

Science and Habitat Restoration Work Group Meeting  
*January 16, 2018*

Meeting Materials:

Meeting Agenda

Meeting Minutes

GWG Priority Projects [not included]

Proposed 2018 ScW/HR Work Plan

ScW/HR Genetics Priorities [spreadsheet not included]

Genetic Monitoring of RGSM: Status of Wild and Captive Stocks in 2017 [presentation]



# Middle Rio Grande Endangered Species Collaborative Program

Est. 2000

## Science and Habitat Restoration Work Group Meeting Agenda

**January 16, 2018, 1:00 PM – 3:00 PM**  
**Location: WEST, Inc. 8500 Menaul NE Suite B-342**

**Conference Call information:**  
**Phone: (712) 451-0011 Passcode: 141544**

- |             |   |                                 |
|-------------|---|---------------------------------|
| 1:00 – 1:05 | Welcome and Introductions   | <i>Debbie Lee</i>               |
|             | ➤ Approval of Agenda  |                                 |
|             | • Introduction of Ashley Tanner                                     |                                 |
| 1:05 – 1:35 | Annual RGSM Genetics Monitoring Update                              | <i>Megan Osborne, UNM</i>       |
| 1:35 – 1:50 | SOW Development Updates   |                                 |
|             | • Tamarisk SOW  | <i>Lynette Giesen</i>           |
|             | • Genetics SOW  | <i>Julie Dickey</i>             |
|             | • Early Life History SOW  | <i>Debbie Lee</i>               |
|             | • Update from Population Monitoring Work Group & Data Analysis Team | <i>Debbie Lee</i>               |
| 1:50 – 2:50 | Development of Science Work Plan (Discussion)                       | <i>Debbie Lee (facilitator)</i> |
|             | • EC Direction  |                                 |
|             | • Task Prioritization   |                                 |
|             | • Task Delegation   |                                 |
|             | ➤ Action Item: Writing Assignments                                  |                                 |
|             | ➤ Decision: Direction to Genetics Subgroups                         |                                 |
| 2:50 – 3:00 | Summary and Next Steps  | <i>Debbie Lee</i>               |
| 3:00        | Adjourn   |                                 |



Middle Rio Grande Endangered Species  
Collaborative Program  
*Est. 2000*

**Science and Habitat Restoration Work Group  
Meeting Minutes  
January 16, 2018 – 1:00 PM – 3:00 PM  
Location: WEST, Inc. – 8500 Menaul Blvd. NE**

**Decisions:**

- The agenda was approved with no objections voiced.
- The group agreed to return to monthly meetings, specifically targeting the 4<sup>th</sup> Tuesday of every month.

**Actions:**

WHO	ACTION ITEM	BY WHEN
WEST	Send out 2017 genetics report and Megan Osborne's presentation	ASAP
USACE (Mick Porter) and NMISC (Grace Haggerty)	Determine what habitat restoration GIS files are available and send to Mo Hobbs and Ashley Tanner	Ongoing
Ashley Tanner and Mo Hobbs	Work to consolidate and develop metadata for GIS map of restoration projects.	Ongoing
Debbie Lee	Revise Proposed 2018 Work Plan Items for ScW/HR review	1-Feb-18
All	Provide any ideas for 2018 SOW development to WEST for consideration at the next ScW/HR meeting	16-Feb-18
Dave Wegner and Mike Marcus	Finish peer review prioritization efforts.	16-Feb-18
Mike Marcus	Find existing habitat restoration SOW for next meeting.	16-Feb-18
Lynette Giesen	Find existing habitat restoration SOW(s) for next meeting.	16-Feb-18
All	Next ScW/HR meeting	27-Feb-18

**Requests/Recommendations:**

- Request that Megan Osborne's genetics presentation and the 2017 genetics report be distributed to the group.
- Request that the group bring ideas for 2018 SOW's to the February ScW/HR meeting, including any existing SOW that may be appropriate for consideration.

- Request that all habitat restoration-related GIS files are sent to Mo Hobbs and Ashley Tanner.
- Request that anyone with funding for projects or people looking to do work in low flow situations in 2018 bring their ideas to the February 9<sup>th</sup> MAT meeting currently scheduled to take place at the NMISC office.

**Next Meeting:**

February 27, 2018

## Meeting Notes

**Presentation:** Genetic Monitoring of Rio Grande Silvery Minnow: Status of Wild and Captive Stocks 2017 – Megan Osborne

Dr. Megan Osborne, UNM, presented the 2017 update on the status of RGSM genetics. Her presentation slides were distributed to the group following the meeting, and will be posted to the Collaborative Program's DBMS.

Primary Conclusions from the presentation:

- Started establishing benchmarks of diversity in response to the genetics peer review.
- Gene diversity and heterozygosity exceeded minimum benchmark levels of diversity in the wild population; heterozygosity approaching lower benchmark in captive population.
- Allelic diversity in the wild population declined in 2017 and was below benchmark levels in the captive population.
- Strong recruitment in fall 2016 and the 2017 genetic effective size increased over recent estimates.

Question and Answer Session:

- Q: Would more samples be better?
  - A: We had more than enough samples for this year, so not really.
- Q: Does the type of water year we're having affect genetics?
  - A: The relationship between water year and genetics is complicated and non-linear.
- Q: How does sample size affect the estimates for reach?
  - A: There are definitely some effects. It's important to acknowledge that the reaches aren't exactly independent of one another, so it's complicated to separate by reach. For example, we would expect genetics in the Isleta reach to be more dynamic given its location.
- Q: Has there been consistency in analysis between work done in the 90's and now?
  - A: Yes, and Dr. Osborne has overseen much of that personally.
- Q: Are the results out of whack with population dynamics for other short-lived species?
  - A: Dr. Osborne doesn't know of a comparable dataset.
- Q: As a manager, should I be concerned about how this population is responding over time?
  - A: Certainly need to be concerned about the loss of diversity we're seeing. It's not a crisis situation, but it is significant to see a loss in both the wild and captive populations. Hatcheries may need to manage differently to account

for that. This will become especially important if/when the wild population declines substantially and you essentially replace that population one with captive fish. The captive propagation program was started with diverse wild stock, so that really helps with where we're at today.

### **SOW Development Updates:**

The ScW/HR heard updates on the scopes of work (SOWs) that had been under development:

- Tamarisk SOW (Lynette Giesen)
  - This SOW was approved at the December Executive Committee meeting, and the EC directed USACE to fund and implement the project. USACE is beginning the contracting process.
  
- Genetics SOW (Julie Dickey)
  - This SOW was completed by the sub-group in December and presented to the EC. The EC approved it, and it was submitted to Reclamation. They are currently considering options for funding it, including as a grant.
  
- Early Life History SOW (Debbie Lee)
  - The Early Life History SOW Subgroup has a meeting scheduled for Monday, January 22, 2018 to discuss this SOW. The group is working to have a draft together for the April EC meeting. The draft will be sent to the ScW/HR for review before the March ScW/HR meeting.
  
- Reanalysis of the Population Monitoring Data (Debbie Lee and Ashley Tanner)
  - The Population Monitoring group decided to undertake this reanalysis in-house and formed a data analysis team (DAT). The data for this effort are currently available and have been sent out to all. WEST is serving as the interim data manager, and Ashley Tanner has been working to prepare the data for use in the next DAT meeting.

### **Update on the Adaptive Management Effort**

Dave Wegner, the Science Coordinator, presented an update on the adaptive management (AM) effort, and gave his thoughts on how AM could work in the Collaborative Program. The group will be developing a consistent definition of adaptive management at our next meeting, which will include expectations and demands. Ultimately, WEST is here to guide the process, but not write the adaptive management and science plans. In the long run, we would like to see the adaptive management plan, regulatory efforts, and science plans come together in a final adaptive management plan for the program. We want to make something unique to and effective for the Rio Grande.

### **Review of the 2018 Proposed Science/Habitat Restoration Work Plan:**

At the December EC meeting, the EC directed the ScW/HR group to develop a proposed work plan for its review, based on the items discussed at the last ScW/HR meeting. The group discussed the items, and generally agreed these were the correct tasks.

- Peer Reviews

- This task would be to complete the prioritization of the most recent peer review panel recommendations (Genetics, Population Monitoring, and RGSM Life History), and then develop a final prioritized list of projects from all the recommendations.
  - Dave Wegner and Mike Marcus agreed to work on finishing the peer review prioritization efforts. This effort was identified as one of the top two priorities for 2018.
- Data Inventory and Consolidation
    - This is a task that WEST has already started. Ashley Tanner had emailed the stakeholders and asked for them to provide information on people, facilities, and data available to the program through their respective organizations. This is an ongoing effort, and Ashley will continue to solicit and organize the provided information.
- GIS Map of Projects
    - The group agreed that a GIS map was one of the top two priorities for 2018. In particular, it was identified that a GIS map was needed to facilitate future restoration work.
    - NMISC and USACE agreed to work together and provide restoration-related GIS layers to Mo Hobbs and Ashley Tanner, who will work to consolidate these data and fill-in missing metadata.
- DBMS Development
    - The DBMS kick-off meeting with USGS is scheduled for January 18, 2018. From that meeting, there will be an update on the process for developing a new DBMS. USGS will want input from the different Collaborative Program users, and the ScW/HR group can be one of the forums for input.
    - The ScW/HR group was asked to begin thinking of a wishlist of functions and how the DBMS interface would look like.
- Habitat Restoration Assessment
    - It was noted that the “increased failure rate of cottonwood pole plantings” mentioned in the proposed Science/Habitat Restoration Work Plan is not a statement that should be universally applied. These failures were potentially just large and more visible. There was interest in determining what factors (i.e. pole source) affected failure or success of these cottonwood pole plantings.
    - Mike Marcus and Lynette Giesen both developed SOW’s in the past that may be applicable to this subject and will bring these SOW’s to the February ScW/HR meeting.
- Additional SOW Development
    - There will be opportunity for the ScW/HR to develop SOWs for funding consideration. Short write-ups will need to be provided to the funding agency by April 2018.
    - The group was reminded of the federal funding cycle, and that planning starts 2-3 years prior to the funds being allocated and available for spending. This should be kept in mind when prioritizing and planning projects.
    - It was noted that the priorities from the peer review panels may be used as a basis for new SOWs.

- There used to be a Collaborative Program science plan that combined the needs and activities for the Science Committee and all the subgroups. Developing a new science plan that incorporates all the listed species and past AM efforts would be a good starting point to identify projects in the future for funding.
- There was a request to develop a database of projects which have been funded, their status, and any results. This can be used to better prioritize future projects.
- ScW/HR members were asked to bring any project ideas to the next meeting for the group to consider.

**Announcements:**

- Grace Haggerty announced there will be a MAT kick-off meeting on February 9, 2018. It is currently scheduled to take place at the NMISC office. They are planning on having hydrology provide updates on what projections are looking like after the February 1 forecast. They are also anticipating a talk from SWCA about 2017 monitoring efforts. The MAT would welcome ideas for project funding or people looking to do work in low flow situations in 2018.

## Meeting Participants

<b>Participant</b>	<b>Organization</b>
Jennifer Bachus	Bureau of Reclamation
Rick Billings	Albuquerque-Bernalillo County Water Utility Authority
Julie Dickey	Western EcoSystems Technology, Inc.
Kim Eichorst	Bosque Ecosystem Monitoring Program
Lynette Giesen	U.S. Army Corps of Engineers
Grace Haggerty	New Mexico Interstate Stream Commission
Mo Hobbs	Albuquerque-Bernalillo County Water Utility Authority
Alison Hutson	New Mexico Interstate Stream Commission
Kathy Lang	City of Albuquerque
Debbie Lee	Western EcoSystems Technology, Inc.
Mike Marcus	Assessment Payers of the Middle Rio Grande Conservancy District
Yasmeen Najmi	Middle Rio Grande Conservancy District
Megan Osborne	University of New Mexico
Matthew Peterson	City of Albuquerque
Mick Porter	U.S. Army Corps of Engineers
Dana Price	U.S. Army Corps of Engineers
Justin Reale	U.S. Army Corps of Engineers
Vicky Ryan	U.S. Fish and Wildlife Service
Summer Schulz	U.S. Army Corps of Engineers
Michael Scialdone	Pueblo of Sandia
Clint Smith	U.S. Fish and Wildlife Service
Ashley Tanner	Western EcoSystems Technology, Inc.
Dave Wegner	Western EcoSystems Technology, Inc.
Wade Wilson	U.S. Fish and Wildlife Service



## **Proposed 2018 Science/Habitat Restoration Work Plan**

### **1. Peer Reviews**

In recent years, the Collaborative Program has sponsored three independent science panels/peer review panels:

- RGSM Life History (February 2017)
- RGSM Genetics Project Peer Review (February 2016)
- RGSM Population Monitoring (December 2015)

The Collaborative Program has undertaken some prioritization of the recommendations from the panel reports, but has not completed these efforts, or looked at prioritizing the recommendations from all three panels as a whole.

Continuing the prioritization effort will help inform the development of a long-term science work plan, as well as an interim work plan for the next year.

### **2. Data Inventory and Consolidation**

Since its inception, the Collaborative Program and its signatories have collected a large amount of data, including (but not limited to) endangered species population numbers, hydrology, water quality, and habitat restoration.

There is a need to inventory what data are available where, and if possible, to consolidate datasets. This will inform science and adaptive management activities in the Program, and minimize duplicate monitoring efforts.

### **3. GIS Map of Projects**

In 2017, the ScW/HR had begun developing a GIS map of all projects in the MRG. Due to Ken Richard leaving NMISC, that effort had stalled. Completing the map development will inform ongoing and future projects, and help with coordination efforts for on-the-ground activities.

### **4. DBMS Development**

In 2018, the Collaborative Program will be developing a new DBMS through an Army Corps contract with USGS. This new DBMS needs to be responsive to the needs of the Program, including its scientists and technical experts. The ScW/HR as a group can work with USGS to develop a list of requirements for the database and data management portion of the DBMS.

### **5. Habitat Restoration Assessment**

At the last ScW/HR meeting, it was raised that the last few years have seen an increased failure rate of cottonwood pole plantings. It was proposed that the group undertake a research project to assess why a habitat restoration project succeeds or fails.

# Genetic Monitoring of Rio Grande Silvery Minnow: Status of Wild and Captive Stocks in 2017



MEGAN OSBORNE & THOMAS TURNER

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THE UNIVERSITY *of*  
NEW MEXICO



## What Is Genetic Monitoring?

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- Tracking genetic diversity over contemporary time scales
- Multiple time points
- Consistent methodology across time series

# Diversity Metrics

## Microsatellites

## MtDNA

Diversity

Gene diversity  
Allelic richness  
Heterozygosity

Haplotype diversity  
Haplotype richness

Effective Size

Variance effective size

MLNE

Moments

TempoFs

Variance effective size

MLNE

Moments

Inbreeding effective size

Linkage disequilibrium

# What are we measuring?

## Allelic diversity

- Number of alleles per locus ( $A$ )
- Dependent on sample size

## Allelic/haplotype richness ( $A_R/n_{ac}$ , $H_R$ )

- Number of alleles/haplotypes per microsatellite/mtDNA locus corrected for unequal sample size

## Bottlenecks and allelic/haplotype diversity

- Depends on the number of alleles and their frequencies
- Rare alleles are most likely to be lost



# What are we measuring?

## Heterozygosity (microsatellites)/ Gene diversity (mtDNA)

- The presence of different alleles at one or more loci on homologous chromosomes. Proportion of heterozygous individuals for a locus in a population.

## Bottlenecks and heterozygosity

- Rate of loss is determined by the genetic effective size of the population during bottleneck
- Rare alleles contribute little to heterozygosity, hence loss of alleles may not be accompanied by loss of heterozygosity



# Genetic Effective Size

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- Size ( $N$ ) of an **idealized population** (equal sex ratio, lifetime variance in number of offspring is binomial, constant population size) that would experience the same degree of **genetic drift** as the observed population ( $N_e$ ).
- Why is it important?
  - $N_e$  determines the amount of variation transmitted from one generation to the next.
- Methods for estimating  $N_e$ 
  - Variance effective size ( $N_{eV}$ ) vs. Inbreeding effective size ( $N_{eI}$ )
  - Provide more accurate estimates (i.e smaller confidence intervals) when  $N_e$  is small and genetic drift is strong
  - Difficult to differentiate large from very large  $N_e$  (i.e. genetic drift is weak) resulting in large or infinite confidence intervals

# Genetic Effective Size

$N_{eV}$  and  $N_{eI}$  provide independent information about effective size

	VARIANCE EFFECTIVE SIZE, $N_{eV}$	INBREEDING EFFECTIVE SIZE, $N_{eI}$
How it is measured	Allele frequency changes	Linkage disequilibrium (non-random association of alleles at different loci)
What it measures	Loss of genetic variation from GENETIC DRIFT	Number of parents for the current generation
Number of temporal samples	2	1
Stable populations	=	=
Population fluctuation Supplementation	≠	≠
Assumptions	<ul style="list-style-type: none"> <li>• Mutation is not important</li> <li>• Alleles selectively neutral</li> <li>• Alleles not in linkage disequilibrium with loci under selection</li> <li>• Samples are drawn randomly no immigration from neighboring populations</li> </ul>	<ul style="list-style-type: none"> <li>• Mutation is not important</li> <li>• Alleles selectively neutral</li> <li>• Alleles not in linkage disequilibrium with loci under selection</li> <li>• Samples are drawn randomly no immigration from neighboring populations</li> <li>• Random mating</li> </ul>



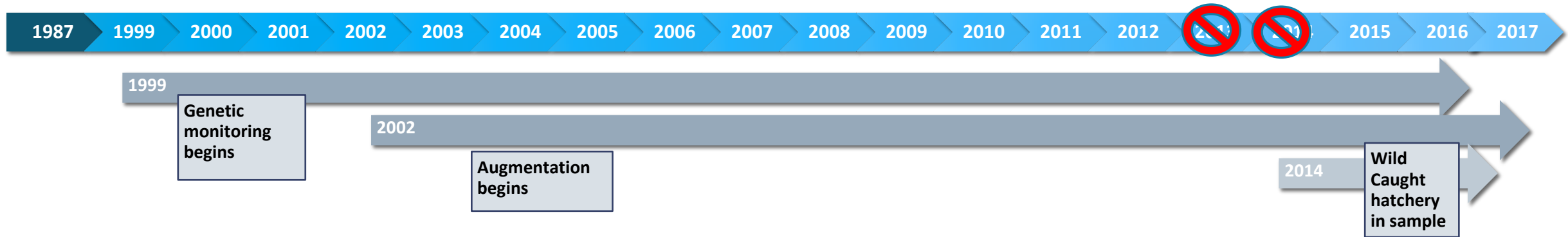
# Why conduct genetic monitoring in RGSM?

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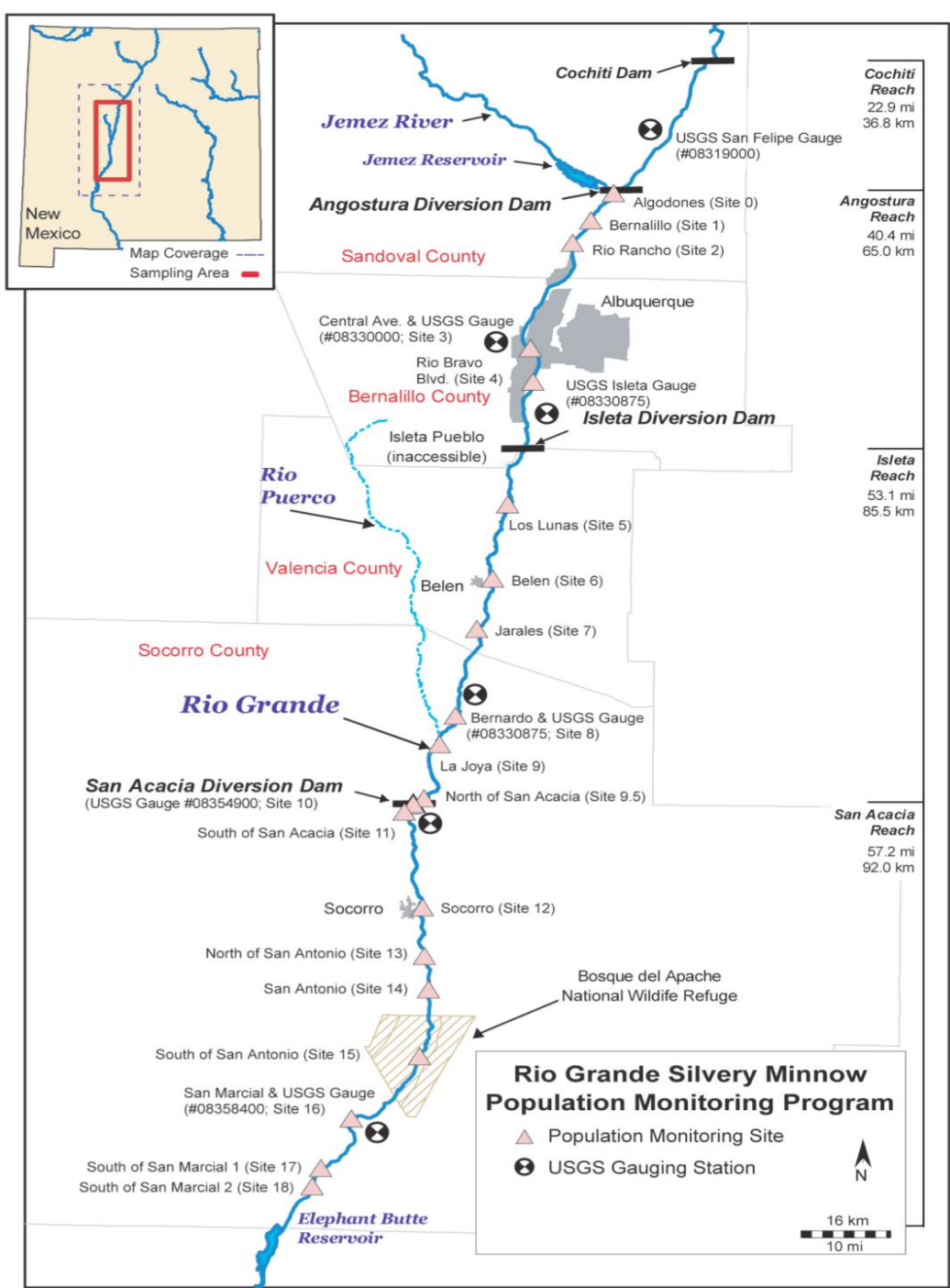


- Short-lived, type III survivorship.
  - Environmental conditions are highly variable
  - Dramatic population fluctuations.
  - Management actions- affect how diversity is distributed
  - Captive propagation and augmentation may increase or decrease diversity and genetic effective size.
- 
- Levels of genetic diversity affected over contemporary time scales.

# Background to RGSM Genetic Monitoring



- Neutral genetic markers:
  - MtDNA-ND4 gene                      Microsatellites (9 loci)
- Representative captive stocks released to the MRG (and to Big Bend)
- **Total = 5448 unmarked fish sampled from the MRG**
  
- **3812 captive bred/reared individuals**



- Unmarked fish sampled from three localities within each river reach
  - Angostura
  - Isleta
  - San Acacia
- Non-destructive sampling
- Total = 5448 unmarked fish sampled from the MRG
- 3812 captive bred/reared individuals

# Objectives

1. Collect samples from 'wild/naturally spawned' RGSM population and captive stocks.
2. Establish benchmarks of diversity using existing data.
3. Determine levels of genetic variability to evaluate temporal trends.
4. Estimate contemporary genetic effective size ( $N_{ev}$  &  $N_{el}$ ) in the wild population to evaluate temporal trends
5. Evaluate genetic effects of captive propagation/augmentation on wild stocks.

# OBJECTIVE 1

Ideal sampling:  
three sites within  
each reach, 50  
samples per site

Year	Angostura	Isleta	San Acacia	Total
<b>2017</b>	<b>159</b>	<b>156</b>	<b>154</b>	<b>469</b>
2016	171	121	128	420
2015	75	33	35	143
2014	5	3	4	12
2013	-	-	-	-
2012	147	215	154	516
2011	71	148	140	359
2010	149	146	151	446
2009	175	153	150	478
2008	165	191	123	479
2007	48	128	42	218
2006	95	143	145	383
2005	190	109	95	394
2004	141	15	6	162
2003	71	65	33	169
2002	67	121	201	389
2001	-	65	63	128
2000	-	-	194	194
1999	-	-	46	46
1987	15	-	28	43

## OBJECTIVE 2: Establish benchmarks of diversity

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- ‘Wild’ (MRG) fish: pooled into one large population ( $n \approx 5000$ )
- Resampled individuals ( $n = 43$ ) to estimate diversity statistics
- Primary interest is maintaining genetic diversity, the one-tailed benchmark corresponds to the lower 5% of the resampled distribution (as opposed to lower 2.5% for a two-tailed).
- The distribution contained above the benchmark corresponds to a conservative null hypothesis of no loss of diversity.

# OBJECTIVE 3

## Microsatellites

- Gene diversity and heterozygosity were UNCHANGED from 2015 and 2016 values
- These metrics exceeded benchmarks
- Allelic diversity declined in 2017 and approached the minimum benchmark

## MtDNA

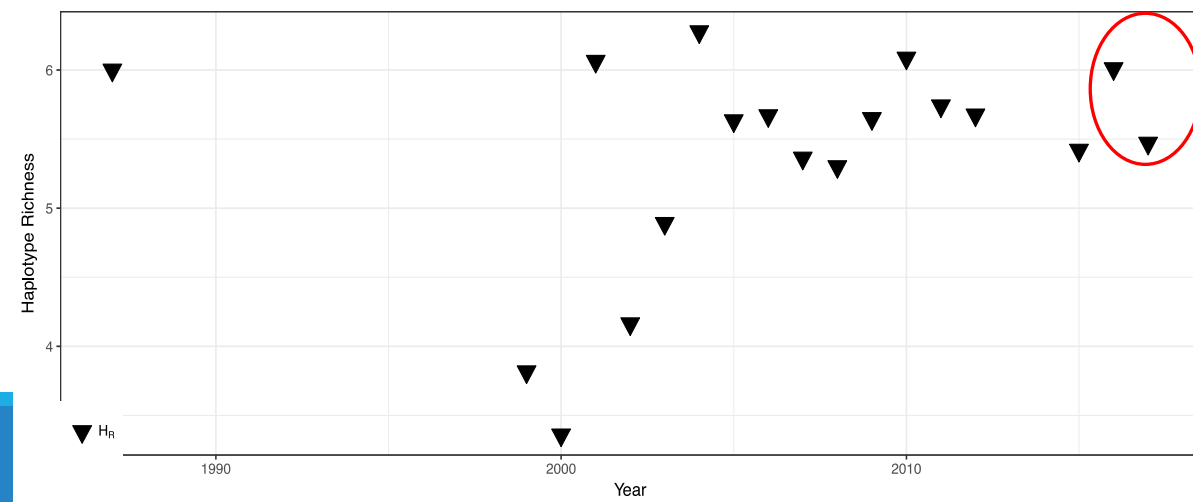
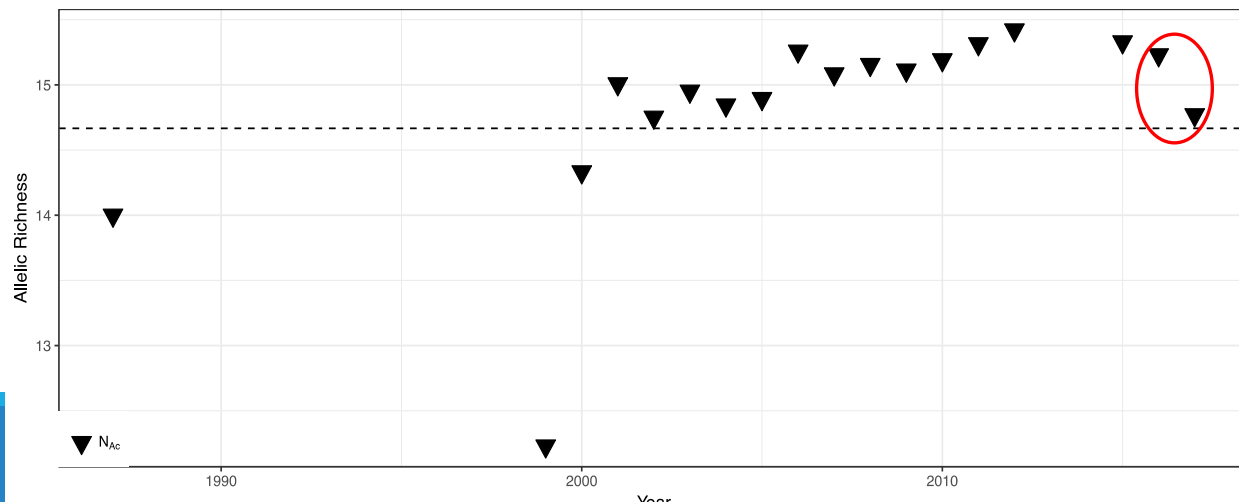
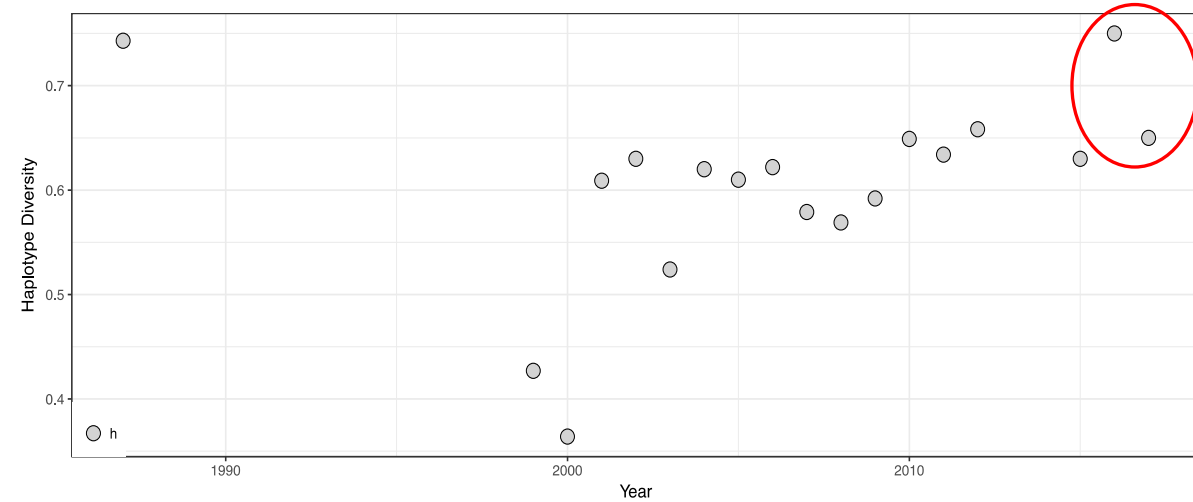
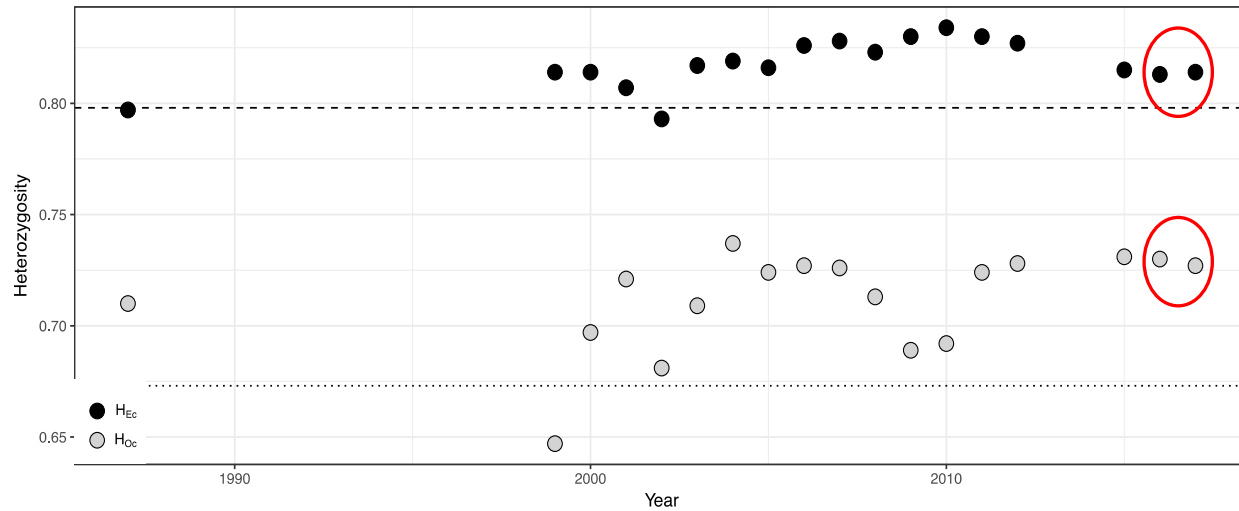
- MtDNA diversity metrics ( $h$  and  $H_R$ ) decreased from 2016 values.
- Detection of three rare haplotypes not seen since 2012.
  - Likely reflects increased number of samples in 2017 > detection of rare alleles
  - Reproductive contribution of old broodstock released in spring of 2016

# OBJECTIVE 3. Estimate genetic diversity in 'wild' population to assess temporal trends

Dashed line- benchmark

## Microsatellites

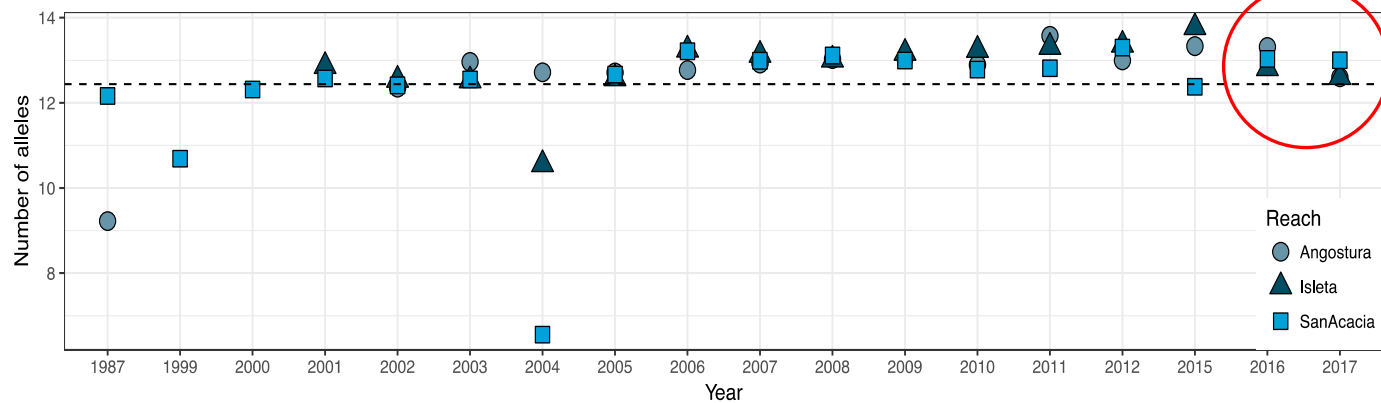
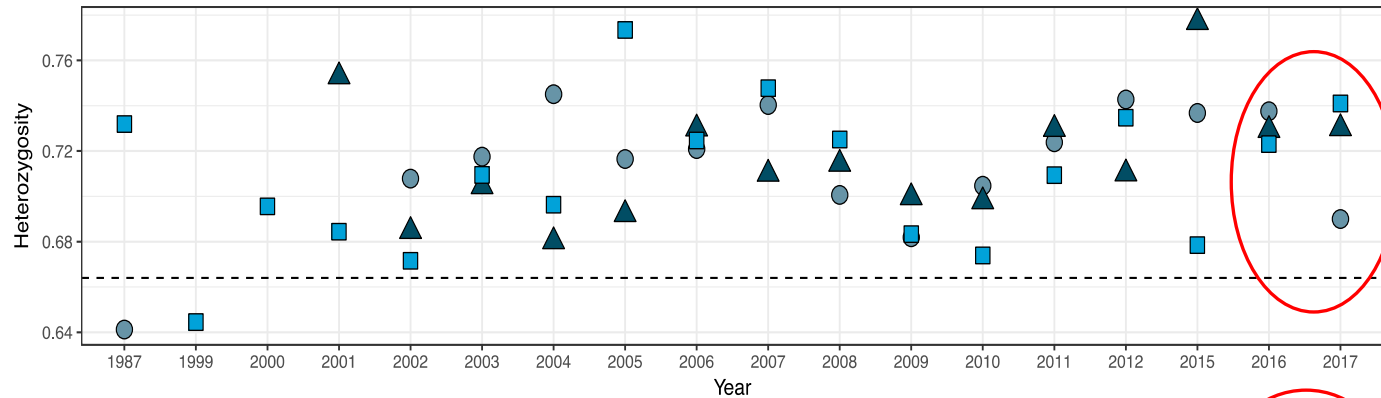
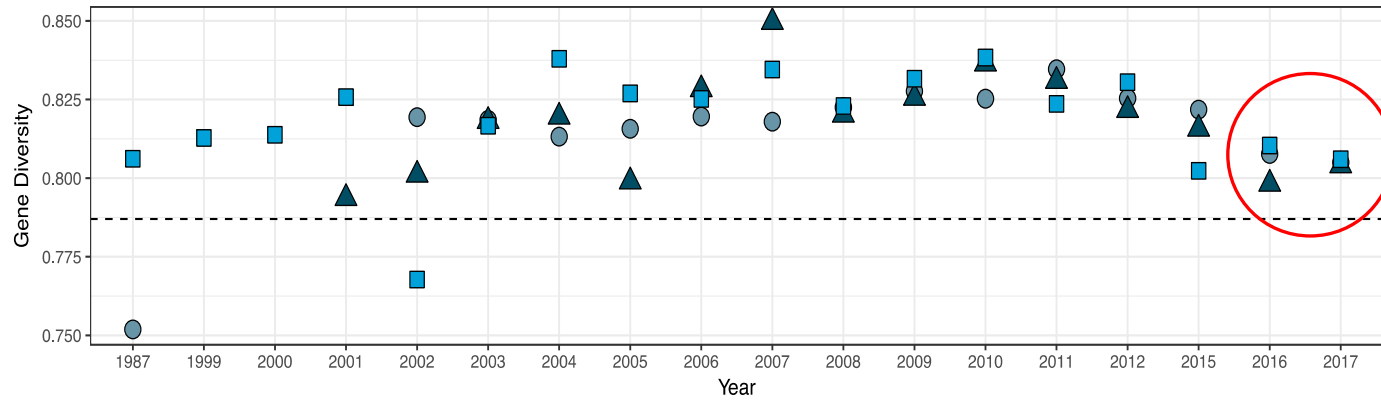
## Mt DNA- ND4





# OBJECTIVE 3

## Diversity by River Reach: Microsatellites



Dashed line- benchmark



Angostura:  $H_{oc}$  declined



Isleta: All metrics stable

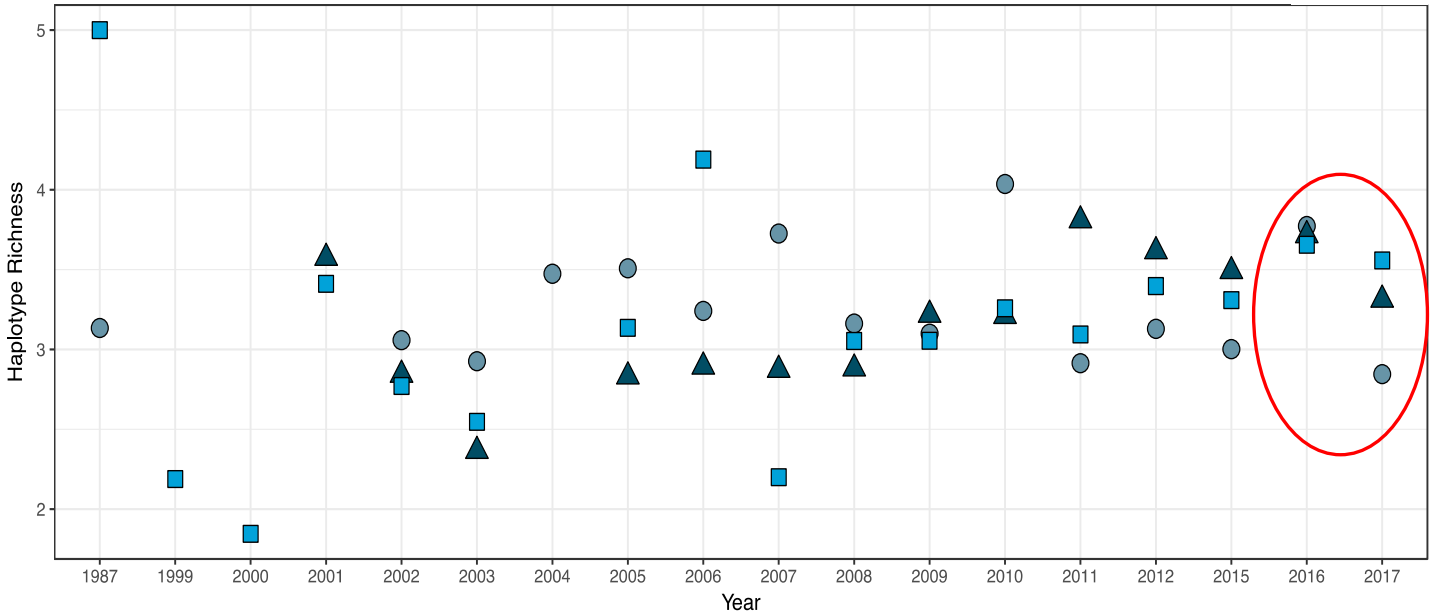
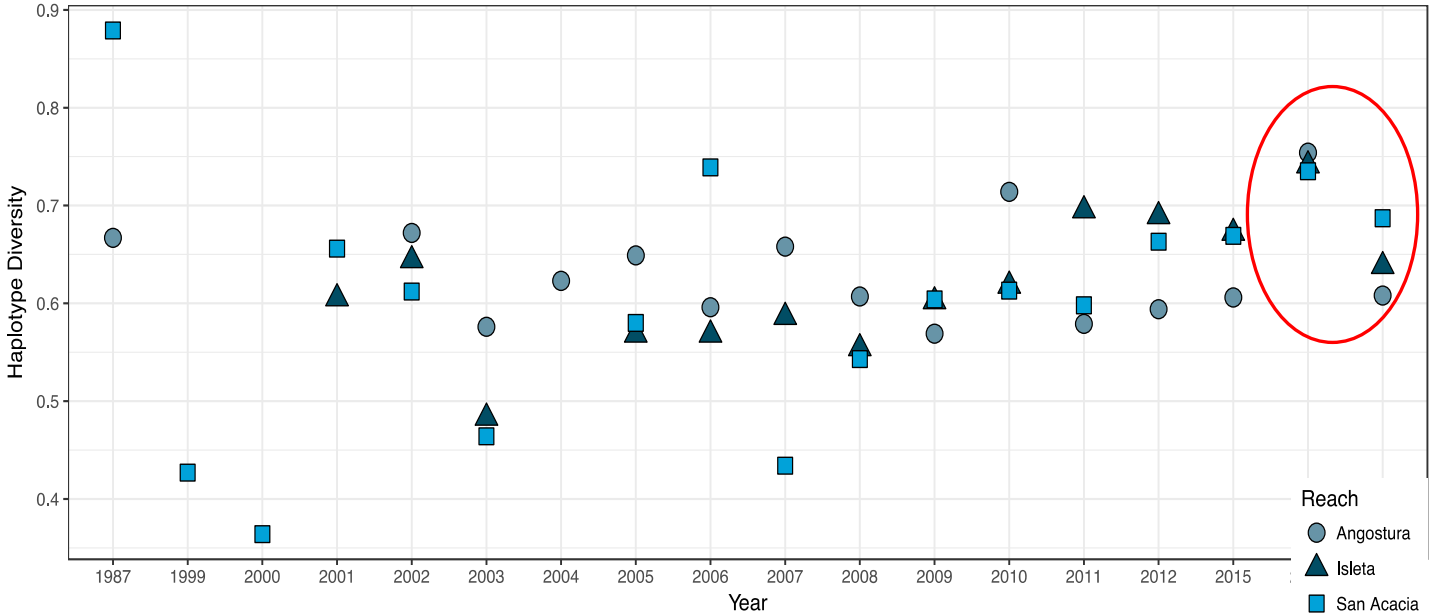


San Acacia: All metrics stable

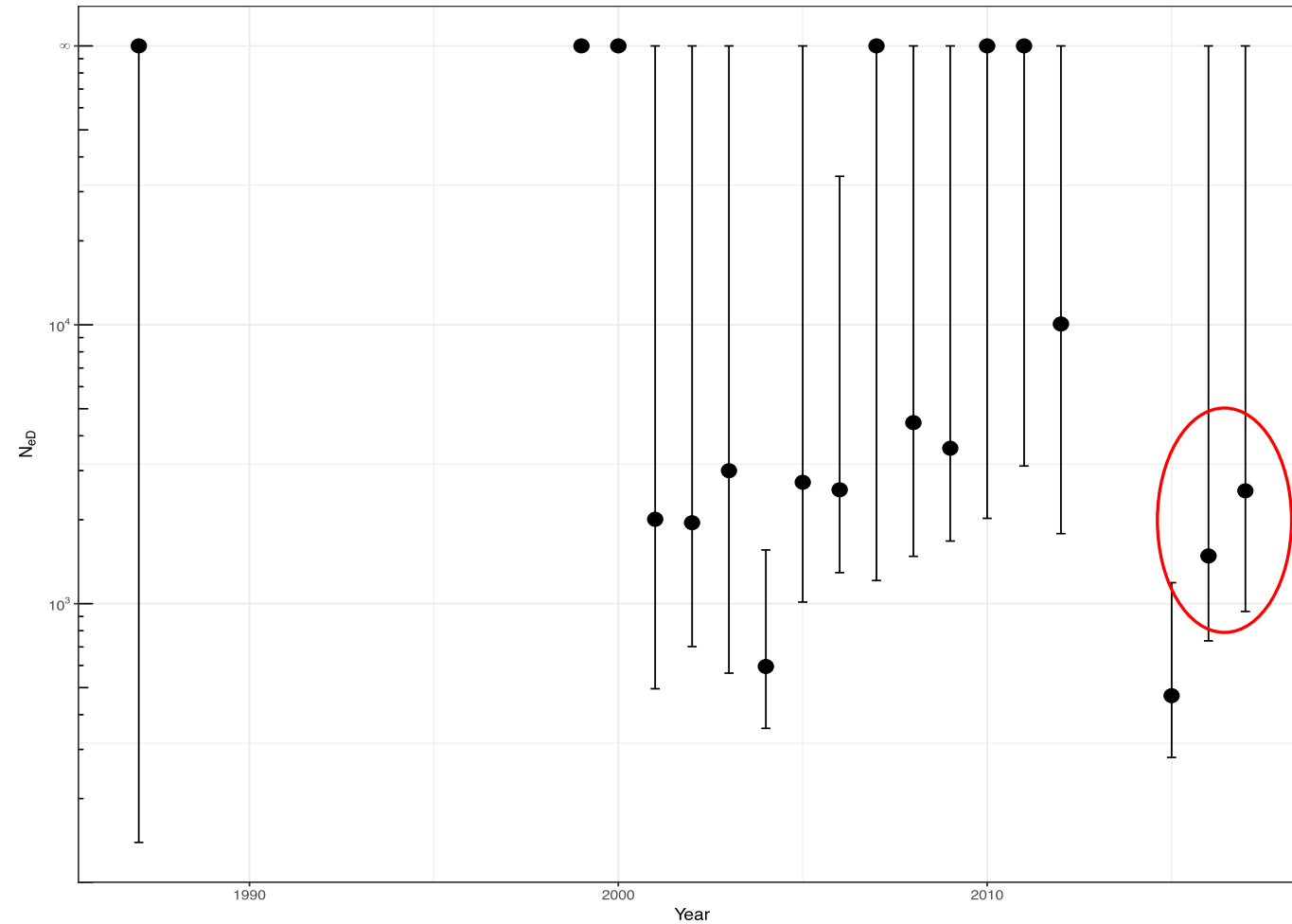
# OBJECTIVE 3

## Diversity by River Reach: Mt-DNA

- MtDNA diversity statistics decreased at the reach level in 2017



# OBJECTIVE 4 Inbreeding Genetic Effective Size



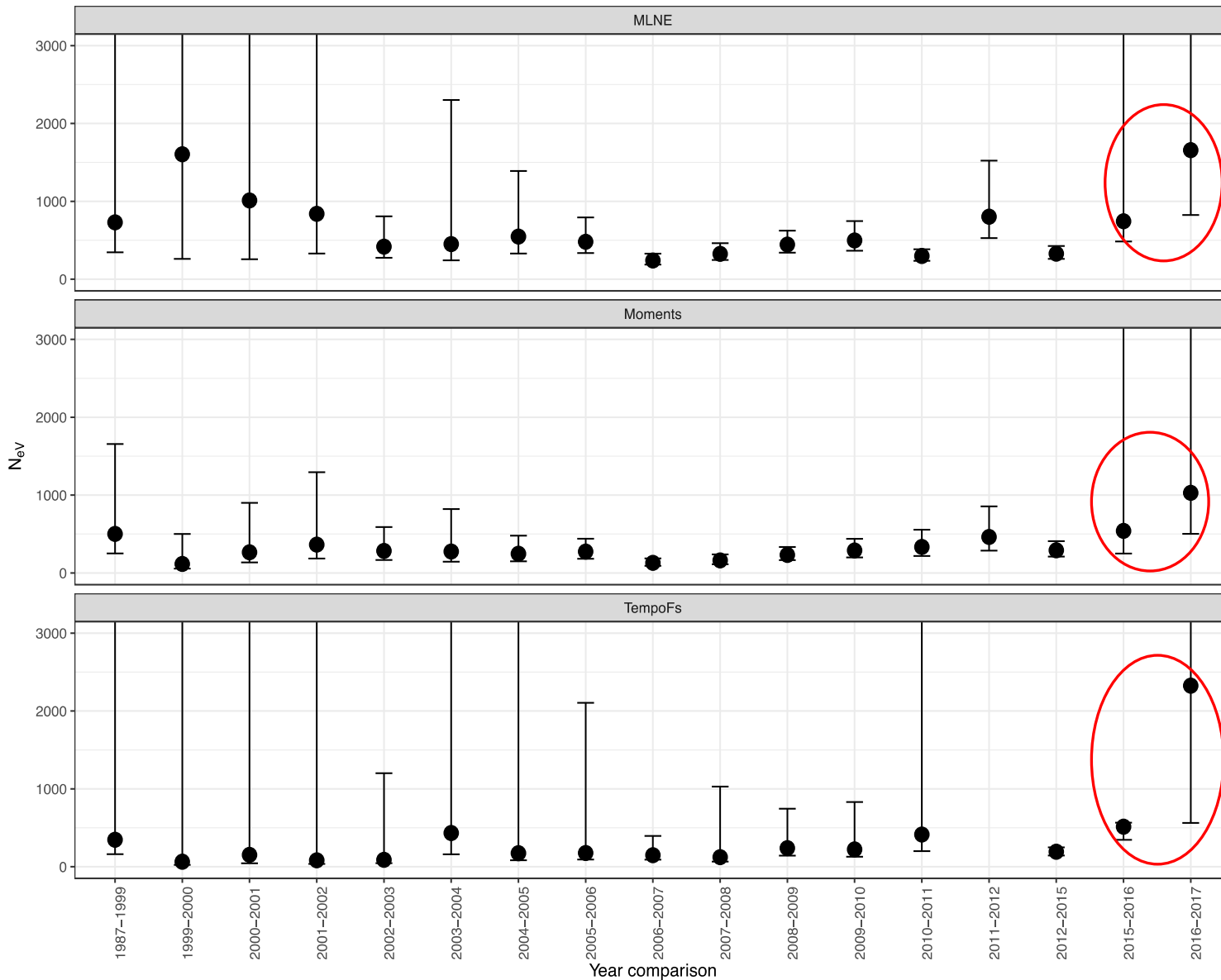
**How it is estimated:** Linkage disequilibrium (non-random association of alleles at different loci)

**What it measures:** Number of parents for the current generation

**Number of temporal samples: 1**

# OBJECTIVE 4

## Trends in $N_{eV}$

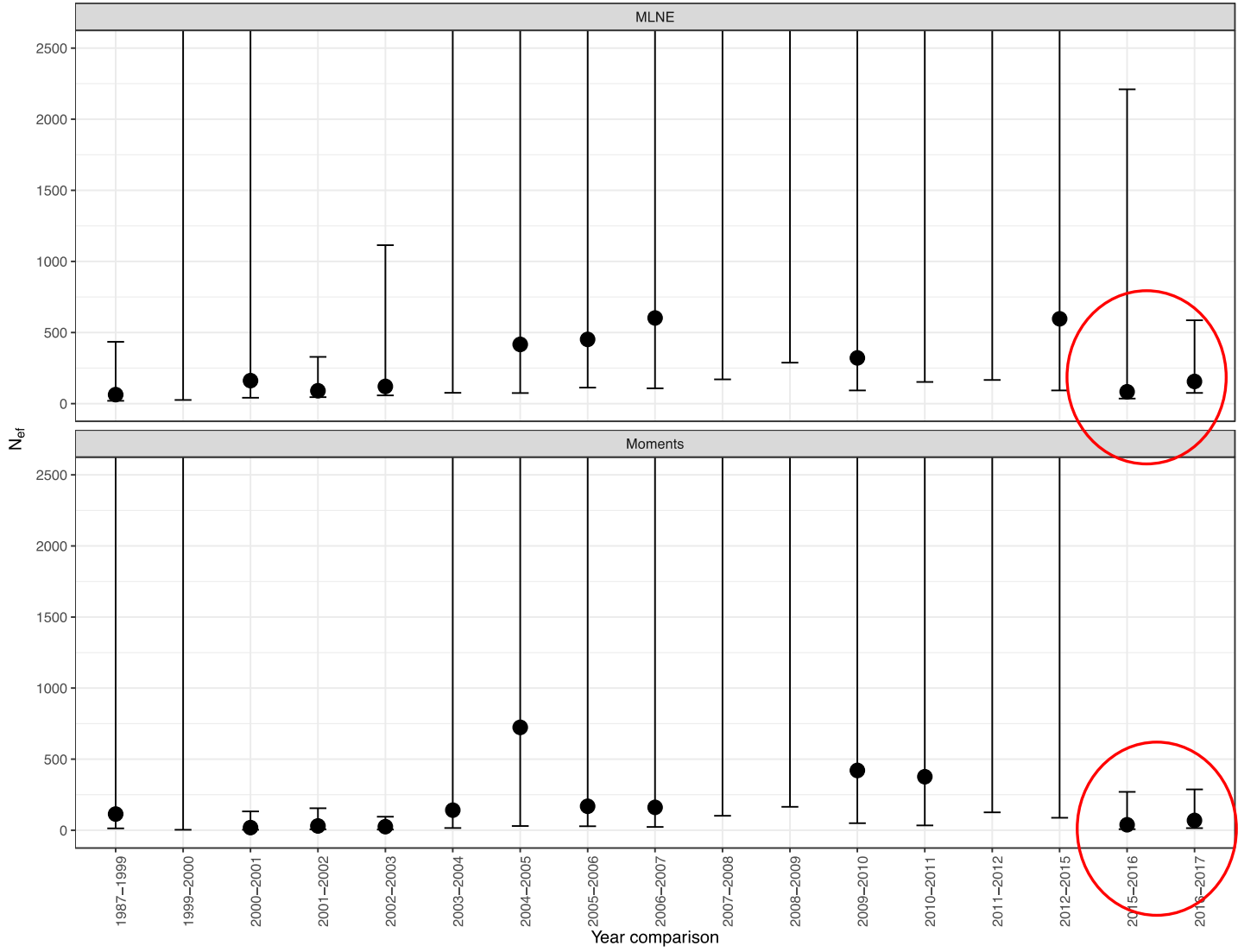


- **How it is estimated:** Allele frequency changes
- **What it measures:** Loss of genetic variation from GENETIC DRIFT
- **Number of temporal samples:** 2
- **Increase in  $N_{eV}$  over previous estimate**

# OBJECTIVE 4

## Female Variance Effective Population Size (mtDNA)

- Marginal increase from 2015-2016 estimate



## OBJECTIVE 5

# Genetic diversity: Captive stocks 2017

Captive spawned	N	$N_{ac}$	$H_{ec}$	$H_{oc}$	$F_{IS}$	$N_{eD}$	-95%	95%	N	$N_h$	h	$H_R$
<b>ABP13-003-04 WC</b>	50	13.8*	0.81	0.70	0.13	407	190	infinite	50	5	0.75	5.00
<b>ABP16-003 CS</b>	39	12.9*	0.83	0.74	0.11	79	50	161	39	5	0.53	5.00
<b>Uvalde 2016</b>	100	12.1*	0.79	0.70	0.11	46	36	62	100	7	0.75	5.17
<b>16CSDX-003</b>	100	13.2*	0.80	0.72	0.10	104	80	141	100	6	0.77	6.10
<b>16CSDX-004</b>	98	10.6*	0.80	0.74	0.08	30	25	37	98	6	0.71	5.28
<b>16CSDX-005</b>	100	12.1*	0.80	0.73	0.09	55	41	75	100	6	0.72	5.09
<b>Global 2017 Hatchery</b>	484	13.8*	0.81	0.73	0.11	179	120	284	484	10	0.74	5.08

- Diversity falls below benchmarks
- Number of alleles is a more sensitive metric of loss of diversity
- Larger number of individuals spawned in captivity to maintain diverse captive populations

# Genetic Diversity: Broodstock

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Captive spawned	N	$N_{ac}$	$H_{ec}$	$H_{oc}$	$F_{IS}$	$N_{eD}$	-95%	95%		N	$N_h$	h	$H_R$
ABQ Biopark-Bs	110	14.2	0.81	0.69	0.15	966	314	infinite		110	5	0.66	4.73
SNARCC- Bs	59	12.7	0.82	0.69	0.16	616	169	infinite		59	7	0.73	6.53

- Allelic diversity falls below benchmarks for both facilities
- Observed heterozygosity also approaches lower benchmark

# Conclusions

- MRG population
  - Gene diversity and heterozygosity exceeded minimum benchmark levels of diversity
  - Strong recruitment in fall 2016, larger effective population size
  - Allelic diversity declined in 2017 and approached benchmark values
    - Replacement of 'wild' population with captive derived stocks
  - Genetic effective size in 2017 increased over recent estimates
    - Reduced genetic drift between 2016 and 2017
    - Strong recruitment
- Captive stocks for release/broodstock
  - Allelic diversity below benchmark levels
  - Broodstock- observed heterozygosity also approaches lower benchmark
  - Increasing the number of individuals used in captive spawning
  - Parentage analysis of fish released in fall 2017



# Acknowledgements

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- ❖ Bureau of Reclamation- funding
- ❖ UNM: Tyler Pilger, Brian Fitzgerald, Mia Coleman, Alyssa Sanchez, Charisa Bell
- ❖ UNM Molecular Biology Facility
- ❖ Museum of Southwestern Biology– Lex Snyder