COMPARISON OF SHORTLEAF PINE FAMILIES AND SEED SOURCES IN SOME OUACHITA NATIONAL FOREST PROGENY TESTS

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Abstract—Shortleaf pine (*Pinus echinata* Mill.) has declined significantly (by over 50 percent) across its range due in part to a lack of both artificial and natural regeneration. A series of shortleaf pine progeny tests, established rangewide from the late 1970s into the early 1990s, offers promise for addressing some of the silviculture and restoration concerns related to this decline. Eighty-four of these shortleaf pine progeny tests were established on the Ouachita and Ozark-St. Francis National Forests. These 33-family (on average), full-sib progeny tests were produced from parent trees growing in the Mount Ida Seed Orchard. These parents originated from three geographic seed source regions in Arkansas and Oklahoma: East Ouachita, West Ouachita, and Ozark. In 2018 and 2019, we remeasured diameter at breast height (d.b.h.), tree height, and survival and recorded general tree health conditions from seven well-stocked progeny tests that were installed in the East and West Ouachita regions. We combined our measurements with those taken in the past to help determine if performance differences over time could be found among these shortleaf pine families. Our preliminary analysis indicated differences in d.b.h., height, and survival—information that should help silviculturists making decisions about which shortleaf families may prove most useful for restoration and tree improvement purposes in the region.

INTRODUCTION

Shortleaf pine (*Pinus echinata* Mill.) has the largest natural range of the four major southern pines, occurring in 22 States from New York to Texas (Little 1971). Shortleaf pine was once the dominant pine species across much of this region due to its adaptability to a large variety of edaphic and climatic conditions (Mattoon 1915, Mohr and Roth 1897). The species is also important for wildlife habitat and timber products such as sawtimber and pulpwood (Lawson 1990, Studyvin and Gwaze 2012). However, changes in land use and forest management practices (for example, fire suppression, conversion to intensely managed loblolly pine, and limited artificial shortleaf pine regeneration), insufficient natural regeneration, and other environmental changes and forest health factors over the last half-century have all contributed to a decline in the coverage and importance of shortleaf pine (Stewart and others 2013, 2015). Although this decline has been ongoing over the last century, the most dramatic losses have occurred since the 1980s, with shortleaf pine acreage down by 52 percent by 2012 (Oswalt 2012).

The ecological and economic importance of shortleaf pine, coupled with its genetic diversity, have made the species an excellent candidate for genetic improvement (Studyvin and Gwaze 2007). Consequently, some tree improvement efforts have been undertaken to improve the performance of the species for timber production (Stewart and others 2016). The Forest Service, U.S. Department of Agriculture has studied the genetics and potential for tree improvement of shortleaf pine since at least the 1950s (Kitchens 1986). This effort included the National Forest System's establishment in the 1960s of a formal shortleaf pine tree improvement program and five first-generation seed orchards (located in Arkansas, Louisiana, Mississippi, North Carolina, and Tennessee) representing 12 geographic zones. Each orchard contained breeding material from at least 50 selected superior clones. In the 1970s, full-sib families were developed through controlled breeding for seed production, progeny testing, and potential second-generation orchard establishment (Zarnoch and others 1994).

Intended to help support the Forest Service's reforestation programs at that time, 155 shortleaf pine progeny tests were installed between 1978 and 1990 on various national forests using seedlings from full-sib families (Studyvin and Gwaze 2007). As part of this effort, 84 shortleaf pine progeny tests were placed in the Ouachita and Ozark-St. Francis National

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Forests using full-sib families from the Mount Ida Seed Orchard in Arkansas (Studyvin and Gwaze 2012). These progeny tests were based on three local (Arkansas and Oklahoma) geographic seed source regions—East Ouachita, West Ouachita, and Ozark. Families were selected on the basis of survival, insect and disease resistance, straightness and form, and height and volume growth. Although the three seed sources were designated by ecotype and were not widely separated by distance, they did capture environmental gradients. For example, the West Ouachita and Ozark regions generally have more severe summer droughts than the East Ouachita, offering an opportunity to disentangle some performance-related differences (La Farge 1991).

Only a couple of researchers have revisited these shortleaf pine progeny tests on the Ouachita and Ozark-St. Francis National Forests. In one study, La Farge (1991) found that the three seed sources were not significantly different for height and survival at age 5, leading him to recommend that the three seed sources be maintained as one population for tree breeding purposes. A later analysis—probably the last done on these shortleaf pine progeny tests—by Studyvin and Gwaze (2012) found a significant difference among families and seed sources for both diameter and height at 10 years of age. They concluded that family selection will be effective due to large family differences for all traits selected.

A shift in agency management priorities (less focus on national forest timber production using plantations and more focus on genetic diversity for resilience) led to most of these progeny plantings being abandoned after the mid-1990s (Crane 2014). However, in recent years shortleaf pine has become a species of conservation concern across its range (Anderson and others 2016, Oswalt 2012). Consequently, efforts are underway to halt, if not reverse, the decline of shortleaf pine using ecosystem restoration, particularly in the national forests of Arkansas and Oklahoma (Guldin 2007). Now that these progeny tests are between 30 and 40 years old, it is desirable to see if additional changes in performance have occurred in the remaining outplantings and if that information can help supplement current management strategies. Therefore, the primary objective of this study was to examine the relative performance of trees in a subset of the shortleaf pine progeny tests located on the Ouachita National Forest to determine if significant differences exist in size and survival among tested families.

MATERIALS AND METHODS

Study Area

The study area was located in the Ouachita National Forest in western Arkansas (fig. 1). The east-to-west running ridges of the Ouachita Mountains are composed of Paleozoic rocks consisting of alternating layers of sandstone and shale. Annual precipitation (primarily rainfall) in these mountains usually ranges between 50 and 60 inches, while annual average temperature ranges from 57 to 61 degrees F (PRISM Climate Group 2013, Pugh and Westerman 2014). The Ouachita Mountains have distinct east-to-west bands of vegetation depending upon parent materials, soil moisture

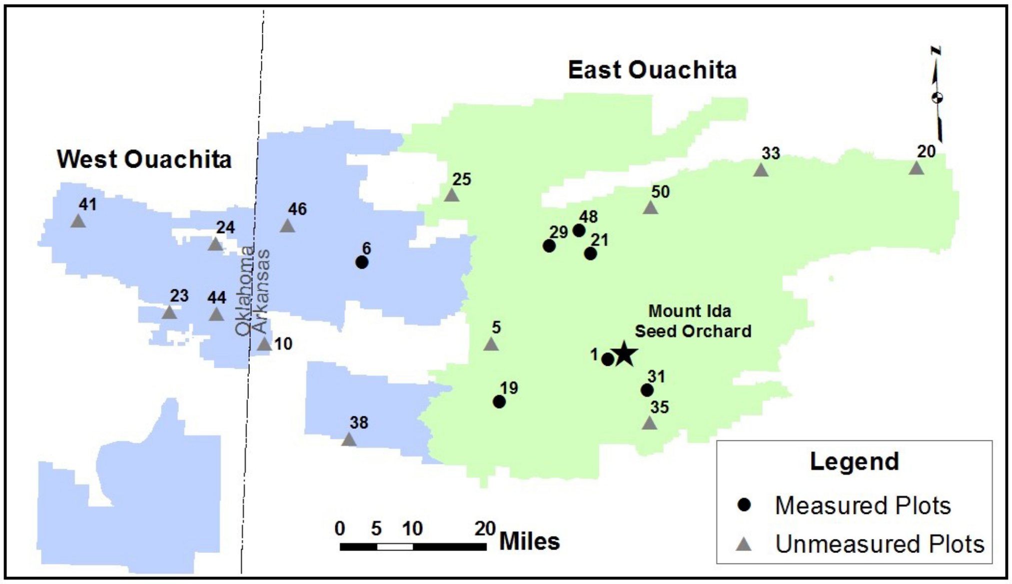

Figure 1—Shortleaf pine progeny test plantings (circles in black and grey triangles) selected for sampling in the East Ouachita (green background) and West Ouachita (blue background) seed source regions. The star symbol denotes the location of the Mount Ida Seed Orchard in the Ouachita National Forest. The circles in black represent the seven progeny test plantings.

availability, and radiation regimes (Foti 2019). The more xeric south-facing slopes, for example, were often covered with pine forests or oak woodlands, while the moister north-facing slopes were covered with denser, more diverse hardwood forests.

Design of Crosses and Outplantings

Details of the original progeny crossing design are presented in La Farge (1991) and Studyvin and Gwaze (2012). In summary, the design of the full-sib shortleaf pine progeny tests was a six-by-six disconnected partial diallel crossing scheme, such that each partial diallel crossing group consisted of six parents, two from each seed source (East Ouachita, West Ouachita, and Ozark). Crossing among all parents using this scheme resulted in 15 groups, which were used to develop 375 full-sib families/crosses. In each of these diallels, there were three crosses between parents from the same seed source, while the other 12 crosses were between parents from different seed sources. To maintain the integrity of the seed sources, care was taken so that crosses used for analysis represented parents of the same seed source and that all crosses were single-pair matings and were unrelated.

The planting design consisted of row plantings (8- by 8-feet) of 10 trees per row (per family, with an average of 33 families in each test) using a completely randomized block design with five replications.[1] Within each test, replicates were not complete as not all families were present in all replicates at that test location. Also not all families were planted in all progeny tests. This planting design was originally installed by the Forest Service and was the basis for two prospective measurements known as first interval evaluation (FIE) and second interval evaluation (SIE) conducted at 5 and 10 years.

Contemporary Remeasurements

Because over the years many of the tests had been heavily damaged or destroyed by ice, insects, fire, wind, or logging, starting in 2018, we chose a subset of the 84 shortleaf pine progeny tests on the Ouachita and Ozark-St. Francis National Forests for further consideration using a multi-step process. First, with a 2013 assessment on the amount of basal area per replicate done by Forest Service contractor and Certified Forest Silviculturist John Blanton, we categorized the still-forested tests into three groups depending on stocking level—excellent [at least two replicates were fully stocked (had at least 100 square feet of basal area per acre of live trees)], good (one replicate was fully stocked), and marginal (no replicates were fully stocked). Of the 20 progeny tests possible on the Ouachita National Forest available (fig. 1), we ended up having 10, 9, and 1 test representing excellent, good, and marginal categories, respectively. Second, we visited the excellent to good tests to determine if any had been destroyed since Blanton's 2013 assessment. Once acceptable progeny tests were located, measurements commenced, with seven being completed by the time of this paper.

In 2018 and 2019, shortleaf pines were identified based on tags placed beside them during planting and their location on maps. All trees in a row (family) were counted either live or dead to account for survival (in terms of percentage). We systematically selected five trees per row in each replicate for diameter at breast height (d.b.h.) measurement (in inches), and two trees were randomly selected to measure total tree height (in feet) from those trees selected for d.b.h. measurement. If a dead or missing tree was encountered, the next live tree would be chosen for both d.b.h. and height measurements. Additionally, status codes were recorded for both live (for example, ice damage, genetic fork, and Ips beetles) and dead trees (for example, dead standing, dead and down, and dead missing).

Statistical Analysis

The statistical analysis used in this study was similar to those used by La Farge (1991) and Studyvin and Gwaze (2012). We employed Proc GLM (General Linear Model) of SAS (SAS Institute Inc. 1989) to estimate if families differed in d.b.h., height, and survival at age 40. Plot means were used for the analysis, and survival was arcsine transformed before the analyses. The GLM was used to account for imbalance of data associated with unequal number of replicates and families. The independent variables tested were full-sib family within seed source and test location. The model assumed was a mixed-effects model, with full-sib family as a fixed effect, test location as a random effect, and a proper error term (random effect) for testing family differences was the family by test location interaction. We chose a subset of families based on their presence in multiple test locations when presenting results related to tree size (for example, descriptive statistics for d.b.h. and height) for the sake of brevity.

RESULTS

We presented results based on the seven progeny tests sampled to March of 2019—six from the East Ouachita and one from the West Ouachita seed source regions. A total of 176 families across the progeny test plantings were sampled in this study, ranging between 4 and 29 per test location (table 1). Of the total families sampled, 140 appeared in only one test, while 36 were represented in more than one test (table 1). Only seven families were found in more than two test plantings, all of which were common in both the East and West Ouachita seed source regions (table 2).

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[1] Personal communication. 2019. B. Rowland, Manager, Mount Ida Seed Orchard, Ouachita National Forest, Mount Ida, AR 71957.

Table 1—Number of families by progeny test and live trees in shortleaf pine progeny plantings on the East and West Ouachita seed source regions

Test	Location	Number of unique families[b]	Number of shared families[c]	Live trees	
				Total	Percent[d]
Test 1	Womble RD	19	9	434	47.7
Test 6	Mena RD[a]	12	31	848	50.5
Test 19	Womble RD	4	31	625	36.3
Test 21	Oden RD	27	9	659	49.1
Test 29	Oden RD	26	7	772	58.9
Test 31	Womble RD	23	6	678	51.8
Test 48	Oden RD	29	5	706	47.7

RD = Ranger District of the Ouachita National Forest.

[a] West Ouachita progeny test.

[b] One hundred and forty families used only in one test.

[c] Thirty-six families were used in more than one test (ranged between two and seven tests).

[d] Percent of planted trees still alive in 2019.

Table 2—Shortleaf pine families appearing in more than two progeny test plantings

Family	Number of tests	Live trees		d.b.h.		Total height	
		Number	Percent[a]	Mean[b]	SD	Mean[b]	SD
				-------------*inches*----------		------------*feet*------------	
103×201	6	155	57.2	10.1 (4.9–14.3)	1.23	61.1 (34–85)	9.87
115×312	6	139	54.8	9.7 (4.6–13.4)	0.89	58.5 (36–82)	10.60
120×333	5	133	62.7	9.5 (4.1–13.6)	0.92	56.4 (38–80)	9.53
233×135	3	78	56.3	11.2 (6.5–17.6)	1.40	65.5 (48–82)	7.52
901×322	7	129	50.1	9.3 (5.1–15.1)	1.31	57.5 (38–79)	10.60
901×620	7	147	49.4	9.4 (4.5–16.8)	0.79	56.6 (37–77)	10.80
913×319	7	164	56.7	9.6 (5.2–13.5)	1.09	57.8 (37–80)	10.30

d.b.h. = diameter at breast height; SD = standard deviation.

[a] Percent of planted trees still alive in 2019.

[b] The numbers in parentheses denote minimum and maximum values for tree d.b.h. and height.

Growth Performance

There was considerable variation in tree size from family to family at age 40 (table 2). Average tree diameter and height among 7 of the 176 families ranged between 9.3 and 11.2 inches d.b.h. [standard deviations (SD) ranged between 0.8 to 1.4 inches] and approximately 56 and 66 feet tall (SD = 7.5 to 10.8 feet), respectively (table 2). Tree size also varied considerably within 7 of the 176 families—tree diameter ranges varied from 8 to 12 inches d.b.h., while tree height ranges varied from 34 to 51 feet (table 2).

The differences among all families sampled were significant for both d.b.h. ($p < 0.001$) and height ($p < 0.05$) (table 3). Consistent with our results, two prior studies conducted at age 5 and 10, respectively, had also found a significant ($p < 0.05$) effect of family on tree height (La Farge 1991) and d.b.h. (Studyvin and Gwaze 2012). For reasons that will be discussed later, no further analysis of growth performance (e.g., d.b.h. and tree height) was conducted.

Survivorship

Forty years after installation, approximately 49 percent of shortleaf pine trees survived in the progeny test plantings visited (table 1). This is a noticeable drop from earlier measurements of these progeny tests, which showed good early survival. At age 5, for example, seedling survival in these progeny tests was above 91 percent (La Farge 1991), while at age 10, mean seedling survival was about 72 percent (Studyvin and Gwaze 2012). A more recent estimate (2012) showed that

Table 3—ANOVAs for d.b.h., total tree height, and survival at age 40

Metric	Source of variation	Degrees of freedom	Type II SS	Mean square	F value	*p*-value
d.b.h.	Family	175	294.50	1.68	1.83	0.0001
	Test	6	173.90	28.90		
	Family × Test	59	64.83	1.09		
Tree height	Family	175	4513.40	25.37	1.03	0.0320
	Test	6	20060.10	3343.30		
	Family × Test	59	1312.10	22.23		
Survival	Family	175	16.15	0.09	2.01	0.0001
	Test	6	3.13	0.52		
	Family × Test	59	5.24	0.08		

d.b.h. is diameter at breast height.

survival rate was about 65 percent (Stewart and others 2016). There appeared to be a slightly higher rate of survival in the only West Ouachita test (approximately 51 percent) as compared to the six East Ouachita tests (approximately 48 percent). Survivorship also varied among families. Of the seven families that were found in more than two tests, mean family survival rate ranged between approximately 49 and 63 percent (table 2). Furthermore, survival differed significantly ($p < 0.001$) among all families (table 3). Neither the test nor family by test interaction variable showed any significant effect on any of the traits examined (table 3).

DISCUSSION

Although the original intent of this study was to more broadly compare these shortleaf pine progeny tests for differences in d.b.h., height, and survival rate, logistical challenges limited our data collection to primarily the East Ouachita tests, with just one test from the West Ouachita source. This constrained our ability to determine the relative success of various families across the three seed sources in the Ouachita and Ozark-St. Francis National Forests. Nevertheless, even this limited sample can suggest a number of important lessons for managers.

For example, Studyvin and Gwaze (2012) recommended maintaining a single breeding population of shortleaf pine rather than three across national forests based on the presence of good families from all seed sources in a prior study. However, our results indicated the persistence of family differences in tree size (growth performance) even 40 years after planting. The large, significant family differences suggest that there were both superior and inferior families within a seed source that may be of utility not only to family-based selection but also to evaluate seed sources determined in the past.

Family differences in survival also persisted through age 40. These results corroborated the findings of Studyvin and Gwaze (2012), who demonstrated a highly significant effect of family on survival at 10 years. However, given the impact of stressors and environmental disturbances, which were not controlled in this study, it would not be appropriate to attribute all survival-related variances to inherent differences among families. Also, we did not have an unbiased sample of these families—after all, we deliberately selected only those tests that had relatively high stocking to help ensure we had as much growth and yield information as possible on the families being tested. Furthermore, because of data imbalance (stated above) and inadequate representation of all families over the study area, we were not inclined to conduct mean separation between families for d.b.h. and height.

Even in these well-stocked progeny tests, the fact that just under half of the shortleaf pine trees have survived after this length of time is not surprising, given decades of losses to competition, disease, insects, and weather events (including multiple severe ice storms and droughts). Indeed, our field observations over the last couple of years (data not shown) while measuring these tests found that more than 75 percent of all live trees had been damaged by ice storms and/or Ips beetles. Losses due to drought may also affect survivorship as a result of changes in environmental conditions. For example, it is hypothesized that the progeny plantings in the West Ouachita seed source region are likely to have better survival than those from the East Ouachita region, ostensibly due to adaptations to summer drought (Studyvin and Gwaze 2012). Unfortunately, we do not have sufficient data at this time to evaluate this hypothesis.

CONCLUSIONS

Despite data limitations associated with partial coverage of study area, and natural disturbances that affected progeny plantings over the decades, we believe these progeny tests can be used to select families with better survivorship, diameter growth, and height performance, with evidence of both superior and inferior families in a given seed source. The observed family differences for all three traits suggest that the selection process for planting should focus on identifying individuals from the superior families for future second- and third-generation tree improvement efforts. However, within the National Forest System, the current objective of the seed orchards is to maximize genetic diversity in support of adaptation and resilience. Multiple selections will therefore need to be maximized and balanced to meet that objective. As more data are available from all seed sources in the future, further comparison of performance of the progeny tests would be beneficial to determine families that are able to withstand environmental stressors for restoration efforts. Such comparisons would also be useful to not only assess seed source influence on important traits but also to evaluate the rationale for seed source determinations for breeding purposes.

In addition to evaluating the value of genetic selections for tree improvement and genetic diversity, old progeny tests offer opportunities to provide additional guidance for shortleaf pine conservation efforts (Stewart and others 2016). For instance, these shortleaf pine progeny tests could be used in conjunction with DNA fingerprinting to better understand the capacity of this species to adapt to future climate change. After all, concerns of the role of changing environments on hybridization rates in shortleaf pine have been raised by others (for example, Crane and others 2019; Stewart and others 2013, 2015).

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