

## ABSTRACT

NORMAN, TRAVIS BRYAN. Impacts on Growth and Quality of Interplanting Loblolly Pine (*Pinus taeda* L.) Seedlings with Clonal Material in the Lower Coastal Plain of North Carolina. (Under the direction of Dr. Bronson P. Bullock.)

Improving the crop-tree potential through the appropriate selection of genetic material along with appropriate silvicultural treatments is essential in increasing the dollar value of plantations. Planting genetically superior clonal varieties with accelerated growth rates and improved timber quality is a potential way to increase the value of plantation forests. However, regenerating with clonal loblolly pine is an expensive investment. One way to reduce the initial investment in regeneration costs while also increasing the potential future dollar value of the stand could be by interplanting loblolly pine clonal varieties with other less genetically superior and less expensive loblolly pine seedlings. By combining these different levels of improved genetics, the clonal varieties can be retained throughout the rotation of the plantation so they will grow to be the more valuable crop-tree trees, while the other genetic stock can be removed during thinnings. The objective of this study is to compare the composition of stands planted as pure clonal blocks to stands interplanted with a mixture of clonal varieties and open-pollinated planting stock.

Survival on both the dry and wet sites was high, but the site productivity differences were very different. In the analysis of the interplanted treatments, the average DBH, total height, and stem volume was significantly different between the two site locations. The average DBH and the predicted outside bark volume was also significantly different at the genotypic level. Overall, when just considering size and volume, the non-clonal genetics outperformed the clonal genetics. To take size and quality into account, crop-tree analysis

was conducted. The average number of clone trees per bed that were considered as potential crop-trees were too low for an interplanting operation to be considered successful, and could not be considered as a feasible investment. In the analysis between the two clonal genetic entries, the differences in average diameter-at-breast-height (DBH), total height, and predicted total outside bark volume (OBV) were significant between site locations. The interaction between site location and clonal genetic entry was also significantly different for all three growth characteristics. There was also a significant difference in DBH between the two clonal genotypes. Based on the results of this research, the non-clonal genetic material was bigger and had better stem quality than the clonal genetic material. Therefore, the additional investment associated with interplanting with these clonal varieties would not be worthwhile.

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Impacts on Growth and Quality of Interplanting Loblolly Pine (*Pinus taeda* L.) Seedlings  
with Clonal Material in the Lower Coastal Plain of North Carolina

by  
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# CHAPTER 1. GENERAL INTRODUCTION

## *Loblolly Pine Genetic Deployment Options*

Loblolly pine (*Pinus taeda* L.) seedlings are planted on over 1 million acres every year (McKeand et al., 2003), and virtually all of the seedlings that are deployed have been genetically improved through the work and efforts of the tree improvement programs in the Southern United States (McKeand et al., 2006). The genetic improvement of trees began in the 1950's when tree breeders and forest product companies collaborated in an effort to produce trees with faster growth along with improved form, and disease and pest resistance. This collaboration and effort resulted in improved growth rates and therefore volume gains, increased rust resistance, and improved wood quality in loblolly pine. It is estimated that improved trees that are planted today are between 10 to 30 percent more productive when compared to unimproved trees (McKeand et al., 2003). It has been estimated that plantation values could increase as high as 30 to 50 percent for open-pollinated families, 40 to 60 percent for full-sib families, and even greater than 60 percent for a tested clone assuming that the appropriate silvicultural techniques are employed (McKeand et al., 2006).

There is a wide variety of seedling genotypes available that are produced by nurseries. This variety of commonly used genotypes includes seed orchard mix families (SOM); single, well-tested open-pollinated (OP) families; single full-sib (FS) families; and single, well-tested clones that are created through vegetative propagation techniques, such as rooted cuttings and somatic embryogenesis (McKeand et al., 2006). Each of these genotypes have differing levels

of genetic homogeneity, with SOM seedlings having the least and the clones having the greatest genetic homogeneity. This variation in genetic homogeneity allows landowners and forest managers to weigh the positive and negative attributes of planting less genetically diverse, yet potentially more productive material (Bridgwater et al., 2005).

Traditionally, seed orchard mixes accounted for the majority of pine plantations in the Southern United States. But, in recent years, the deployment strategy has shifted to specific open-pollinated families which have been planted extensively. In 2002, open-pollinated families accounted for 59 percent of all loblolly pine plantations (McKeand et al., 2006). However, full-sib and clonal deployments have also been increasing across the South. Therefore, with this change in deployment strategies, the potential productivity per acre has increased, due to the increased growth (volume) on the same amount of area. With the increased production potential there is also a decrease in the genetic diversity of the landscape, this decrease in genetic diversity presents the issue of having a higher potential risk to landowners. The risks that are associated with decreased genetic diversity include native and exotic invasive forest pests that tend to prefer large even-age forests. According to Waring and O'Hara (2005), landscapes consisting of stands that are similar in size and age are more susceptible to damage from a particular pest than if the landscape were comprised of stands and forests that vary in size and age classes. The potential implications and risks associated with large landscapes with limited genetic diversity will continue to be an important issue. Although, with the experiences to present, the risk from narrowing the genetic base in plantations has been minimal (McKeand et al., 2003).

With loblolly pine beginning its fourth generation of tree improvement, landowners and forest managers have more options available now than ever before when they want to consider planting or reforesting with loblolly pine. Due to the increased gains in productivity, improved quality, and disease and pest resistance, stands are now more productive and have higher quality crop-trees. Since there is a large amount of genetic variation in growth and adaptability remaining within the species, loblolly pine tree breeding will continue to produce significant improvements in the future generations of selections (McKeand et al., 2003).

### *Loblolly Pine Tree Improvement*

Tree improvement refers to the application of forest genetics principles within a given silvicultural system for the purpose of improving the genetic quality of the forest, and the goal of tree improvement is to enhance the genetic value of the population while also maintaining genetic diversity (Williams, 2010). Historically, foresters did not view trees as typical plants having systems of heredity similar to all other organisms. Genetic variability was ignored, and it was somehow felt that a tree's development depended almost entirely on the environment in which it was grown. Only within the past 60 years has there been a general recognition that tree parentage is important and that changes and improvements in tree growth and quality can be made through breeding and parental control (Zobel & Talbert, 1984).

When loblolly pine breeding programs were becoming established in the 1950's, the breeding programs were initiated with large numbers of selections from wild stands and

unimproved plantations (White, 1992). From the beginning of the tree improvement programs in the South, the focus has been on selecting, breeding, testing, and planting trees that provide landowners and land managers with the greatest return on their investments (Zobel, 2005). Practically all of the nearly 1 billion loblolly pine seedling that are currently planted annually come from tree improvement programs (McKeand et al., 2006).

The southern United States has been referred to as having become the “wood basket” of the United States (Wear & Greis, 2002). The agrarian culture, available land, favorable political and social attitudes towards production forestry, productive soils, and a moderate climate are all favorable attributes for the advancement of plantation forestry in the South (Allen et al., 2005). The South became the “wood basket” of the United States, between 1953 and 1997, because the South’s timber production more than doubled (McKeand et al., 2003). The Southern region of the U.S. now produces more timber than any other country in the world. Today, foresters in the Southern United States are responsible for more than 75 percent of the nation’s tree planting and more than 95 percent of the seedlings are genetically improved loblolly and slash pine (McKeand et al., 2007). The significant increase in the South’s timber production over the years can be attributed to the advances in silvicultural techniques and technology and forest tree improvement. There are many ways to evaluate the investments in southern tree improvement (e.g. Porterfield et al. 1975; van Buijtenen 1984; Talbert et al. 1985; McKeand et al. 2006). At present, every analysis that has been conducted concludes that the returns on the investment in breeding and planting genetically improved loblolly pine are very high (McKeand et al., 2007).

### *Silviculture in the Southeast Coastal Plain*

Silviculture is defined as the practice of controlling the establishment, growth, composition, health, and quality of a forest to meet diverse needs and values (Nyland, 2002). Throughout the South, silvicultural techniques can vary considerably depending on the intensity of management that the landowner wants to pursue on their land. Generally, silvicultural practices consist of site preparation, competitive vegetation management, thinning regimes, and stand fertilization. Furthermore, silviculture systems are not just vital for maintaining healthy stands of trees, but the choice of silvicultural inputs also plays an integral part in the quality of the trees at the time of harvest.

Land owners in the Lower Coastal Plain are confronted with a host of problems that forest and land managers in other physiographic regions do not encounter (Fox et al., 2007). In the lower coastal plain, poorly drained soils are predominant across a majority of the landscape. In addition to the concerns of controlling vast amounts of competing vegetation, the seasonal water tables can be high and are sometimes at or very near the soil surface. Therefore, as a result, survival and growth of planted seedlings can be very poor (Fox et al., 2007). In order to help lower the water table and increase drainage, many areas in the South were ditched and drained. In fact, the first large-scale drainage project for forestry in the Southern United States was on the Hofmann Forest in eastern North Carolina in the 1930s (Fox et al., 2007). By the 1950s, it was evident that substantial increases in survival and growth rates of pine stands located on naturally wet soil were a direct result of removing the excess water from these sites (Schlaudt 1955, Miller and Maki 1957, Maki 1960).

Significantly large growth responses were reported in several studies, ranging from 80 percent to 1,300 percent as a result of the drainage of excess water (Terry and Hughes, 1975). This increased growth response, as a result from draining the excess water from forest stands, led to the widespread drainage of many forested wetlands in the Atlantic and Gulf Coastal Plain, in the 1960s and 70s (Fox et al., 2007).

Even though drainage ditches significantly lower the water table, the reduced evapotranspiration rates in young plantations allows for extended periods of time where the soils were saturated during the winter months, which led to decreased seedling survival and growth (Burton, 1971). McKee and Shoulders (1970) found that by creating an elevated microtopography and improving soil aeration, seedling growth was dramatically increased. As a result, foresters began bedding sites using fire plows that were modified to produce a raised planting site for seedlings (Bethume 1963, Smith 1966). Bedding became the standard site preparation practice to be used on poorly drained soils (Fox et al., 2007).

The control of competing vegetation in a pine plantation is fundamental to ensure high levels of survival and vigorous trees. In the lower coastal plain, hardwood and herbaceous vegetation will strongly compete with young seedlings. Therefore, the control of the competing vegetation can lead to significant gains in the species of interest. By controlling the amount of hardwood competition, the growth of pine trees can increase by more than 100% (Burkhart and Sprinz, 1984). In order to effectively control competing vegetation, there are a wide variety of mechanical and chemical methods that can be used. Some commonly used mechanical methods include roller-drum chopping, prescribed burning, shearing, and disking (Fox et al., 2007). One of the commonly prescribed

silvicultural techniques in eastern North Carolina is to apply herbicides several months prior to planting seedlings. Usually, a mixture of imazapyr and sulfometuron methyl is sprayed during the late summer, which will kill the existing vegetation and prevent any seedlings from germinating.

In the Lower Coastal Plain, poorly drained Ultisol soils are very common, and are generally considered to be phosphorous deficient. Even though drainage will substantially improve uniformity and site quality, these phosphorous deficient soils in the Lower Coastal Plain will hinder the survival and growth of young seedlings. There are several studies that have concluded that phosphorous or phosphorous and nitrogen fertilization mixtures resulted in significant growth responses (Pritchett et al. 1961, Gent et al. 1986, Jokela et al. 1991, Jokela and Stearns-Smith 1993). Fox et al. (2004) also observed that fertilization with phosphorous and nitrogen on poorly drained soil types resulted in significantly increased tree height and overall volume growth by as much as 25 percent. Given that such gains were observed as a result of fertilization, phosphorous and nitrogen fertilization prior to stand establishment has become a very common silvicultural prescription in the Lower Coastal Plain. Diammonium phosphate (18-46-0) applied at 200 pounds per acre is a commonly used fertilization regime before stand establishment.

It has been well documented and observed that thinning significantly affects the size and quality of loblolly pine at time of harvest (Burkhart and Bredenkamp 1989). The bole volume of individual trees will be larger in stands that have been thinned when compared to stands that have not been thinned (Baldwin, et al., 2000). The spacing between trees also has a significant effect on the stem quality of loblolly pine at the time of harvest. Plantations that

were planted at the widest spacing had greater branch biomass, branch diameters, longer crown lengths, and lower overall stem quality than the plantations planted at higher densities (Baldwin et al., 2000).

### *Hypothesis and Objectives*

Somatic embryogenic seedlings are presumably faster growing and have better growth and quality characteristics, but they are much more expensive than full-sib and half-sib genetics. With somatic embryogenic seedling costing up to \$500 per thousand, regenerating in a monoclonal stand represents a very significant cost. Therefore, many land managers decide to plant different genetic material to avoid higher regeneration costs, thereby missing the opportunity of having a higher return at the end of the rotation. However, there are some possible solutions to this problem. One potential way that land managers could take advantage of the potential benefits of using somatic embryogenic seedlings while also decreasing their initial investment in regeneration costs could be by interplanting somatic embryogenic loblolly pine seedlings, with other less genetically superior and less expensive loblolly pine seedlings. By interplanting these different levels of improved genetics, the clonal varieties can be retained throughout the rotation of the plantation so they can grow to be more valuable crop-trees trees, while the other genetic stock can be removed during thinning operations.

It was very important that the design of this study should follow local forest management practices that are common in the Coastal Plain of North Carolina. Therefore, the study was planted at a density of 436 trees per acre (TPA). With the clonal genetics,

ideally, being kept as the future crop-trees throughout the rotation in the interplanted treatments, the clonal genetics were evenly distributed throughout the plot at a density of 109 TPA. Assuming that all of the clone trees survived and were kept throughout the rotation, the stand density would be evenly distributed throughout the stand.

In this study, the hypotheses of different genotypes planted on different sites are (1) the clonal genetics will outperform the open-pollinated and seed-orchard-mix genetic entries, and (2) in the pure monoclonal blocks, there will be more high quality trees because there are more “good” trees present to compensate for the trees planted on lower quality micro sites within a plot. Based on the hypotheses, the objective of this study is to compare the composition of stands planted as clonal blocks to stands interplanted with a mixture of clonal seedlings and open-pollinated seedlings in loblolly pine.

Both individual-stem and stand-level traits are compared in this study. This study is based on an established set of growth and yield block plots that can be used to research differences in the two planting regimes. Ultimately, the objective of this study is to learn if it is possible to interplant clonal genetics among less superior genetics with the intent of retaining the clonal genetics as crop-trees to the final rotation age of the plantation.

## CHAPTER 2. IMPACTS ON GROWTH AND QUALITY OF INTERPLANTING LOBLOLLY PINE SEEDLINGS WITH CLONAL MATERIAL IN THE LOWER COASTAL PLAIN

### INTRODUCTION

Due to the successful improvement of loblolly pine (*Pinus taeda* L.), it has become a very economically and environmentally important species in the southeastern United States. Loblolly pine is the primary plantation species that is used for economically valuable products such as pulp, paper and sawtimber (Schultz, 1999; Rahmana et al., 2003; Zhou and Buongiorno 2004; Roth et al. 2007; McKeand et al. 2006; Xion et al., 2010; Zhang et al., 2010; Subedi et al., 2012). Over 1 million acres are planted with genetically improved loblolly pine annually, which equates to approximately 904 billion cubic feet of stemwood volume being produced from 1969 to 2007 (McKeand et al., 2012).

Tree improvement programs have been focusing on increasing the value of forest plantations in the southeastern United States for more than 50 years. Due to the fact that intensive timber production is primarily focused on fewer acres of highly managed land, not only increasing the volume, but increasing the value of harvested timber is a high priority for silvicultural improvements. Improvements in stem quality can also be made to further improve economic value. In a study on improving sawtimber production in loblolly pine through genetic improvements, the potential dollar value of loblolly pine was increased by as much as 162% over local checks (Cumbie et al., 2012). Therefore, improving the genetic

sawtimber potential along with silvicultural treatments is essential in increasing the potential dollar value of plantations.

Clonal forestry has the potential to present more uniformity and increased growth that will increase gains in productivity to higher levels (Mullin and Park, 1992; McKeand et al., 2003; Baltunis et al., 2007). The process of somatic embryogenesis (SE) may obtain larger gains when compared to seed orchard technology due to the higher selection intensity and that it captures both additive and non-additive genetic effects (Lstiburek et al., 2006). Therefore, planting a genetically superior seed stock such as clonal loblolly pine has the potential to increase the potential dollar value of plantation forests due to accelerated growth rates and good timber quality. However, clonal loblolly pine seedlings are very expensive relative to the price of other seedlings. The cost of clonal variety seedlings is 5 to 6 times higher than seedlings from open-pollinated families (see <http://www.arborgen.us/uploads/catalog/Digital-Arborgen-catalog.pdf> as an example).

One way to lessen the initial investment in seedlings while also increasing the potential dollar value of the forest stand, would be by interplanting loblolly pine clonal varieties having superior growth and stem form characteristics, with other less genetically superior, and therefore less expensive, loblolly pine seedlings. By mixing these genetics, the clonal varieties can theoretically be retained throughout the rotation of the plantation so they will grow to be the more valuable crop-trees at the end of the rotation, while the other genetic stock can be removed during thinnings.

The objective of the Hofmann Forest Interplanting Study is to compare the composition of stands planted as pure clonal blocks to stands interplanted with a mixture of

clonal seedlings and open-pollinated seedlings in loblolly pine. Both individual-stem and stand-level traits will be compared. This study uses established growth and yield block plots to research any differences in the two planting regimes.

## MATERIALS AND METHODS

### *Study Site and Experimental Design*

The Hofmann Forest Interplanting study was established in February of 2007 and aims to test the efficacy of interplanting highly-selected clonal material with seedlings from a seed orchard mix and an open-pollinated family, in loblolly pine on both the individual stem- and stand-level basis. The genetic entries that were used in this study are representative of very good performing genetics that were commonly planted when the study was established in 2007. As a matter of fact, some of the genetics that were used in this study are still widely planted due to their great performance and quality.

There are two different site locations in this study. The study sites are located on the Hofmann Forest in Onslow and Jones County, North Carolina ( $34^{\circ}52.27'N$ ,  $77^{\circ}17.17'W$  and  $34^{\circ}52.24'N$ ,  $77^{\circ}20.6'W$ ) and are referred to as the “Dry Site” and the “Wet Site” respectively. The dry site is located on Gramp Slocum Road, and the wet site is located on Roper Road. Both site locations were chosen to be used for this study because they are representative of the different types of site conditions that are found on the Hofmann Forest and in the Coastal Plain of North Carolina. The wet site was assumed to be more variable than the dry site, allowing us to better test the performance of clonal varieties in competition

with conventional seedlings. The elevation ranges from near sea level to 111 feet on the forest, however, the study sites are topographically uniform with an average elevation of 45 feet above sea level (Appendix A). Mean annual temperature ranges from 59 to 71°F, and mean annual precipitation ranges from 40 to 55 inches. The soils on the dry site consists of a Pantego mucky loam (fine-loamy, siliceous, semiactive, thermic Umbric Paleaquults) and a Rains fine sandy loam (Fine-loamy, siliceous, semiactive, thermic Typic Paleaquults). The soil on the wet site is a Croatan muck (Loamy, siliceous, dysic, thermic Terric Haplosaprists) (USDA, NRCS available at: <http://websoilsurvey.nrcs.usda.gov/> accessed 02/01/2014). The soils on both sites are considered very poorly drained with a water table very near the surface. Due to the wet soil conditions, both the wet and dry site were previously ditched and drained to remove excess water. The dry site was ditched and drained in 2006, while the wet site was ditched and drained in 2005. The dry site was more extensively ditched than the wet site, allowing the dry site to drain more effectively. Additionally, both sites were bedded to provide the study trees optimum growing conditions. Prior to the establishment of this study, the land use of these sites consisted of natural pine stands.

The Interplanting study consists of 6 total replications, with 3 replications being on a very good quality dry site and the other 3 replications being on a poorer quality and presumably more variable wet site. Each of the replications consists of 3 planting treatments for each of the 2 clones used in this study: 1) pure clonal block, 2) interplanting clonal and seed orchard mix (SOM), and 3) interplanting clonal and open pollinated (OP) seedlings. All of the treatments were planted with an initial density of 436 trees per acre (TPA) at a 5 x 20 ft spacing. In the interplanting treatments, the clones were each planted at an initial density

of 109 TPA (20 x 20 ft) while the SOM and OP seedlings were planted in between the clones (Appendix B). The following genetic entries were planted: two clones (C1, C2), one Seed Orchard Mix (SOM), and one open-pollinated (OP) family. The clonal material used in this study were reported to be top-performing clones and were propagated by somatic embryogenesis by CellFor, Inc. The seed orchard mix seedlings are a Coastal Elite Family Mix from the North Carolina Forest Service that are a mixture of parent trees that were wind pollinated. Finally, the open-pollinated family (assumed to be half-sib) was created by collecting seed from a single, fast-growing selection in an open-pollinated seed orchard. This family has been extensively tested and is widely planted throughout the Lower Coastal Plains of the Southeast.

The design of the Interplanting study was set up as a Randomized Complete Block Design (RCBD) with a 3x2 factorial; the planting regime (pure vs. mixed 1 and mixed 2) is one treatment and the clonal material another (C1 and C2). Each genetic entry and planting regime was randomly assigned within each replication. Each plot consists of 100 trees planted on a 5x20 feet spacing, spanning 5 beds. The design summary is:

- 2 locations (wet and dry site)

- 3 replications within each location

- 3 planting treatments (pure clonal block and 2 interplantings – SOM and OP)

- 2 genetic entries (Clones 1 and 2)

- 100 tree block plots

There are 3,600 trees over all plots, replications, and locations. The total size for each replication is 1.4 acres. The total area for each location is approximately 4.1 acres, with the

whole study being about 8.4 acres. Each research area was clearly labeled with the corners of each replication and each plot labeled with a tag and post. Each planting spot was marked with a pin flag for each of the appropriate genetic entries.

Fertilizer, herbicide applications, and volunteer removal were conducted to promote stand growth and reduce competing vegetation from confounding the results of the study. Prior to planting, both of the sites were fertilized with liquid Diammonium Phosphate in a banded application prior to bedding at elemental rates of 10-35-0 with an application rate of 200 pounds per acre. Both sites were also fertilized with liquid Boron in a banded application prior to bedding with an application rate of 0.51 pounds per acre. In 2005, both sites received an aerial broadcast herbicide treatment with a mixture of 48 ounces per acre of Chopper, 32 ounces per acre of Garlon 4, and 5 quarts per acre of MOS. In the spring of 2007, prior to planting, both study sites received another herbicide treatment with a mixture of 4 ounces per acre of Imazapyr 4SL and 2 ounces per acre of SFM 75. Every other year, volunteer pine and hardwood seedlings were manually removed by student workers. In year six, in order to improve access and further reduce the competing vegetation the an 8-foot wide drum chopper was passed between the beds.

### *Measurements*

Initial measurements (Age 1) were taken in December 2007. The measurements included total height, ground-line diameter, and initial tree survival. The total height and survival were assessed on all experimental trees. In subsequent years at ages 2, 4, and 6, total tree height and diameter-at-breast height (DBH was only taken on trees at least 4.5 feet

tall) and were measured during the dormant season. Diameter-at-breast (DBH) was measured using diameter tapes to the nearest hundredth of an inch. Total height was measured using Haglof Vertex Hypsometers to the nearest one-tenth of a foot. The predicted individual tree volume outside bark was calculated using the equations of Sherril, et al. (2011) from measurements taken in the winter of 2012 at age 6. All of the measurement data were recorded on Dell PDAs. The DBH, total height, and mortality scores at age 6 were recorded during the months of March and early April, before stem elongation began.

### *Survival Assessment*

Mortality assessments were completed during each measuring event. The mortality scale is as follows:

(0) = Dead.

(1) = Stressed/defective.

(2) = Healthy.

It is worth noting that some of the mortality and defects within the study could be attributed to Hurricane Irene in 2011. To insure that the results of the study would not potentially be biased due to mortality, overall percent survival was calculated for each measuring event (years 1, 2, 4, and 6). Percent survival was also calculated and evaluated for both study site locations for each measuring event. Overall, in year 6, 9.8% of the trees in the study were reported as being dead, and 9.9% were reported as being stressed or defective.

## *Estimating Site Quality*

Site quality as measured by site index indicates the productive capacity of a specific area of forest land for a single species or group of species as classified by forest types. The accepted method in the United States for determining forest site quality is on the basis of average total height attained by dominant and co-dominant trees at certain ages, termed site index. Total height is used because it is relatively easy to measure, there is little or no change if the stand is opened by thinning or injury, and it is little affected by stand density (Rolfe et al., 2003). To calculate estimates of site index, the dynamic site model that was developed by Dieguez-Aranda et al. (2006) was used by incorporating the dominant heights from the age 6 data. Dieguez-Aranda et al. defines the site index as the average top height, which is the average height of the dominant and codominant trees (2006). This site index model was chosen due to the fact that it was generated from loblolly pine plantations that were planted with improved genetics, had logical behavior, and showed polymorphism and parsimony (Dieguez-Aranda et al., 2006). The site index at base age 25 was calculated by applying the age 6 dominant/co-dominant heights to a dynamic site model. The equation used was:

$$Y = \frac{85.74 + X_0}{1 + 4474/X_0 t^{-1.107}}, \quad (1)$$

where  $Y$  is the predictor height (feet) at age  $t$ , and  $X_0$  is given by:

$$X_0 = 1/2 \left( Y_0 - 85.74 + \sqrt{(Y_0 - 85.74)^2 + 4 \times 4474 Y_0 t_0^{-1.107}} \right), \quad (2)$$

For estimating site index, the dominant and co-dominant heights were calculated by averaging the heights of all the trees that were ranked in the tallest 50 percent in each replication within each planting treatment on both the wet and dry sites. Again, trees that

were scored as being dead or stressed were excluded from this analysis. On average, trees were taller on the dry site when compared to the tree heights on the wet site. To calculate the overall dominant and co-dominant tree height for each site, all 3 replications on each site were averaged. Site indices were projected to a base age of 25 years for each genetic entry within each planting treatment across both site locations.

### *Crop-tree Assessment*

In the spring of 2013, an assessment was done to evaluate the crop-tree potential in the study trees. By doing a crop-tree potential assessment, quality is taken into account with the size of the trees. Crop-tree potential was scored using a 1 to 4 scale that was very similar to the one used by Cumbie et al. (2012), with one being the best and four being the worst quality. Several factors contributed to the crop-tree potential score, including height, DBH, branch angle, branch diameter, and straightness. The scoring scale is as follows:

- (1) = High-quality crop-tree: no quality defects in the first 1.5 logs (24 ft) of the tree.
- (2) = Crop-tree: minor defects in the first 1.5 logs but still likely to be a crop-tree. Minor defects could include minor sweep (less than 3 in), high forks (above first log or 16 ft), and small ramicorn branches.
- (3) = Pulpwood: defects present such as low forks, major ramicorn branches, large branches in the crown greater than 2.5 inches, branch angles over 45 degrees, below average volume, sweep greater than 3 inches.
- (4) = non-merchantable/non-crop-tree: multiple major stem defects such as stem rust, forking, poor branching characteristics, or extremely poor growth.

Any trees that were scored as being a 1 or 2 could be retained for the entire rotation as crop-trees, while any trees that received a score of 3 or 4 would ideally be removed in thinning operations.

After collecting the crop-tree assessment data, the overall scoring proportions were calculated for each genetic entry across all planting treatments and both study site locations in order to discern the quality of each of the genetic entries on each study site location. The percentage of average total number of clones that were scored as crop-trees within each interplanting treatment was also calculated across both study site locations.

A top 5 and top 10 ranking assessment was also conducted. This ranking assessment calculated the average frequency of clonal crop-trees per bed that were among the largest 5 and largest 10 crop-trees per bed (out of a total of 20 trees per bed per plot), with respect to DBH, total height, predicted total volume, and crop-tree score across all interplanting treatments within each study site location. These frequencies were then analyzed to determine if the average clonal frequencies per bed were significantly different from 5, being that there are 5 clone trees planted in each bed of the interplanting treatments (Appendix B). This crop-tree ranking analysis takes both size and quality of each tree into consideration, and will help determine whether or not interplanting clonal genetic material with non-clonal genetic material can be implemented successfully.

### *Statistical Analysis*

Prior to conducting any of the following analyses, all of the collected data were examined for errors and distributions via exploratory data analysis. Also, any study trees that were scored as being dead or stressed were removed from the analysis. In the mixed treatment analysis and clonal analysis, all calculations and significance tests were conducted in PROC GLM (SAS/STAT software v 9.3, SAS Institute, Inc.) using a significance level (alpha-level) of 0.05 as a determination of significance. In the crop-tree analysis, all significance tests were conducted in PROC UNIVARIATE (SAS/STAT software v 9.3, SAS Institute, Inc.), using a significance level (alpha-level) of 0.05 as a determination of significance. Coefficients of variation (CVs) were calculated at the plot level and across all genetic entries and planting treatments using SAS analytical software. Given that there are several different analyses being conducted in this study, it was acknowledged that multiplicity could be a potential source of error.

### *Interplanting Treatment Analysis*

The ANOVA for the mixed treatment analysis was used to test the DBH, total height, predicted total volume, and the coefficient of variation of each of the three growth characteristics of both clonal varieties with the open-pollinated family and seed orchard mix genetics within each planting treatment across both sites. For this analysis the pure clonal blocks were dropped from the analysis. After conducting this ANOVA analysis, differences

of least square means were also calculated in order to determine any significant pairwise comparisons. The linear model for this analysis was:

$$Y_{ijklm} = \mu + \alpha_i + \beta(\alpha)_{j(i)} + \gamma_k + (\alpha\gamma)_{ik} + (\beta(\alpha)\gamma)_{j(i)k} + \delta_l + (\alpha\delta)_{il} + (\gamma\delta)_{kl} + (\alpha\gamma\delta)_{ikl} + (\beta(\alpha)\delta)_{j(i)l} + (\beta(\alpha)\gamma\delta)_{j(i)kl} + \varepsilon_{ijklm} \quad (3)$$

Where  $Y_{ijklm}$  is the observed total volume, total height, or DBH;  $\alpha_i$  is the main effect of the  $i^{th}$  site ( $i = 1, 2$ );  $\beta(\alpha)_{j(i)}$  is the nested effect of  $j^{th}$  replication within the  $i^{th}$  site;  $\gamma_k$  is the main effect of the  $k^{th}$  clonal variety;  $(\alpha\gamma)_{ik}$  is the interaction between the  $i^{th}$  site and the  $k^{th}$  clonal variety;  $(\beta(\alpha)\gamma)_{j(i)k}$  is the interaction between the nested effect of the  $j^{th}$  replication within the  $i^{th}$  site and the  $k^{th}$  clonal variety;  $\delta_l$  is the main effect of the  $l^{th}$  planting treatment;  $(\alpha\delta)_{il}$  is the interaction between the  $i^{th}$  site and the  $l^{th}$  planting treatment;  $(\gamma\delta)_{kl}$  is the interaction between the  $k^{th}$  clonal variety and the  $l^{th}$  planting treatment;  $(\alpha\gamma\delta)_{ikl}$  is the interaction between the  $i^{th}$  site, the  $k^{th}$  clonal variety, and the  $l^{th}$  planting treatment;  $(\beta(\alpha)\delta)_{j(i)l}$  is the interaction between the nested effect of the  $j^{th}$  replication within the  $i^{th}$  site and the  $l^{th}$  planting treatment; and  $\varepsilon_{ijklm}$  is the random error associated with the model and is assumed to be distributed  $N(0, \sigma^2)$ .

### *Clonal Analysis*

The ANOVA for the clonal analysis was used to test the DBH, total height, total volume, and the coefficient of variation for each of the three growth characteristics of just the two clonal varieties across the pure and mixed treatments on each site. After conducting this

ANOVA analysis, differences of least square means were also calculated in order to determine any significant pairwise comparisons. The linear model was:

$$Y_{ijklm} = \mu + \alpha_i + \beta(\alpha)_{j(i)} + \gamma_k + (\alpha\gamma)_{ik} + (\beta(\alpha)\gamma)_{j(i)k} + \delta_l + (\alpha\delta)_{il} + (\gamma\delta)_{kl} + (\alpha\gamma\delta)_{ikl} + (\beta(\alpha)\delta)_{j(i)l} + (\beta(\alpha)\gamma\delta)_{j(i)kl} + \varepsilon_{ijklm} \quad (4)$$

Where  $Y_{ijklm}$  is the observed total volume, total height, or DBH;  $\alpha_i$  is the main effect of the  $i^{th}$  site ( $i = 1, 2$ );  $\beta(\alpha)_{j(i)}$  is the nested effect of  $j^{th}$  replication within the  $i^{th}$  site;  $\gamma_k$  is the main effect of the  $k^{th}$  clonal variety;  $(\alpha\gamma)_{ik}$  is the interaction between the  $i^{th}$  site and the  $k^{th}$  clonal variety;  $(\beta(\alpha)\gamma)_{j(i)k}$  is the interaction between the nested effect of the  $j^{th}$  replication within the  $i^{th}$  site and the  $k^{th}$  clonal variety;  $\delta_l$  is the main effect of the  $l^{th}$  planting treatment;  $(\alpha\delta)_{il}$  is the interaction between the  $i^{th}$  site and the  $l^{th}$  planting treatment;  $(\gamma\delta)_{kl}$  is the interaction between the  $k^{th}$  clonal variety and the  $l^{th}$  planting treatment;  $(\alpha\gamma\delta)_{ikl}$  is the interaction between the  $i^{th}$  site, the  $k^{th}$  clonal variety, and the  $l^{th}$  planting treatment;  $(\beta(\alpha)\delta)_{j(i)l}$  is the interaction between the nested effect of the  $j^{th}$  replication within the  $i^{th}$  site and the  $l^{th}$  planting treatment; and  $\varepsilon_{ijklm}$  is the random error associated with the model and is assumed to be distributed  $N(0, \sigma^2)$ .

#### *Variability between planting treatments*

In forestry, stand uniformity is highly desirable from a management and quality perspective. Therefore, measures of variability such as coefficients of variation ( $CV = \frac{S}{\bar{x}}$ ), are an important way for foresters to determine if there are significant amounts of variability within a stand. So, another ANOVA analysis was conducted to test for significant

differences in the coefficient of variation in DBH, total height, and predicted total outside bark volume between the 6 planting treatments across both study site locations. The linear model for this analysis was:

$$Y_{ijklm} = \mu + \alpha_i + \beta(\alpha)_{j(i)} + \gamma_k + \delta_l + (\gamma\delta)_{kl} + \varepsilon_{ijklm} \quad (5)$$

Where  $Y_{ijklm}$  is the CV for predicted total volume, total height, or DBH;  $\alpha_i$  is the main effect of the  $i^{th}$  site ( $i = 1, 2$ );  $\beta(\alpha)_{j(i)}$  is the nested effect of  $j^{th}$  replication within the  $i^{th}$  site;  $\gamma_k$  is the main effect of the  $k^{th}$  clonal variety;  $\delta_l$  is the main effect of the  $l^{th}$  planting treatment;  $(\gamma\delta)_{kl}$  is the interaction between the  $k^{th}$  clonal variety and the  $l^{th}$  planting treatment; and  $\varepsilon_{ijklm}$  is the random error associated with the model and is assumed to be distributed  $N(0, \sigma^2)$ .

#### *Crop-tree analysis*

As mentioned above, for the crop-tree analysis, a top 5 and top 10 ranking assessment was conducted using the crop-tree scores that were collected during measurements (out of a possible 20 per bed). This ranking assessment calculated the frequency of clonal crop-trees per bed that were among the largest 5 and largest 10 crop-trees per bed, with respect to DBH, total height, predicted total volume, and crop-tree score across all interplanting treatments within each study site location. These frequencies were then analyzed to determine if the average clonal frequencies per bed were significantly different from 5, being that there are 5 clone trees planted in each bed of the interplanting treatments (Appendix B). All significance tests were conducted using PROC UNIVARIATE (SAS/STAT software v 9.3, SAS Institute, Inc.), using a significance level (alpha-level) of 0.05 as a determination of

significance. By using this analysis, it can be determined if the average number of clonal crop-tree per bed, with respect to the three growth characteristics and quality, are significantly different than 5.

## RESULTS

### *Summary Statistics*

At age 6, across both study site locations, the average DBH, total height, and predicted volume of the trees were 5.34 inches in diameter, 28.0 feet in height, and 2.24 cubic feet in volume (Appendix C, Table 1). The average DBH, total height, and predicted volume on the dry site was greater than on the wet site. The average DBH, total height, and predicted volume for the dry site were as follows; 5.6 inches, 29.6 feet, and 2.49 cubic feet. While the average DBH, total height, and predicted volume for the wet site were as follows; 5.03 inches, 26.0 feet, and 1.93 cubic feet (Appendix C, Table 2).

Overall, survival at age 6 years was 90.2% across both the wet and dry sites (Appendix D, Figure 1). This was approximately 7 percent lower than the year 1 survival of 97.1%. However, it is evident that there is lower survival rates on the wet site when compared to the dry site. In year 6, the survival on the wet site had decreased to 83.5% from 95.5% in year 1 (Appendix D, Figure 2). But, higher mortality rates were expected for the wet site due to the fact that it is more poorly drained. In comparison, the survival rate of the dry site only decreased from 98.6% in year 1 to 96.9% in year 6 (Appendix D, Figure 2).

Site productivity was estimated by projecting the average dominant and codominant heights to the base age of 25. Overall, site productivity was significantly different between the dry and wet sites at age 6, with the dry site having a higher average site index than the wet site. On the dry site, Clone 2 was taller than all the other families across all treatments on average (Appendix C, Table 3). As a result, the site index for Clone 2 is projected higher than the other genotypic families with average site indices of 99.6 feet in the open-pollinated treatment, 100.1 feet in the pure clonal treatment, and 99.5 feet in the seed-orchard-mix treatment (Appendix E, Figure 1). The open-pollinated genetic entry had the second highest average site index of 98 feet, while Clone 1 and the seed-orchard-mix had the third and fourth highest average site index respectively. Clone 2 had a slightly higher average projected site index in the pure clonal treatment when compared to its respective interplanting treatments. However, Clone 1 had a higher average projected site index in the interplanting treatments. Overall, all the genotypes were very productive on the dry site, as site index at age 25 was greater than 90 feet for all families (Appendix E, Figure 1).

On the wet site, the site index was significantly lower than the dry site across all genetic entries. Interestingly, Clone 1 had the highest average site index across all interplanting and pure clonal treatments with average site indices of 93.2 feet in the open-pollinated treatment, 92.5 feet in the pure clonal treatment, and 89.5 feet in the seed-orchard-mix treatment (Appendix E, Figure 2). The open-pollinated genetic entry, again, had the second highest average projected site index, while Clone 2 and the seed-orchard-mix had the third and fourth highest average projected site index respectively. Again, on the dry site, Clone 2 had a higher average projected site index in the pure clonal treatment when

compared to its respective interplanting treatments. Contrary to what was observed on the dry site, Clone 1 had a slightly higher average projected site index in the open-pollinated treatment (93.2 ft) than in the pure clonal treatment (92.5 ft), and the seed-orchard-mix treatment (89.5 ft) (Appendix E, Figure 2). Overall, these genotypes were very productive, as the site index at age 25 was greater than 80 feet for all genetic entries (Appendix E, Figure 2).

### ***Interplanting Analysis***

#### *Effects of interplanting on the DBH, total height, and volume growth between clonal and non-clonal genetic entries*

DBH differed for the main effect of site location ( $P < 0.0001$ ) and the main effect of genetic entry ( $P < 0.0001$ ) (Table 1). Overall, all of the genetic entries on the dry site had larger diameters than what was found on the wet site (Appendix C, Table 3). In the Least Squares Means analysis, the only genetic entries that were not significantly different from each other were the open-pollinated (OP) and seed-orchard-mix (SOM) genetic entries (Appendix F, Table 1). The clonal genetic entries were significantly different ( $P = 0.0122$ ) (Appendix F, Table 1). On the dry site, the average DBH for Clone 2 was larger than the average DBH for Clone 1. Conversely, on the wet site, the average DBH was larger for Clone 1 than Clone 2 (Appendix C, Table 3). The OP genetic entry had a significantly larger average DBH than either of the two clonal genotypes ( $P = 0.0155$ ,  $< 0.0001$ ). The SOM genetic entry also had a significantly larger average DBH than either of the two clonal genotypes ( $P < 0.0001$ ).

For total height of the stem, the test for significance found that the main effects of site location and replication were significant ( $P < 0.0001$ ,  $0.0488$ ) (Table 2). The nested effects of replication within site and replication by treatment within site were significant ( $P = 0.0106$ ,  $P = 0.024$ ). Unlike DBH, total height was not significantly different between individual genetic entries ( $P = 0.0751$ ). Overall, the average total heights across all genetic entries were larger on the dry site when compared to the wet site (Appendix C, Table 3).

In the test for significance for predicted total outside bark volume, the main effects of site location and genetic entry were significant ( $P < 0.0001$ ) (Table 3). The overall average total predicted volume was larger on the dry site when compared to the wet site (Appendix C, Table 3). In the Least Squares Means analysis, Clone 1 and Clone 2, and the OP and SOM genotypic families were not significantly different (Appendix F, Table 2). Although the clonal genetic entries were not significantly different ( $P = 0.0998$ ), Clone 2 had larger average total volumes than Clone 1 on the dry site, and vice versa on the wet site (Appendix C, Table 3). Furthermore, the OP genetic entry had larger average predicted total volumes than the SOM genetic entry, overall. The OP and SOM genetic entry were significantly different from both of the clonal genotypes (Appendix F, Table 2). The overall average predicted total volumes for the OP and SOM genetic entries were larger when compared to the average predicted total volumes for both clonal genotypes (Appendix C, Table 3).

*Effects of interplanting on the variability in DBH, total height, and Volume growth of clonal and non-clonal genetic entries*

In the test for significance for variability between clonal and non-clonal genetic entries, using plot-level CVs, all three growth characteristics had significant differences in variability by study site locations (Tables 4, 5, and 6). Predicted total outside bark volume also had significant differences for the main effect of genetic entry, the interaction between interplanting treatment and genetic entry, and the interaction between replication and treatment within site (Table 6). There were no significant differences in variability between Clone 1 and Clone 2 (Appendix C, Table 4), but there were significant differences in the variability between Clone 1 and Clone 2 in the OP interplanting treatment ( $P=0.0178$ ) (Appendix C, Table 4). Across both site locations, Clone 1 had a lower average coefficient of variation than Clone 2 in the OP interplanting treatments (Appendix C, Table 4). It was also observed that the OP genetic entry had significantly different coefficients of variation than Clone 2 in the OP interplanting treatments ( $P=0.0064$ ), with Clone 2 having more variability than the OP genetic entry. The differences in the coefficients of variation between the SOM genetic entry and Clone 2 in the OP interplanting treatments were also significant ( $P=0.0008$ ) (Appendix C, Table 4). As mentioned earlier, Clone 2 in the OP interplanting treatments were more variable than the SOM genetic entry (Appendix C, Table 4). Overall, the non-clonal genetic entries had less variability than the clonal genetic entries in the interplanting treatments.

### *Crop-tree Assessment and Analysis*

In the analysis of the crop-tree scores, there were large differences between site locations in the number of clonal trees that were scored as being of a high enough overall quality (scored as 1 or 2) to be considered as a potential crop-tree in the future (Appendix G, Figures 1, 2, 3, and 4). Overall, the percentage of trees that were qualified as being a crop-tree were higher on the dry site when compared to the wet site across all genotypes (Appendix G, Figures 3 and 4).

The percentage of the total number of clones that were scored as crop-trees within each of the four interplanting treatments also differed between the two site locations. On the wet site, Clone 1 had the highest frequency of clonal crop-trees in the SOM interplanting treatment (41.8%), whereas Clone 2 had a substantially lower crop-tree frequency in the same interplanting treatment (17.7%) (Appendix G, Figure 2). There was a similar trend found in the OP interplanting treatments, with Clone 1 having a higher crop-tree frequency (30.9%) than Clone 2 (20.8%) (Appendix G, Figure 2). However, on the dry site, Clone 1 exhibited the highest clonal crop-tree frequency in the OP interplanting treatment (44.1%), while Clone 2 had the lowest crop-tree frequency (32.4%) (Appendix G, Figure 1). Similar to the trend found on the wet site, Clone 1 also had a higher crop-tree frequency in the SOM interplanting treatment when compared to Clone 2 (Appendix G, Figure 1). Overall, Clone 1 had higher crop-tree frequencies across all interplanting treatments and site locations.

Figures 1 and 2 illustrate the mean number of clone trees that occur in each bed that were ranked among the top 5 crop-trees with respect to DBH, total height, and predicted total

outside bark volume for each site. On the dry site (Figure 1), there is a higher average frequency of clone trees present in the top 5 crop-trees within each bed than on the wet site (Figure 2). Within the dry and wet sites, the mean frequencies of clone trees per bed appear to perform relatively similarly with respect to each growth characteristic and interplanting treatment. The differences in mean frequencies with respect to each of the growth characteristics is more variable than the mean frequencies observed on the wet site (Figures 1 and 2). The largest average frequency of clonal crop-trees per bed in the top-5 ranking was on the dry site in the SOM-Clone 2 interplanting treatment (2.5) for total height (Figure 1). On the wet site, the largest average frequency of clonal crop-trees per bed in the top-5 ranking was 0.8 in the SOM-Clone 1 and OP-Clone 1 interplanting treatments. In the SOM-Clone 1 interplanting treatment, all three growth characteristics had an average clonal crop-tree frequency per bed of 0.8. While in the OP-Clone 1 interplanting treatment, DBH was the only growth characteristic with a value of 0.8 (Figure 2).

After viewing the average frequencies for the top-5 assessment, the frequencies were analyzed to determine if they were significantly different from 5. In theory, if the clonal genetic entries were the best trees, then the average number of clonal crop-trees per bed would be very close to 5, and would not be significantly different from 5, being that there are 5 clone trees planted in each bed of the interplanting treatments (5 beds per plot). However, for all three growth characteristics across all of the interplanting treatments on both study site locations, all the average frequencies of clonal crop-trees within the top-5 ranking were significantly different from 5 ( $P < 0.0001$ ) (Tables 7, 8, and 9).

The mean number of clone trees that occur in each bed that were ranked among the top 10 crop-trees with respect to DBH, total height, and predicted total outside bark volume for each site was also calculated (Figures 3 and 4). On the dry site, there is a higher average frequency of clone trees that are present in the top 10 crop-trees within each bed than on the wet site. Within each of the two site locations, the average frequencies of clone trees per bed appear to perform relatively similarly with respect to each growth characteristic and interplanting treatment. As observed in the top-5 ranking, the average frequencies with respect to each of the growth characteristics on the dry site is more variable than the average frequencies observed on the wet site (Figures 3 and 4). The largest average frequency of clonal crop-trees per bed in the top-10 ranking was observed on the dry site in the OP-Clone 1 interplanting treatment (3.0) for total height (Figure 3). On the wet site, the largest observed average frequency of clonal crop-trees per bed in the top-10 ranking was 1.0 in the SOM-Clone 1 and OP-Clone 1 interplanting treatments. In both the SOM-Clone 1 and OP-Clone 1 interplanting treatments, all three growth characteristics had the mean value of 1.0 (Figure 4). Again, after viewing the average frequencies for the top-10 ranking assessment, the frequencies were analyzed to determine if they were significantly less than 5. Theoretically, if the clonal genetic entries were the best trees, then the average number of clonal crop-trees per bed would be very close to 5, and would not be significantly different from 5, being that there are 5 clone trees planted in each bed of the interplanting treatments. However, for all three growth characteristics across all of the interplanting treatments on both study site locations, all the average frequencies of clonal crop-trees within the top-10 ranking were still found to be significantly different than 5 ( $P < 0.0001$ ) (Tables 10, 11, and 12).

The proportions of crop-trees within each planting treatment on the dry and wet sites are illustrated in figures 5 and 6 respectively. Again, there were substantial differences in the proportions of crop-trees between the dry and wet site. The wet site (Figure 6) had significantly fewer trees that received a crop-tree score of 1 than what was observed on the dry site across all genetic entries (Figure 5). Overall, Clone 1 had the largest proportion of clonal crop-trees in the OP interplanting treatment, while Clone 2 had the lowest proportion of clonal crop-trees that were in the SOM interplanting treatment on the dry site (Figure 5). Contrarily, Clone 1 had the largest proportion of clonal crop-trees in the SOM interplanting treatment, while Clone 2 had the lowest proportion of clonal crop-trees in the OP interplanting treatment on the wet site (Figure 6). It was interesting to observe the differences in the proportions of Clone 1 and Clone 2 in the pure clonal treatments. In the pure clonal planting treatments on the dry site, the mean number of crop-trees per bed for Clone 1 was higher than Clone 2. However, on the wet site, Clone 2 had a greater mean number of crop-trees per bed than Clone 1.

### ***Clonal Analysis***

#### *Effects of interplanting on the DBH, total height, and volume growth of clonal genetic entries*

At age 6, tests for significance showed that diameter-at-breast height (DBH) were significantly different between the two clonal genotypes, as well as between sites (Table 13). In fact, DBH was the only growth characteristic that was significantly different between the two clones ( $P=0.0315$ ) across the sites. The interaction between the two site locations and

the two clonal genotypes were significantly different for DBH ( $P=0.0323$ ). However, there was no significant interaction between the clonal genotypes that were interplanted with the open-pollinated (OP) and seed-orchard-mix (SOM) families ( $P=.2438$ ). On the dry site, Clone 2 had a slightly higher average DBH than Clone 1 (Appendix C, Table 3).

Conversely, on the wet site, Clone 1 had a higher average DBH than Clone 2 (Appendix C, Table 3). The differences in DBH between the Clone 1 and Clone 2 on the wet and dry sites were all significantly different, except for Clones 1 and 2 on the dry site (Appendix H, Table 1).

There were significant differences in total height between the dry and wet sites ( $P < 0.0001$ ), and for the interaction between the two sites and the two clonal genotypes ( $P = 0.006$ ) (Table 14). Unlike DBH, the total height differences between the two clones were not significant, as was the interaction between the clones and their respective interplanting treatments (Table 14). The differences in total height between Clone 1 and Clone 2 on the wet and dry sites all showed significant differences, except for Clones 1 and 2 on the dry site ( $P=0.0886$ ) (Appendix H, Table 2). On the dry site, Clone 2 had a slightly taller average total height than Clone 1 (Appendix C, Table 3). Although, on the wet site, Clone 1 had a significantly taller average height than Clone 2 ( $P=0.0005$ ).

For the predicted outside bark volume, the test for significance showed that the main effect of site location ( $P < 0.0001$ ), and the interaction between clonal genotypes and site location was significant ( $P=0.0284$ ) (Table 15). The main effect of clonal genotype and the interaction between clonal genotype and interplanting treatment were not significant (Table 15). On the dry site, the average predicted total volume for Clone 2 was slightly larger than

Clone 1 (Appendix C, Table 3). However, the difference in predicted total volume between the clonal genotypes on the dry site was still not significant ( $P=0.3754$ ) (Appendix H, Table 3). On the wet site, Clone 1 had significantly higher average predicted total volume than Clone 2 (Appendix H, Table 3; Appendix C, Table 3). On the wet and dry site, both of the clonal genotypes had greater predicted total volume growth in the pure clonal treatment when compared to the clonal genotypes in the interplanting treatments. Furthermore, the differences in predicted total outside bark volume all proved to be significantly different, except for Clone 1 and 2 on the dry site (Appendix H, Table 3).

#### *Variability in DBH, total height, and volume of clonal genetic entries*

In the tests for significance for variability (using the plot level coefficients of variation) between individual clonal genetic entries, DBH, total height, and predicted total volume were all found to only have significant amounts of variation between site locations (Tables 16, 17, and 18). Overall, all three growth characteristics had greater variability on the wet site when compared to the dry site (Appendix C, Table 4).

In the test for significance for variability between the interplanted and pure clonal planting treatments (using the plot level coefficients of variation), there were no significant differences in variability found between the interplanted treatments and the pure clonal treatments for all three growth characteristics (Tables 19, 20, and 21). Again, there were significant differences in variability found between the two study site locations for all three growth characteristics ( $P<0.0001$ ) (Tables 19, 20, and 21). However, for DBH, there were also significant differences found for the main effect of clonal genetic entry ( $P=0.0393$ ), the

nested effect of replication within site ( $P=0.0004$ ), and the interaction effect of planting treatment by clonal genetic entry ( $P=0.0146$ ) (Table 19). Predicted total volume also had significant differences for the interaction effect of planting treatment by clonal genetic entry ( $P=0.0230$ ) (Table 21).

## DISCUSSION

### *Interplanting Analysis*

#### *Effects of interplanting on the DBH, total height, and volume growth between clonal and non-clonal genetic entries*

Overall, it was interesting, and surprising, that across both site locations, the OP and SOM genetic entries had larger average diameters and total predicted volumes than either of the two clonal genetic entries in the mixed plots. According to our hypothesis, the clonal varieties were expected to be more productive growers than the other genotypic families based on the performance trials that were conducted on these specific clonal genotypes prior to the establishment of this study. On average, both clonal genotypes performed greater in the pure monoclonal planting treatments across all three growth characteristics when compared to the clonal genotypes in the interplanting treatments. In similar studies, this can be explained by the fact that in monoclonal treatments all trees were of equal competitiveness and therefore utilized resources similarly to maximize growth, whereas in the interplanting treatments interactions of genotypes of varied competitiveness resulted in the suppression of the clonal genotypes (Sharma et al., 2008; Stovall et al., 2013). Therefore, being that the OP

and SOM genetic entries grew larger and outcompeted both of the clonal genetic entries in the interplanting treatments, interplanting clonal genetics cannot be justified when using these specific genetic combinations with respect to DBH, total height, and predicted volume growth.

As mentioned earlier, there were significant differences in the main effects of site location and genetic entry ( $P\text{-val}<0.0001$ ) for DBH and total predicted outside bark volume. Total height was also found to be different between site locations ( $P\text{-val}<0.0001$ ). But, it was also found that the effects of replication, replication with site location, and the interaction of replication and planting treatment within site location were significantly different for total height. This suggests that site conditions have a large impact on the overall growth and productivity of trees despite their level of genetic homogeneity. Although total height was not found to be significantly different between individual genetic entries, there is a slight trend between the average DBH and total heights that suggests that the clonal genotypes allocated more growth to total height rather than DBH. This growth trend can be explained due to the reason that many improved genetic stock are selected based on initial height growth to overcome competing vegetation more successfully. It was observed that there was a significant difference in DBH growth between the two clonal genetic entries. According to genetic theory and other studies, clones should be expected to display a higher degree of interaction with the environment than full-sib or half-sib families, due to the fact that there is no genetic variance within a clone (Allard and Bradshaw, 1964; Bridgwater and Stonecypher, 1978).

*Effects of interplanting on the variability in DBH, total height, and Volume growth of clonal and non-clonal genetic entries*

In the analysis between both clonal and non-clonal genotypes, there were also significant differences in variation (as measured by the coefficient of variation) between two site locations across all three growth characteristics. Furthermore, there were significant differences between genetic entries for predicted total outside bark volume. On average, the clonal genotypes exhibited more variation than the OP and SOM families that were planted for this study across all growth characteristics. Variation was substantially higher on the wet site when compared to the dry site, which was to be expected being that the wet site is more variable in terms of site quality.

*Crop-tree Assessment and Analysis*

Overall, the poorer and more variable site conditions of the wet site reduced the potential crop-tree qualities across all genetic entries, and therefore, reduced the quantity of trees that would potentially be retained as future crop-trees at the end of rotation. Other studies have found similar results for differences in crop-trees potential between site locations (Cumbie et al., 2012). This suggests that foresters and land managers should strongly take site quality and site conditions into consideration prior to choosing the appropriate genetic stocks to deploy. As expected, it was observed that the average number of clonal crop-trees per bed were greater in the pure clonal planting treatments than in the interplanting treatments. However, this is due to the fact that there are more clone trees within each bed in the pure clonal planting treatments than in the interplanting treatments,

which means that the probability of having clonal crop-trees is greater in the pure clonal planting treatments.

It was interesting to see how the crop-tree proportions for the clonal genetic entries also differed between site locations. On the dry site, in the pure clonal planting treatments, the slower growing Clone 1 had a larger average total number of crop-trees per bed than, the faster growing, Clone 2. Although, the pure Clone 1 planting treatment had fewer trees that received a potential crop-tree score of 1 than Clone 2 in the pure clonal treatments. Clone 1 also had a larger number of trees that received a potential crop-tree score of 2 (Figure 5). On the wet site, in the pure clonal planting treatments, the slower growing Clone 2 had a greater total number of crop-trees per bed than, the faster growing, Clone 1. But, Clone 2 had fewer trees that received a potential crop-tree score of 1 than in the pure Clone 1 treatment. The pure Clone 2 treatment, however, had more trees that received a crop-tree score of 2 than what was observed in the pure Clone 1 treatment (Figure 6). While this would suggest that some clonal genotypes perform better in different site conditions, it would also suggest that faster growth rates are not always conducive to higher quality potential crop-trees. Other studies have shown that if crop-tree quality is of importance, some of the faster growing genotypes may be less desirable, whereas some genotypes with a slightly slower growth rate have a greater proportion of crop-tree quality trees at age 6 (Cumbie et al., 2012). It is also worth mentioning that, across both site locations, there were more average total clonal crop-trees per bed in the SOM interplanting treatments, with the exception of the OP and Clone 1 interplanting treatment on the dry site. This would suggest that the SOM family used in this

study did not compete as aggressively with the clonal genotypes as the OP family (Figures 5 and 6).

In theory, in the top-5 and top-10 clonal crop-tree rankings per bed, the average number of clonal crop-trees within each bed should be relatively close to 5. However, as observed earlier, the average number of clonal crop-trees within each bed were all significantly less than 5. Therefore, there are far too few clonal crop-trees per bed for an interplanting operation such as this to be considered successful. For example, using the best case scenario that was observed in the SOM and Clone 2 interplanting treatment, only half of the interplanted clones in each bed could potentially be considered as a crop-tree to be retained for the rest of the rotation. With the current cost of clonal seedlings being very high (~\$400 per thousand), to only retain approximately half of the clones within each bed would be a poor investment. Therefore, if value toward higher quality crop-trees is an important objective for a landowner, and based on the overall differences in growth and stem quality between these individual genotypes that has been observed in these interplanting treatments, a landowner should not use interplanting with these genotypes. Furthermore, given the increased cost associated with establishing monoclonal stands, a landowner probably would not use these specific clonal genotypes on these sites. However, the process of landowners being paid for the overall quality, and not just the overall quantity, of timber on their lands is an evolving and complicated challenge. Of the genotypes that were used, and of the site locations that were used in this study, it is clear that the best genotype to plant on better quality sites is the OP genetic entry, which had the best overall volume growth, exceptional crop-tree potential, and excellent survival rates. On lesser quality and more variable sites,

the best genotype to plant was the SOM. Although volume growth and crop-tree potential were found to be second to OP, SOM had a substantially higher survival rate than OP. Regardless of what genotypes one may choose to plant, it is important to emphasize that the best genotypes should be planted on the best sites.

It should be noted that this study included only 4 genotypes, which were, and in some cases still are, among some of the best genotypes available when this study was established in 2007. Yet there are numerous other loblolly pine genetics options available today, some of which may be more productive and of greater stem quality than the genotypes planted in this study. Furthermore, over the past several years, Tree Improvement Cooperatives have developed elite genetic material that was not yet available at the establishment of this study, some of which should best the top genotypes in this study. Additionally, crop-tree potential was assessed during the early spring of age 7, consequently assessments cannot exactly be considered to be true representation of crop-tree quality (Cumbie et al., 2012). Although, it is important to state that tree improvement programs can and do accurately assess other growth and stem traits as early as 4-years-old. With this in mind, it is assumed that assessing crop-tree potential in juvenile stands is a dependable indicator of characteristics at rotation age.

## ***Clonal Analysis***

### *Effects of interplanting on the DBH, total height, and volume growth of clonal genetic entries*

For DBH, the significant difference in the main effect of clonal genotype ( $P\text{-val}=0.0315$ ) and the interaction between site location and clonal genotype ( $P\text{-val}=0.0323$ ) suggests that some clonal varieties of loblolly pine perform better in terms of diameter growth than others. This would also suggest that some clonal varieties, such as Clone 2, perform better on sites with dryer and more uniform site conditions than others, while some clonal varieties, such as Clone 1, may perform better on wetter and more variable sites than others. Similarly, results for clonal genotypes by site location interactions have been found in other studies for loblolly pine (McKeand et al., 2006; Isik et al., 2003). Given the differences observed in site productivity shown earlier, the interaction between the clonal varieties and site location was expected. Due to the fact that there is no genetic variance within a clone, the clones should be expected to display a higher degree of interaction with the environment than the full-sib or half-sib families (Allard and Bradshaw, 1964; Bridgwater and Stonecypher, 1978). The significant main effect of site location, and site location by clonal genotype interaction for total height ( $P\text{-val}=0.006$ ), and predicted total outside bark volume ( $P\text{-val}=0.0284$ ) would, again, suggest that site conditions have very significant effects on the growth and performance of different clonal varieties.

The difference in the two clonal genotypes in crop-tree scores was interesting, especially when compared across the two study locations. Overall, the dry site had significantly more trees that received crop-tree scores of 1 and 2 when compared to the wet

site. On the dry site, both clonal varieties had very similar numbers of trees that received a crop-tree score of 1. However, there were more trees in the Clone 1 genotype that received a crop-tree score of 2 (over 50%) than what was observed for Clone 2 (over 40%). On the wet site, both clonal varieties had similar numbers of trees with a crop-tree score of 1 (under 5%), with Clone 1 having slightly more than Clone 2. But, contrary to what was observed on the dry site, Clone 2 had slightly more trees with a crop-tree score of 2 than Clone 1. This would suggest that, depending on site conditions, some clonal genotypes may grow better and have greater potential crop-tree quality than other clonal genotypes. Furthermore, according to the observed crop-trees score proportions for both of the clonal genotypes, differences in site conditions will have a significant impact on the overall growth and potential economic value of loblolly pine.

#### *Variability in DBH, total height, and Volume of clonal genetic entries*

Variability between individual clonal genetics as measured by coefficients of variation (CVs) was only found to be significant between site locations across all three growth characteristics. This difference in variability between site locations was anticipated due to the very different conditions between the two sites. It was interesting, however, to observe that there was no significant difference in CVs between the two clonal genetic entries across all planting treatments. It was also interesting to observe that, overall, both clonal genetics had lower average CVs in the pure clonal planting treatments than what was observed in the interplanting treatments. In similar studies, it was found that in monoclonal treatments, all trees were of equal competitiveness, and therefore, utilized resources similarly

to maximize growth, whereas in the interplanting treatments interactions of genotypes of varied competitiveness resulted in the suppression of the clonal genotypes (Sharma et al., 2008; Stovall et al., 2013). Because all of the trees competed more evenly with each other and utilized site resources more similarly than in the interplanting treatments, the clonal genotypes in the monoclonal planting treatments tended to grow more uniformly than the clones in the interplanting treatments.

As mentioned previously, there was no significant differences in variability found between the interplanted and pure clonal planting treatments across all three growth characteristics. This suggests that even though there are differing levels of competition in the interplanting treatments, there is still no significant difference in variability between the interplanted treatments and the pure clonal planting treatments with respect to all three growth characteristics. For this analysis, the differences in variability between the two study site locations were significant for all three growth characteristics. This significant difference between the study site locations was expected given the differing levels of site quality. The significant differences found for DBH between the clonal genetic entries implies that one of the clones is more uniform in DBH growth when compared to the other clone. For predicted total volume, the significant differences found in the interaction between planting treatment and clonal genetic entry also implies that the average volume for one of the clones is more uniform in predicted total volume than the other clone across the different planting treatments. It was interesting to observe that the variability in total height growth was only significantly different between the two study site locations. This implies that total height growth was uniform across all genetic entries and planting treatments.

## CONCLUSIONS

At both the stand-level and individual stem-level, we examined the growth and uniformity of genotypes with varying amounts of genetic diversity while also quantifying differences in productivity among four loblolly pine genotypes. We tested two hypotheses; (1) the clonal genetics will outperform the open pollinated and seed-orchard-mix genetic entries, and (2) in the pure monoclonal blocks that were planted, there will be more high quality trees because there are more “good” trees present to compensate for the trees planted on lower quality micro sites within a plot. Based on the results, the OP and SOM genetic entries consistently out competed the clonal genetics across both site locations and with substantial differences in uniformity between site locations. There were no instances where either of the clones were more productive than the other genetic entries. Thus, our results show evidence to reject the first hypothesis that the clonal genetics will outperform the OP and SOM genetic entries.

Our assessment of the crop-tree potential for the pure clonal blocks and the interplanted treatments consistently demonstrated that there were more clonal crop-trees within each bed in the pure clonal blocks than what was observed in the interplanting treatments. Furthermore, there were not enough clonal crop-trees within each bed of the interplanting treatments to be considered worth the additional cost of clonal genetic stocks. Therefore, our results show substantial evidence to support the second hypothesis that in the pure monoclonal blocks that were planted, there will be more high quality trees because there are more “good” trees present to compensate for the trees planted on lower quality micro

sites within a plot. Consequently, we conclude that interplanting with these loblolly pine genetics, on these sites, would not be a worthwhile investment.

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Table 1: F-tests of fixed effects of clonal varieties with open-pollinated and seed orchard mix genetics within each interplanting treatment (OP and SOM) on each site for DBH (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	6.8797	6.8797	97.63	< <b>.0001</b>
Rep	2	0.1200	0.0600	0.80	0.458
Rep(Site)	2	0.0725	0.0363	0.48	0.622
Treatment	1	0.1042	0.1042	1.39	0.248
Site*Treatment	1	0.0136	0.0136	0.18	0.673
Genetic entry	3	5.3408	1.7803	23.71	< <b>.0001</b>
Treatment*Genetic Entry	1	0.0591	0.0591	0.79	0.381
Rep*Treatment(Site)	4	0.5135	0.1284	1.71	0.172
Error	32	2.4027	0.0543		

Table 2: F-tests of fixed effects of clonal varieties with open-pollinated and seed orchard mix genetics within each interplanting treatment (OP and SOM) on each site for total height (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	262.4591	262.4591	116.25	< <b>.0001</b>
Rep	2	15.0115	7.5057	3.32	<b>0.049</b>
Rep(Site)	2	23.7686	11.8843	5.26	<b>0.011</b>
Treatment	1	0.8014	0.8014	0.35	0.556
Site*Treatment	1	0.1293	0.1293	0.06	0.812
Genetic entry	3	17.0992	5.6997	2.52	0.075
Treatment*Genetic entry	1	1.7542	1.7542	0.78	0.385
Rep*Treatment(Site)	4	29.3653	7.3413	3.25	<b>0.024</b>
Error	32	72.2479	2.2577		

Table 3: F-tests of fixed effects of clonal varieties with open-pollinated and seed orchard mix genetics within each interplanting treatment (OP and SOM) on each site for predicted total outside bark volume (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	5.1164	5.1164	94.17	< <b>.0001</b>
Rep	2	0.3538	0.1769	3.26	0.516
Rep(Site)	2	0.2837	0.1419	2.61	0.089
Treatment	1	0.0416	0.0416	0.77	0.388
Site*Treatment	1	0.0174	0.0174	0.32	0.576
Genetic entry	3	1.6365	0.5455	10.04	< <b>.0001</b>
Treatment*Genetic entry	1	0.0402	0.0402	0.74	0.396
Rep*Treatment(Site)	4	0.2891	0.0723	1.33	0.280
Error	32	1.7385	0.0543		

Table 4: F-tests of fixed effects of clonal varieties with open-pollinated and seed orchard mix genetics within each interplanting treatment (OP and SOM) on each site for the coefficient of variation in total height (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	323.52	323.52	44.82	< <b>.0001</b>
Rep	2	11.85	5.93	0.82	0.449
Rep(Site)	2	12.11	6.06	0.84	0.4414
Treatment	1	2.72	2.72	0.38	0.5436
Site*Treatment	1	5.39	5.39	0.75	0.394
Genetic Entry	3	12.55	4.18	0.58	0.6326
Treatment*Genetic Entry	1	14.00	14.00	1.94	0.1733
Rep*Treatment(Site)	4	58.78	14.70	2.04	0.1129
Error: MS(Error)	32	231.00	7.22		

Table 5: F-tests of fixed effects of clonal varieties with open-pollinated and seed orchard mix genetics within each interplanting treatment (OP and SOM) on each site for the coefficient of variation in **DBH** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	697.83	697.83	51.79	<b>&lt;.0001</b>
Rep	2	11.65	5.82	0.43	0.6528
Rep(Site)	2	41.98	20.99	1.56	0.2262
Treatment	1	6.95	6.95	0.52	0.4777
Site*Treatment	1	16.79	16.79	1.25	0.2727
Genetic Entry	3	114.57	38.19	2.83	0.0537
Treatment*Genetic Entry	1	28.76	28.76	2.13	0.1538
Rep*Treatment(Site)	4	101.23	25.31	1.88	0.1384
Error: MS(Error)	32	431.18	13.47		

Table 6: F-tests of fixed effects of clonal varieties with open-pollinated and seed orchard mix genetics within each interplanting treatment (OP and SOM) on each site for the coefficient of variation in **predicted total outside bark volume** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	2471.53	2471.53	64.56	<b>&lt;.0001</b>
Rep	2	4.50	2.25	0.06	0.943
Rep(Site)	2	36.08	18.04	0.47	0.6285
Treatment	1	27.78	27.78	0.73	0.4006
Site*Treatment	1	30.78	30.78	0.8	0.3766
Genetic Entry	3	375.08	125.03	3.27	<b>0.0339</b>
Treatment*Genetic Entry	1	127.29	127.29	3.33	0.0776
Rep*Treatment(Site)	4	718.39	179.60	4.69	<b>0.0043</b>
Error: MS(Error)	32	1224.97	38.28		

Table 7: Top-5 clonal crop-tree ranking analysis with respect to **DBH**, tested to see if the average frequency of crop-trees per bed is significantly different than 5. Significant P-values are in bold.

Location	Interplanting Treatment	Mean	t-value	Pr > t
Dry	SOM_C2	0.6	-23.13	<b>&lt;.0001</b>
	SOM_C1	0.6	-33.61	<b>&lt;.0001</b>
	OP_C2	0.8	-24.06	<b>&lt;.0001</b>
	OP_C1	0.8	-15.03	<b>&lt;.0001</b>
Wet	SOM_C2	0.5	-34.00	<b>&lt;.0001</b>
	SOM_C1	0.8	-17.28	<b>&lt;.0001</b>
	OP_C2	0.5	-18.90	<b>&lt;.0001</b>
	OP_C1	0.8	-18.87	<b>&lt;.0001</b>

Table 8: Top-5 clonal crop-tree ranking analysis with respect to **total height**, tested to see if the average frequency of crop-trees per bed is significantly different than 5. Significant P-values are in bold.

Location	Interplanting Treatment	Mean	t-value	Pr > t
Dry	SOM_C2	2.5	-13.20	<b>&lt;.0001</b>
	SOM_C1	1.7	-10.99	<b>&lt;.0001</b>
	OP_C2	1.5	-18.07	<b>&lt;.0001</b>
	OP_C1	1.3	-17.39	<b>&lt;.0001</b>
Wet	SOM_C2	0.6	-26.94	<b>&lt;.0001</b>
	SOM_C1	0.8	-17.28	<b>&lt;.0001</b>
	OP_C2	0.6	-18.72	<b>&lt;.0001</b>
	OP_C1	0.7	-18.70	<b>&lt;.0001</b>

Table 9: Top-5 clonal crop-tree ranking analysis with respect to **predicted total outside bark volume**, tested to see if the average frequency of crop-trees per bed is significantly different than 5. Significant P-values are in bold.

Location	Interplanting Treatment	Mean	t-value	Pr > t
Dry	SOM_C2	1.1	-15.12	<b>&lt;.0001</b>
	SOM_C1	0.8	-24.06	<b>&lt;.0001</b>
	OP_C2	0.9	-25.02	<b>&lt;.0001</b>
	OP_C1	0.9	-19.20	<b>&lt;.0001</b>
Wet	SOM_C2	0.5	-35.50	<b>&lt;.0001</b>
	SOM_C1	0.8	-17.28	<b>&lt;.0001</b>
	OP_C2	0.6	-18.72	<b>&lt;.0001</b>
	OP_C1	0.7	-20.69	<b>&lt;.0001</b>

Table 10: Top-10 clonal crop-tree ranking analysis with respect to **DBH**, tested to see if the average frequency of crop-trees per bed is significantly different than 5. Significant P-values are in bold.

Location	Interplanting Treatment	Mean	t-value	Pr > t
Dry	SOM_C2	2.0	-15.37	<b>&lt;.0001</b>
	SOM_C1	2.1	-12.86	<b>&lt;.0001</b>
	OP_C2	2.1	-13.32	<b>&lt;.0001</b>
	OP_C1	2.7	-7.00	<b>&lt;.0001</b>
Wet	SOM_C2	0.8	-21.00	<b>&lt;.0001</b>
	SOM_C1	1.0	-13.66	<b>&lt;.0001</b>
	OP_C2	0.7	-15.03	<b>&lt;.0001</b>
	OP_C1	1.0	-13.66	<b>&lt;.0001</b>

Table 11: Top-10 clonal crop-tree ranking analysis with respect to **total height**, tested to see if the average frequency of crop-trees per bed is significantly different than 5. Significant P-values are in bold.

Location	Interplanting Treatment	Mean	t-value	Pr > t
Dry	SOM_C2	2.7	-9.13	<b>&lt;.0001</b>
	SOM_C1	2.4	-9.53	<b>&lt;.0001</b>
	OP_C2	2.3	-12.65	<b>&lt;.0001</b>
	OP_C1	3.0	-6.48	<b>&lt;.0001</b>
Wet	SOM_C2	0.8	-21.00	<b>&lt;.0001</b>
	SOM_C1	1.0	-13.66	<b>&lt;.0001</b>
	OP_C2	0.7	-15.03	<b>&lt;.0001</b>
	OP_C1	1.0	-13.66	<b>&lt;.0001</b>

Table 12: Top-10 clonal crop-tree ranking analysis with respect to **predicted total outside bark volume**, tested to see if the average frequency of crop-trees per bed is significantly different than 5. Significant P-values are in bold.

Location	Interplanting Treatment	Mean	t-value	Pr > t
Dry	SOM_C2	2.3	-17.83	<b>&lt;.0001</b>
	SOM_C1	2.1	-13.32	<b>&lt;.0001</b>
	OP_C2	2.1	-13.32	<b>&lt;.0001</b>
	OP_C1	2.8	-6.21	<b>&lt;.0001</b>
Wet	SOM_C2	0.8	-21.00	<b>&lt;.0001</b>
	SOM_C1	1.0	13.66	<b>&lt;.0001</b>
	OP_C2	0.7	-15.03	<b>&lt;.0001</b>
	OP_C1	1.0	-13.66	<b>&lt;.0001</b>

Table 13: F-tests of fixed effects of individual clones with the main effects of site and treatment (Pure, OP, and SOM) along with interactions for **DBH** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	7.1633	7.1633	128.46	<b>0.0003</b>
Clone	1	0.5848	0.5848	10.54	<b>0.0315</b>
Treatment	2	0.1741	0.0870	0.48	0.6247
Site*Clone	1	0.5753	0.5753	10.37	<b>0.0323</b>
Clone*Treatment	2	0.2275	0.1137	2.05	0.2438

Table 14: F-tests of fixed effects of individual clones with the main effects of site and treatment (Pure, OP, and SOM) along with interactions for **total height** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	264.8059	264.8059	31.91	<b>0.0046</b>
Clone	1	4.5604	4.56047	3.84	0.1217
Treatment	2	8.5747	4.2874	1.93	0.1585
Site*Clone	1	33.8092	33.8092	28.45	<b>0.006</b>
Clone*Treatment	2	6.9217	3.4609	2.91	0.1658

Table 15: F-tests of fixed effects of individual clones with the main effects of site and treatment (Pure, OP, and SOM) along with interactions for **predicted total outside bark volume** (significant P-values are in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	5.2428	5.2428	31.83	<b>0.0049</b>
Clone	1	0.2026	0.2026	3.64	0.1292
Treatment	2	0.1220	0.0601	0.84	0.4410
Site*Clone	1	0.6282	0.6282	11.27	<b>0.0284</b>
Clone*Treatment	2	0.1360	0.0680	1.22	0.3857

Table 16: F-tests of fixed effects of individual clones with the main effects of site and treatment (Pure, OP, and SOM) along with interactions for the **coefficient of variation in DBH** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	701.7854	701.7854	26.96	<b>0.0066</b>
Clone	1	40.2227	40.2227	2.28	0.2058
Treatment	2	5.1686	2.5843	0.78	0.4635
Site*Clone	1	9.0897	9.0897	0.51	0.5129
Clone*Treatment	2	91.6373	45.8186	2.59	0.1896

Table 17: F-tests of fixed effects of of individual clones with the main effects of site and treatment (Pure, OP, and SOM) along with interactions for the **coefficient of variation in total height** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	359.7940	359.7940	34.07	<b>0.0043</b>
Clone	1	7.2325	7.2325	0.44	0.5422
Treatment	2	15.8601	7.9300	1.32	0.2792
Site*Clone	1	20.1758	20.1758	1.24	0.3287
Clone*Treatment	2	21.4380	10.7189	0.66	0.5669

Table 18: F-tests of fixed effects of individual clones with the main effects of site and treatment (Pure, OP, and SOM) along with interactions for the **coefficient of variation in predicted total outside bark volume** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	2330.3133	2330.3133	98.76	<b>0.0006</b>
Clone	1	165.0077	165.0077	2.88	0.1647
Treatment	2	62.3176	31.1587	0.60	0.5524
Site*Clone	1	49.2494	49.2494	0.86	0.4061
Clone*Treatment	2	291.6184	145.8092	2.55	0.1934

Table 19: F-tests of fixed effects of pure clonal planting treatments and interplanted treatments with the main effects of site and treatment along with interactions for the **coefficient of variation in DBH** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	444.3664	444.3664	79.23	< <b>.0001</b>
Rep(Site)	4	114.1410	28.5352	5.09	<b>0.0004</b>
Treatment	2	2.9303	1.4652	4.73	0.7722
Clone	1	26.5225	26.5225	0.26	<b>0.0393</b>
Treatment*Clone	2	56.4667	28.2333	5.03	<b>0.0146</b>

Table 20: F-tests of fixed effects of pure clonal planting treatments and interplanted treatments with the main effects of site and treatment along with interactions for the **coefficient of variation in total stem height** (significant P-values indicated in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	191.7302	191.7302	40.03	< <b>.0001</b>
Rep(Site)	4	40.0954	10.0238	2.09	0.1118
Treatment	2	6.9632	3.4816	0.73	0.4933
Clone	1	6.8644	6.8644	1.43	0.2425
Mixture*Clone	2	7.2200	3.6100	0.75	0.4810

Table 21: F-tests of fixed effects for of pure clonal planting treatments and interplanted treatments with the main effects of site and treatment along with interactions the **coefficient of variation in predicted total outside bark volume** (significant P-values in bold).

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Site	1	1408.1256	1408.1256	65.37	< <b>.0001</b>
Rep(Site)	4	191.4684	47.8671	2.22	0.0955
Treatment	2	54.1120	27.0560	1.26	0.3022
Clone	1	73.8740	73.8740	3.43	0.0759
Mixture*Clone	2	174.6233	87.3116	4.05	<b>0.0230</b>

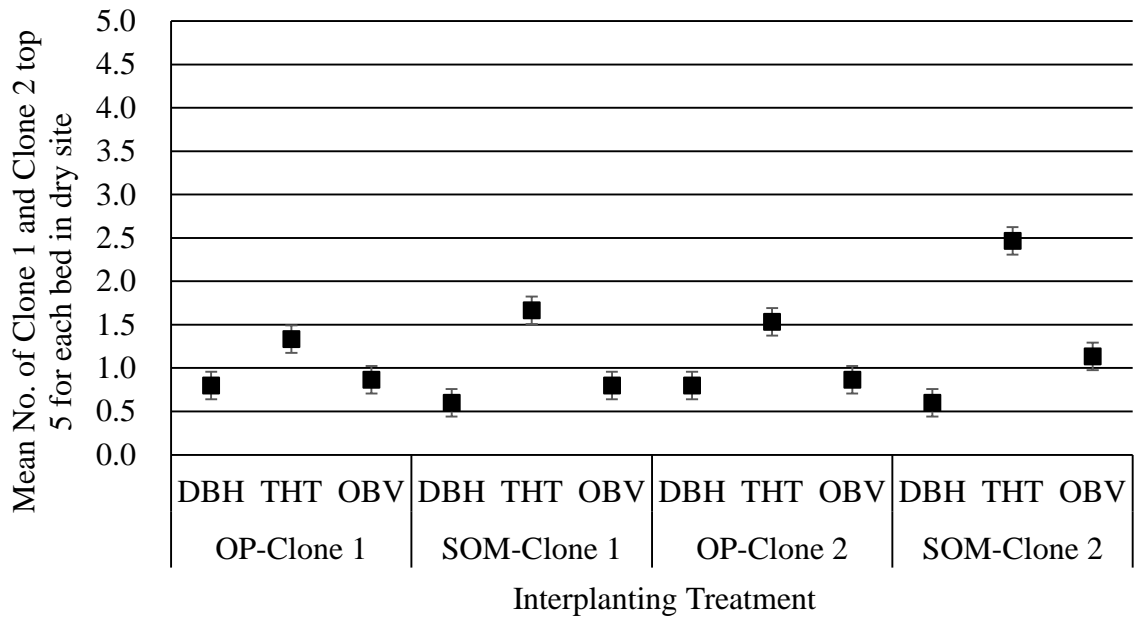


Figure 1: Mean number of clones in each bed on the dry site that were classified to be crop-trees that were ranked in the top 5 of each growth characteristic. (DBH = diameter at breast height, THT = total height, OBV = outside bark volume).

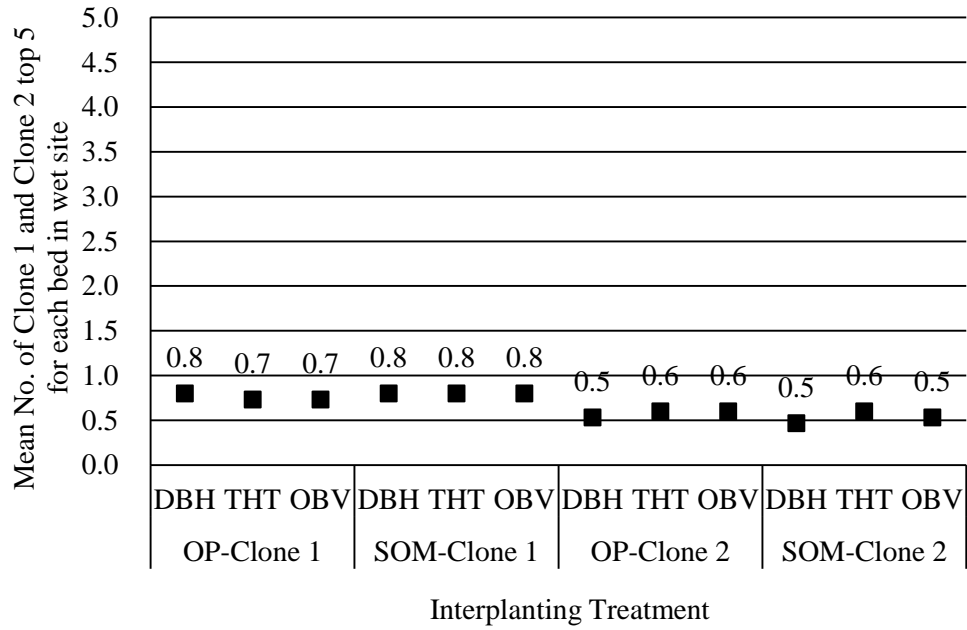


Figure 2: Mean number of clones in each bed on the wet site that were classified to be crop-trees that were ranked in the top 5 of each growth characteristic. (DBH = diameter at breast height, THT = total height, OBV = outside bark volume).

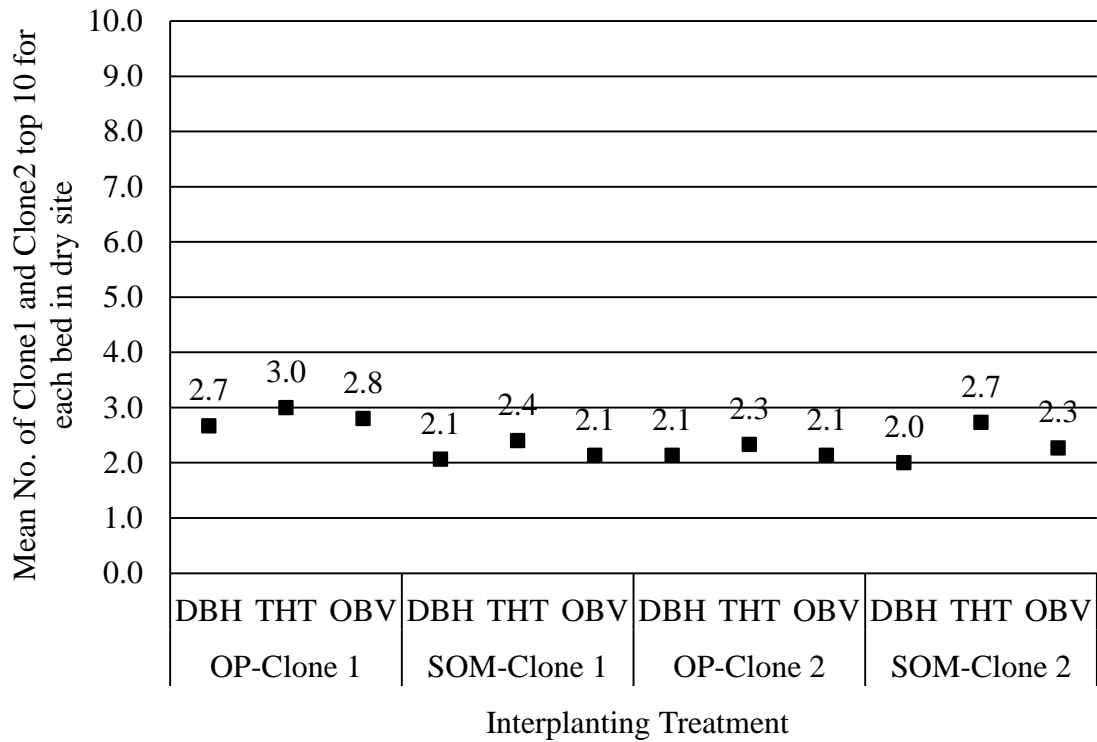


Figure 3: Mean number of clones in each bed on the dry site that were classified to be crop-trees that were ranked in the top 10 of each growth characteristic. (DBH = diameter at breast height, THT = total height, OBV = outside bark volume).

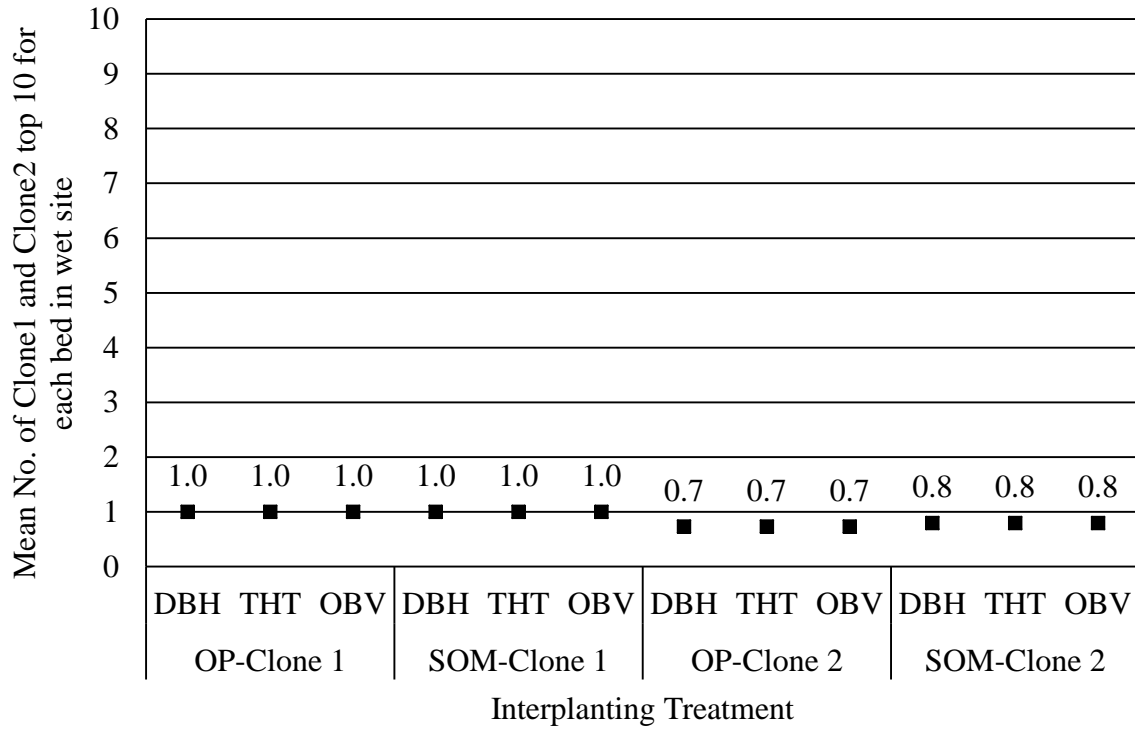


Figure 4: Mean number of clones in each bed on the wet site that were classified to be crop-trees that were ranked in the top 10 of each growth characteristic. (DBH = diameter at breast height, THT = total height, OBV = outside bark volume).

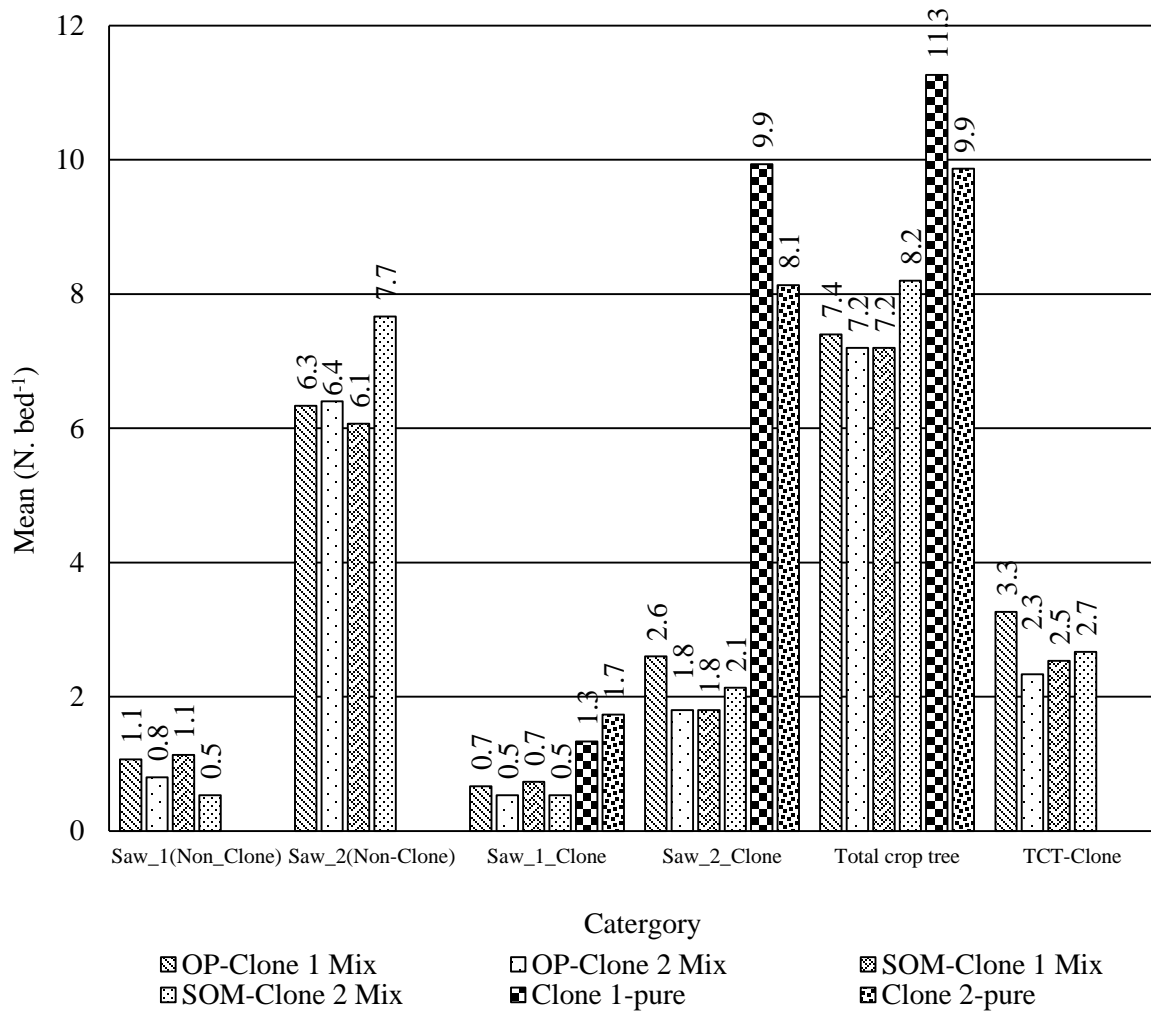


Figure 5: Crop-tree grade (1 and 2) proportions within each planting treatment on the dry site. For example, Saw\_1 (non\_clone) and Saw 2 (non\_clone) are all the OP and SOM trees that were classified as being a crop tree with respect to interplanting treatment. Saw\_1\_Clone and Saw\_2\_Clone are only the clonal genetics that were classified as being a crop tree with respect to pure and mixed planting treatments.

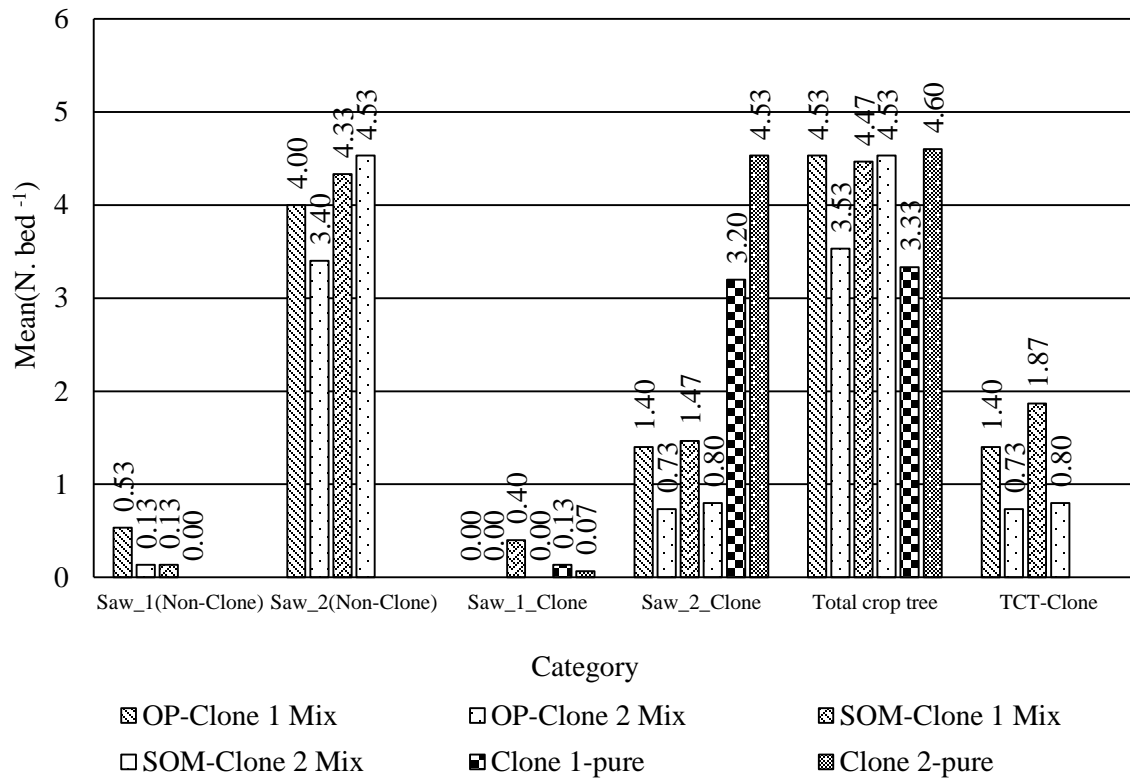
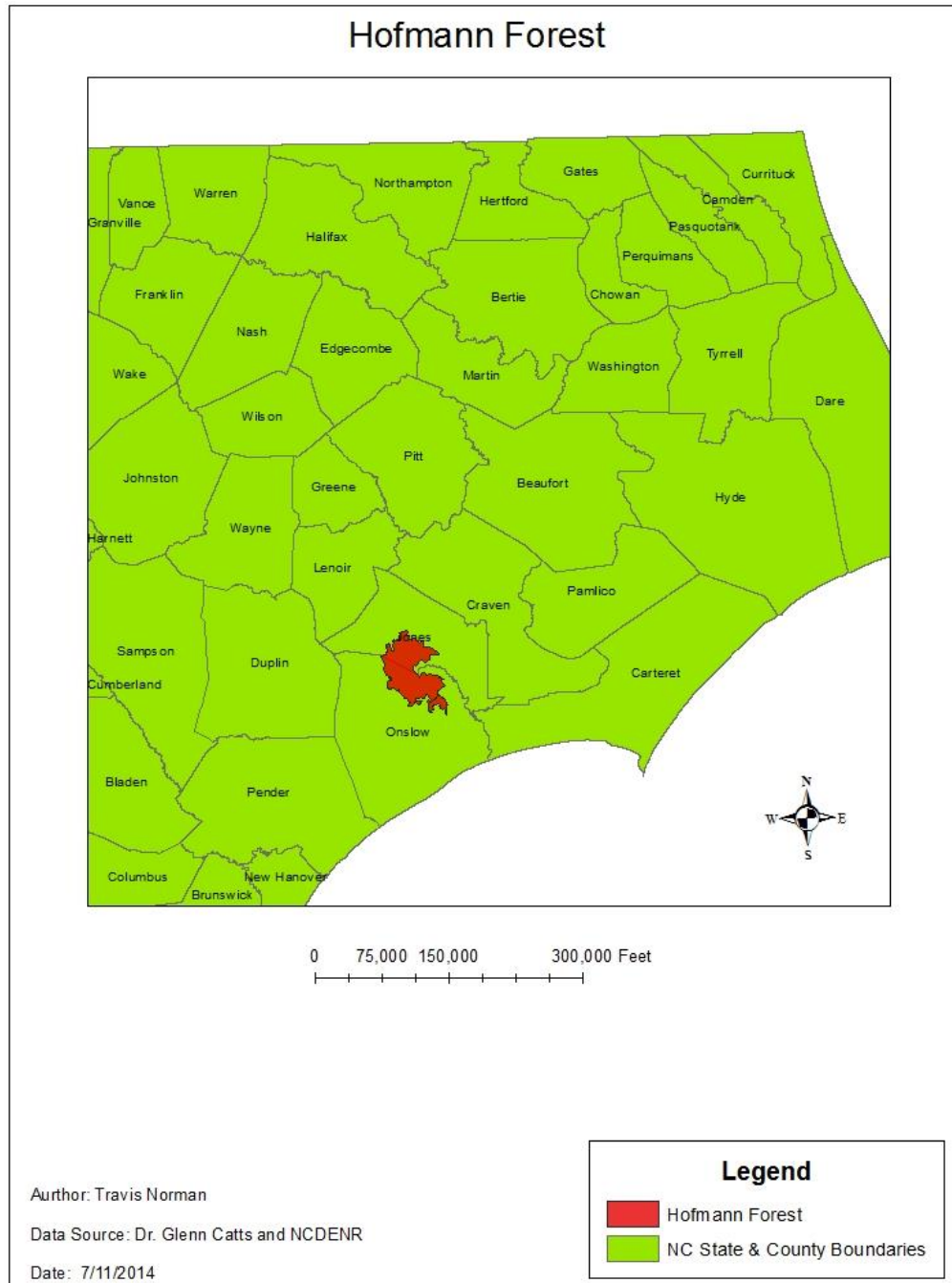


Figure 6: Crop-tree grade (1 and 2) proportions within each planting treatment on the wet site. For example, Saw\_1 (non\_clone) and Saw 2 (non\_clone) are all the OP and SOM trees that were classified as being a crop tree with respect to interplanting treatment. Saw\_1\_Clone and Saw\_2\_Clone are only the clonal genetics that were classified as being a crop tree with respect to pure and mixed planting treatments.

## APPENDICES

Appendix A: Location of the Hofmann Forest in eastern North Carolina



Appendix B: Example of replication layout with genetic entry codes.

Dry Site (FMU 811) - Replication 1 (planted Feb. 3, 2007)															Gramp Stocum Road				
Row	Bed 1	Bed 2	Bed 3	Bed 4	Bed 5	Bed 6	Bed 7	Bed 8	Bed 9	Bed 10	Bed 11	Bed 12	Bed 13	Bed 14	Bed 15				
1	SOM	C1	SOM	C1	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	C1				
2	SOM	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
3	C1	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
4	SOM	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
5	SOM	C1	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
6	C1	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
7	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
8	SOM	C1	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
9	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
10	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
11	C1	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
12	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
13	SOM	C1	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
14	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
15	C1	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
16	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
17	SOM	C1	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
18	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
19	C1	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
20	SOM	SOM	SOM	SOM	C1	C1	C1	C1	C1	C1	OP	OP	OP	OP	OP				
21	C2	OP	C2	OP	C2	OP	OP	OP	OP	OP	C2	OP	OP	OP	C2				
22	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
23	C2	OP	C2	OP	C2	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
24	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
25	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
26	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
27	C2	OP	C2	OP	C2	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
28	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
29	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
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31	C2	OP	C2	OP	C2	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
32	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
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34	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
35	C2	OP	C2	OP	C2	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
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38	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
39	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				
40	C2	OP	C2	OP	C2	OP	OP	OP	OP	OP	OP	OP	OP	OP	OP				

### Appendix C: Summary Statistics

Table 1: Average overall diameter-at-breast-height (DBH), total height (THT), and predicted total outside bark volume at age 6.

N	DBH (in)	Total Height (ft)	Total Volume (ft <sup>3</sup> )
2889	5.3	28.0	2.2

### Appendix C: Summary Statistics

Table 2: Average overall diameter-at-breast-height (DBH), total height (THT), and predicted total volume with respected to study site location at age 6.

Location	N	DBH (in)	Total Height (ft)	Total Volume (ft <sup>3</sup> )
Dry	1610	5.6	29.6	2.5
Wet	1280	5.0	26.0	1.9

Appendix C: Summary Statistics

Table 3: Mean diameter at breast height (DBH), total height (THT), and predicted outside bark volume with respect to site, planting treatment, and genetic entry at age 6. Standard deviations indicated inside parentheses.

Site	Treatment	Genetic Entry	N	DBH (in)	THT (ft)	Volume (ft <sup>3</sup> )
Dry	OP C1 Mix	OP	195	5.85 (0.85)	29.87 (3.77)	2.72 (0.88)
		Clone 1	71	5.20 (0.81)	29.52 (3.38)	2.17 (0.64)
	OP C2 Mix	OP	189	5.74 (0.92)	30.05 (3.57)	2.65 (0.87)
		Clone 2	71	5.21 (0.98)	30.83 (3.35)	2.31 (0.91)
	C1 Pure	Clone 1	264	5.40 (0.80)	28.95 (3.10)	2.29 (0.72)
		Clone 2	272	5.43 (0.88)	31.06 (3.76)	2.48 (0.84)
	SOM C1 Mix	Clone 1	68	5.12 (0.74)	29.88 (3.36)	2.13 (0.67)
		SOM	212	5.85 (0.86)	28.34 (2.95)	2.59 (0.76)
	SOM C2 Mix	Clone 2	64	5.36 (0.88)	31.44 (3.33)	2.44 (0.79)
		SOM	204	5.87 (0.70)	28.36 (2.82)	2.58 (0.67)
Wet	OP C1 Mix	OP	147	5.55 (0.99)	28.31 (4.01)	2.39 (0.93)
		Clone 1	57	4.97 (1.10)	27.66 (4.31)	1.97 (0.87)
	OP C2 Mix	OP	142	5.22 (1.19)	25.13 (4.18)	1.98 (0.90)
		Clone 2	52	4.23 (1.14)	24.09 (4.81)	1.38 (0.73)
	C1 Pure	Clone 1	222	5.15 (1.04)	27.54 (4.24)	2.08 (0.81)
		Clone 2	223	4.59 (1.17)	25.85 (4.99)	1.67 (0.84)
	SOM C1 Mix	Clone 1	55	4.73 (1.25)	25.87 (4.51)	1.76 (0.89)
		SOM	154	5.18 (1.20)	24.68 (3.68)	1.93 (0.87)
	SOM C2 Mix	Clone 2	57	4.38 (1.04)	25.18 (4.17)	1.47 (0.71)
		SOM	171	5.31 (1.09)	24.70 (3.89)	1.98 (0.77)

Appendix C: Summary Statistics

Table 4: Average coefficient of variation for diameter at breast height (DBH), total height (THT), and predicted outside bark volume with respect to site, planting treatment, and genetic entry at age 6.

Site	Treatment	Genetic Entry	N	DBH	THT	Volume
Dry	OP C1 Mix	OP	195	14.48	12.62	32.23
		Clone 1	71	15.65	11.44	29.52
	OP C2 Mix	OP	189	15.99	11.88	32.71
		Clone 2	71	18.78	10.86	39.29
	C1 Pure	Clone 1	264	14.81	10.7	31.32
		Clone 2	272	16.16	12.09	33.9
	SOM C1 Mix	Clone 1	68	14.52	11.25	31.52
		SOM	212	14.68	10.39	29.3
	SOM C2 Mix	Clone 2	64	16.36	10.58	32.4
		SOM	204	11.87	9.93	26.16
Wet	OP C1 Mix	OP	147	17.81	14.18	39.08
		Clone 1	57	22.13	15.6	43.82
	OP C2 Mix	OP	142	22.78	16.63	45.37
		Clone 2	52	26.82	19.98	53.1
	C1 Pure	Clone 1	222	20.26	15.38	39.14
		Clone 2	223	25.45	19.32	50.38
	SOM C1 Mix	Clone 1	55	26.46	17.44	50.27
		SOM	154	23.17	14.93	45.02
	SOM C2 Mix	Clone 2	57	23.71	16.55	48.37
		SOM	171	20.59	15.76	38.95

## Appendix D: Survival Assessment

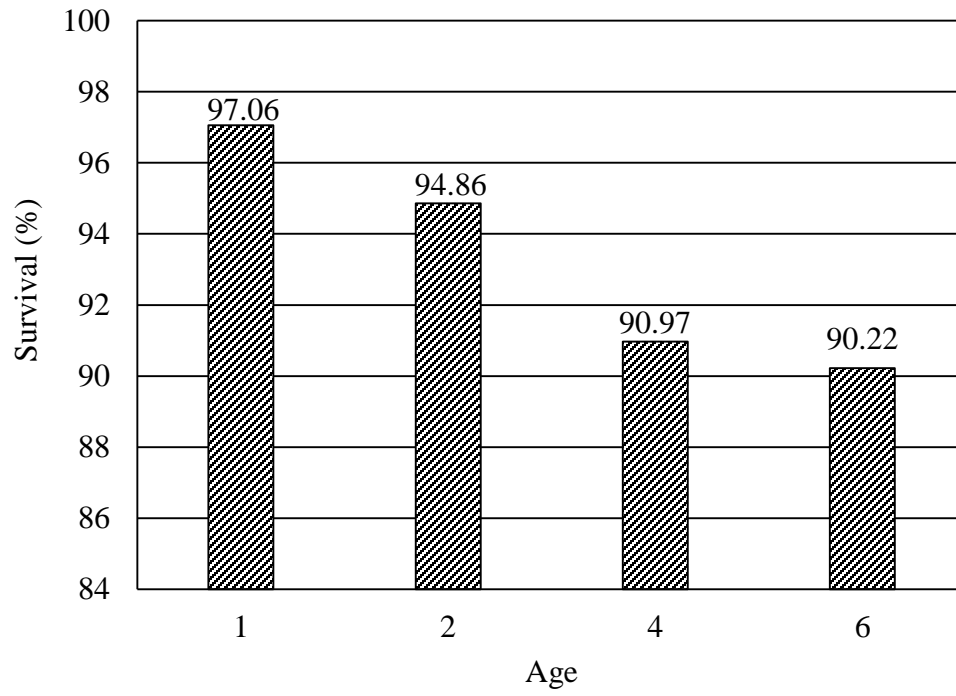


Figure 1: Survival by age over all sites and replications.

Appendix D: Survival Assessment

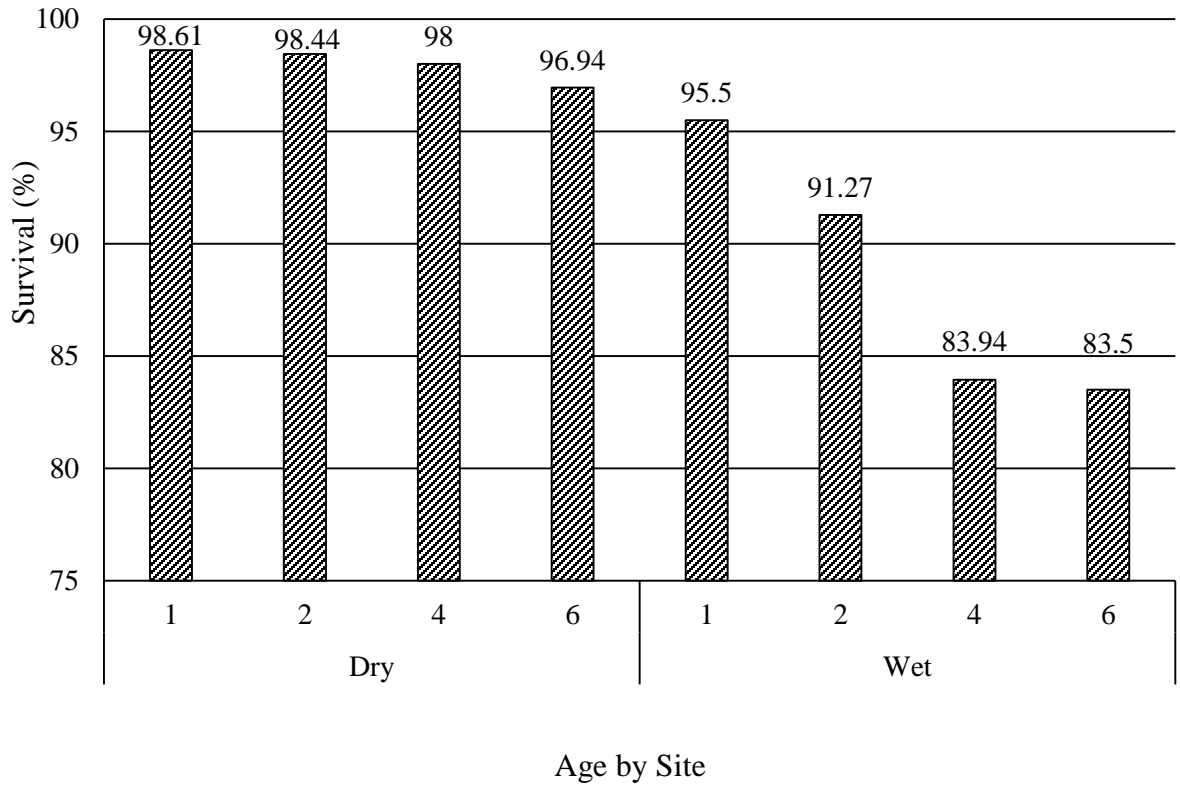


Figure 2: Overall percent survival by age and by site.

Appendix D: Survival Assessment

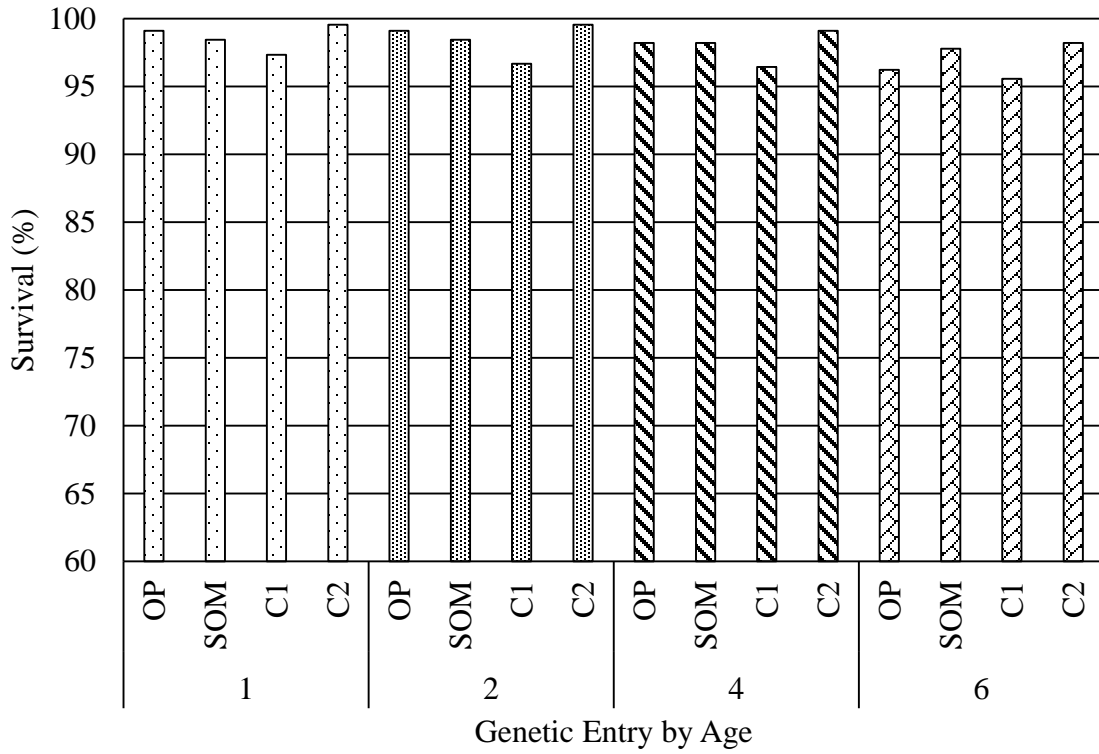


Figure 3: Overall percent survival by age and genetic entry on the dry site.

### Appendix D: Survival Assessment

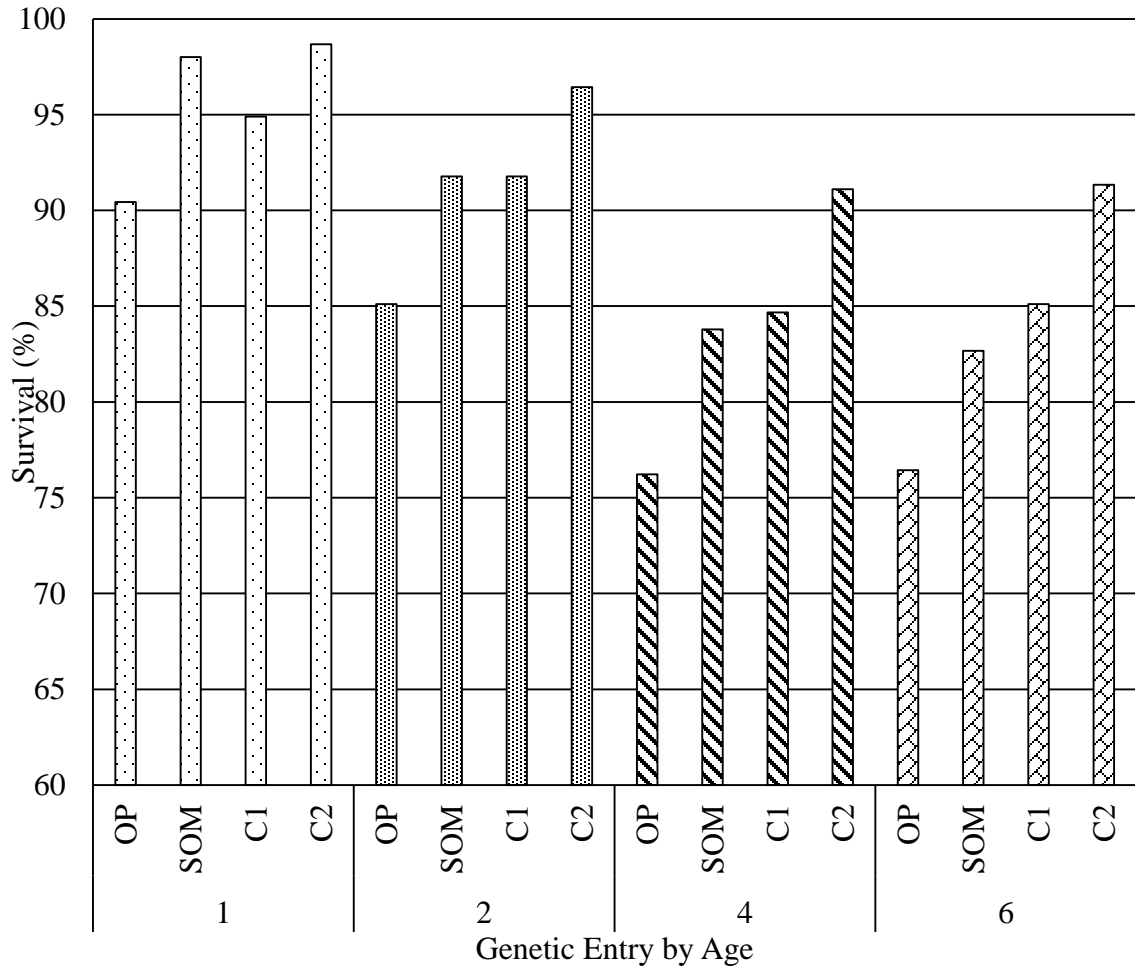


Figure 4: Overall percent survival by age and genetic entry on the wet site

Appendix E: Site Productivity Assessment

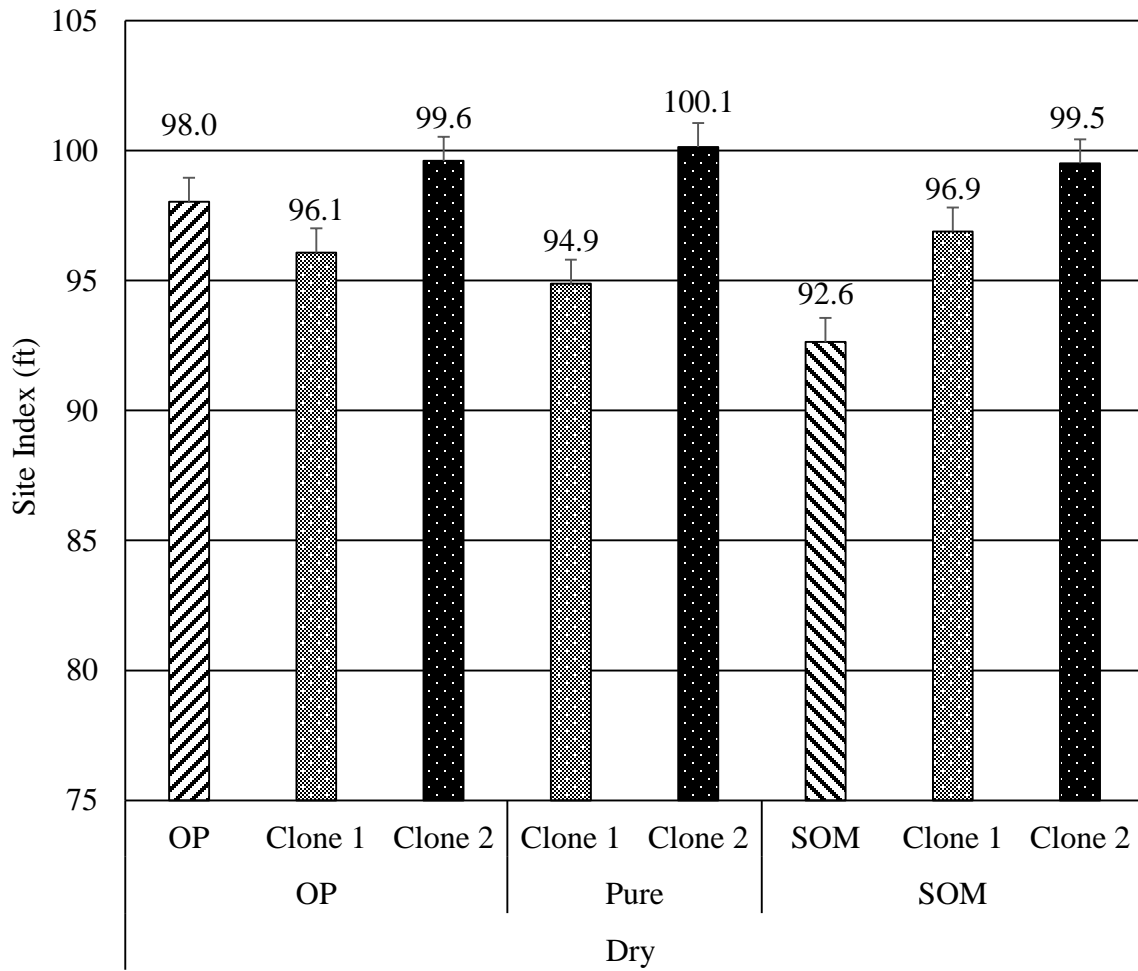


Figure 1: Predicted site index at age 25 on the dry site across all genetic entries within each planting treatment. Heights were predicted using age 6 dominant and codominant heights.

Appendix E: Site Productivity Assessment

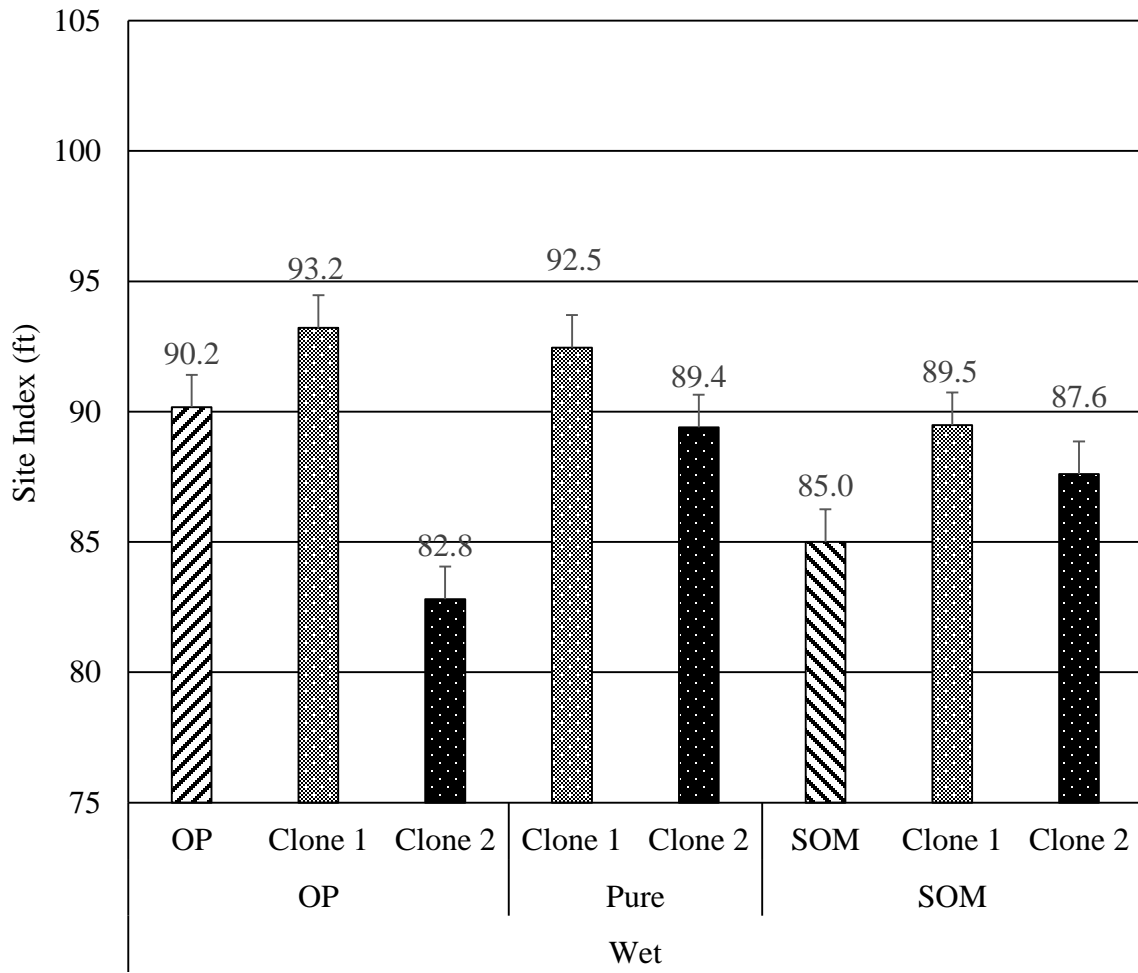


Figure 2: Predicted site index at age 25 on the wet site across all genetic entries within each planting treatment. Heights were predicted using age 6 dominant and codominant heights.

## Appendix F: Interplanting Treatment Analysis

Table 1: Differences of least square means of fixed effects of individual clones with open-pollinated and seed orchard mix genetics with all pairwise comparisons for **DBH**. For example, the difference between the dry site mean (5.41 inches) and the wet site mean (4.65 inches) is significant at  $P < 0.0001$ . The difference between Mixture\*Family mean OP-Clone 1 (4.98 inches) and SOM-Clone 1 (4.75 inches) is not significant.

Differences of Least Squares Means												
Effect	Site	Mixture	Genetic Entry	Clone	Mean	Site	Mixture	Genetic Entry	Clone	Mean	DF	Pr >  t
Site	Dry				5.41	Wet				4.65	47	< <b>0.0001</b>
Clone				1	4.87				2	4.57	47	<b>0.0122</b>
Mixture* Family		OP		1	4.98		OP		2	4.59	47	<b>0.0175</b>
Mixture* Family		OP		1	4.98		OP	OP		5.33	47	<b>0.0155</b>
Mixture* Family		OP		1	4.98		SOM		1	4.75	47	0.1539
Mixture* Family		OP		1	4.98		SOM		2	4.55	47	<b>0.0107</b>
Mixture* Family		OP		1	4.98		SOM	SOM		5.36	47	<b>0.0095</b>
Mixture* Family		OP		2	4.59		OP	OP		5.33	47	< <b>0.0001</b>
Mixture* Family		OP		2	4.59		SOM		1	4.75	47	0.3039
Mixture* Family		OP		2	4.59		SOM		2	4.55	47	0.8386
Mixture* Family		OP		2	4.59		SOM	SOM		5.36	47	< <b>0.0001</b>
Mixture* Family		OP	OP		5.33		SOM		1	4.75	47	<b>0.0002</b>
Mixture* Family		OP	OP		5.33		SOM		2	4.55	47	< <b>0.0001</b>
Mixture* Family		OP	OP		5.33		SOM	SOM		5.36	47	0.8062
Mixture* Family		SOM		1	4.75		SOM		2	4.55	47	0.2203
Mixture* Family		SOM		1	4.75		SOM	SOM		5.36	47	< <b>0.0001</b>
Mixture* Family		SOM	SOM		5.36		SOM		2	4.55	47	< <b>0.0001</b>

Appendix F: Interplanting Treatment Analysis

Table 2: Differences of least square means of fixed effects of individual clones with open-pollinated and seed orchard mix genetics with all pairwise comparisons for **predicted total volume outside bark**. For example, the difference between the dry site mean (2.34 ft<sup>3</sup>) and the wet site mean (1.63 ft<sup>3</sup>) is significant at P<0.0001. The difference between Mixture\*Family mean OP-Clone 1 (2.01 ft<sup>3</sup>) and SOM-Clone 1 (1.84 ft<sup>3</sup>) is not significant.

Differences of Least Squares Means												
Effect	Site	Mixture	Genetic Entry	Clone	Mean	Site	Mixture	Genetic Entry	Clone	Mean	DF	Pr >  t
Site	Dry				2.34	Wet				1.69	47	< <b>0.0001</b>
Clone				1	1.93				2	1.77	47	0.0998
Mixture* Family		OP		1	2.01		OP		2	1.77	47	0.0802
Mixture* Family		OP		1	2.01		OP	OP		2.25	47	<b>0.0488</b>
Mixture* Family		OP		1	2.01		SOM		1	1.84	47	0.2286
Mixture* Family		OP		1	2.01		SOM		2	1.77	47	0.0785
Mixture* Family		OP		1	2.01		SOM	SOM		2.15	47	0.2482
Mixture* Family		OP		2	1.77		OP	OP		2.25	47	<b>0.0002</b>
Mixture* Family		OP		2	1.77		SOM		1	1.84	47	0.5662
Mixture* Family		OP		2	1.77		SOM		2	1.77	47	0.9916
Mixture* Family		OP		2	1.77		SOM	SOM		2.15	47	<b>0.0026</b>
Mixture* Family		OP	OP		2.25		SOM		1	1.84	47	<b>0.0015</b>
Mixture* Family		OP	OP		2.25		SOM		2	1.77	47	<b>0.0002</b>
Mixture* Family		OP	OP		2.25		SOM	SOM		2.15	47	0.2935
Mixture* Family		SOM		1	1.84		SOM		2	1.77	47	0.5592
Mixture* Family		SOM		1	1.84		SOM	SOM		2.15	47	<b>0.0142</b>
Mixture* Family		SOM	SOM		2.15		SOM		2	1.77	47	<b>0.0025</b>

## Appendix F: Interplanting Treatment Analysis

Table 3: Differences of least square means of fixed effects of individual clones with open-pollinated and seed orchard mix genetics with all pairwise comparisons for **total stem height**. For example, the difference between the dry site mean (29.1 feet) and the wet site mean (24.4 feet) is significant at  $P < 0.0001$ . The difference between Mixture\*Family mean OP-Clone 1 (28.1 feet) and SOM-Clone 1 (27.2 feet) is not significant.

Differences of Least Squares Means												
Effect	Site	Mixture	Genetic Entry	Clone	Mean	Site	Mixture	Genetic Entry	Clone	Mean	DF	Pr >  t
Site	Dry				29.1	Wet				24.4	47	< <b>0.0001</b>
Clone				1	27.7				2	26.7	47	0.1401
Mixture*Family		OP		1	28.1		OP		2	26.6	47	0.1002
Mixture*Family		OP		1	28.1		OP	OP		26.8	47	0.1005
Mixture*Family		OP		1	28.1		SOM		1	27.2	47	0.3041
Mixture*Family		OP		1	28.1		SOM		2	26.8	47	0.1457
Mixture*Family		OP		1	28.1		SOM	SOM		25.7	47	<b>0.0031</b>
Mixture*Family		OP		2	26.6		OP	OP		26.8	47	0.7936
Mixture*Family		OP		2	26.6		SOM		1	27.2	47	0.5213
Mixture*Family		OP		2	26.6		SOM		2	26.8	47	0.8412
Mixture*Family		OP		2	26.6		SOM	SOM		25.7	47	0.2222
Mixture*Family		OP	OP		26.8		SOM		1	27.2	47	0.631
Mixture*Family		OP	OP		26.8		SOM		2	26.8	47	0.9758
Mixture*Family		OP	OP		26.8		SOM	SOM		25.7	47	0.0739
Mixture*Family		SOM		1	27.2		SOM		2	26.8	47	0.6583
Mixture*Family		SOM		1	27.2		SOM	SOM		25.7	47	0.0548
Mixture*Family		SOM	SOM		25.7		SOM		2	26.8	47	0.1491

## Appendix F: Interplanting Treatment Analysis

Table 4: Differences of least square means of fixed effects of individual clones with open-pollinated and seed orchard mix genetics with pairwise comparisons for the **coefficient of variation in predicted total outside bark volume**. For example, the difference between the dry site mean (30.71) and the wet site mean (45.06) is significant at  $P < 0.0001$ . The difference between Mixture\*Family mean OP-Clone 1 (36.84) and SOM-Clone 1 (39.29) is not significant.

Differences of Least Squares Means												
Effect	Site	Mixture	Genetic Entry	Clone	Mean	Site	Mixture	Genetic Entry	Clone	Mean	DF	Pr >  t
Site	Dry				30.71	Wet				45.06	47	< <b>0.0001</b>
Clone				1	38.07				2	42.39	47	0.0971
Mixture* Family		OP		1	36.84		OP		2	45.76	47	<b>0.0178</b>
Mixture* Family		OP		1	36.84		OP	OP		36.73	47	0.9726
Mixture* Family		OP		1	36.84		SOM		1	39.29	47	0.4970
Mixture* Family		OP		1	36.84		SOM		2	39.01	47	0.5487
Mixture* Family		OP		1	36.84		SOM	SOM		34.36	47	0.4275
Mixture* Family		OP		2	45.76		OP	OP		36.73	47	<b>0.0064</b>
Mixture* Family		OP		2	45.76		SOM		1	39.29	47	0.0796
Mixture* Family		OP		2	45.76		SOM		2	39.01	47	0.0676
Mixture* Family		OP		2	45.76		SOM	SOM		34.36	47	<b>0.0008</b>
Mixture* Family		OP	OP		36.73		SOM		1	39.29	47	0.4138
Mixture* Family		OP	OP		36.73		SOM		2	39.01	47	0.4680
Mixture* Family		OP	OP		36.73		SOM	SOM		34.36	47	0.3532
Mixture* Family		SOM		1	39.29		SOM		2	39.01	47	0.9360
Mixture* Family		SOM		1	39.29		SOM	SOM		34.36	47	0.1201
Mixture* Family		SOM	SOM		34.36		SOM		2	39.01	47	0.1425

Appendix F: Interplanting Treatment Analysis

Table 5: Differences of least square means of fixed effects of individual clones with open-pollinated and seed orchard mix genetics with pairwise comparisons for the **coefficient of variation in total stem height**. For example, the difference between the dry site mean (10.57) and the wet site mean (15.76) is significant at  $P < 0.0001$ . The difference between Mixture\*Family mean OP-Clone 1 (13.12) and SOM-Clone 1 (13.97) is not significant.

Differences of Least Squares Means												
Effect	Site	Mixture	Genetic Entry	Clone	Mean	Site	Mixture	Genetic Entry	Clone	Mean	DF	Pr >  t
Site	Dry				10.57	Wet				15.76	47	< <b>0.0001</b>
Clone				1	13.54				2	13.73	47	0.8683
Mixture*Family		OP		1	13.12		OP		2	14.83	47	0.2783
Mixture*Family		OP		1	13.12		OP	OP		13.41	47	0.8274
Mixture*Family		OP		1	13.12		SOM		1	13.97	47	0.5857
Mixture*Family		OP		1	13.12		SOM		2	12.63	47	0.7541
Mixture*Family		OP		1	13.12		SOM	SOM		11.98	47	0.4028
Mixture*Family		OP		2	14.83		OP	OP		13.41	47	0.2999
Mixture*Family		OP		2	14.83		SOM		1	13.97	47	0.5846
Mixture*Family		OP		2	14.83		SOM		2	12.63	47	0.1656
Mixture*Family		OP		2	14.83		SOM	SOM		11.98	47	<b>0.0417</b>
Mixture*Family		OP	OP		13.41		SOM		1	13.97	47	0.6802
Mixture*Family		OP	OP		13.41		SOM		2	12.63	47	0.5629
Mixture*Family		OP	OP		13.41		SOM	SOM		11.98	47	0.2003
Mixture*Family		SOM		1	13.97		SOM		2	12.63	47	0.3927
Mixture*Family		SOM		1	13.97		SOM	SOM		11.98	47	0.1477
Mixture*Family		SOM	SOM		11.98		SOM		2	12.63	47	0.6326

## Appendix F: Interplanting Treatment Analysis

Table 6: Differences of least square means of fixed effects of individual clones with open-pollinated and seed orchard mix genetics with pairwise comparisons for the **coefficient of variation in DBH**. For example, the difference between the dry site mean (15.04) and the wet site mean (22.66) is significant at  $P < 0.0001$ . The difference between Mixture\*Family mean OP-Clone 1 (18.78) and SOM-Clone 1 (19.89) is not significant.

Differences of Least Squares Means												
Effect	Site	Mixture	Genetic Entry	Clone	Mean	Site	Mixture	Genetic Entry	Clone	Mean	DF	Pr >  t
Site	Dry				15.04	Wet				22.66	47	<b>&lt; 0.0001</b>
Clone				1	19.34				2	21.14	47	0.2385
Mixture* Family		OP		1	18.78		OP		2	22.77	47	0.0689
Mixture* Family		OP		1	18.78		OP	OP		17.54	47	0.5044
Mixture* Family		OP		1	18.78		SOM		1	19.89	47	0.6032
Mixture* Family		OP		1	18.78		SOM		2	19.51	47	0.7351
Mixture* Family		OP		1	18.78		SOM	SOM		17.38	47	0.4494
Mixture* Family		OP		2	22.77		OP	OP		17.54	47	<b>0.0076</b>
Mixture* Family		OP		2	22.77		SOM		1	19.89	47	0.1842
Mixture* Family		OP		2	22.77		SOM		2	19.51	47	0.1332
Mixture* Family		OP		2	22.77		SOM	SOM		17.38	47	<b>0.0061</b>
Mixture* Family		OP	OP		17.54		SOM		1	19.89	47	0.2093
Mixture* Family		OP	OP		17.54		SOM		2	19.51	47	0.2929
Mixture* Family		OP	OP		17.54		SOM	SOM		17.38	47	0.9123
Mixture* Family		SOM		1	19.89		SOM		2	19.51	47	0.8554
Mixture* Family		SOM		1	19.89		SOM	SOM		17.38	47	0.1796
Mixture* Family		SOM	SOM		17.38		SOM		2	19.51	47	0.2547

## Appendix G: Crop-tree Assessment and Analysis

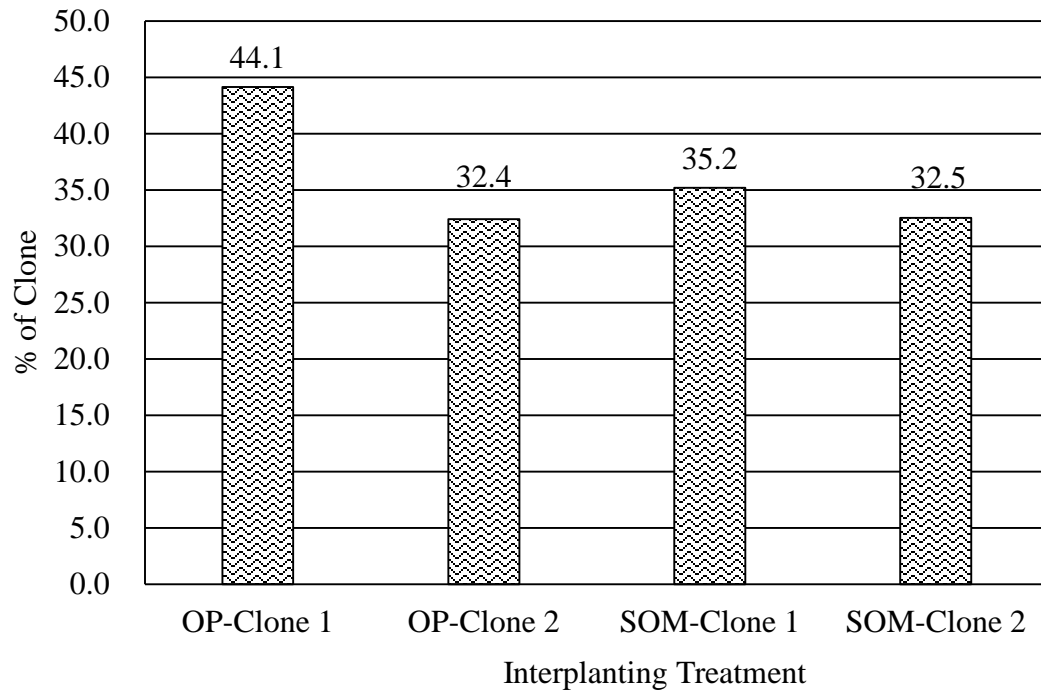


Figure 1: Total clone trees (%) that were graded as crop-trees (crop-tree scores 1 or 2) within each interplanting treatment on the dry site.

Appendix G: Crop-tree Assessment and Analysis

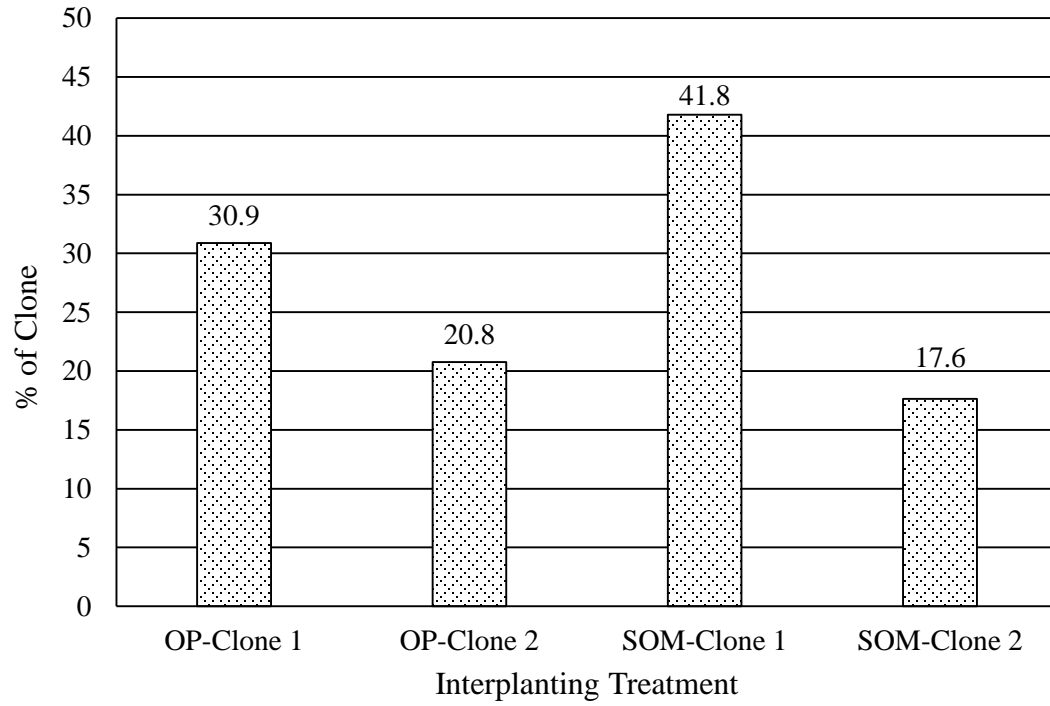


Figure 2: Total clone trees (%) that were graded as crop-trees (crop-tree scores 1 or 2) within each interplanting treatment on the wet site.

Appendix G: Crop-tree Assessment and Analysis

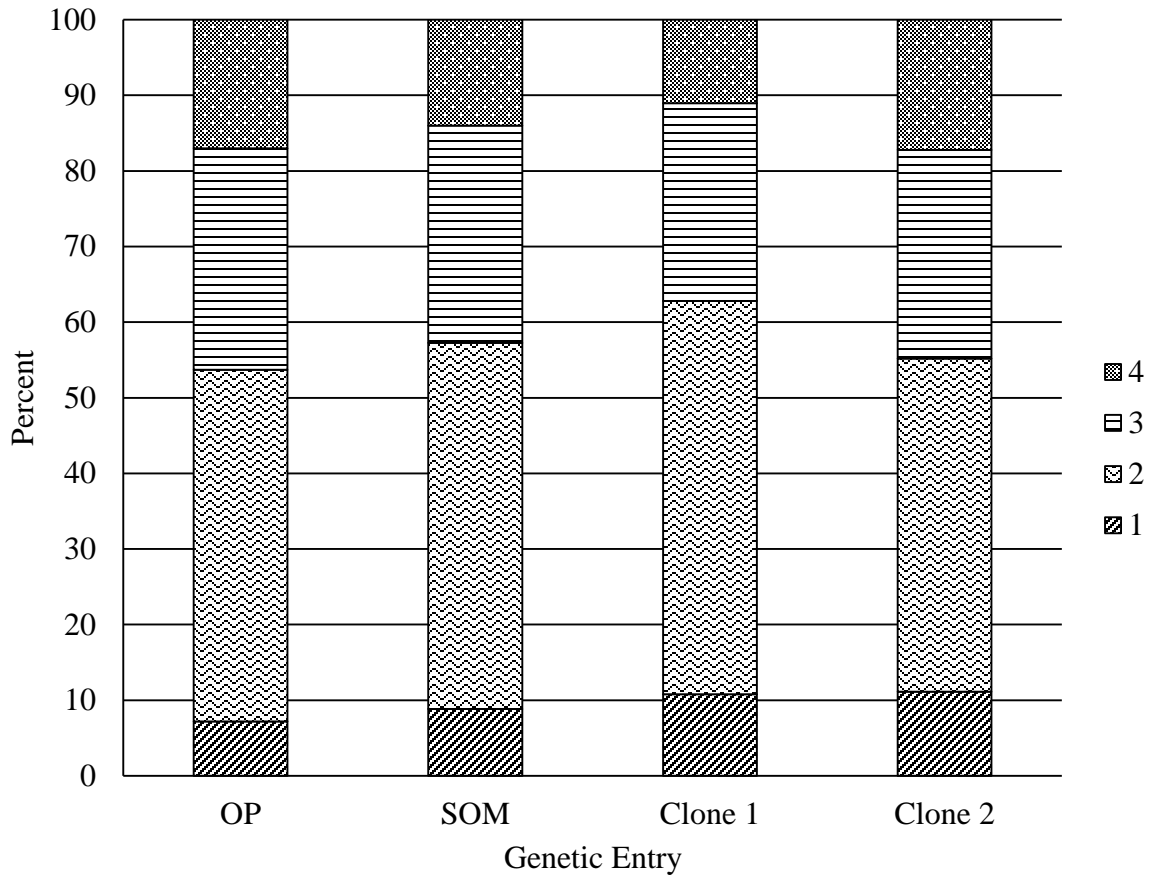


Figure 3: Crop-tree scores for all genetic entries in dry site, expressed as a percentage.

### Appendix G: Crop-tree Assessment and Analysis

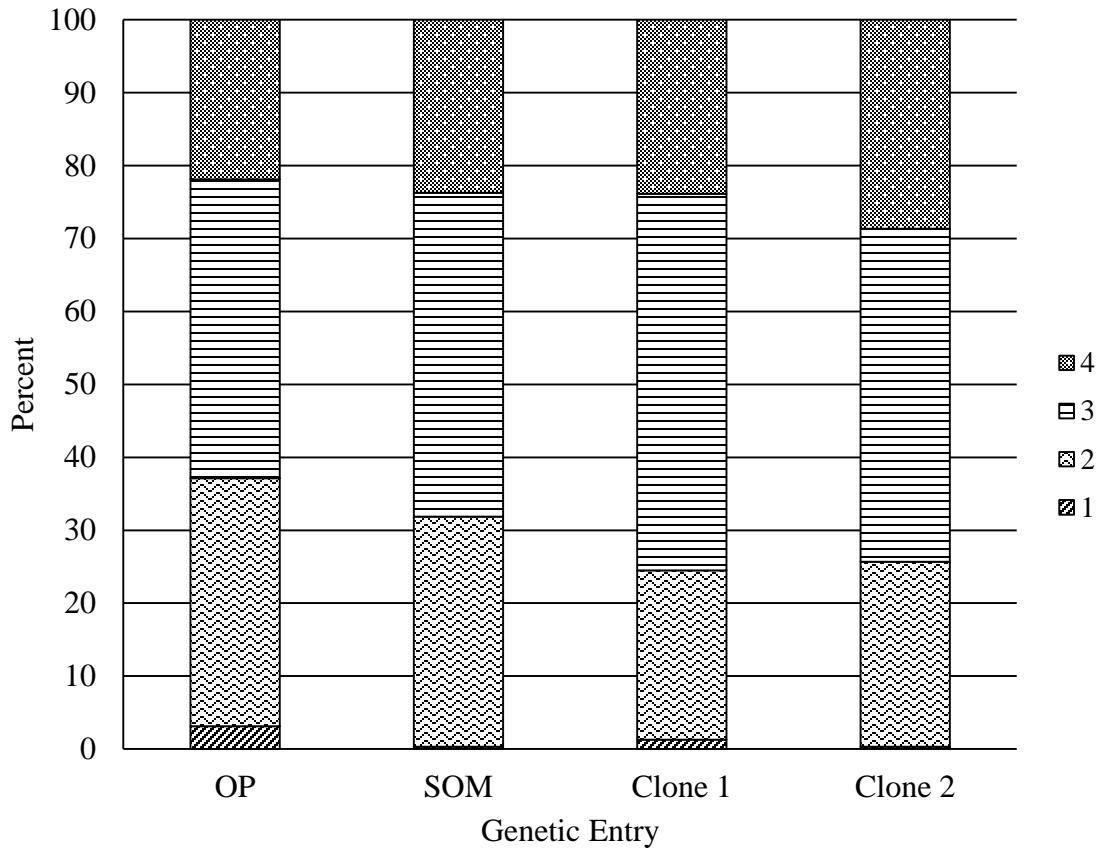


Figure 4: Crop-tree scores for all genetic entries in the wet site, expressed as a percentage.

## Appendix H: Clonal Analysis

Table 1: Differences of least square means of fixed effects of individual clone genetics with pairwise comparisons for **DBH** (in). For example, the difference between the dry site mean (5.36 inches) and the wet site mean (4.63 inches) is significant at  $P < 0.0001$ . The difference between Site\*Clone mean Dry-Clone 1 (5.36 inches) and Dry-Clone 2 (5.35 inches) is not significant.

Differences of Least Squares Means								
Effect	Site	Clone	Mean	Site	Clone	Mean	DF	Pr >  t
Site	Dry		5.36	Wet		4.63	59	< <b>0.0001</b>
Site*Clone	Dry	1	5.36	Dry	2	5.35	59	0.9918
Site*Clone	Dry	1	5.36	Wet	1	4.83	59	<b>0.0029</b>
Site*Clone	Dry	1	5.36	Wet	2	4.42	59	< <b>0.0001</b>
Site*Clone	Dry	2	5.35	Wet	1	4.83	59	<b>0.003</b>
Site*Clone	Dry	2	5.35	Wet	2	4.42	59	< <b>0.0001</b>
Site*Clone	Wet	1	4.83	Wet	2	4.42	59	<b>0.0159</b>

## Appendix H: Clonal Analysis

Table 2: Differences of least square means of fixed effects of individual clone genetics with pairwise comparisons for **total height** (feet). For example, the difference between the dry site mean (29.09 feet) and the wet site mean (24.66 feet) is significant at  $P < 0.0001$ . The difference between Site\*Clone mean Dry-Clone 1 (28.59 feet) and Dry-Clone 2 (29.60 feet) is not significant.

Differences of Least Squares Means								
Effect	Site	Clone	Mean	Site	Clone	Mean	DF	Pr >  t
Site	Dry		29.09	Wet		24.66	59	< <b>0.0001</b>
Site*Clone	Dry	1	28.59	Dry	2	29.60	59	0.0886
Site*Clone	Dry	1	28.59	Wet	1	25.75	59	< <b>0.0001</b>
Site*Clone	Dry	1	28.59	Wet	2	23.58	59	< <b>0.0001</b>
Site*Clone	Dry	2	29.60	Wet	1	25.75	59	< <b>0.0001</b>
Site*Clone	Dry	2	29.60	Wet	2	23.58	59	< <b>0.0001</b>
Site*Clone	Wet	1	25.75	Wet	2	23.58	59	<b>0.0005</b>

## Appendix H: Clonal Analysis

Table 3: Differences of least square means of fixed effects of individual clone genetics with pairwise comparisons for **predicted total volume outside bark**. For example, the difference between the dry site mean (2.32 ft<sup>3</sup>) and the wet site mean (1.70 ft<sup>3</sup>) is significant at P<0.0001. The difference between Site\*Clone mean Dry-Clone 1 (2.27 ft<sup>3</sup>) and Dry-Clone 2 (2.37 ft<sup>3</sup>) is not significant.

Differences of Least Squares Means								
Effect	Site	Clone	Mean	Site	Clone	Mean	DF	Pr >  t
Site	Dry		2.32	Wet		1.70	59	< <b>0.0001</b>
Site*Clone	Dry	1	2.27	Dry	2	2.37	59	0.3754
Site*Clone	Dry	1	2.27	Wet	1	1.86	59	<b>0.0003</b>
Site*Clone	Dry	1	2.27	Wet	2	1.53	59	< <b>0.0001</b>
Site*Clone	Dry	2	2.37	Wet	1	1.86	59	< <b>0.0001</b>
Site*Clone	Dry	2	2.37	Wet	2	1.53	59	< <b>0.0001</b>
Site*Clone	Wet	1	1.86	Wet	2	1.53	59	<b>0.0023</b>

## Appendix H: Clonal Analysis

Table 4: Differences of least square means of fixed effects of individual clone genetics with pairwise comparisons for **coefficients of variation of DBH**. For example, the difference between the dry site mean (15.16) and the wet site mean (22.37) is significant at  $P < 0.0001$ . The difference between Site\*Clone mean Dry-Clone 1 (14.71) and Dry-Clone 2 (15.62) is not significant.

Differences of Least Squares Means										
Effect	Site	Treatment	Clone	Mean	Site	Treatment	Clone	Mean	DF	Pr >  t
Site	Dry			15.16	Wet			22.37	59	< <b>0.0001</b>
Clone			1	17.90			2	19.63	59	0.0872
Site*Clone	Dry		1	14.71	Dry		2	15.62	59	0.5191
Site*Clone	Dry		1	14.71	Wet		1	21.10	59	< <b>0.0001</b>
Site*Clone	Dry		1	14.71	Wet		2	23.65	59	< <b>0.0001</b>
Site*Clone	Dry		2	15.62	Wet		1	21.10	59	<b>0.0003</b>
Site*Clone	Dry		2	15.62	Wet		2	23.65	59	< <b>0.0001</b>
Site*Clone	Wet		1	21.10	Wet		2	23.65	59	0.0748
Mxture*Clone		OP	1	17.38		OP	2	20.94	59	<b>0.0205</b>
Mxture*Clone		Pure	1	17.01		OP	2	20.94	59	<b>0.0356</b>
Mxture*Clone		OP	2	20.94		SOM	2	17.74	59	<b>0.0363</b>

## Appendix H: Clonal Analysis

Table 5: Differences of least square means of fixed effects of individual clone genetics with pairwise comparisons for **coefficients of variation of total stem height**. For example, the difference between the dry site mean (10.76) and the wet site mean (15.92) is significant at  $P < 0.0001$ . The difference between Site\*Clone mean Dry-Clone 1 (11.00) and Dry-Clone 2 (10.51) is not significant.

Differences of Least Squares Means										
Effect	Site	Treatment	Clone	Mean	Site	Treatment	Clone	Mean	DF	Pr >  t
Site	Dry			10.76	Wet			15.92	59	< <b>0.0001</b>
Clone			1	12.97			2	13.70	59	0.2796
Site*Clone	Dry		1	11.00	Dry		2	10.51	59	0.6063
Site*Clone	Dry		1	11.00	Wet		1	14.94	59	<b>0.0002</b>
Site*Clone	Dry		1	11.00	Wet		2	16.89	59	< <b>0.0001</b>
Site*Clone	Dry		2	10.51	Wet		1	14.94	59	< <b>0.0001</b>
Site*Clone	Dry		2	10.51	Wet		2	16.89	59	< <b>0.0001</b>
Site*Clone	Wet		1	14.94	Wet		2	16.89	59	<b>0.045</b>
Mxture*Clone		SOM	2	12.18		OP	2	14.38	59	<b>0.0335</b>
Mxture*Clone		Pure	2	14.55		SOM	2	12.17	59	0.0599

## Appendix H: Clonal Analysis

Table 6: Differences of least square means of fixed effects of individual clone genetics with pairwise comparisons for **coefficients of variation of predicted total outside bark volume**. For example, the difference between the dry site mean (31.22) and the wet site mean (44.36) is significant at  $P < 0.0001$ . The difference between Site\*Clone mean Dry-Clone 1 (30.43) and Dry-Clone 2 (32.02) is not significant.

Differences of Least Squares Means										
Effect	Site	Treatment	Clone	Mean	Site	Treatment	Clone	Mean	DF	Pr >  t
Site	Dry			31.22	Wet			44.36	59	< <b>0.0001</b>
Clone			1	36.04			2	39.54	59	0.0817
Site*Clone	Dry		1	30.43	Dry		2	32.02	59	0.5699
Site*Clone	Dry		1	30.43	Wet		1	41.66	59	<b>0.0002</b>
Site*Clone	Dry		1	30.43	Wet		2	47.07	59	< <b>0.0001</b>
Site*Clone	Dry		2	32.02	Wet		1	41.66	59	<b>0.0012</b>
Site*Clone	Dry		2	32.02	Wet		2	47.07	59	< <b>0.0001</b>
Site*Clone	Wet		1	41.66	Wet		2	47.07	59	0.0578
Mxture*Clone		OP	1	35.77		OP	2	42.27	59	<b>0.0325</b>
Mxture*Clone		Pure	1	34.36		OP	2	42.27	59	<b>0.0337</b>
Mxture*Clone		OP	2	42.27		SOM	2	35.50	59	<b>0.0264</b>