ERROR STRUCTURES IN BIPLOT ANALYSIS OF MULTI-ENVIRONMENT TRIALS

<u>M. Balzarini¹</u>, F. Casanoves², R. Macchiavelli³

¹Universidad Nacional de Córdoba, Córdoba, Argentina ²CATIE, Turrialba, Costa Rica ³University of Puerto Rico, Mayagüez, Puerto Rico.

Email: mbalzari@agro.uncor.edu

Multi-Environment yield trials (MET) are crucial tools to recommend cultivars in plant breeding. Because of the genotype-by-environment interaction (GEI), METs are conducted in various environments using designs which involve several replications (plots) for each genotype at each environment. Biplot analysis from additive main effects and multiplicative interaction (AMMI) models, as well as site regression (SReg) models, are commonly used for visualizing GEI. Frequently, biplots parameters are estimated under error structures which are too simple. Instead of the model mean structure, mixed models have been suggested to taking into account within-trial spatial correlation among plots as well as between-trial residual variance heterogeneity. This work describes the analysis of GEI in a series of METs studying yields of peanut. For each database, we analyzed GEI by means of AMMI and SReg models with and without modeling spatial plot correlations and residual variance heterogeneity. The MET-specific best fit and the corresponding biplot for exploring GEI are interpreted. The heterogeneity of residual variances across trials is dominant. The inclusion of correlations and variance heterogeneity results in better model fits in most cases and modifies the interpretation of some GE patterns.