

MODELING GENETIC IMPROVEMENT EFFECTS ON GROWTH AND VALUE OF FOREST PLANTATIONS

Harold E. Burkhart

Department of Forest Resources and Environmental Conservation, Virginia Tech, Blacksburg, VA

Genetic improvement has resulted in increased growth rates, improved tree-stem quality, and enhanced value of forest plantations. In the case of loblolly pine, genetically improved material ranging from open pollinated to control pollinated to clonal is available, but the cost of the seedlings varies significantly. Landowners and forest managers need reliable information on expected productivity – in terms of both wood quantity and quality – to make informed decisions on selection of planting stock, silvicultural treatments, and rotation ages. Early work with data from provenance and open pollinated plantings indicated that an adjustment in site index was sufficient to account for changes in stand basal area, volume and mortality (Buford and Burkhart, 1987). As genetic improvement has advanced, modification of site index alone is not adequate due to changes in tree allometry (height-diameter relationships), tree stem form and quality, disease resistance, and other factors.

Analyses were carried out to examine height-age relationships in a loblolly pine genetics screening trial. Further analyses of height-diameter relationships, height and diameter distributions, and stem quality were conducted using data from block plantings of open-pollinated (OP), control-pollinated (CP), and clonal stock established at two initial planting densities.

MATERIALS AND METHODS

The genetics screening trial consisted of 120 clonal genetic varieties in 10 single-tree blocks (Sabatia and Burkhart, 2013a). The clones were rooted cuttings developed by MeadWestvaco Company from a controlled cross between two half-sib families. The study was established in the spring of 1994 on an old-field site near Summerville, South Carolina, in the Atlantic Coastal Plain physiographic region. Initial spacing was 2.74 m by 2.74 m with two rows of buffer trees around the study. Height data used were obtained from clones with at least five ramets that had no history of damage or extreme suppression by age 15. Eighty-six of the 120 clones in the study satisfied these criteria.

Data were also obtained from a block-planted experiment established with four genetic varieties in spring of 2002 to investigate the effects of planting density (PD) on stand level growth and development. The study, near Summerville, South Carolina, in the Atlantic Coastal Plain

physiographic region, was established on a cutover site and was a completely randomized factorial design with four levels of genetic variety treatment of (OP, CP, and two clones) and two levels of PD treatments (680 trees/ha (TPH) and 1360 TPH). The study consisted of 24 contiguous 0.1781 ha plots as experimental units on which the inner 0.0526 ha was the measurement plot. Site preparation and management of competing vegetation and nutritional deficiencies on the study plots was done according to operational management prescriptions. Each 0.1781 ha experimental plot had 10 beds each 48.2 m long and spaced 3.7 m apart. Trees along the beds were spaced 4 m from each other in the 680 TPH PD treatment and 2 m from each other in the 1360 TPH plots. The 0.0526 ha measurement plot was made up of the inner six beds with the inner 6 trees per bed in the 680 TPH PD and the inner 12 trees per bed in the 1360 TPH density. Diameters and heights were measured during the 2009-10 dormant season when the stands were eight years old.

RESULTS AND DISCUSSION

The effects of genetic variety on the parameters of the height-age relationship were investigated for the 86 clones using the Chapman-Richard's height-age equation

$$H_{iA} = \beta_1(1 - \exp(-\beta_2 A))^{\beta_3} + \varepsilon_{iA} \quad (1)$$

where H_{iA} is the total height of the i^{th} genetic variety at age A , β_1 is the asymptotic height parameter, β_2 is the rate parameters, β_3 is the shape parameter, and ε_{iA} is a normally distributed zero-expectation random error due to the total height observed at age A . The effect of clone on the height-age relationship was modeled by incorporating random effects on parameters of Equation (1).

Although the best fit was obtained by including random effects for both the asymptote and the shape parameters, there was no practical effect of varying the shape parameter on the resultant site index curves. Hence one can assume that the site curves are anamorphic and that an adjustment in level alone is sufficient for accounting for differences in site index of these clones.

Using data from the block planting at two densities with four genotypes, effects of genetic improvement on the tree height-diameter relationship were investigated using the equation form

$$H_i = \beta_0 \times \exp(\beta_1 D_i^{-1}) + \varepsilon_i \quad (2)$$

where H_i is the total height and D_i the diameter at breast height of the i^{th} tree; β_0 is the upper asymptote parameter and β_1 is the rate parameter; and ε_i is the random stochastic error due to the i^{th} tree ($\varepsilon_i \sim N(0, \sigma_\varepsilon^2)$). Genetic variety exhibited a significant effect on both the rate and

asymptote parameters. Planting density had a significant effect on the rate parameter but not on the asymptote parameter. Due to the effect of the PD on the parameter β_1 , the effect of genetics on the parameters was investigated separately for the two PDs. Data from the three replicates of each genetic variety in a PD level were combined for use in fitting the equations. The two clones were taller for a given diameter and the variance of height within a given diameter was less than that of OP and CP material (Sabatia and Burkhart, 2013b).

When fitting two-parameter Weibull distribution functions to the diameter data for the four genotypes, the means and variances were similar. However, as expected from the foregoing results on height-diameter relationships, the height distributions for the two clones were shifted to the right (Sabatia and Burkhart, 2013b).

Improvements in stem form and straightness were clearly evident in the two clones. Furthermore, forking and fusiform rust incidence was essentially eliminated in the clones while occurring, respectively, at rates of 8 and 11 percent in OP and 2 and 9 percent in CP trees.

When incorporating genetic improvement relationships in growth and yield models, analysts must take the model architecture into account. Interrelationships among model components are complex and changes to any of the equations can have effects on other components.

Acknowledgements: Data used in this study were obtained from study plots established by MeadWestvaco. The contribution of ArborGen in maintaining the studies, collecting data, and providing helpful review is gratefully acknowledged. Financial support for data collection and analysis was provided by the Forest Modeling Research Cooperative at Virginia Tech and the National Science Foundation Center for Advanced Forestry Systems.

REFERENCES

Buford, MA and HE Burkhart. 1987. Genetic improvement effects on growth and yield of loblolly pine plantations. *For. Sci.* 33:707-724.

Sabatia, CO and HE Burkhart. 2013a. Modeling height development of loblolly pine genetic varieties. *For. Sci.* 59:267-277.

Sabatia, CO and HE Burkhart. 2013b. Height and diameter relationships and distributions in loblolly pine stands of enhanced genetic material. *For. Sci.* 59:278-289.