

Genetic diversity and distribution of coastal wolves in Northern British Columbia

Michelle Hoang¹, Ramona Maraj², Gretchen Roffler³, Shelley Marshall⁴, and Mark Boyce¹

¹University of Alberta, Dept. of Biological Sciences ²Parks Canada, Chrysalis Ecological ³Alaska Department of Fish and Game ⁴British Columbia Ministry of Forests, Fish and Wildlife

M. Hoang

Introduction

- Wolves in coastal British Columbia and Southeast Alaska are genetically, morphologically, and functionally distinct from mainland conspecifics^{1,2,3,4}
- Close evolutionary history between coastal wolves in British Columbia and Southeast Alaska⁵
- Recent petition to list coastal wolves in Southeast Alaska under the Endangered Species Act
- Current literature lacks understanding of genetic variation and gene flow between coastal wolf populations in British Columbia and Southeast Alaska



Figure 1. Wildlife camera photo of wolf responding to hair snag board treated with Mega Musk lure. Image from Mark Boyce.

Objectives

- Characterize the genetic differentiation and distribution of coastal wolves in Northern British Columbia
- Examine landscape connectivity to identify how corridors and geographical features might increase or decrease genetic continuity between subpopulations

Study Area

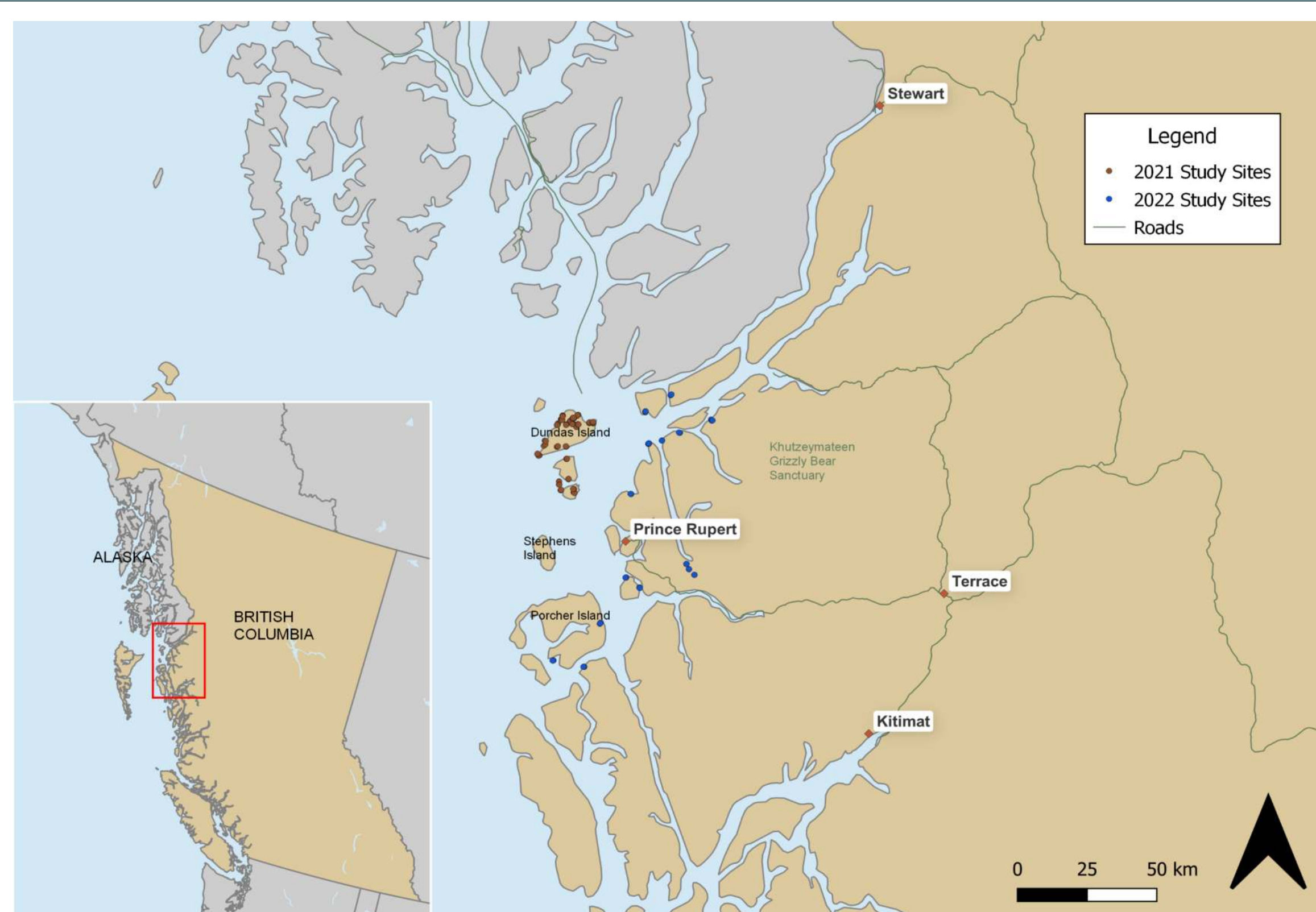


Figure 2. Map of study area in Northern coastal British Columbia.

Methods: DNA Sample Collection

- Increase sampling effort for upcoming field season
- Deploy non-invasive hair snag boards
- Apply 5mL Mega Musk lure on boards to evoke scratch-and-rub response
- Sampling will occur in 12-day rotations
- To prevent cross-contamination between sampling intervals, hair boards will be torched between rotations
- Wolf scat collected opportunistically

Year	Number of hair boards	Number of hair samples	Number of scat samples
2021	110	154	8
2022	71	134	8



Methods: DNA Genotyping and Analyses

- All DNA extraction and genotyping conducted at Wildlife Genetics International in Nelson, British Columbia
- Use a vetted set of 24 microsatellite loci
- Calculate allelic diversity and mean observed and expected heterozygosity using FSTAT v.2.9.3 and hp-rare 1.0^{6,7}
- Identify populations and conduct assignment tests according to genetic clusters using STRUCTURE v2.3.3 and GENELAND v3.3.0^{8,9}

Methods: Landscape Connectivity

- Use omnidirectional circuit theory models to compute landscape connectivity
- Habitat attribute layers will include forest cover, digital elevation models, bathymetry data, ocean currents
- Resistance layers will include terrain ruggedness, distance between islands, forestry logging data
- Combine genotype data and connectivity maps
- Identify potential corridors and areas of genetic continuity

References

(1) Weckworth et al. *Molecular Ecology*. 2005, 14, 4. (2) Stronen et al. *BMC Ecology*. 2014, 14, 1. (3) Darimont and Paquet. Prepared for the Raincoast Conservation Society. 2000. (4) Muñoz-Fuentes et al. *Journal of Biogeography*. 2009, 36, 8. (5) Weckworth et al. *PLoS ONE*. 2011, 6, 5. (6) Goudet. University of Lausanne, Dorigny, Switzerland. 2001. (7) Kalinowski. *Molecular Ecology Notes*. 2005, 5, 187-189. (8) Pritchard et al. *Genetics*. 2000, 155, 945-959. (9) Guillot et al. *Molecular Ecology Notes*. 2005, 5, 712-715.

Preliminary Results

Individual	Number of recaptures	Sample type	Sex
g2332-58	6	Hair	M
g2332-68	1	Hair	M
g2332-71	6	Hair, Scat	M

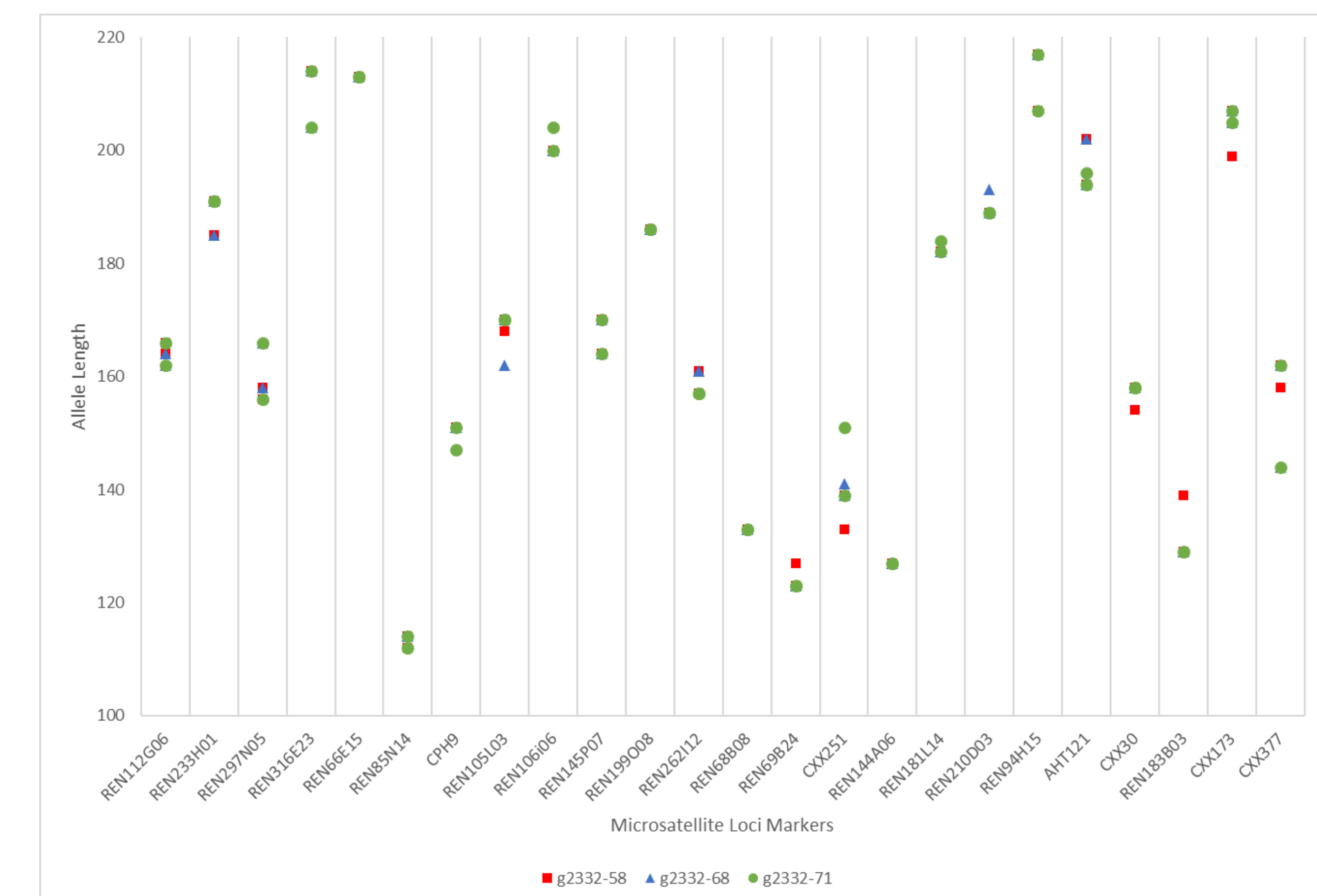


Figure 3. Allelic diversity of 3 genotyped male wolves using a vetted set of 24 microsatellite loci.

- Results from 2021 samples, awaiting report for 2022 samples
- Among these 72 datapoints there were 39 heterozygous genotypes, for an initial estimate of 54% heterozygosity
- More genetic variability in this population than expected for long-term isolated small population

Management Implications

- Results from this project will help inform the petition listing in Southeast Alaska
- Document trans-boundary interactions of coastal wolves to enhance management of the subspecies

Funding Sources

