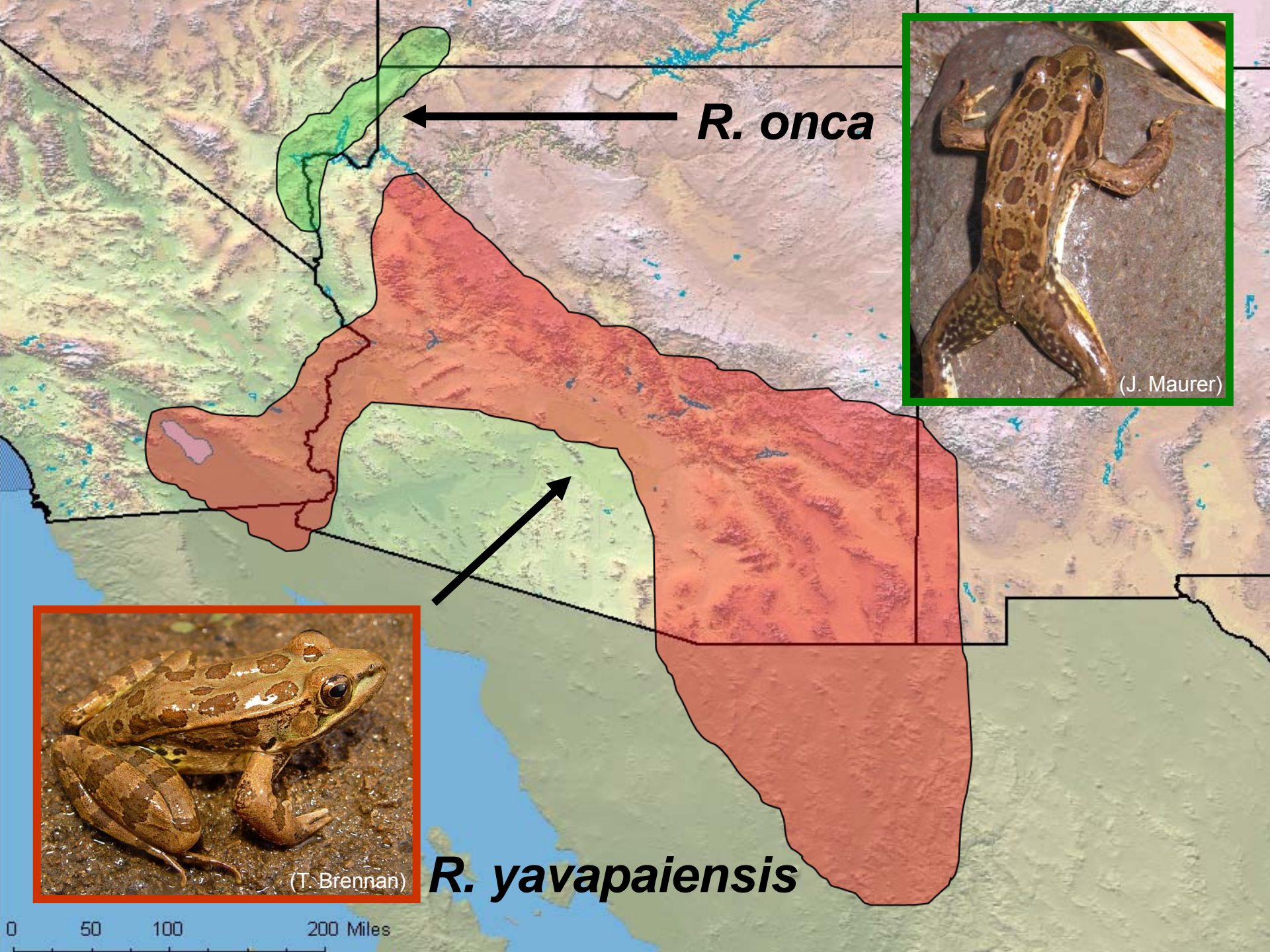


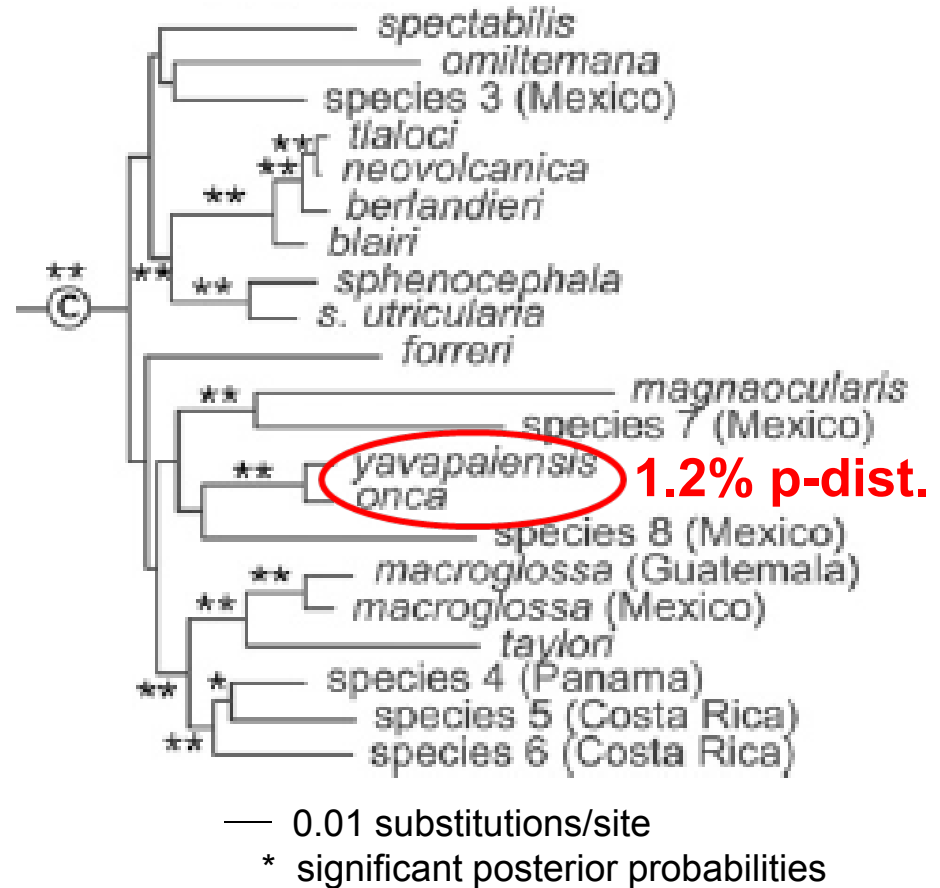
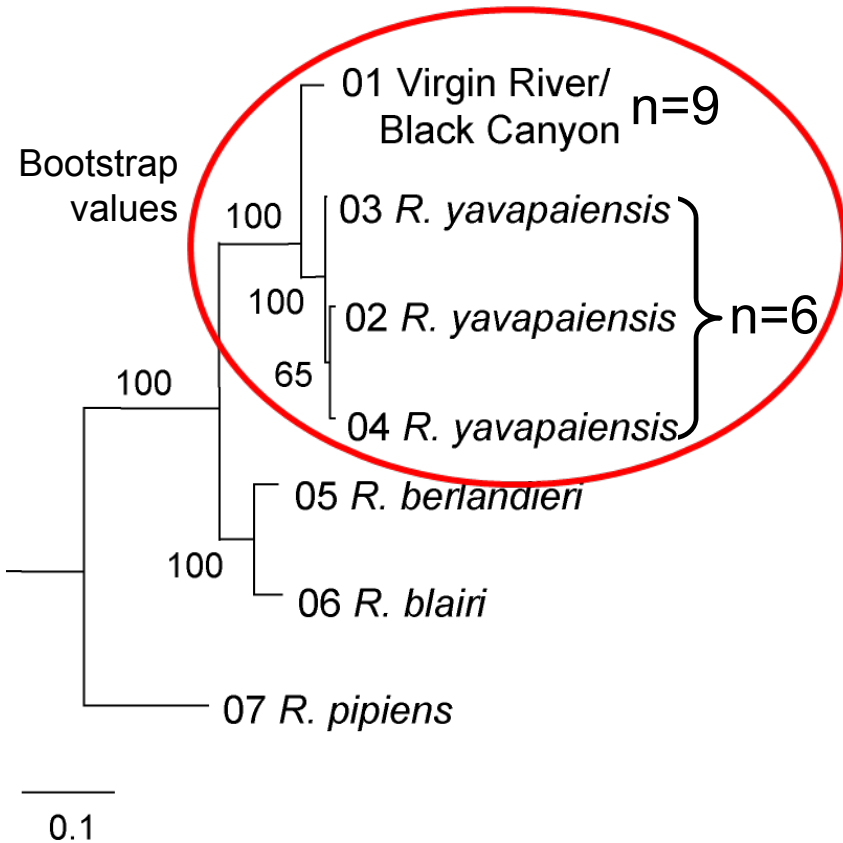
Current Knowledge on the Phylogeography of Relict and Lowland Leopard Frogs



V. Hemmings, J. Jaeger, M. Sredl,
M. Schlaepfer, R. Jennings,
D. Bradford and B. Riddle

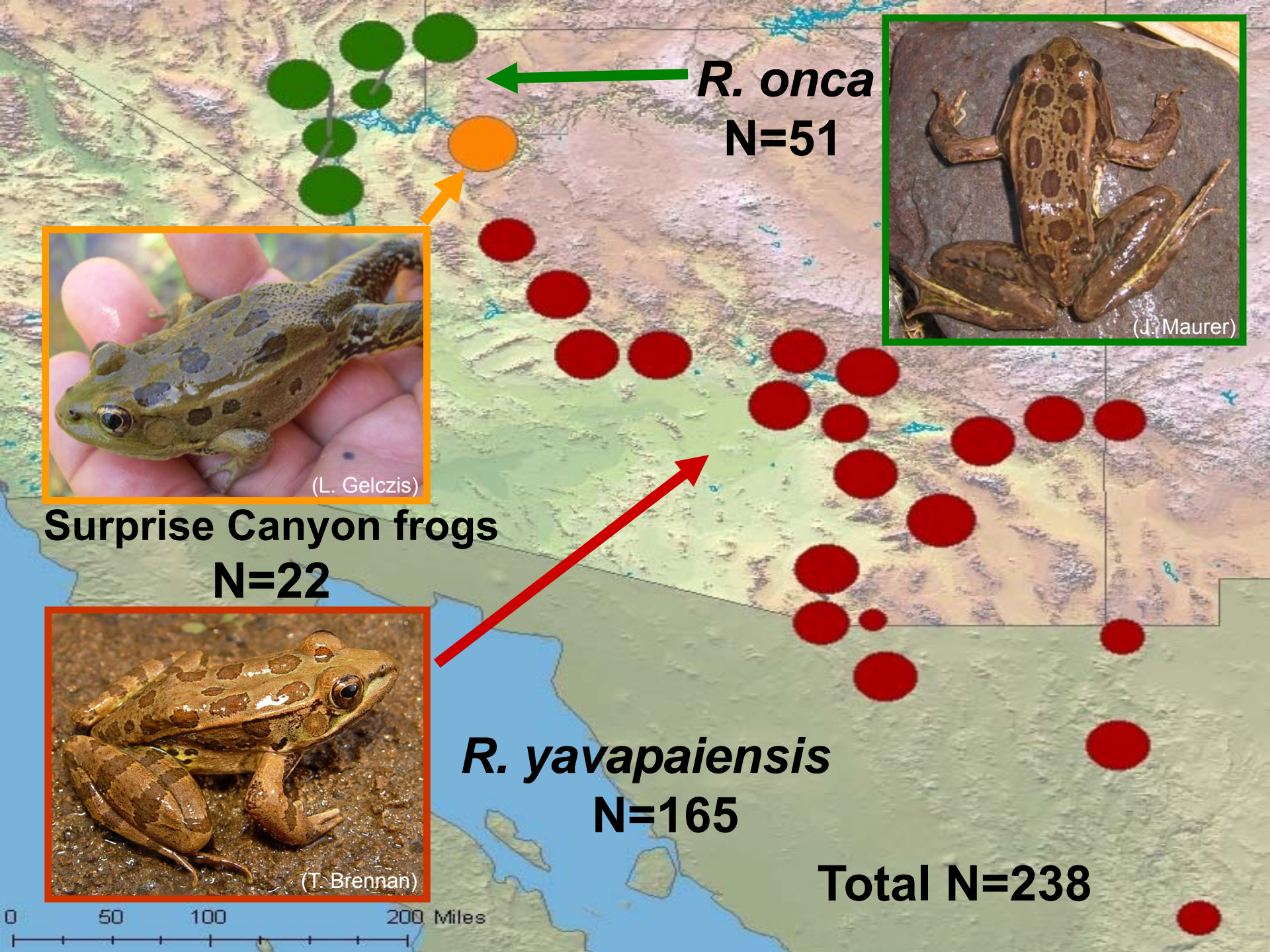


Previous Phylogenetic Work



Maximum Likelihood Haplotype Tree based on 1137 bp of mtDNA Control Region (Jaeger et al. 2001)

Portion of Maximum Likelihood Tree based on 1962 bp of 12s and 16s ribosomal mtDNA (Hillis and Wilcox 2005)



R. onca
N=51



Surprise Canyon frogs
N=22



R. yavapaiensis
N=165

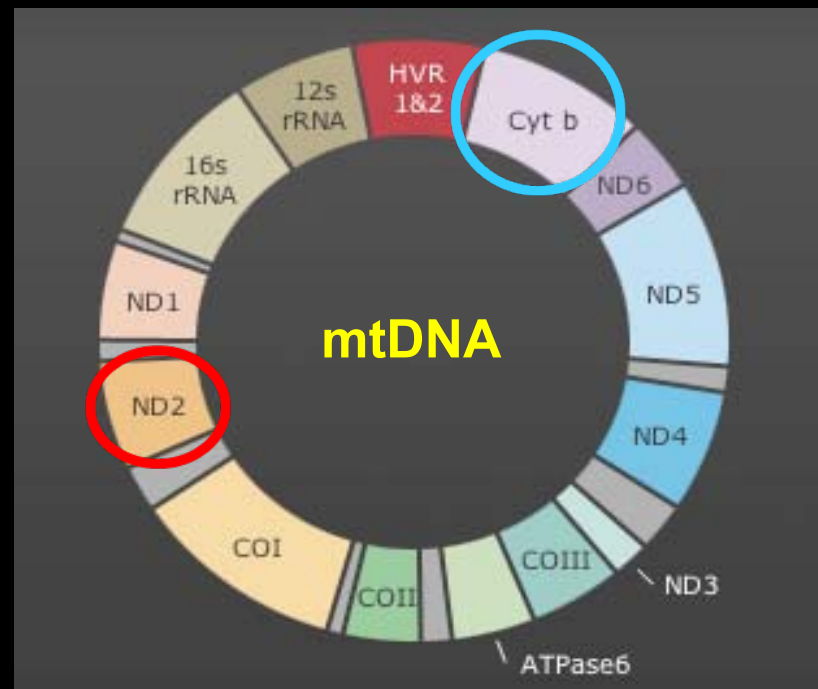
Total N=238

0 50 100 200 Miles

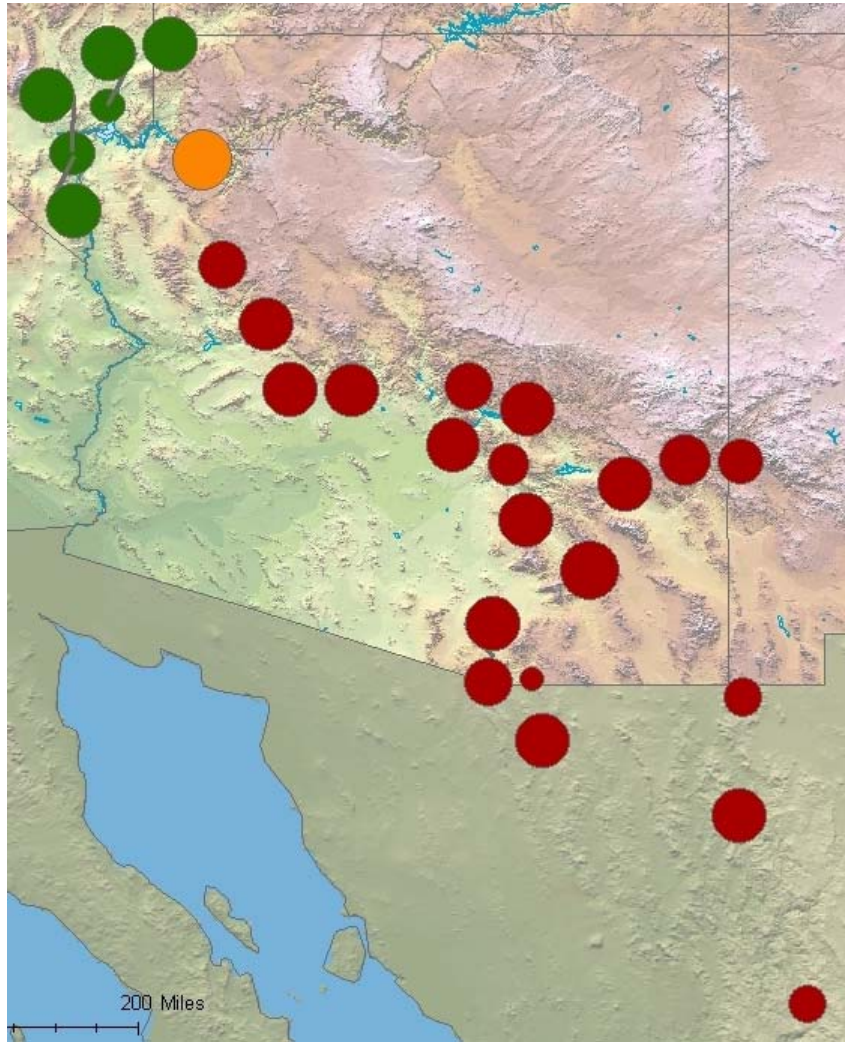
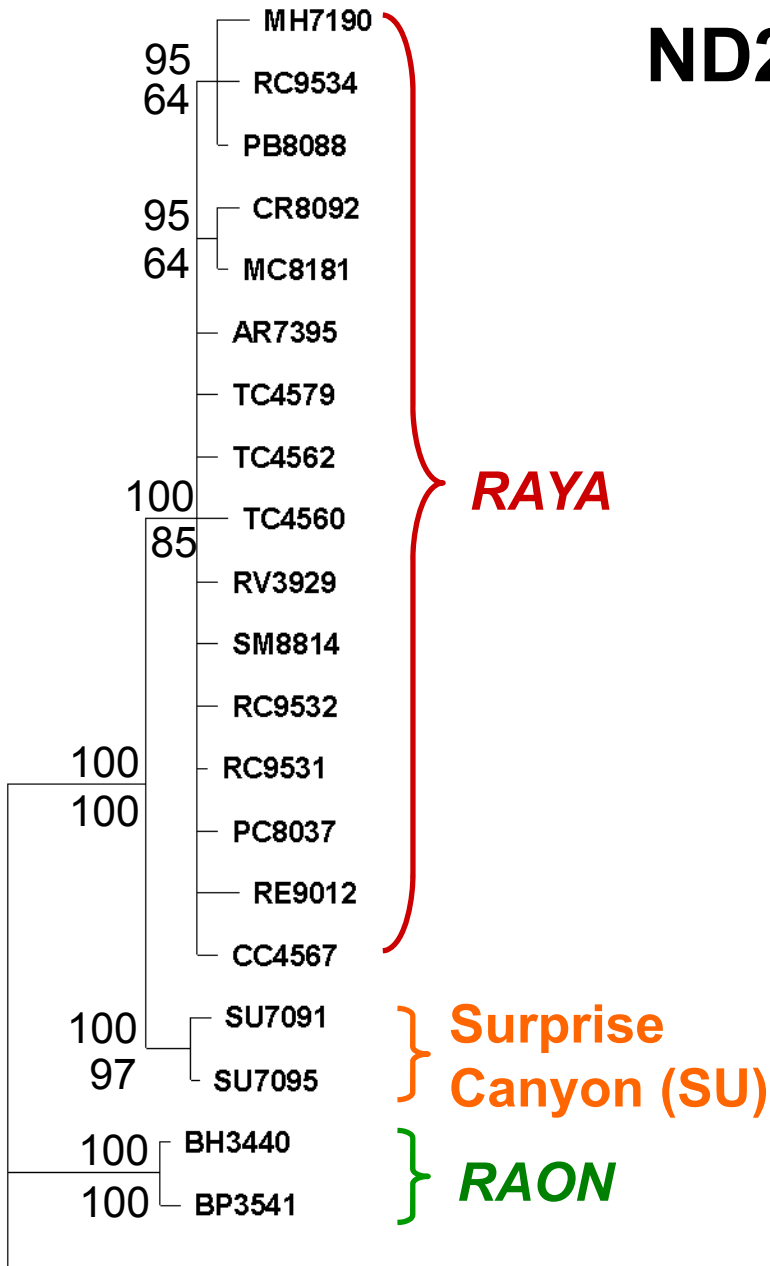
Methods

- Genomic DNA from toe and tail clips
- Amplified mtDNA – ND2 and Cyt b
- Double-stranded automated sequencing
- Phylogeographic and population genetic programs

1035bp ND2
962bp Cyt b



ND2 Bayesian Inference Tree



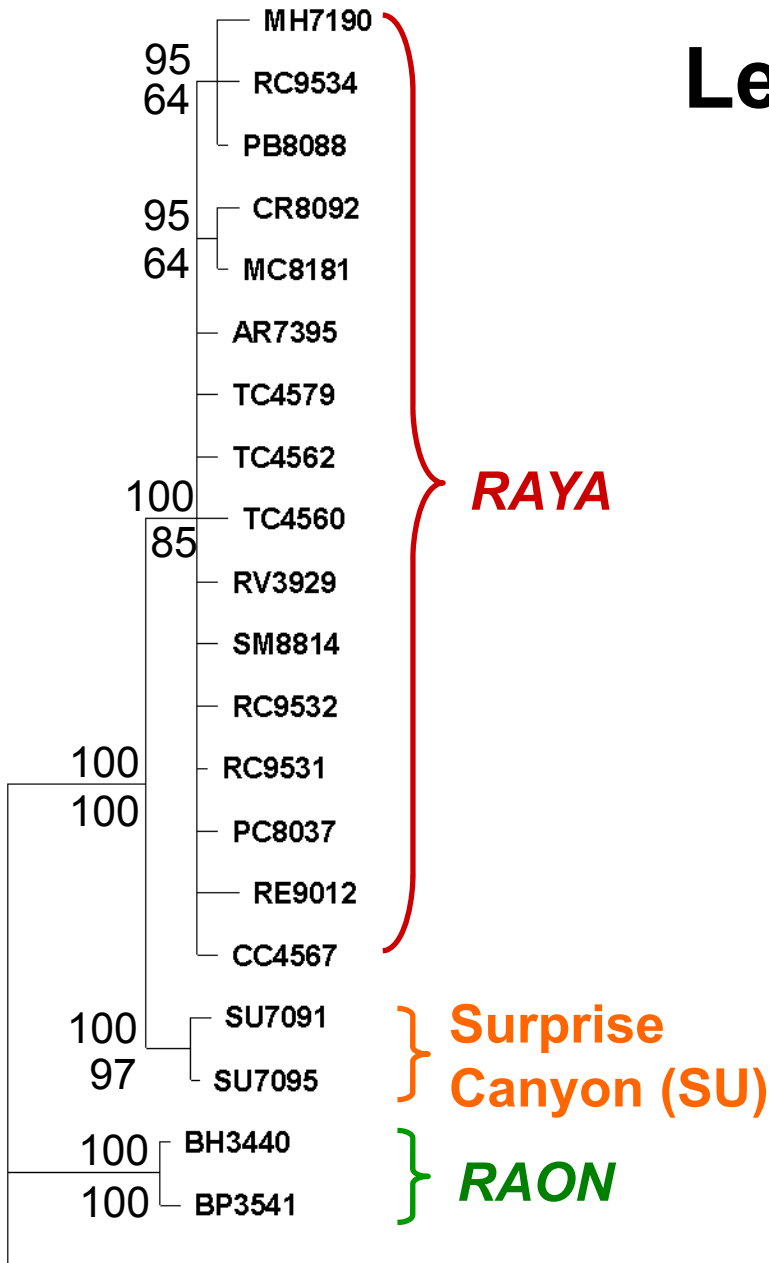
Posterior probability (upper values)
MP bootstrap support (lower values)

Level of ND2 Sequence Divergence

Pairwise p-distances

$$RAON : RAYA + SU = 2.8\%$$

$$RAYA : SU = 0.7\%$$



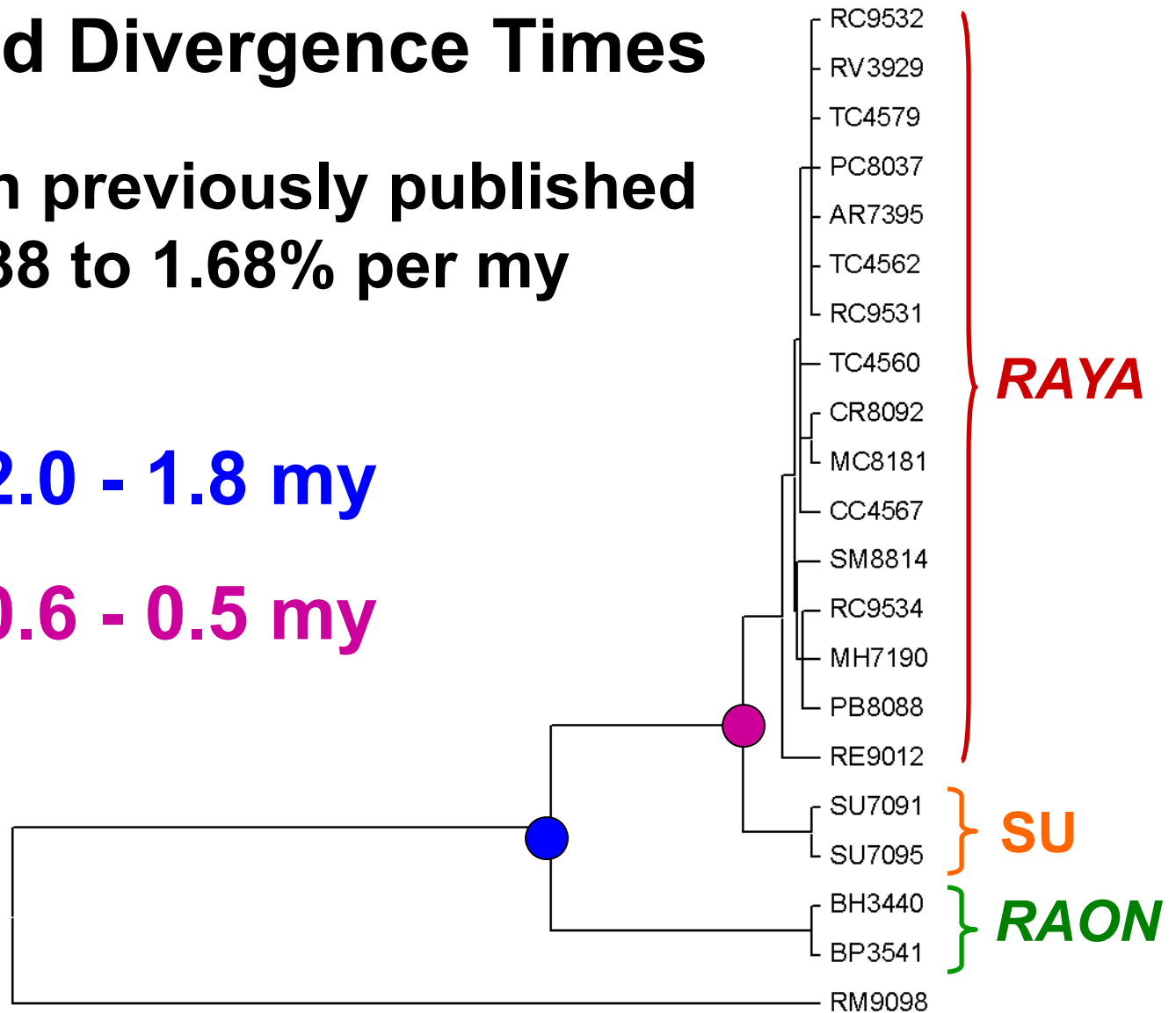
RM9098

Estimated Divergence Times

Based on previously published rates: 1.38 to 1.68% per my

● ~ 2.0 - 1.8 my

● ~ 0.6 - 0.5 my

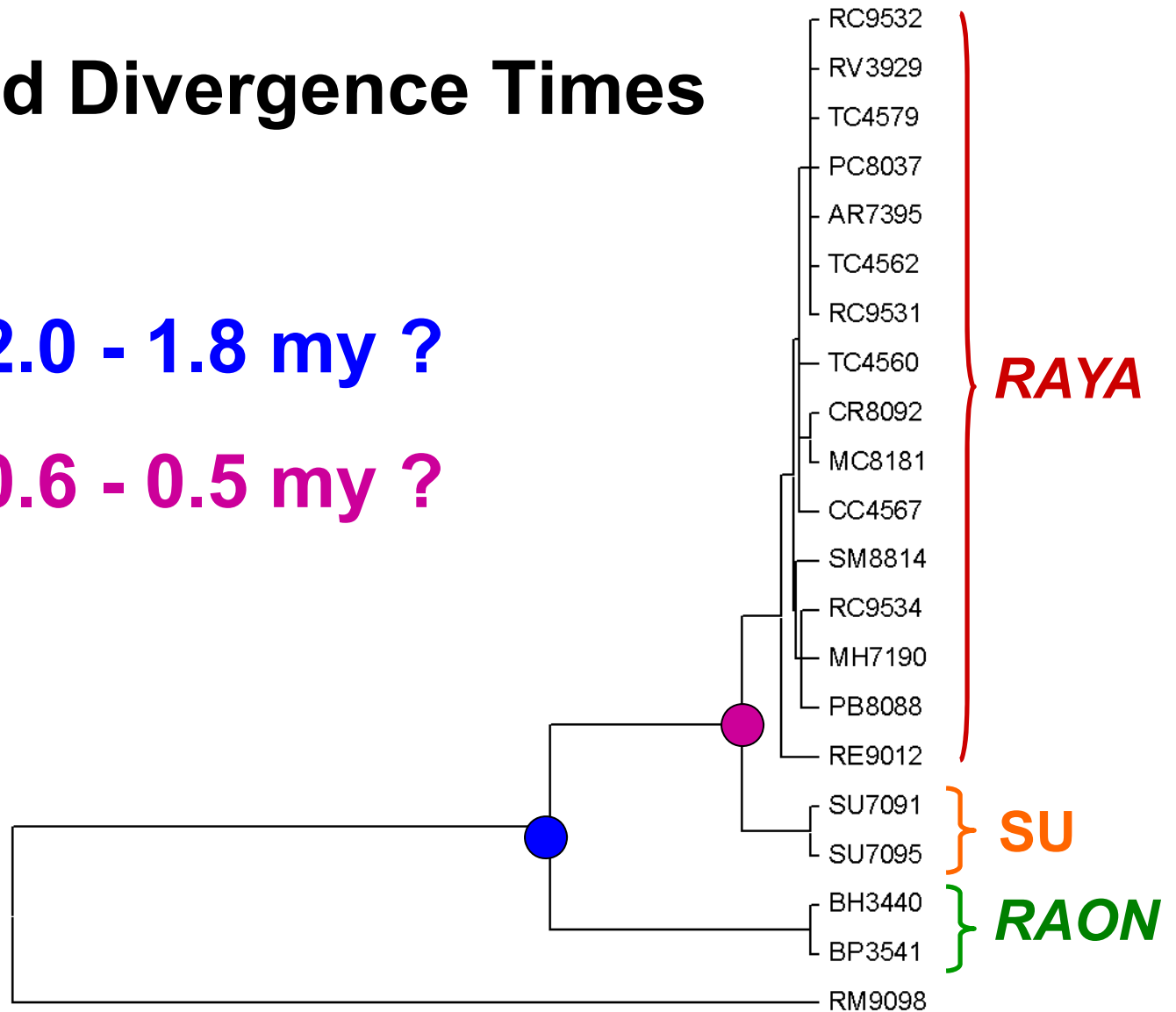


ND2 Neighbor-Joining haplotype tree

Estimated Divergence Times

● ~ 2.0 - 1.8 my ?

● ~ 0.6 - 0.5 my ?

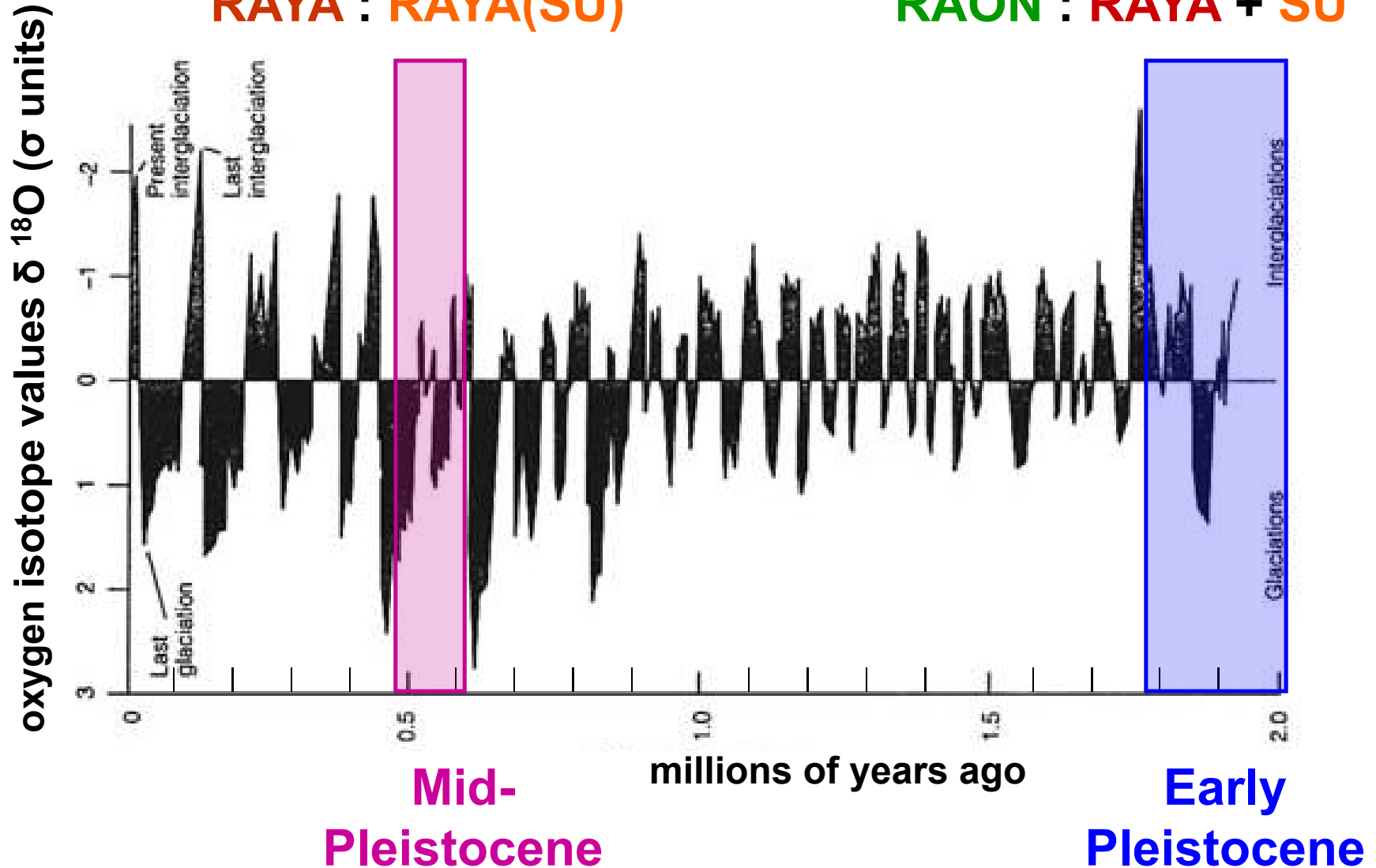


ND2 Neighbor-Joining haplotype tree

Quaternary Climatic Oscillations

RAYA : RAYA(SU)

RAON : RAYA + SU



(Figure: Skinner & Porter 1995)

ND2 Sequence Variation

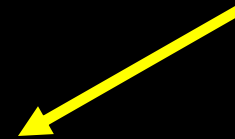
	<u>RAON</u>	<u>RAYA (w/o SU)</u>
Haplotype diversity (h)	0.41 L	0.65 H
Nucleotide diversity (π)	0.0004 L	0.001 L

	Low h	High h
Low π	Recent population bottleneck	Population bottleneck followed by rapid population expansion

Low h is < 0.5 , Low π is < 0.005 (Grant and Bowen 1998)

Neutrality Tests

	<u>RAON</u>	<u>RAYA (w/o SU)</u>
Tajima's D (P-value)	1.1066 (0.88)	-1.7099 (0.01)*
Fu's Fs (P-value)	1.5166 (0.68)	-9.0673 (0.003)*



population expansion

population bottleneck – population expansion

selective sweep

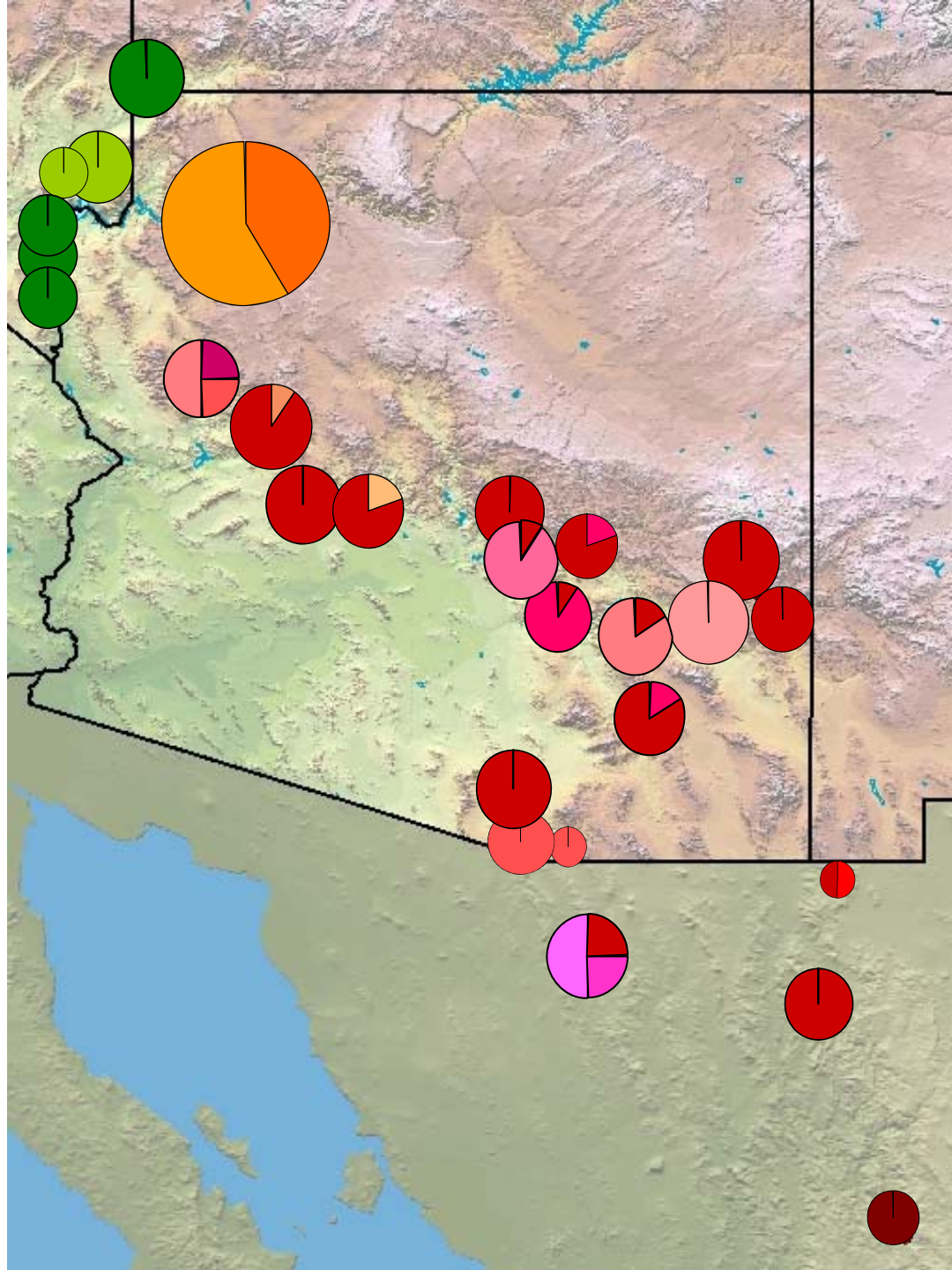
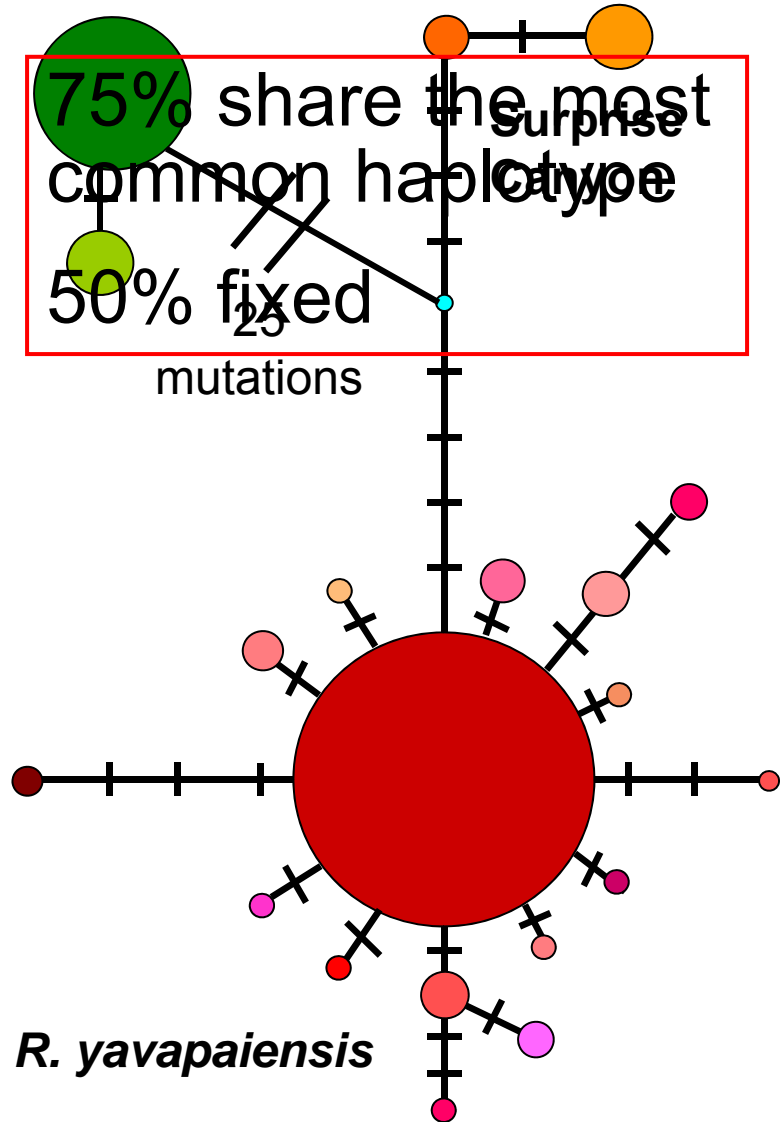
* Significant

ND2 Haplotype Network

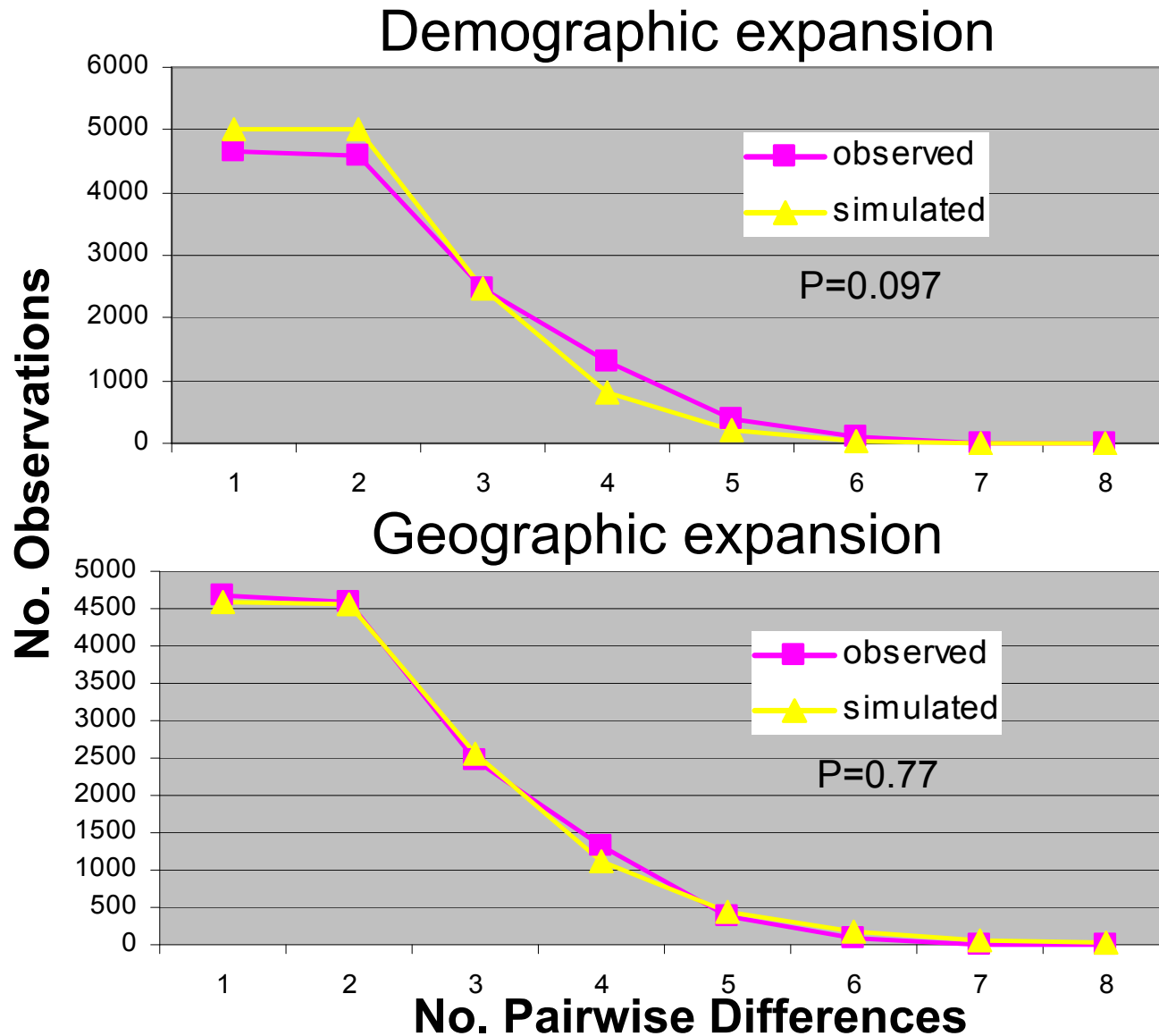
R. onca

75% share the most common haplotype

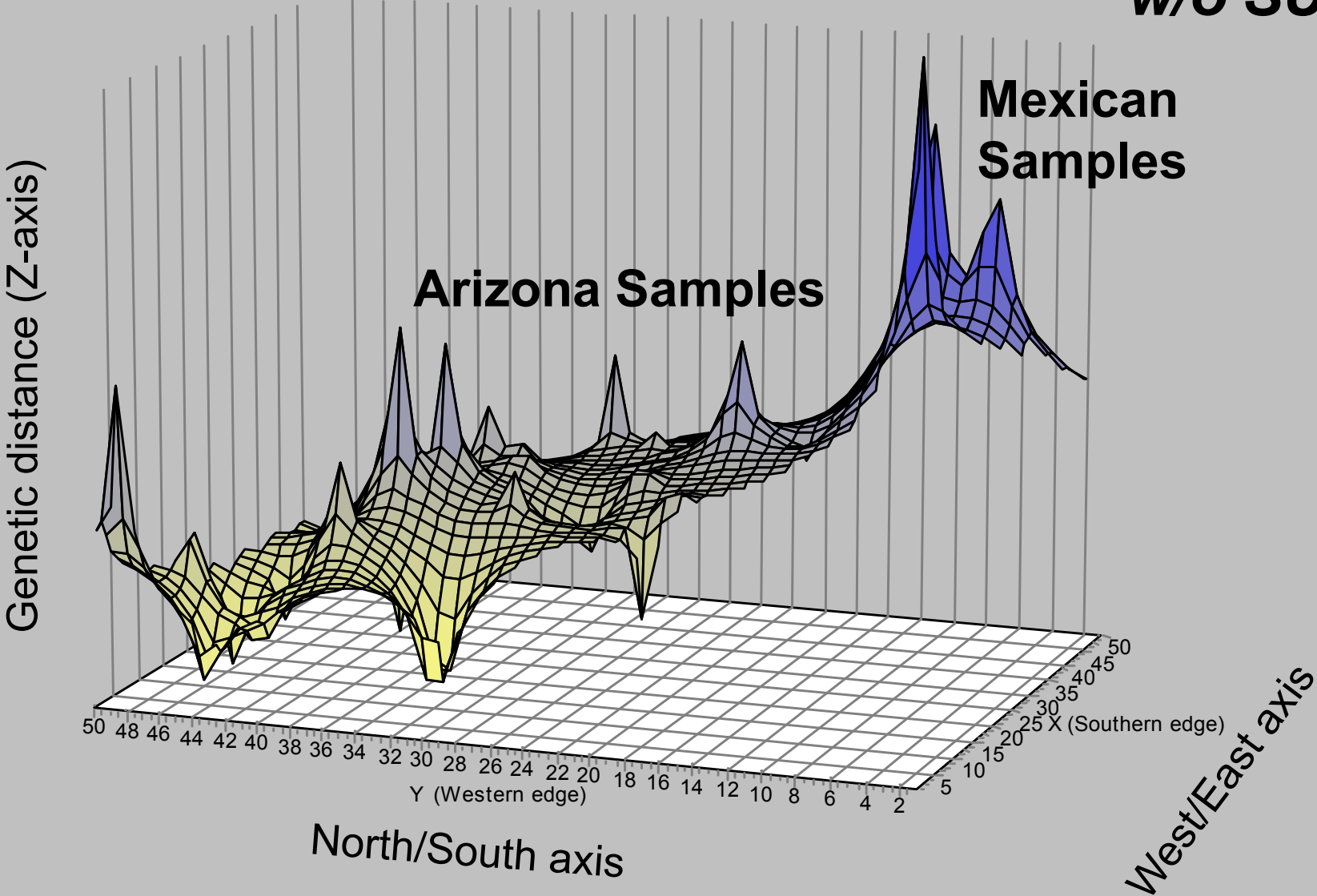
50% fixed mutations



Mismatch distribution - *R. yavapaiensis* w/o SU

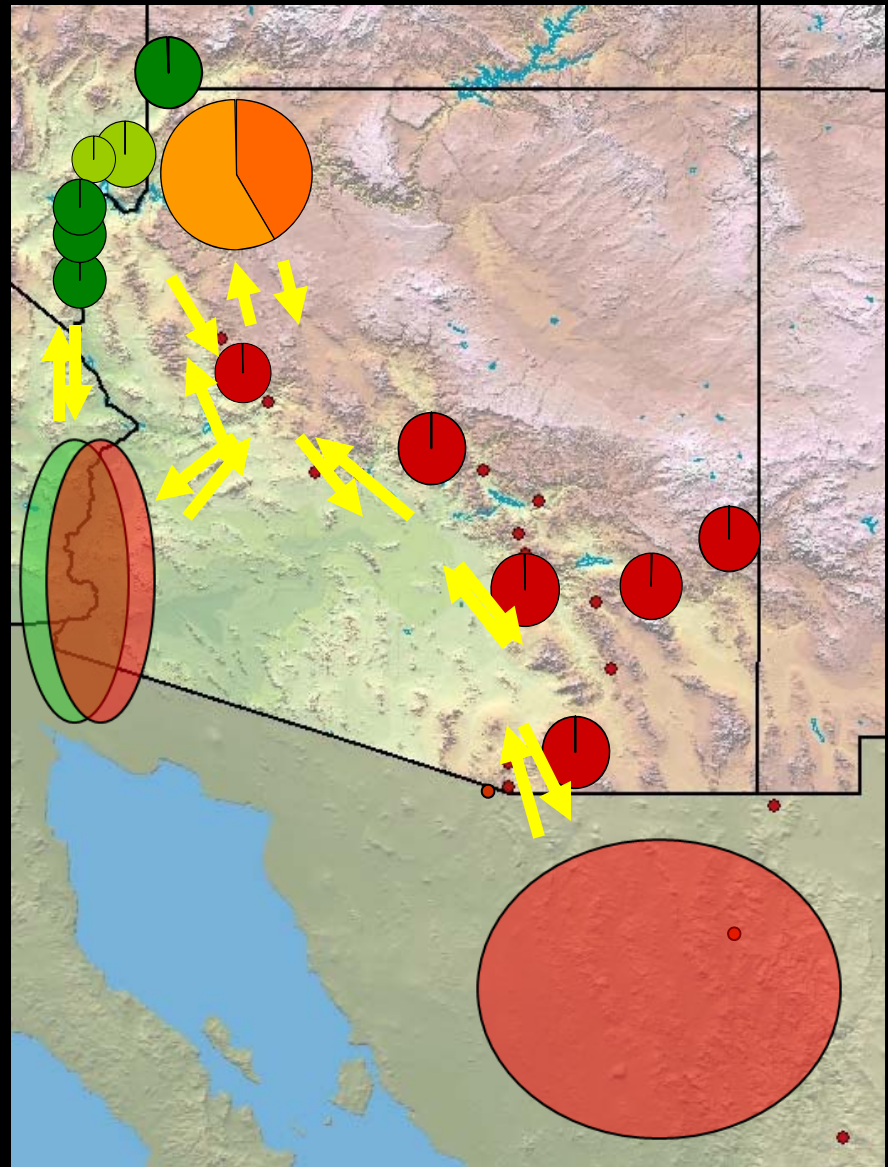


Landscape Shape Interpolation – *R. yavapaiensis* w/o SU



Phylogeography and Population Structure

Complex history of range expansion, contraction, and isolation



Many Thanks!

Charles Drost
Lisa Gelczis
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Charles Painter
SaBR group

