Patterns of genetic variability and differentiation of Garry oak (*Quercus garryana* Dougl. ex Hook) on Vancouver Island, Canada

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Garry oak (Quercus garryana Dougl. ex Hook) is a deciduous tree species considered endangered throughout its range in British Columbia, Canada. Today Garry oaks account for less than 0.3% of the province's land coverage, yet they still exist as a keystone species, housing more plant species than any other land-based ecosystem in coastal BC. The current distribution of Garry oak meadows range from the Pacific Coast of southcentral California to the northern peripheral boundary of south-central Vancouver Island. Coniferous forest, urban encroachment, and changes in disturbance regime continue to threaten these ecosystems by impacting the spatial distribution and population composition. This study investigates the biogeography of Garry oaks using genetic techniques to quantify patterns of gene flow. One hundred and twenty-one tree samples were collected across four locations in the Nanaimo region on Vancouver Island. Each sample was genotyped using six nuclear microsatellite loci. To infer age class within individual sampling sites, each population was divided into largest and smallest diameter breast height (DBH) sized cohorts. Overall, allelic variation was low to moderate, ranging from 3.00 to 7.50 alleles per locus with an average of 4.375 (+ 0.389 SE) across all loci. A Global F_{ST} of 0.06 and 0.085 averaged over all loci suggests significant departures from the Hardy-Weinberg equilibrium (P < 0.05) in all four populations and size Given that this data suggests low levels of cohorts respectively. differentiation within populations and high levels of gene flow between populations, this may reflect an adaptive potential for Garry oaks in response to future climate change events.