Appendix 1.

METHODS

DNA extraction and genotyping details

We prepared hair samples for extraction by selecting 10 guard hairs when available and supplementing with five underfur hairs per missing guard where needed. When no guard hairs were present in a sample, 30 underfur hairs were chosen.

For microsatellite genotyping, we labeled primers with FAM, HEX, HEX, TET, or NED dye groups. We amplified DNA on a MJ Research PTC-100 thermocycler with PCR reagent concentrations optimized for each primer pair (Table A1.1). We utilized a quality control protocol that involved subsampling each sample and removing samples that were poor quality or had three or more alleles at a locus (Paetkau 2003). This protocol has previously resulted in error rates of 0.002-0.005 per locus per sample (Kendall et al. 2009).

The amelogenin locus for sex determination was amplified using 10 pM of each primer (Forward:CAGCCAAACCTCCCTCTGC Reverse:CCCGCTTGGTCTTGTCTGTTG), 200uM dNTPs, and 0.9 units of Taq polymerase on a MJ Research PTC-100 thermocycler. We distinguished between male and female individuals using gel electrophoresis with female sample producing a single 280bp fragment and male samples producing a 280 and a 217 bp fragment. To avoid Y allele dropout, we only sexed samples that produced high confidence scores for all other microsatellite loci (Paetkau 2003). This method has previously produced error rates of 0.0007 per locus per sample (Kendall et al. 2009).

Hardy Weinberg proportions

Deviations from Hardy Weinberg equilibrium (HWE) were investigated with the web-based version of Genepop (Rousset 2008). Identifying deviations is important as they can provide information on population size, gene flow, and the presence of selection (Allendorf et al. 2012). Additionally, HWE is an essential assumption underlying the model-based clustering algorithms performed by STRUCTURE and Geneland (Pritchard et al. 2000, Guillot et al. 2005).

Connectivity and Resistance Estimation with Mantel tests

Initially, we utilized partial Mantel tests in R (version 3.2.4, 2018) package ecodist to identify individual landscape variables that explained a significant proportion of variation in the genetic distance variable beyond that explained by geographic distance alone.

RESULTS

Global deviation from HWE found in one genetic group
We found significant (p < 0.05) heterozygote deficiency at three loci (G10C, p = 0.017; G10L, p = 0.026; and MSUT2, p = 0.030 in population G3, G2, and G1 respectively). We observed significant (p < 0.05) heterozygote excess at four loci: G10B (p = 0.028) and G10U (p = 0.040) in population G1, and MU59 (p = 0.023) and X145P07 (p = 0.030) in population G3. Using global HWE tests, we did not find any populations with a significant heterozygote deficit, whereas G1 was the only population that showed significant (p < 0.050) global deviation from HWE in the form of heterozygote excess (p = 0.015). This heterozygote excess suggests that G1 may be receiving gene flow from other areas or represents the unification of previously separated populations (Allendorf et al. 2012). Though these deviations from HWE can be problematic for the use of STRUCTURE and Geneland, deviation is only globally present in one genetic group and the breaks between groups are confirmed with sPCA, a method that does not require the assumptions of HWE to be met (Jombart 2008).

**Initial Mantel tests showed high multicollinearity between variables**

We validated modern and archaeological surfaces separately using partial Mantel tests, which identified only waterways (p = 0.001), fish traps (p = 0.010), and Indigenous language family boundaries (p = 0.010) as being significant beyond the influence of geographic distance. However, we found a high level of multicollinearity between the resulting significant variables (waterways and fish traps (Mantel R = 0.817), which prohibited the testing of models with all variables simultaneously against the genetic distance matrix using multiple regression of distance matrices (MRM).


Figure A1.1 Delta $K$ plot identifying the most probable $K$ using the Evanno method as implemented in Structure Harvester for the results of STRUCTURE analysis.
Figure A1.2 Spatial grizzly bear population structure map produced by Bayesian clustering model implemented in Geneland. High population membership is indicated by yellow and cream colors and genetic discontinuities between populations are represented by dense contour lines. A) Spatial output for G1. B) Geneland spatial output for G2. C) Geneland spatial output for G3.
Figure A1.3 Spatial Principal Components Analysis of grizzly bear population structure for male and female bears conducted with a A) Delauney Connection Network and producing B-D) three representations of the first score and E-F) two eigenvalue plots.
Figure A1.4 Spatial Principal Components Analysis of grizzly bear population structure for female bears conducted with a A) Delauney Connection Network and producing B-D) three representations of the first score and E-F) two eigenvalue plots.
Figure A1.5 Spatial Principal Components Analysis of grizzly bear population structure for male bears conducted with a A) Delauney Connection Network and producing B-D) three representations of the first score and E-F) two eigenvalue plots.
Figure A1.6 Commonality analysis beta weights with filled circles indicating significant beta weights for the A) archaeological surface with 95% bootstrap confidence intervals. (F1=Language family residuals, F2=Fish trap residuals, F3=Midden residuals, F4=Ice and snow residuals, F5=Waterway residuals, F6=Ruggedness residuals) and B) the modern surface with 95% bootstrap confidence intervals. (F1 = Modern settlement residuals, F2 = Forestry residuals, F3 = Ice and snow residuals, F4 = Waterway residuals, F5 = Ruggedness residuals).
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Table A1.2 Primary sources for archaeologically recorded shell middens and fish traps in the study area

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Table A1.3 Observed and expected heterozygosity for North American grizzly bear populations. (Abbreviations: $H_E$ = expected heterozygosity; $H_O$ = observed heterozygosity; $N$ = sample size)

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<th>Sampling Area</th>
<th>N</th>
<th>$H_O$</th>
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$^1$Proctor (2005), $^2$Paetkau (1998)
Anonymous, 2001. Site form for fish trap Weeteeam Bay (FdTg-6) on file at the BC Archaeology Branch, Victoria.


Foster, J., and D. Coombes, 1980. *Site form for Fish trap FfTa-1* on file at the BC Archaeology Branch, Victoria.


Radke, B., and G. Radke, 2005. *Archaeological Fish traps and site forms submitted to the BC Archaeology Branch.* Site forms and map illustrations on file at the BC Archaeology Branch, Victoria.


