Recruitment history, current health and conservation genetics of butternut (Juglans cinerea) populations in Great Smoky Mountains National Park

Amanda M. Parks1, Michael A. Jenkins1, Keith E. Woeste2, Michael E. Ostry3

1 Department of Forestry and Natural Resources, Purdue University, West Lafayette, IN
2 USDA Forest Service, Northern Research Station, Hardwood Tree Improvement and Regeneration Center, Purdue University, West Lafayette, IN
3 Northern Research Station, USDA Forest Service, St. Paul, MN

Abstract
In recent decades, butternut populations throughout eastern North America have been decimated by butternut canker, a disease caused by the fungal pathogen Ophiognomonia clavigignenti-juglandicola. Disease mortality, poor regeneration in contemporary forests, and hybridization with Japanese walnut threaten the survival of butternut throughout its historic range. Successful conservation of butternut requires a better understanding of its current survival, conditions under which regeneration occurs, and its genetic integrity where it co-occurs with Japanese walnut. In addition, genetic diversity and gene flow between isolated populations should be assessed to determine best management practices and priorities. We assessed butternut populations within Great Smoky Mountains National Park (GSMNP) to determine recruitment history of populations, post-canker survivorship, and degree of hybridization with Japanese walnut. We used National Park Service monitoring records to locate and collect health data for 202 butternut trees across 19 watersheds within GSMNP. Tree core samples were taken from a subset of individuals throughout the Park to assess the pattern of recruitment for the current populations. Leaf samples were collected from hybrid butternut for analysis to determine the frequency of hybridization. Based upon our results, butternut populations in GSMNP have declined dramatically due to disease mortality and thirty years of minimal regeneration. Tree core samples revealed continuous recruitment since Park establishment (1934) until around 1980, after which regeneration declined drastically across all watersheds. Initial genetic analyses indicate that butternut-Japanese walnut hybrids comprise a small portion of the total trees sampled. The presence of healthy trees and low rates of hybridization offer hope that the trees in GSMNP may contribute to efforts to develop and reestablish disease-resistant populations of this threatened tree species. In the next phase of this study, we will genotype all individuals at 15 microsatellite loci to determine the genetic diversity and population genetic structure to evaluate gene flow patterns among populations that have become increasingly isolated due to disease mortality.

Introduction
Within Great Smoky Mountains National Park, after several decades of disease, butternut remain in diffuse populations throughout the Park. In this portion of our study, our objectives were as follows:
1. Assess the survivorship and current health conditions of remaining trees;
2. Determine the degree of hybridization (if any) of J. cinerea with J. ailantifolia;
3. Determine the age structure of J. cinerea populations and recruitment pattern since Park establishment.

Methods
Field Collection
Butternut location database, compiled by NPS during the late 1980’s and 1990’s; Our samples: 202 butternut sampled across 19 watersheds; Survivorship over the past 2 decades estimated from number of trees that were not found or found dead in our survey; Collected GPS location, dbh, and several health rating measures for each individual; Leaf samples from 168 trees for genetic analysis.

Genetic Analysis
DNA extracted from fresh leaves; All individuals assessed using markers developed to distinguish butternut from butternut-Japanese walnut hybrids (Zhao & Woeste 2010); 1 chloroplast marker; 3 nuclear markers.

Results

Methods

Discussion

Acknowledgments

References

Figure 1: Map of GSMNP with locations of butternut samples. Hybrids shown in red.

Figure 3: Butternut seedling (top), butternut with arborist clingshot, used for leaf sampling (middle), core sample extraction (bottom).

Figure 4: Graph of butternut recruitment pattern, determined by aging tree core samples. 4a: Recruitment dates of combined butternut, in 5 year increments, 61 samples total. 4b: Recruitment dates divided by watershed for the 4 intensively sampled populations, 42 samples, distributed as shown in legend.

Figure 5: Distribution of ratings of butternut for 4 health measures.

Figure 6: Percentage of butternut mortality by watershed (left) and number of basal cankers by watershed (right).