

# Negotiating a Fragmented Landscape: Does the Spatial Configuration of Habitat Patches Drive Pika Dispersal Patterns?

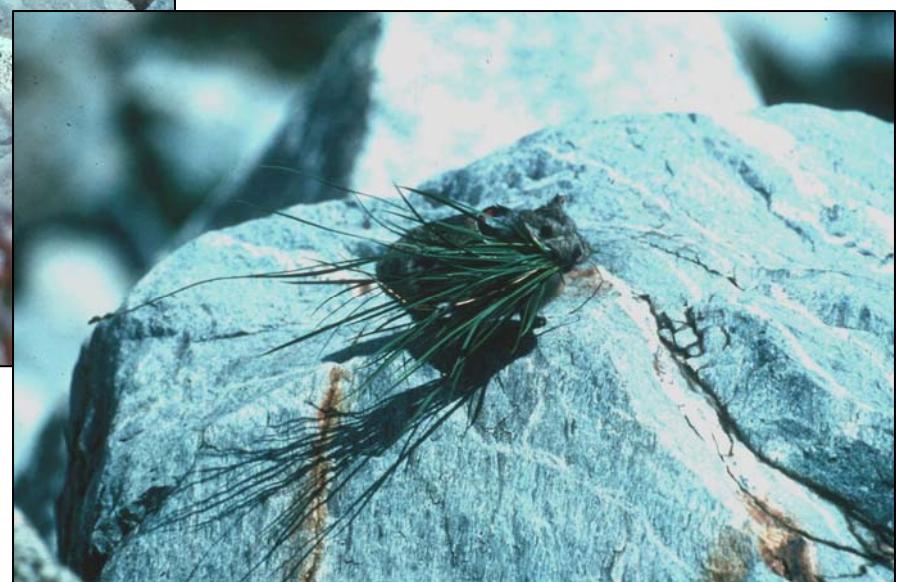


Mary Peacock<sup>1</sup> Susan Merideth<sup>1</sup> Chris Ray<sup>2</sup> Eileen Hickey<sup>1</sup> and  
Peter Brussard<sup>1</sup>

<sup>1</sup>University of Nevada, Reno and <sup>2</sup>University of Colorado, Boulder

## Natural History

- Non-hibernating lagomorphs
- Talus obligates
- Narrow range of thermal tolerance
- Individually territorial
- Grazing and haying diets



# The spatial scale of fragmentation varies



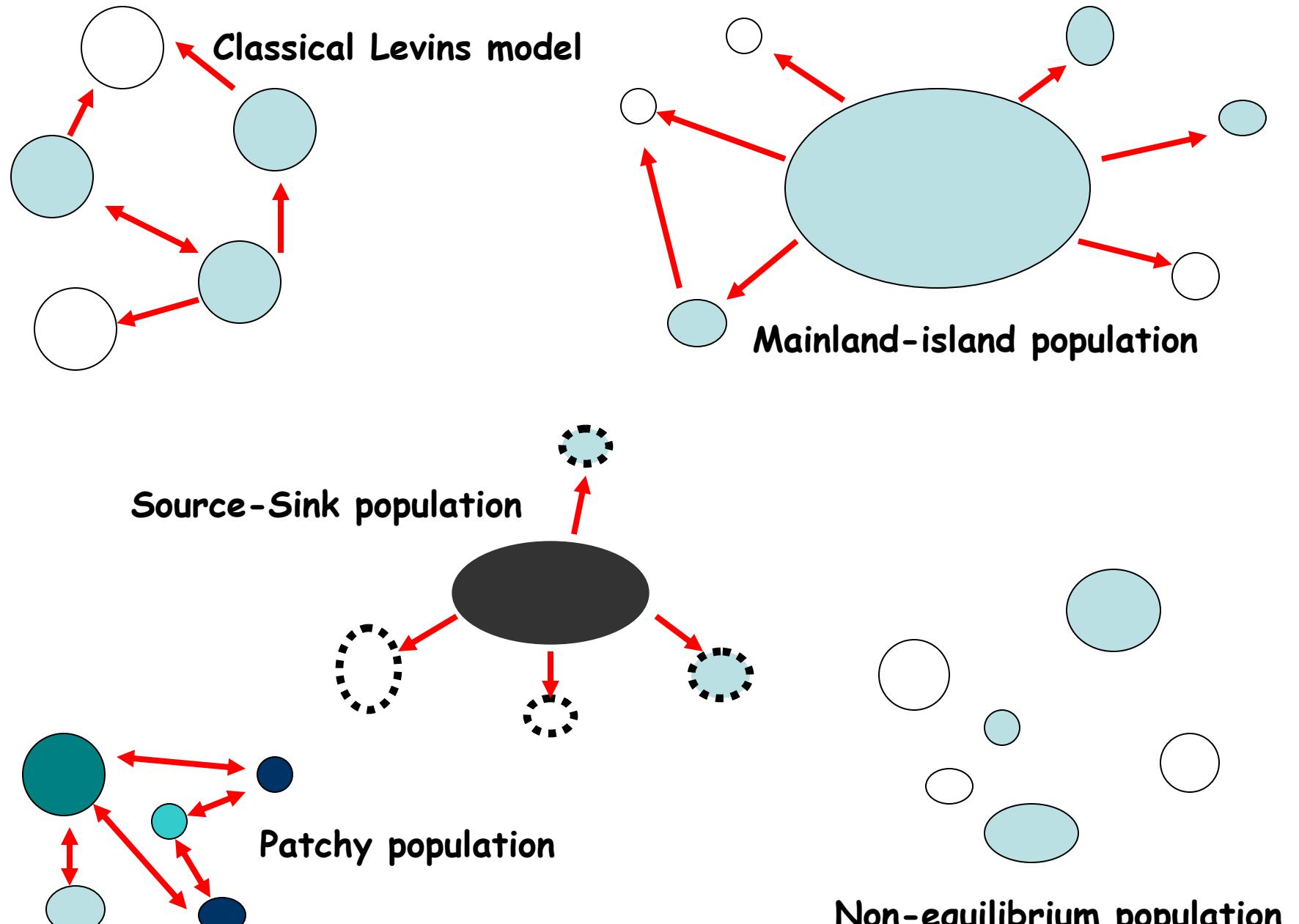
Large talus patches in semi-continuous habitat



Small habitat patches in highly fragmented habitat

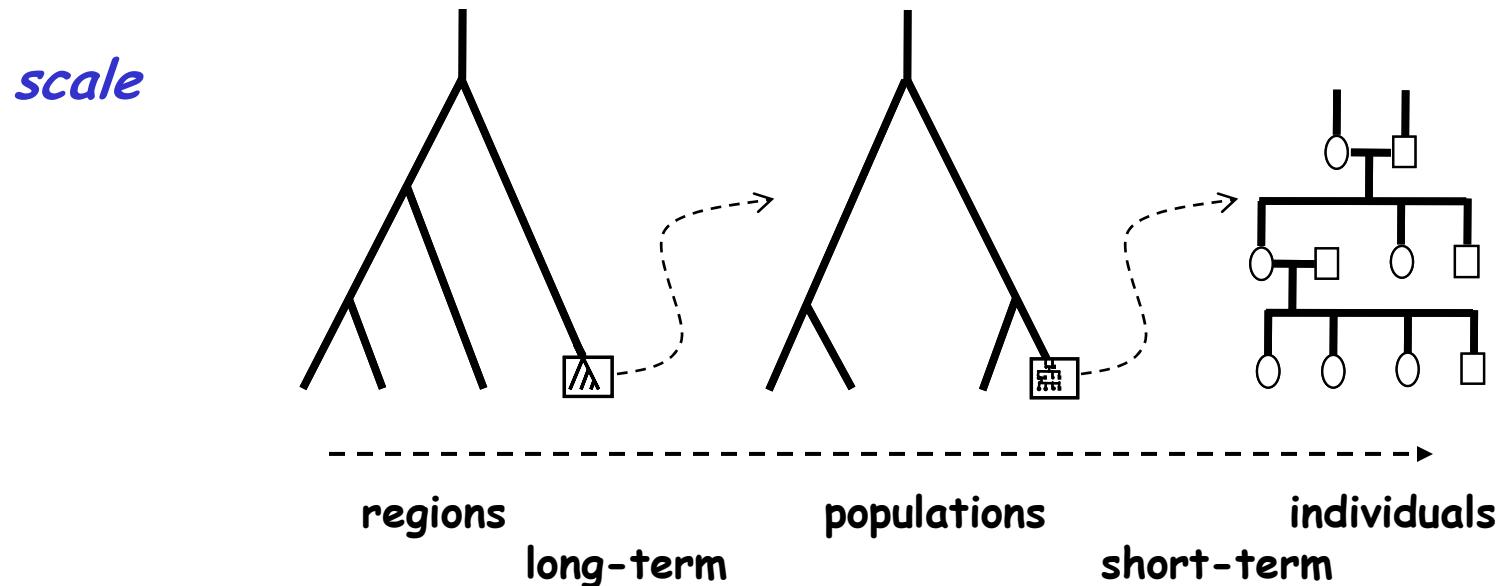
# Metapopulation Concept

- Theoretical construct used to understand effect of habitat fragmentation on population dynamics
- Model to guide reserve design

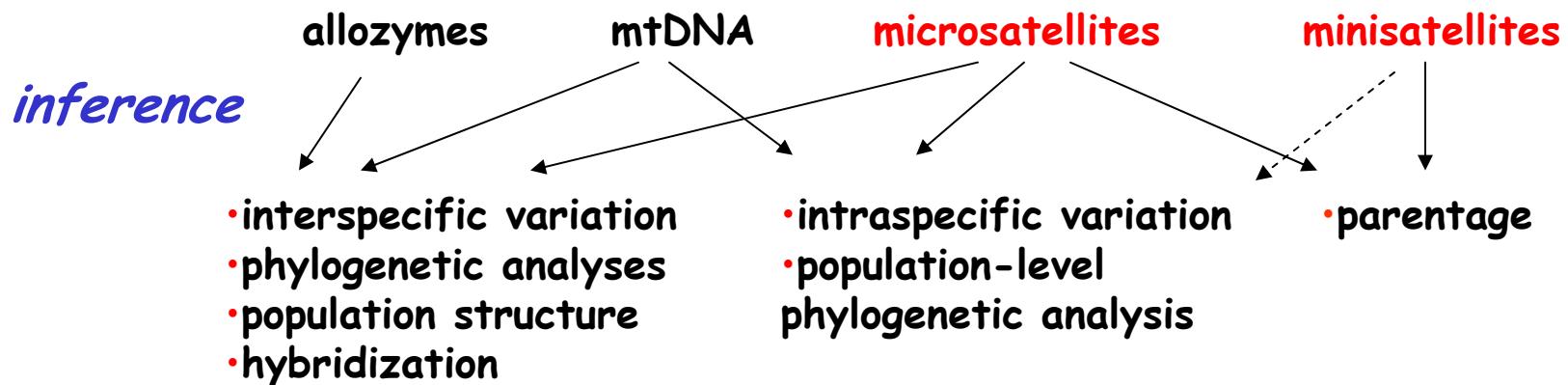


*(Adapted from Harrison and Taylor 1997)*

# genetic tools for inference of population structure

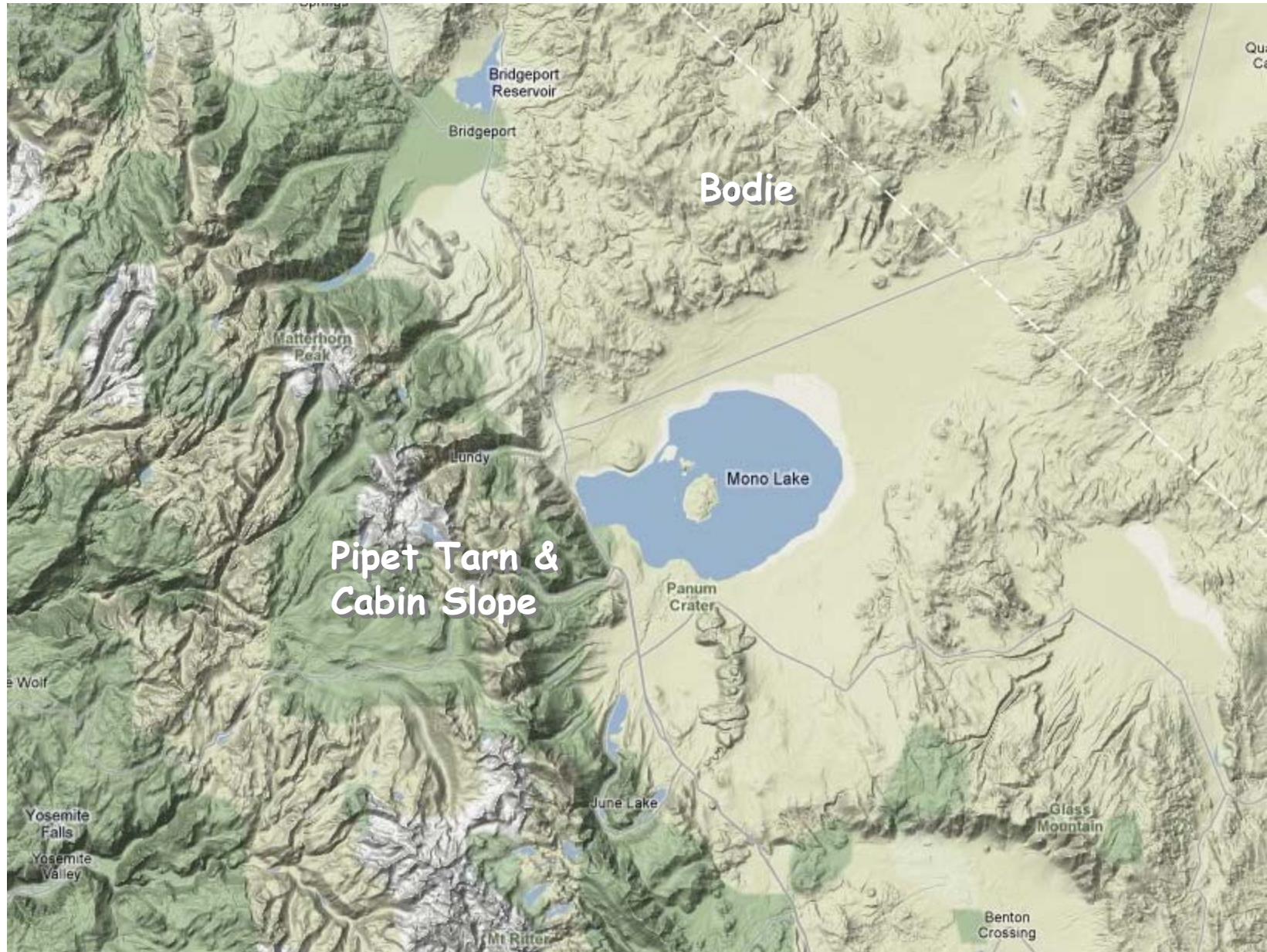


## *genetic marker*



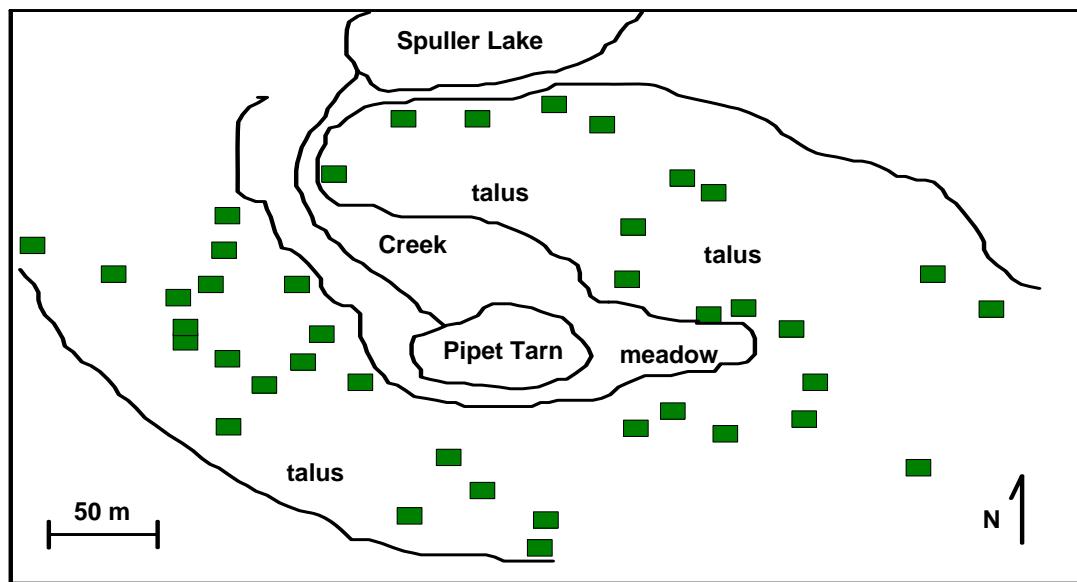
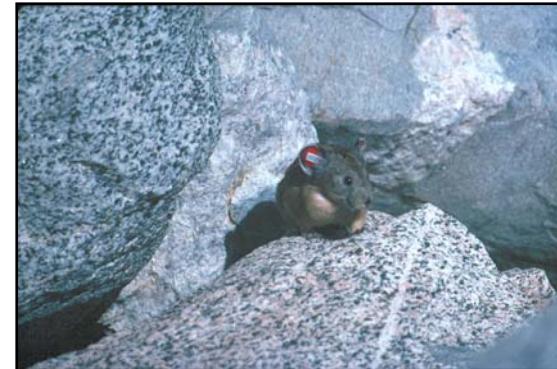


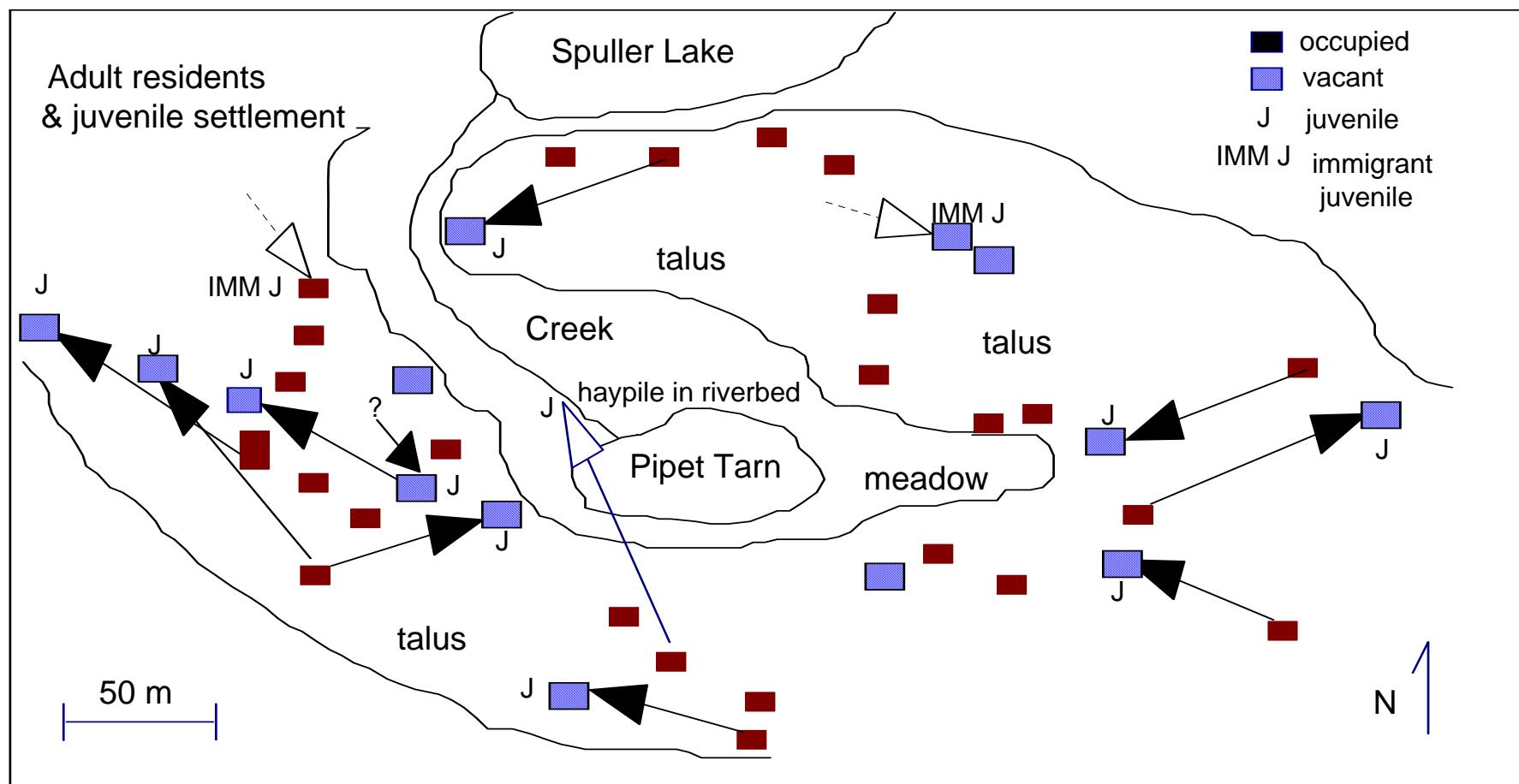
1. Pipet Tarn and Cabin Slope
2. Bodie Hills
3. Ruby Mountains and East Humboldt Range





Pipet Tarn in the  
Harvey Monroe Hall Natural Area





Peacock, M. M. 1997. *Behavioral Ecology* 8: 340-350.



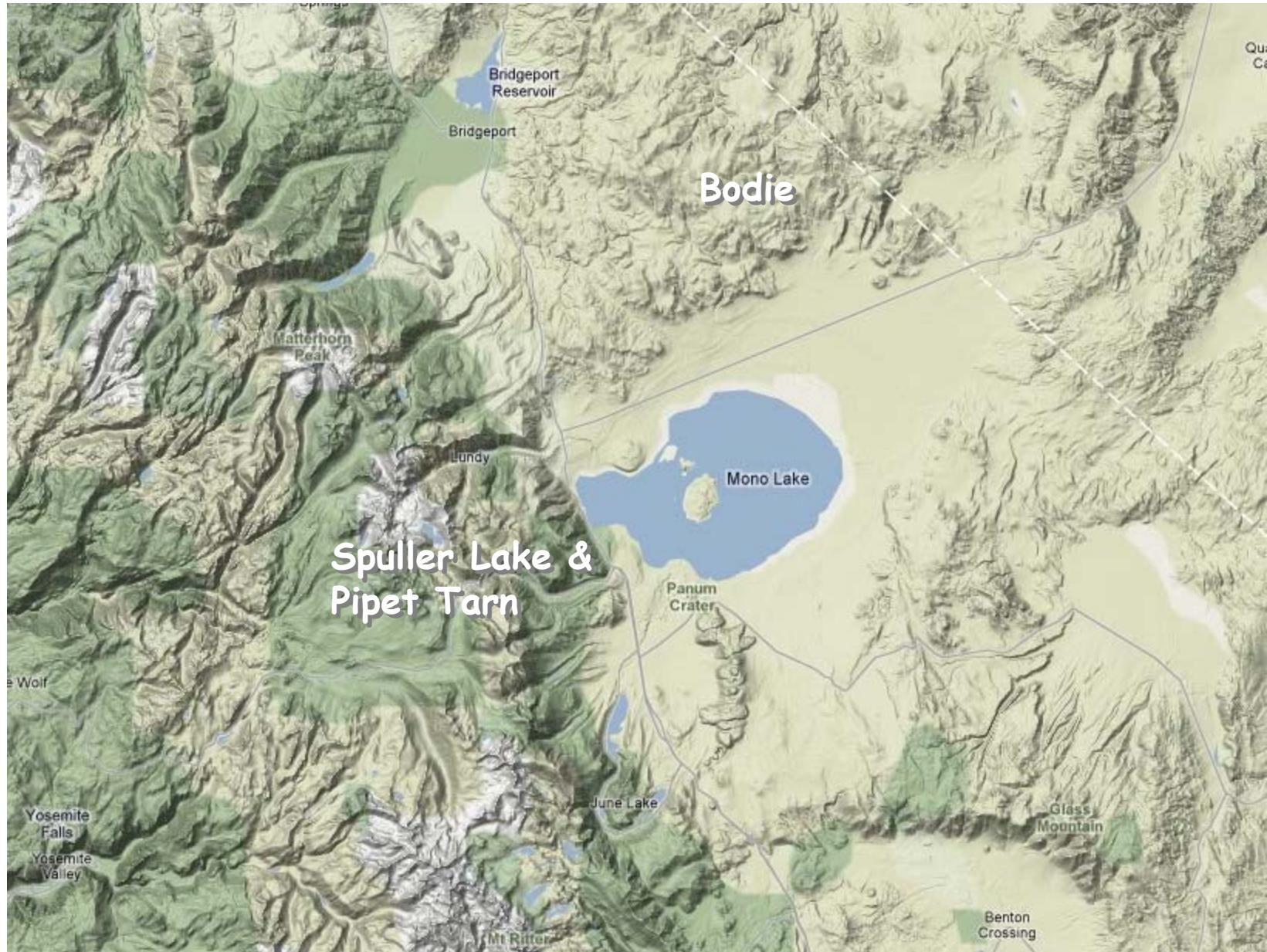
	Juveniles		Adults		Totals		Percentage
	M	F	M	F			
Born at Pipet Tarn	6	7			13		27.5
Probable short distance dispersers			6	4	10		25.0
Intermediate dispersal distance (?)	1	3	7	6	17		42.5
Long distance dispersers (2 km)	1	1			2		5.0

# Pipet Tarn - multilocus minisatellite data

- population-wide band-sharing  $D = 0.359$   
 $(D = 2N_{AB}/N_A + N_B)$
- Average Heterozygosity = 0.706
- Pairwise  $F_{ST} = 0.105$   
(Pipet Tarn and Cabin Slope separated by 2 km)
- $Nm = 1.3$



Peacock, M. M. and A. T. Smith. 1997. *Oecologia* 112:524-533.

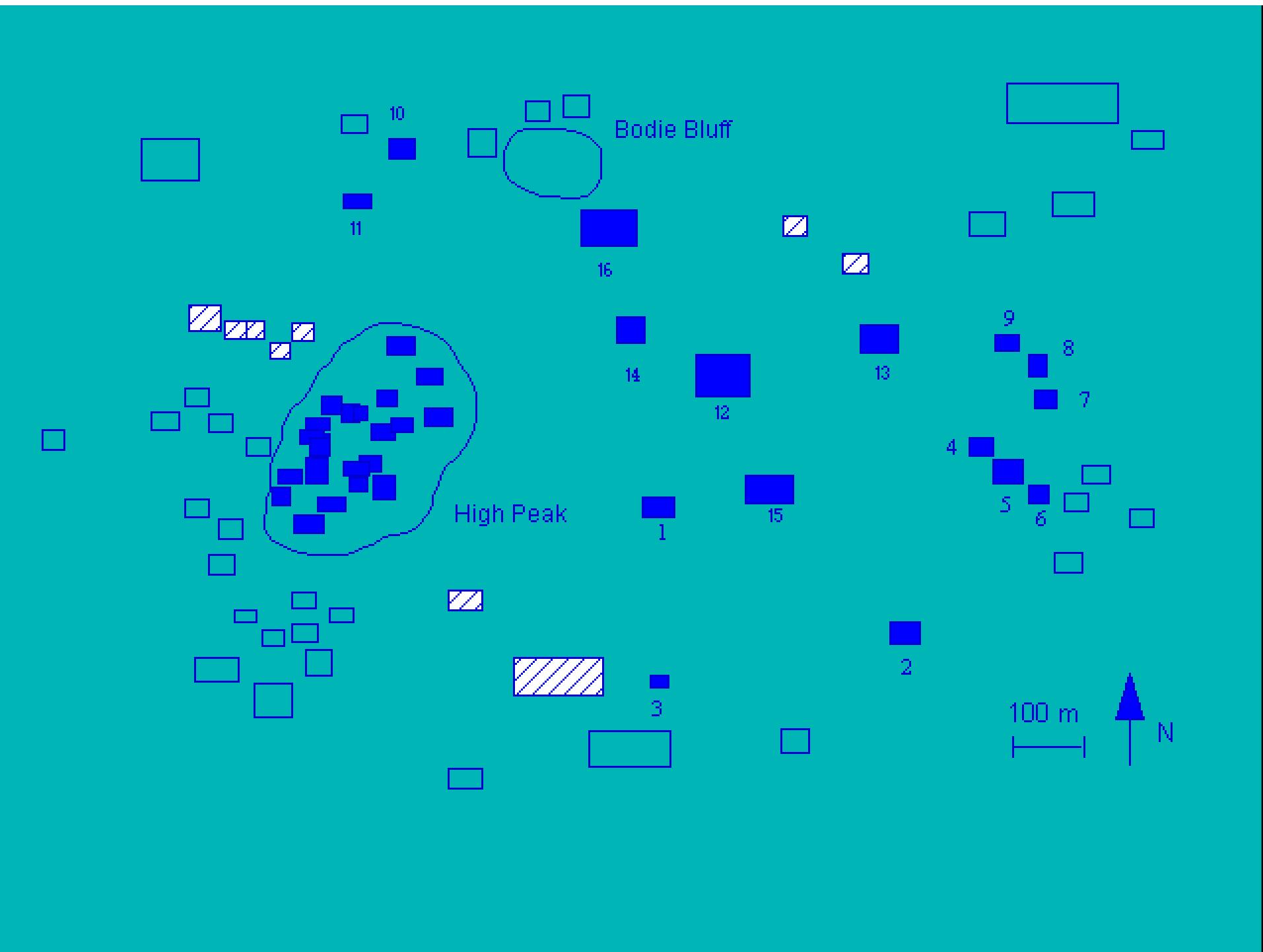


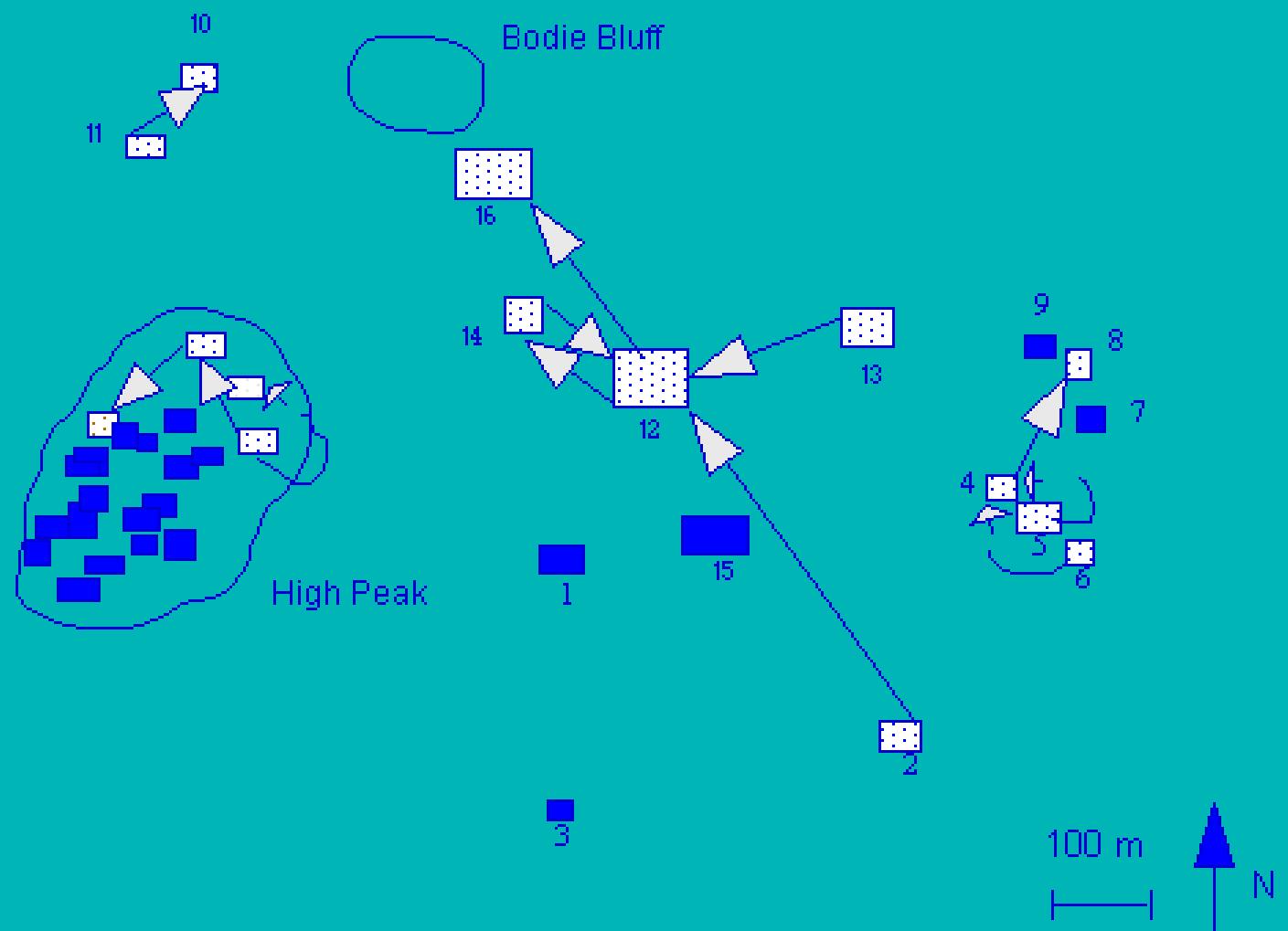
## Bodie Hills

- Sagebrush steppe ecosystem
- Pika habitat = mine tailings
- 2-10 residents per tailings patch
- High Peak mainland ~ 50 residents

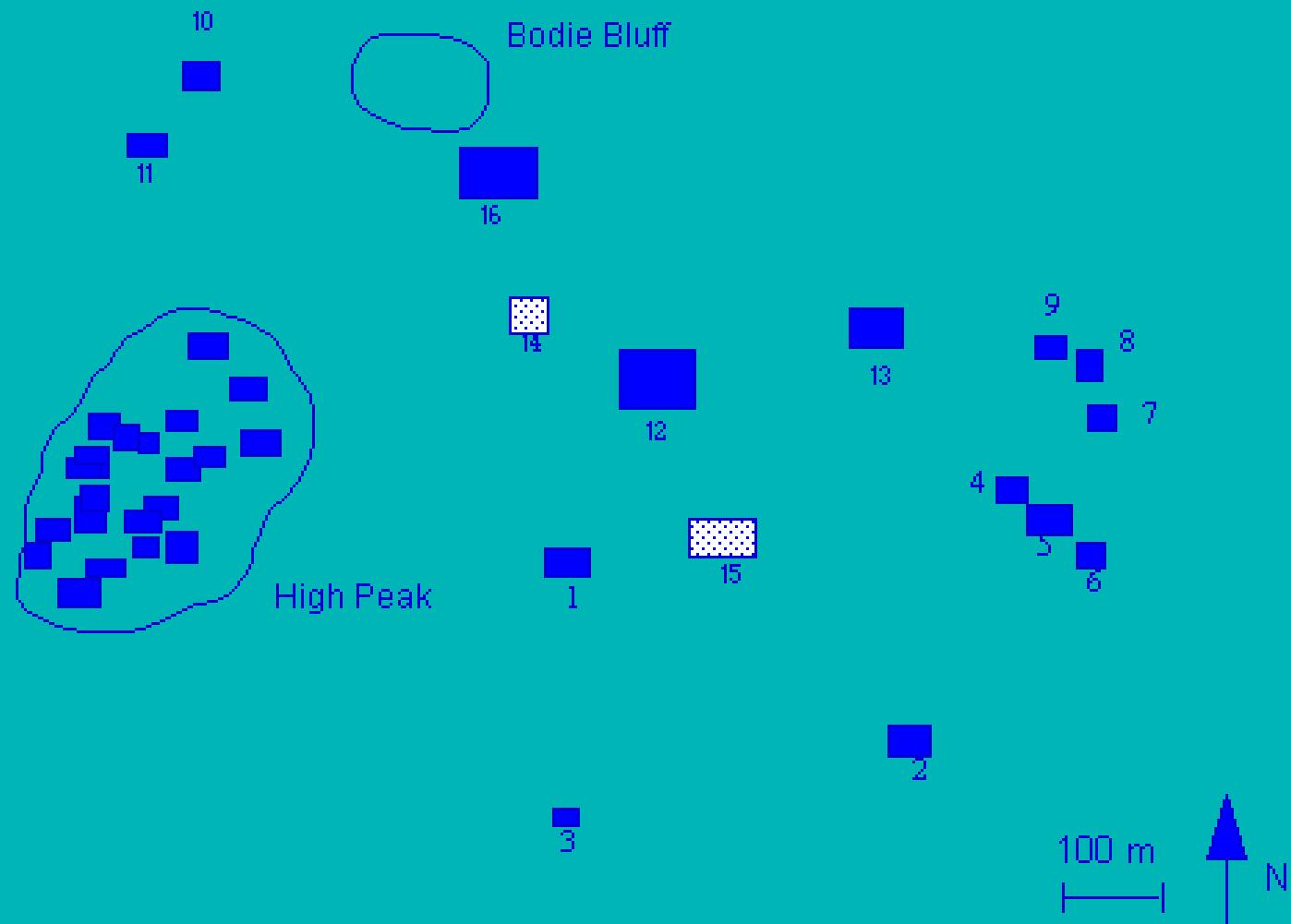


Peacock, M. M. and A. T. Smith. 1997. *Oecologia* 112:524-533.

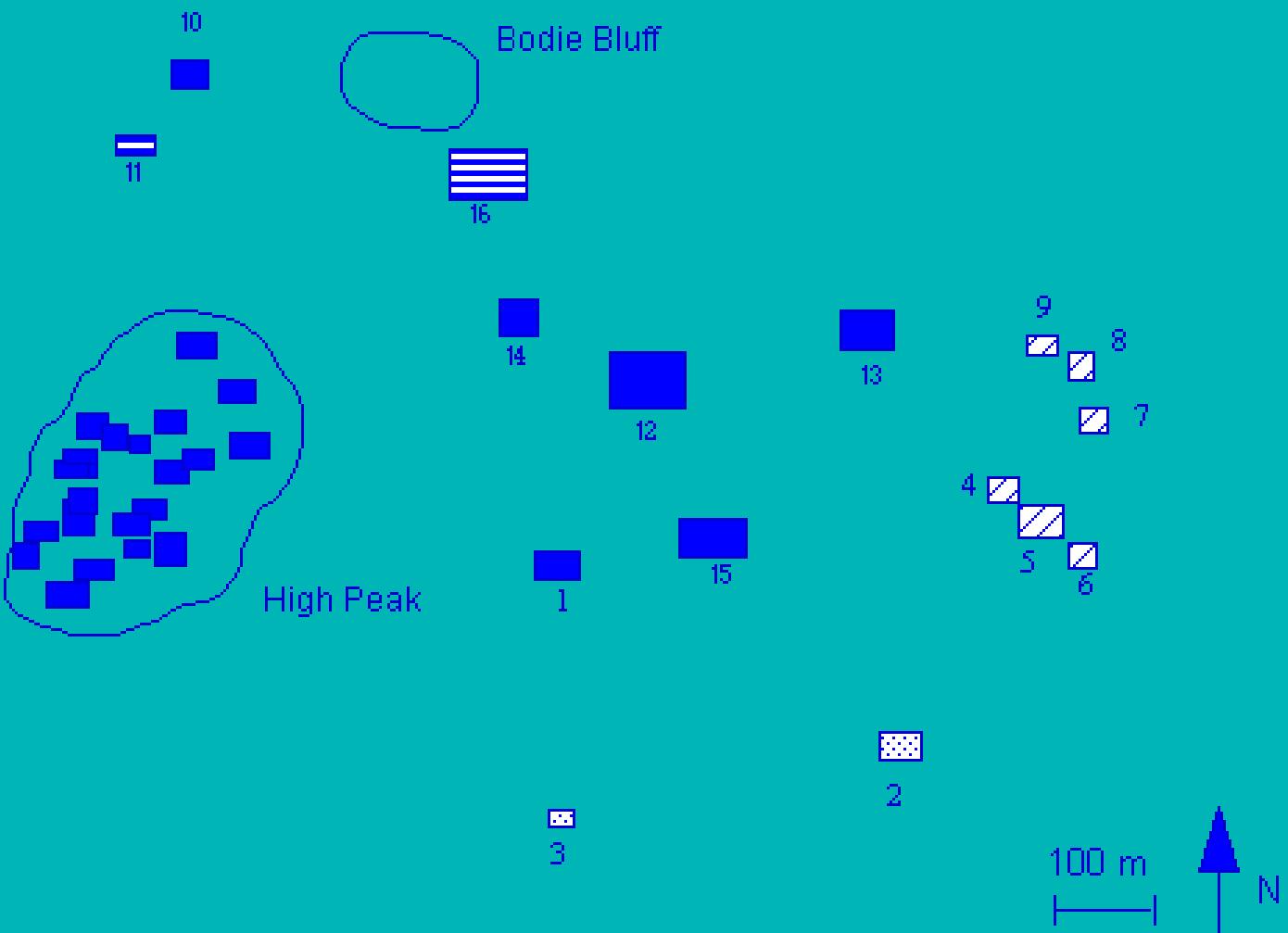


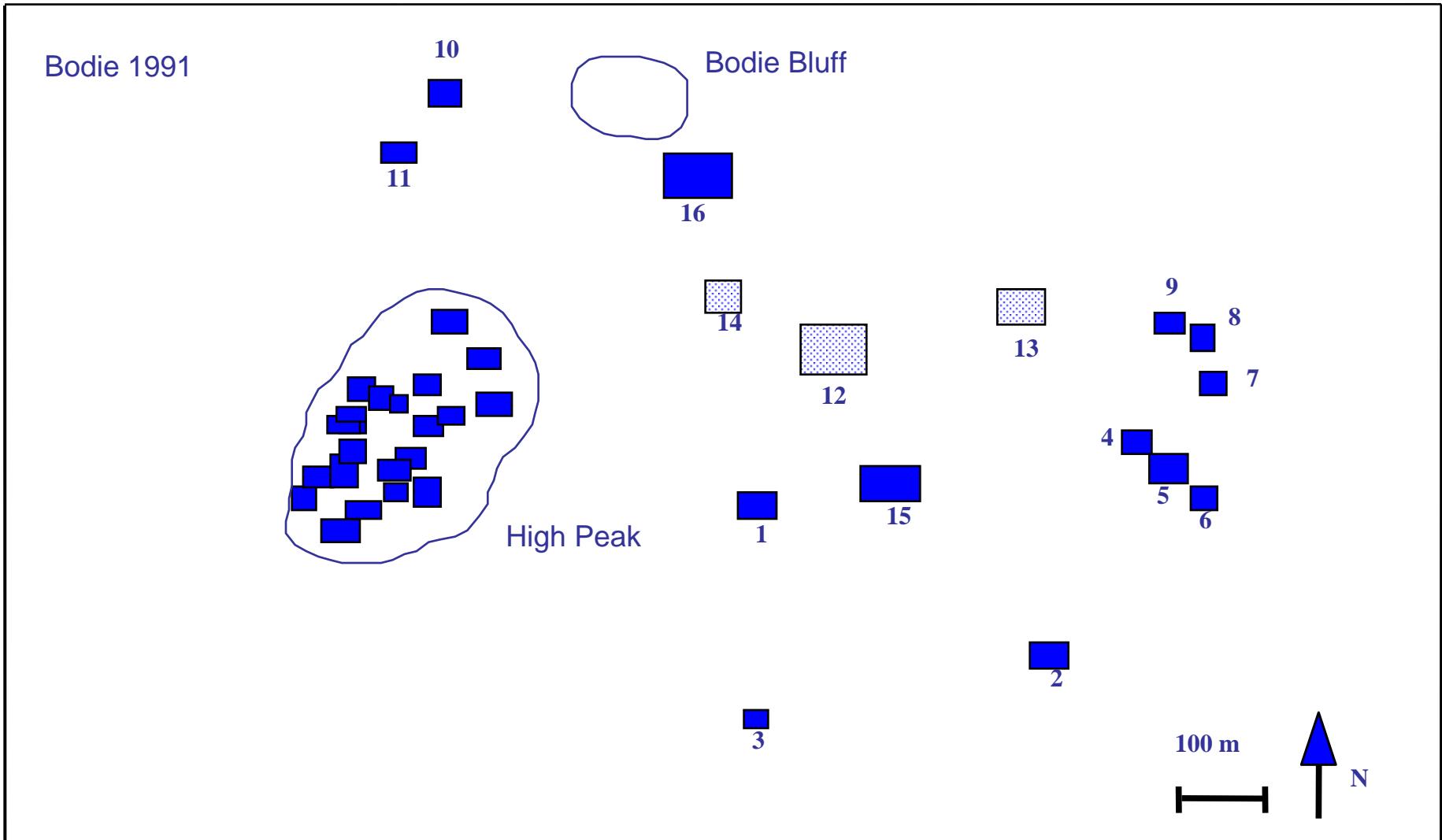


Bodie 1990

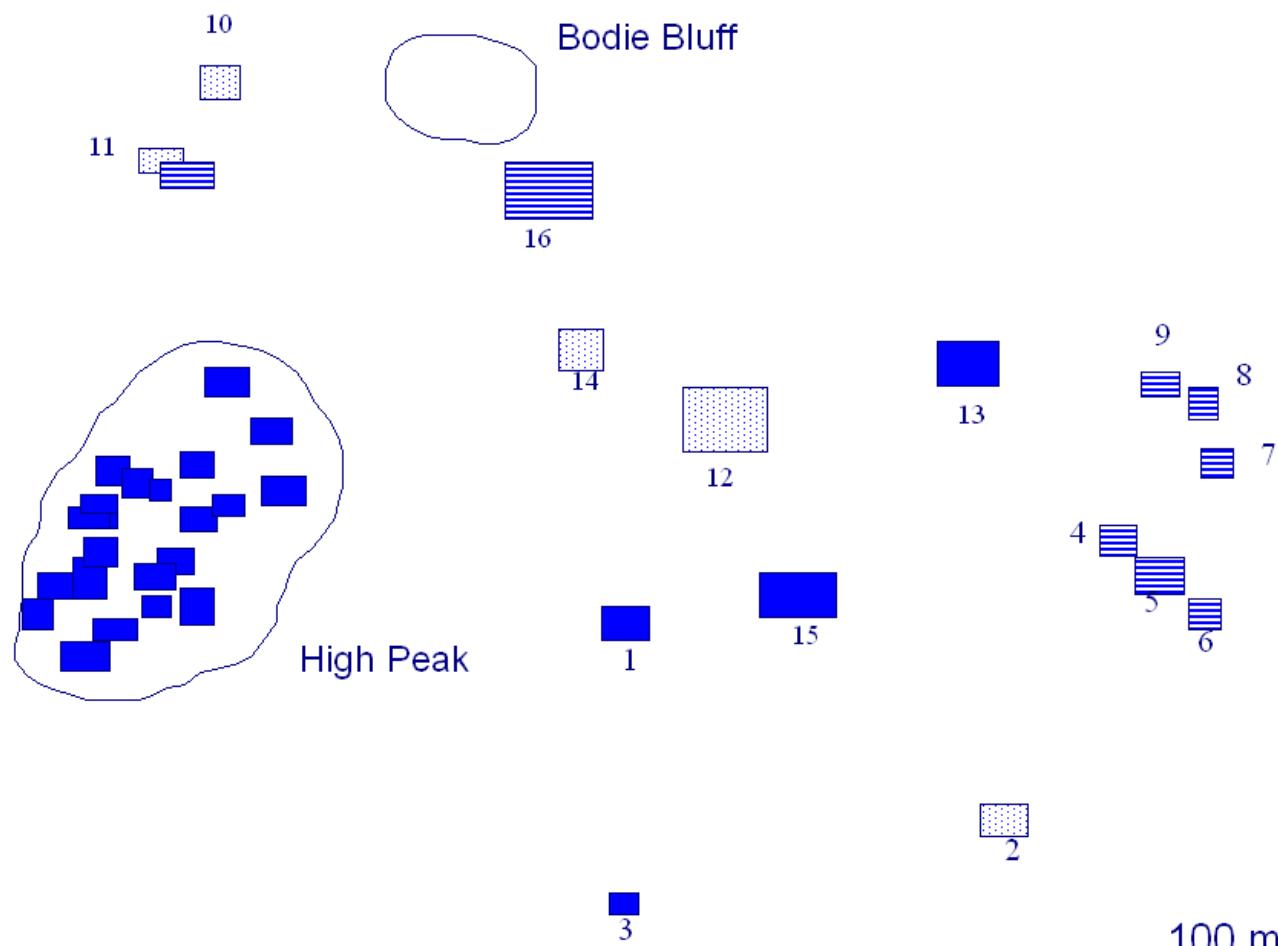


Bodie 1990





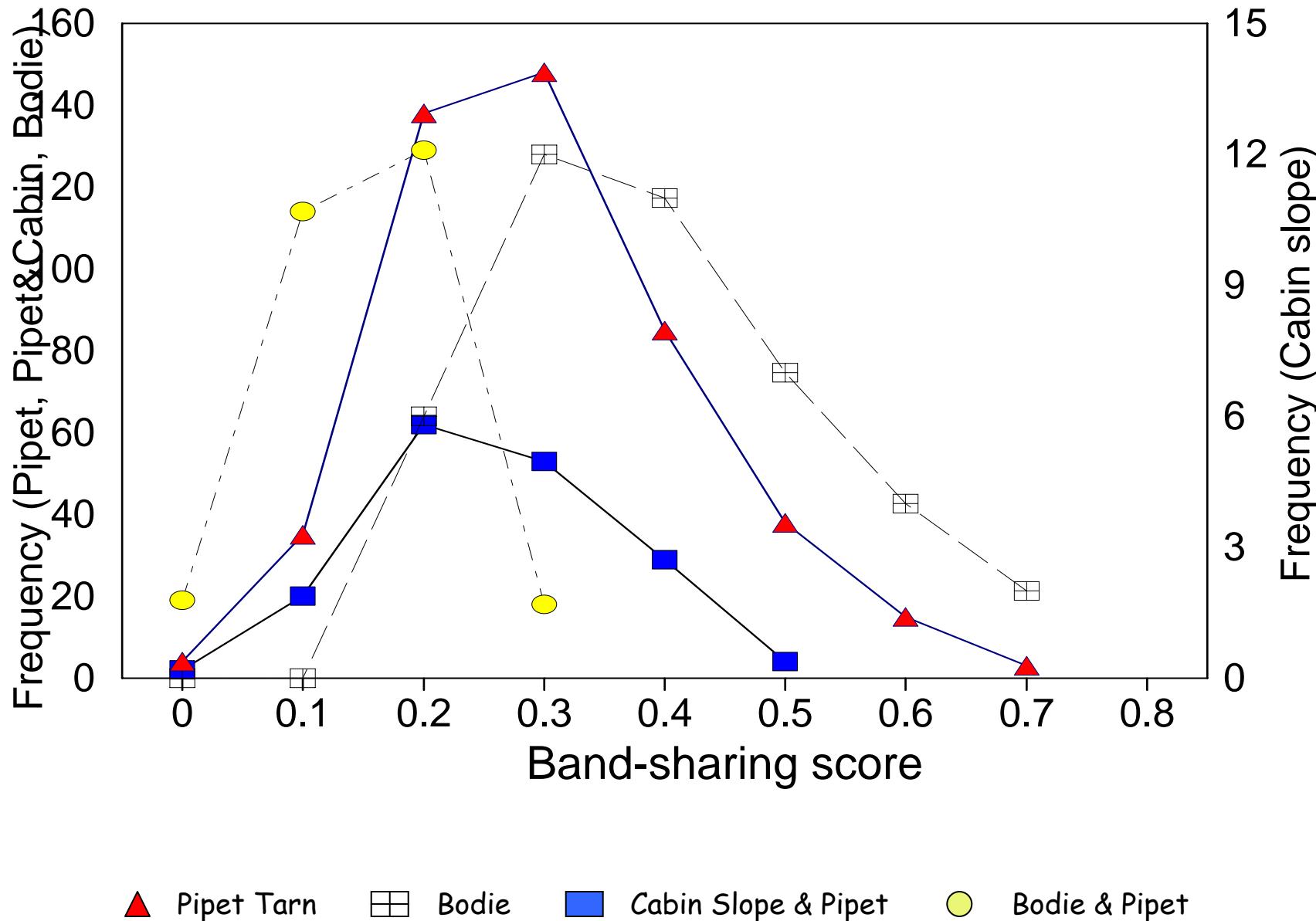
Bodie 1991



## Bodie Hills - multilocus minisatellite data

- Population-wide band-sharing  $D = 0.483$
- Average Heterozygosity = 0.736



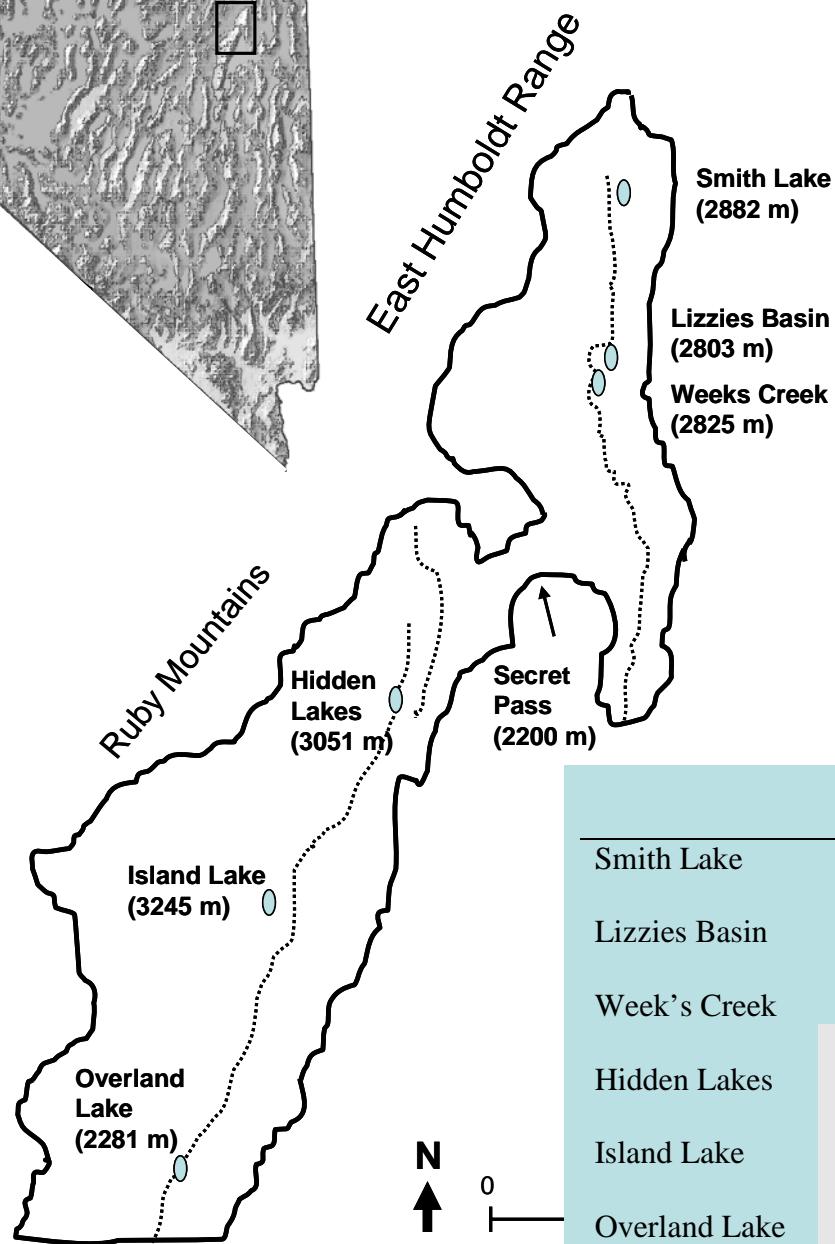
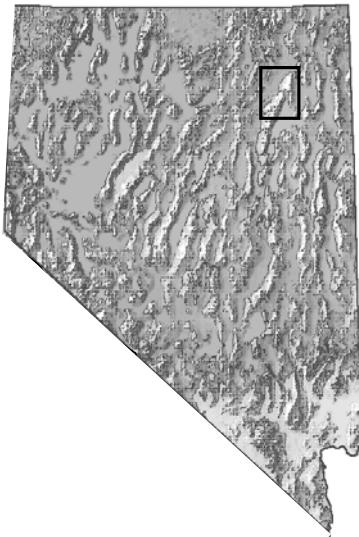


So - What does this tell us?

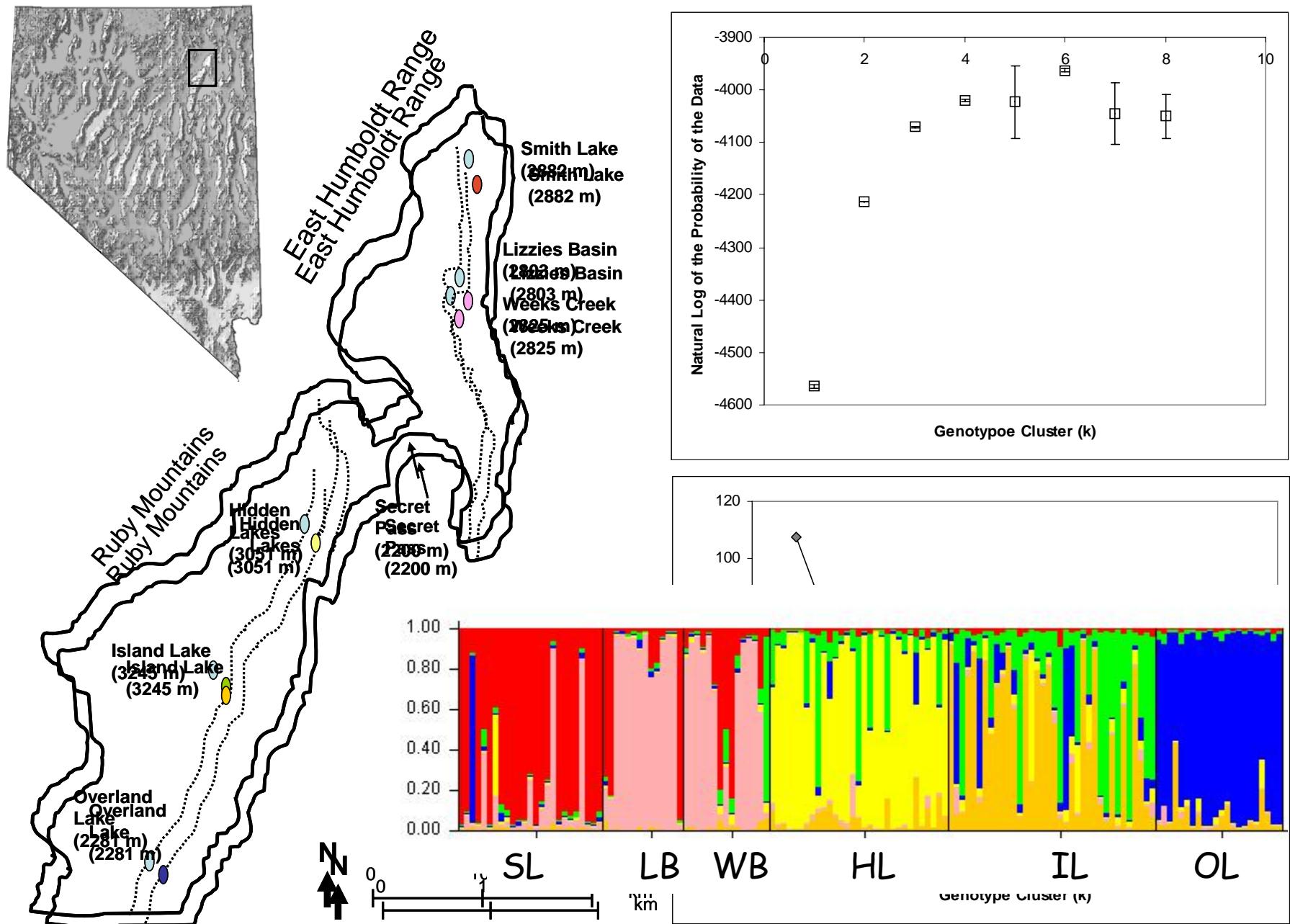
## Ruby and East Humboldt Mountains Ranges

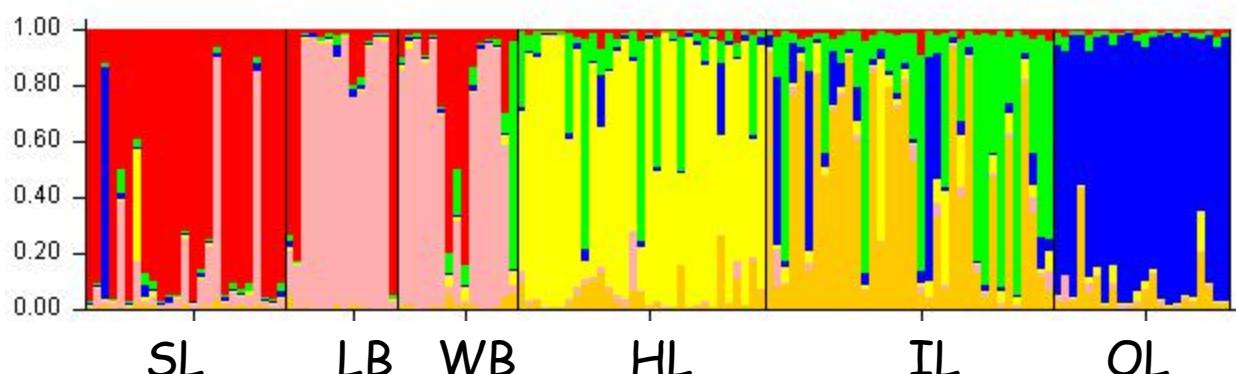
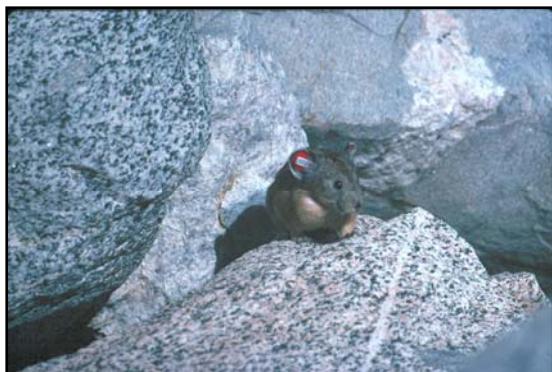
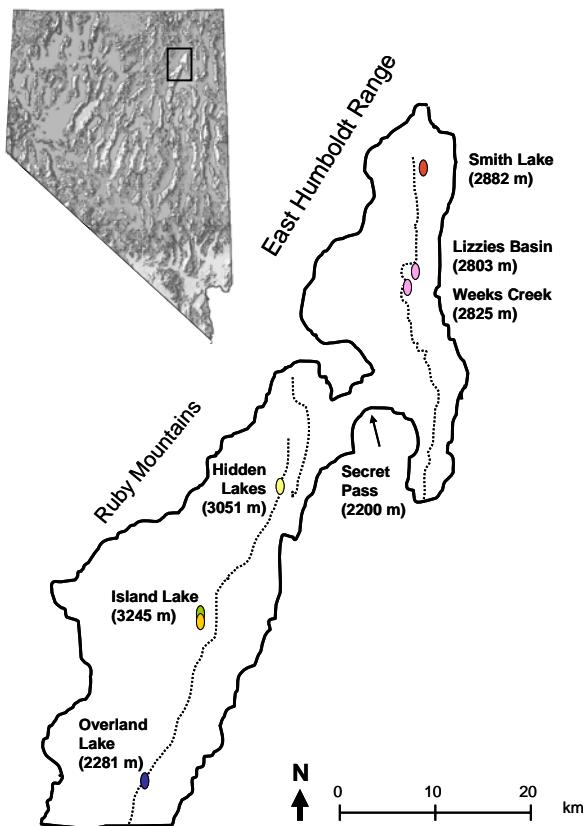
Pikas remain in only the highest elevation  
Mountain ranges in Nevada





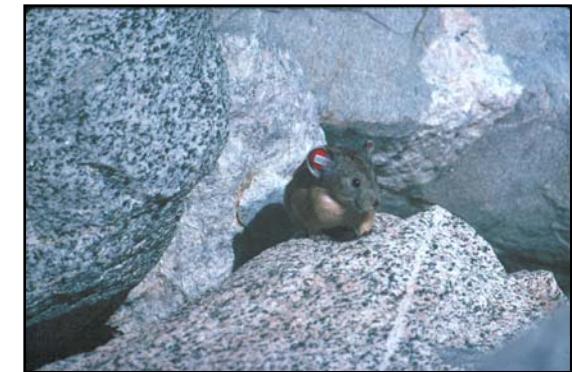
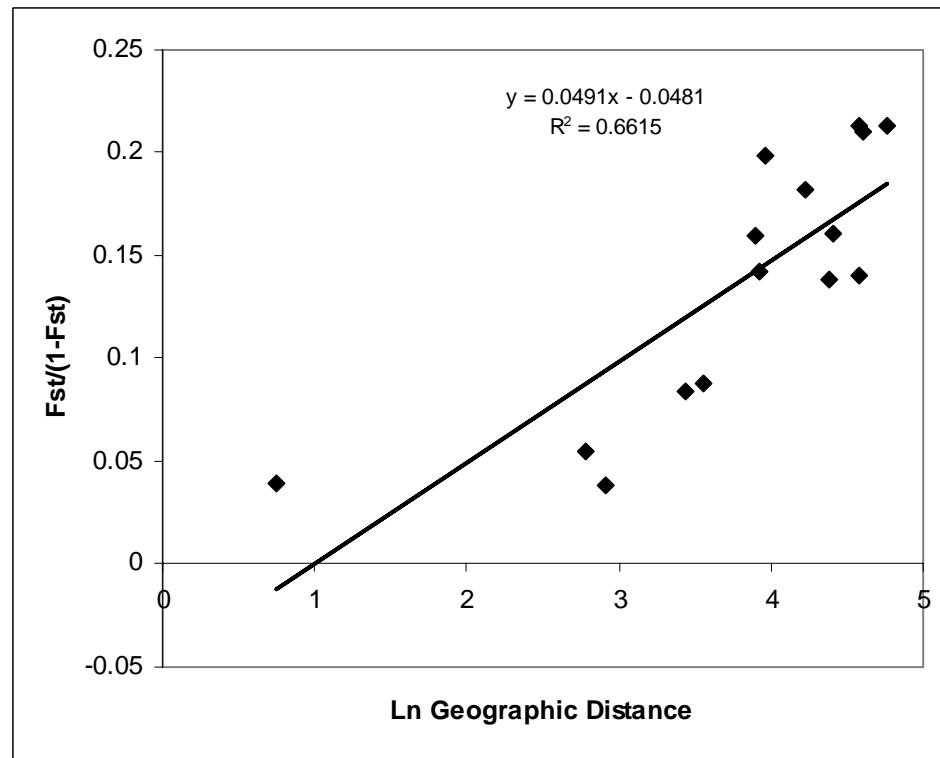
	Smith Lake	Lizzies Basin	Week's Creek	Hidden Lakes	Island Lake	Overland Lake
Smith Lake						
Lizzies Basin		16.2				
Week's Creek		18.3	2.1			
Hidden Lakes	68.8	52.6	50.6			
Island Lake	98.1	81.9	79.9	31.3		
Overland Lake	116.6	99.5	97.5	49.3	34.9	



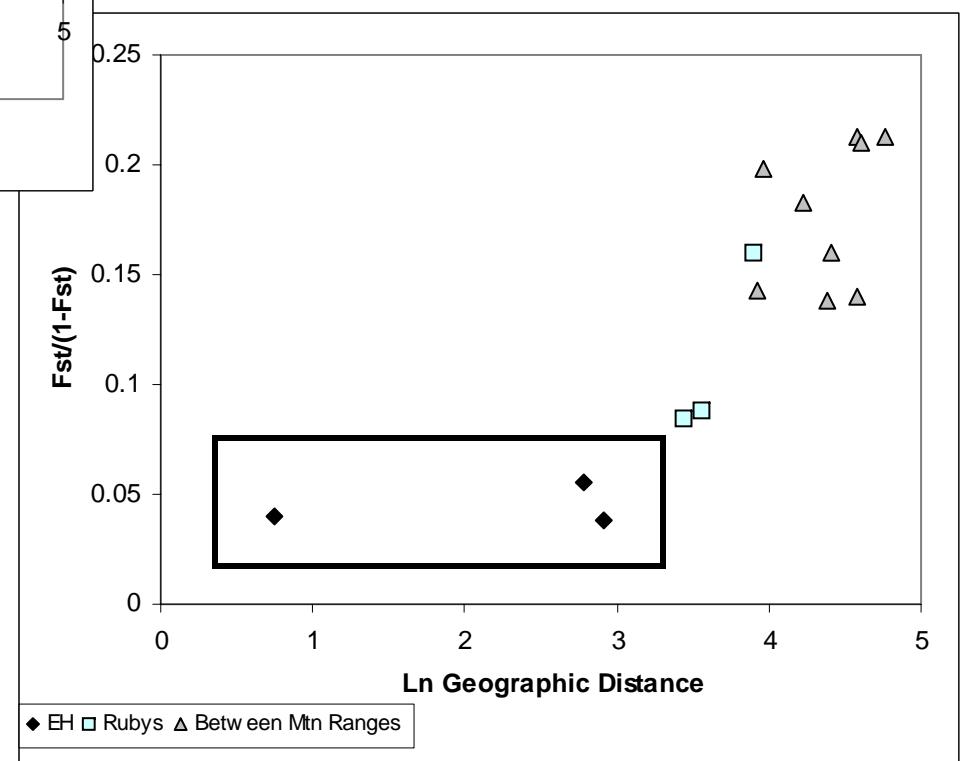


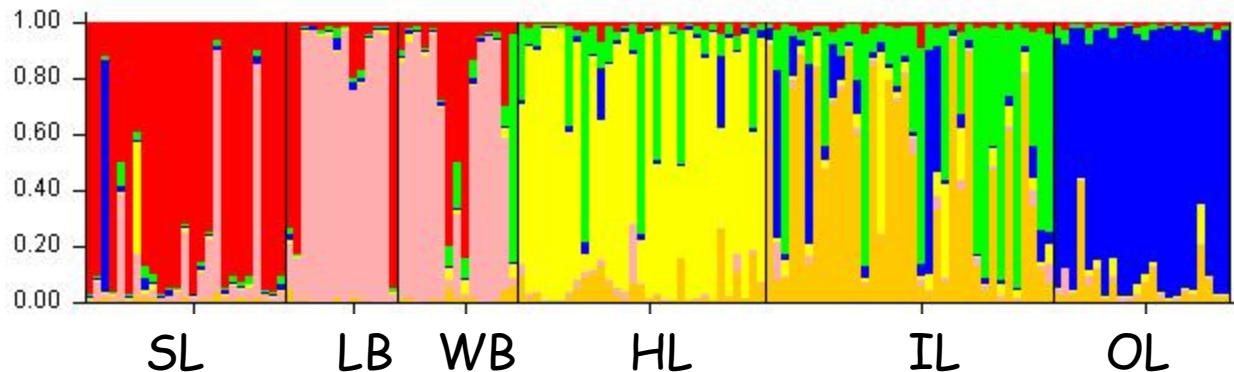
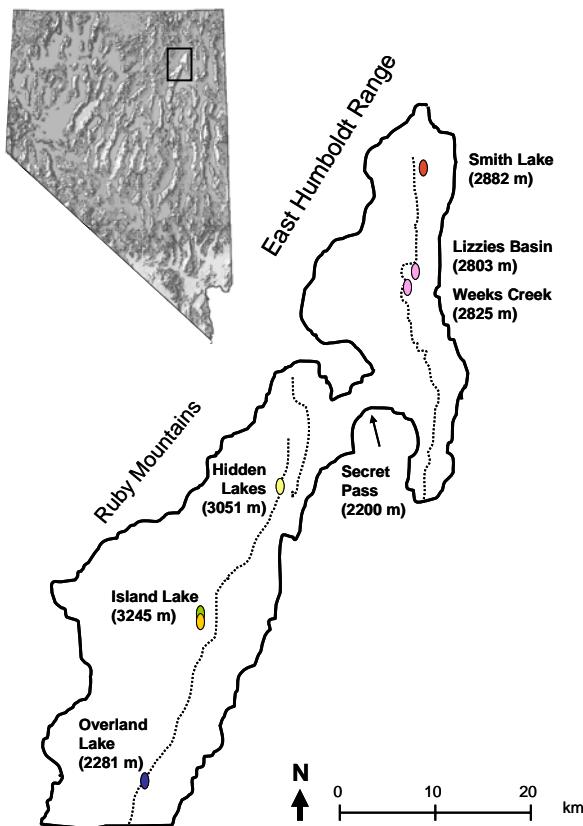
Pairwise  $F_{ST}$  estimates among genotype clusters. All genotype clusters are significantly differentiated ( $P = 0.003$ , corrected for multiple comparisons after 300 permutations) except where indicated by asterisk (\*).

	East Humboldt Range		Ruby Mountains		
	SL (red)	LB&WB	HL	IL	IL&HL
LB&WB (pink)	0.038				
HL (yellow)	0.146	0.149			
IL (mustard)	0.151	0.164	0.097		
IL&HL (green)	0.132	0.151	0.079	0.038*	
OL (blue)	0.162	0.151	0.128	0.091	0.094



Genetic Neighborhoods < 20 km

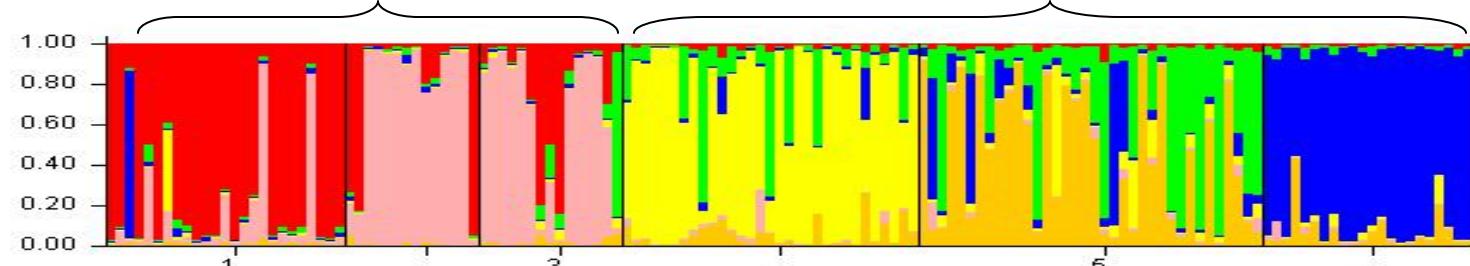




Effective Population Size ( $N_e$ ) and 95% confidence interval estimated for each genotype cluster indicated by color and location.

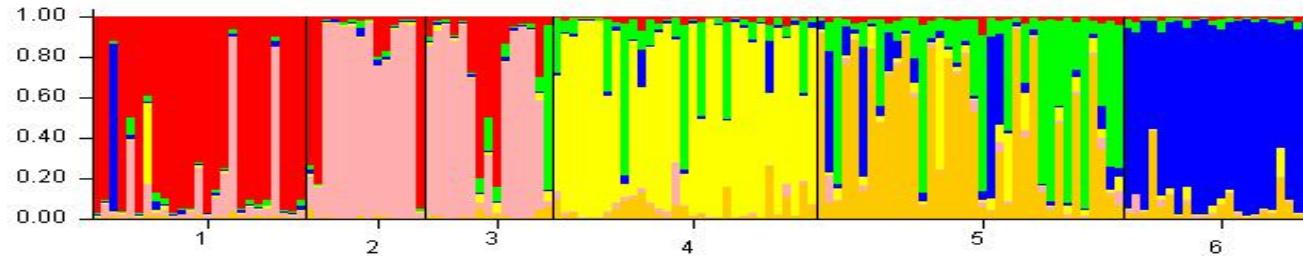
Genotype Cluster	$N_e$	95%CI
East Humboldt Range 1 (red)	18.5	(14.8 23.9)
2 (pink)	13.8	(11.6 16.7)
Ruby Mountains		
3 (yellow)	26.6	(21.1 34.9)
4 (green)	29.5	(20.2 51.3)
5 (mustard)	12.9	(10.6 16.3)
6 (blue)	30.5	(22.7 44.2)

## Heterozygosity per locus per population (genotype cluster)



	SL (red)	LB&WB (pink)	HL (Yellow)	IL (mustard)	HL&IL (green)	OL (blue)
OCP2	0.703	0.853	0.729	0.831	0.781	0.824
OCP3	0.073	0.078	0.457	0.512	0.421	0.476
OCP4	0.868	0.885	0.836	0.779	0.799	0.621
OCP5	0	0	0.394	0.093	0.053	0.171
OCP9	0.818	0.913	0.8	0.837	0.855	0.874
OCP10	0	0.082	0.477	0.497	0.426	0.486
OCP11	0.739	0.557	0.695	0.599	0.671	0.607
OCP12	0.753	0.677	0.72	0.716	0.735	0.726
OCP13	0.637	0.707	0.472	0.548	0.531	0.294
OCP14	0.254	0.086	0.366	0.526	0.488	0.341
OCP15	0.795	0.836	0.571	0.725	0.67	0.676
OCP16	0.469	0.442	0.289	0.343	0.442	0.491
OCP18	0.04	0.089	0.518	0.279	0.327	0.51
Average	0.473	0.477	0.563	0.560	0.554	0.546

## Number of alleles per locus per genotype cluster.



	SL (red)	LB&WB (pink)	HL (yellow)	IL (mustard)	HL&IL (green)	OL (blue)
OCP2	6	9	8	7	6	12
OCP3	2	2	2	2	2	2
OCP4	12	11	12	8	9	4
OCP5	1	1	2	2	2	2
OCP9	11	15	11	11	10	14
OCP10	1	2	3	2	2	2
OCP11	5	3	5	5	4	5
OCP12	6	4	5	5	6	6
OCP13	5	6	3	4	4	6
OCP14	2	3	3	4	2	2
OCP15	6	6	4	5	6	4
OCP16	2	2	2	2	2	2
OCP18	2	2	3	3	4	4
Total	<b>61</b>	<b>66</b>	<b>63</b>	<b>60</b>	<b>59</b>	<b>65</b>



## Conclusions