Genetic Interrelationships among Populations of *Gila cypha* in the Colorado River Ecosystem

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Relationships among Populations of Humpback Chub (HBC)

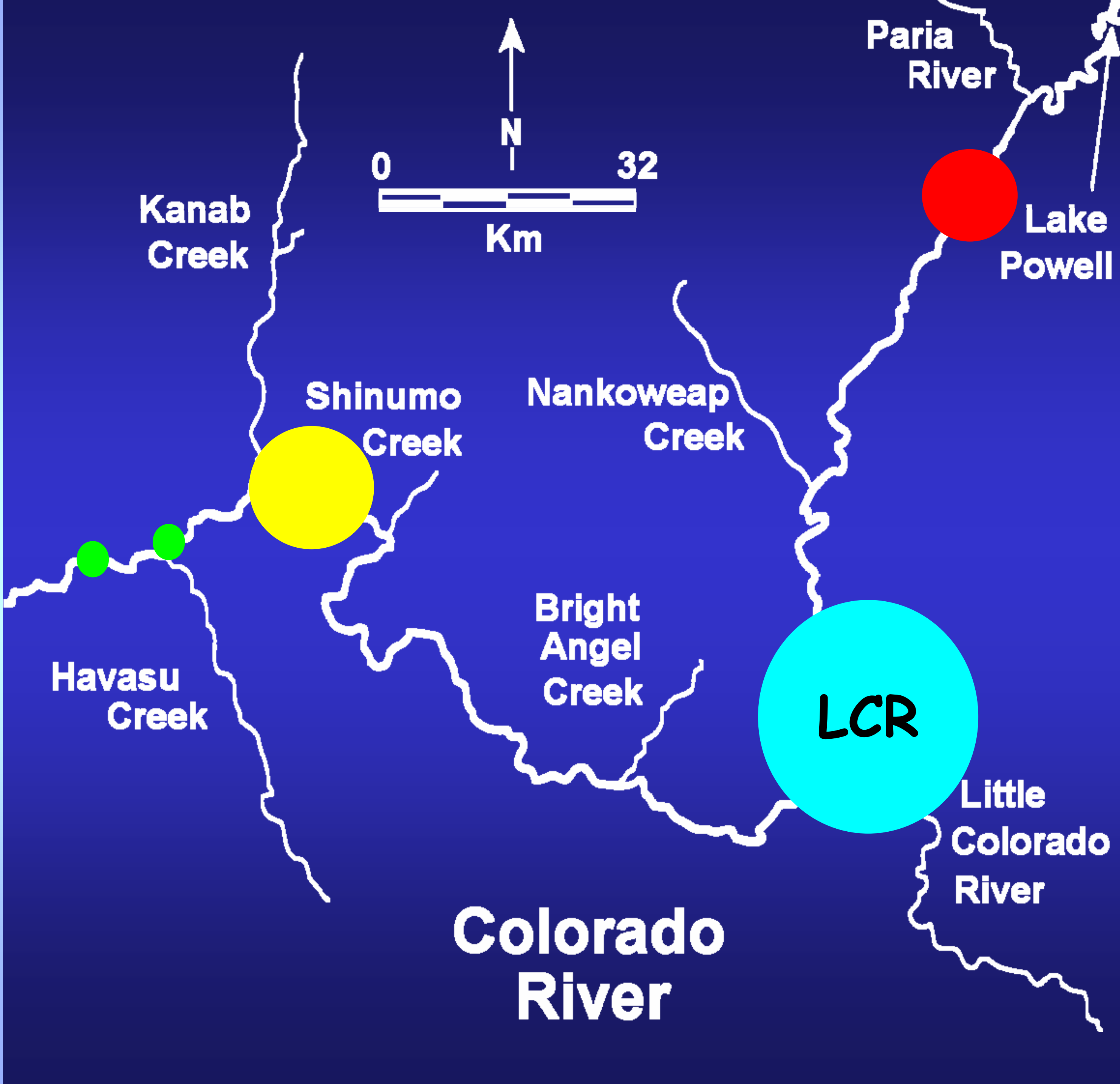
Humpback Chub (*Gila cypha*)

HBC in Grand Cn

9 locations

=

aggregates

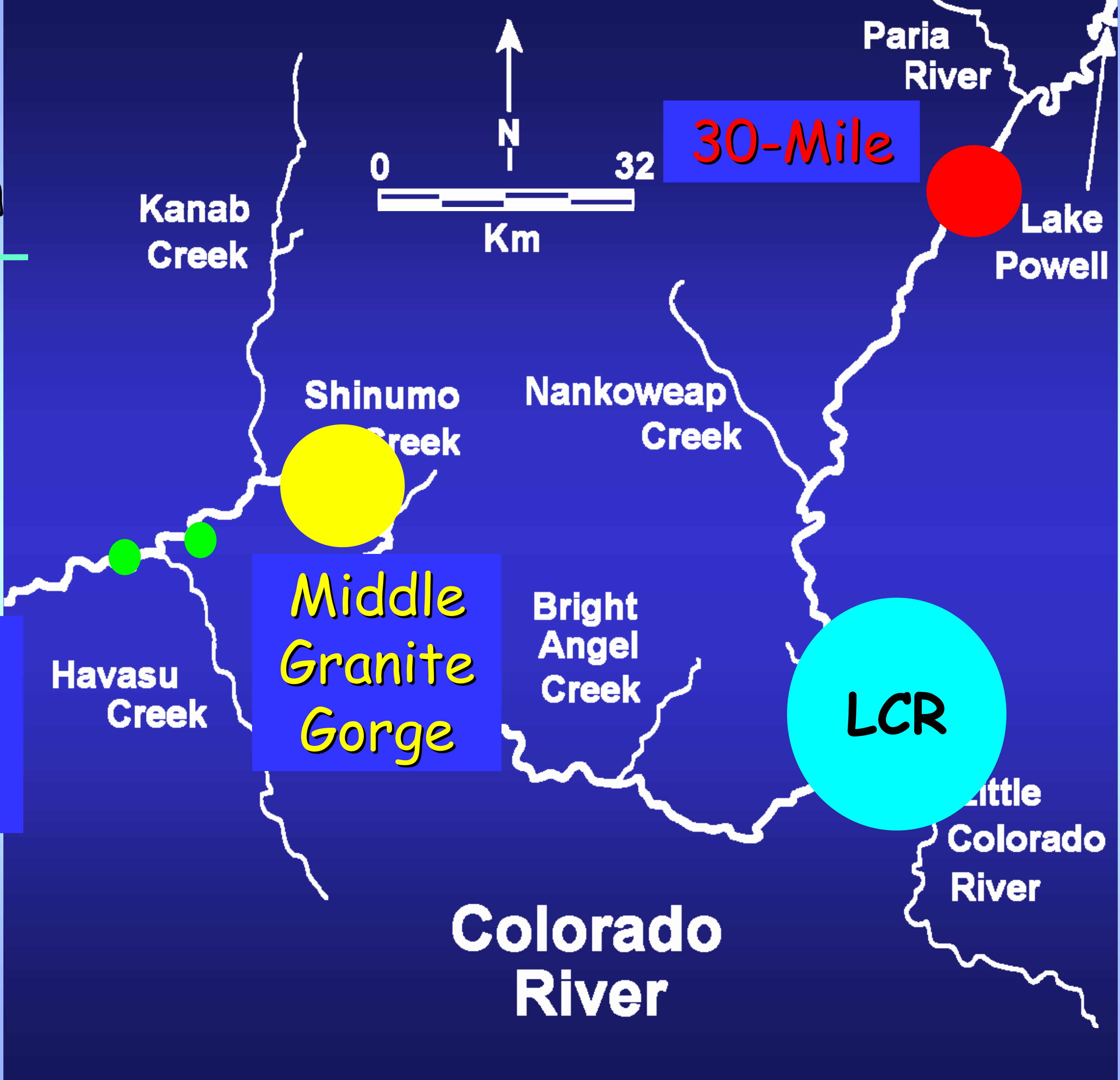


Gila cypha in Grand Canyon

- Do aggregates represent discrete populations ?
  - migration among aggregates?
  - local reproduction?
  - local recruitment?

HBC in Grand Cn

locations



Gila cypha in Grand Canyon

- Relationships among 9 "aggregates"?
- Mainstem / LCR continuum ?
    - 30-Mile vs LCR?
    - LCR vs Middle Granite Gorge
    - LCR vs Western Grand Canyon

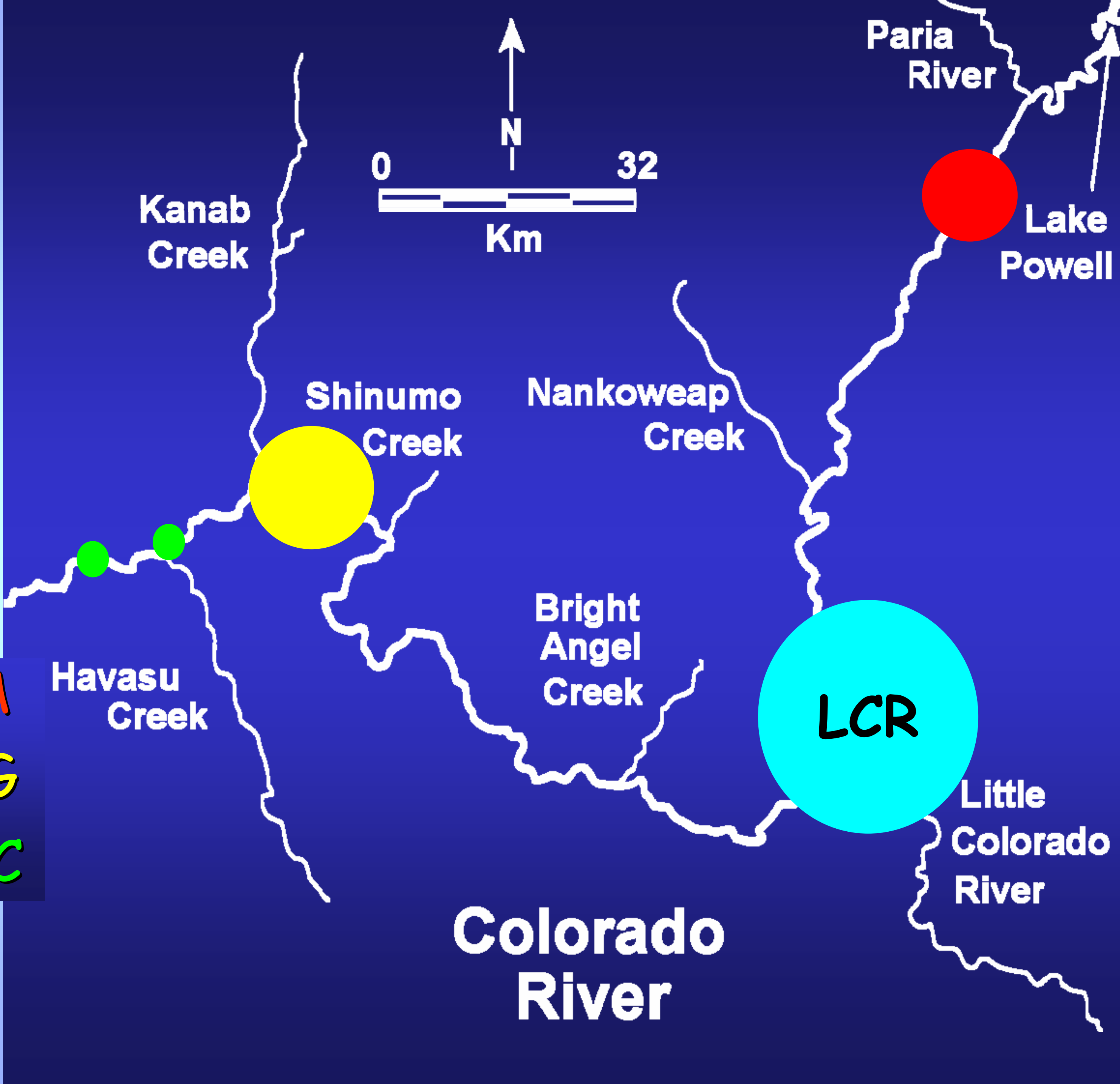
HBC in Grand Cn

aggregates

LCR vs 30M

LCR vs MGG

LCR vs WGC

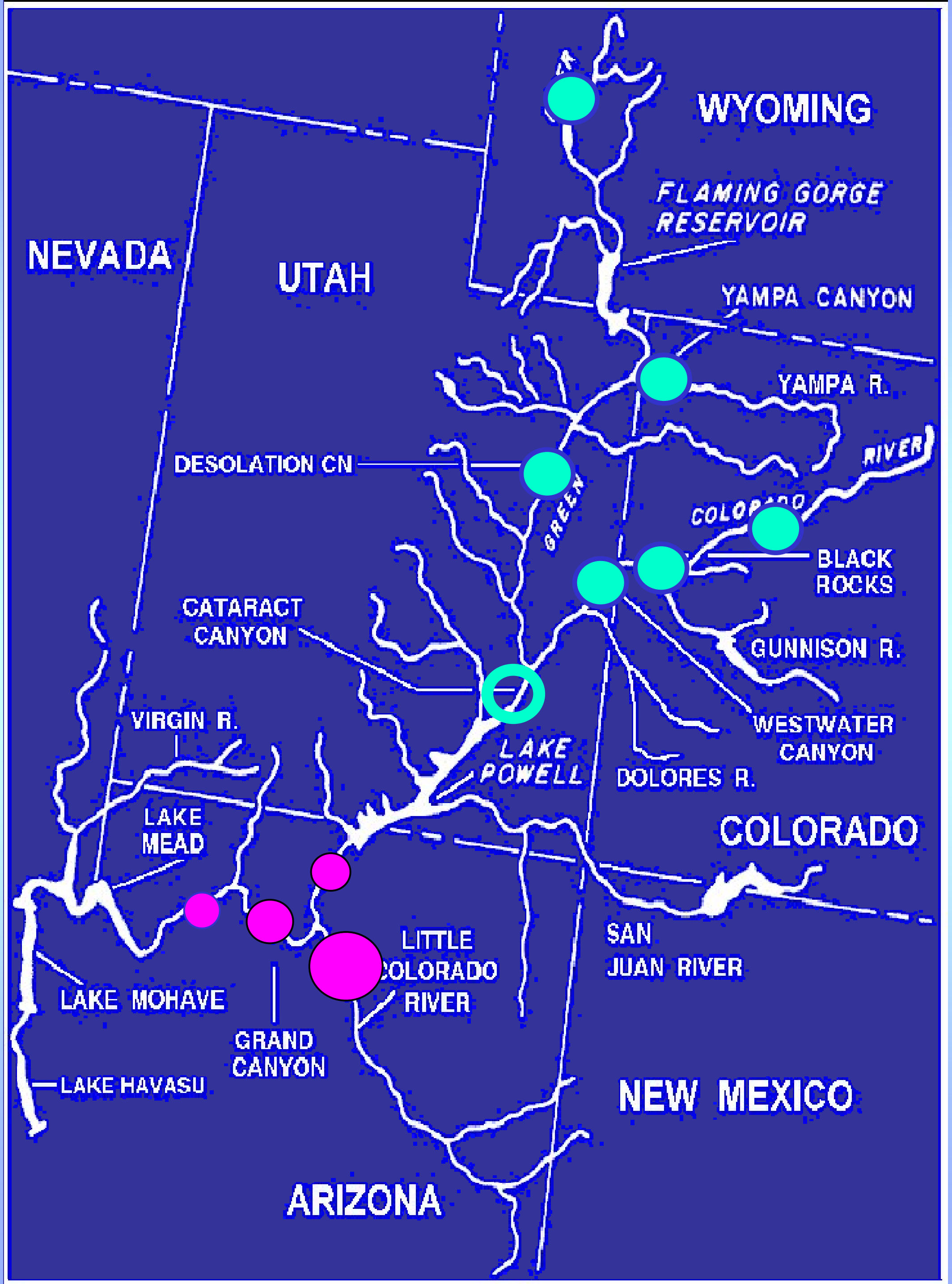


Gila cypha in Grand Canyon

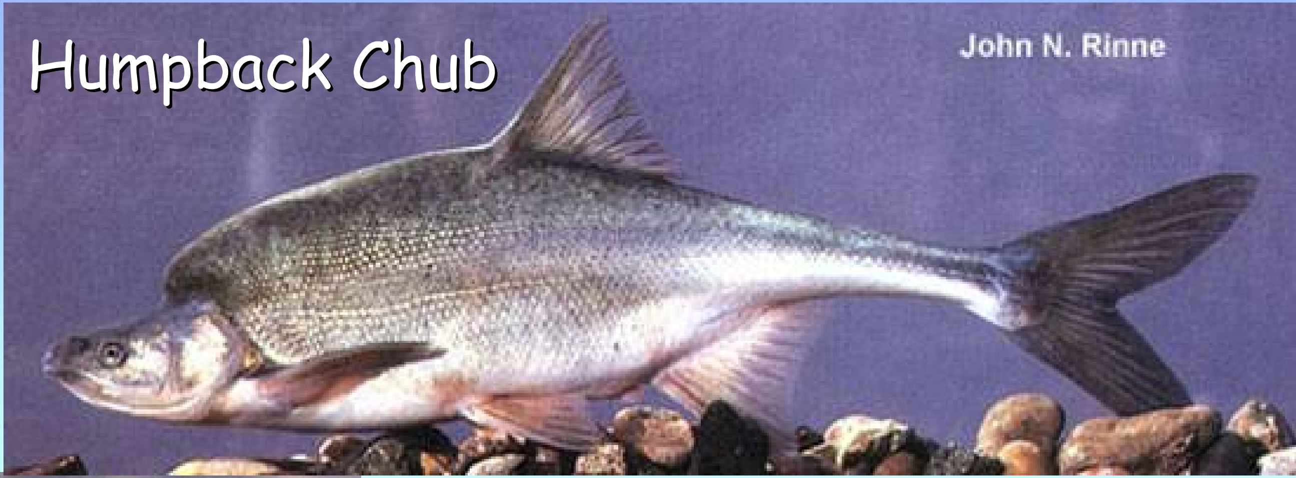
- Examine population structure of *Gila cypha*
  - genetic interrelationships among aggregates in Grand Canyon
- Is there a baseline?
  - how much differentiation to expect?
  - which methods to use?

Gila cypha in Colorado River Basin

- ● Upper Basin
- ● Grand Canyon



Colorado R *Gila*



Humpback Chub

John N. Rinne

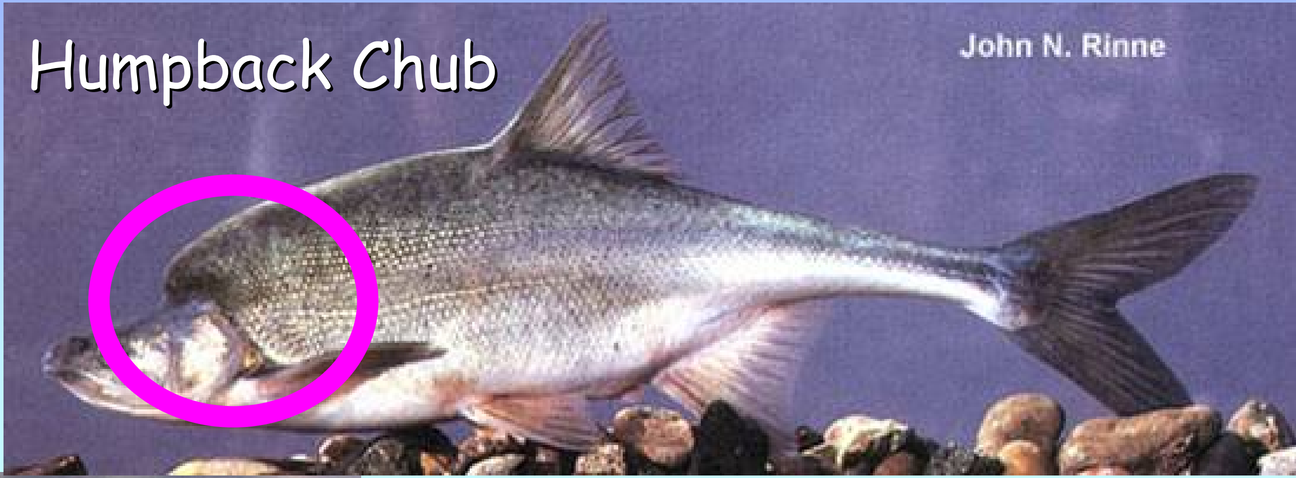
Roundtail Chub

John N. Rinne

Bonytail

John N. Rinne

Colorado R *Gila*


Humpback Chub

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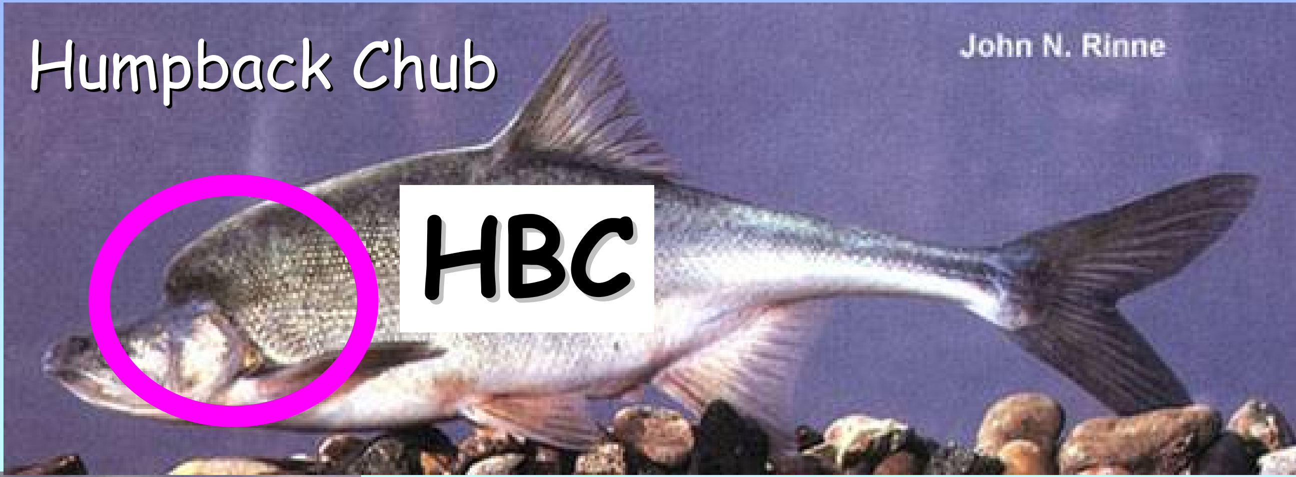
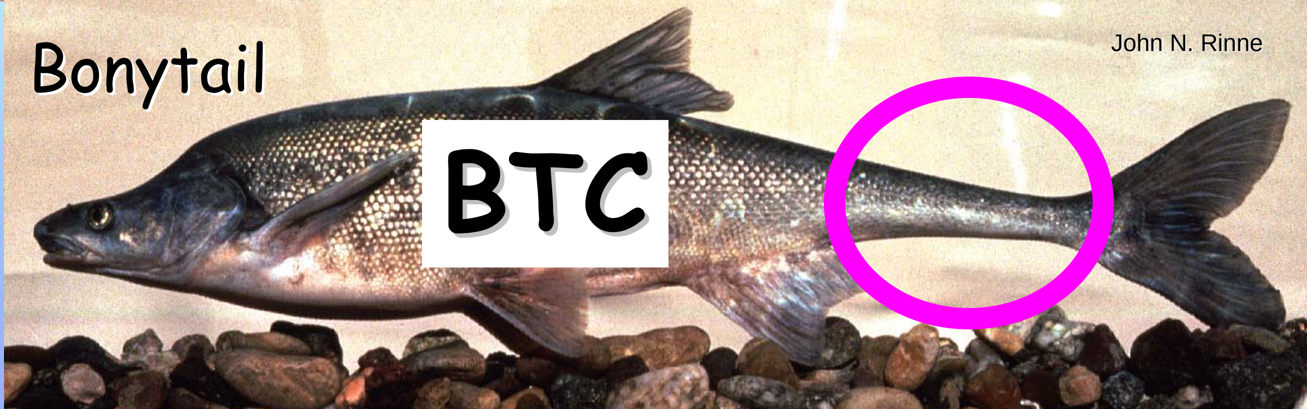
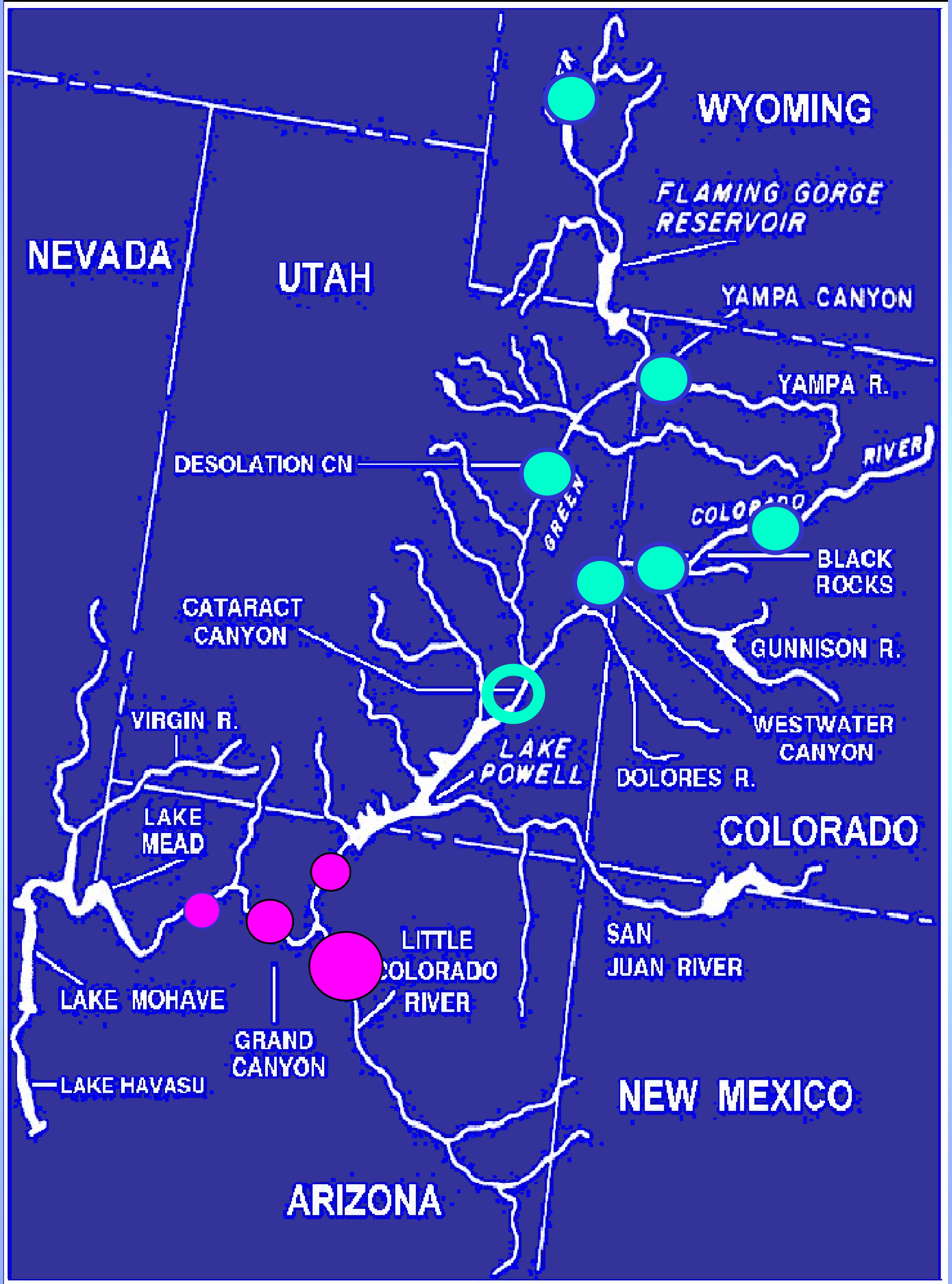




Entire Basin

● Upper Basin
- HBC
- RTC

● Grand Canyon
- HBC



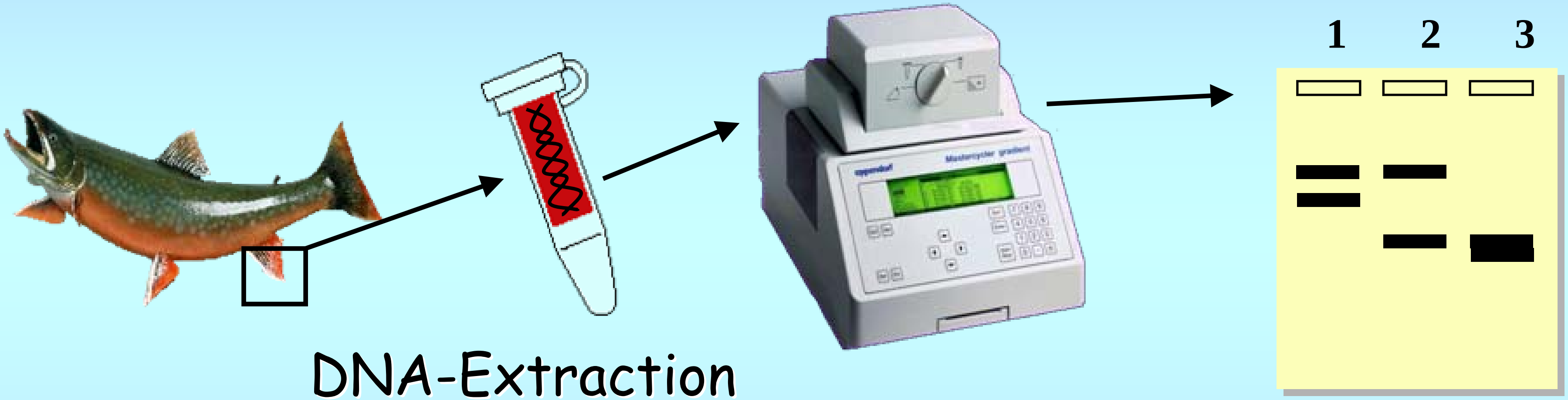
Study Objectives

- Examine population structure among *Gila* in the Colorado River Ecosystem

- genetic interrelationships of populations at

    - spatial scales (= population structure)
    - temporal scales (= evolutionary history)

Approach: Molecular Genetic Methods



Tissue collection

DNA-Extraction

DNA Amplification
(PCR)

Electrophoresis

Molecular Genetic Methods

- mitochondrial DNA sequence analysis
  - >> evolutionary history
    - >> long-term conservation goals (ESUs)

- microsatellite DNA analysis
  - >> population structure
    - >> management units (MUs)

Msat Loci & Sample Sizes

- high variability
  - \+ population-level analyses
  - \- # alleles >> # sample sizes
- codominant inheritance
  - \+ species ecology (e.g., introgression)
  - \- larger sample size to encapsulate pop. variation

Sampling: Grand Canyon

- 9 aggregates / 234 HBC

- 30-Mile Springs	11
- Little Colorado River	77
- Lava to Hance	8
- Shinumo Ck	26
- Stephen's Aisle	7
- Randy's Rock	80
- Kanab Ck	4
- Havasu Ck	11
- Western Grand Cn	10

Table 5

Sampling: Upper Basin

- 5 locations / 186 HBC + 208 RTC

	HBC	RTC
- Yampa R	7	56
- Desolation Cn	51	19
- Black Rocks Cn	51	43
- West Water Cn	77	59
- 15-mile Reach	-	31

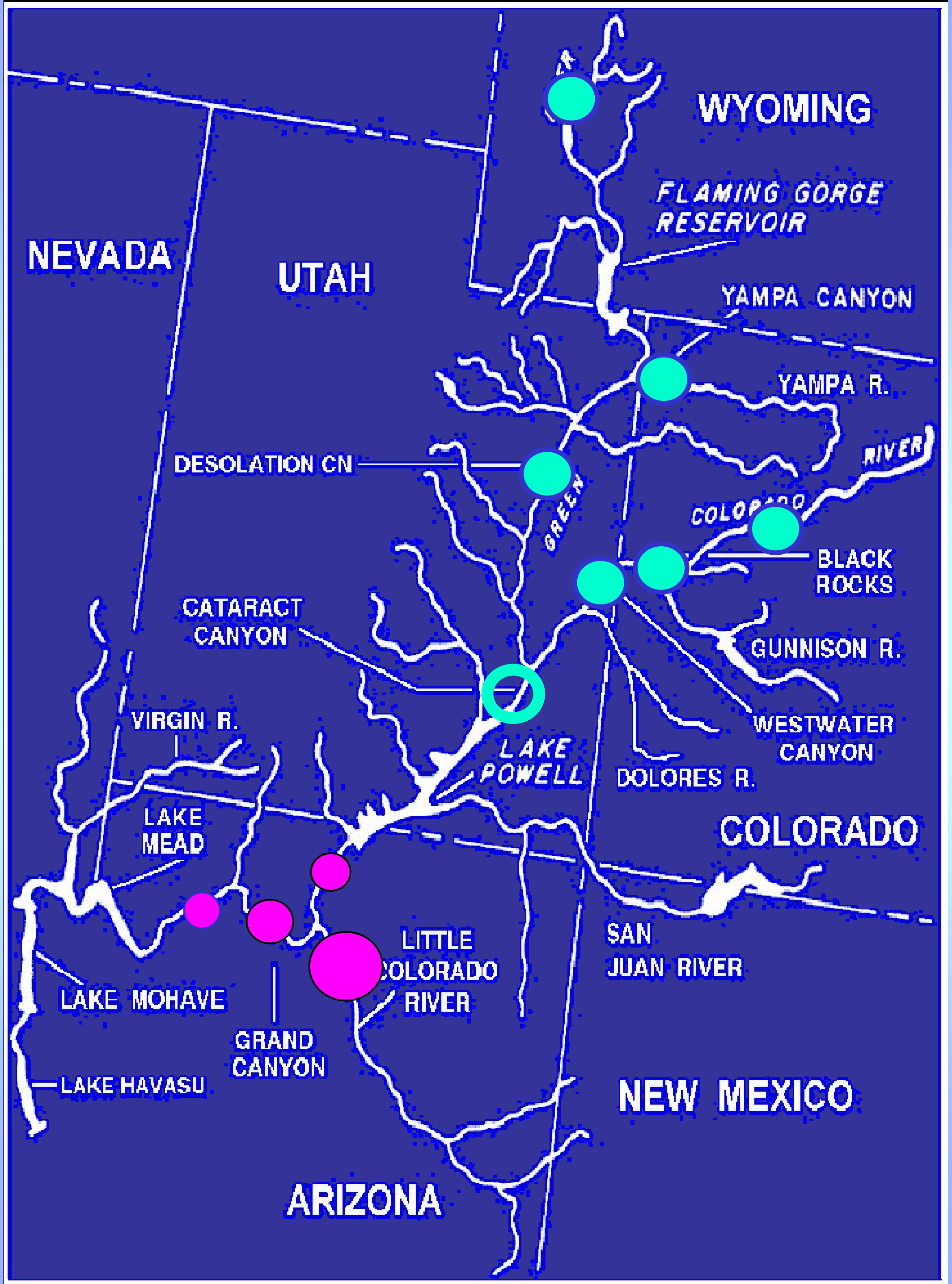
Table 5

Sampling

● **Upper Basin**
208 RTC
186 HBC

● **Grand Canyon**
234 HBC

● **Broodstock**
15 BTC



Results: mtDNA Analysis

- 8 HBC/RTC with BTC haplotypes in

HBC Desolation Cn	2 (21)
HBC 30-Miles	2 (9)
HBC LCR	2 (46)
HBC Randy's Rock	2 (44)
RTC Desolation Cn	1 (22)

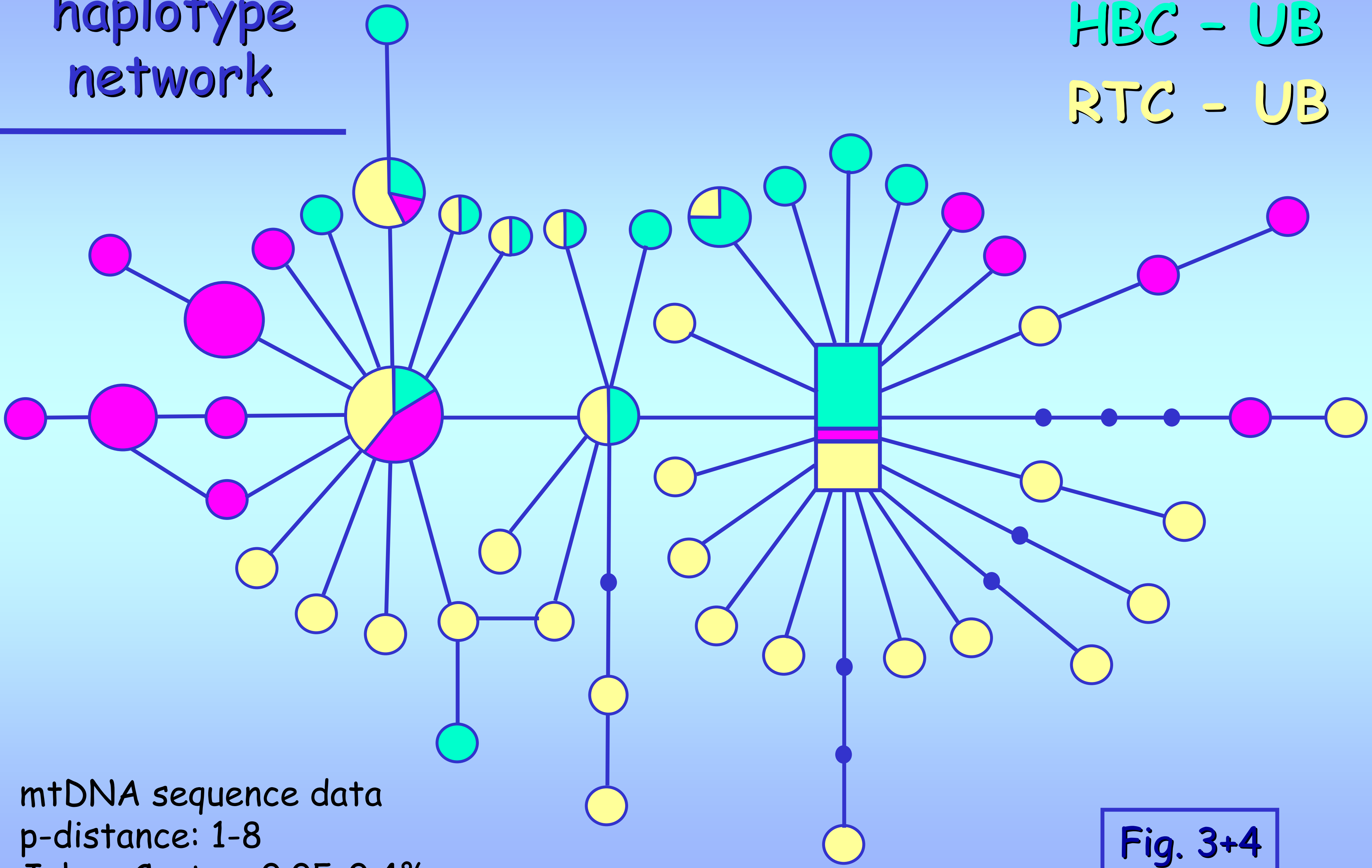
Table 2

Parsimony haplotype network

HBC - GC

HBC - UB

RTC - UB



mtDNA sequence data
p-distance: 1-8
Jukes-Cantor: 0.05-0.4%

Fig. 3+4

Mitochondrial DNA Analysis

Comparison	% Sequence Divergence
HBC_{UB} / HBC_{GC}	no difference
HBC / RTC_{UB}	~ 0.1% (negligible)
BTC / HBC+ RTC_{UB}	~ 5%
RTC_{UB} / RTC_{LB}	~ 4%
Ptychocheilus / *Gila*	~ 6%

Table 3

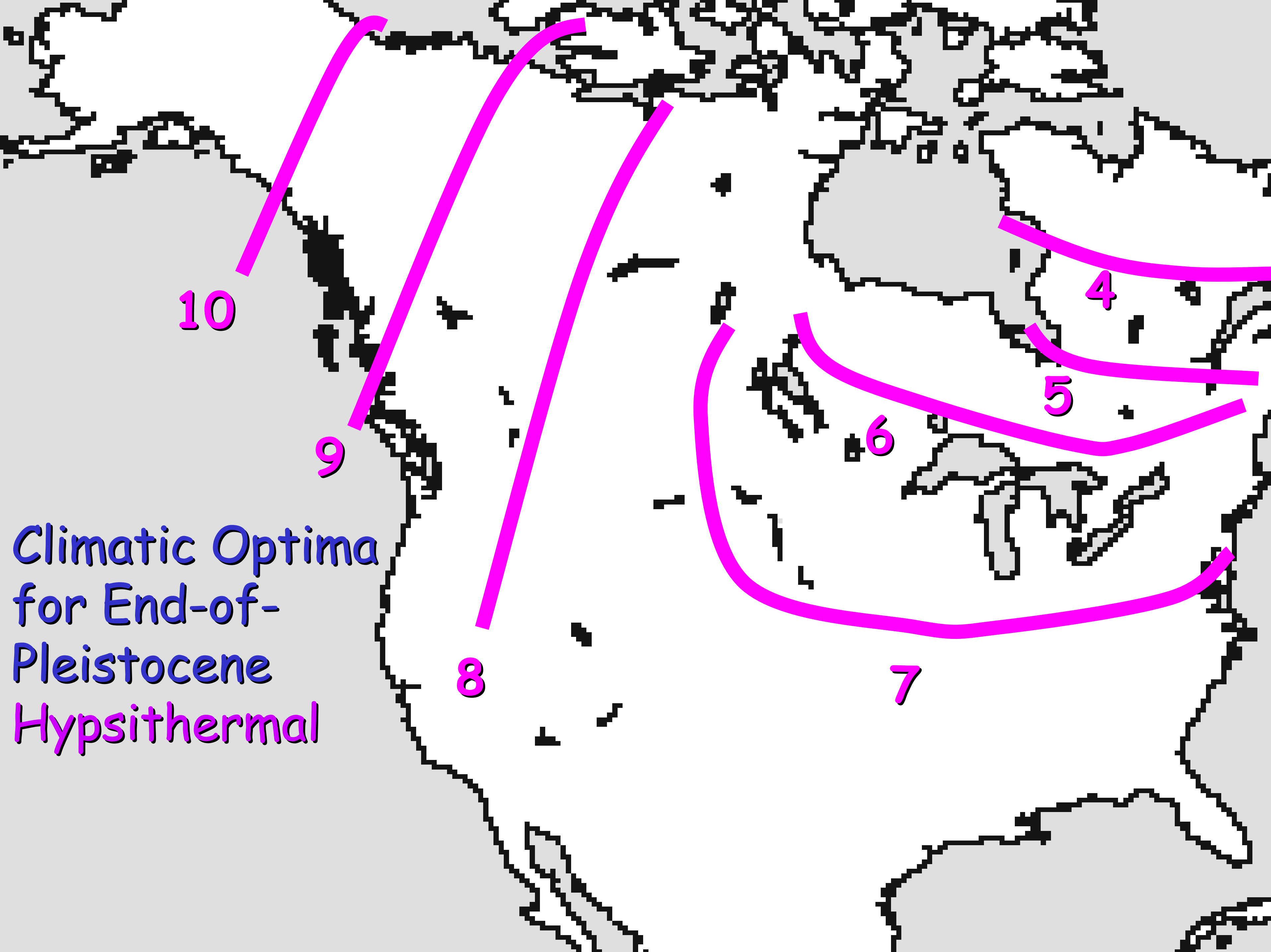
Results: mtDNA Analysis

- many haplotypes
  but low divergence among haplotypes
- historic population bottleneck
  thus low effective population size Ne
- population expansion since bottleneck
  re-colonization of upper basin

Table 2 + 4

mtDNA + Colorado River Fishes

- Douglas, Brunner, Douglas (2003)
  Freshwater Biology PDF available
- Drought in "recent" geologic time had
  severe impacts on Colorado River fishes



Climatic Optima for End-of-Pleistocene Hypsithermal

Historic Demography & Management

- Historic Population Bottleneck
  - Low effective population size Ne
  - Shorter evolutionary time scale
  - Different molecular approaches

Results: Msat Analysis - Diversity

- High allelic diversity within populations
- Moderate to high levels of heterozygosity
- Unique alleles for populations, basins, species

Table 7 + 8, Appendix 5 + 6

Results: Msat Analysis - Diversity

- Allele frequencies between populations show differences (Bonferroni correction)

…… but

  - sample size effects!

Table 9

Conclusion (1)

- Data support recognition of six MUs

(1) HBC_{GC} : Marble/Grand Cn

(2) HBC_{DES} + RTC_{DES} : Desolation Cn

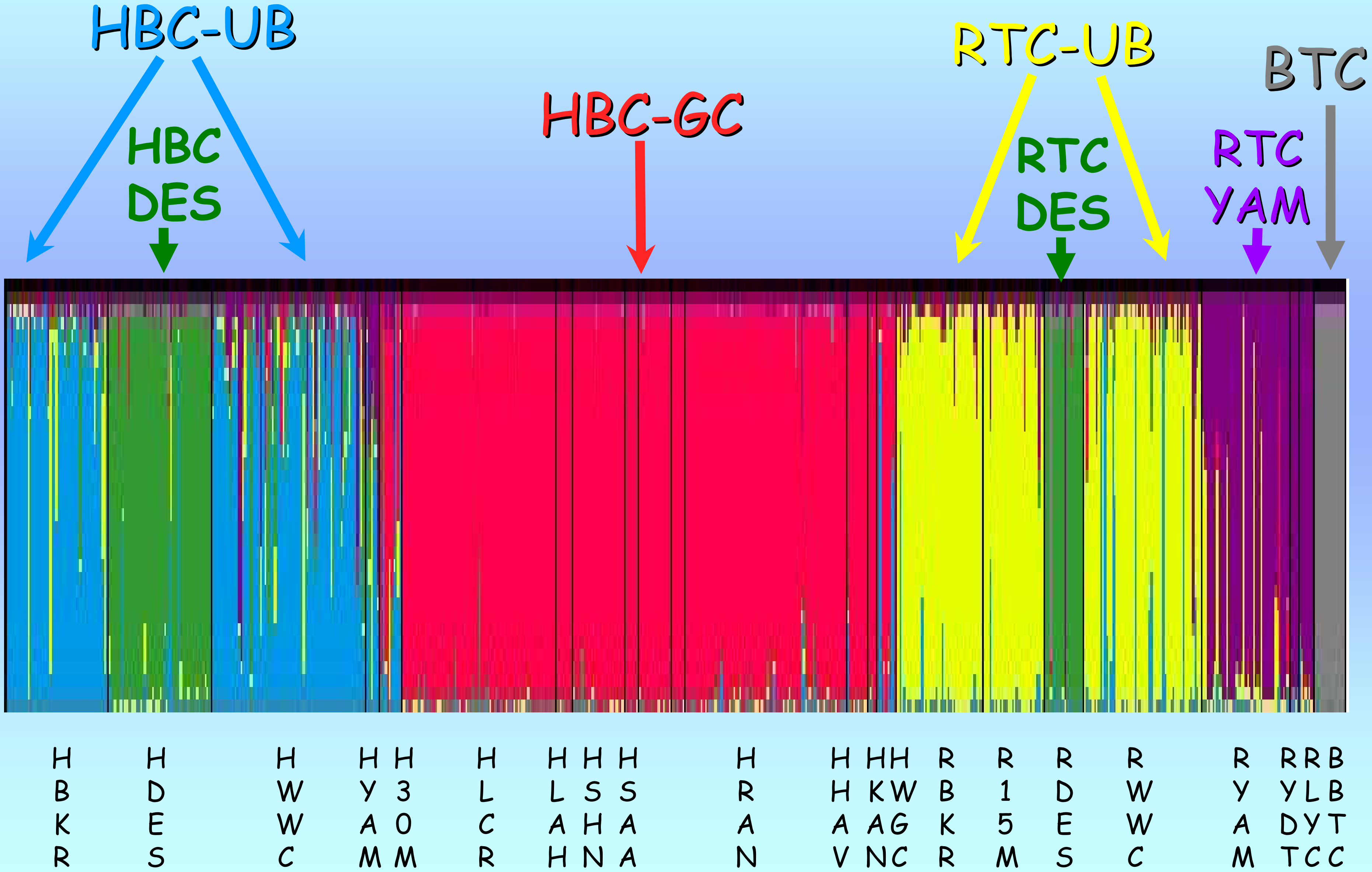
(3) HBC_{UB} : upper basin

(4) RTC_{UB} : upper basin (except Yampa R)

(5) RTC_{YR} : Yampa R

(6) BTC : Bonytail

msat - STRUCTURE: 6 Clusters



Gila cypha – Upper Basin

- Populations:
  - Yampa River
  - Desolation Cn
  - Black Rocks Cn
  - Westwater Cn
  - Cataract Cn

Table 9 = sig.
GP2,3,6,7

Table 9 = ns, GP1

no samples

Conclusion (2)

- HBC in Marble/Grand Cn genetically similar

  - aggregates connected by geneflow

    pairwise tests non-significant
    GP5 = genepool identified by TFPGA

    Table 9

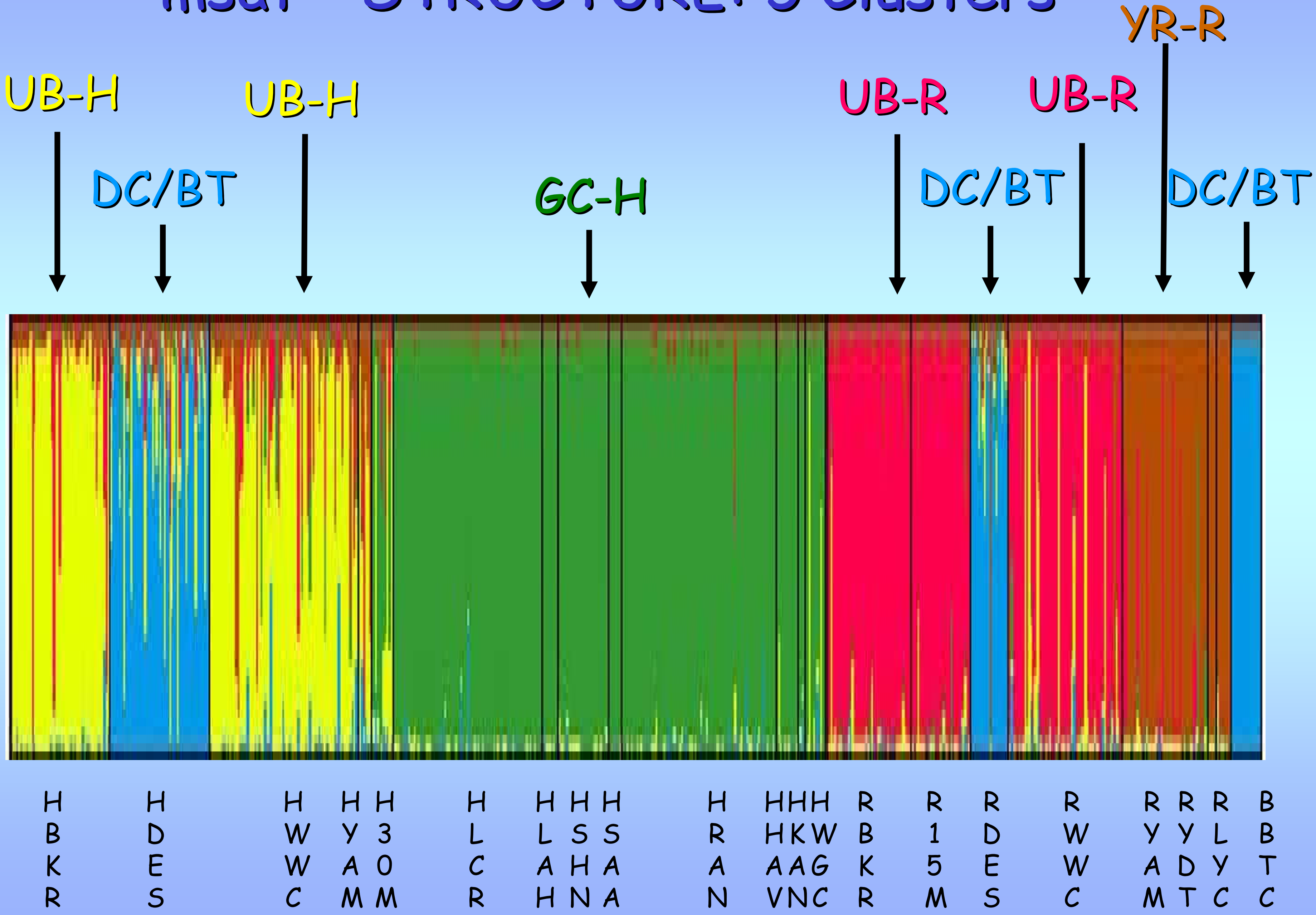
>> downstream drift of larvae + juveniles

>> LCR likely primary source

>> occasional local reproduction

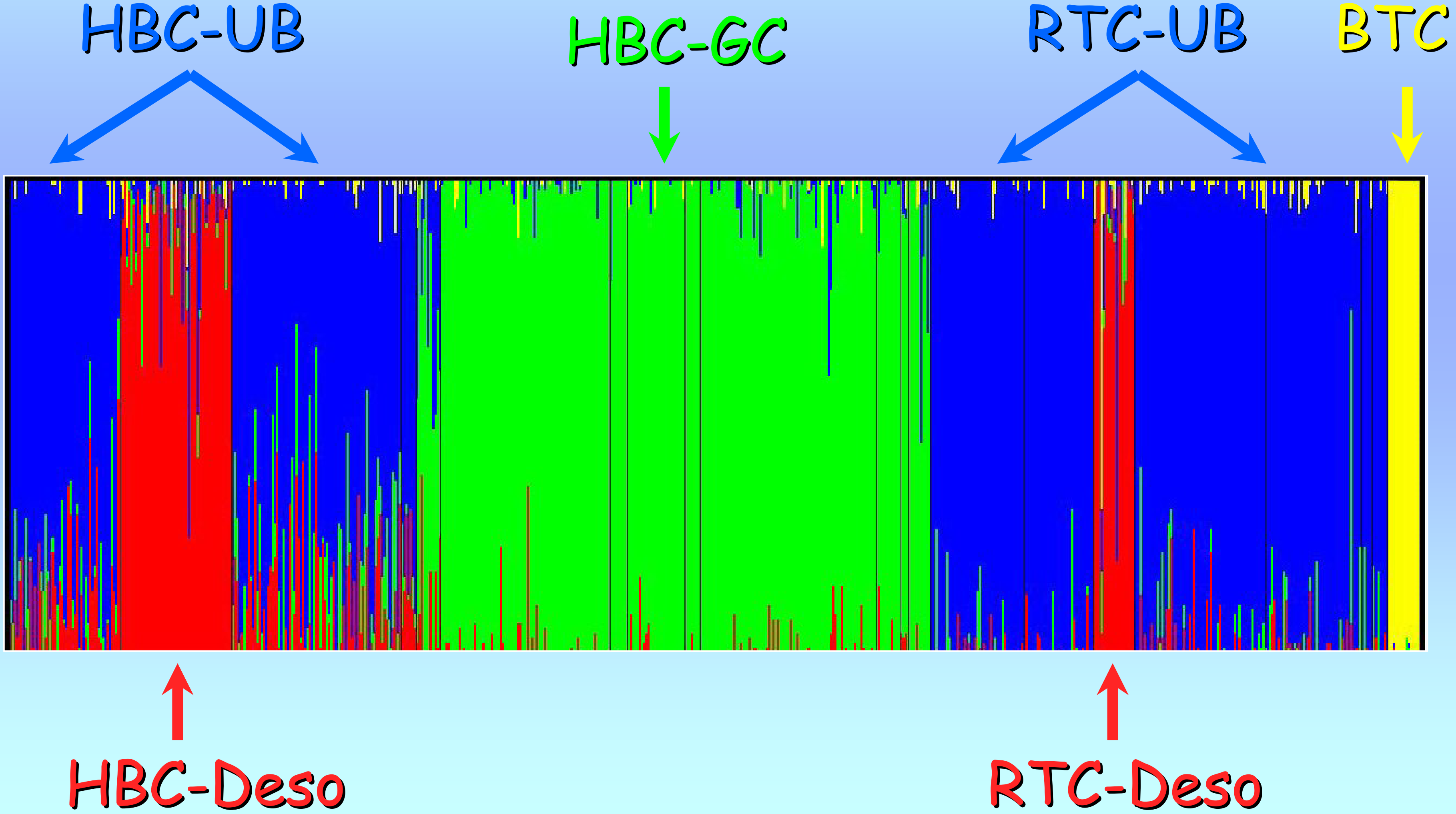
msat – STRUCTURE: 5 Clusters

F7



msat - Bayesian Assignment Test

Four-Group Clustering (Program BAPs)


HBC-UB

HBC-GC

RTC-UB

BTC

HBC-Deso

RTC-Deso

Conclusion (3)

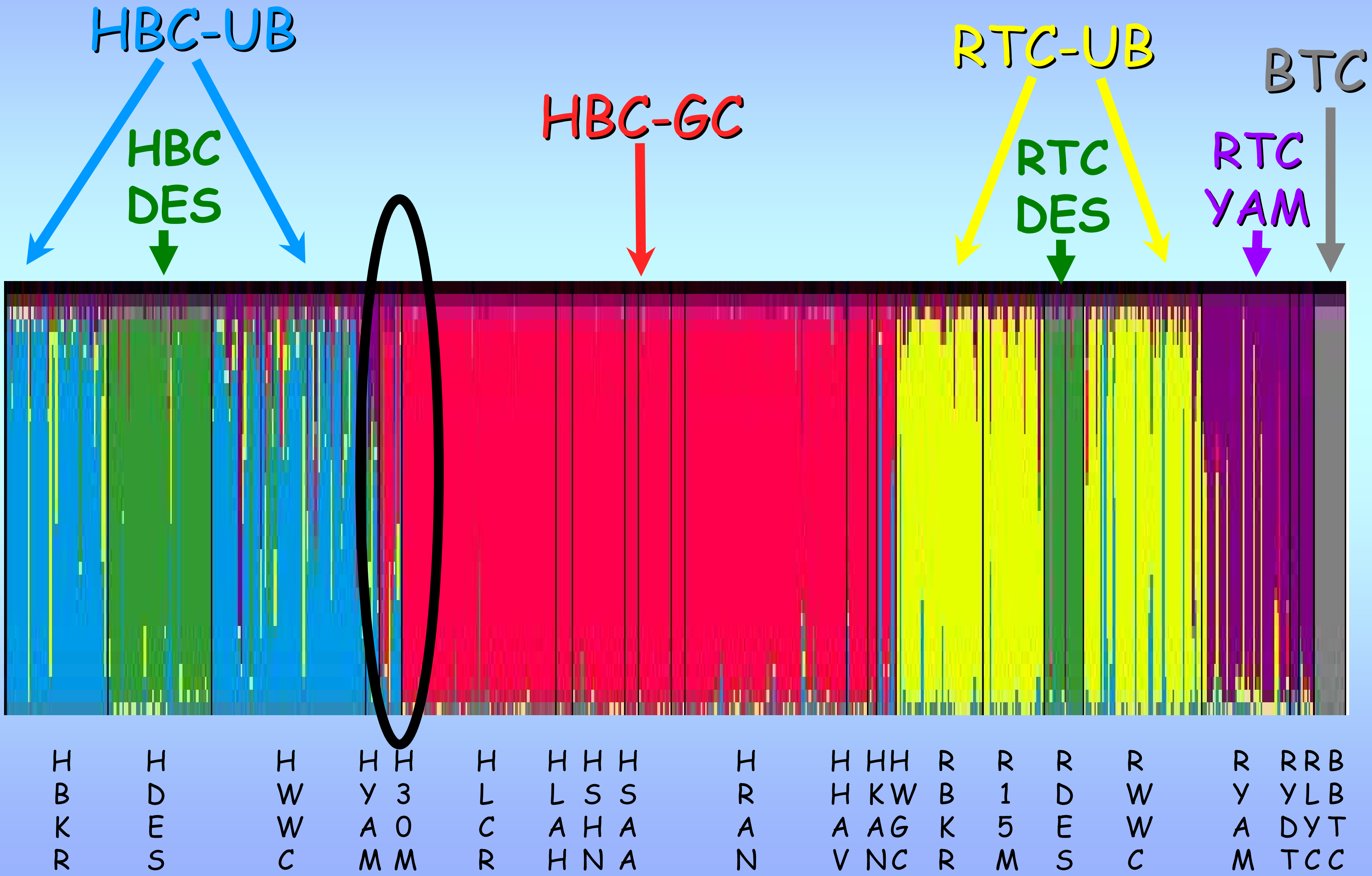
- 30-Mile population in Marble Cn
  - admixture with BTC (mtDNA) — Table 2
  - association with HBC_{UB} — Table 11, Fig 8
  - distinct genepool — Table 9 = GP4

>> occasional local reproduction — Valdez & Masslich 1999

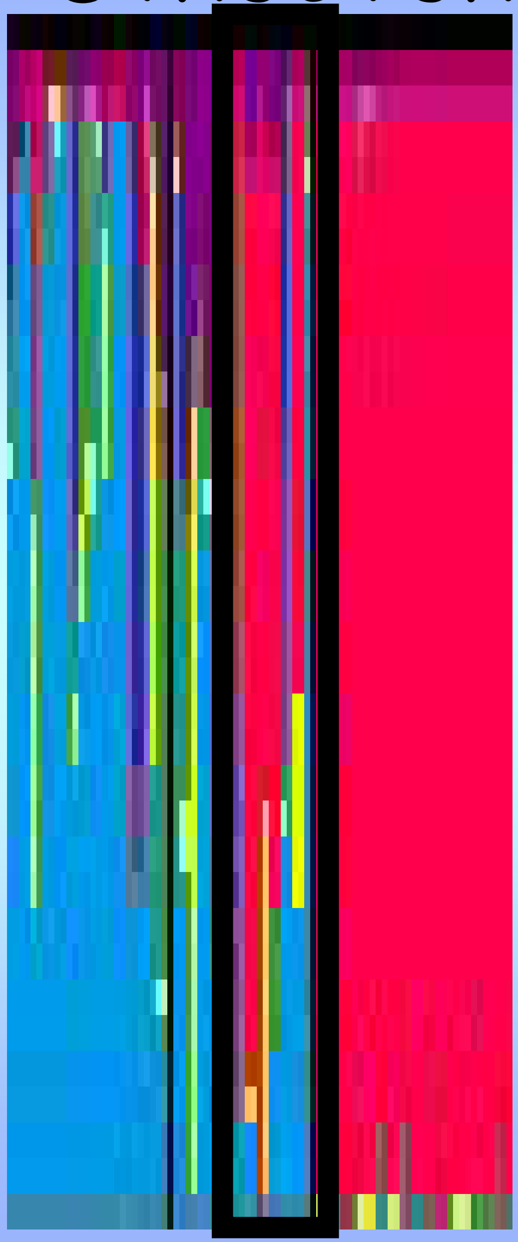
BUT – small sample size, low pop. number

msat - STRUCTURE: 6 Clusters

Fig 8



msat – STRUCTURE: 6 Clusters



HBC – 30-Mile

DES
RTC_{UB}
RTC_{YR}

HBC-UB

HBC-GC

Conclusion (4)

- Upper Basin HBC / RTC

  - RTC in Yampa River forms distinct cluster

Table 11, Fig 7+8

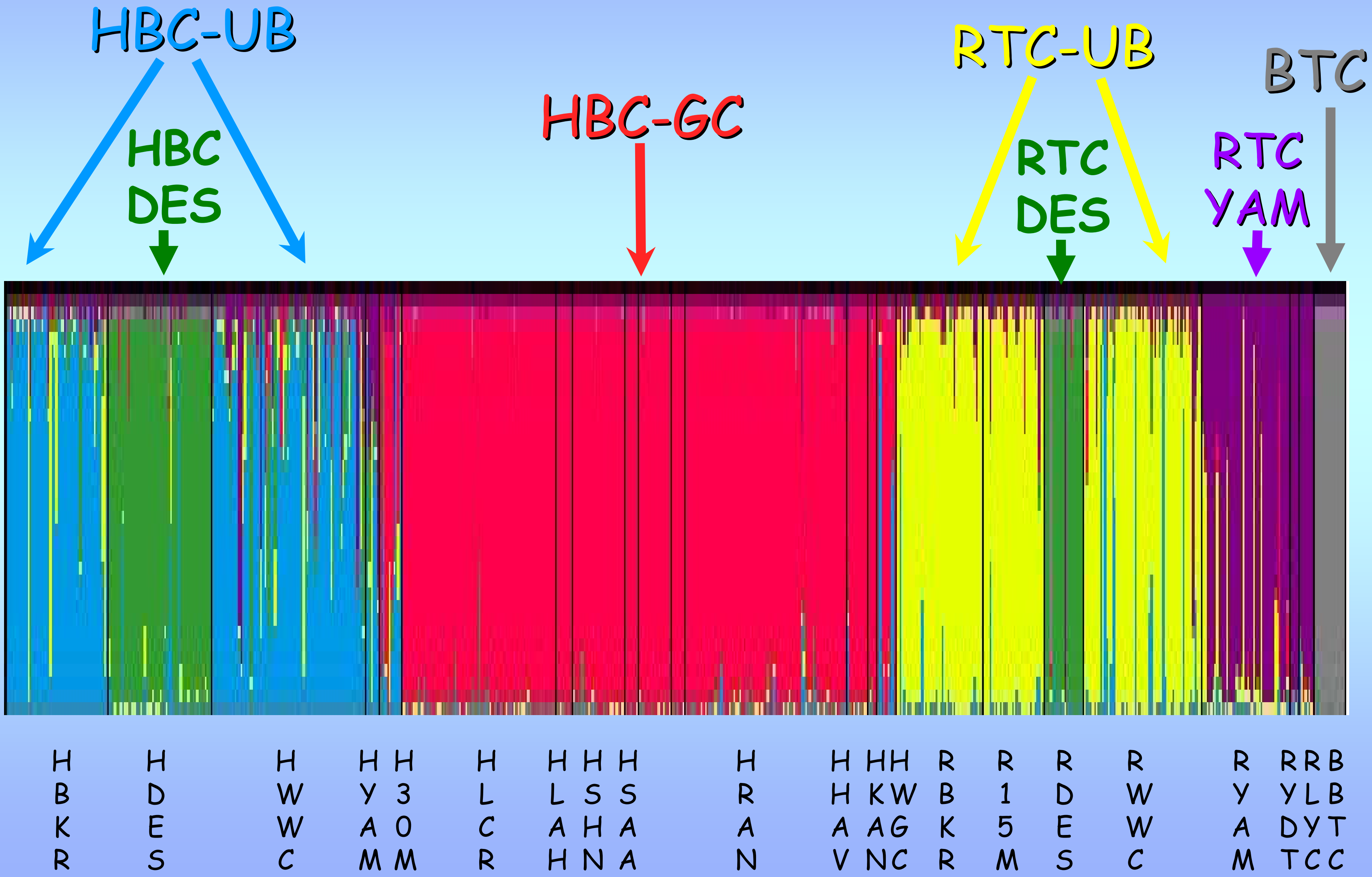
>> different from other Upper Basin RTC

Table 9 = GP7

BUT – small sample size for HBC Yampa R

msat - STRUCTURE: 6 Clusters

Fig 8



Conclusion (5)

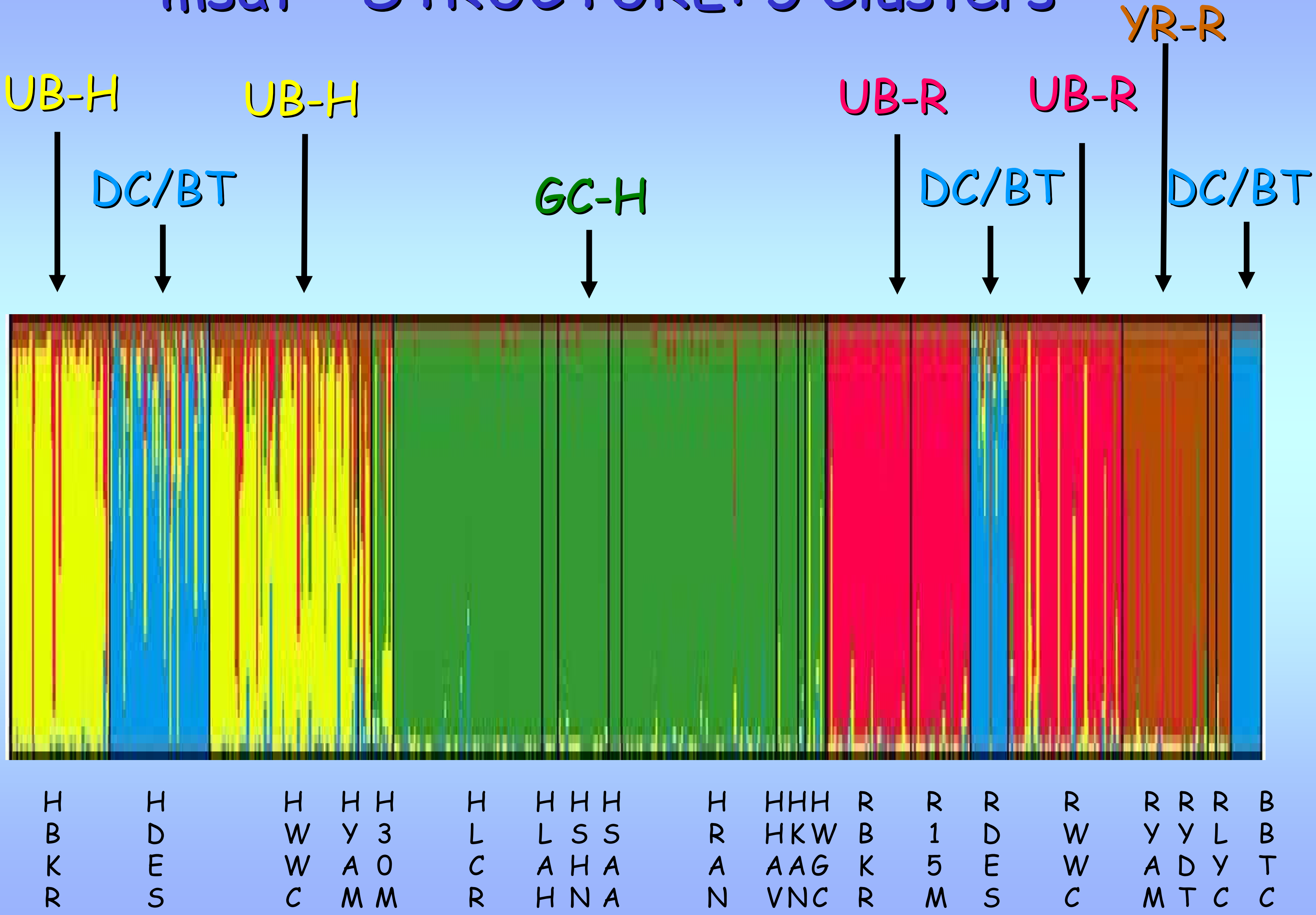
- Bonytail
  - admixture with HBC

>> historic signal of introgression

>> stronger signal Desolation Canyon

BAPs - Fig 5

msat - STRUCTURE: 5 Clusters

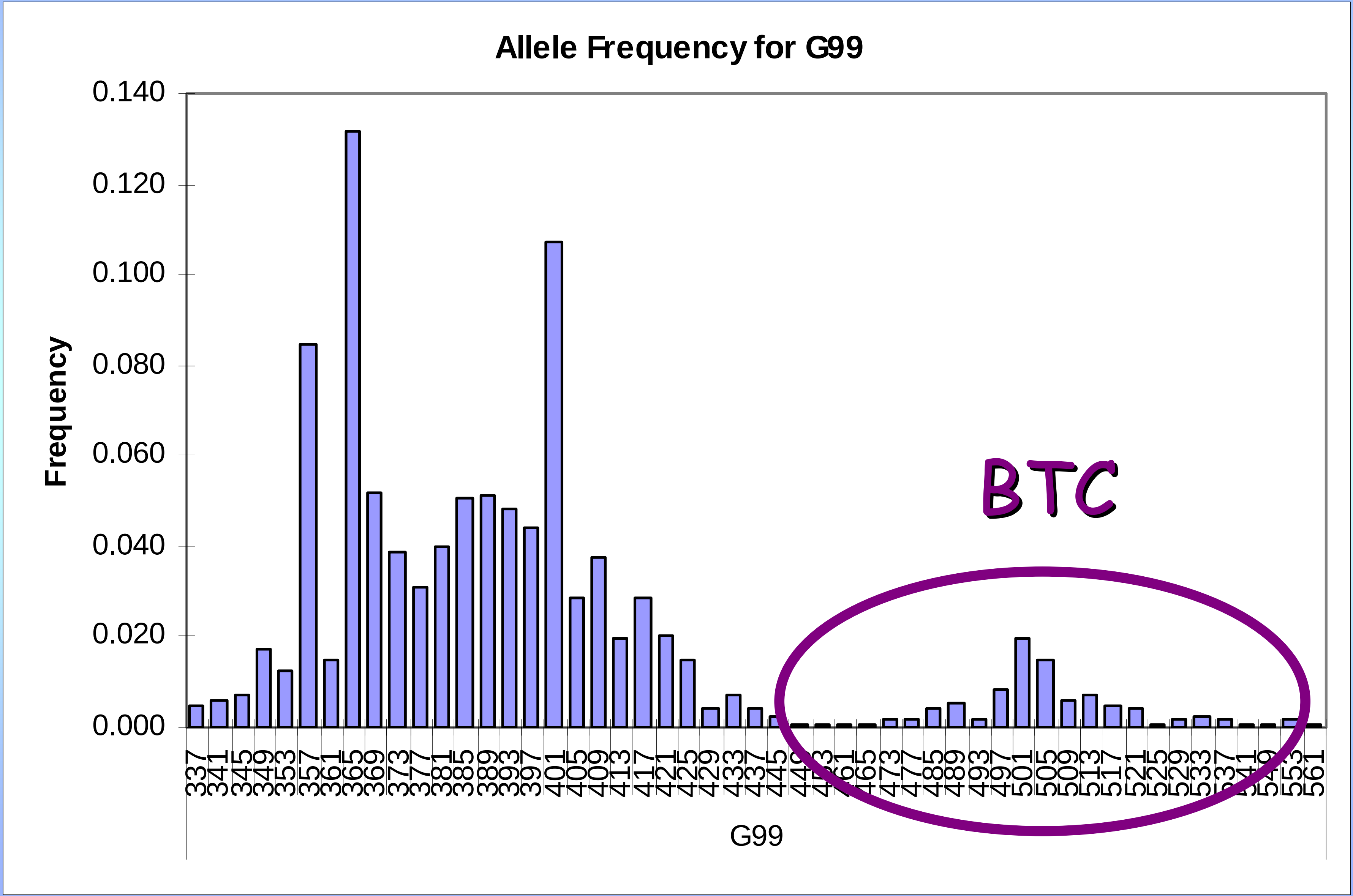


Msat Analysis - Admixture

- **Bonytail**
  - characteristic allele size ranges

some BTC in HBC
some HBC/RTC in BTC

Conclusion (5)



Compendium

- mtDNA reflects evolutionary history
  - admixture HBC / RTC
- msat also reflect morphology
  - distinct morphs
  - locality effect

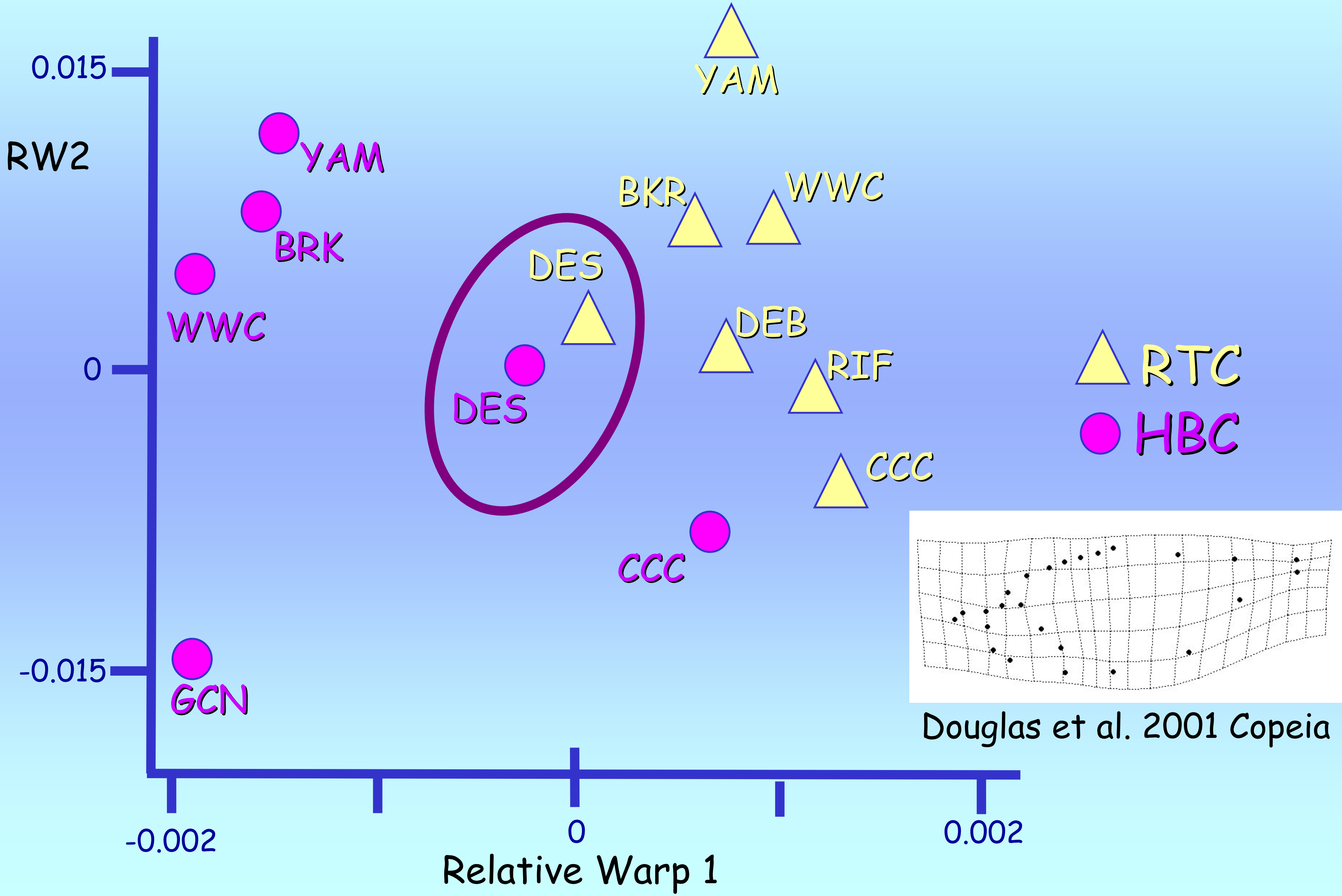
Species <u>still</u> described morphologically

Morphology & *Gila*

- Morphometric Characters (museum specimen)
  - Discriminant Function Analysis
  - Adults: 95% allocated to species
  - Juveniles: 97% allocated to RTC or HBC/BTC

Douglas et al. 1998 TAFS

Shape Variation: Relative Warp Analysis



Douglas et al. 2001 Copeia

Thank You!