GxE interaction in interspecific *Urochloa* hybrids using factor analytic models

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Introduction

• Environmental factors influence plant phenotypes shaping the expression of forages.
• The ability to test genotypes in multiple environments is critical in a breeding program because important traits are strongly influenced by the environment.
• Nutritional quality is essential in forage breeding because it affects the rate of live weight gain in livestock as well as the quality of end products such as milk and meat.
• There is scarce information on the environmental effect on agronomic and nutritional quality traits in tropical forages.

Objective

Analyze the genotype-by-environment interaction in a breeding population of interspecific *Urochloa* hybrids (*U. brizantha × U. decumbens × U. ruziziensis*) evaluated for agronomic and nutritional quality traits across four locations in Colombia, using factor analytic mixed models.

Materials & Methods

Genotypes and experimental design: In 2019-2020, 103 apomictic genotypes and 7 checks (Basilisk, Caporal, Cayman, Cobra, Marandú, Mulato II, Toledo) were evaluated in 4 locations: Agrosavia Research Centers of Turipaná (Cereté, Córdoba) and Nataima (Espinal, Tolima); Alliance Americas Hub (Palmira, Valle) and research plots in Llanos (Puerto Gaitán, Meta). Each plot made up of four plants arranged in a rectangular alpha lattice design with 110 treatments and 22 blocks (10 units/block, 11 blocks/rep, 2 reps).

Traits: Five evaluations were performed in each environment. Agronomic traits such as plant biomass, plant height, plant area, and fresh and dry weight; and nutritional quality traits were evaluated. Agronomic traits will be presented.

Statistical Analysis

• The phenotypic data was analyzed using R. ASReml-R (v4) (Butler, 2018) and lme4 (Bates et al., 2015) were used to fit Linear Mixed Models (LMM).
• The genotype was taken as a fixed factor to obtain best linear unbiased estimators (BLUEs), and as a random factor to obtain, BLUPs, genotypic variances, and broad-sense heritability (Cullis et al. 2006).
• Two multi-enviromental trial (MET) models were fitted: an alpha-lattice MET for calculating overall parameters (random components and heritabilities), a second one for knowing the GxE pattern was incorporating a Factor Analytic structure of order 2 (FA2) and the variance matrix for the residuals was assumed to be the block diagonal.
• For the FA2 MET, the genotype and GxE factors are combined into a single compound model factor of genotype nested within the environment: gen(trial)ij. This formulation then allows us to specify the pattern of genotypic variances within environments and the correlation structure for the effects of a common genotype across environments (Isik, F., Holland, J., & Maltecca, C. 2017).

Results
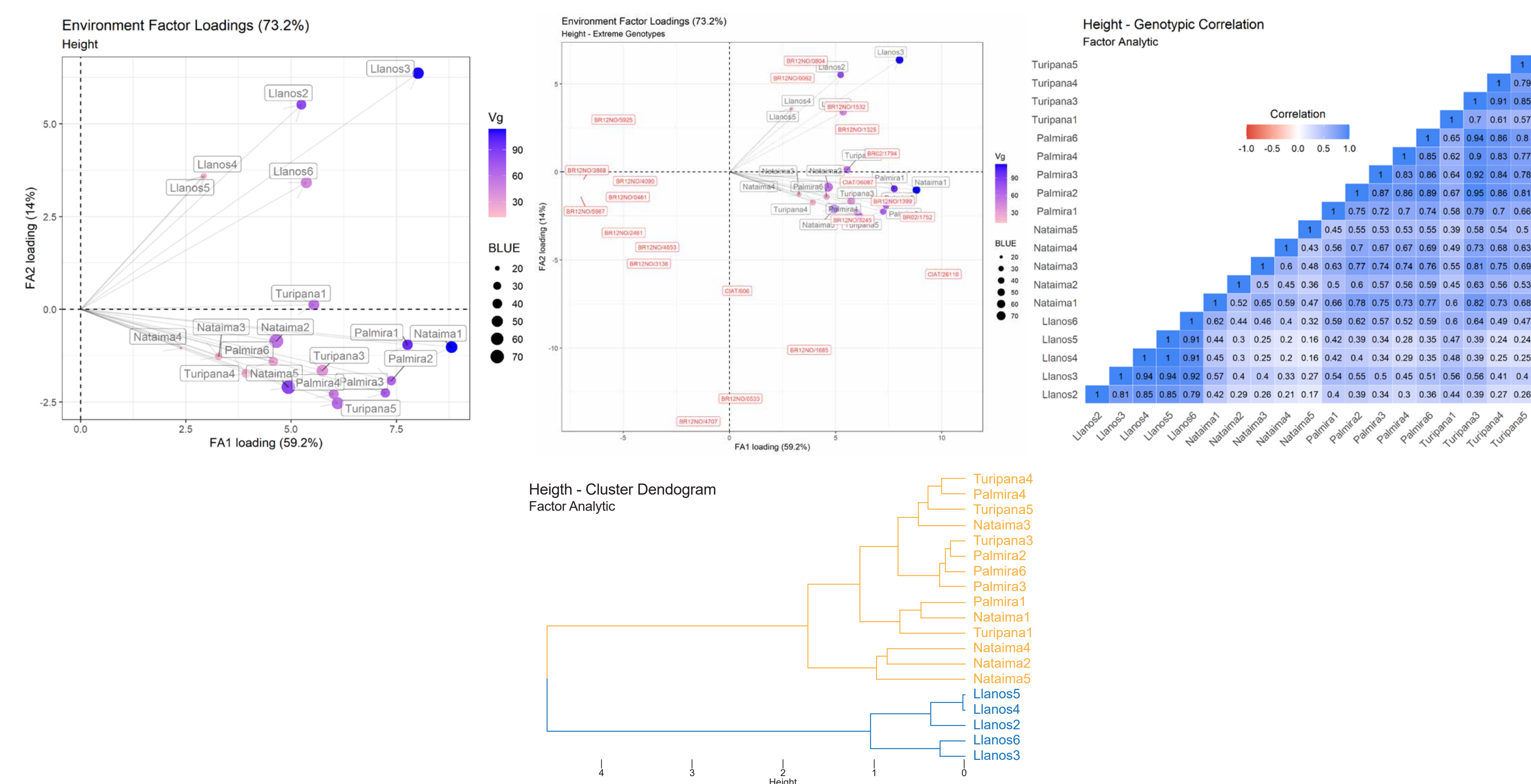
Conclusions

• Broad sense heritability was high for all traits (h2 >0.69).
• Phenotypic correlations among traits ranged from 0.26 to 0.93.
• Genetic correlations among environments showed different ranges depending on the variable evaluated.
• The factor analytic analysis revealed that two factors explained > 60% of genetic variance in all traits and that 80% of environments were clustered in the first factor.
• Factor analytic biplot indicates that Llanos location differed strongly from other locations evaluated.
• Based on the results obtained, the factor analytic analysis is a useful tool to stratify environments and identify *Urochloa* cultivars adapted to different ecological niches.

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