

STRUCTURE OF THE RESIDUAL COVARIANCE MATRIX AND IMPLICATIONS ON THE SELECTION OF *Brachiaria humidicola* PROGENIES

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In the analyses of trials with genotypes of *B. humidicola* (syn. *Urochloa humidicola*) under several cuts the split-plot-in-time model or structure of the residual covariance matrix (R) compound symmetry (CS) has been used. However, some studies have shown that the anticipated choice of the R matrix structure may not be adequate. The aim of this study was to evaluate various R matrix structures and verify its implications on selection of *B. humidicola* progenies. We evaluated 52 progenies of *B. humidicola* under nine cuts in a randomized complete block design with eight replications. The plot size was 1,0 m². We analyzed the data of dry matter yield (Kg.ha⁻¹) by a mixed model approach considering twelve different structures of the R matrix. The Bayesian Information Criterion (BIC) was used as fit statistic of the models. Besides, we compared the models by genetic variance estimates, Spearman's rank correlation between BLUPs, coincidence and genetic gain with selection of five and ten best progenies. The unstructured matrix (UN) was the best structure of the R matrix according to BIC. This result demonstrated that the assumptions of covariance homogeneity are not appropriate. The genetic variance was significant for all models, but the estimates did not differ significantly among the models. The estimates and standard error of this parameter were 20428±4848.67 (CS) e 12943±3738.17 (UN), respectively. There were not expressive alterations in progenies classification among the fitted models. The Spearman's correlations were higher than 0.97. There was a correspondence of 80% between CS and UN models for the best five progenies, while for ten progenies this coincidence was 70%. The expected genetic gains among models were 16% on average for selection of the five best progenies and 14% for ten of them. We concluded that there were small alterations in the ranking of progenies for the fitted models. Nevertheless we observed that the breeding values presented smaller prediction standard error for the best model (i.e. UN). Theoretically the best model indicated by BIC results in more realistic estimates of parameters and predictions of the breeding values.

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