

ANALYSIS AND SELECTIONS OF THE CFGRP 4TH CYCLE SLASH PINE TREE IMPROVEMENT

Salvador A. Gezan, Gregory L. Powell, Andrew D. Sims, Matias Kirst and Gary F. Peter

University of Florida, Gainesville, FL, USA

During 2016-2017 the Cooperative Forest Genetics Research Program (CFGRP) of the University of Florida performed a large and detailed statistical analysis to make its 4th-cycle selections. This analysis combined a total of 24 field trials located in the southeastern United States. The variables considered for this analysis included individual tree volume increment and rust score. The trials considered were a mixture of polimix tests (PMX I and PMX II) and full-sib trials (FS) measured at ages ranging from 4 to 8 years since planting.

After data validation and checking, a multi-trial environment analysis was performed that considered for each of the sites its corresponding design effects (replicates, row, column or incomplete blocks within replicate), together with an additive-by-trial effect that was flexible enough to consider a different additive variance per sites and a single type-B genetic correlation between sites. In addition, a family term and its interaction with trial was incorporated, together with a different error variance for each trial. This model allowed to combine different levels of 'genetic signal' from each of the trials into a single analysis.

Breeding values were obtained across all trials, which were later used to select parents (backward selection) and offspring (forward selections). The latter were only performed in the full-sib trials established in 2012. Selections were restricted to have individuals from each of the breeding groups, with limitations on the numbers of individuals per family. A selection index based on 50/50 for volume and rust was used to select the best genotypes.

Preliminary results indicate of this large analysis resulted in a narrow-sense heritability of 0.20 and 0.25 with type-B correlations of 0.73 and 0.88 for volume and rust, respectively. These statistics are similar to those previously reported in other genetic studies of slash and loblolly pine, and they allow for selections of genotypes that produce interesting gains across all planting area. A total of 399 selections were identified with 34 backward and 365 forward selections distributed across the eight breeding groups and all trials. These selections will be evaluated and later used for planning future crosses to establish the new generation for the 5th cycle.

Contact Information: Salvador A. Gezan, School of Forest Resources and Conservation, University of Florida, 363 Newins-Ziegler, P.O. Box 110410, Gainesville, FL 32611, Phone: 846-0133, Email: sgezan@ufl.edu