

---

# Growth and Yield Differences in Pure- Versus Mixed-Family Stands: Six-Year Results From Slash and Loblolly Pine Trials

---

Christina Staudhammer

Brian Roth

Luis Osorio

*School of Forest Resources and Conservation*

---

# Background – elite pine families

- Growing elite fast-growing pine families can create sustained economic yield over a smaller landbase
- Families that show high growth potential and disease resistance in progeny trials are selected
- Pure plantings of single families or clones are becoming more common, but there are outstanding research questions

---

# Do individual families planted in mixtures correlate well with pure family-block installations?

1. Do elite families of loblolly/slash pine yield more per unit area when grown in pure or mixed family plantings?
2. Can estimates of stand level attributes (i.e., BA per unit area, TPA, DBH) in pure plantings be predicted from mixed plots?
3. Does spacing, silvicultural intensity, genotype or species influence the relationship between pure and mixed plantings?
4. How long can valid stand-level estimates based on mixed plantings be made in pure plots before inter-genotypic competition begins?

---

# Presentation Outline

- Introduction
- Objectives
  - Long-term vs. short-term
- Materials & Methods
  - Layout & Statistical tools
- Results
  - Mortality, yield, forest structure
- Conclusions
  - Implications for forest plantation managers

# Objectives

***To explore the differences between growth and yield of pure- and mixed-family stands in terms of:***

- Genetics
  - Full-sib family
- Silviculture
  - Initial spacing, silviculture intensity, and their interactions
- Stand structural diversity
  - dbh distributions

# Materials: Pine Productivity INteraction on Experimental Sites (PPIInES) Study



---

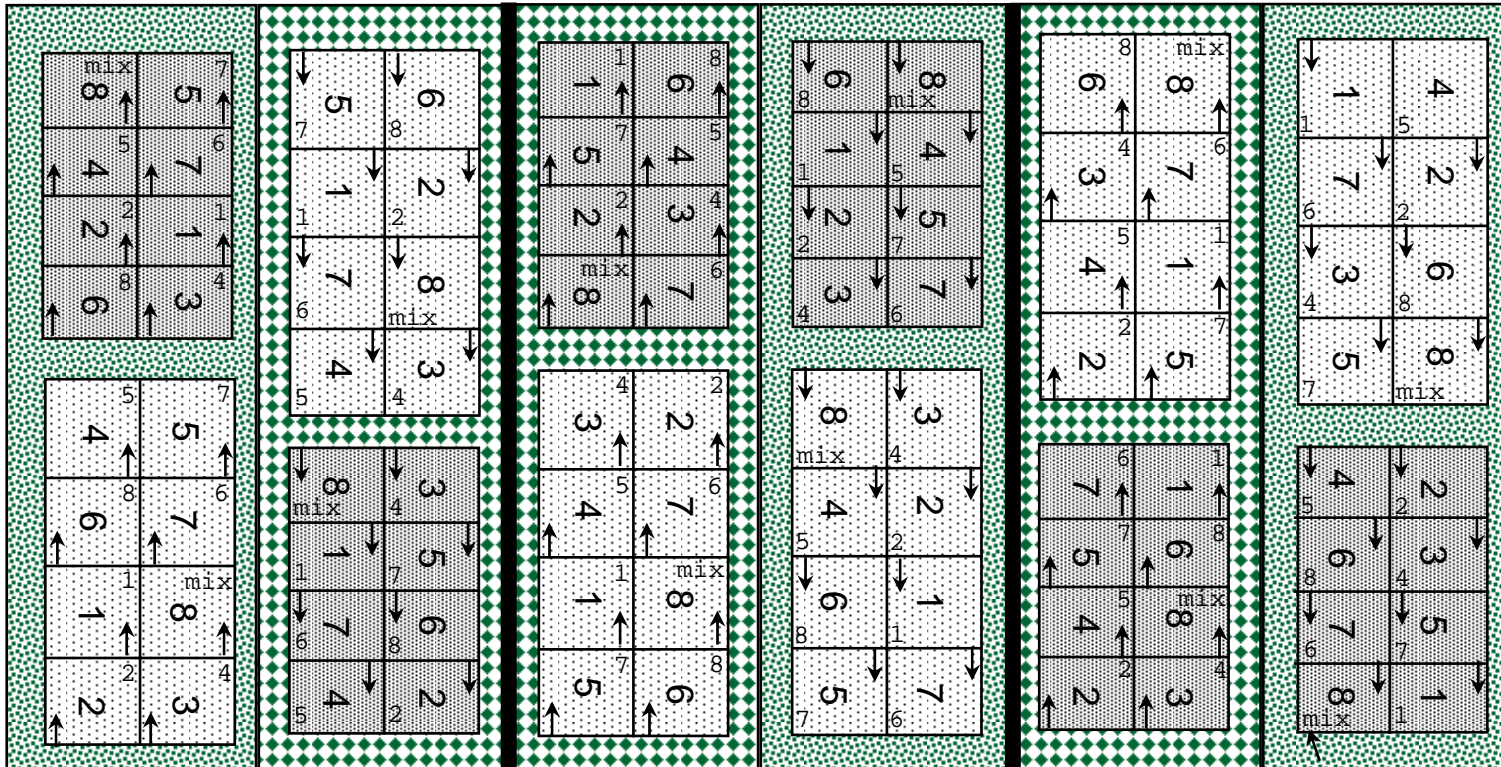
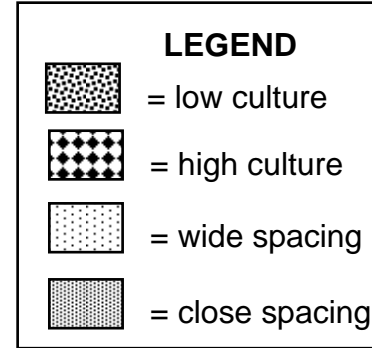
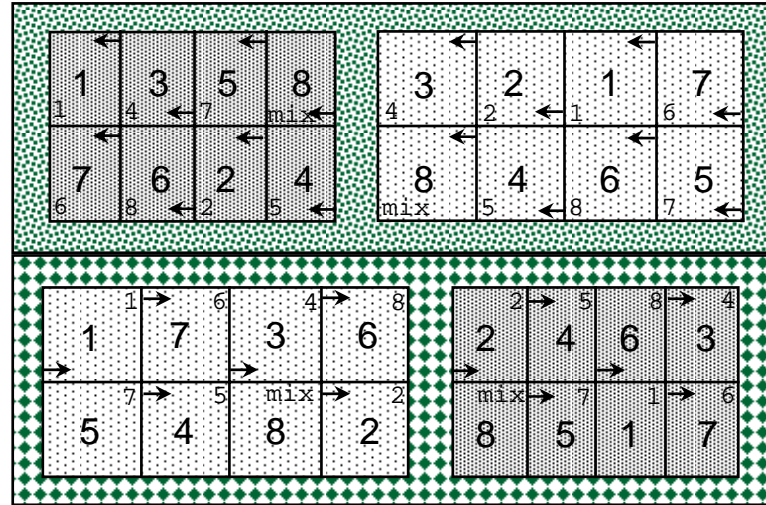
# Materials: Pine Productivity Interaction on Experimental Sites (PPIInES) Study

- Trials installed at five locations in the southeast
  - Separate analyses for loblolly (Bunnell, Sanderson, and Waverly) and slash (Perry and Waldo) sites
- Two planting densities
  - 2990 and 1330 tph
- Two levels of culture
  - Intensive and ‘operational’
- Six full-sib loblolly, five full-sib slash families
- “Pure plots” of one family versus “Mixed plots” of five/six elite families

# Methods: Experimental Design

- Replicated Randomized Complete Block Design with “pseudo-split-plot” culture x density, split-split plot deployment and family
  - four blocks
  - replicated in five locations: Bunnell, Perry, Sanderson, Waldo, Waverly
  - Main plot was “pseudo-split-plot” culture over spacing
    - high (intensive) vs. low (operational)
    - 9' x 9' (2.7m x 2.7m) vs. 4' x 9' (1.2m x 2.7m)
  - Sub-plot was deployment: mixed vs. pure
  - Sub-sub-plot was family: six Loblolly families, five Slash families

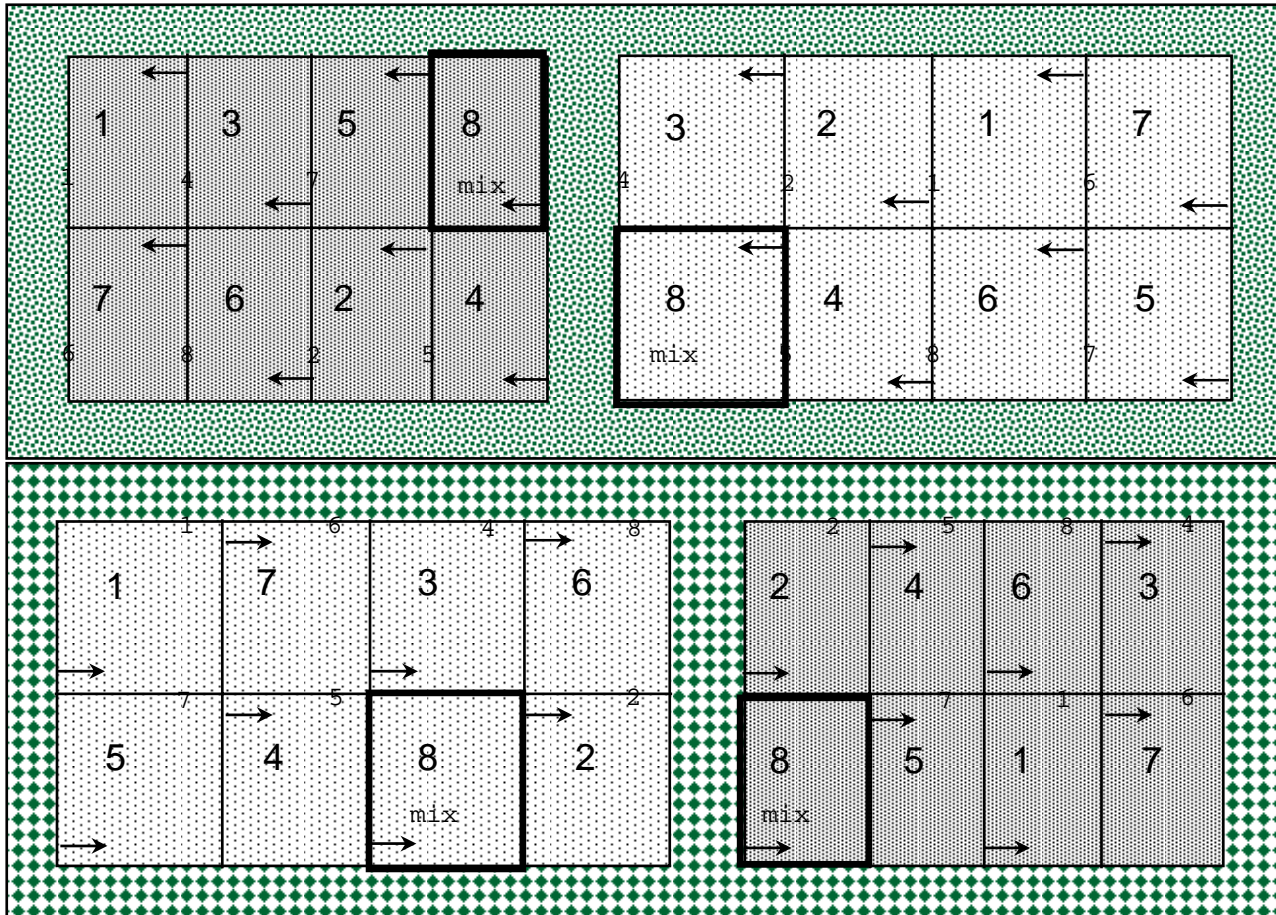
# Example Location (Sanderson)







Example  
Location  
(Sanderson)



# Example Block



## LEGEND

-  = low culture
-  = high culture
-  = wide spacing
-  = close spacing

---

# Measurements

- 48 measured trees per plot, surrounded by treated buffer trees
  - Diameter measured on all trees at year 2, 3/4, 5, and 6
  - Condition codes for dead/dying trees
  - Soil analysis, foliar analysis, etc.

# Statistical Analyses – growth & yield measures

- Diameter
- Basal area per hectare
  - Basal area per tree/average growing space in plot
  - Assumed mortality had uniform impact across plot
- Annual mortality rate
  - Proportion of trees dying each year
- Live trees per hectare
  - Number of stems per family in plot/initial growing space of family in plot
  - Weighted by number of initial stems in plot
- Disease/damage presence
  - Presence of disease/damage in any year

# Statistical Analyses – models

- Mixed model framework with repeated measures to account for correlation between trees within plots, measurements over time
  - Diameter, Basal area per hectare, live trees per hectare modeled with normal response
  - Annual mortality rates and disease presence modeled with lognormal response
- Nested random effects for block, block\*culture, block\*culture\*density, etc. to account for hierarchical restriction of randomization

# Statistical Analyses – stand structure

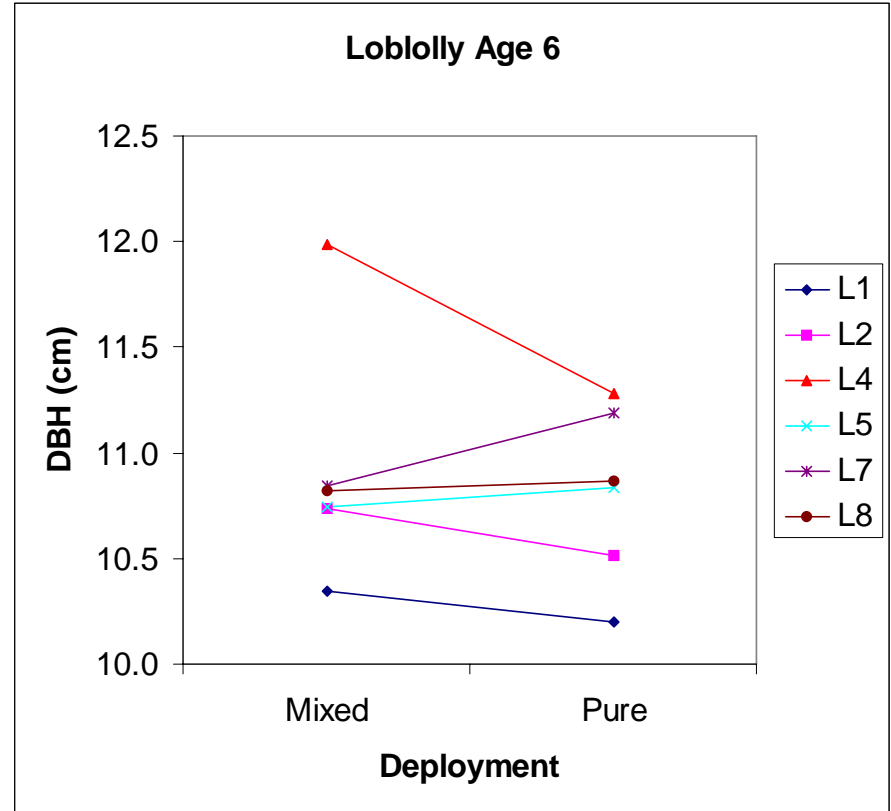
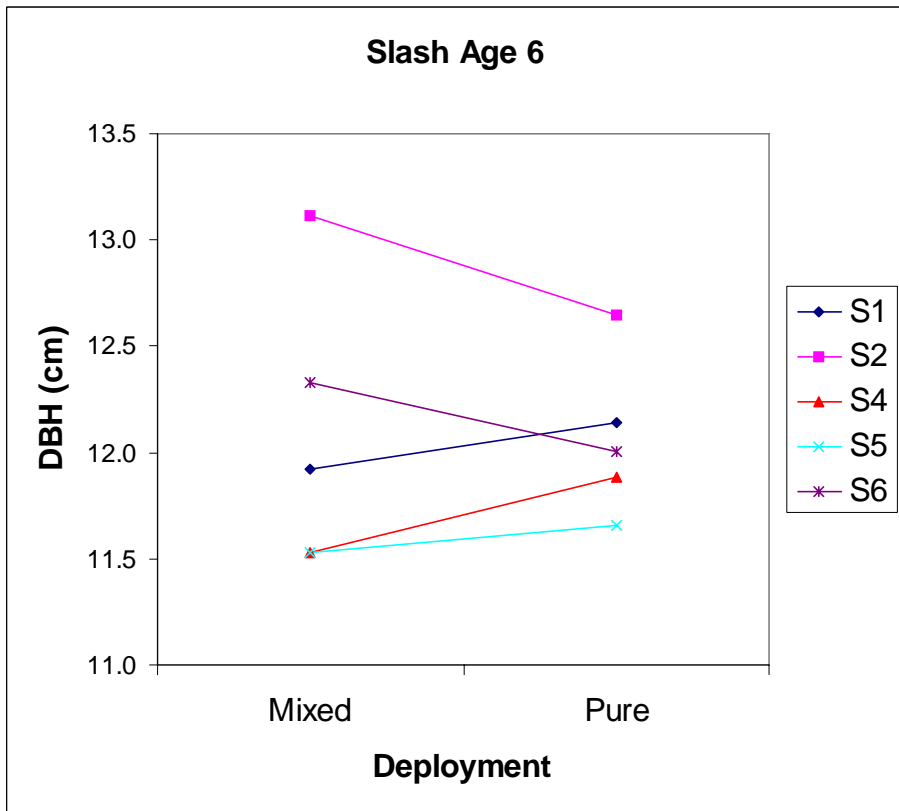
- Stand structural diversity was analyzed using diameter distributions
  - Shape and scale parameters from fitted Weibull distributions
  - Robust statistics
    - IQR, median, etc.
  - Parametric methods
    - Mean, standard deviation, skewness, kurtosis
  
- To account for low numbers of trees in each family in mixed plots:
  - Observations were adjusted to eliminate block effects and combined at trial x culture x density x family level
  - Weights accounted for the original numbers of trees in each family that were planted

---

# Results – Individual Tree Diameter

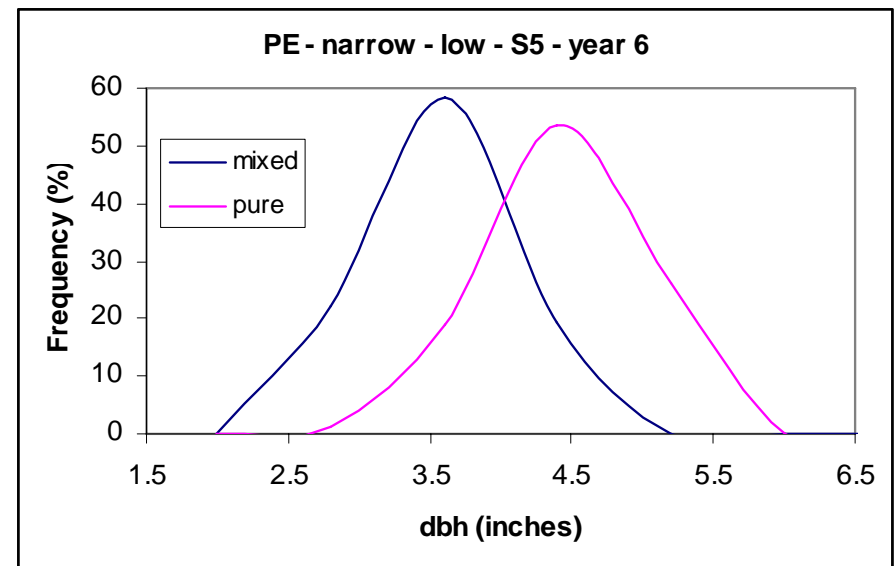
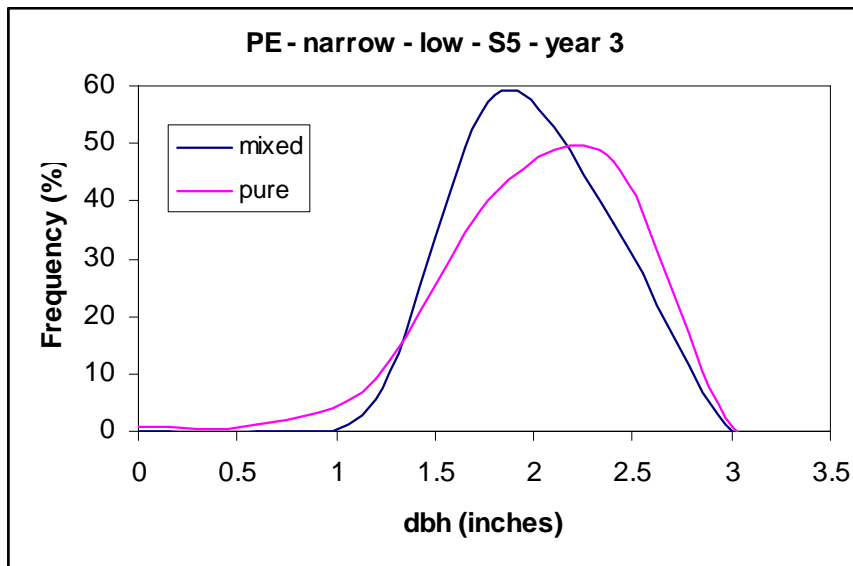
- Significant family x deployment interaction in year 5-6, but virtually no “cross-over” interactions (i.e., consistent by year)
- Some families performed better in mixed versus pure plots
- Mixed plots had larger range of average dbh x family
  - Best performing families grew larger at the expense of the smallest ones when growing in an intimate mixture

# DBH of mixed vs. pure plots by family (all sites combined, age 6)



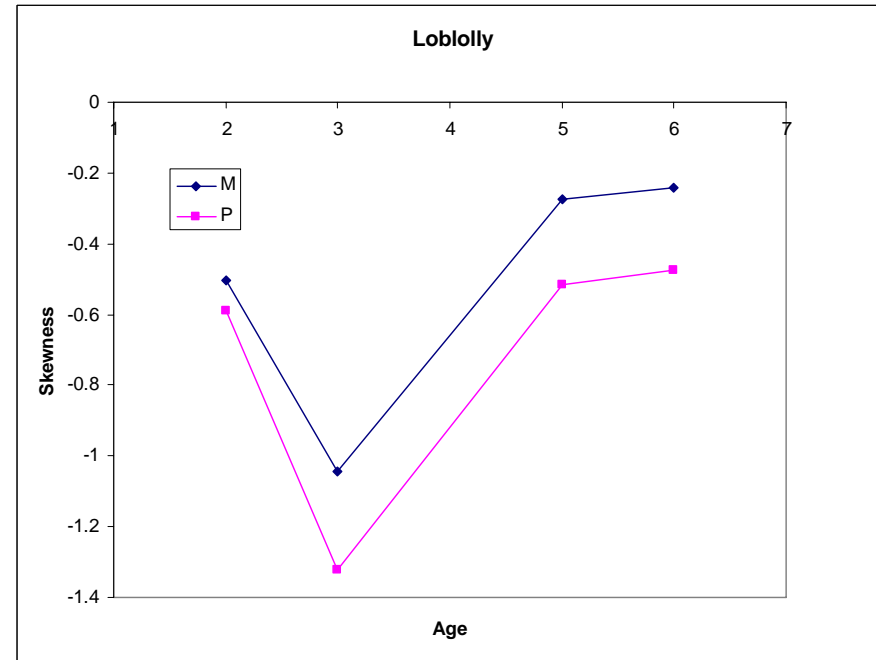
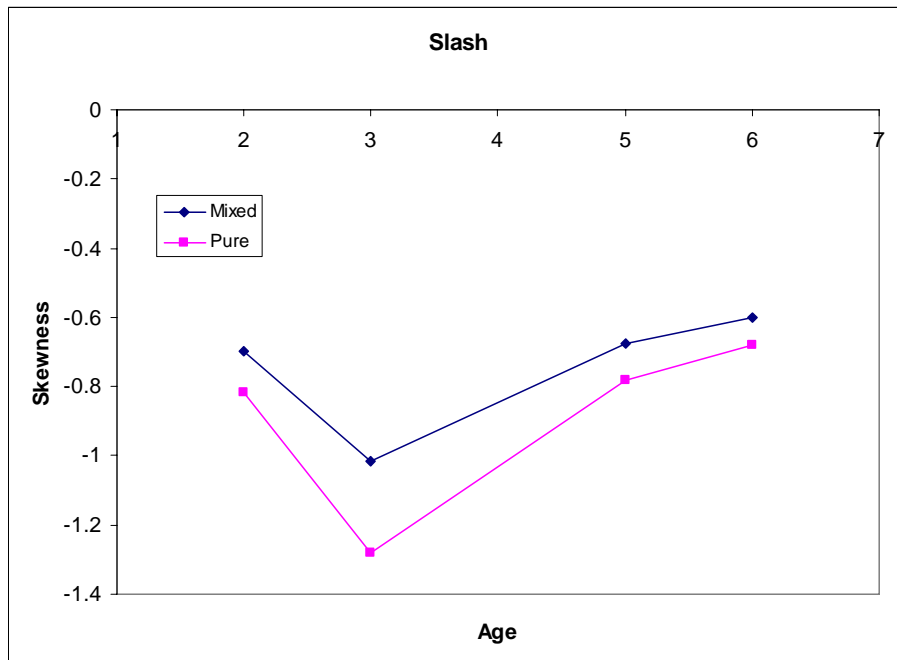
# Dbh distribution (example plot in Perry – narrow spacing, low culture, family S5 in year 3 vs. year 6)

- At younger ages, pure plots were significantly more skewed left than mixed plots



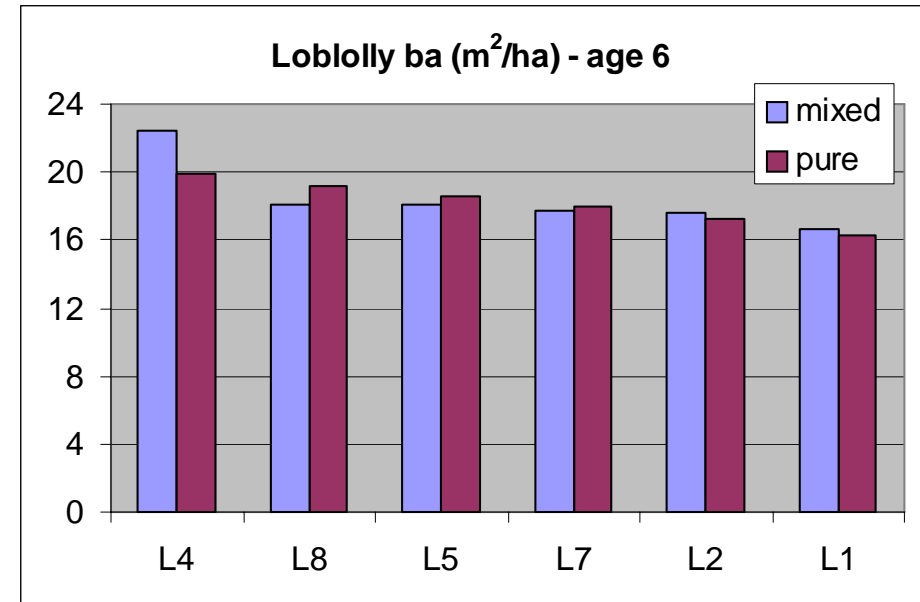
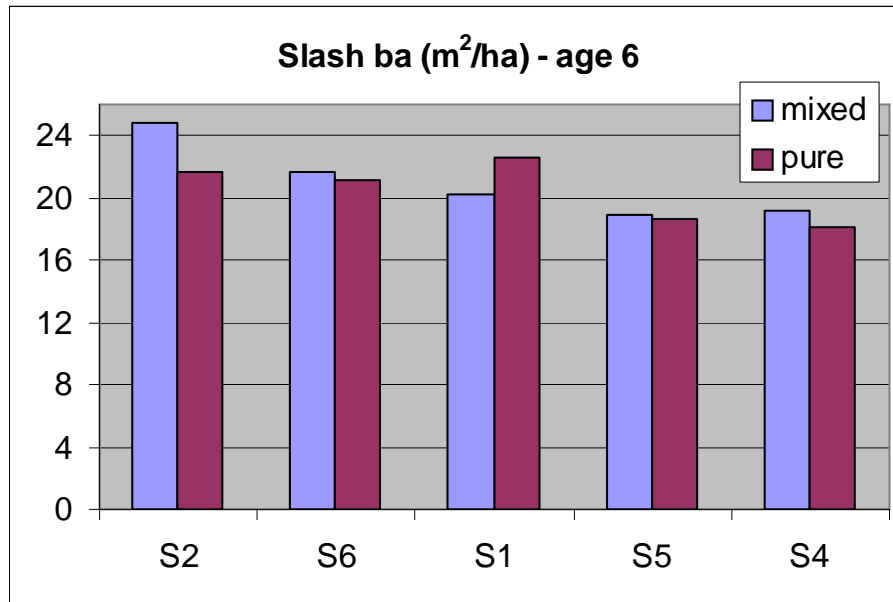
# Skewness of Dbh distribution – mixed vs. pure plots by year (all sites combined)

- Effect fades after age 3, possibly due to disease induced mortality of small trees



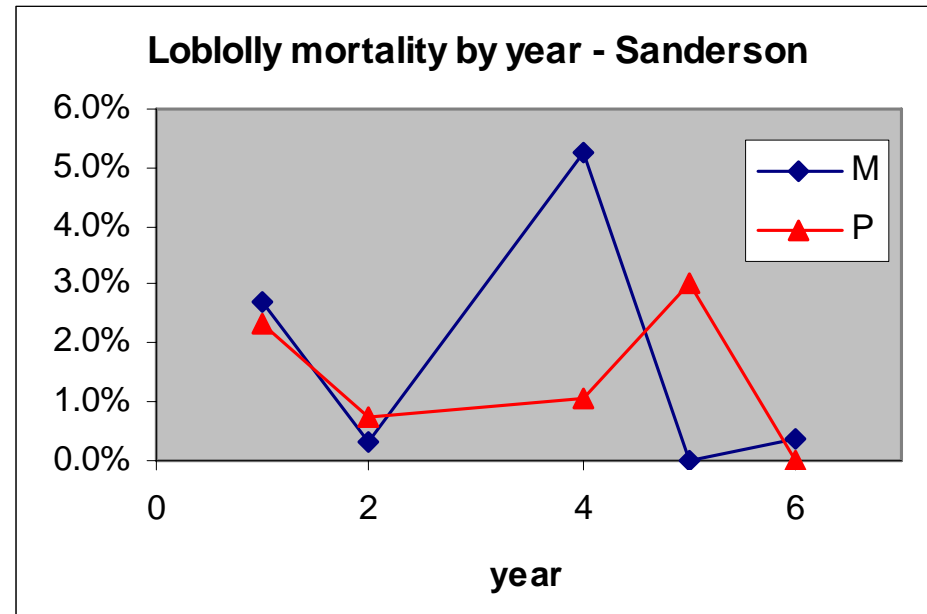
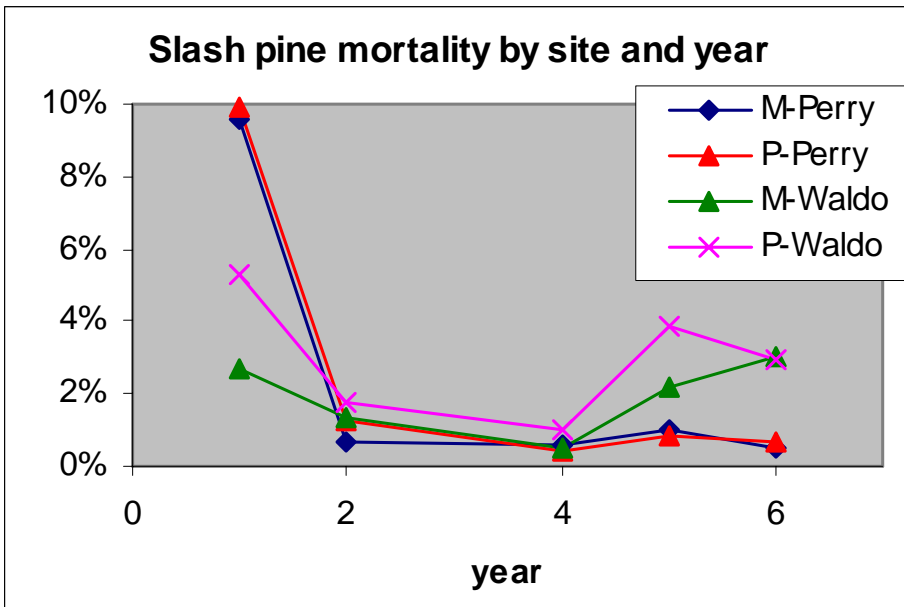
# Results – Basal area per acre

- Significant interaction between family and deployment at age 5-6
- Inconsistent effects by family, trial location



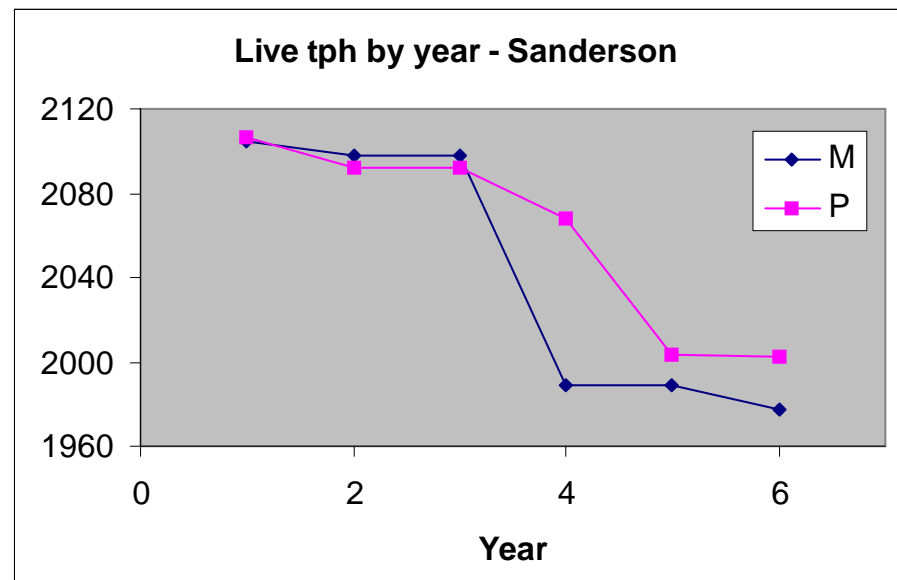
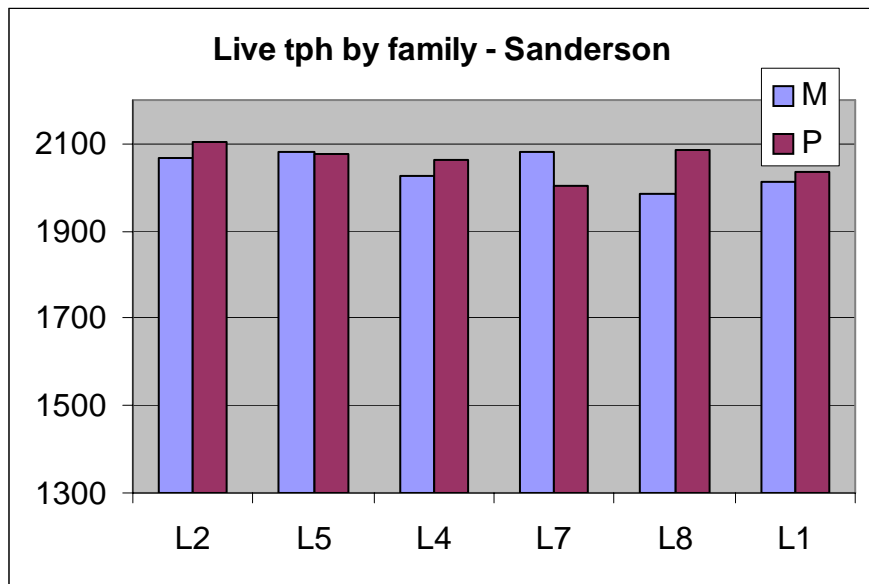
# Results – Annual mortality rate

- Annual mortality rates had significant trial x deployment x year interactions in Perry, Waldo, Sanderson
  - In Perry (slash), high mortality in first year
  - In Sanderson (lob), mixed/pure mortality at age 4/5



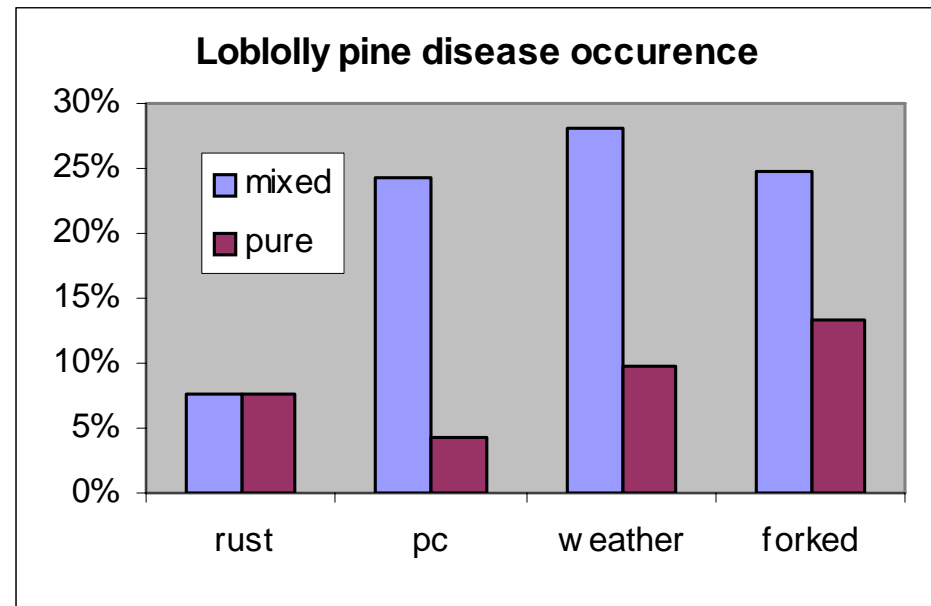
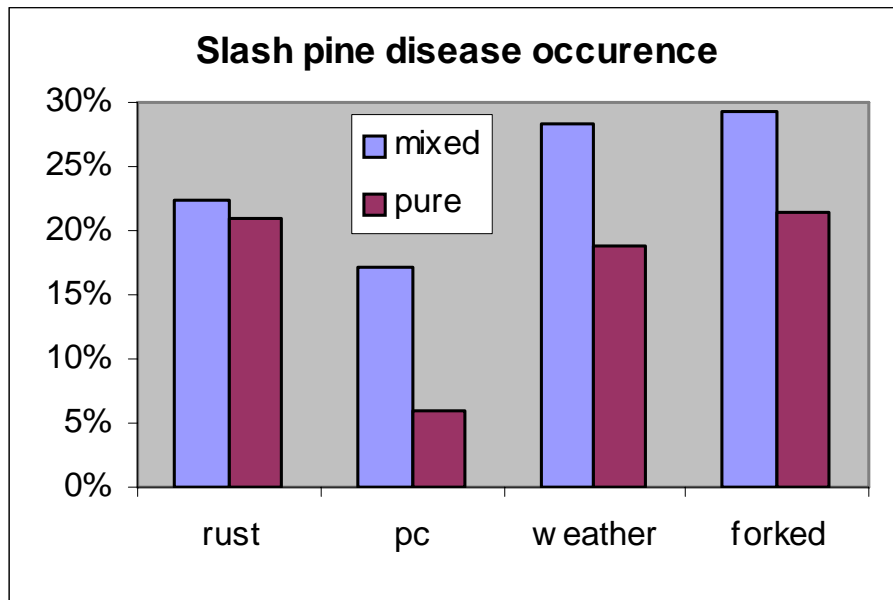
# Results – Live trees per hectare (tph)

- Significantly effects of deployment x year and deployment x family in Sanderson (none elsewhere)
  - Most families had higher tph in pure plantings
  - Mixed plot mortality pulse earlier than pure plot



# Results – Disease/damage incidence (occurrence over all years)

- Mixed plots were far more susceptible to pitch canker, weather damage, and forking (all years)



# Summary and conclusions

- ❑ No interaction of deployment with silvicultural intensity or spacing
- ❑ Competition between trees occurs fairly early in intimate mixtures with the fastest growing genotypes growing larger at the expense of slower growers
  - This may produce an upward bias in the prediction of rapidly growing genotypes in pure plots as early as 5 years at densities between 1330 tph and 2990 tph
- ❑ Predictions from mixed plots can be confounded by mortality due to diseases
  - This may interact with deployment method

---

# Implications for forest resource managers

- Estimates from intensively managed single-tree genetic field trials were representative of what we may find in trials under less intensive management
- Care must be taken in using mixed single tree plots for pure plot performance estimates, as they may not be representative after the onset of competition
- Localized disease or weather events can confound results from mixed to pure plots

---

# Future directions

- Analyses should take into account location of trees to properly account for changes in growing space
- Random sample of tree heights will allow volume comparisons
  
- Are there missing covariates?
- What will change with year 7 measurement: Is it too early to say *anything*?

---

# Acknowledgements

- Forest Biology Research Cooperative
- Drs. Eric Jokela and Timothy Martin
- Florida Agricultural Experiment Station