

TRABALHOS CIENTÍFICOS

## AREA TEMÁTICA: MELHORAMENTO VEGETAL

## 162 - BIPLOT ANALYSIS OF PHENOTYPIC STABILITY IN UPLAND COTTON GENOTYPES IN MATO GROSSO

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## **Resumo:**

The breeding program of EMBRAPA Cotton aims to develop more productive genotypes with higher-quality fibers. To achieve this, a large number of genotypes (G) is tested annually in different environments (E), before final recommendation and multiplication. In most cases, these environments vary substantially, and there are interactions between genotypes and environments (GE), that arise from differential genotypic responses to the environment. Understanding GE interactions affords an assessment of the real impact of selection and ensures greater reliability when recommending genotypes to maximize productivity and other agronomic traits of interest in a specific location or group of environments. The GGE biplot model is best suited to identifying mega-environments, selecting representative and discriminative environments, and appointing more adapted and stable genotypes to specific environments. In contrast, AMMI analysis can be used efficiently for identifying superior environmental conditions for the agricultural holding (selection of growing regions) and higher mean performance genotypes. To date, the GGE biplot method has been used to investigate GE interactions in several crops, but has not been applied to upland cotton in Brazil. Thus, the aim of this study is to investigate the association between AMMI and GGE biplot methods and select cotton genotypes that simultaneously contain high seed cotton yield and stability in environments of Mato Grosso State. Eight cotton cultivar competition experiments were conducted during the 2008/2009 crop season in Mato Grosso State. Soil and climate features of each environment are shown in Table 1. The experimental design was a randomized complete block with 16 genotypes (BRS ARAÇA, BRS BURITI, BRS 286, FMT 701, FM 993, FM 910, DELTA OPAL, IPR JATAI, LD CV 05, LD CV 02, BRS CEDRO, NUOPAL, CNPA MT 05 1245, CNPA MT 04 2080, CNPA MT 04 2088, and BRS 293) and four replicates of each genotype x environment combination. Each experimental unit consisted of four rows 5 m long, spaced 0.9 m apart, with a density of 9 plants/m. In each experimental unit, seed cotton yield was evaluated in two central rows, corrected to 13% moisture, and extrapolated to kg/ha. Seed cotton yield data for each genotype were analyzed individually with ANOVA, with genotypes as fixed effects and the environments as random effects. The relationship between the largest and smallest MS of the residuals from the individual ANOVAs did not exceed the ratio 7:1, permitting a joint analysis of trials.Data were then analyzed for adaptability and stability with the AMMI and GGE biplot methods. The genotypes DELTA OPAL (G7), and BRS BURITI (G2) were the most unstable and contributed the most towards GE interaction (Figure 1). The genotypes BRS ARAÇÁ (G1), LD CV 05 (G9), and LD CV 02 (G10), had lower coordinates on the PC1 axis (were most stable), and therefore contributed the least towards GE interaction. BRS ARAÇÁ (G1) and LD CV 05 (G9) performed above the overall mean. The environment Pedra Preta (PET) had higher mean yield and proved to be more unstable. Environments Campo Novo dos Parecis (CNP), Sapezal (SAP), and Nova Ubiratã (NUB) presented the lowest scores on the PC1 axis, and were thus considered the most stable.

## **Palavras-chave:**

AMMI, GGE Biplot, GE Interaction, Gossypium hirsutum