Impact of repatriation on genetic variation in the Lake Mohave population of razorback sucker

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Objective

Use molecular markers (microsatellites, mtDNA) to monitor impact of management on genetic diversity



Sampling

- 15 years worth of data!!!
- Larvae (1997-2011)
 - 259 collections, 6347 individuals
- Adults
 - 303 wild fish
 - 922 repatriates (stocked 1992 2011)





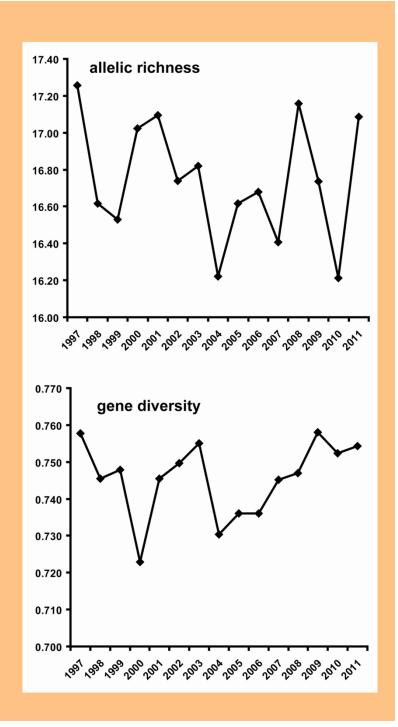
Statistics

- Allelic Richness: The number of alleles per locus corrected for sample size
- Gene Diversity: A measure of genetic variation in a population (expected frequency of heterozygous individuals)

Microsatellite DNA variation within larval samples over time

- Nuclear DNA variation is being maintained by this sampling strategy
- Allelic richness
 - r = 0.007, P = 0.914
- Gene diversity

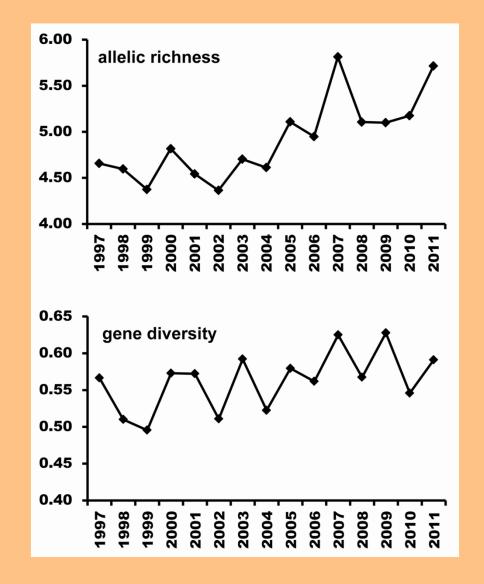
- r = 0.007, P = 0.918



mtDNA variation within larval samples over time

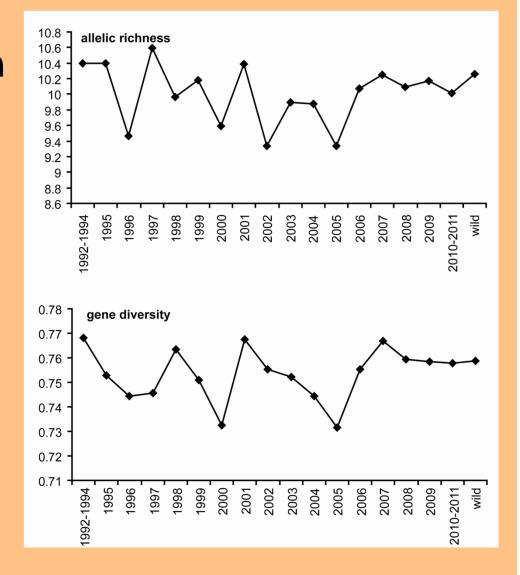
- mtDNA variation is actually being increased by this sampling strategy!
- Allelic richness
 - r = 0.212, P = 0.001
- Gene diversity

- r = 0.119, P = 0.064



Microsatellite variation within repatriate samples over time

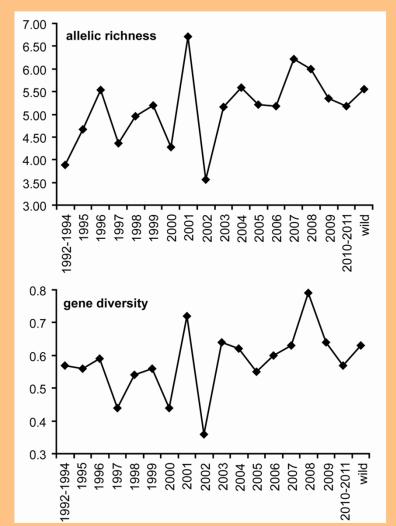
- Nuclear DNA variation is being maintained by this sampling strategy
- Allelic richness
 - r = 0.005, P = 0.935
- Gene diversity
 r = 0.005, P = 0.938



mtDNA variation within repatriate samples over time

- mtDNA variation is actually being increased by this sampling strategy!
- Allelic richness
 - r = 0.449, P = 0.071
- Gene diversity

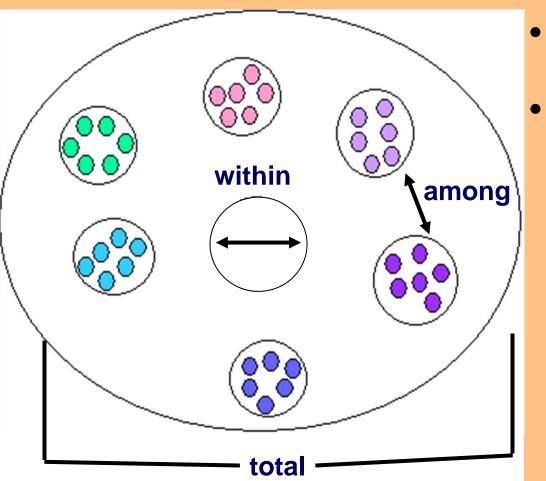
- r = 0.397, P = 0.124



Transmission of variation from larvae to repatriates?

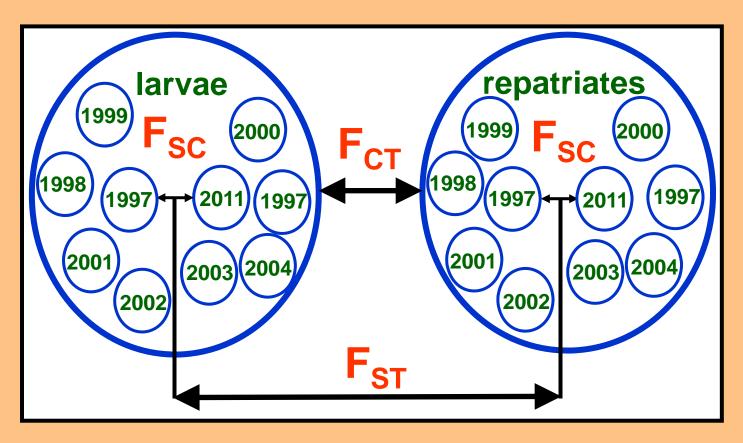
- Look for differences in allele frequencies among life history stages
- Use F-statistics

F-statistics



- Subpopulations (S) are made up of individuals (I)
- Can examine several components affecting random mating
 - between individuals within subpopulations (IS)
 - among individuals relative to the total population (IT)
 - among subpopulations (ST)

Partitioning among sample variation (F_{ST})



F_{ST} = divergence among all life stages
 F_{SC} = divergence among temporal samples within life stages
 F_{CT} = divergence among regions corrected for temporal variation within life stages

Distribution of mtDNA variation among larvae, adults, and repatriates

SOURCE

Among groups	F _{ST} = 0.003
Among samples within groups	$F_{SC} = 0.004$
Among larvae, repatriates, and adults	F _{CT} = -0.001

No differences among larvae, repatriates, and adults!

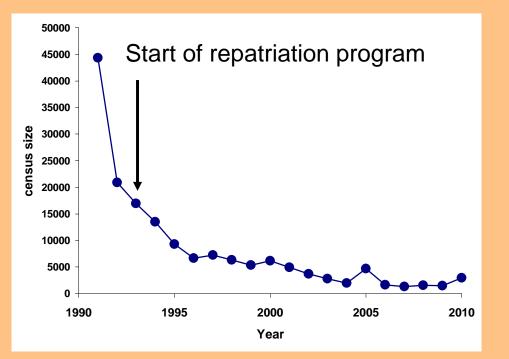
Conclusions

- All measures of genetic variation consistent among samples of larvae and repatriates
- Variation is being transmitted from larvae to repatriates
- Increasing levels of genetic variation over time



Still have a problem!!!

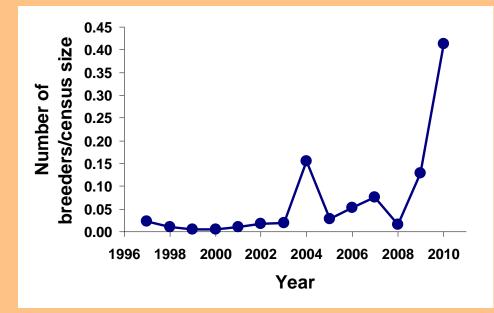
Despite all of our efforts, population size continues to decline



At this point, more than 155,500 young fish have been repatriated, with estimated annual survivorship of ca. 1%

Still have a problem!!!

Genetic variation is increasing because a higher proportion of the population is contributing



- Problem ability to maintain genetic variation is constrained by population size
- This will lead to a loss of variation, resulting in decreased adaptability and potential issues with inbreeding

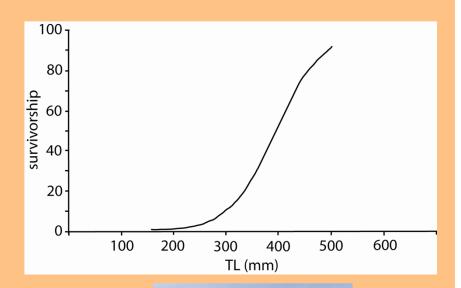
Still have a problem!!!

Size matters

Difficult to grow up fish to >400 mm in a timely manner

Even so, striped bass are large enough to eat even the largest razorback suckers

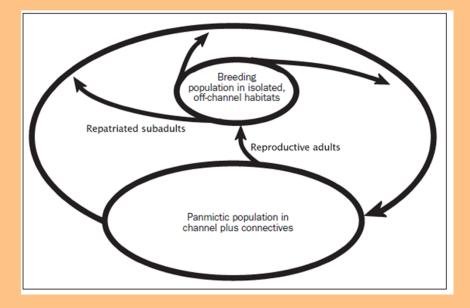
SOLUTION: refuges where can develop appropriately age structured populations

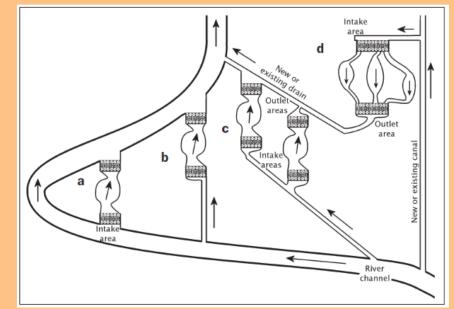




Solution: Off-channel habitats (Minckley et al. 2003)

- Develop isolated off-channel habitats
- Refugia for reproduction
- Interchange individuals with main river





Off-channel habitats

- Need some basic life history information
 - How many individuals do we use in each pond?
 - How often do we exchange them?
 - How does reproductive success vary across individuals and years?
- Demographic and genetic information is essential for design of and informed management of backwater populations