



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), stands treated with selection (for uneven-aged), and stands with 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. These stands are 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 that will be able 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.

Progress in 2022

Most of the research activities in 2022 were spent on laboratory work, including genomic DNA extraction, PCR primer pair optimization, and amplification through multiplex PCR. The DNA isolated from all the 718 sugar maple leaf samples passed quantity and quality assessments. Multiplex PCR involved amplifications of various combinations of the 11 primers representing Expressed Sequence Tag-derived Simple Sequence Repeat Markers. Polymorphism information content was calculated and indicated that each of the 11 genetic markers were informative. Genotype accumulation curve analysis showed that the data have at least the minimum number of loci necessary to discriminate between individuals in populations. The rest of the year was spent on preliminary data analysis. The dataset was used to estimate genetic diversity indices such as total number of alleles, allelic richness, observed heterozygosity, expected heterozygosity, and inbreeding coefficient. Each index for the shelterwood and selection systems was compared with the unmanaged stands according to size class (seedling, juvenile and mature) and state (NY, VT, NH, and ME). Preliminary results indicated that the selection and shelterwood stands both generally showed decreased genetic diversity compared to the unmanaged stands, but their impacts differed based on size, class, and state.

Physiognomy



Slide from the presentation on the preliminary insights of silvicultural practices on the genetic diversity of sugar maple in the Northern Forest by Seona Yun and Namjoo Heo.

Problems or Changes

The laboratory portion proceeded as expected but took longer due to additional steps required to ensure we have high quality DNA. Manual inspection of the electropherograms from Cornell showed that three samples (two from NY and one from VT) had many low-quality peaks. Thus, these samples were removed from the dataset and treated as missing data resulting in 715 samples for further genetic analysis. The final sample size is still robust, so we can proceed to the analysis as planned.

Plans for 2023

We will continue to analyze our data relative to the various genetic diversity indices as one (all combined) analysis, as well as separately by breaking the dataset into subsets based on various parameters. We plan to submit at least two papers for publication and present our results to appropriate scientific meetings e.g., Northern Hardwood Conference in New Brunswick on August 1-3, 2023. A project extension will allow us to engage in community outreach, particularly for forest managers and other stakeholders, as another way of disseminating our findings and their practical implications for forest management.

Collaboration

Preliminary interpretations of the results have been done and presented to graduate students and colleagues at SUNY-ESF through Ecolunch, our regular, informal departmental seminar by post-doctoral associates, Dr. Seona Yun and Dr. Namjoo Heo. (See figure above.)