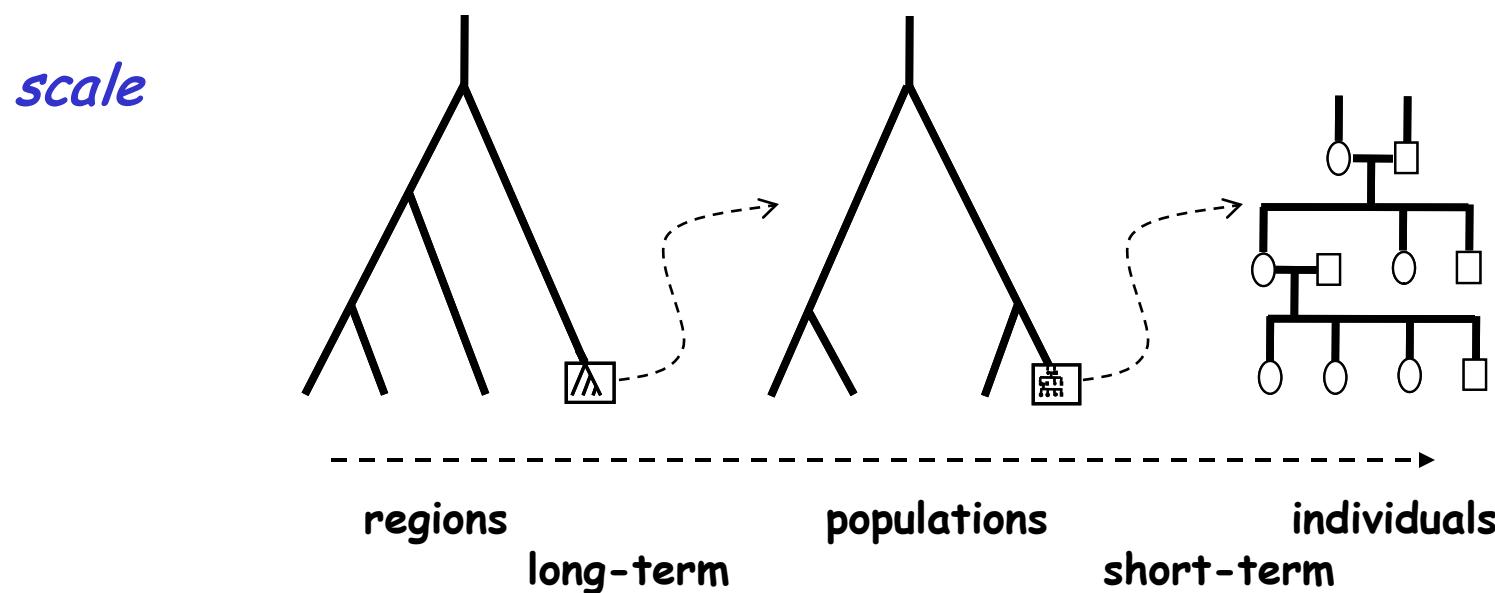
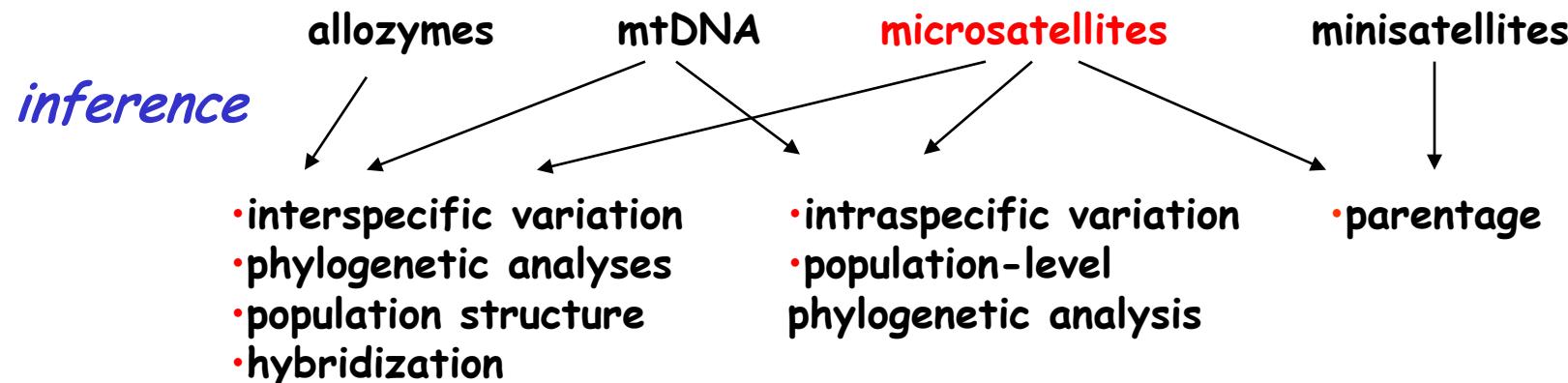


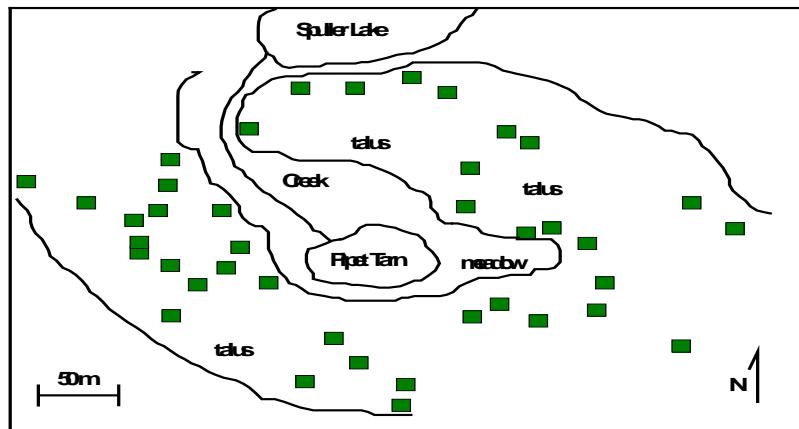
genetic tools for inference of population structure



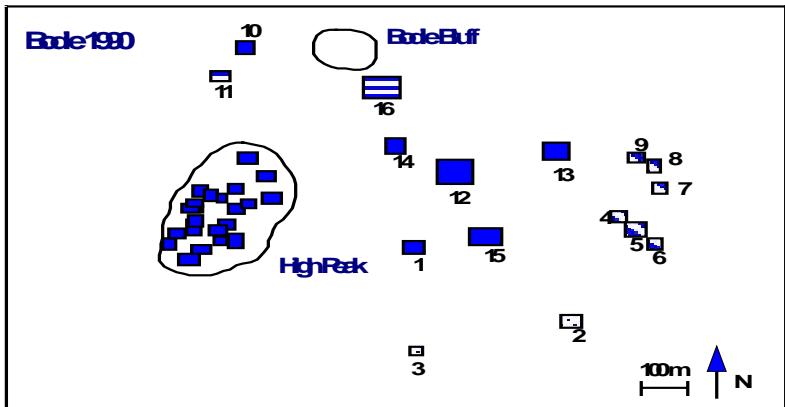
genetic marker



Continuous habitat $H = 0.706$ ($N = 18$)



Highly subdivided $H = 0.736$ ($N = 24$)



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

Nuclear minisatellite data

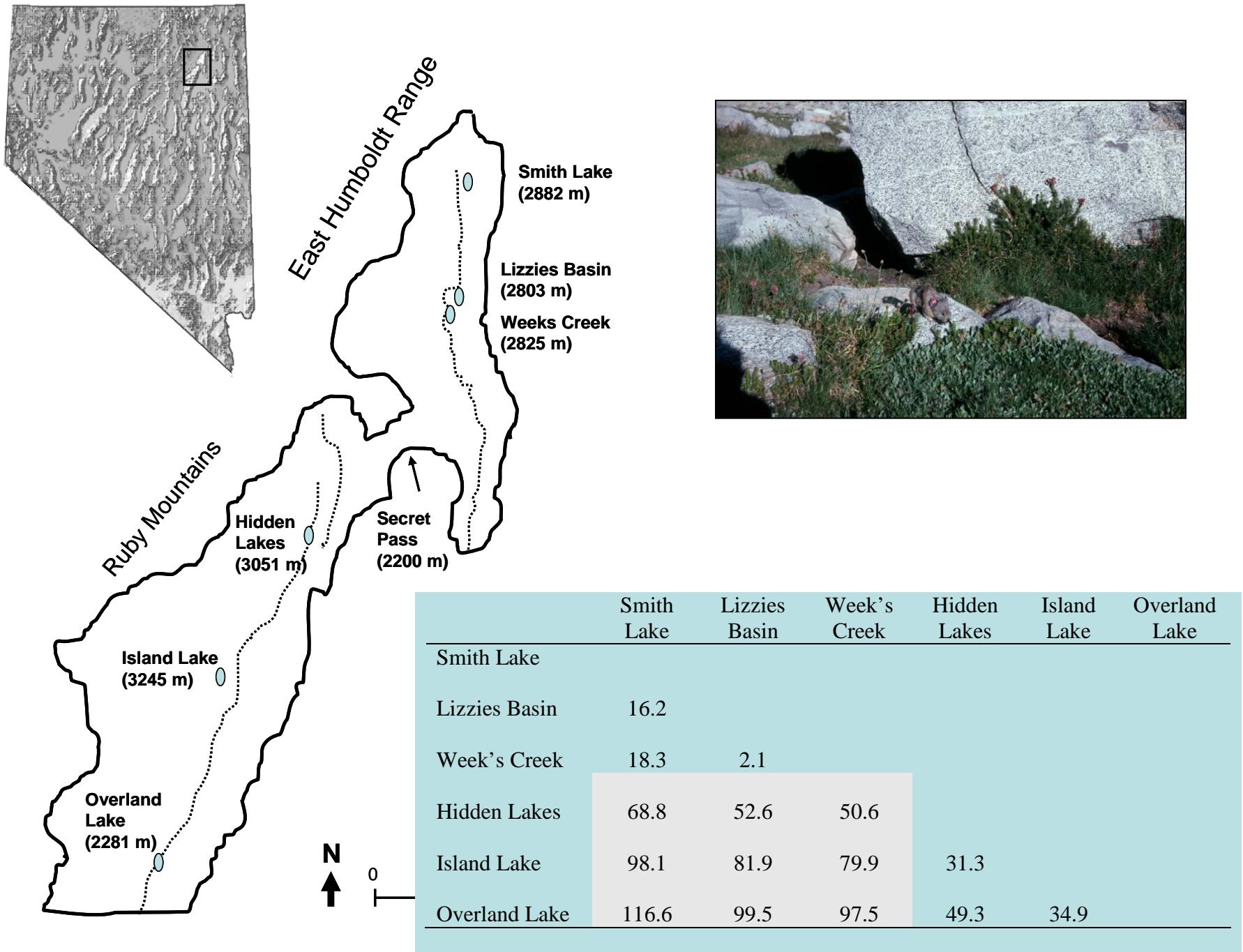
- population-wide band-sharing $D = 0.359$ ($D = 2N_{AB}/N_A + N_B$)
- mean band-sharing among non-relatives $D = 0.336$ (first-order relatives excluded)
- $F_{ST} = 0.105$
- $Nm = 1.3$ ($FST = 1/[4(Nm+Nu)] +$

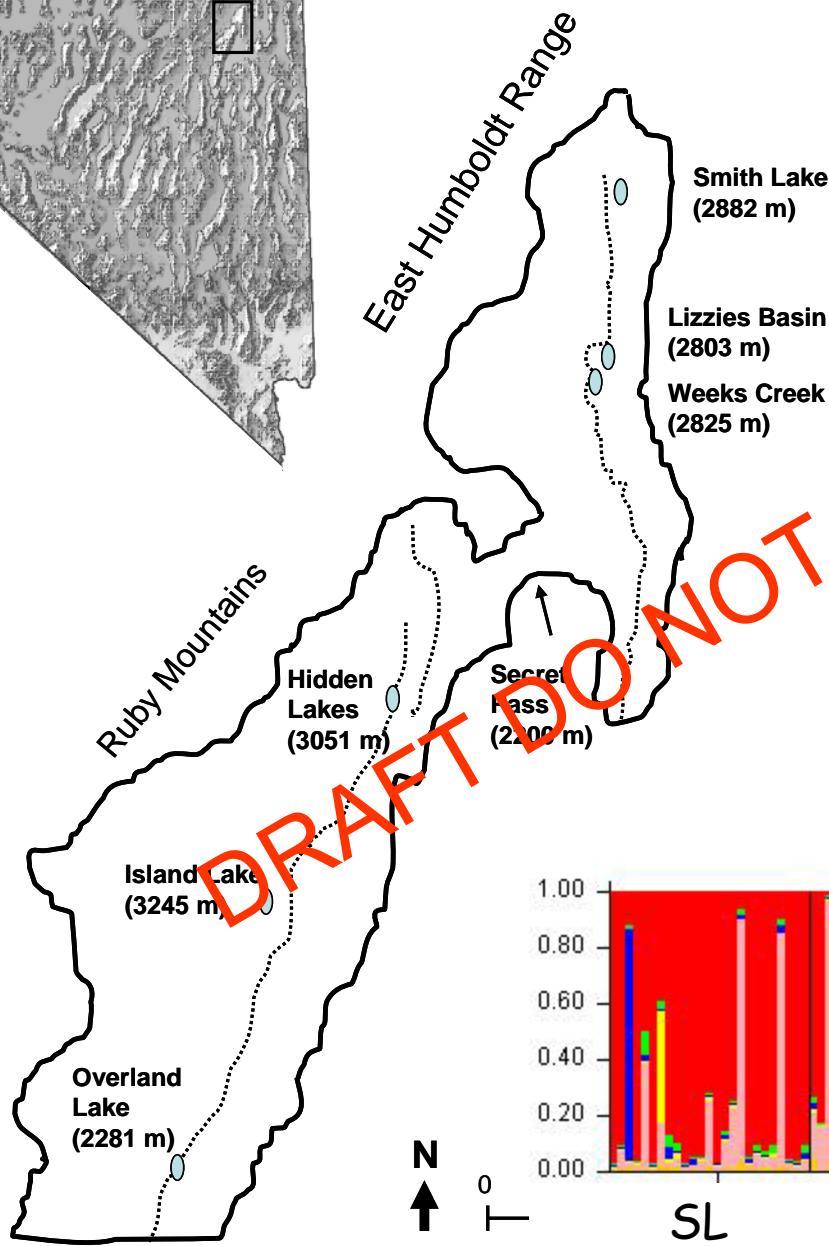
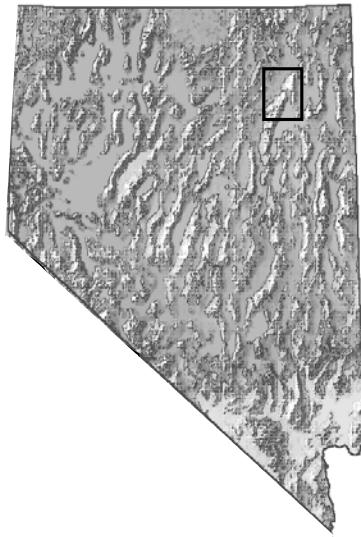


Peacock, M. M. 1997. *Behavioral Ecology* 8: 340-350.



	Juveniles		Adults		Totals		Percentage
	M	F	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





Pairwise F_{ST} analysis. All populations are significantly differentiated from each other at $P = 0.003$ (corrected for multiple comparisons) obtained after 300 permutations.

	SL	LB	WB	HL	IL
LB	0.052				
WB	0.037	0.038			
HL	0.154	0.165	0.125		
IL	0.123	0.138	0.121	0.078	
OL	0.169	0.174	0.176	0.138	0.081

