

New York's Melting Pot : Forest Fragmentation Effects

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INTRODUCTION

• At an unfathomable rate since the Industrial Era, **2/3** of the world's forest has been cleared making forest fragments now a more common fixture in the landscape than the once vast expanses of intact forest that covered the Earth.

• Forest fragmentation, mainly anthropogenic deforestation, has been linked to regional species extinctions and reductions in the genetic diversity of the surviving populations¹. Likewise, a decrease in the biota providing ecosystem services can similarly be responsible for fluctuations in ecosystem stability.

• Most studies on the effects of fragmentation on plant diversity have been conducted in experimental communities² or grassland ecosystems³.

It is critical to quantify the effects that forest fragmentation has on the biotic diversity of a community to be able to predict the environmental responses from pressures such as climate change and other disturbances that disrupt environmental stability.

Hypothesis:

• Theory states that larger islands will harbor the highest species diversity⁴; do forest fragments behave the same as islands?

• Biotic diversity, as well as genetic diversity, of larger "islands" should be higher due to a greater availability of resources and space for biota to coexist.

OBJECTIVES

Evaluate the effects forest fragmentation has on the genetic diversity of a keystone species, red oak (*Quercus rubra*), and on the plant species diversity of New York State's deciduous temperate forest.

Sites:



Figure 1. In New York State's Hudson Valley, analogous forest remnants were chosen as sampling sites. The New York Botanical Garden (NYBG 50 acres, small red dot), Louis Calder Center (LCC 113 acres, medium red dot), and Black Rock Forest (BRF 3830 acres, large red dot) allow the study to be conducted along a size gradient.

METHODS

We addressed these questions using two approaches:

1. Genetic Approach: Microsatellite analysis was performed on DNA extracted from the leaves of 16 adult red oak trees and 16 red oak saplings from each of the 3 forest fragments.
2. Taxonomic Approach: Collaborating with the forest managers at each site, existing forest censuses were used to estimate tree diversity at the species level.

RESULTS: 1. Genetic Approach

Red Oak STR:

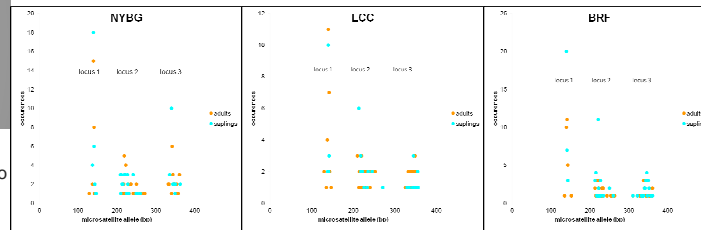


Figure 2. Using primers that bind to specific microsatellite regions of DNA, we are able to amplify genetic markers within the DNA extracted from the red oak leaves. The different alleles present in each individual provide a means to construct genetic profiles that are unique to each sample; here they are pooled and a profile was created for each forest fragment. Separated into adults and saplings, the dots represent alleles that were detected at each locus. Each site shares a similar pattern of microsatellite alleles. This may reflect the fact that they were once part of the same forest, and therefore, the same population, prior to the fragmentation event(s).

Rift in Time:

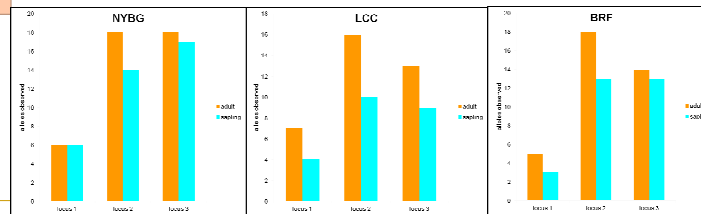


Figure 3. Overall, a reduction in the number of alleles was observed at each microsatellite locus between the older and the younger generation; this was seen at every forest fragment. Logically one can infer that the older trees were all part of the once unfragmented contiguous forest predating any fragmentation. The younger generation, which inhabit forest fragments or forest "islands", is showing reduced genetic diversity.

RESULTS: 2. Taxonomic Approach

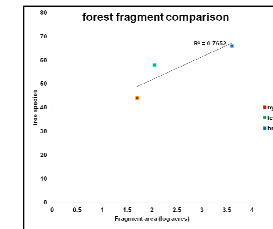


Figure 5. The forest censuses were filtered to compile an inclusive list of tree species. By comparing the number of tree species found at each forest fragment along an area-size gradient we see that larger forest fragments can house more tree species.

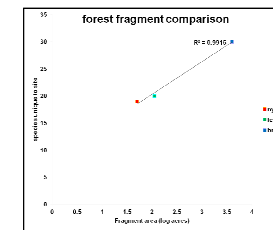


Figure 6. The list of tree species was then filtered once more to include only tree species that were unique to the forest fragment. Comparing the number of tree species unique to the forest fragments along an area-size gradient elaborates on the results illustrated in Fig5; larger forest fragments house more unique tree species.

CONCLUSION

• Genetic diversity of a keystone species, *Q. rubra*, has seen a reduction as an effect of forest fragmentation but a weak correlation to the size-area of the forest fragment was seen. We think that by increasing the number of sites a stronger association can be made.

• As predicted by the Theory of Island Biogeography, a higher number of tree species are able to coexist on forest "islands" that are larger; research on non-woody species is the next step in this study.

Short term effects of forest fragmentation, like deforestation, are easy to spot and can blatantly alter an ecosystem's landscape but until the long-term effects that cause ecosystem instability are understood we won't be able to detect signs of nor diagnose at risk ecosystems.

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