GGE BIPLOT ANALYSIS IN MULTI-ENVIRONMENT TRIALS AND HARVESTS FOR LEAF DRY MATTER YIELD IN *PANICUM MAXIMUM* JACQ. (syn. *MEGATHYRSUS MAXIMUS* JACQ.)

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INTRODUCTION

Among the main forage grass crops in Brazil, guinea grass (*Panicum maximum* Jacq.) stands out due to it is excellent yield performance, adaptation and good forage quality. In forage evaluations, if the most important traits are strongly influenced by the genotype x environment (GxE) interaction, a larger number of environments may be necessary.

OBJECTIVE

The objective of this research was to verify the effect of GxE interaction, as well as to obtain information about the number of harvests per environment required for genotype selection in the context of multi-environment and multi-harvest trials (MET) for leaf dry matter yield (LDMY).

MATERIAL AND METHODS

❖ Evaluation was performed with 23 genotypes: 14 genotypes selected from the genebank, four selected hybrids and five cultivars as checks (Aruana, Milênio, Mombaça, Tanzânia and Massai), in 11 harvests, under rainy and dry seasons.

❖ A randomized complete block design (RCBD) was used with three replications. Plots were 6 rows of 4.0 m length, occupying an area of 12 m^2, with spacing of 0.5 m between rows and 2.0 m of distance between plots.

❖ Statistical analysis: REML/BLUP procedure were implemented in ASReml-R. Visual grouping of the locations associated with the genotypes were obtained through the GGE Biplot analysis performed by GGEBiplotGUI-R package and the scores of the first two principal components (PC1 and PC2) were used to display two-dimensional biplot. Pair-wise Spearman correlations of cumulative harvests were computed to obtain the ideal number of harvests.

Figure 1. Representation of geographic distribution of the series of trials of guinea grass regarding latitude (Lat) and longitude (Long) for the sites in Brazil: Mato Grosso do Sul (MS), Distrito Federal (DF), Rondônia (RO), Acre (AC), and Rio de Janeiro (RJ).
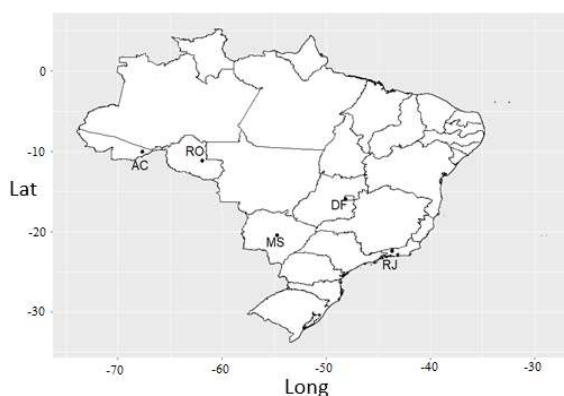
RESULTS

Figure 2. a) GGE biplot of "which-won-where" that relates the environments to the genotypes of better performance for identification of mega-environments; **b)** Spearman correlations among the means of the accumulated values of harvests (1_4 to 1_11) for each site (AC, DF, MS, RJ, RO).

a)

b)
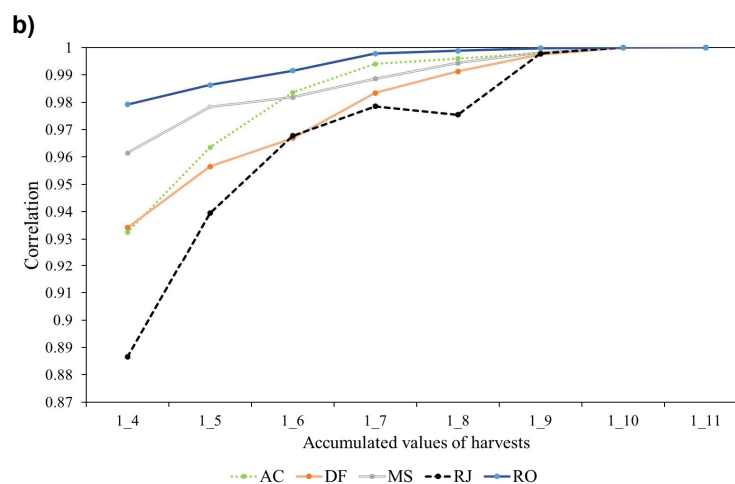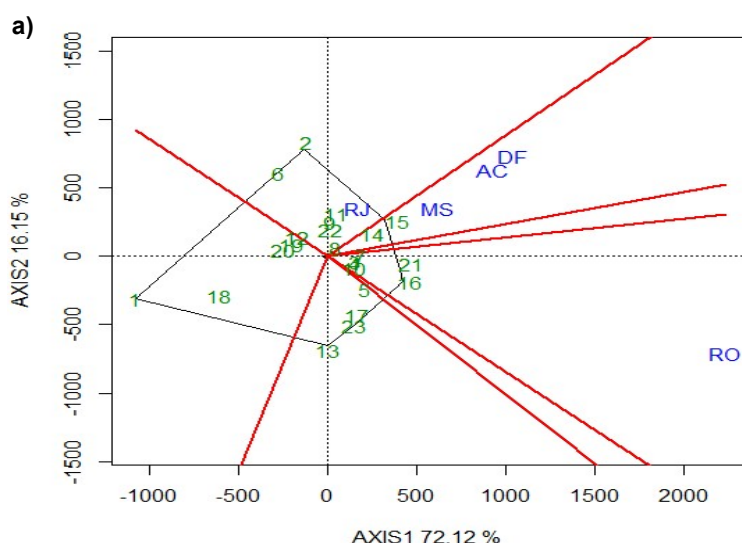
CONCLUSION

To perform the genotype selection for the LDMY trait, seven harvests per environment were representative and enough to discriminate genotypes. These results show us the importance of studying the GxE interaction effects in MET analysis, to support the forage breeders in the context of genotype selections and improve the P. maximum breeding programs.