Modeling the variance-covariance matrix of genetic and residual effects in a *Panicum maximum* genome wide selection experiment

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Abstract:
Panicum maximum stands out among the tropical forage species due to its high biomass yield and excellent nutritional quality, providing high animal performance. The improvement of sexual plant population of *P. maximum* by recurrent selection increases the probability of releasing superior cultivars. In this work, we aimed to model variance-covariance matrices for genetic (**G**) and residual (**R**) effects in a spaced plant experiment to obtain adjusted means that will be used in a recurrent genomic selection program. The experiment was conducted in an augmented block design, with 570 sexual plants as treatments and three cultivars as controls in six blocks. Individual plants were evaluated in eight clippings for total green matter (TGM), leaf dry matter (LDM), stem dry matter (SDM), and regrowth capacity (RC). The analyses were performed using the software GenStat*16th*. The treatments were separated into two groups: regular, where the effects were assumed as random and controls, where the effects were assumed as fixed. Matrices **G** and **R** were analyzed considering five different structures: Identity (ID), Diagonal (DIAG), Autoregressive(1) (AR1), Power (P) and Unstructured (UNST). We also used the kinship matrix between individuals, obtained with the R package AGHmatrix, to model their genetic effects. The model selection was performed based on the AIC and BIC criterion. For all traits, the inclusion of the kinship matrix improved the fit of the model. The best structures obtained for matrix **G** (genetic effects for clippings) were P for TGM and LDM, DIAG for SDM and AR1 for RC. The matrix **R**, which contains the residual effects for clippings, blocks and mothers, was modeled using DIAG⊗DIAG⊗DIAG for TGM and LDM, and DIAG⊗DIAG⊗ID for SDM and RC. With these structures defined, it was possible to obtain the adjusted means of these traits, which will be used in a forthcoming genomic selection study.

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