Genomic selection in a seedling seed orchard of the *Eucalyptus urophylla* using microsatellite markers*

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Eucalyptus urophylla is one of the most important species for the planted forest sector in Brazil due to characteristics of productivity, adaptation and rusticity. Seedling seed orchards (SSO) are one of the most common used types to produce improved seeds for forest breeding programs. The selection is usually made by BLUP procedure in a progeny test in order to transformation in a SSO. However, selection based on molecular markers associated with the individuals phenotype has aroused great interest, especially, due to high selective accuracy and efficiency that accelerate this process. Thus, the aim of this study was to evaluate the prediction of genetic genomic value of microsatellite loci in *E. urophylla*. For this, 298 mothertrees in a SSO of *E. urophylla*, located in the Fazenda de Ensino, Pesquisa e Extensão, in Selvíria, Mato Grosso do Sul state, were genotyped with 20 microsatellite markers (SSR) EMBRA. The total height was measured at 23 years old trees, with mean of 44.2 meters. To estimate the genetic value we used the Random (Ridge) Regression BLUP (RR-BLUP/GWS) method. The total number of alleles were 304, with mean of the 1.42. The herdability used for prediction was 0.82. The predictive capacity (rgf) was 0.5574 and the selective accuracy in the selection population (rgg) was 0.6155. The accuracy showed moderate values indicating that selection based on genomic genetic value can be performed, but with caution.