

OPTIMIZATION OF GENOMIC SELECTION MODELS FOR SLASH PINE ADVANCED BREEDING POPULATION

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Productivity of Southern pines plantations have dramatically increased over the past decades in part because of the development of genetically improved materials (McKeand et al. 2003). Tree breeding cooperatives have played a major role in enabling and facilitating that effort. Among these, the Cooperative Forest Genetics Research Program (CFGRP) from the University of Florida has been breeding mostly slash and loblolly pine for a single breeding zone, encompassing the natural variation that exists in four million hectares of timberlands and using traditional breeding approaches (White et al. 1993). More recently, phenotypic prediction of growth and disease traits based on high-throughput genomic information has been proposed to increase the efficiency and accelerate pine breeding programs. Simulated and experimental data have suggested that genetic gains in selection efficiency can range from 50% up to 200% when using genomic prediction approaches (Resende et al. 2012a).

In this work we describe the comparison of accuracy of genomic selection models generated from different single nucleotide polymorphism (SNP) sets, obtained from sequence capture/next generation sequencing technology, and applying various SNP identification and filtering parameters. The genotypic information was obtained from two populations: (1) the CFGRP 3rd cycle slash pine full-sib progeny test, where 1000 trees from 60 different crosses among 37 parents were genotyped, and (2) the CFGRP 2nd cycle Florida loblolly pine test, with 2000 genotyped individuals, representing 45 full-sib families derived by crossing 28 parents. From a total of 80,000 probes previously designed for *P. taeda* by RAPID genomics LLC, an optimized subset of 12,000 were selected based on quality of the SNPs obtained from the parental trees. Phenotypic data such as tree height and diameter was obtained by end of the fourth from slash pine population. Genomic selection models for growth traits were developed using Genomic-BLUP (VanRaden 2008), and estimation of prediction performance was done using a ten-fold cross validation. The SNP filtering parameters were additionally evaluated by genetic parameters (inbreeding, genetic gain and variance) of the selected populations obtained by each genomic selection model. The accuracy of genomic selection models will be presented, including the comparison to pedigree-based BLUP prediction models for non-genotyped families.

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