Introduction

Pondberry (Lindera melissifolia) is an endangered aromatic shrub in the Laurel family. It grows, often in clonal patches, in seasonally flooded forests in seven southeastern states. The U.S. Fish and Wildlife Service’s Recovery Plan requires the identification of self-sustaining populations. Use of molecular genetic markers can aid in this identification by determining several important conservation genetic factors: genetic relatedness between populations, which populations are reproductively isolated, and whether their genetic diversity is maintained over time.

Materials and Methods

For DNA isolation one leaf was sampled from each of about 1500 plants at 14 sites in 10 locations (see map). The western populations were in AR and MS, the eastern populations in AL, GA, SC and NC. Eleven microsatellite DNA markers were used to genotype each plant. Microsatellite markers (called Simple Tandem Repeats or STRs in human genetics) are highly variable and have alleles (variant forms) that differ from each other by discrete size classes. This feature makes them ideal for parentage, population genetic and phylogenetic analyses. The genotyping results revealed 408 unique genotypes (non-clonal individuals) which were then used in various genetic analyses.

Results

East vs West

All 14 sampled populations were genetically distinct from each other. There is an ancient divide between the eastern and western regions, which may have arisen from two separate glacial refugia. The patterns of diversity within and between regions are consistent with the regional natural history of pondberry: expansive flood plains in the west promoted high gene flow between large populations, while the topography and hydrology of scattered local depressions of the east promoted smaller, more isolated populations having restricted gene flow.

So, you been here long?

In the western populations genetic relatedness decreases as a function of distance out to about 150m-200m. (There weren’t enough data for such analyses in the east.) At short range distances genetic relationships were often highly spatially structured. Theory and studies with other species suggest that greater spatial structure evolves with increasing age of a stand. Thus spatial genetic bubble maps could be used to determine relative ages of pondberry sites, e.g. newer sites will have little structure – few or no “bubbles”. These data are consistent with pondberry being an insect pollinated, bird and gravity dispersed, clonal species.

Daddy, what’s a population?

Neighborhood size (N_e, the number of neighbors within a continuous population that randomly mate with each other) was estimated to be ~50-60 unique genotypes (non-clonal, mating plants). By one definition this describes the maximum extent of a breeding population, where an adjacent neighborhood of the same size would give the minimum measurable genetic difference between populations. Neighborhood size will vary with the sex ratio (males and females are different plants), age and clonal genotype ratio.

The (genetic) future of pondberry

Demographic and ecologic factors are the main determinants of whether populations on the edge slip into extinction. But even if these factors are favorable insufficient genetic diversity spells trouble in the long run. Fortunately for most pondberry populations genetic diversity is high and inbreeding is low to non-existent. These data will be used to run population genetic simulations and determine which, if any, populations may be headed for a genetic fall from grace.