

Phenotyping and association genetics for the ADAPT2 population of loblolly pines

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Introduction

Loblolly pine (*Pinus taeda*) trees phenotypes may be inherited in different ways, some traits may be inherited independently, and others may be 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.

Methods

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.

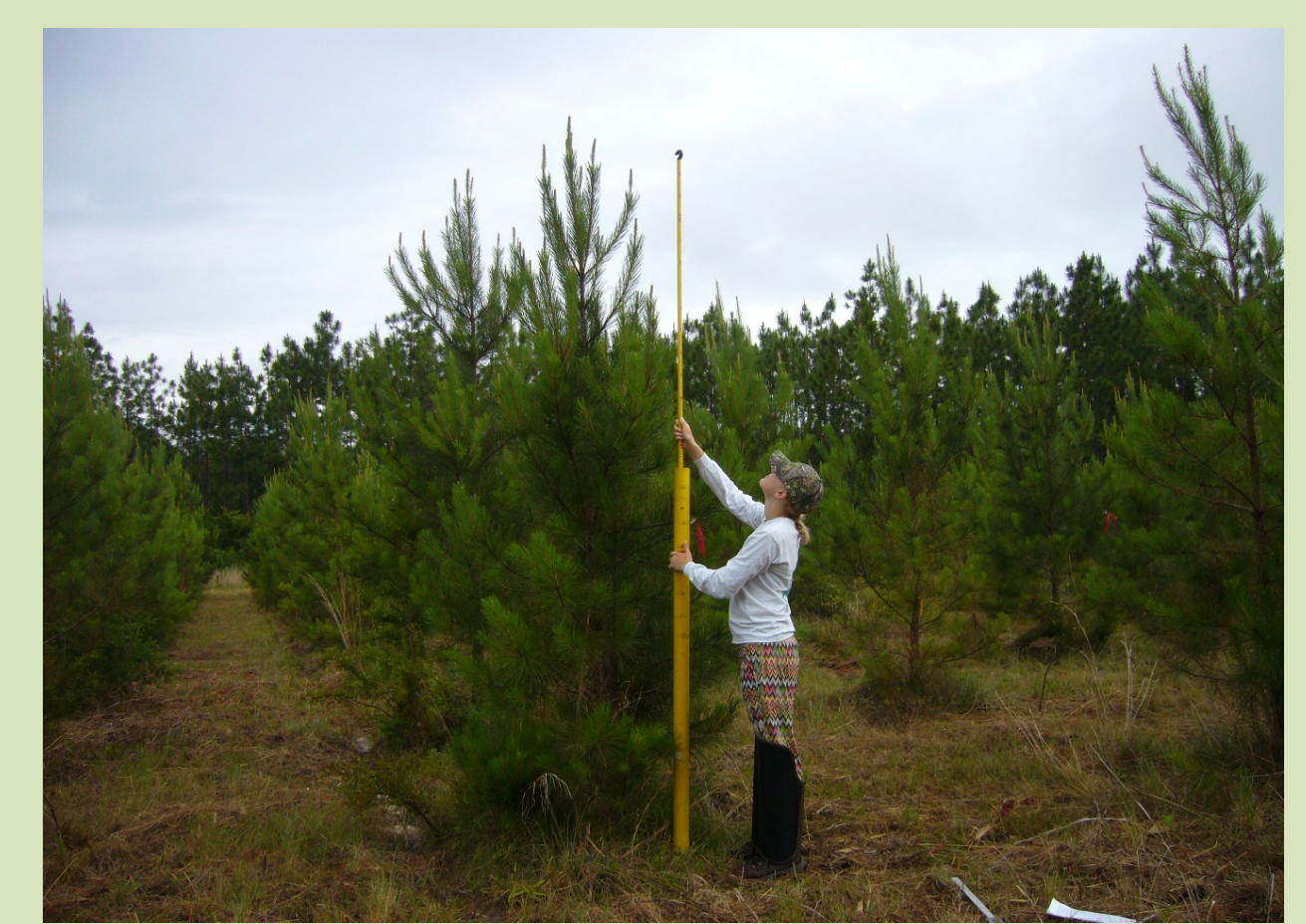
Conclusion

High phenotypic variation exists among the ADAPT 2 population and the clonal repeatability reflects the heritability of the traits investigated.

Phenotypic and Clonal Correlations Among the Traits Investigated

	Specific leaf area	Mean branch angle	Crown width	Total height	Diameter
Specific leaf area	--	Not significant	Not significant	Not significant	Not significant
Mean branch angle	Not significant	--	1.05e-2	Not significant	Not significant
Crown width	Not significant	Not significant	--	0.56	0.58
Total height	Not significant	Not significant	0.52	--	0.80
Diameter	Not significant	5.74e-3	0.53	0.82	--

Table 1: phenotypic and clonal correlations among the traits investigated $\alpha = 0.05$.



Results

The repeatability for the traits measured were high. Branch angle and crown width both had an r value of 1.00, total height was 0.70, diameter was 0.74, and specific leaf area was 0.47. For phenotypic and clonal correlations among the traits investigated, there were significant r^2 values at $\alpha = 0.05$ [Table 1].

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