Landscape effects on gene flow for a climate-sensitive montane species, the American pika

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Keywords: Landscape genetics, Mantel tests, causal modeling, CDPOP

Pika landscape genetics

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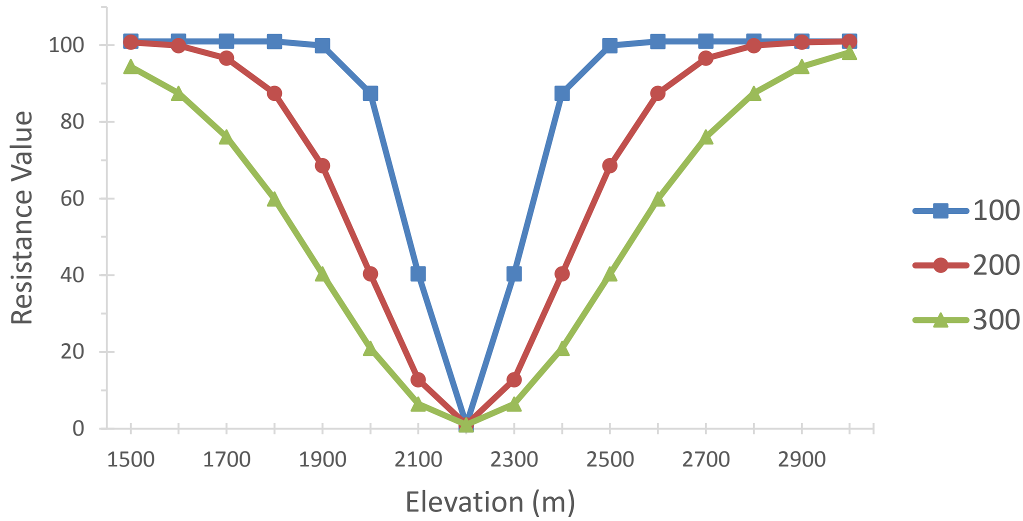
Supporting Information

Equation S1: Landcape resistance as a function of elevation; Inverse Gaussian function:

$$R = R_{max} + 1 - R_{max} * e^{\frac{-(Elev.-E_{opt})^2}{2*E_{SD}^2}}$$

where R_{max} is the maximum resistance, E_{opt} is the optimal elevation, and E_{SD} is the standard deviation about the optimal elevation. Parameter values tested are as follows: R_{max}= 2, 10, 100, 500, and 1000; E_{opt}= 1950, 2050, 2150, 2250, 2350, 2450, and 2550 m; E_{SD}= 100, 200, 300 m.

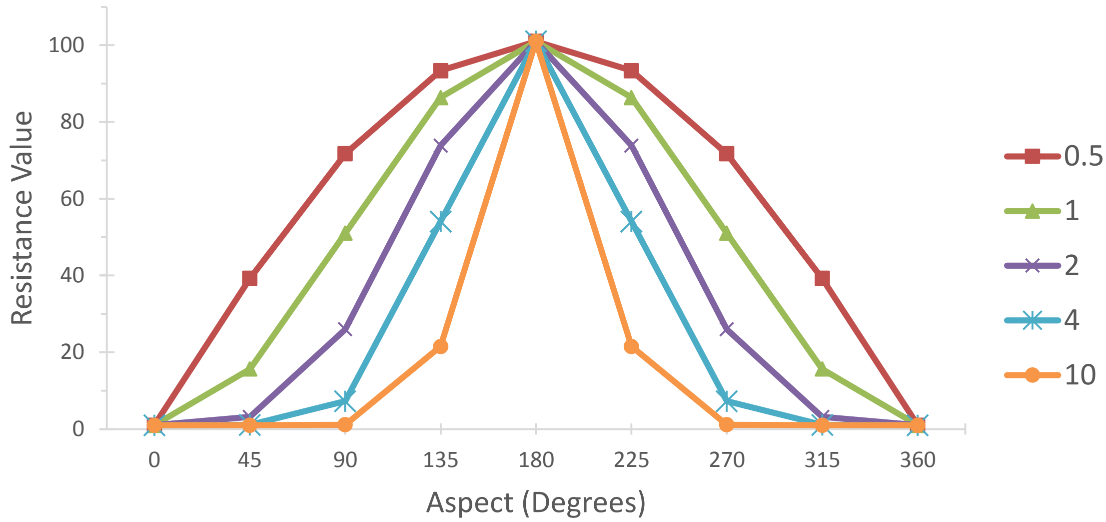


The above figure illustrates the resistance hypotheses with an optimal elevation of 2200 m and an R_{max} of 100. Series names are E_{SD}values. Higher values of E_{SD} represent lower contrast.

Equation S2: Landcape resistance as a function of aspect; Modified heat load index

$$R = \left[\frac{1 - \cos\left(\theta - \theta_{opt}\right)}{2}\right]^{x} R_{max} + 1$$

where θ_{opt} is the hypothesized optimal aspect such that resistance increases toward R_{max} (at $\theta_{opt} + 180°$) according to a curve governed by x. We tested aspects in 45° increments from 0° to 315°, five values of x, and four values oR_{max}f. Parameter values tested are as follows: x = 0.5, 1, 2, 4, and 10; R_{max}= 2, 10, 100, 500, and 1000. Flat areas, pixels with a value of -1, were reclassified as $R_{max}/2$.

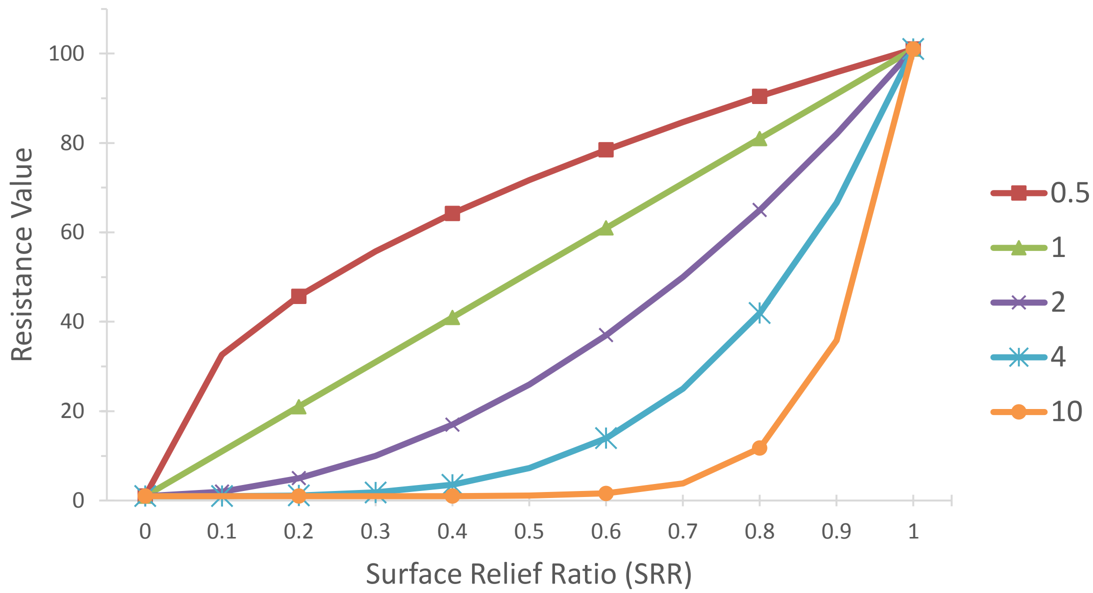


The above figure illustrates the resistance hypotheses with an optimal aspect of 0° and an R_{max} of 100. Series names are x values. Higher values of x represent higher contrast.

Equation S3: Landcape resistance as a function of Topographic Complexity

$$R = (SRR^{x})R_{max} + 1$$

We calculated surface relief ratio (SRR) within a radius of 3, 20, and 50 cells. Values range from 0 for low topographic complexity to 1 for high topographic complexity. Parameter values tested are as follows: x = 0.5, 1, 2, 4, and 10; R_{max}= 2, 10, 100, 500, and 1000.



The above figure illustrates the resistance hypotheses for topographic complexity with an R_{max} of 100. Series names are x values. Higher values of x represent higher contrast.

Table S1. Details for each microsatellite locus, including original source. Primer sequences and GenBank accession numbers are given for those loci that were designed from published clone sequences only. PCR product sizes are provided for Crater Lake National Park as well as those observed across multiple study sites. Multiplex panel ID and PCR conditions are consistent across all study sites[†]. Number of Alleles and expected heterozygosity are provided for Crater Lake only.

Locus	Primer sequence (5'-3')	GenBank Accn #	Repeat sequence	Product size† (bp)	CRLA Product size (bp)	Multiplex panel	Cycles	$T(a)$ (°C)	CRLA Alleles	CRLA H_e
OCC03	F-TGTGCTAAGATGCTAGACACTCCA R-CTAACTGCCAAACCCAGGACT	EU665185	AC	140-168	150-168	1	35	58	8	0.79
OCC04	F-GCCAGAATGATGTACACACACAC R-CGATTGGCCTTTCAAATGAGT	EU665186	AC	158-192	170-178	1	35	58	5	0.70
OCP04	Peacock et al. 2002		ATAG	193-249	205-237	1	35	58	8	0.64
OCP07	Peacock et al. 2002		AC	268-304	278-292	1	35	58	7	0.63
OCP20	F-GACAGAGGGATGGGAAGACA R-ATGTGGGAGATCCAGCAGAG	GQ461715	AG	120-164	136-156	1	35	58	9	0.77
OCP03	F- CAGCCATCTGGACAATGAAAC R- TGACAGTTTGACAGAGGGAAGTAA	AF487494	CTAT	126-174	134	1	35	58	1	0.00
OCC09	F-CAGTGATTCGCATAAGGTAAAGAT R-Zgurski et al. 2009	EU665189	AC	137-165	143-153	2	35	62	5	0.63
OCP14	F-TCTCTCCATAAACCTGACTTTCCAA R-CCAAGGGATCCTGGAGCGTTA	GQ461709	TATC	132-178	150-170	2	35	62	6	0.78
OCP21	F-TCACTCCTTGGCACATCTCA R-TCTGTTGGATGAATGGGGTTA	GQ461716	TATC	142-174	146-170	2	35	62	6	0.78
OCP01	Peacock et al. 2002		AG	286-342	308-310	2	35	62	2	0.05
OCP02	Peacock et al. 2002		GATA	379-435	391-415	2	35	62	7	0.65
OCP08	Peacock et al. 2002		AG	209-261	219-223	2	35	62	3	0.54
P7	Li et al. 2009		AC	139-185		2	35	62	0	0.00
OCP05	F-TGAACCAGCAGTCAGAAGACA R-Peacock et al. 2002	AF487496	TATC	156-196	172-192	3	32	58	6	0.77
OCP12	F-GCAGGTCTTTGGGGAATAAAA R-CCTGCTCTACAACCATCTGGA	GQ461707	TAGA	184-248	208-232	3	32	58	6	0.68
OCP17	F-TGAGGGAGAGCCAAAGACCAA R-GCTTCAGGAGACTGACCCAACC	GQ461712	GA	182-232	198-206	3	32	58	2	0.02
OCP18	F-TGACTTCCATAGTGGCTGCAC R-AAATCCCAGGGGCTGTGGAA	GQ461713	TCA	112-148	121-139	3	32	58	2	0.05
OCC02	Zgurski et al. 2009		AC	128-160	128-144	3	32	58	2	0.02
OCP27	F-AGGGACAATGGGAAAACTTGT R-TCTGGGCTCCTAGCTTCAGAT	GQ461721	AG	171-223	171-175	3	32	58	3	0.66
OCP06	F-Peacock et al. 2002 R-CCCAAAAACTGACACACAGGT	AF487497	TAGA	181-252	213-229	4	35	58	5	0.76
OCP11	F-TTGCCTGTTTACCATGCTTTG R-TGGCTATCTGACGAGTGAACC	GQ461706	TAGA	152-192	164-184	4	35	58	5	0.66

Table S1 continued.

Locus	Primer sequence (5'-3')	GenBank Accn #	Repeat sequence	Product size† (bp)	CRLA Product size (bp)	Multiplex panel	Cycles	$T(a)$ (℃)	CRLA Alleles	Hexp
OCP09	Peacock et al. 2002		TAGA	201-317	253-313	4	35	58	14	0.90
OCP16	F-GCCATTTGGGGAATGAAGCA R- GGCATGTCTGGCAAAAGCTG	GQ461711	ATC	118-154	127	4	35	58	1	0.00
OCP24	F-ACGTTGTATCTGTCTAGGAAACAAGTC R-ACCAGATCGGGTTGCCACAG	GQ461718	GATA	162-202	186-202	4	35	58	5	0.74

†PCR product sizes are for Crater Lake National Park (NP), Grand Teton NP, Rocky Mountain NP, Lassen Volcanic NP, Yosemite NP, Craters of the Moon National Monument and Preserve, Yellowstone NP, Lava Beds National Monument, Great Sand Dunes NP and Preserve, Sheldon National Wildlife Refuge, and Hart Mountain National Antelope Refuge (Castillo and Epps, unpublished data).

Table S2. Final multivariate models from the optimization with partial Mantel correlation after partialling out the IBD model for (1) PCA and (2) Bray-Curtis percent dissimilarity genetic distance metrics. Model parameters, partial mantel correlation, and p values are shown. Model parameters for topographic complexity refer to equation S3. The variable selection was the same, but variable parameters differed. As with the PCA genetic distance, a similar model with the converse trend in R_{max}, model 3, was equally well supported for Bray-Curtis percent dissimilarity.

Model	Topographic Complexity	Water	Aspect	partial Mantel r	p
(1) T + W	low $x = 2$, $R_{max} = 3$	classified, $R_{max} = 100$	-	0.22	0.00
(2) T + W	low $x = 2$, $R_{max} = 1001$	unclassified, $R_{max} = 2$	-	0.20	0.00
(3) T + W	low $x = 2$, $R_{max} = 101$	classified, $R_{max} = 50$	-	0.20	0.00

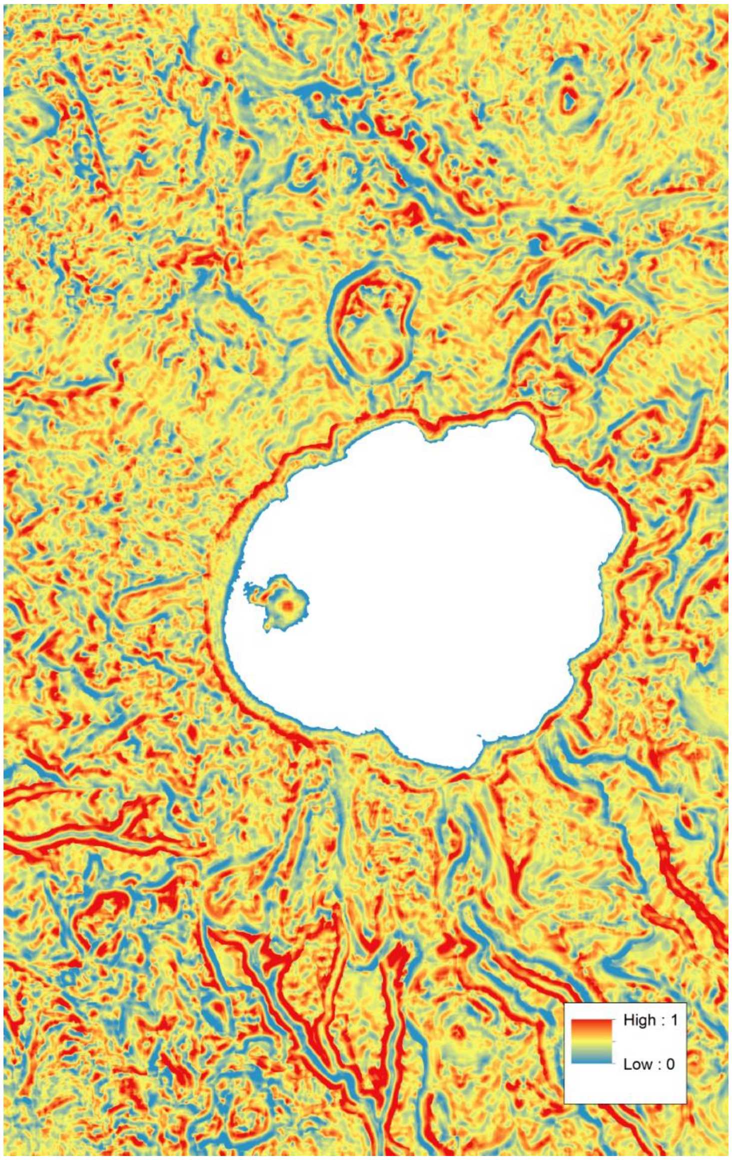


Figure S1: Map of the analysis frame within Crater Lake National Park showing surface relief ratio, a measure of topographic complexity. Values represent surface complexity for each pixel calculated using a radius of 20 pixels.

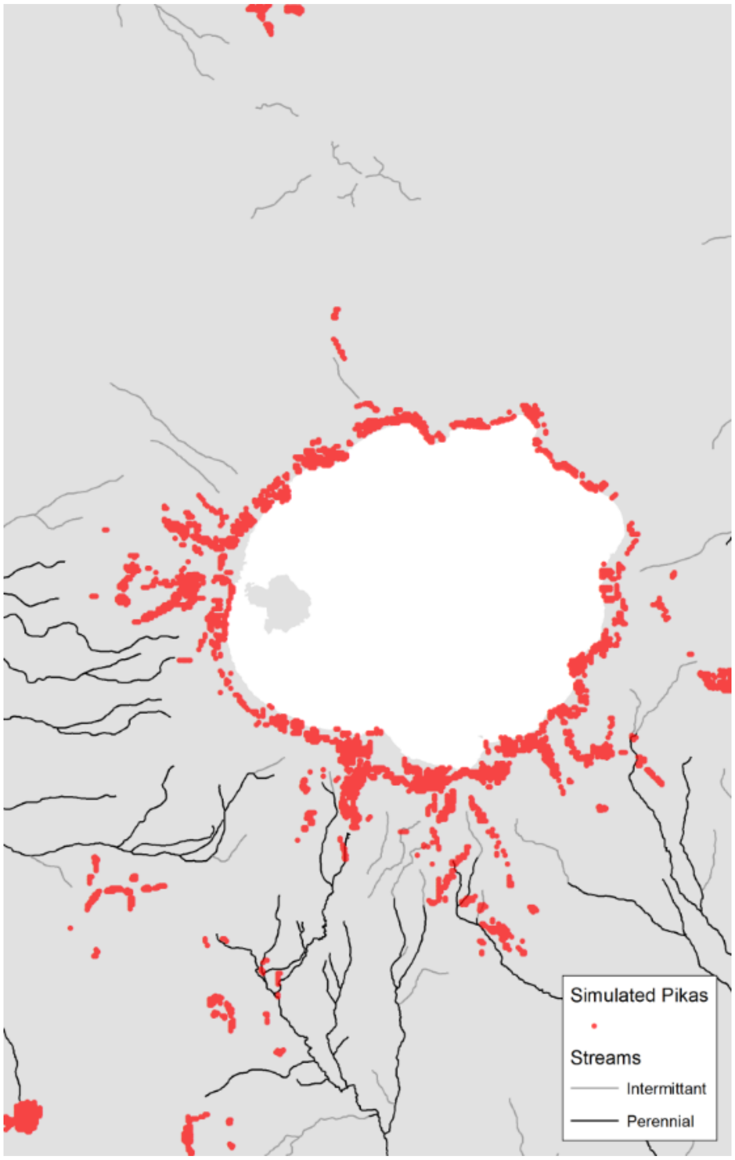


Figure S2. Map of the analysis frame within Crater Lake National Park showing the location of streams and simulated pikas.

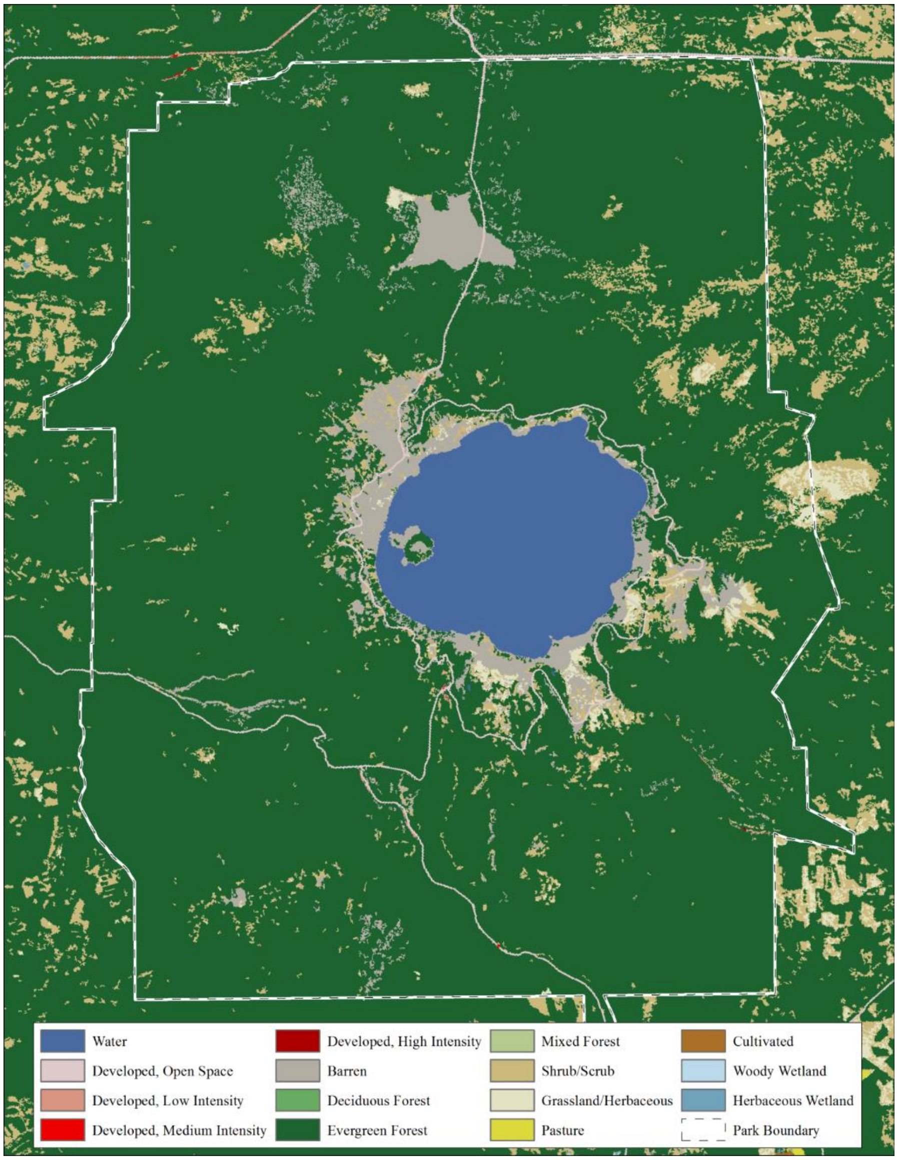


Figure S3. Map of Crater Lake National Park showing land cover categories from the 2006 National Land Cover Dataset.

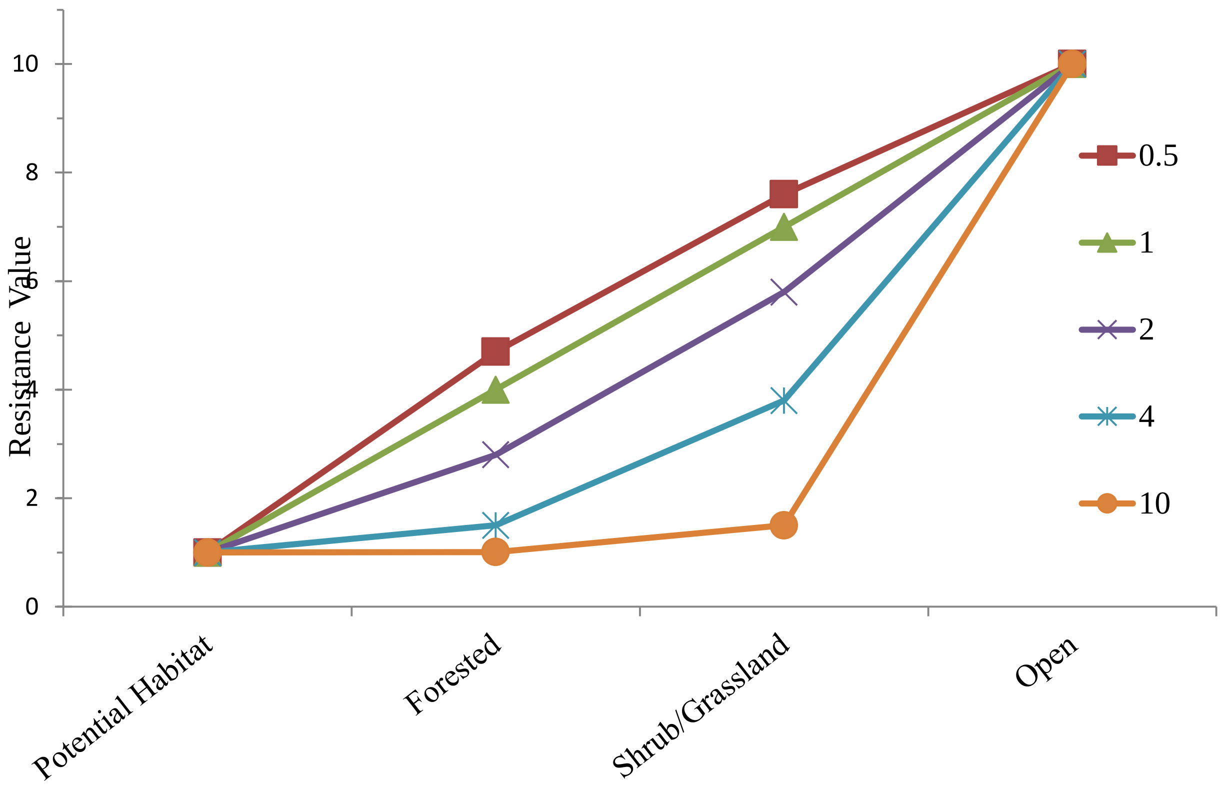


Figure S4. Resistance values for each land cover category ranked according to cover, with lowest rank assigned to land cover types that provide greater cover. The figure shows hypotheses with an R_{max} = 10 and series names are x values.

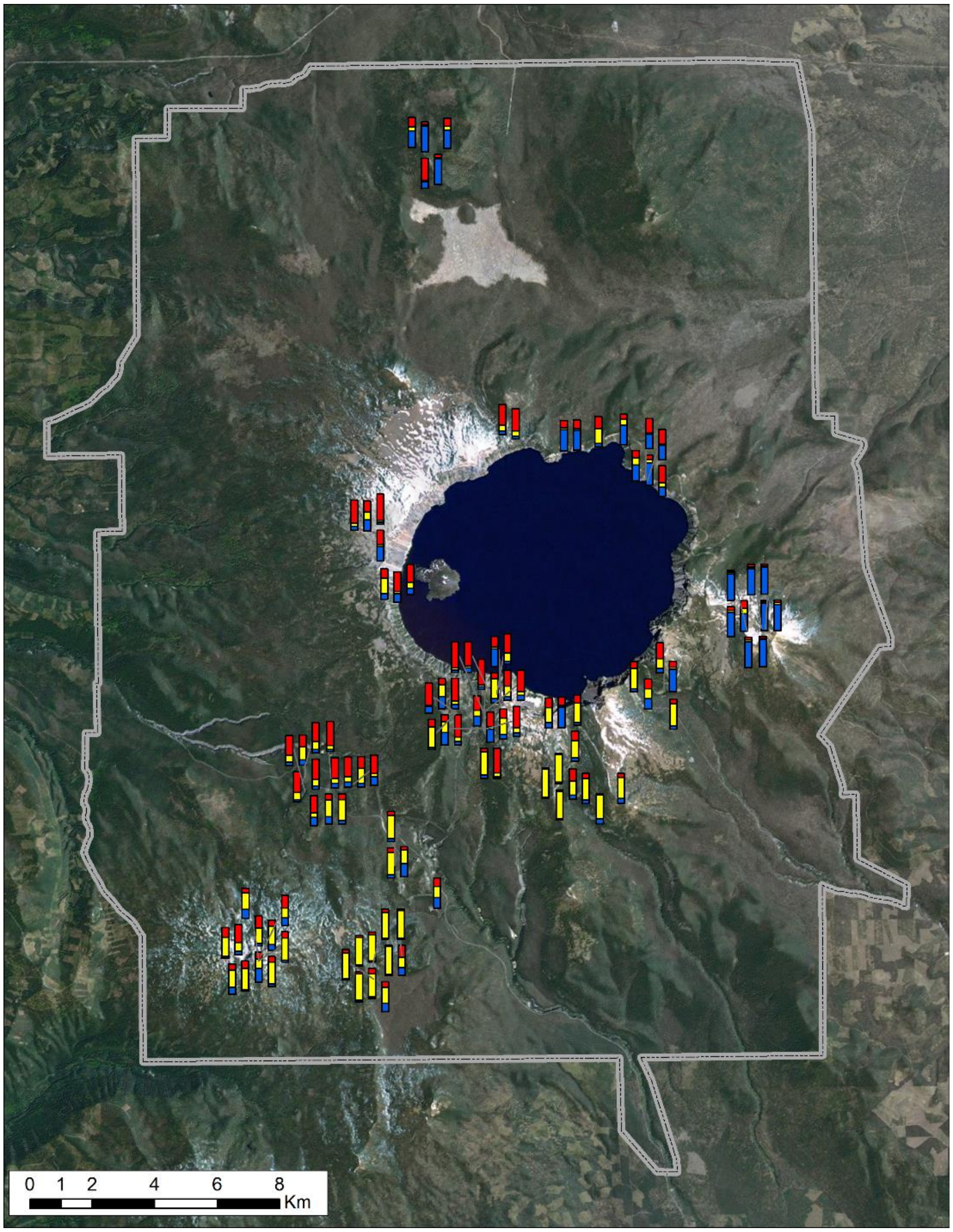


Figure S5. Population genetic structure of pikas at Crater Lake National Park. Results from STRUCTURE suggest there are three genetic groups (ΔK method) with gene flow among geographic clusters. Bar graphs represent individual pikas and colors represent the proportion of assignment to each of the three populations identified by STRUCTURE (q value). The best number of populations was determined using STRUCTUREHARVESTER to analyze results for 20 runs each for K = 1-10. Q values were determined from all 20 runs using CLUMPP.

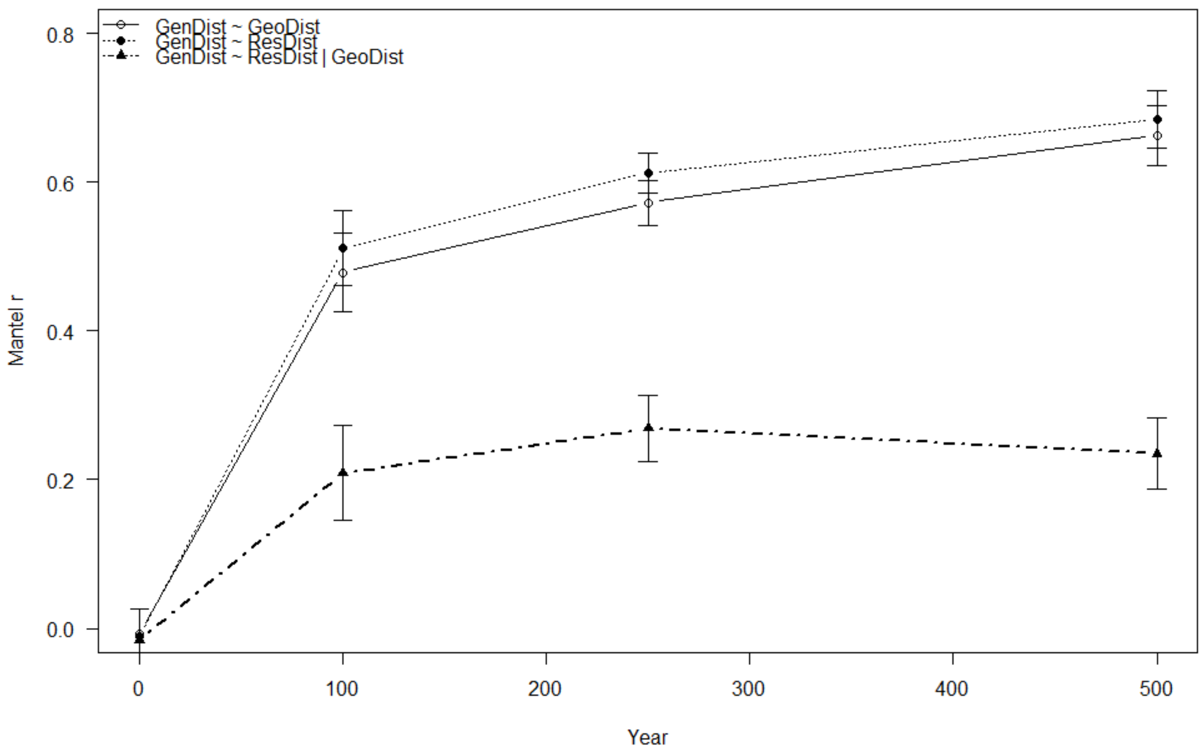


Figure S6: Correlation between genetic distance and geographic distance (open circle, solid line), resistance distance (solid circle, dotted line), and resistance distance after partialling out geographic distance (solid triangle, dashed line), averaged across all ten MC replicates. Whiskers represent 95% confidence intervals. The correlation for all three tests asymptotes around 250 generations. We considered the first 250-300 generations "burn in".