NATURALIZED CHINESE CHESTNUT (*CASTANEA MOLLISSIMA*): STAND DYNAMICS, ROOT DISTRIBUTIONS, AND GENETIC RELATIONSHIPS

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Background

American chestnut (*Castanea dentata*) was an important tree species in the eastern North American forest until near extirpation by a fungal disease called chestnut blight. The American Chestnut Foundation (TACF) has been working to breed a blight-resistant chestnut by hybridizing American and Chinese chestnuts.

The ideal hybrids resemble American chestnut morphologically, but incorporate the Chinese chestnut genetic blight resistance. TACF intends to deploy these 'Restoration Chestnuts' to the forest. Research has focused on characteristics of *C. dentata*, but success of Restoration Chestnuts will also depend on the *C. mollissima* characteristics that are expressed. While *C. mollissima* has been studied in plantation settings, nearly nothing is known about silvics, genetics, and performance of naturalized *C. mollissima* in North American forests.
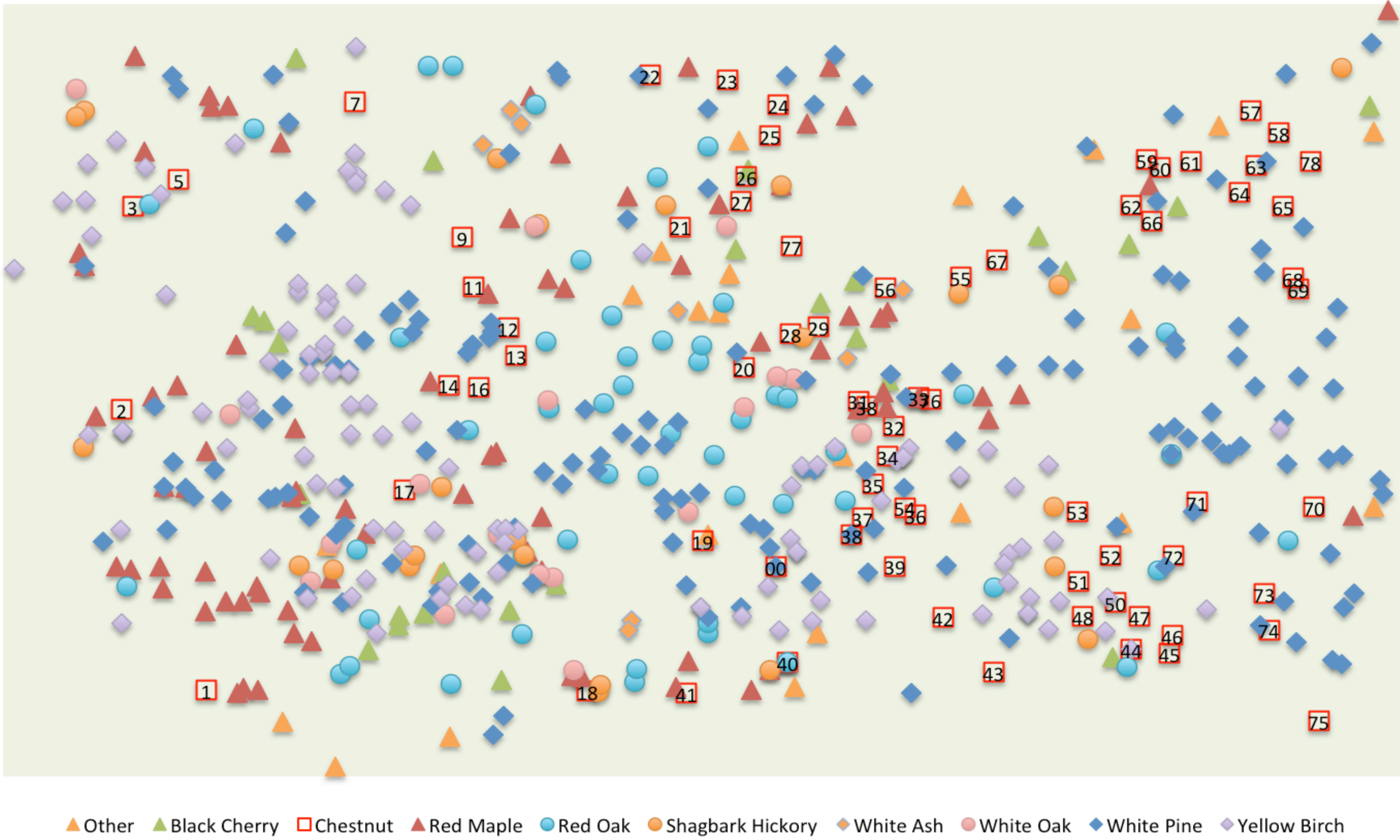
Introduction

On a Connecticut property known as the Sarah Cunningham estate, there is an orchard of *C. mollissima* trees whose offspring have established in an adjacent forest. We investigate how these *C. mollissima* trees were able to establish, survive, and compete so effectively, given that such an extensive naturalization of the species has not been reported elsewhere in the United States.

Our investigation:
1) STAND DYNAMICS (stand development and spatial patterns of the forest)
2) ROOT DISTRIBUTIONS (the relationship between below- and above-ground competition dynamics based on mapping and root forensics)
3) GENETIC RELATIONSHIPS (gene flow from parents to offspring by microsatellite analysis, looking for evidence of selection pressure in offspring)

S. Cunningham Forest

Legend: Other, Black Cherry, Chestnut, Red Maple, Red Oak, Shagbark Hickory, White Ash, White Oak, White Pine, Yellow Birch

STAND DYNAMICS

Methods

1) Map was made of this 1 ha. forest by measuring polar coordinates from the center of the plot
2) Tree species were determined and DBH measured
3) Ripley's K and Cross K analyses were used to determine spatial distribution of all forest trees and chestnut compared to other forest trees
4) Tree cores were taken to determine age and growth history of chestnut

Results

Species Stem Counts:

Species	Count	Species	Count
White Pine	168	Bigtooth Aspen	6
Yellow Birch	108	Eastern Redcedar	4
Red Maple	80	American Elm	3
Chinese Chestnut	73	Apple (domestic)	3
Red Oak	50	Alternate-leaf Dogwood	2
Black Cherry	27	Burningbush	2
Shagbark Hickory	24	Flowering Dogwood	1
White Oak	18	Honeysuckle	1
White Ash	8	Sassafras	1

Basal Area by Species

Size Class Distribuions

Ripley's K: Distribution of All Forest Trees

Ripley's Cross K: Chestnut vs. Other Trees

Conclusions

1) Chinese chestnut is a codominant canopy species which composes 20% of the basal area of this forest and is one of the most numerous species. It appears to compete effectively with native North American species in this location.
2) Tree ring counts verified that forest chestnut were of similar age, about 40-50 years old, grew rapidly for most of their lives, and show slowed, suppressed growth in the last 20 years coinciding with canopy closure.
3) Chestnut mostly occurs in the middle size classes, with the only larger species being white pine. There is no recruitment in the smaller size classes, probably due to competition with shade-tolerant species and deer predation.
4) Ripley's K analysis shows spatial clustering of all trees in the forest, which is expected in a natural, unmanaged forest stand. Chestnut clusters with other forest trees, again indicating that fits the typical patterns of forest dynamics of natural, native species.

UPCOMING RESULTS

GENETIC RELATIONSHIPS

1) DNA was extracted from all chestnut from parents in the orchard and offspring in the forest.
2) An array of 16 microsatellite loci and the computer program CERVUS are being used to determine:
   1) Relatedness within the parent population
   2) Relatedness within the offspring population
   3) Parentage of the forest offspring
3) Based on these analyses, we will determine how much selection pressure is evident in the offspring, which may assist in Chinese chestnut parent selection for future hybrid breeding

ROOT DISTRIBUTIONS

1) Soil samples were taken at regular intervals and depths throughout the forest site, and the fine roots were removed.
2) DNA was extracted from the roots, and these samples were taken to the Smithsonian Museum of Natural History.
3) Based on DNA barcoding markers developed in that lab, the species of each root sample was determined.
4) Inverse modeling uses the species of each root, weights of root samples, the location of the sample, and the map of above-ground stems to determine the below-ground distributions of species.
5) Considering the importance of rhizosphere dynamics and conditions to species survival and growth, and considering how difficult it has been to study below-ground interactions, this new technique could give us access to a new wealth of forest ecology information.