

Modeling Genetic Gain in Douglas-fir Growth Models

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Growth modeling of genetic gain has typically taken one of three approaches: site index adjustment, effective age computation, or growth modifiers. Each method involves certain assumptions that may or may not be easily tested with available data. We used the growth multiplier procedure to estimate the impact of genetic tree improvement on long-term growth. The reason for using this method was that we were limited to single-tree-plot progeny test data which can be used in individual tree / distance independent growth models. Such models, such as ORGANON and FVS, are frequently used in the Pacific Northwest. While growth modifiers can be used in other model constructs, the progeny test data provide sufficient information to modify the individual tree model.

Genetic-gain multipliers were calculated based on the BLUP breeding values of parent trees and the incremental growth measurements of the progeny tests from which the BLUP values were obtained. Results from our study suggest that constant genetic-gain multipliers can be used for stands 10 years and older; however, multipliers need to be increased for younger stands. How the multipliers are used depends on stand age and whether actual stand data or a “typical” tree list is used. The genetic gain reflected in the input tree list is as important as the multiplier in many situations. Growth projections for some example stands indicate that the percentage of volume gain in improved stands will decrease sharply between age 10 and 20 years as higher early gains give way to lower gains later in the rotation; however, absolute gains continue to increase during this time period. Gain projections are sensitive to the maximum stand density allowed by the model, raising the question of whether tree improvement increases maximum density or only allows the maximum to be reached earlier in the rotation.