GENETIC CONTROL OF GROWTH AND SHOOT PHENOLOGY IN LOBLOLLY PINE (*PINUS TAEDA* L.) CLONAL TRIALS DURING THE SECOND AND SIXTH GROWING SEASONS

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Pine genetic improvement programs in the Southeast United States have resulted in the development of loblolly pine material with increased yield and disease resistance (Li et al., 1999). Most traits of interest are related to growth, wood properties or disease resistance and are usually multigenic. In addition, growth and crown traits have been very well characterized in loblolly pine and their genetic architecture is well known (Baltunis et al., 2006; Emhart et al., 2007; Hodge and White, 1992). In contrast, the genetic architecture of phenology traits is less well known, despite the increased interest in forestry research, particularly in anticipation of changes in global climate patterns (Hanninen and Tanino, 2011). There is evidence that growth phenology traits are under genetic control (Jayawickrama et al., 1998), but these have not been well characterized. In this study, we compare second-year growth and phenological traits from two loblolly pine sites from a clonal study consisting of 71 full-sib families, including some high-performing elite genotypes, and we estimate their genetic correlations with sixth-year growth measurements.

MATERIAL AND METHODS

Measurements of growth and phenological traits were taken from two populations of 71 full-sib families obtained from crosses among 36 selected parents and located in Palatka, Florida and Cuthbert, Georgia. The crosses were obtained using a circular mating design and consisted of rooted cuttings and seedlings from each family planted in a randomized incomplete block design with four replications. Growth and flush measurements from both sites consisted of total height at years 2 and 6, average crown width at year 6, diameter at year 6, number, average and sum of flush lengths at year 2, as well as number of stem units (NSU) and mean stem unit length (MSUL) at year 2. Phenology traits measured at the Palatka site at year 2 were: growth initiation, cessation, duration and rate, whereas only cessation was recorded during the second growth season in the Cuthbert site.

Broad-sense and narrow-sense heritability estimates were obtained for cuttings and seedlings for all traits in both sites and growing seasons. Genetic correlations were estimated among all traits within a site as well as across sites (type B correlations).

RESULTS AND DISCUSSION

Measurements for growth, flush descriptors and phenological traits were obtained for 3472 cuttings and 928 seedlings at the Cuthbert site, and for 3656 cuttings and 824 seedlings at the Palatka site. The mean heights observed during the second (2.24-3.27 m) and sixth-year (6.5-
8.4) measurements in Palatka and Cuthbert were similar to those previously reported, whereas mean crown width and diameter ranges between 1.41 and 1.98 m and 10.1 and 13.5

cm, respectively. Mean flush lengths were 36.9 cm in Cuthbert and 24.9 cm in Palatka (Figure 1), whereas the number of flushes remained fairly constant between the two sites (5.39 and 5.35 for Cuthbert and Palatka, respectively, suggesting that differences observed in height were mainly due to flush length and not number of flushes. Higher values for growth traits in Cuthbert with respect to Palatka may be due to more favorable growth conditions in Cuthbert for loblolly pine cuttings and seedlings, as both sites have different soil types and environmental conditions (Parisi, 2006).

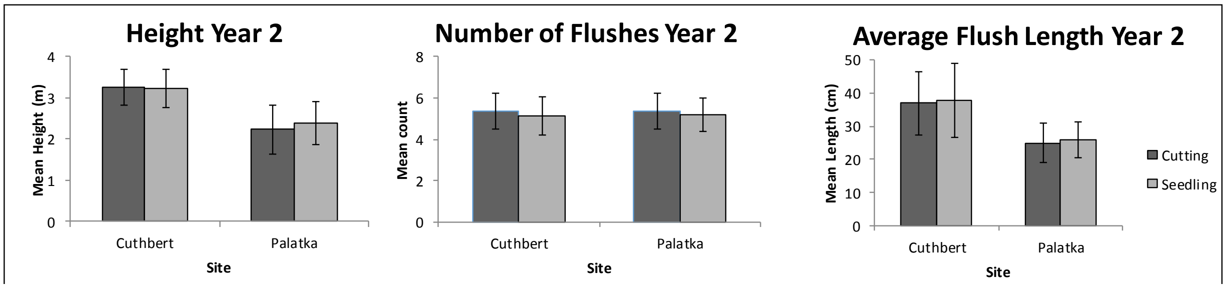

Figure 1. Mean height, number of flushes and average flush length in the second growth season for cuttings and seedlings in Palatka, FL and Cuthbert, GA. Error bars correspond to standard deviations from the mean.

Heritability estimates in cuttings from both sites were moderate to high for most growth and flush traits, with broad-sense heritabilities ranging between 0.35 and 0.68 in Cuthbert and 0.27 and 0.52 in Palatka. These estimates are consistent with those from previous reports in loblolly pine and other conifers (Hodge and White, 1992) and are suggestive of strong genetic control. For phenology traits, cessation showed the lowest heritability in both populations, with 0.0025 and 0.078 in Cuthbert and Palatka, respectively (Table 1), suggesting that there is a strong environmental influence for this trait, whereas shoot initiation is likely to be more under genetic control.

Table 1. Broad-sense heritabilities for different growth, flush and phenological traits in loblolly pine cuttings during the second and sixth growth seasons for the Cuthbert and Palatka sites. Numbers in parenthesis correspond to standard errors.

Site	Height year 2	Height year 6	Crown Width year 2	DBH year 6	Number Flush year 2	logAvFL year 2	Sum FL year 2	MSUL year 2	NSU year 2	Initiation year 2	Duration year 2	Cessation year 2	Growth Rate year 2
Cuthbert	0.68 (0.17)	0.35 (0.11)	0.67 (0.17)	0.53 (0.15)	0.49 (0.15)	0.39 (0.12)	0.49 (0.15)	0.37 (0.11)	0.27 (0.09)	-	-	0.0025 (0.0048)	-
Palatka	0.32 (0.088)	0.52 (0.047)	0.27 (0.078)	0.45 (0.12)	0.43 (0.12)	0.31 (0.97)	0.36 (0.07)	0.21 (0.076)	0.17 (0.062)	0.74 (0.17)	0.19 (0.058)	0.078 (0.028)	0.34 (0.046)

Strong genetic correlations (r>0.6) were observed in cuttings for a given site between second year growth traits (height, diameter and sum of flush length) and sixth year height and diameter in Palatka. Correlations were slightly lower in the Cuthbert site. This suggests that such traits could be potentially important for early selection of material in breeding programs. Type B genetic correlations were also high (r>0.64) between Palatka and Cuthbert for a given trait. The high correlations suggest low genetic by environment (G x E) interactions and could represent an advantage for deployment in these two sites, as the material may likely have a similar performance in these locations.

Even though much is known on the genetic architecture of growth traits in loblolly pine, much less is known on shoot phenology. In this study, genetic analysis of shoot phenology in the Palatka site showed that most phenology traits have moderate to strong heritability values, and are thus likely to be under strong genetic control, with the exception of cessation, which showed very low heritability, and is therefore more likely to be under strong environmental influence. Phenology traits and their relationship to growth are useful for understanding how the timing of growth events is affected in different environments. Further knowledge on these relationships can be useful for modeling tree growth in new sites or under different environmental conditions, particularly as global climate is predicted to continue changing in the near future.

Acknowledgments: Funding was provided by the Forest Biology Research Cooperative (FBRC) the Cooperative Forest Genetic Research Program (CFGRP), the Fullbright-Bunge&Born fellowship and the National Institute of Agriculture Technology (INTA) of Argentina (L.M.P). Additional support was provided by Greg Powell and Fabian Hergenreder for taking measurements during the second growth season; and by Plum Creek Timber Company and Mead Westvaco Corporation for providing the measurements from the sixth growth season, as well as the land and general management for the study sites in Palatka and Cuthbert, respectively.

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