

## Effects of the Decline of the American Chestnut and Harvesting on Genetic Diversity of Northern Red Oak in Western North Carolina

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Sustainable forestry requires assessment and preservation of genetic diversity. The maintenance of genetic diversity within a species is important for three central reasons: genetic diversity is necessary to retain resistance to climatic change and pest invasion; protection of species is needed to promote a stable ecosystem; and the maintenance of allelic diversity is important for potential value in future breeding practices. *Quercus rubra* (L.) (northern red oak) (NRO) is the most economically important hardwood species in western North Carolina. Despite efforts to facilitate NRO regeneration, success in western North Carolina has been very poor and the decline in population sizes may be resulting in loss of genetic diversity. This study used nine microsatellite markers to determine if NRO populations in western North Carolina have experienced a change in genetic diversity following two different ecosystem changes; 1) after harvesting, and 2) after the disappearance of the American chestnut (*Castanea dentata* L.) overstory from the southern Appalachian forests. Cambial samples were collected from approximately 250 northern red oak individuals located in four sites that have been harvested and four sites that have not been harvested since the demise of the American chestnut in the Nantahala National Forest. All of the sites used in this study were historically American chestnut dominated, and each harvested site was located within a mile of an unharvested site of similar forest type. Sampled NRO trees include those that were established when American chestnut was still the dominant overstory species, individuals that have established since the loss of the American chestnut, and individuals established pre- and post-harvest of a stand. The hypotheses tested in this study were; 1) genetic diversity of pre-chestnut blight northern red oak trees does not differ from that of trees established after the decline of the chestnut; 2) genetic diversity of northern red oak stands before and after harvesting does not differ. Population genetic variation was analyzed using ANOVA, as well as autocorrelation analysis. The relative genetic diversity of the population was quantified in terms of allele frequencies, observed heterozygosities ( $H_o$ ), expected heterozygosities ( $H_e$ ), effective number of alleles ( $A_e$ ), and fixation index ( $F$ ). Genetic structure was quantified using  $F$ -statistics. This presentation will summarize preliminary results of this study, and will offer preliminary conclusions.