Growth and Growth Efficiency of Loblolly and Slash Pine Hybrid Stands

Jennifer Lauture

June 2017

CFGRP and FBRC Hybrid Site

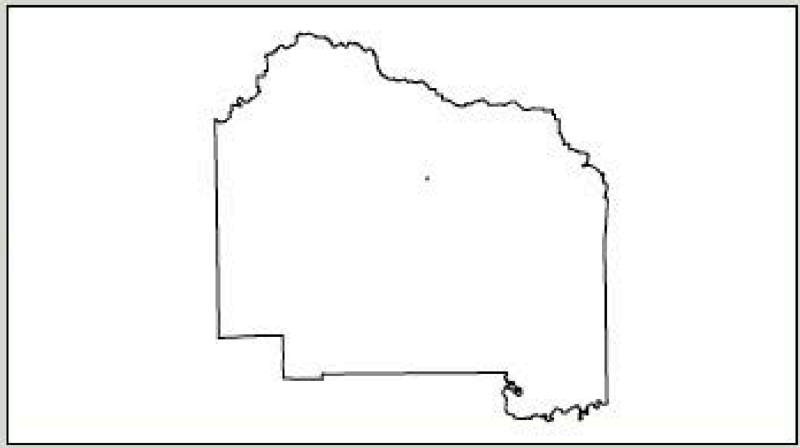
- Well field pseudo-backcross hybrid study
  - Planted in 2012
  - Location: Murphree Well Field Site Gainesville, Florida
- 3420 total trees planted
  - Replicate 1: conventional management scenario
  - Replicate 2: high intensity fertilization
- Families
  - Pure loblolly OP
  - Pure slash OP
  - Pseudo backcross loblolly
  - Pseudo backcross slash - 2

Wellfield - Loblolly and Slash Pine Backcross Hybrids

Source: Esri, DigitalGlobe, GeoEye, Earthstar Geographics, CNES/Airbus DS, USDA, USGS, AEX, Getmapping, Aerogrid, IGN, IGP, swisstopo, and the GIS User Community

Author: Jennifer Lauture
Date: April 28, 2016

Scale
1:10,000

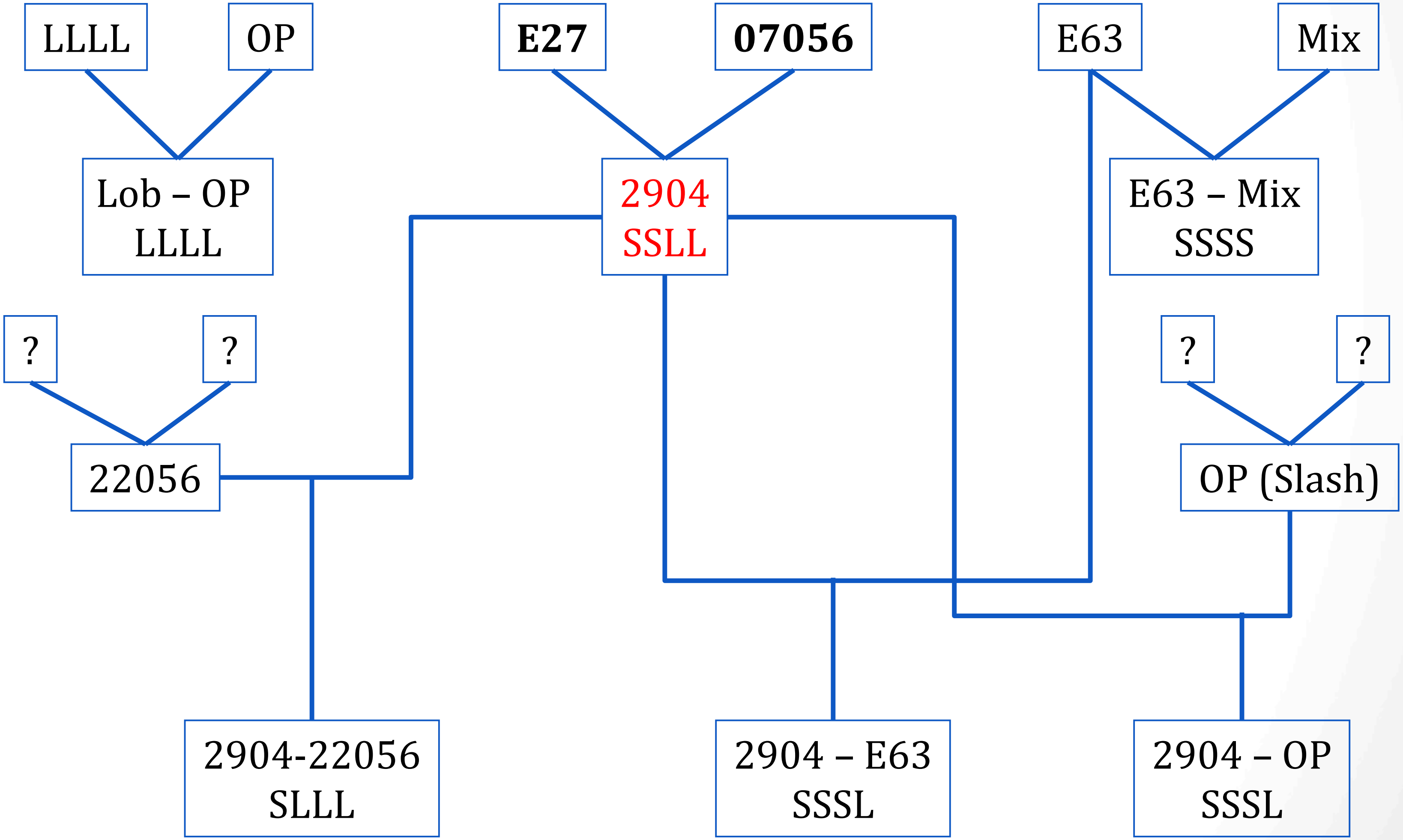


Wellfield Backcross
Hybrid Test

🟦 Replicate 1
🟧 Replicate 2
▭ Alachua County

Source: ESRI and U.S. Census Bureau
Projection Information:
Albers Conical Equal Area

Experimental Design and Methodology – Planted Hybrids



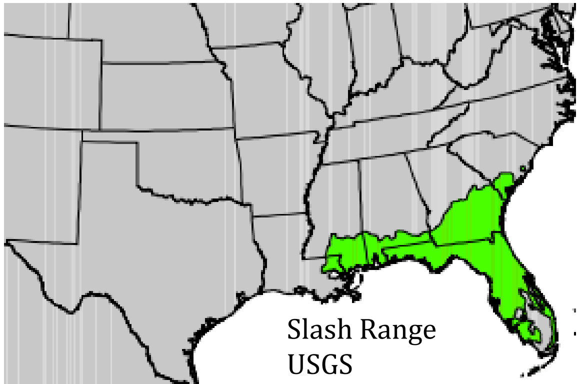
Study Objectives

- Analyze efficiency and genetic control of phenotypic traits
- Assess how growth traits are affected in backcrossed hybrids

Differences Between Slash and Loblolly Pine

Slash Pine

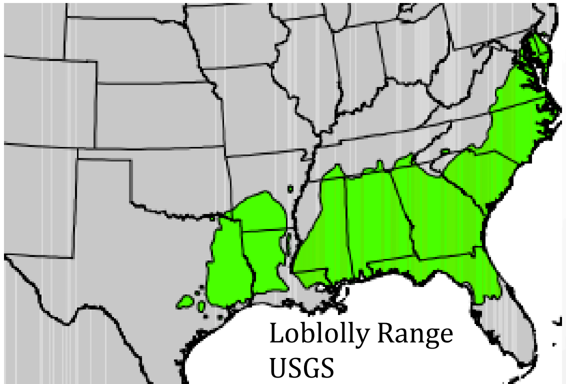
- Better growth in very poorly drained sites
- More resistant to wind damage
- Better stem form
- Smaller crown
- 14 million acres in the U.S.



Slash Range
USGS

Loblolly Pine

- More responsive to nutrient management
- More resistant to fusiform rust
- More productive during early developmental stages
- Larger crown
  - More secondary branching
- 30 million acres in the U.S.

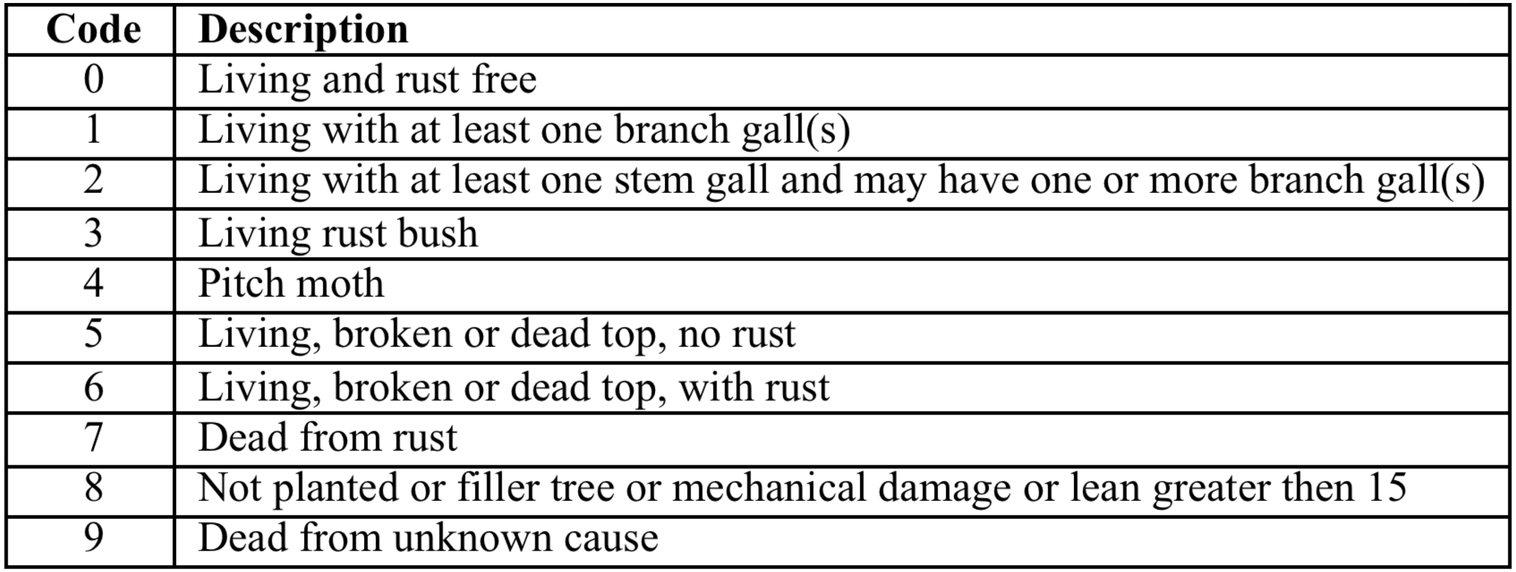


Loblolly Range
USGS

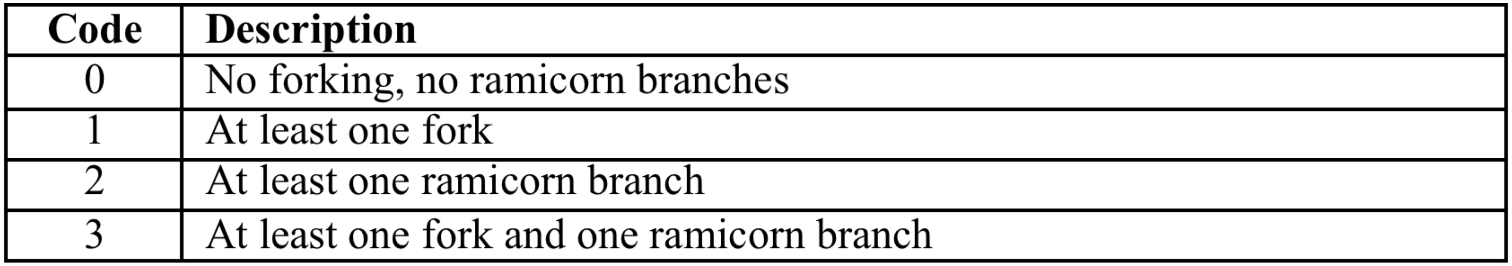
Phenotypic Traits Measured – Year 3

- Status: disease and mortality
- Stem form
- Height (ft)
- DBH (in)
- Crown length along and across planting bed (ft)
- Number of primary branches
- Number of primary branches at node 3 and 5
- Number of secondary branches at node 3 and 5

Status and Stem Form Codes



Code	Description
0	Living and rust free
1	Living with at least one branch gall(s)
2	Living with at least one stem gall and may have one or more branch gall(s)
3	Living rust bush
4	Pitch moth
5	Living, broken or dead top, no rust
6	Living, broken or dead top, with rust
7	Dead from rust
8	Not planted or filler tree or mechanical damage or lean greater then 15
9	Dead from unknown cause



Code	Description
0	No forking, no ramicorn branches
1	At least one fork
2	At least one ramicorn branch
3	At least one fork and one ramicorn branch

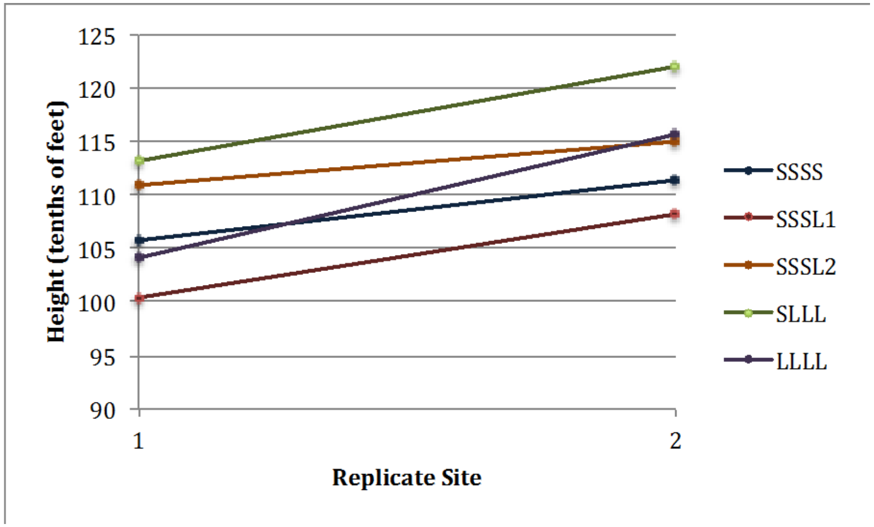
Linear Mixed Model

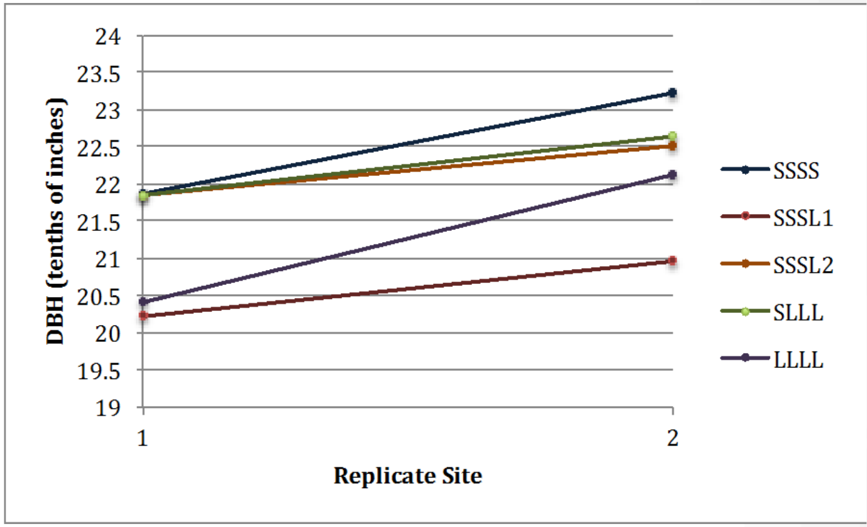
- Y = Rep + Family + Rep:Block
  - Rep: fixed replicate plot (1 to 2) effect
  - Family: fixed family effect
  - Rep:Block: Fixed replicate plot by block (1 to 95) effect
- Used to calculate least squares means

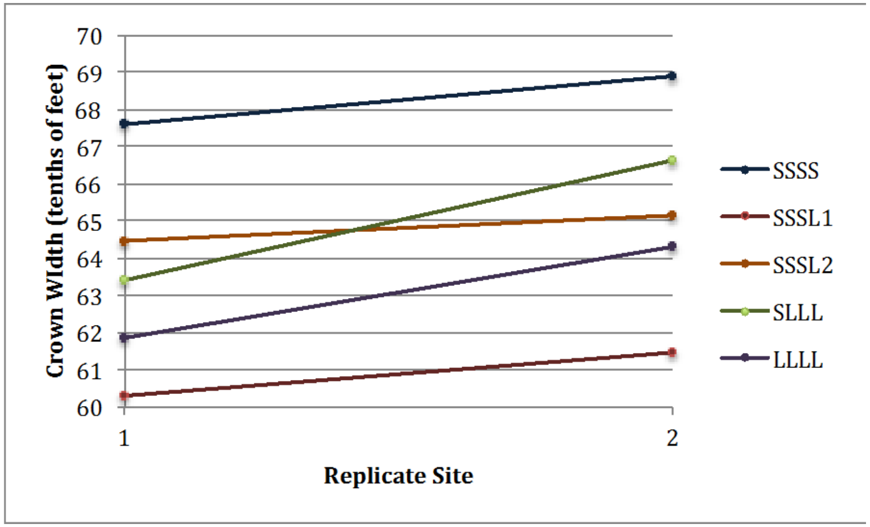
Summary Data Year 3

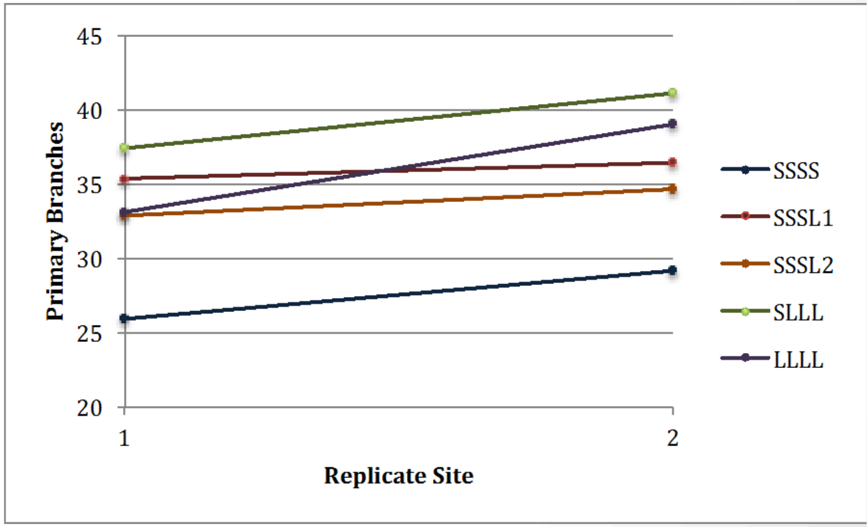
Year 3 Measurements				
	SSSS	**SSSL**	**SLLL**	**LLLL**
Height (tenths ft)	108.61 (1.25)	104.21 (1.97)	117.32 (0.79)	109.99 (1.33)
		113.13 (1.03)		
DBH (tenths in)	22.52 (0.31)	20.47 (0.49)	22.15 (0.20)	21.31 (0.33)
		22.20 (0.26)		
Crown (tenths ft)	68.19 (0.68)	60.81 (1.10)	64.80 (0.43)	63.03 (0.72)
		65.03 (0.57)		
Primary Branch	27.48 (0.47)	35.72 (0.76)	39.17 (0.29)	36.58 (1.09)
		33.82 (0.39)		
Primary Branch Node 3	2.64 (0.08)	3.16 (0.13)	2.97 (0.05)	3.20 (0.18)
		2.77 (0.07)		
Secondary Branch Node 3	9.28 (0.93)	23.71 (1.50)	29.22 (0.58)	27.74 (2.14)
		14.74 (0.77)		
Primary Branch Node 5	2.89 (0.08)	3.18 (0.13)	3.46 (0.05)	3.84 (0.18)
		3.46 (0.07)		
Secondary Branch Node 5	5.85 (0.87)	17.39 (1.40)	25.00 (0.54)	28.67 (1.99)
		10.13 (0.72)		

Genotype by Environment Effects?

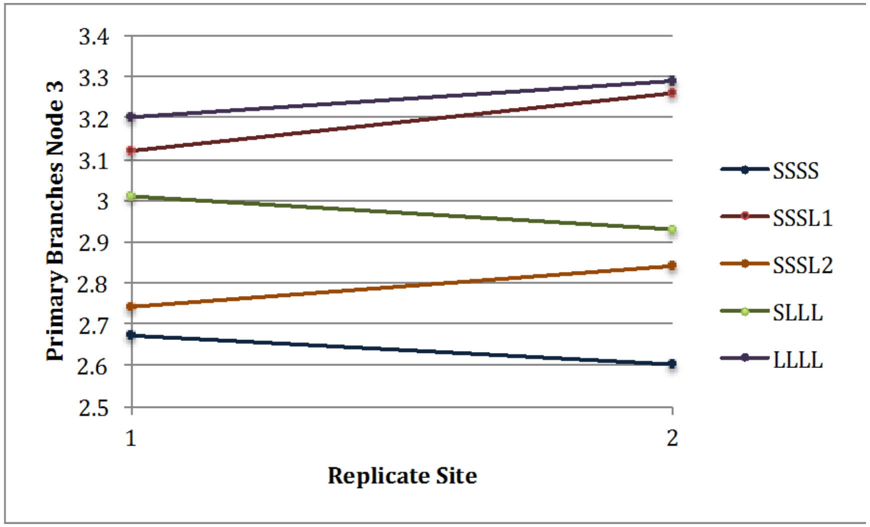


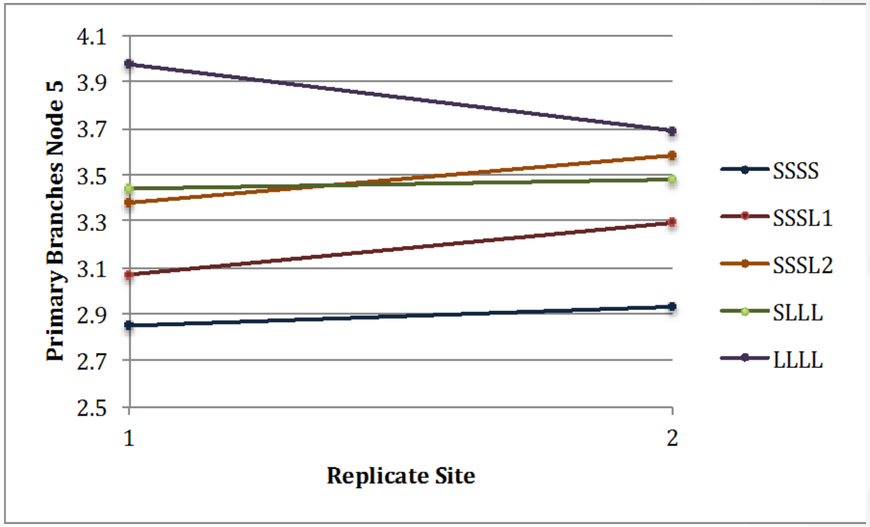


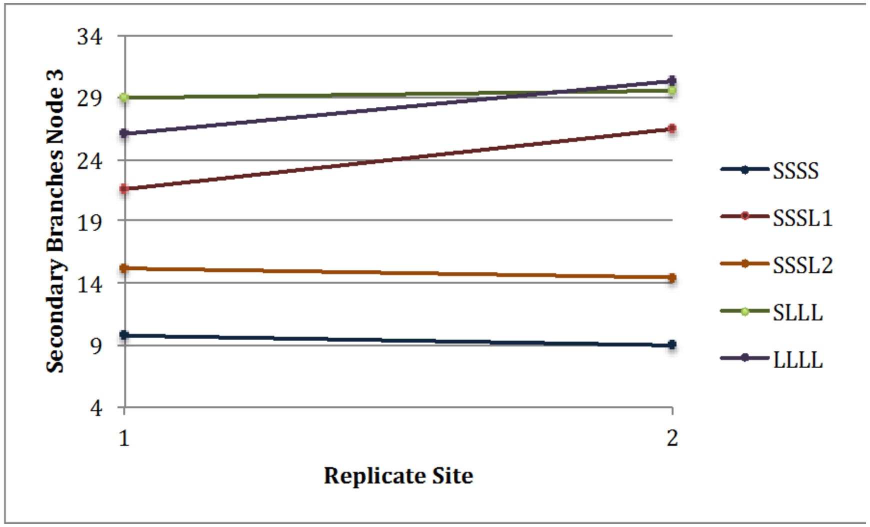


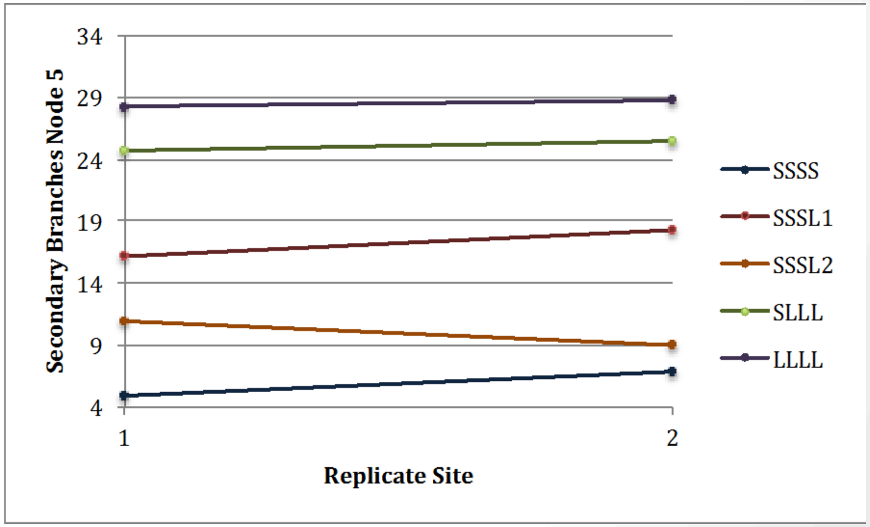


Genotype by Environment Effects?









Growth Efficiency – Year 3

Year 3 Measurements				
	SSSS	**SSSL**	**SLLL**	**LLLL**
Height/Crown	1.65 (0.01)	1.85 (0.02)	1.88 (0.01)	1.80 (0.01)
		1.85 (0.01)		
DBH/Crown	0.33 (0.003)	0.35 (0.005)	0.34 (0.002)	0.34 (0.003)
		0.35 (0.003)		
Primary Branch/Crown	0.41 (0.008)	0.60 (0.012)	0.61 (0.005)	0.58 (0.018)
		0.53 (0.006)		

Mortality – Year 1

1st Year Survival				
Family	**Total Planted**	**Total Mortality**	**% Mortality**	**% Survival**
SLLL	1254	35	2.8%	97.2%
SSSL1	214	16	7.5%	92.5%
SSSL2	1083	300	27.7%	72.3%
SSSS	517	17	3.3%	96.7%
LLLL	449	20	4.5%	95.5%
Total	3517	388	11%	89%

Disease and Mortality – Year 3

Disease and Mortality Status By Environment				
Family	**Rust**	**Rust Mortality**	**Pitch Moth**	**Mortality**
SLLL	8.97%	0.06%	1.73%	0.47%
Replicate 1	4.06%	0.06%	0.94%	0.18%
Replicate 2	4.91%	0%	0.79%	0.29%
SSSL1	1.17%	0%	0.32%	0.21%
Replicate 1	0.56%	0%	0.12%	0.12%
Replicate 2	0.61%	0%	0.20%	0.09%
SSSL2	2.96%	0.03%	1.72%	2.08%
Replicate 1	1.67%	0.03%	0.73%	0.99%
Replicate 2	1.29%	0%	0.99%	1.08%
SSSS	2.46%	0.18%	1.17%	0.44%
Replicate 1	1.11%	0.12%	0.56%	0.18%
Replicate 2	1.35%	0.06%	0.61%	0.26%
LLLL	0.56%	0%	0.42%	0.20%
Replicate 1	0.15%	0%	0.23%	0%
Replicate 2	0.41%	0%	0.18%	0.20%
Total	16.12%	0.27%	5.36%	3.39%

Stem Form – Year 3

Stem Form By Environment

Family	None	Forking	Ramicorn Branching	Both
SLLL	11.38%	5.55%	15.69%	5.74%
Replicate 1	6.12%	2.81%	7.97%	2.52%
Replicate 2	5.26%	2.74%	7.72%	3.22%
SSSL1	2.63%	0.84%	2.30%	0.42%
Replicate 1	1.44%	0.48%	1.02%	0.16%
Replicate 2	1.18%	0.35%	1.28%	0.26%
SSSL2	13.01%	3.12%	5.96%	0.86%
Replicate 1	6.12%	1.53%	3.70%	0.57%
Replicate 2	6.89%	1.59%	2.26%	0.29%
SSSS	9.57%	1.44%	4.08%	0.26%
Replicate 1	4.88%	0.67%	1.88%	0.13%
Replicate 2	4.69%	0.77%	2.20%	0.13%
LLLL	5.59%	1.59%	5.45%	0.86%
Replicate 1	2.78%	0.89%	2.55%	0.41%
Replicate 2	2.81%	0.70%	2.90%	0.45%
Total	42.18%	12.54%	33.48%	8.14%

Individual Pedigree Model

- $Y_{ij} = \mu + R_i + Ri{:}B_j + ped(I) + e_{ij}$
  - Y_{ij} corresponds to the phenotypic trait in the i^{th} replicate (i = 1 to 2) and i^{th} replicate by j^{th} block (j = 1 to 95)
  - R_i corresponds to the fixed replicate effect
  - $Ri{:}B_j$ corresponds to the fixed replicate by block effect
  - ped(I) corresponds to the random individual pedigree effect
  - e_{ij} corresponds to the random residual effects
- Narrow sense heritability
  - $h^2 = V_A / V_P$
  - V_A equal to additive variation (variance component for the individual pedigree effect) and V_P equal to the total phenotypic variation (total variance component)

Heritability – Year 3

Year 3 Measurements		
Phenotypic Trait	**Narrow Sense Heritability**	**Standard Error**
Height (tenths of ft)	0.094	0.058
DBH (tenths of in)	0.046	0.043
Crown (tenths of ft)	0.102	0.065
Primary Branch	0.194	0.071
Primary Branch Node 3	0.059	0.055
Secondary Branch Node 3	0.133	0.050
Primary Branch Node 5	0.100	0.063
Secondary Branch Node 5	0.195	0.070

Summary and Conclusion

- Slash pine has the largest crown and DBH
- Loblolly backcross is the tallest
- Branch measurements
  - Loblolly and loblolly backcross have more secondary branching
- Growth efficiency
  - Backcross families were more growth efficient
- Disease
  - Loblolly more susceptible to fusiform rust
- Stem form
  - Loblolly backcross has poorer stem form

Summary and Conclusion

- Genotype by environment interaction observed for nearly all traits
  - With the exception of DBH
- Low heritabilities observed for traits after 3rd growing season

Future Research

- Compare oleoresin flow in backcrossed hybrids with slash pine trees
    - Short-term oleoresin yield
- Calculate heritability of oleoresin flow traits among families

Acknowledgements

- Dr. Gary Peter
- Dr. Salvador Gezan
- Greg Powell
- CFRGP
- FBRC
  - Kari Hurst
  - Joshua Cucinella

Literature Cited

- Muñoz Del Valle, P.R., D.A. Huber, and J.R. Butnor. 2011. Phenotypic analysis of first year traits in a pseudo-backcross {(slash x loblolly) x slash} and the open-pollinated families of the pure-species progenitors. Tree Genetics and Genomes 7: 183-192.

- Xiao Y., E. Jokela, T.L. White. 2003. Species differences in crown structure and growth performance of juvenile loblolly and slash pine. Forest Ecology and Management 174: 295–313.