Effective Population Sizes for *Gila cypha* in the Colorado and Green Rivers

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DNA as a Data Archive

- ✓ DNA accumulates mutations over time
- ✓ It can thus serve as a data archive for the deciphering of past events
- ✓ Population trends, for example, can now be interpreted across deep ecological time
- ✓ Before we show how these data can be so unlocked, we must first lay groundwork

1: Effective Population Size (Ne)

- ✓ **Hardy-Weinberg equilibrium** – involves a series of idealized assumptions for a population
- ✓ These are: >50:50 sex ratio >panmixia
  >infinite pop. size >no selection
- ✓ **Premise**: No real population can be expected to obey all the assumptions that pertain to an "idealized" Mendelian population

2: Effective Population Size (Ne)

- Genetic variability is instead affected by parameters that vary in time and space:
  - sex ratio
  - small breeding groups
  - variable fertility
  - numerical fluctuations
- Furthermore, not all individuals in a population contribute gametes to the next generation

3: Effective Population Size (Ne)

- The approach to calculating Ne takes these variables into consideration
- Ne thus represents the numerical size an ideal ("Hardy-Weinberg") population must have to accommodate the inbreeding values and levels of genetic variability observed in the study population

4. Effective Population Size (Ne)

- ✓ Hardy-Weinberg equilibrium thus serves as a barometer to evaluate how a population deviates from an idealized baseline
- ✓ In this sense, Ne converts socially and demographically variable populations into a common currency that can be evaluated among species

5. Effective Population Size (Ne)

- ✓ Ne is an important consideration in conservation genetics, and has been utilized in:
  - › Maintenance of hatchery brood stocks
  - › Management of large fisheries
  - › Monitoring small, natural populations
- ✓ Populations with low Ne are prime candidates for adaptive management

Recent Advances in Calculating Ne

- Molecular genetics wed with microcomputers
- DNA sequences aligned and Ne calculated by indirect methods
- Begin with a genealogy of individuals
- Modify it by Monte Carlo sampling to produce a likelihood curve and likelihood estimates of 2Nem (m=mutation rate/site/generation)

Sampling of *G. cypha*

Blackrocks (Colorado River) = 16

Desolation Cn. (Green R.) = 20

Westwater Cn. (Colorado R.) = 20

Yampa Cn. (Green R.) = 20

Little Colo. R. (Grand Cn.) = 20

Shinumo Ck. (Grand Cn.) = 20

Randy's Rock (Grand Cn.) = 20

Geographic locations of the seven HBC populations evaluated in this study

Overview of Genetics

ND2 -- 589 bp

ATPase 8 -- 168 bp

ATPase 6 -- 474 bp

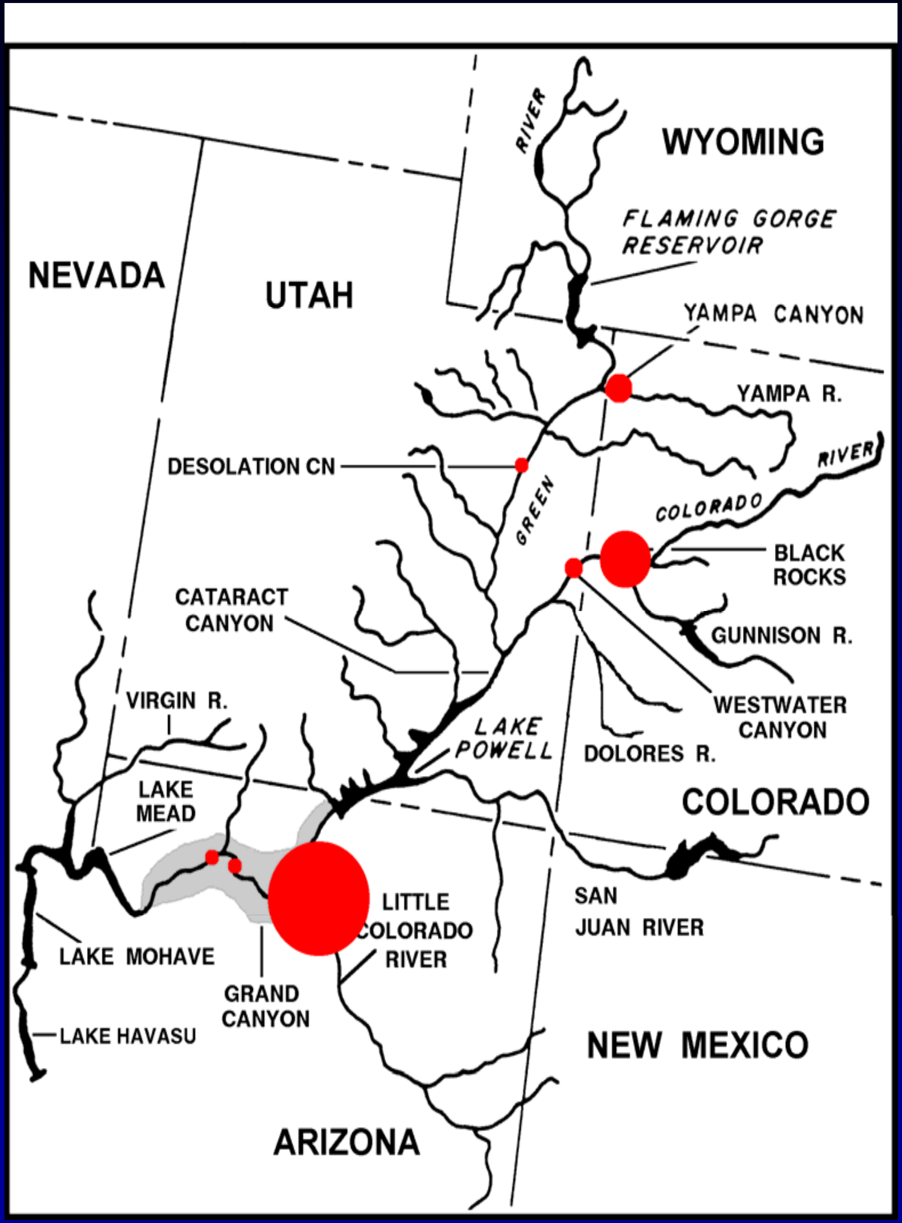
D-loop -- 616 bp

TOTAL -- 1,847 bp mtDNA

sequenced for 136 adult G. cypha

across 3 mt-genes and one mt-region

Relative sizes of historic "effective populations" at each of the seven populations of HBC (as judged by Ne)



Overview of Ne

- ✓ Data suggest that effective population sizes for HBC were larger in the historical past than current population sizes are today
- ✓ In the historical past, movements between basins appeared minimal
- ✓ Movements also minimal within basins

Relative sizes of historic "effective populations" at each of the seven populations of HBC (as judged by Ne)