GENOMIC SELECTION IN LOBLOLLY PINE

Marcio F. R. Resende Jr.,[1] Patricio R. Munoz, Juan Jose Acosta, Gary F. Peter, John Davis, Marcos D.V. Resende, Dario Grattapaglia, and Matias Kirst

[1]Genetics and Genomics Program, University of Florida, Gainesville, FL

Genomic Selection (GS) is a method of predicting the genetic value of an individual based on high-density marker data. The application of GS in early selection is particularly valuable for long-lived, perennial tree species. We report the first assessment of the utility of GS in a forest species, the conifer *Pinus taeda* (*Loblolly pine*). A set of 800 individuals, clonally replicated in four sites, were genotyped with 3983 SNPs and phenotyped for Diameter at Breast Height (DBH) and total height (HT). Prediction models were developed using a Genomic BLUP (Best Linear Unbiased Prediction) procedure. The prediction models were validated in all four sites and across different ages and the accuracy of those models was calculated. GS model accuracies remained high across environments within the same breeding zone. However, models generated at early ages did not perform well to predict phenotypes at age 6. The selection efficiency per unit time is 53–118% higher using GS compared to phenotypic selection, assuming a conservative reduction of 50% in the length of the breeding cycle. These results demonstrate the feasibility and remarkable gain that can be achieved by incorporating GS in breeding program of conifers and long-lived perennial species.