Assessing past epicormic dynamics in pole-size white oak logs with CT scanning

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Introduction

White oak (*Quercus alba* L.) is one of the most valuable and ubiquitous tree species in the Central Hardwoods Forest Region. It is well-known for its tendency to form epicormic sprouts, which can lead to decreased log values. All epicormic branches in oaks produce an epicormic trace in the wood that reflects past epicormic development. We used CT scanning to analyze the dynamics of epicormic traces in young oak trees. Our main objective was to assess the relative impacts of tree vigor and genetics on epicormic development.

Methods

Site selection

White oak logs for this study were removed as part of a crop tree release treatment in two 28 year old white oak progeny tests in Indiana (Table 1), at the Harrison-Crawford State Forest (HC) (38˚ 15' N, 86˚ 15' W) and the Jasper-Pulaski Fish and Wildlife Area (JP) (41˚ 09' N, 86˚ 54' W). Both stands had never been thinned; some pruning has occurred at the HC site. Parentage of each tree in these progeny tests is known and a large number of families are present at both sites.

Table 1. General characteristics of the two white oak progeny tests prior to treatment.

Site	Number of scanned trees	Basal area (ft^2/ac.)	Mean DBH (in.)	Site index (ft. at 50 yr.)
HC	32	96.8	5.6	70
JP	16	95.4	6.8	65

Tree selection

In 2006, all trees in the plantations were ranked qualitatively for epicormic branching; family averages for these rankings were calculated and families with the highest, lowest and median values were assigned to corresponding epicormic classes. A subset of families from these classes that were present at both sites were selected for study. Within selected families, individuals were identified based on canopy classes, with the objective of selecting trees of high and low vigor for analysis. External counts of epicormic branches were made on the bottom 12-foot section of each selected tree in January and February of 2010 (Fig 1a); trees were then felled and the second 4-foot section was removed for CT scanning.

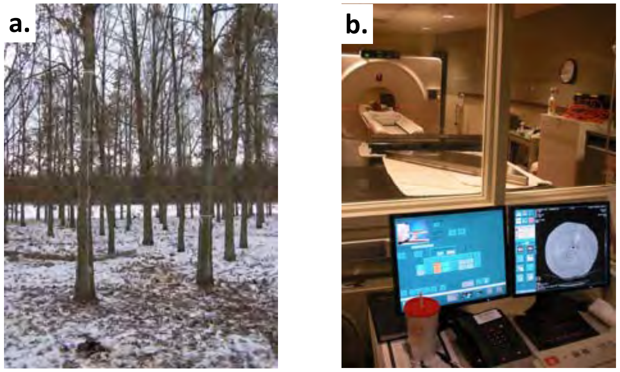

Figure 1. a) Residual crop tree (l.) and tree for scanning (r.) prior to treatment. b) CT scanner and simultaneous reconstruction of the log being scanned.

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CT scanning and data analysis

Logs were scanned using a GE Lightspeed QX/i multislice helical CT scanner (Fig 1b). Images were collected at 5 mm intervals; each scanned log consisted of approximately 240 images. Resulting images were analyzed manually using ImageJ software with the cell-counter plugin. Epicormic structures were characterized by their size, development and origin (Fig 2). Primary traces originated at the pith of the main stem and secondary traces originated at the pith of another branch. We used a non-parametric Kruskall-Wallis test with multiple comparisons (PROC NPAR1WAY, SAS Institute, Inc., Cary, NC, USA) to make initial determinations of differences in the composition of epicormic structures between canopy classes and epicormic classes. For analysis, trees were grouped into upper (dominant and codominant) and lower (intermediate and suppressed) canopy classes.

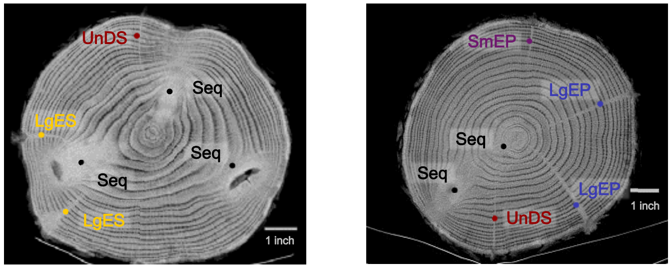

Figure 2. Examples of two CT scanned log images with tallied epicormic structures. *Seq*: Sequential branch knot, *UnDS*: Undeveloped secondary epicormic trace, *SmEP*: Small developed primary epicormic trace (< ¼ in. diameter), *LgEP*: Large developed primary epicormic trace (> ¼ in. diameter) *LgES*: Large developed secondary epicormic trace.

Results

Differences between sites

- Epicormic variables were not significantly different between sites (Fig 3).
- Broad scale environmental differences probably had little impact on epicormic sprouting.
- The production of sequential branches at both sites was nearly identical.

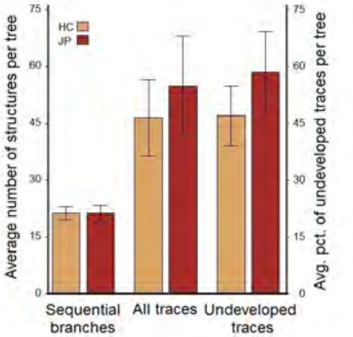

Figure 3. Characteristics of internal epicormic structures at the two sites. Bars represent ±1 s.e.

Differences among canopy classes

- No significant differences in epicormic dynamics were noted between lower and upper canopy classes (Fig 4).
- There was high variability among individuals within crown classes.
- Upper crown classes had slightly more undeveloped traces and slightly fewer large epicormics.
- Differences in epicormic dynamics might be more pronounced if a more precise measure of vigor was used to assign vigor classes.

Differences among epicormic classes

- There were significant differences only between family groups rated as low and high epicormic sprouters (Fig 4).
- The low epicormic class maintained a higher proportion of undeveloped epicormic traces and fewer large epicormic branches.
- Variability was high among individuals within each epicormic class.

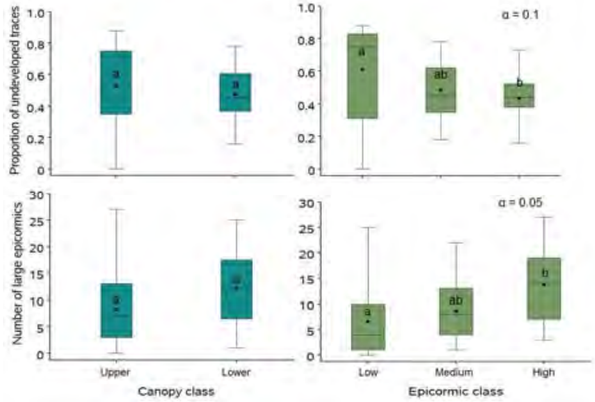

Figure 4. Boxplots of epicormic variables for scanned logs by canopy class and epicormic class. Solid dots signify class means. Letters indicate the significance of differences between means; where significant differences occurred, the level of significance is noted in the upper right hand corner of the graph.

Future Directions

- We will use generalized linear models to assess vigor in terms of quantitative variables, such as DBH increment and crown volume.
- We will also test the interaction of tree vigor and epicormic class in terms of the already analyzed variables.
- Further genetic studies are needed to test individual families or clones, rather than groups of families.

Conclusions

1. There are no significant differences in epicormic structural development between upper and lower crown classes.
2. There is some evidence of differences in epicormic production between families.
3. Significant variability is evident in both these instances, suggesting that more complex interactions regulate epicormic bud development and sprouting.