Computer Simulation of Marker-Directed Population Improvement

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The wide range of commercially important traits in forest-tree breeding may be referred to as complex. The complex nature should in theory ask for a situation-specific approach to improvement to make the tree breeding as efficient as possible. However, the most common approach in real programs is to treat all traits as purely polygenic, assuming the infinitesimal model. The objective of our research is to quantitatively evaluate the marker-directed population improvement breeding strategy. In this strategy, the complex nature of commercial traits is reflected in predicting both polygenic and QTL additive effects, and combining these into a single criterion (BLUP value) prior to the selection. We first review the development of the method and challenges arising in outbred species, particularly forest trees. Later, we present the first results of computer simulation, where the main variables are the density of markers flanking to the quantitative trait loci, and the relative effect of QTL loci to the trait’s expression. The strategy is compared to control scenarios under pure polygenic inheritance model. We focus on a single breeding population and respective genetic response and diversity over a number of consecutive generations. Finally, we discuss the future development of this strategy.