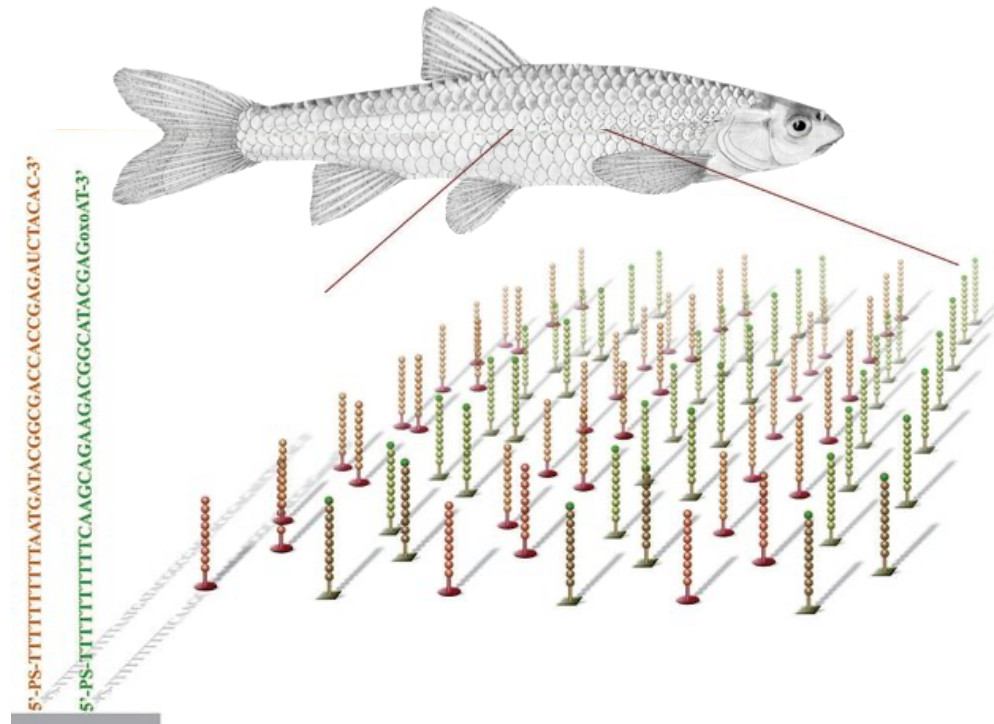


# The Next Generation of Rio Grande Silvery Minnow Genetic Monitoring



THE UNIVERSITY of  
NEW MEXICO



Museum of  
Southwestern  
Biology

Guilherme Caeiro-Dias  
gcaeirodias@unm.edu



Thomas Turner  
turnert@unm.edu



Megan Osborne  
mosborne@unm.edu

- Guilherme Caeiro-Dias:
  - Post-doc researcher in Turner Lab. Dep. of Biology, UNM
  - Bioinformatics
  - Population genomics
  - Conservation genomics



# The Next Generation of RGSM Genetic Monitoring

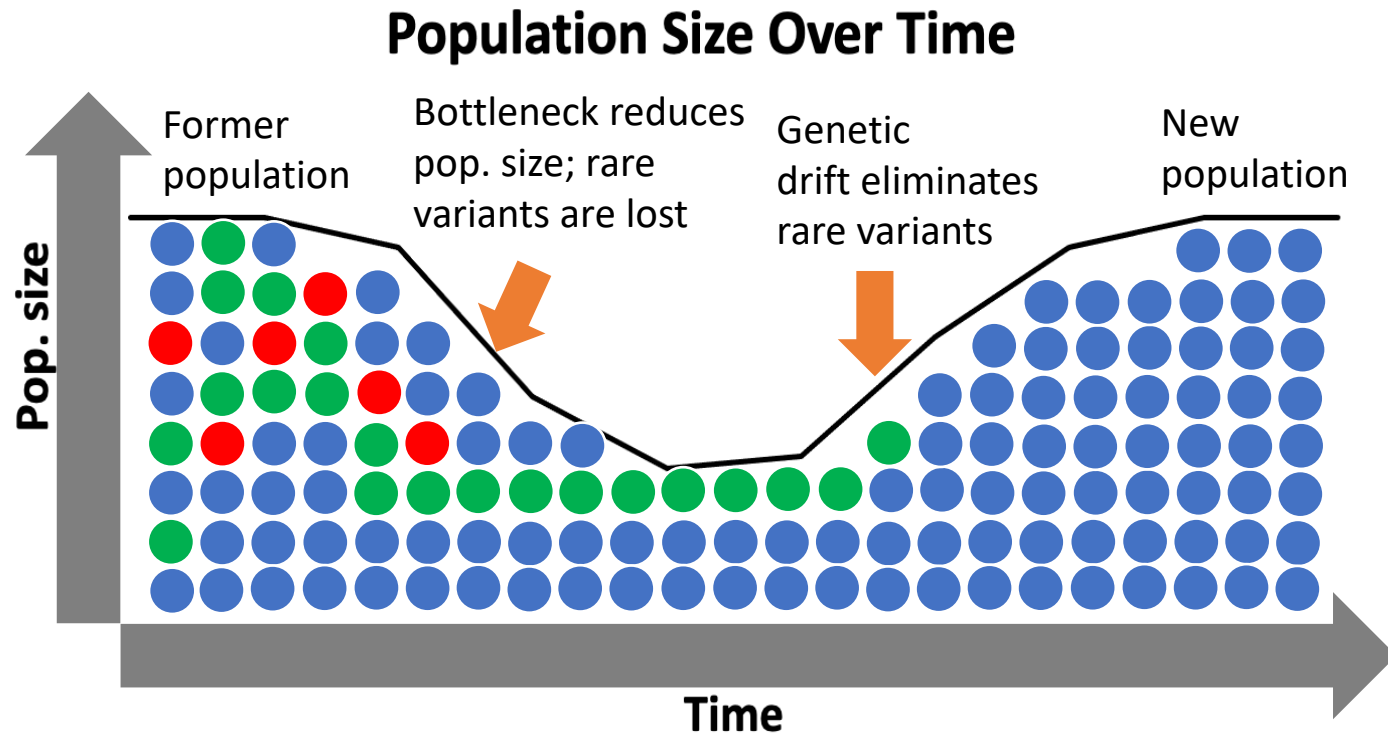
## Presentation plan:

- I. Populations change over time
- II. 20 years of RGSM genetic monitoring
- III. What can thousands of markers tell about RGSM genetic diversity?
- IV. Main Findings
- V. What next?





# Populations change over time



- Abundance; Distribution; Rate of change; ...
- Demographic factors influence genetic diversity;
- Population history;
- Natural selection;
- Intrinsic traits.
- The RGSM is particularly susceptible to demographic fluctuations

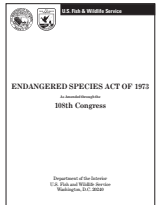




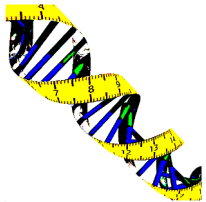
# 20 years of RGSM genetic monitoring

- 🐟 Monitoring tracks changes;
- 🐟 RGSM population changes has been monitoring in the last decades;
- 🐟 Genetic monitoring commenced in 1999.

ESA listing



Genetic monitoring begins



Augmentation begins



1994

1999

2000

2001

2002

2003

2004

2005

2006

2007

2008

2009

2010

2011

2012

2013

2014

2015

2016

2017

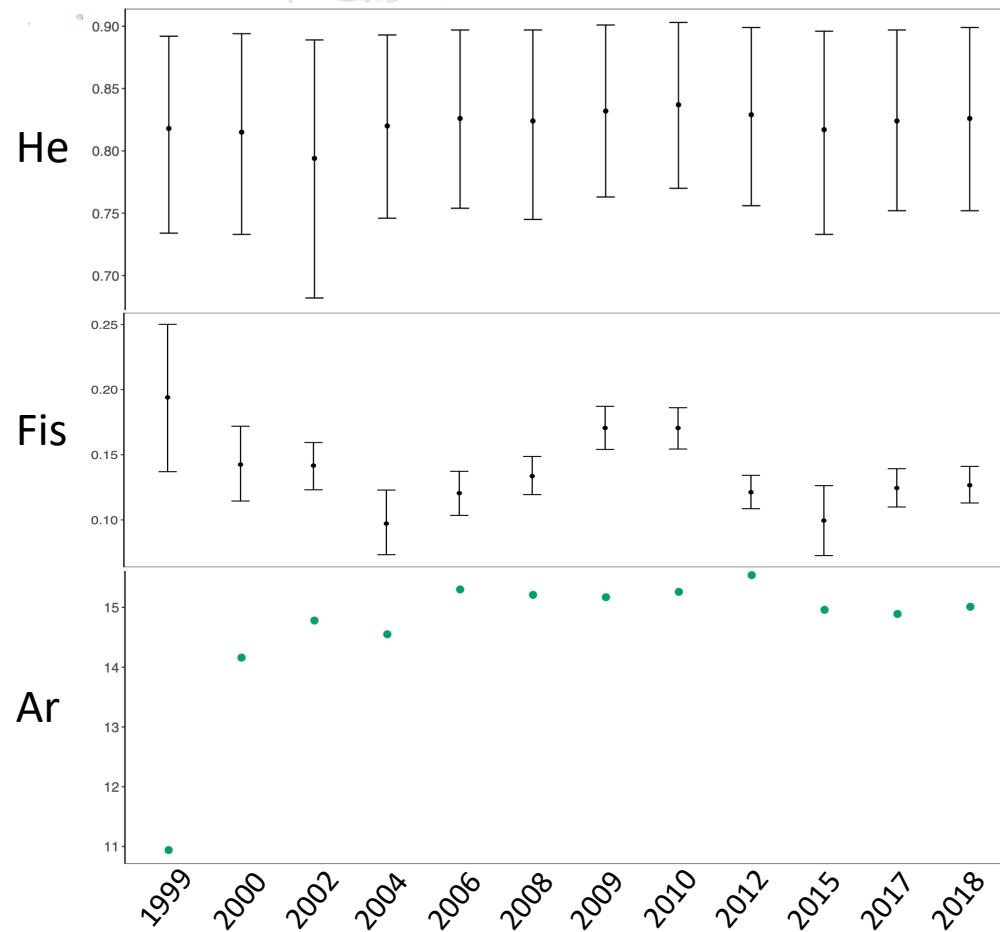
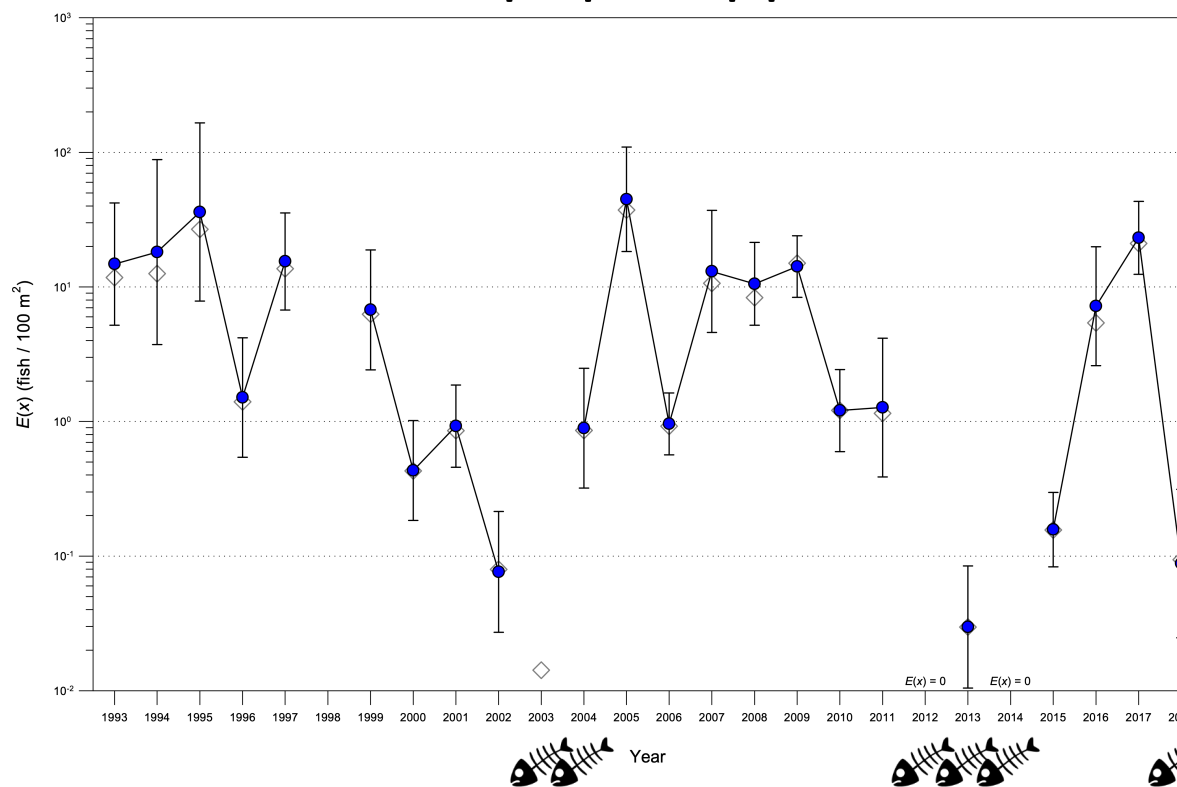
2018

2019

2020


# 20 years of RGSM genetic monitoring

- 🐟 Genetic diversity maintained
- 🐟 Attributed to pop. supplementation.





# What thousands of markers can tell about RGSM genetic diversity?

 RADseq: 2983 genetic markers (loci) containing 5329 variable nucleotides (SNPs);

 Proxy for genomic diversity;

 Detection of changes in genomic composition at microevolutionary scales (few generations).







# What thousands of markers can tell about RGSM genetic diversity?


## Genetic Diversity:

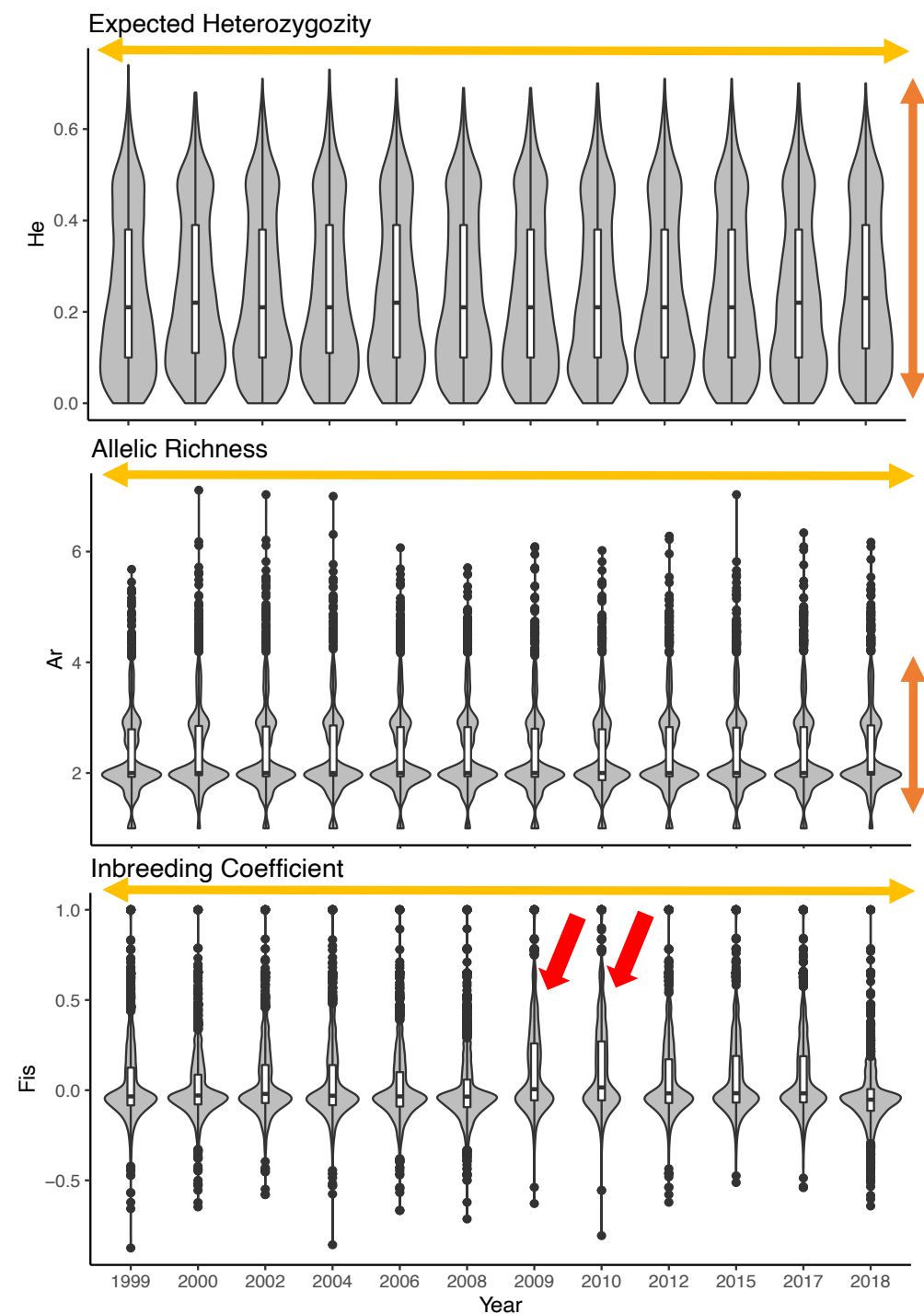
 Similar diversity across time; 

 He and Ar variable across the genome; 

  $F_{is} \approx 0$ ;

  $F_{is}$  increased in 2009 and 2010; 

 What happened in those years?





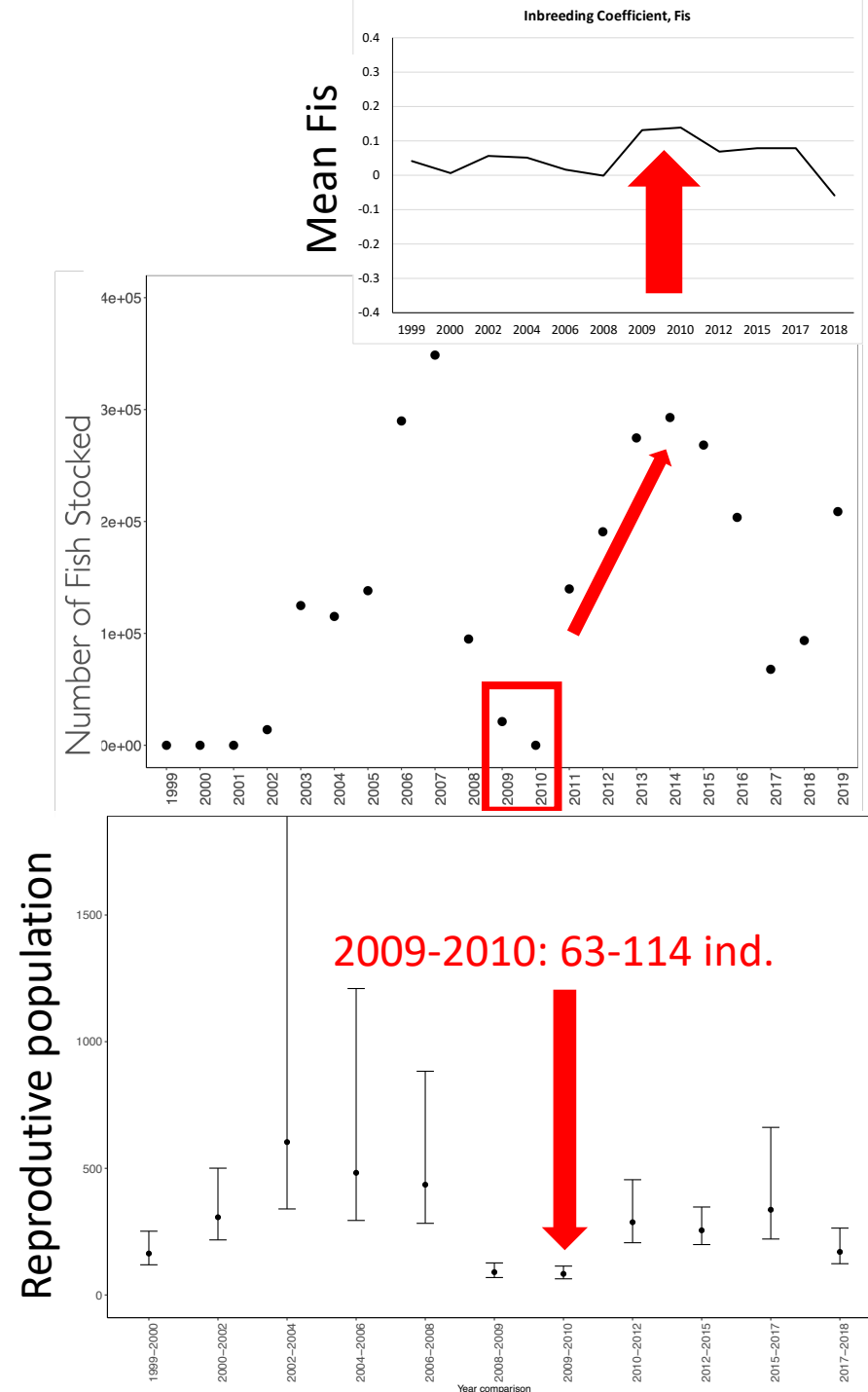


# What thousands of markers can tell about RGSM genetic diversity?



## Inbreeding:

- What happened in 2009 - 2010?
- Low fish stock;
- Low reproductive population;
- After 2010 supplementation increased;
- Inbreeding decreased to “normal” levels.





# What thousands of markers can tell about RGSM genetic diversity?

## Genomic variance - $F_{ST}$



Variance of allele frequencies between years

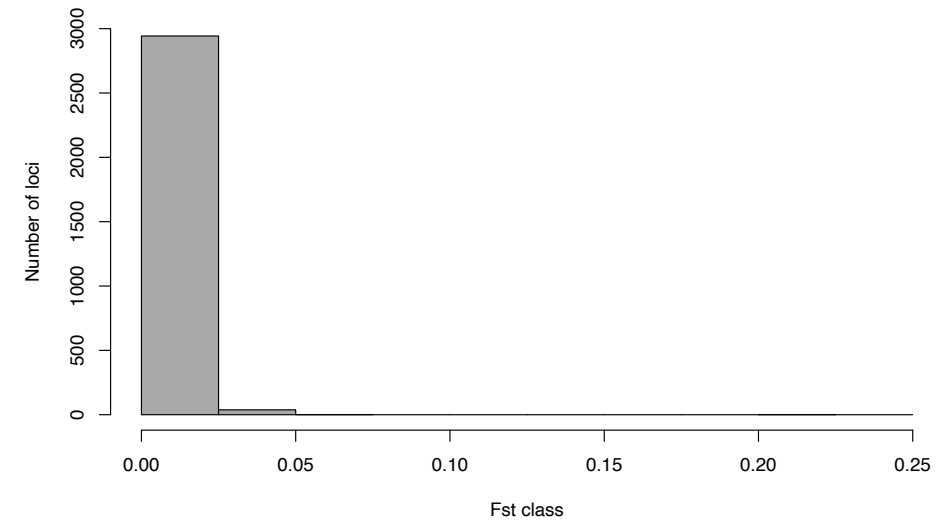


Most loci without variation in allele frequencies across time



A few loci with small allele frequency changes

Fst histogram










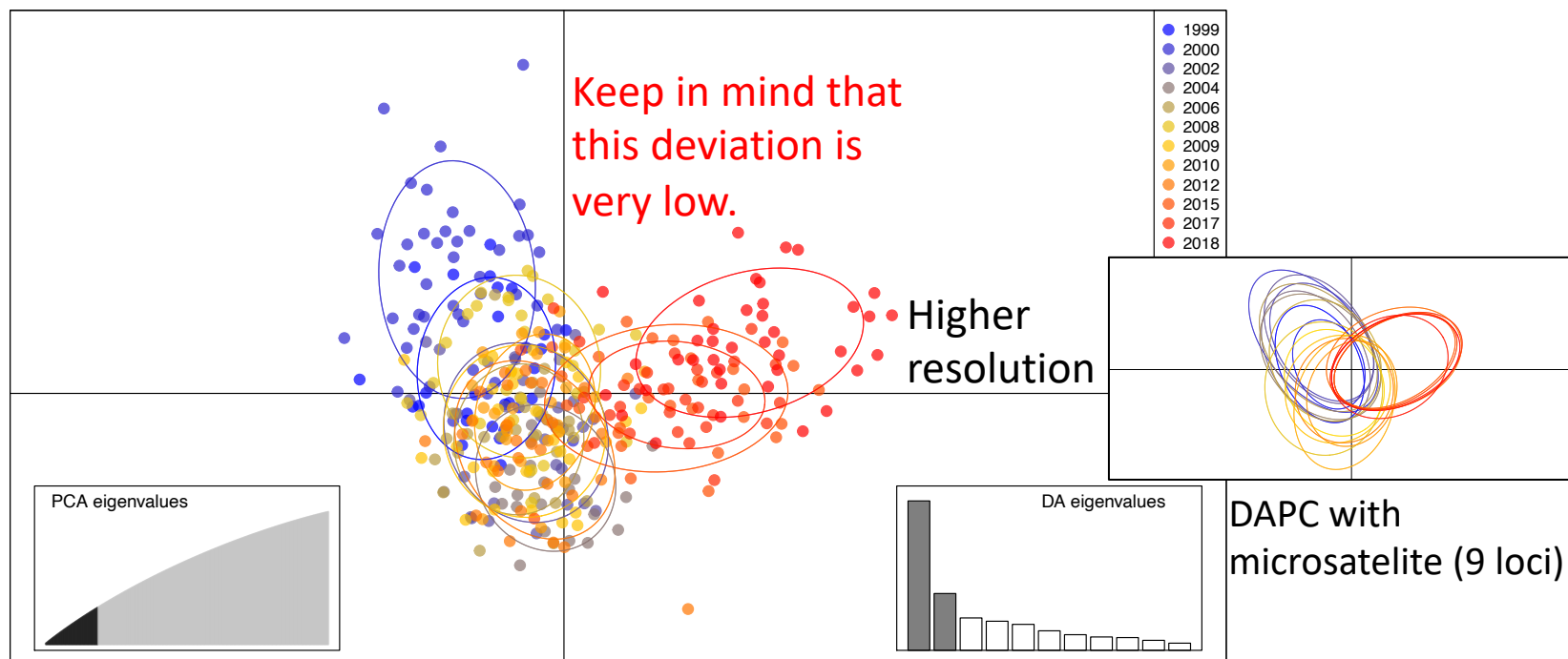
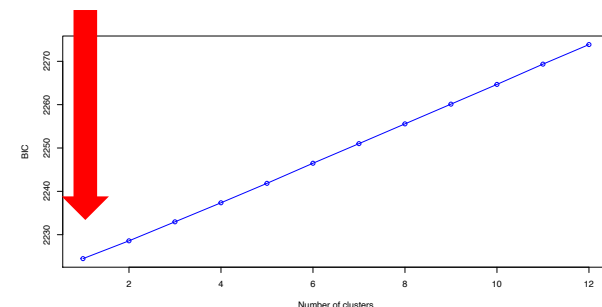
What thousands of markers can tell about RGSM genetic diversity?



## Temporal genetic Structure - DAPC

-  1 genetic cluster;
-  2015 - 2018 pops deviate along x-axis;
-  What happened between 2012 and 2015?

Lower BIC = Best #groups to describe the data





What thousands of markers can tell about RGSM genetic diversity?

## Temporal genetic Structure - DAPC



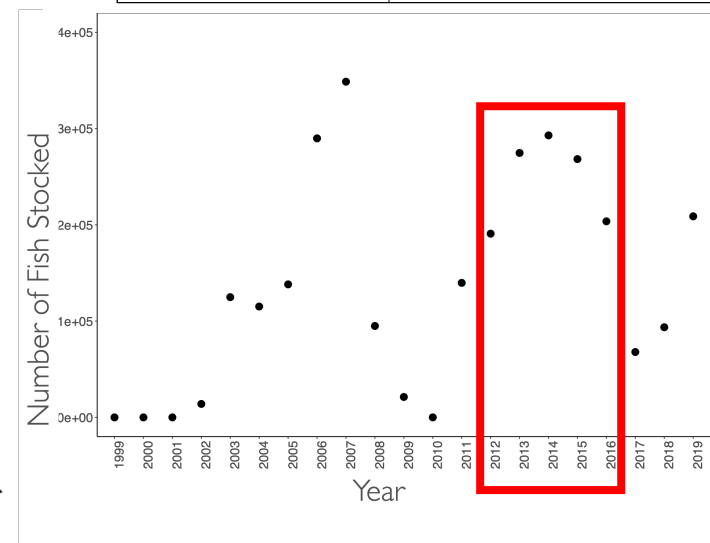
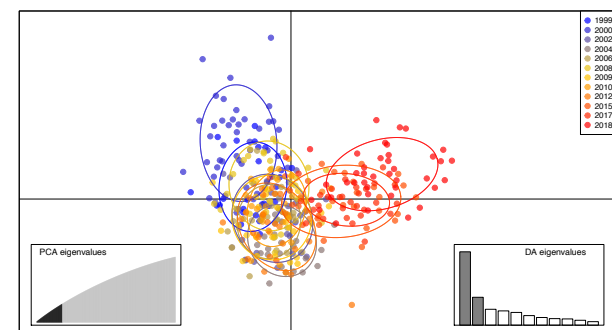
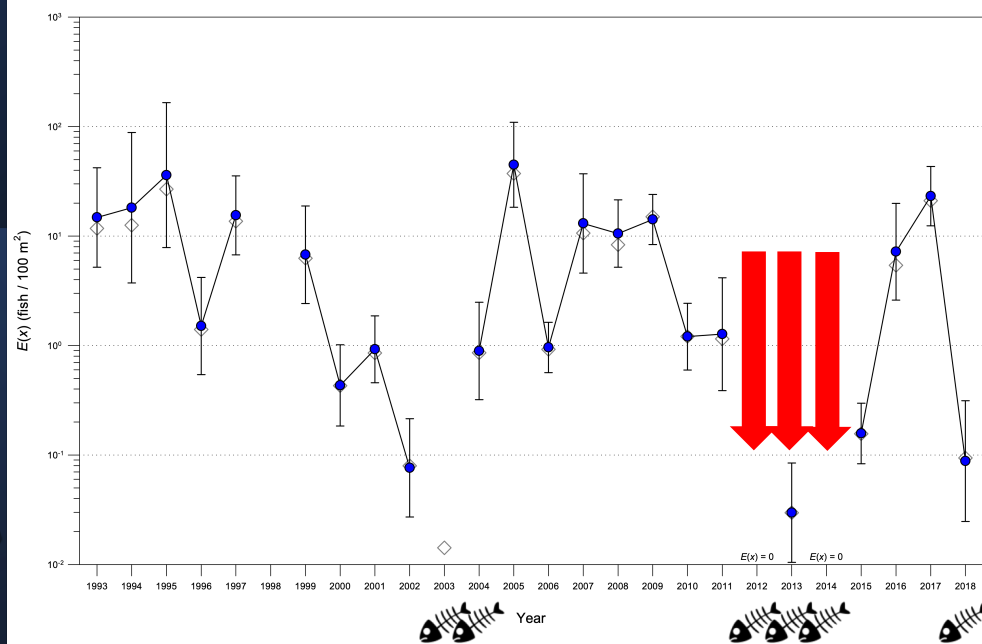
What happened between 2012 and 2015?



Major pop collapse 2012 – 2014;








Large number of captive reared fish were stocked, preventing major shifts in genomic composition.





# What thousands of markers can tell about RGSM genetic diversity?

## Main findings

-  Genomic diversity similar across years;
-  Inbreeding levels reverted after supplementation;
-  Augmentation prevented loss of diversity and major shifts on genomic composition during severe bottleneck;
-  Genomic composition shifts seems to be ongoing;
  -  Analysis of next years important to check if the trend continues.

# What next?

- Selection of a subset of markers adequate for genetic monitoring:
  - Why?
    - Keep most informative loci;
    - Replicability;
    - Costs.
  - How?
    - **Genotyping in Thousands by sequencing – Gtseq;**
    - Uses next-generation sequencing like RAD-seq Allows to amplify and sequence specific loci in many individuals;
    - Main restriction - efficient for relatively small loci panel (<500).

# Acknowledgments

---

- Dominique Aló, Melissa Benavides Christine Cooper, Melvin Foster, Melissa Martinez, Tamara Max, Tracy Diver, Alana Sharp, Sierra Netz, Jesse Trujillo, Ian Cunning, Thien Le, Samantha Sanchez, Michelle Sandoval, Hailey Conover, Jesse Perez-Baca, Brennan Davis, Alyssa Sanchez, Helene Martinez, Mia Coleman, Brain Fitzgerald, Charisa Bell, Sam McKitrick, Madison Paulk, Tyler Pilger, Alex Cameron, David Camak.
- Museum of Southwestern Biology: Emily DeArmon, Alexandra Snyder.
- UNM Molecular Biology Facility.
- UNM Centre for Advanced Research Computing – CARC.
- ASIR (S. Platania, R. Dudley, M. Farrington).
- Southwestern ARCC (M. Ulibarri, W. Wilson, W. Knight).
- ABQ BioPark (K. Lang, K. Ward, C. Altenbach).
- LLSMR (A. Hudson).



Guilherme Caeiro-Dias  
gcaeiroidias@unm.edu



Thomas Turner  
turnert@unm.edu



Megan Osborne  
mosborne@unm.edu

**Thank you**



THE UNIVERSITY of  
NEW MEXICO

