

Phenotyping and association genetics for the ADAPT2 population of loblolly pines

Nathalie A Reilly¹, Mengmeng Lu², C. Dana Nelson², and Carol Loopstra²

¹Department of Biology and Marine Biology, University of North Carolina Wilmington, Wilmington, North Carolina

²Department of Forest Genetics, Texas A&M University, College Station, Texas

ABSTRACT: Different phenotypes of loblolly pine (*Pinus taeda*) trees may be inherited in different ways, with some traits inherited independently, and others inherited where one trait depends on the presence of another trait. This research addressed the problem of repeatability, or heritability, of different phenotypes for loblolly pine trees. The ADAPT2 population study was initiated at the Harrison Forrest at the Southern Institute of Forest Genetics, MS in the spring of 2011 using rooted cuttings from 384 unrelated loblolly pine trees. Phenotypic measurements of total height, diameter, crown width, branch angle, and specific leaf area were taken for each tree. A mixed model analysis using JMP Pro 11 statistical software was used to assess clonal effects for the measured traits. Repeatability for measured traits were high: branch angle and crown width ($r = 1.00$), total height ($r = 0.70$), diameter ($r = 0.74$), and specific leaf area ($r = 0.47$). For phenotypic and clonal correlations among the traits investigated, there were significant r^2 values (the cut off P value was 0.05) between crown width and total height (0.56), crown width and diameter (0.58), total height and crown width (0.52), total height and diameter (0.8), diameter and crown width (0.53), and diameter and total height (0.82). There is a high phenotypic variation among the ADAPT 2 population and the clonal repeatability reflects the heritability of the traits investigated.

KEYWORDS: *Pinus taeda*, genetics, heritability, repeatability, clonal effects