement of these species.
- A **broader range of genotypes will be evaluated** to identify additional LMFs that can be adopted globally.

References

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Acknowledgments

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