Development of a Microsatellite Library for the Eastern Hemlock, *Tsuga Canadensis*

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ABSTRACT

Eastern hemlock, *Tsuga canadensis*, is a vital component of the eastern North American forest, providing important habitat for songbirds and small mammals (Yamasaki et al. 2000, Young et al. 2002), browse for deer and other herbivores (Anderson and Loucks 1979), and temperature moderation important for native brook trout in first and second order streams (Ross et al. 2003). Over the last 20 years, widespread decline and mortality of hemlock in the eastern United States has occurred, particularly in association with hemlock woolly adelgid (*Adelges tsugae*) infestations. In order to mitigate hemlock decline, an important first step is to determine the genetic structure of the existing hemlock populations. This will be accomplished using a library of microsatellite markers recently being developed at our facility.

Microsatellites occur throughout a species' genome and are comprised of segments of repeated DNA with a short (usually 1-6 nucleotides) repeat length, are highly unstable, and mutate at high rates compared to other genetic markers. These differing numbers of repeats at a microsatellite constitute alleles and are inherited in a Mendelian fashion. Divergence of allele frequencies between populations occurs over time due to new mutations and drift while migration leads to a homogenization of allele frequencies. Effects of natural selection may overcome these forces by causing selection of an allele at a specific locus.

Screening individuals with microsatellite markers allows these allele frequencies to be measured and can reveal a multitude of information about the species being studied. Microsatellites have been used for genetic mapping, linage analyses of disease susceptibility genes, paternity and kinship analysis, early cancer detection, and the probability of sample identity at both the individual and population levels. In the study of entire populations, microsatellites are also useful in determining the degree of hybridization between closely related species, interspecies and inter-population variation, estimating effective population size, degree of population structure including both the amount of migration between subpopulations and genetic relationships among the various subpopulations (Murray 1996).

For eastern hemlock, these markers will facilitate identification of native variants that are resistant to infestation effects of hemlock woolly adelgid and allow the effectiveness of recovery strategies, such as genetic engineering of resistance genes and intergression of congeneric genomes into *T. canadensis*, to be monitored.