Genetic monitoring of razorback sucker in the Lower Colorado River: Status report

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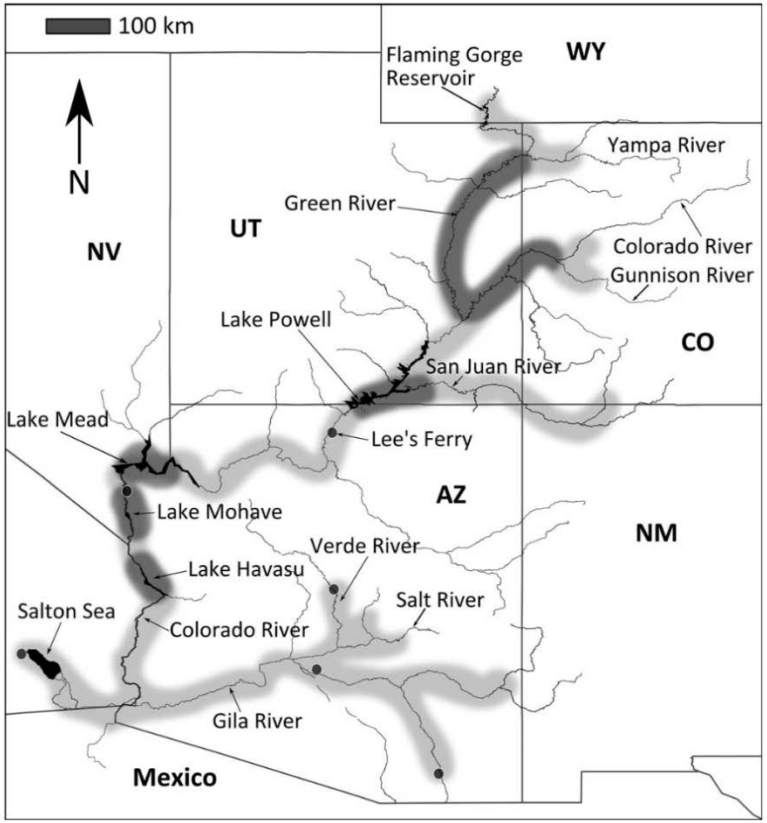
Funded by:

Razorback sucker (RASU)

- Endemic to Colorado River system
  - Formerly very abundant in main channels throughout the drainage
- Focus here on:
  - Lake Mohave
  - Reach 3 (Lake Havasu)
  - Lake Mead

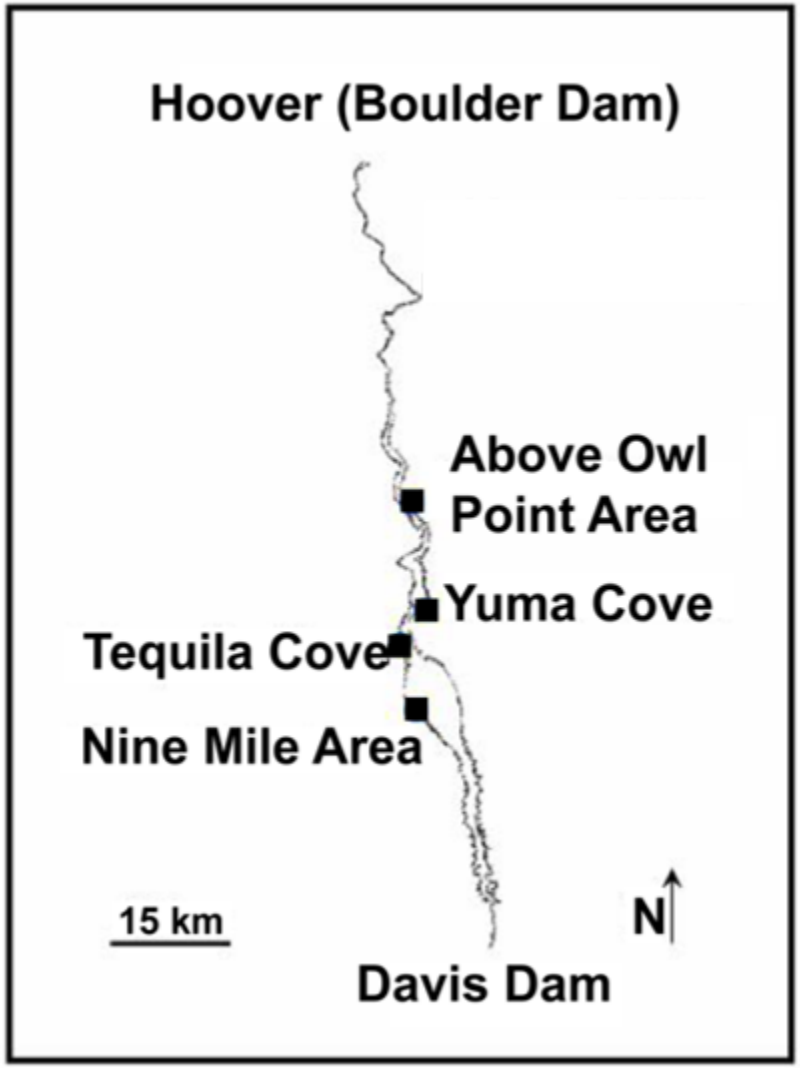


Marsh et al. 2015, *Copeia*

Objective

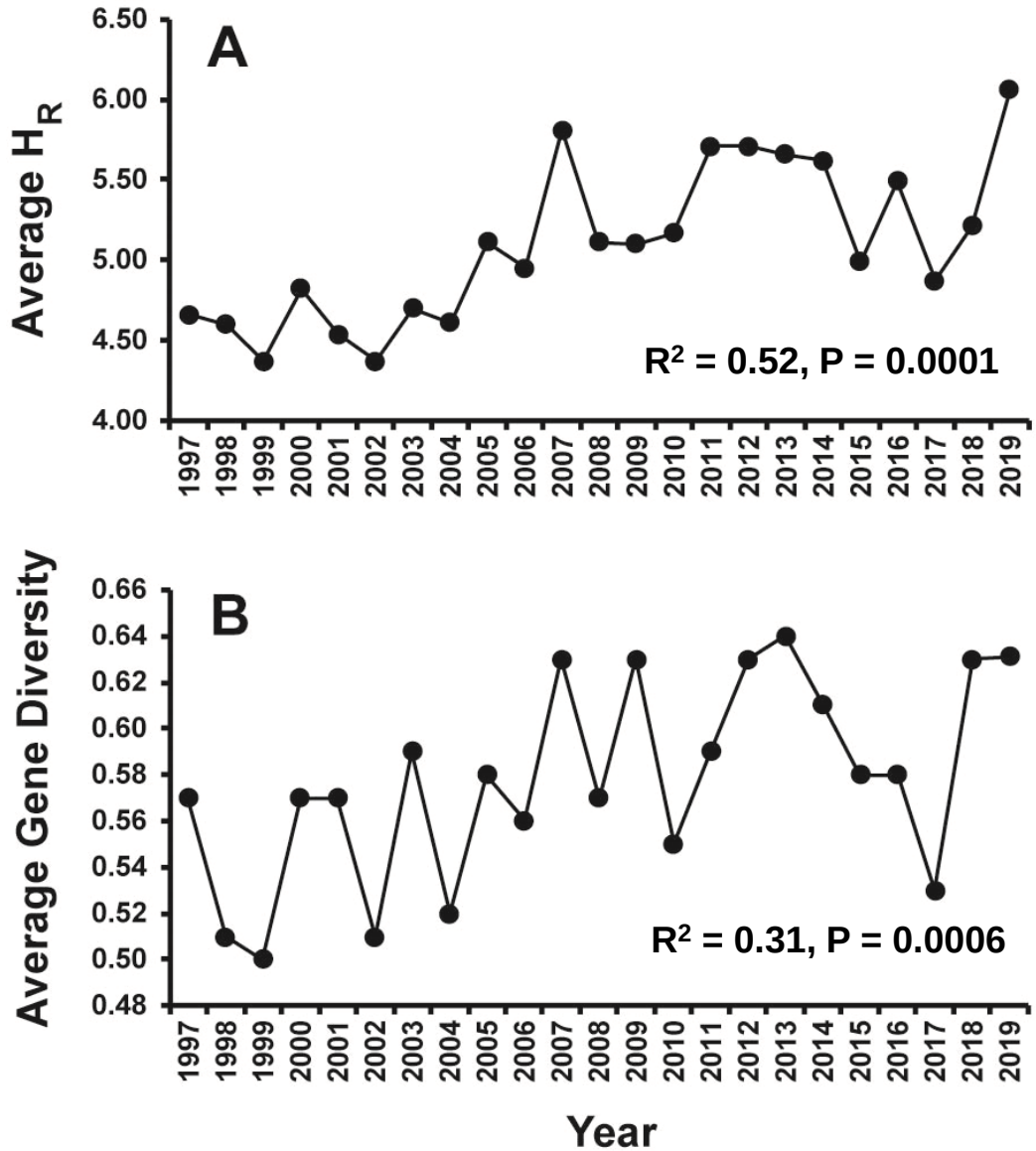
- Use molecular markers (microsatellites, mtDNA) to monitor levels of genetic diversity
- Monitoring has been ongoing from 1997 – 2019
- Summary of results

Lake Mohave - regions sampled

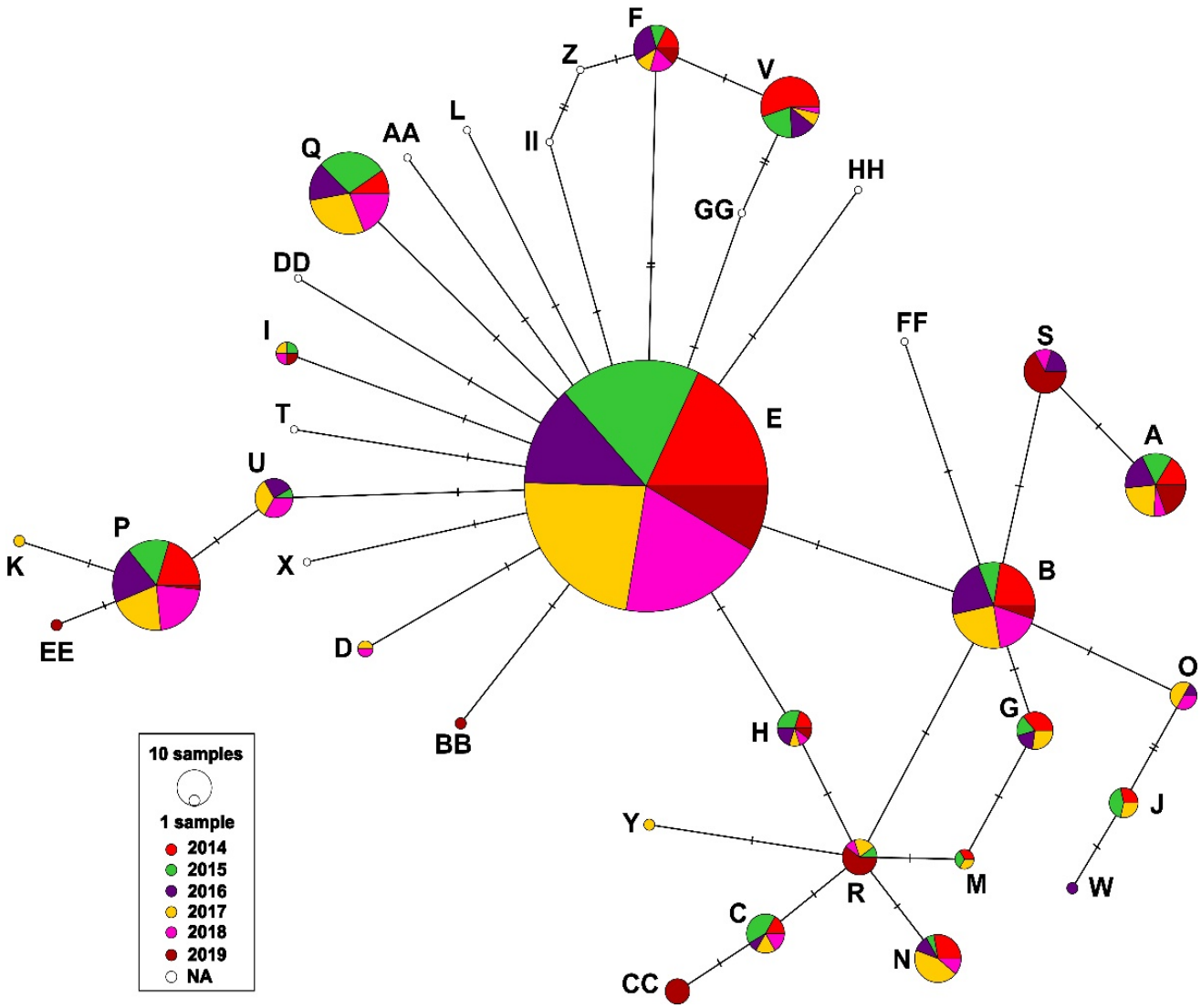


Lake Mohave

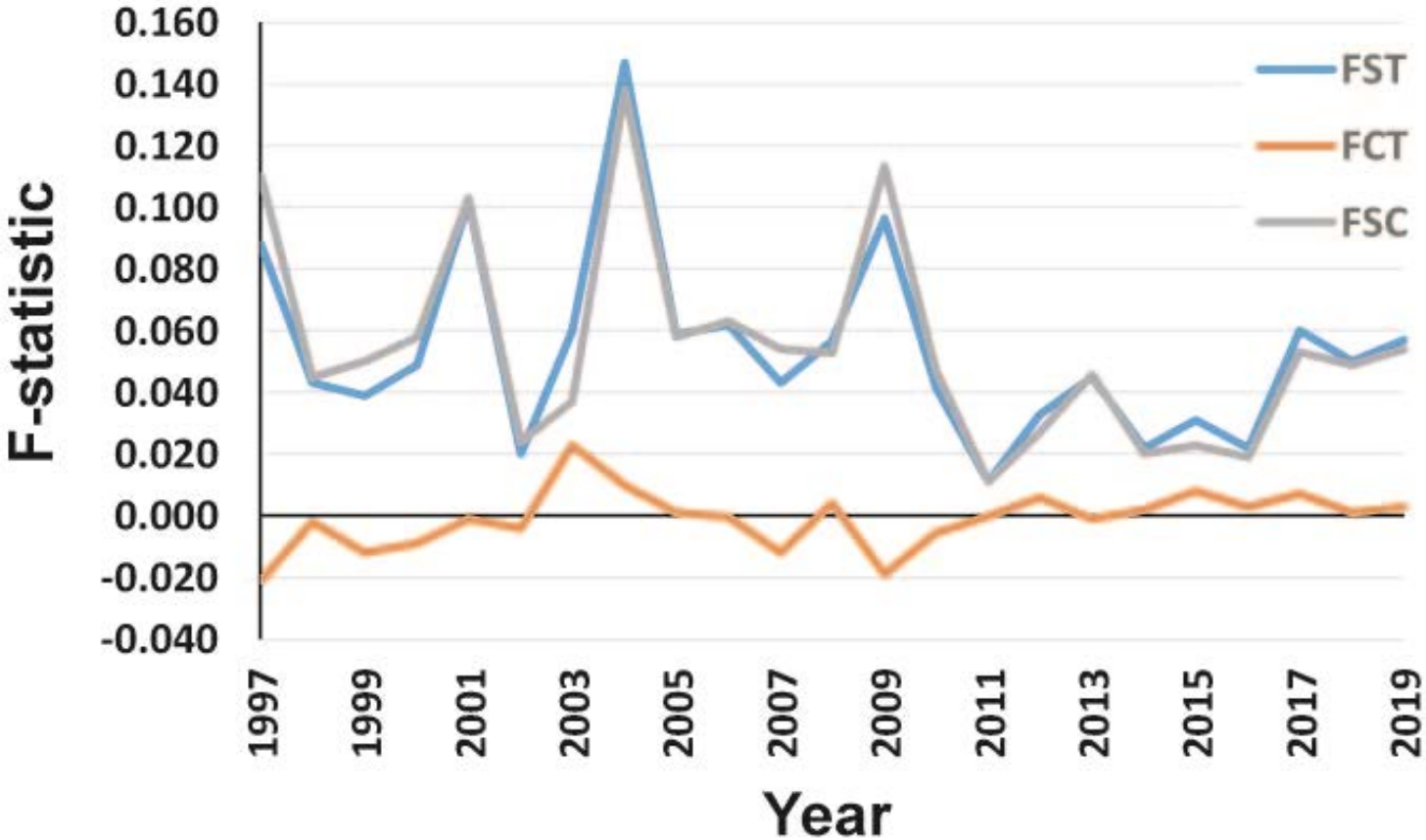
- 23 years worth of data (1997 – 2019)
- Genetic diversity has been maintained (or increased) by using wild-caught larvae



Haplotypes 2014 -2019



Distribution of mtDNA variation within and among regions



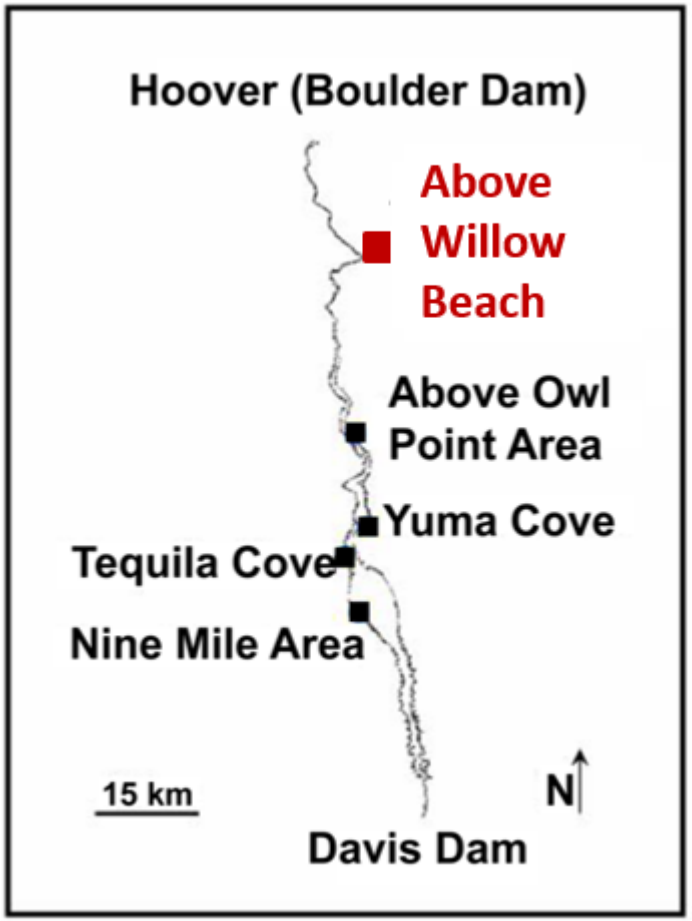
F_{ST} = total contribution differences among samples

F_{CT} = differences among four regions

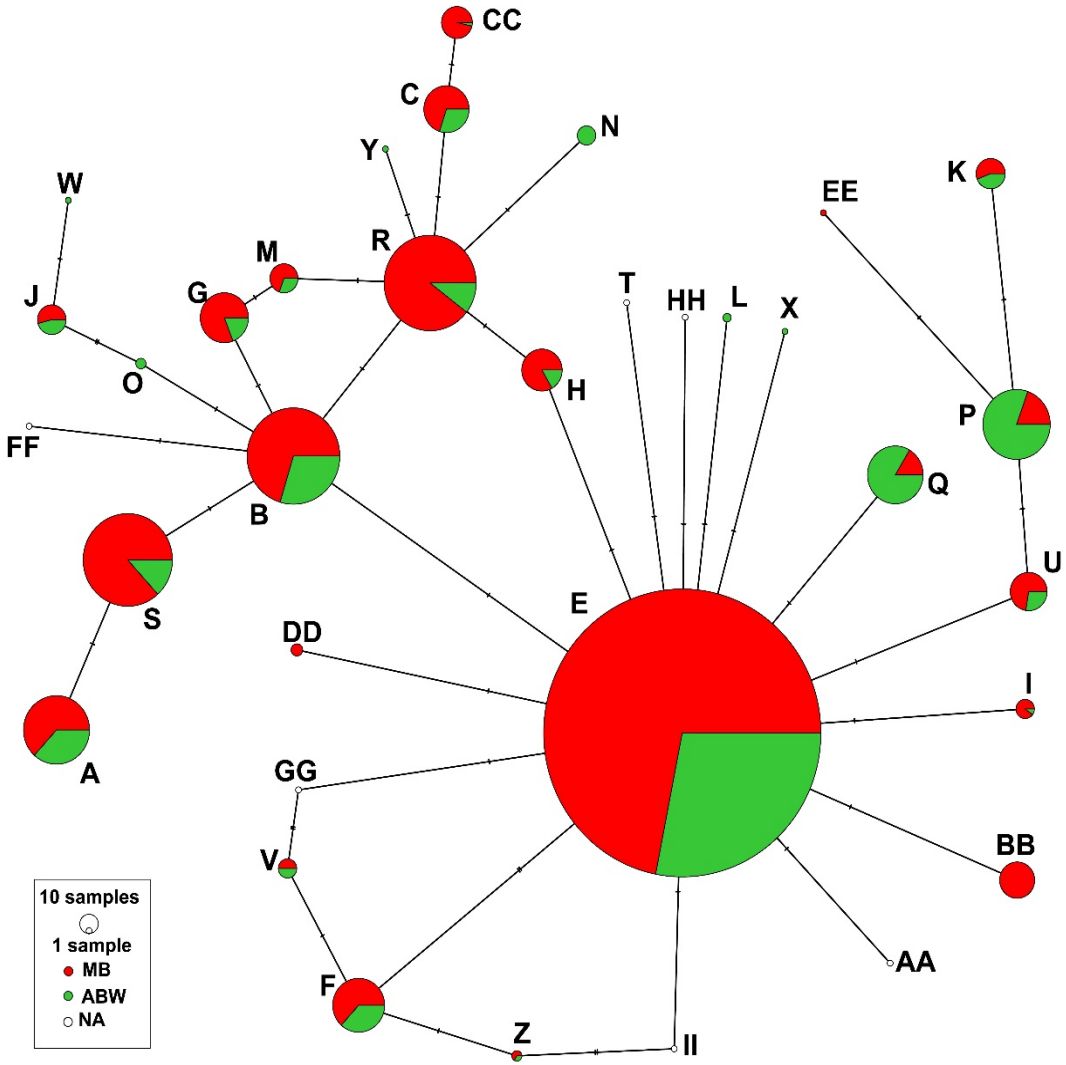
F_{SC} = among samples within regions

Include region above Willow Beach (since ca. 2014)

Jeff Lantow, Layne Huber, and the MSCP staff

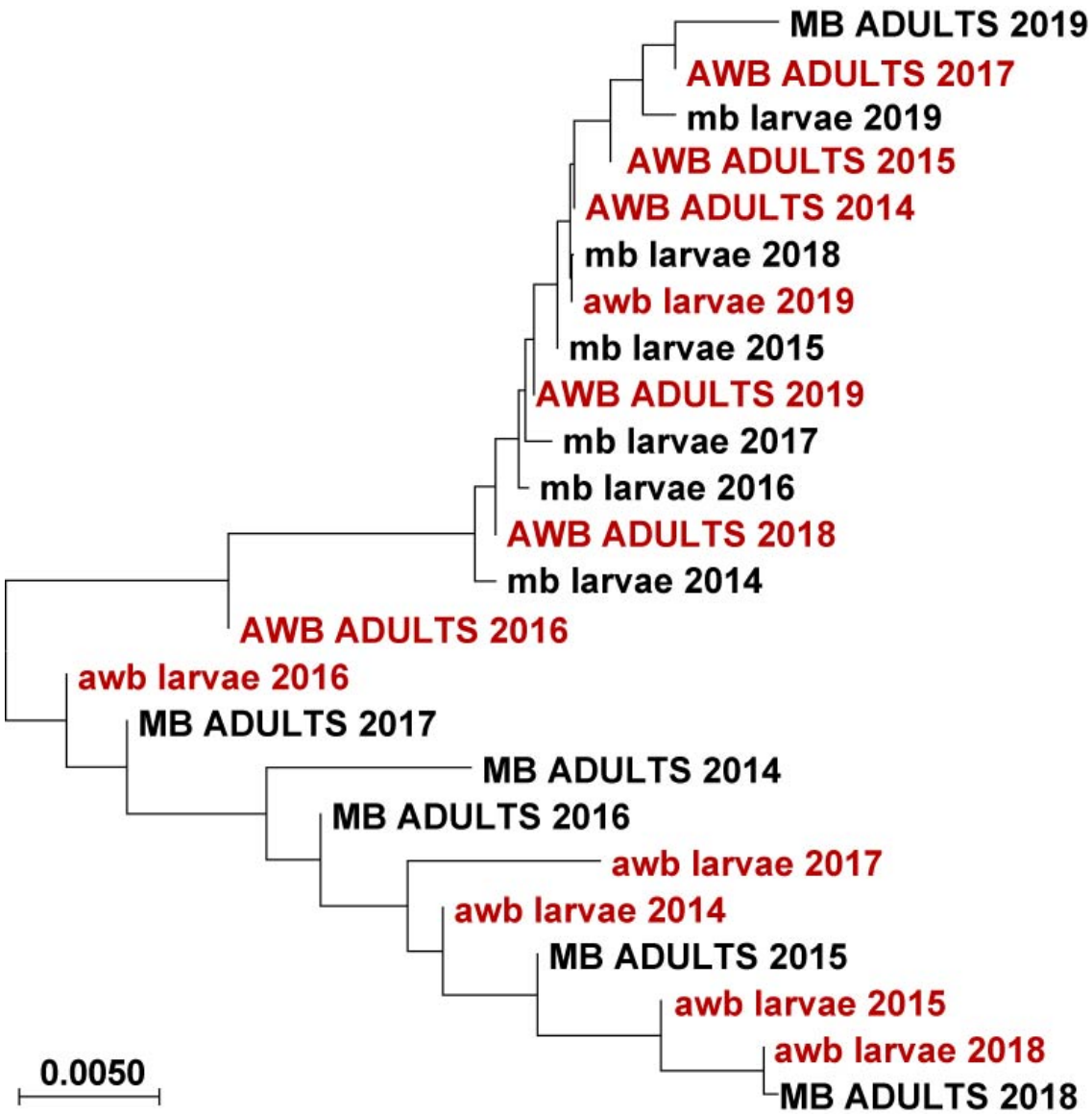


Similar to main basin of L Mohave



- 2014-2019 larval samples
- Proportional to sample sizes
  - MB = 2756
  - AWB = 1136
- Some differences for moderate alleles
  - P and Q

AWB similar to main basin of L Mohave

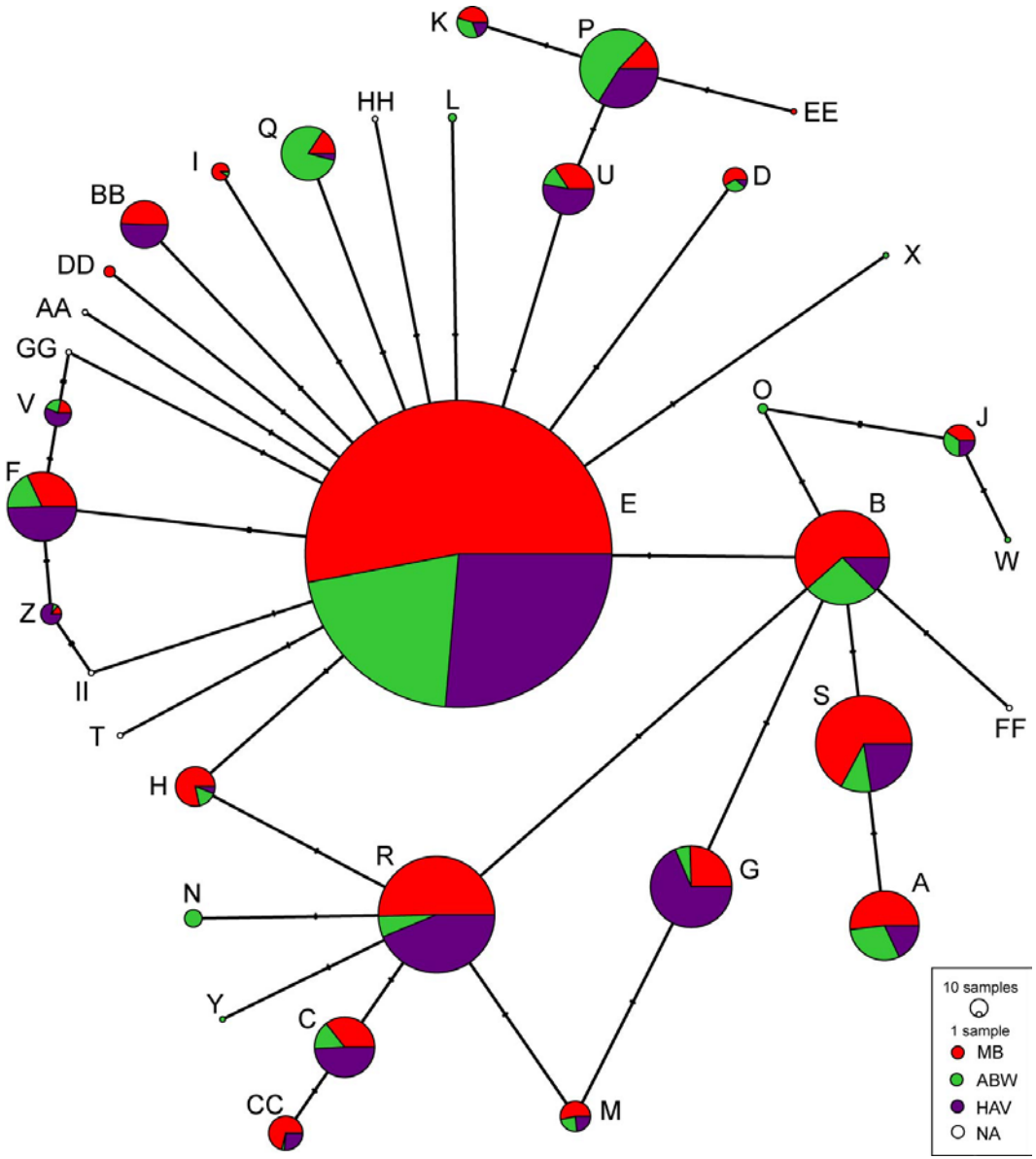


Conclusions: Lake Mohave

- All measures of genetic variation consistent among samples of larvae, repatriates, and source wild fish
- Levels of mtDNA variation increased and appear to be stable
- Samples from above Willow Beach similar to main basin and have increased estimated population size

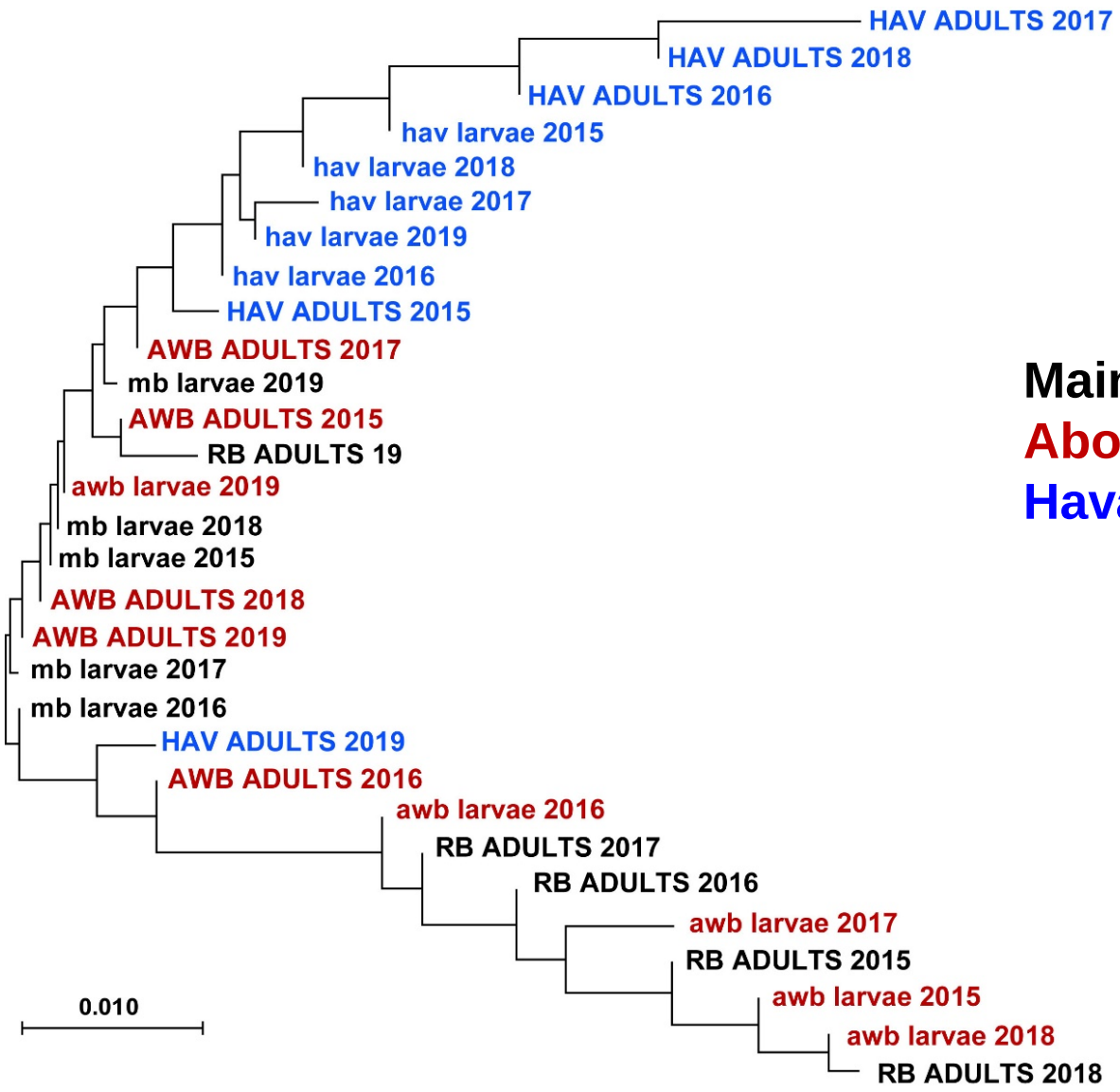
Lake Havasu region (Reach 3)

- Mixed stock
- HAV also diverse
  - Similar # of haplotypes to Lake Mohave
  - Different frequencies of haplotypes



Sample Sizes
MB = 2756
AWB = 1136
HAV = 1630

Clustering of all samples



Main basin Mohave
Above Willow Beach
Havasu

Conclusions – Reach 3

- Samples from Reach 3 show similar levels of genetic variation to Lake Mohave
- Larval and adult samples from Reach 3 genetically distinct from those found in Lake Mohave
- Likely reflects different sources of this population
  - Early stockings from the hatchery
  - Recently augmented with fish from Lake Mohave or backwaters

Lake Mead

- RASU thought to be extirpated in the 1970s
- Re-appeared in late 1980s to early 1990s
  - Unlike other locations subadults have been found
- Bottleneck
  - Significantly less genetic diversity than Lake Mohave

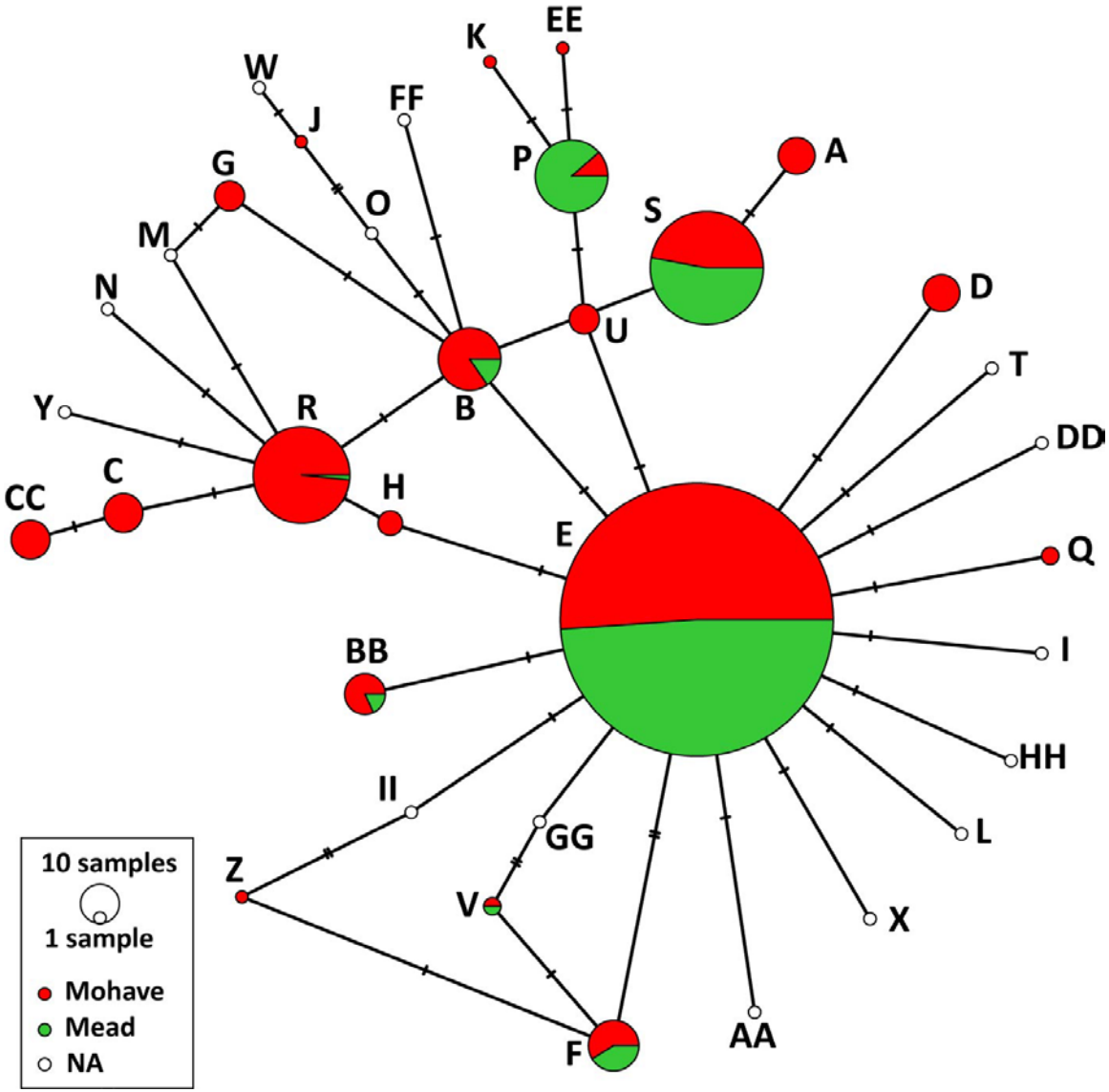
	mtDNA		
Location	**N**	**N_h**	**diversity**
Lake Mead			
Adults			
1988	16	**2***	**0.13 +/- 0.11***
2002	29	5	0.66 +/- 0.07
2011	15	**2***	**0.25 +/- 0.13***
2012	61	**3***	0.51 +/- 0.04
2013	51	**4***	0.55 +/- 0.04
2014	61	**4***	**0.46 +/- 0.06***
2015	24	5	0.63 +/- 0.07
2016	60	**5***	0.50 +/- 0.06
2017	39	**3***	0.47 +/- 0.06
2018	50	**5***	**0.35 +/- 0.08***
2019	40	**6***	0.63 +/- 0.07
Larvae			
1997	25	**3***	0.61 +/- 0.06
2002	57	**6***	0.76 +/- 0.03
2012	50	**2***	**0.15 +/- 0.06***
2013	78	**5***	0.53 +/- 0.04
2014	47	**3***	0.44 +/- 0.06
2015	77	**4***	**0.47 +/- 0.06***
2016	81	**4***	**0.50 +/- 0.04***
2017	85	**4***	0.54 +/- 0.05
2018	309	**4***	0.54 +/- 0.03
2019	333	**8***	**0.45 +/- 0.03***
Lake Mohave			
Adults - 2000	49	11	0.64 +/- 0.08
Larvae - 2011	120	14	0.60 +/- 0.05

* statistically significant ($P < 0.05$) by resampling

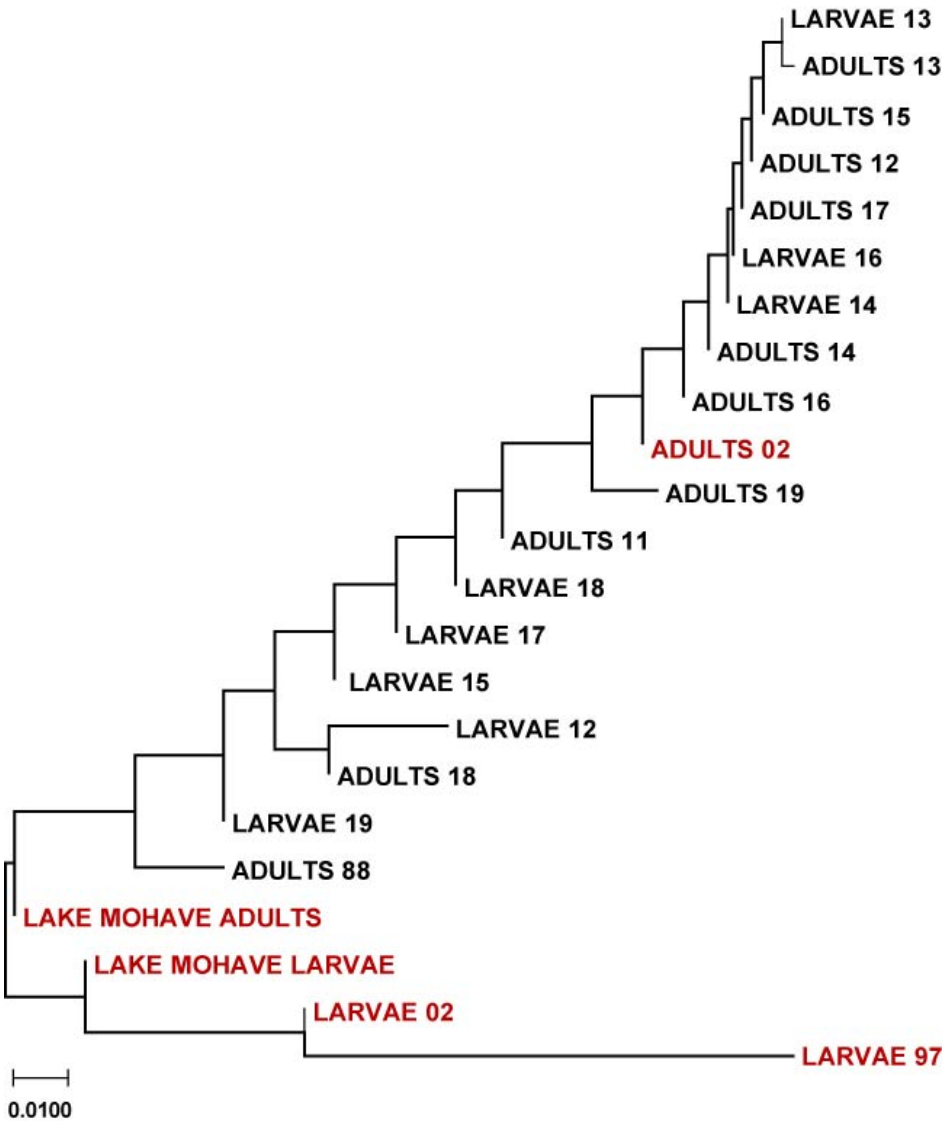
Distribution of haplotypes - 2019

- Fewer haplotypes than Lake Mohave
- Different frequencies of haplotypes
  - P and S

Sample Sizes
Mohave = 460
Mead = 333



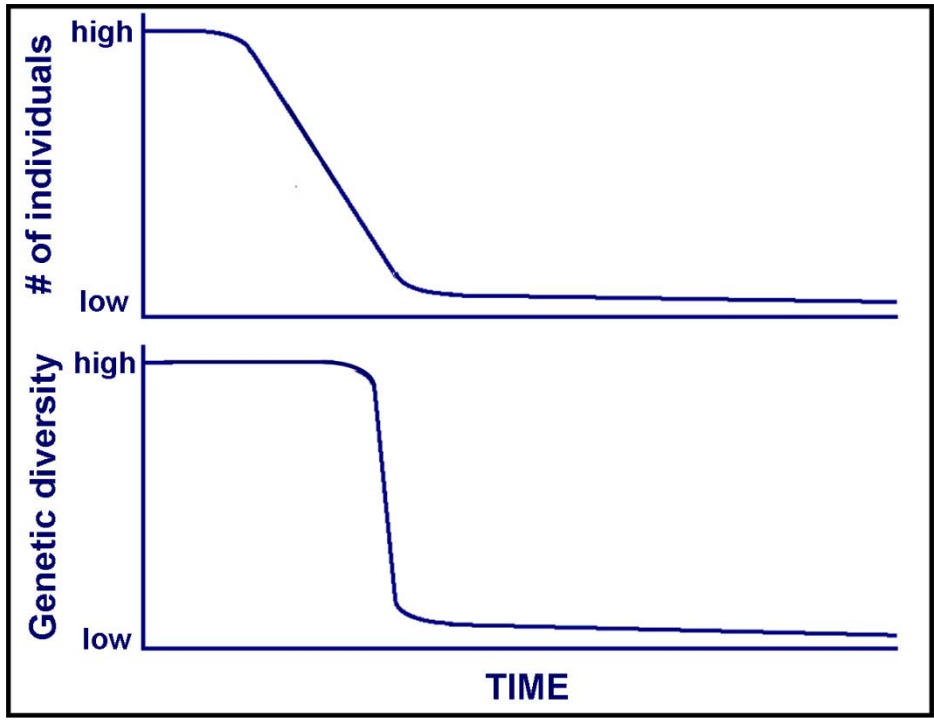
Variation among annual samples



Lake Mohave Pre-2010

Post-2010

Conclusions

Lake Mead (Reach 1)

- RASU in Lake Mead have diverged from Lake Mohave
  - Impact of drift due to small population size?
  - We have seen most flannelmouth-razorback sucker hybrids at the Colorado River inflow, increased influx from Grand Canyon?
  - Other geographic effects?