

Ex Situ Management in *Quercus oglethorpensis*

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Introduction

The most effective way to prevent the loss of plant genetic diversity is within the natural populations, known as *in situ* conservation. However, *ex situ* conservation strategies may also be necessary to help support *in situ* conservation efforts.¹ Some *ex situ* methods include seed banking, tissue culture and cryopreservation. Although seed banking is the most cost effective and commonly used method, it does not work for all species. The species which cannot be seed banked are known as "exceptional species" and they need to be maintained as living collections.² However, just like small populations in the wild, living collections are susceptible to genetic and demographic threats (e.g., genetic drift and inbreeding), and therefore they need to be managed to avoid these potential issues.³ In this study, we focused on *Quercus oglethorpensis* (Oglethorpe oak) an exceptional species that is endemic to southeastern United States. We examined the genetic variability of wild populations across the entire species range, and then compared the genetic diversity of the wild population to the *ex situ* living collection.

Species Information



- The Oglethorpe oak is listed as threatened on IUCN's red list. It is one of fifteen threatened oaks in North America.⁴
- Quercus oglethorpensis* is threatened by habitat loss due to development and clear-cut logging
- Most of the *Q. oglethorpensis* plants in living collections were collected from populations in the eastern portion of the range, while the western populations are not yet represented or represented by only a few individuals

Figure A.) *Q. oglethorpensis* at Chicago Botanic Garden production greenhouse.

Methods

- Perform DNA extraction from *Q. oglethorpensis*
- PCR allowed us to amplify specific regions of DNA
- Neutral microsatellites were used to quantify data
- Analysis using GenAlEx, compared populations
 - F statistic
 - Observed and expected heterozygosity
 - The amount of private alleles per population.

Objectives

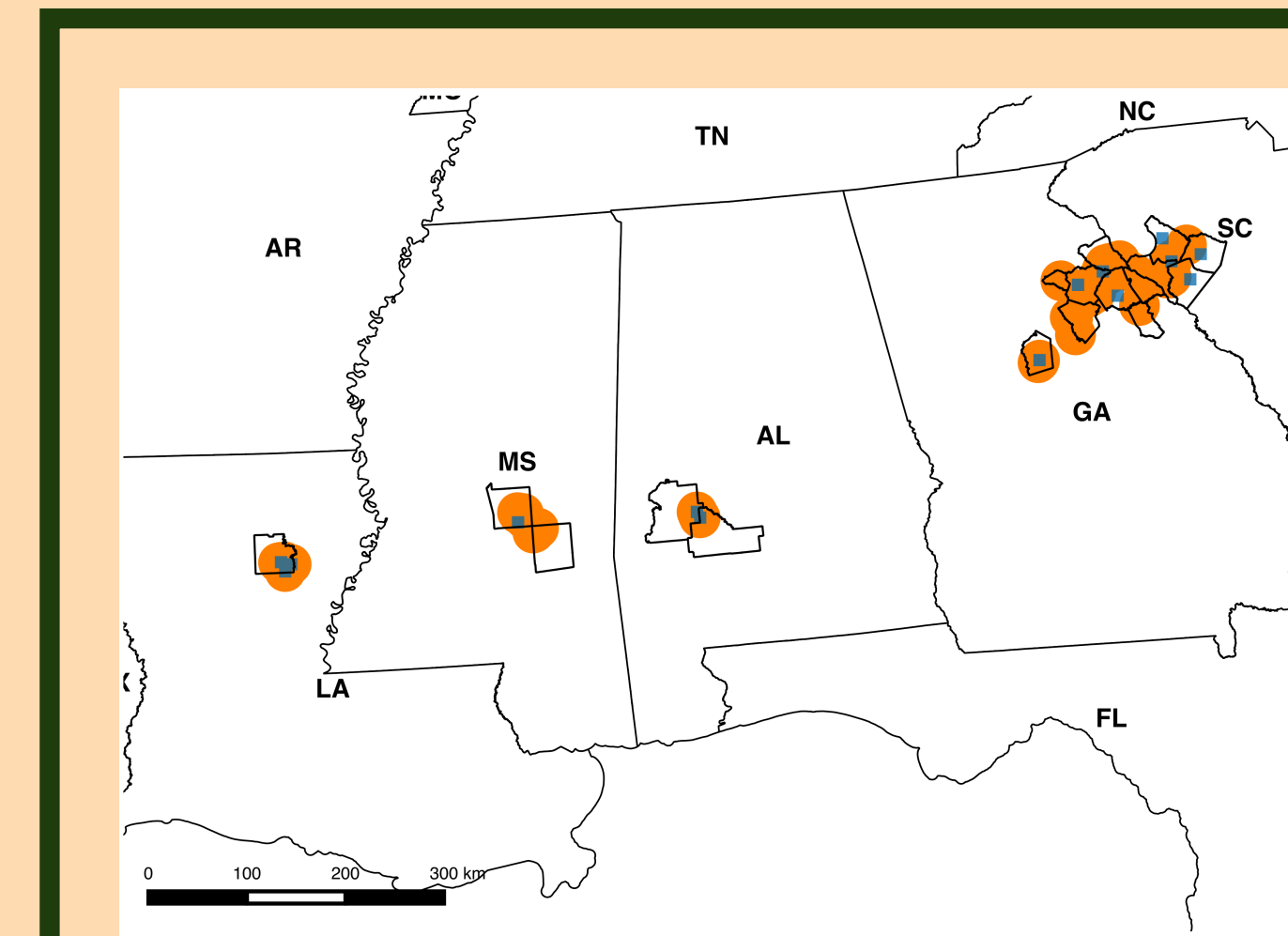


Figure B.) This map represents the range of *Q. oglethorpensis* populations.

The objective of this project is to examine the genetic variation between *Quercus oglethorpensis* in both *ex situ* and *in situ* populations. It may be likely that the genetic diversity found in *ex situ* collections is low compared to those *in situ*. It is also expected that with an increased maintenance of genetic diversity, living collections will be more demographically stable, potentially aiding in future reintroduction efforts.

Results

Locality	County	State	Mean Alleles per loci (NA)	Mean Effective Alleles (NE)	Genetic Diversity (HE)	Private Alleles
Copenhagen Hills Preserve (COP)	Caldwell	LA	6.250	3.250	0.555	0
Reasource management Services (RMS)	Caldwell	LA	6.750	4.523	0.659	0
Bienville National Forest (BIE)	Scott	MS	7	3.592	0.705	2
County Road 14- Catherine (CAT)	Marengo	AL	9.25	3.406	0.600	3
Buffalo Mill Road- Buffalo Creek (BUF)	Oglethorpe	GA	8	2.882	0.604	4
Goosepond Road - Goosepond Creek (GOS)	Oglethorpe	GA	2.500	2.250	0.469	0
Monticello Glades (MOT)	Jasper	GA	8.250	3.499	0.565	4
Sumter National Forest (SUM)	McCormick	SC	7.250	3.060	0.610	2
Wild Population Average	N/A	N/A	6.906	3.308	0.596	N/A
Ex situ	N/A	N/A	10.750	3.942	0.624	4

Figure C.) Representation of genetic diversity (through various indicators) across the subpopulations that *Quercus oglethorpensis* can be found at. Organization is based on population locality (west to east). All subpopulations are compared to the *ex situ* diversity.

Population	Mean Alleles Per Loci (NA)	Mean Effective Alleles (NE)	Genetic Diversity (HE)	Private Alleles
Ex situ	10.750	3.942	0.624	4
Wild	15.750	4.229	0.683	24

Figure D.) Genetic diversity within the overall wild population is compared to that found *ex situ*.

Results

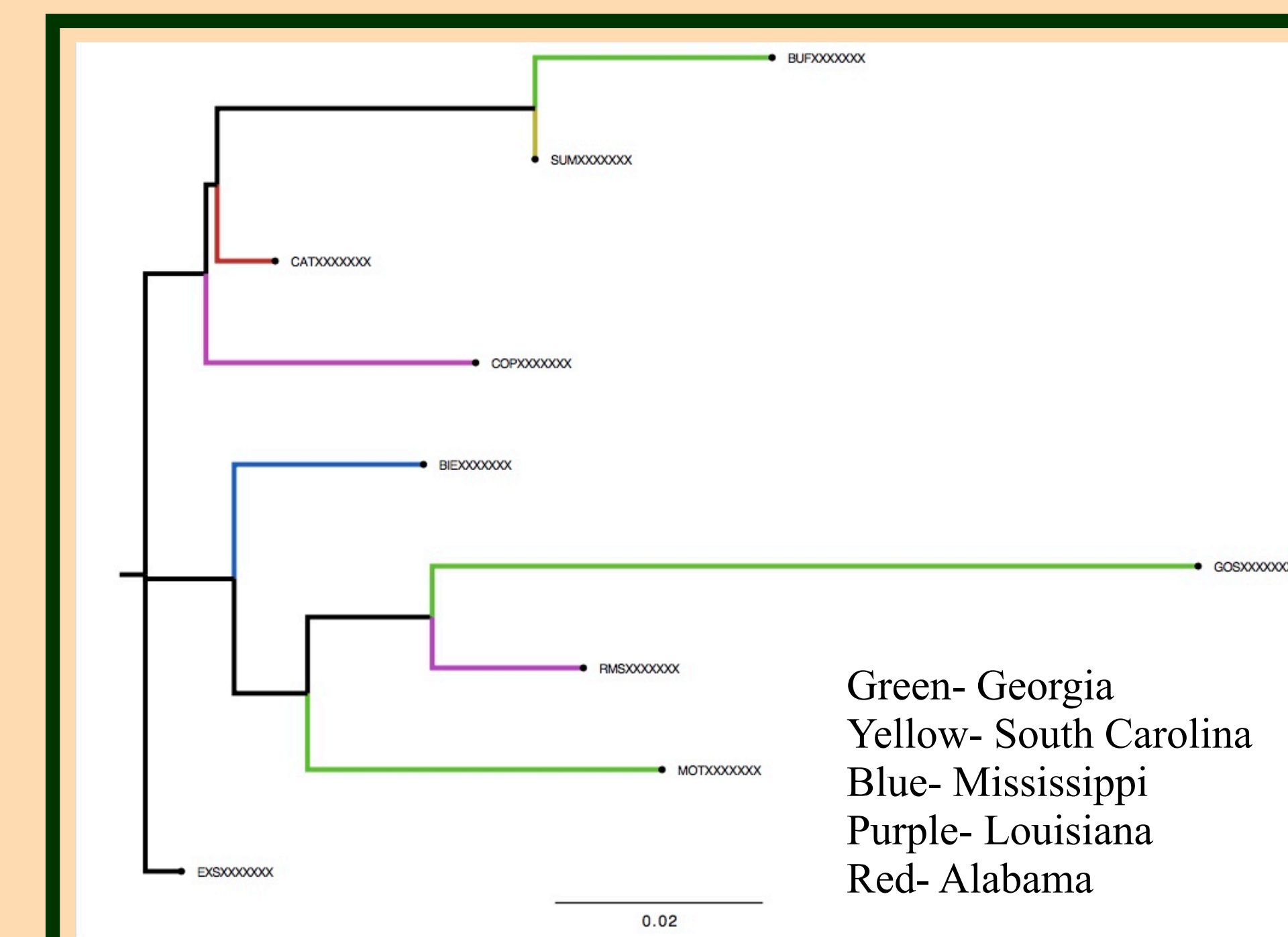


Figure E.) F statistic values were converted to phylogenetic tree to represent the genetic relationship within the nine subpopulations.

Conclusion

The wild population of *Q. oglethorpensis* contained more genetic diversity when compared to the *ex situ* living collection. To make this comparison, we combined all wild subpopulations into a single population that represented the total extant genetic diversity of the species. However, when the *ex situ* living collection is compared to individual wild subpopulations the living collections represent greater genetic diversity. This is because the *ex situ* living collections represents plants from multiple wild populations across the species range.

We also found that the mean number of alleles per loci was higher in wild population as well as the number of private alleles. This suggests that wild populations contain diversity that is not yet represented in living collections. In order to maximize the amount of diversity in *ex situ* collections, seed collecting must be done at various sites across the entire range of the species.

F statistic analysis along with Figtree helped visualize the population differentiation. The phylogenetic tree suggest that when sampling for an *ex situ* collection geographic distance between sites may only have marginal impact on increasing genetic representation. It would be expected that sites with greater proximity would be more genetically similar. However, this is not the case for *Quercus oglethorpensis*. Subpopulations of this oak are scattered across the south east U.S. Population fragmentation may be one of the causes to the unsuspected relatedness of the eight subpopulations. Sampling should be done across the population range to ensure that all potential diversity is caught.

Acknowledgements

I would like to thank Jordan Wood for allowing me to assist him in his research. I would also like to give thanks to the Plant Biology & Conservation Research Experiences for Undergraduates - From Genes to Ecosystems (Supported by NSF award DBI-1461007). Finally, thank you Cedric McDaniel for helping with DNA extractions.



Works Cited

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