Measuring resistance to chestnut blight (*Cryphonectria parasitica*) and American chestnut (*Castanea dentata*) morphology of backcrossed hybrids in Lesesne State Forest

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Background

C. dentata filled a social and ecological niche in Eastern hardwood forests rivaled by few hardwood species to date. Restoration of C. dentata depends on establishing resistance to C. parasitica in the species (Diskin, 2005).

Backcross breeding introduces blight resistance through hybridization with resistant Chinese chestnut (Castanea mollissima).

Success of backcross breeding depends on selecting individuals that express blight resistance while resembling their *C. dentata* parent (Westbrook,

2019). Genetic testing or fieldbased observation indices determine this



Figure 1: Recapture of *C. dentata* genome through 3 generations of backcrossing.

Image from PA-TACF Chapter, 2016.

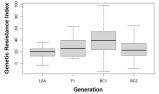


Figure 2: Blight resistance in Lesesne State Forest, 2 generations of backcrossing. Indicative of *C. mollissima* genetic content in hybrids.

Objectives

- Measure phenotypic blight resistance and C. dentata morphology in C. dentata backcrossed hybrids in Lesesne State Forest.
- Identify correlation between field-based indices and genetic data (genetic resistance index and *C. dentata / C. mollissima* genome content)

Methods



Setting: Lesesne State Forest, Virginia. Data collected May-October 2022. Evaluated 600 trees by observable traits indicative blight resistance and *C. dentata* morphology. Genetic data provided by Jared Westbrook.



Image 2 & 3: Examples of *C. dentata* (left) and *C. mollissima* (right) morphology. Leaf serration, shape, and shine shown. Leaf pubescence, petiole angle, and tree form also observed, not pictured. Image 3 by Zhangzhugang (板栗, 杭州植物园), 2018.

Methods, cont.



Image 4 & 5: Cankers caused by chestnut blight fungus, C. parasitica. Blight resistance evaluated by canker size, containment, depth, and appearance. Evaluation also included presence of exposed wood, canopy or stem death, stump sprouts, and blight sporulation (not pictured).

Image 5 shows cross section of deep canker with swelling and scar tissue.

Results

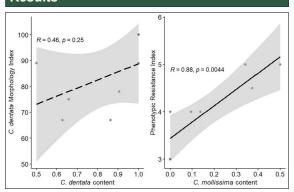


Figure 3: Correlation between *C. dentata* genome content and *C. dentata* morphology index. No significance found.

Figure 4: Correlation between *C. mollissima* genome content and phenotypic resistance index. Strong and significant correlation found.

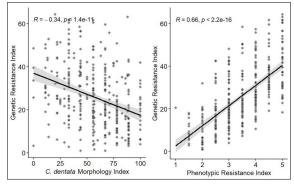


Figure 5: Weak correlation between *C. dentata* morphology and genetic resistance index. Significance found.

Figure 6: Correlation between *C. dentata* morphology and genetic resistance index.

Weak but significant.

Results, cont.

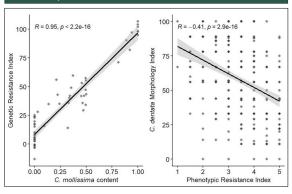


Figure 7: Correlation between *C. mollissima* genome content and genetic resistance index. Strong and significant correlation found.

Figure 8: Correlation between phenotypic resistance index and C. dentata morphology index. Moderate, significant correlation found.

Conclusion

- The Phenotypic Resistance Index is a successful measure of blight resistance in the field and is correlated with both the genetic-based resistance index and C. mollissima genotypic content.
- The C. dentata Morphology index is not an effective estimate of C. dentata genotypic content in the field.
- The C. dentata Morphology index should be improved upon in order to correlate significantly with genetic data.
- This study was limited by the amount of Whole Genome Sequencing data available for the trees evaluated.
- Increasing the correlation between field-based indices and genetic data offers an opportunity to increase the success and progress of the C. dentata backcross breeding program without requiring extensive genetic testing.

References

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