

## GENOMIC PREDICTION OF ADDITIVE AND NON-ADDITIVE EFFECTS USING GENETIC MARKERS AND PEDIGREES IN PINES BREEDING

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Pedigrees and dense markers panels have been used to predict genetic merit of individuals in plant and animal breeding. Initially, models accounted only for additive effects. However, the prediction of non-additive effects is important for many plant breeding systems. In this study we evaluated prediction models that include or ignore non-additive effects, for traits with different genetic architectures. The models tested were based either on genetic markers or pedigree information, or both. The models used to compute the genetic marker information were: Reproducing Kernel Hilbert Spaces (RKHS), additive- and additive-dominance-BayesA. Theoretically RKHS can predict additive and non-additive effects confounded (whole genotypic values). Model performance was assessed for the traits tree height (HT) at 6 years of age, diameter at breast height (DBH) and rust resistance, measured in 923 loblolly pine individuals from a structured population of 71 full-sib families genotyped with 4722 genetic markers. We also simulated a population with similar genetic properties, and evaluated the performance of models for six simulated traits with distinct genetic architectures (polygenic and oligogenic traits with three dominance levels). The simulated population were derived from a pine breeding program, originated from selections made in a natural population with  $N_e=10,000$ . The model that included only genetic markers produced similar results to models that combined pedigree and marker information. Both models also provided substantially better predictions than pedigree-only models. The additive-BayesA provided higher accuracies for rust resistance and in simulated additive-oligogenic traits. On the other hand, the inclusion of dominance in BayesA leads to higher accuracies in simulated additive-dominant oligogenic traits. For DBH and HT the RKHS based models showed higher accuracies. In the polygenic simulated traits RKHS were similar than BayesA models. Our results indicate that the capacity of prediction using genomic information is dependent on the number of genes controlling the trait. Considering that, BayesA performs the best for traits with few genes with major effects. We also show that the presence of non-additive effects influences the prediction accuracy since additive-dominant-BayesA and RKHS overcame additive-BayesA in traits with non-additive effects.

Keywords: Polygenic, Oligogenic, RKHS, BayesA, pines.

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