

PATTERNS OF POST-GLACIAL RECOLONIZATION OF NORTHERN RED OAK (*QUERCUS RUBRA* L.)

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Quercus rubra is a dominant species in the forests of east central North America and is a source of valuable hardwood. The purpose of our research is to detect the impact of postglacial recolonization patterns on contemporary population substructure. We hypothesize that the species has undergone two reductions of effective population size: a natural reduction about 18,000 years ago, during the Wisconsinian glaciation and an anthropogenic reduction during European colonization. After the glacier retreated, trees surviving in southern and western refugia recolonized the northeastern United States and Canada. We hypothesize that during this recolonization process a loss of organelle genetic diversity occurred due to genetic drift. Thus, we expect to see genetic diversity diminish as a function of distance north from the southernmost advance of the Wisconsinian ice sheet. An alternative hypothesis is that genetic diversity will peak in the middle of the contemporary range as a result of mixing two refugial source populations: a population west of the Mississippi River and a population south of the Ohio River. We are using PCR-RFLP of three intergenic regions in oak chloroplast DNA sequences to test this hypothesis. The maternally inherited chloroplast genome will retain the signal of postglacial migrations even after considerable contemporary disturbance. For our preliminary survey we chose sites with histories of minimal human disturbance within the last one hundred years. We have detected only three haplotypes north of the glaciation line (fig. 1). Most Northern sites had either haplotype I or haplotype II. Haplotype V was locally abundant at one Indiana site and occurred at four other sites north of the glaciation line. We detected only one haplotype in each of the two northernmost sites in Wisconsin (15 trees/site). These data support the first hypothesis.

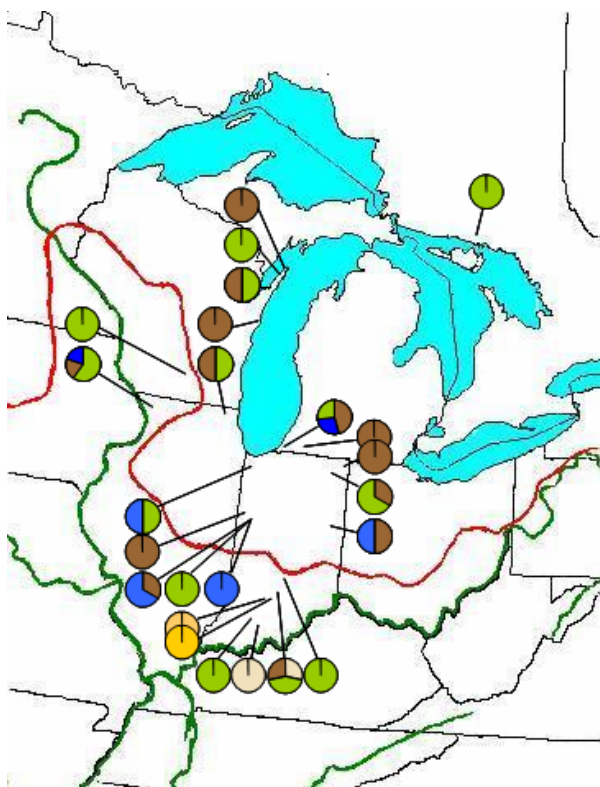


Figure 1.—Geographic distribution and frequencies of haplotypes at each site. Haplotypes I, II, III, IV and V are represented as brown, green, beige, yellow and blue, respectively. The maximum advance of Wisconsinian ice sheet indicated by the red line.

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