Quantifying the Genetic Impacts of Forest Management Strategies on Sugar Maple (Acer saccharum) in the Northern Forest

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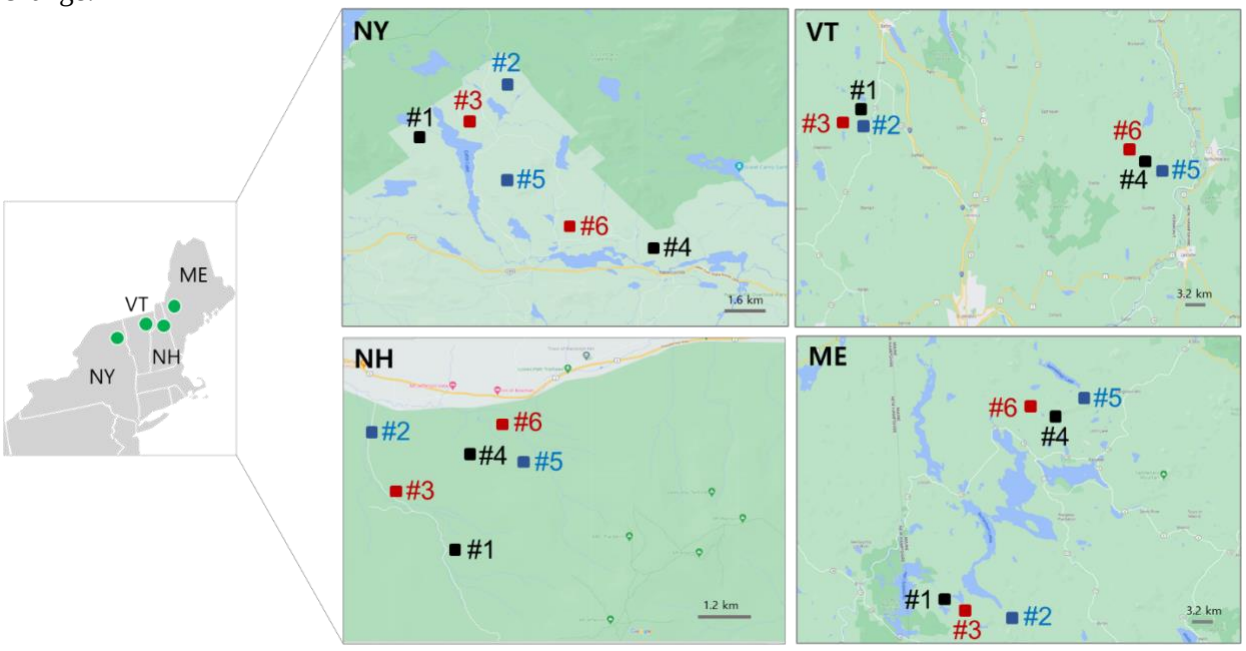
Project abstract

To examine how forest management practices affect genetic diversity of sugar maple, NSRC researchers will quantify the effect of two common management strategies (even-aged and uneven-aged) on northern hardwood stands with a strong sugar maple component. Managers use both practices to achieve a variety of objectives; however, no one has explored their impacts on tree genetic diversity. Researchers will measure differences in genetic diversity between stands treated with shelterwood (for even-aged) and selection (for uneven- aged) methods and no management within the last 100 years (as the control group) by examining three age classes (seedlings, saplings, and mature trees) per stand, with two replications in each of the four Northern Forest states.

Researchers will use sugar maple genetic markers that are subjected to natural selection and related to the fitness of individual trees. They will analyze 720 leaf samples across the Northern Forest to quantify metrics of genetic diversity within and between stands and states in relation to each tree age class under each management practice. Findings will help refine management practices, such as identification of trees or stands that are genetically diverse and ideal for use as seed stocks for regeneration or restoration and of pollen sources for assisted pollination to genetically enrich future generations. Results will provide baseline information for the level of sugar maple diversity and serve as the start of a Forest Genetic Resource Monitoring program for the Northern Forest to detect potentially harmful changes to forest adaptability. Genetically-sound harvesting practice is central to sustainable management of forest resources, especially the "genetic resource" that allows population and species-level adaptations to change.



Study sites/sampling locations. The numbers indicate the control and experimental stands (in two replicates): unmanaged (black), shelterwood (red), and selection (blue).

NSRC Progress Report 2021

Progress in 2021

The research team conducted fieldwork from June to July 2021 to collect sugar maple leaf samples across the Northern Forest (Figs. 1 and 2). In consultation with the appropriate forest managers and landowners, sampling was done from Huntington Wildlife Forest (NY), White Mountain National Forest (NH), North Greensboro (VT), and the Seven Islands property in Rangeley (ME). Two of the sampling locations were managed by state and national governments (SUNY-ESF, NY and US Forest Service, NH) while the other two were owned by private entities (LandVest, VT and Seven Islands Land Company, ME). In each location, samples were obtained from two geographically separated sites (≥1 km apart) as replicates (Fig. 1). Each site included a control group (unmanaged stand) and two experimental groups (selection and shelterwood stands). Using extendable tree pruners, fresh leaves were randomly collected from several individuals (≥ 5 m apart) of each age class: seedlings (two leaves), saplings (12-20 cm DBH) and mature trees (≥ 25 cm DBH) per stand. Ten individuals were sampled from all stands except for one stand in NY where only 8 samples were available. A total of 718 sugar maple leaf samples were collected across the northern forest. The leaf samples were stored in individual tea bags with silica gel and transported to SUNY-ESF for DNA isolation. Genomic DNA were successfully extracted from all the samples. Primers for PCR (Polymerase Chain Reaction) were designed, and the conditions optimized for 11 out of the 14 EST-based genic microsatellite markers. PCR products were checked through electrophoresis.

Problems or changes

The project generally proceeded as planned with only a couple of issues: 1) only 8 samples (instead of 10) were collected from one of the stands in NY due to insufficient number of appropriate individuals; and 2) 3 out of the 14 potential microsatellite markers will be excluded from the analysis because it was found that they exhibit null alleles producing significant deviations from Hardy-Weinberg Equilibrium and thus, will cause bias in genetic diversity analysis. The uneven sample size and reduced number of microsatellite markers will not affect the results and strength of the study.

Plans for 2022

The next step will involve a lot of laboratory work by performing PCR amplifications of the 11 primer pairs against each of the 718 samples, followed by assessments of their quantity and quality. To reduce the total number of PCR runs, multiplex PCR will be performed on the optimized PCR conditions. The amplified PCR products will be sent to Cornell Institute of Biotechnology for automated fragment analysis using the Applied BioSystems 3730xl DNA Analyzer. Following receipt of the raw data, we will determine the number, sizes, and frequency of alleles for each PCR products using GeneMapper v4.0 software and then manually construct the data matrix.

Data analysis will constitute most of our activities for the second half of 2022. We will quantify the various metrics of genetic diversity within stands, states and for the entire Northern Forest in relation to each of the management practices and age classes. Statistical analyses will be used to compare various parameters including total number of alleles, number of unique alleles, percentage polymorphic loci, observed and expected heterozygosity, etc. We will also quantify the various metrics of genetic divergence between stands, states, and entire Northern Forest region in relation to the management practices and age classes. This part will be accomplished through analysis of parameters such as molecular variance, discriminant and principal components analyses, genetic distance, population genetic structure, gene flow, degree of inbreeding, occurrence of bottleneck, and others. We hope to finish data analysis and begin data interpretation towards the end of 2022.