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## SPATIAL TREND CORRECTION: CHANGES IN THE RANKING OF SOYBEAN CULTIVARS

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### RESUMO

Soybean [*Glycine max* (L.) Merrill] is a crop of great economic importance, due to its high levels of protein and oil. In soybean breeding, experiments are carried out in experimental designs in order to predict the genotypic values of individuals. These designs make it possible to isolate the environmental variability, so that the best genotypes can be selected. However, this environmental variation is not totally isolated in the evaluation of treatments/genotypes and can inflate the error variance. This problem can be circumvented by the use of robust statistical analyses, such as spatial analysis. This analysis uses data from individual plots and allows for a separate spatial covariance structure and error variance for each observation. We evaluated the potential of a robust spatial model to correct grain yield data from a trial of soybean cultivars. In this way, the spatial trends and the prediction of genotypic values were measured by the change in the ranking of the genotypes, when comparing the basic model with the spatial one. The trial was installed in Maracaju, MS, in a randomized complete block design with three replications. The total plot consisted of five lines of 12 meters in length, spaced 0.5 m apart. The useful plot was formed by three central lines of 11 m. The treatments were represented by 58 genotypes in the 2021/22 crop year. The basic model and the spatial model were compared regarding the estimates of the Akaike (AIC) and Bayesian (BIC) information criteria proposed by Verbyla. Subsequently, the significance of the models was evaluated using the likelihood ratio test (LRT). In addition, the Spearman correlation coefficient was calculated between the models and the coincidence index (CI) and heritability, based on genotypic values (BLUP's). The use of the spatial model improved the heritability estimate, reducing the variance estimates of the prediction errors, based on the lower values of AIC (2290.52) and BIC (2312.39). There was a change in the ranking of the ten best genotypes, with a correlation of 0.64 and a CI of 0.62. Thus, the use of the spatial model improved the estimates of genotypic values, bypassing the spatial heterogeneity.

**PALAVRAS-CHAVE:** spatial analysis, prediction of genotypic values, robust spatial model, heritability, heterogeneity, grain yield

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