

## THE EFFECT OF THE BLUP BREEDING VALUES IN GENOMIC SELECTION ACCURACY

Patricio R. Munoz,<sup>1</sup> Dudley A. Huber, Marcio Resende, Matias Kirst, Tania Quesada, and Gary F. Peter

<sup>1</sup>School of Forest Resources and Conservation, University of Florida, Gainesville, FL

In tree and cattle breeding populations, pedigree errors have been estimated to be ~ 10%. Even minimal errors in pedigree can cause an underestimate of the additive variance and a decrease in the BLUP breeding value (BV) prediction accuracy. Traditionally, a relationship matrix (A) derived from the pedigree is used in mixed model prediction of BV (Henderson 1972). The A matrix has the expected relationship values between individuals (i.e. 0.5 for full-sib) but does not account for variation caused by Mendelian segregation among individuals (Mrode 2006). Simulations have demonstrated that the observed relationship matrix (ORM) derived from a panel of SNPs can be used to correct pedigree relationships. In addition, use of the ORM rather than the A matrix in the BLUP analysis of phenotypic data yields less biased estimates of the true heritability and more accurate predictions of BV.

Predictions of BV with traditional BLUP analysis from phenotypic data are the input for construction of prediction models based solely on genotypic information, genomic selection (GS) (Meuwissen et al. 2001). Posteriorly, BVs are correlated with GS-predictions to assess the accuracy of the GS models. Thus, bias in BVs and/or pedigree errors should decrease GS accuracy.

The objectives of this study are to construct the ORM from SNP data available from a small pine breeding population to first compare the accuracy on the BV prediction by using the original pedigree in BLUP and by using a pedigree corrected using the ORM. Second to determine the effect on the GS accuracy using these sets of BVs. Evaluate the effect of incorporating the ORM directly in the BLUP BV prediction. And to evaluate the effect on GS accuracy when using BV that have confounded non-additive effects.

The data correspond to a clonal population of loblolly pine phenotyped at six years for total height (HT) and genotyped with SNPs markers. The ORM was constructed based on a recently published method. BLUP analysis were performed in ASReml (Gilmour et al. 2006), and GS was performed using the RR-BLUP method (Meuwissen et al. 2001). Accuracies for BV predictions were obtained following Mrode (2006) and GS accuracy was calculated as the correlation between the BLUP-BV and the GS-BV (Goddard et al. 2009).

When compared to traditional BLUP with the original pedigree, using the ORM corrected pedigree increase heritability from 0.26 to 0.31, BLUP-BV accuracy from 0.80 to 0.85, and GS accuracy from 0.64 to 0.77. An additional increase in GS accuracy (3%) could be reached if the ORM is incorporated directly in the BV predictions by BLUP. Finally ignoring non-additive effects on the BV prediction by BLUP and using those BV in GS generate a considerable decrease in GS accuracy (33%).