



Genetic monitoring in Rio Grande Silvery Minnow using Genotyping-in- Thousands by Sequencing

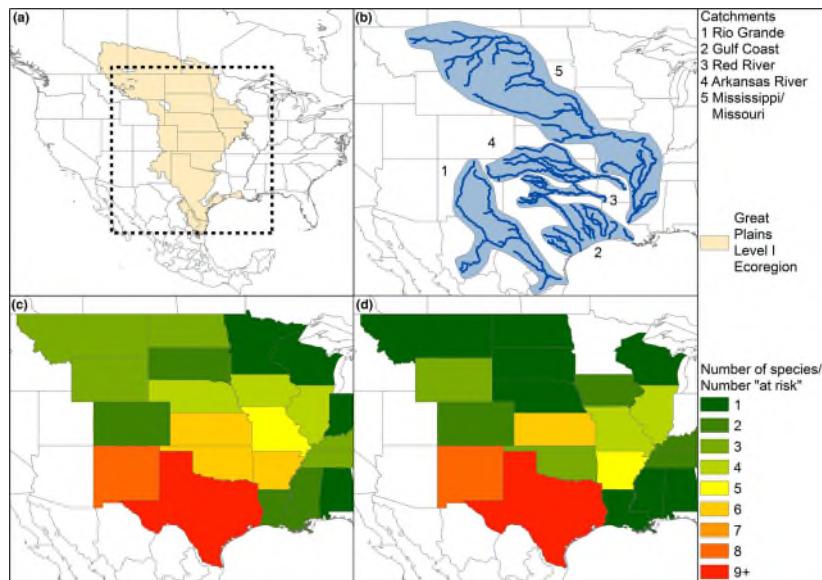


M. Osborne, G. Caeiro-Dias, T. Turner



Pelagic broadcast spawning minnows

Drought results in recruitment failure of Rio Grande silvery minnow (*Hybognathus amarus*), an imperiled, pelagic broadcast-spawning minnow



Rapid intensification of the emerging southwestern North American megadrought in 2020–2021

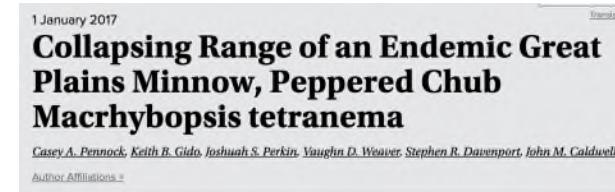
A. Park Williams¹, Benjamin I. Cook^{2,3} and Jason E. Smerdon²

Freshwater Biology

ORIGINAL ARTICLE | Open Access

No quarter: Lack of refuge during flow intermittency results in catastrophic mortality of an imperiled minnow

Thomas P. Archdeacon¹ & Justin K. Reale¹



Extreme drought causes fish recruitment failure in a fragmented Great Plains riverscape

Joshua S. Perkin¹, Trevor A. Starks, Casey A. Pennock, Keith B. Gido, Garrett W. Hopper, Skyler C. Hedden

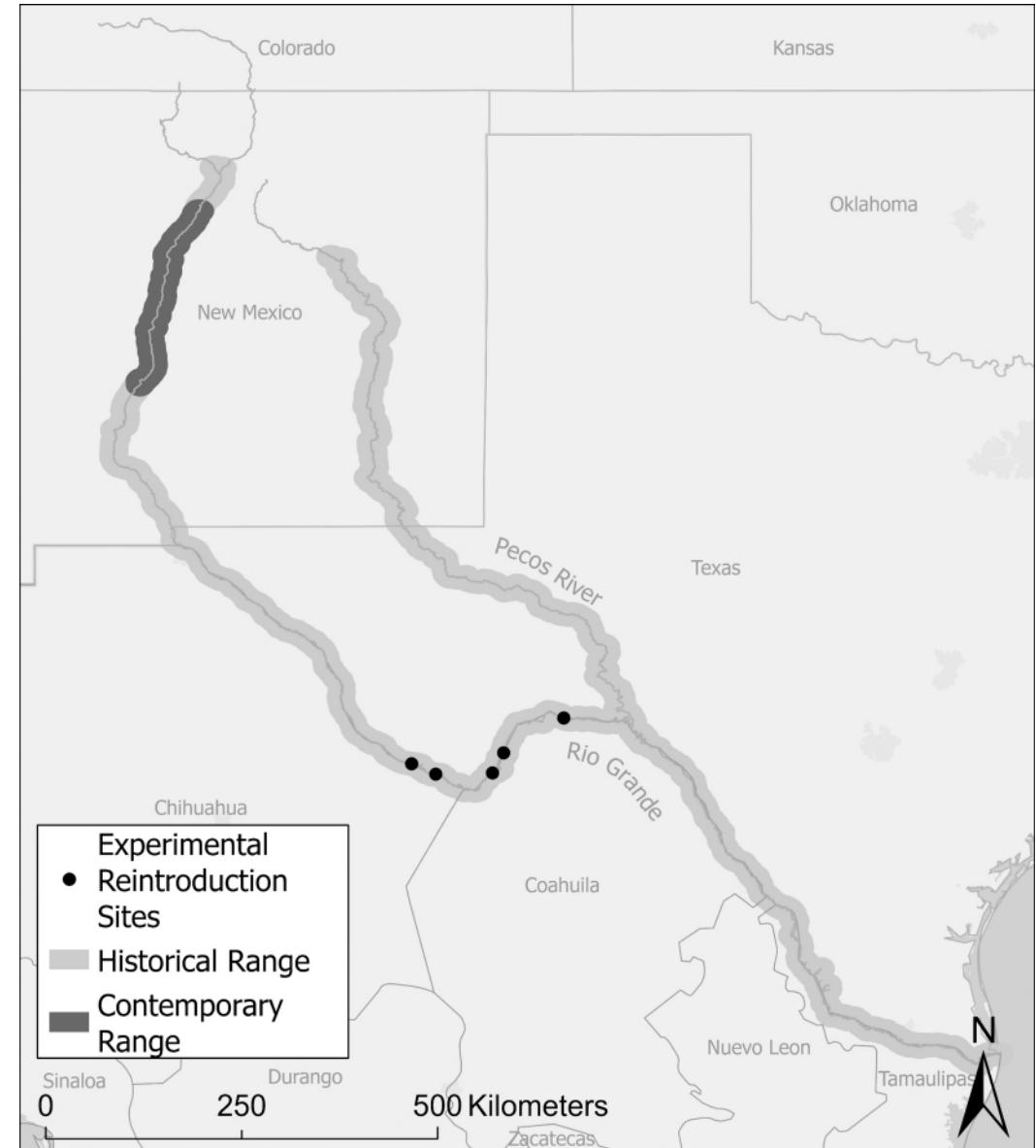
First published: 05 June 2019 | <https://doi.org/10.1002/eco.2120>



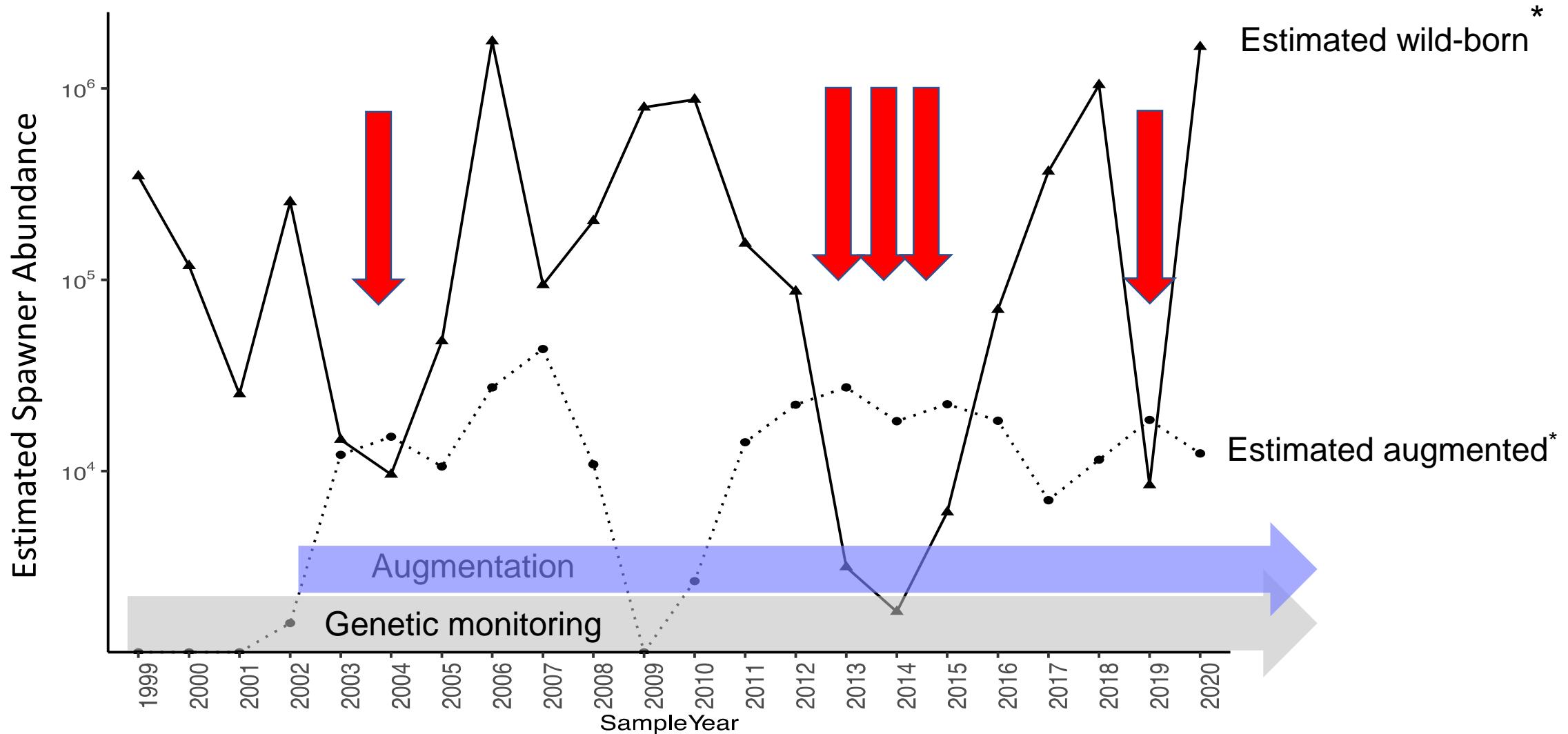
Rio Grande silvery minnow (*Hybognathus amarus*)

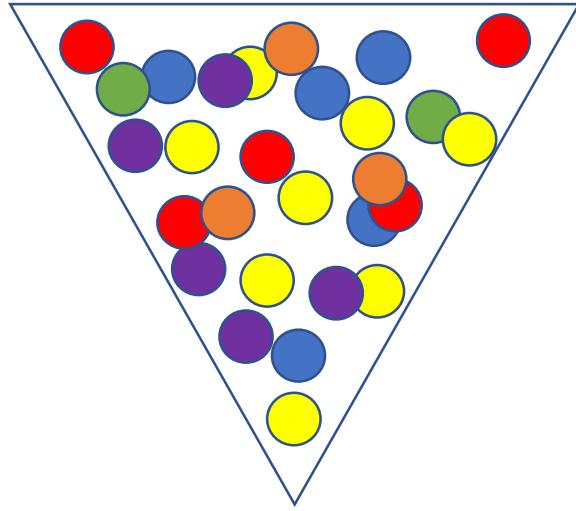
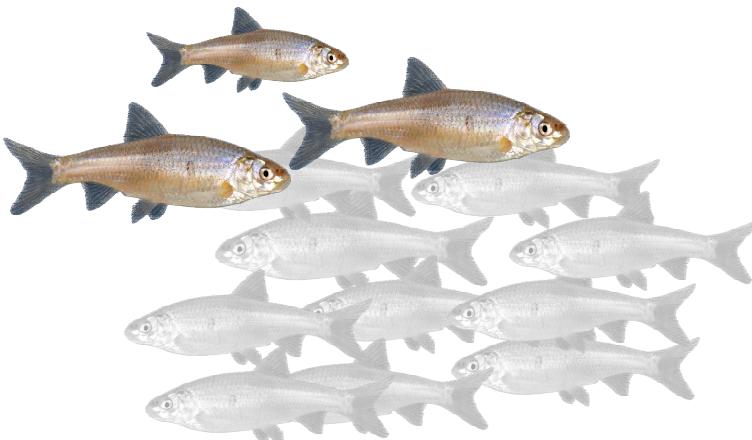
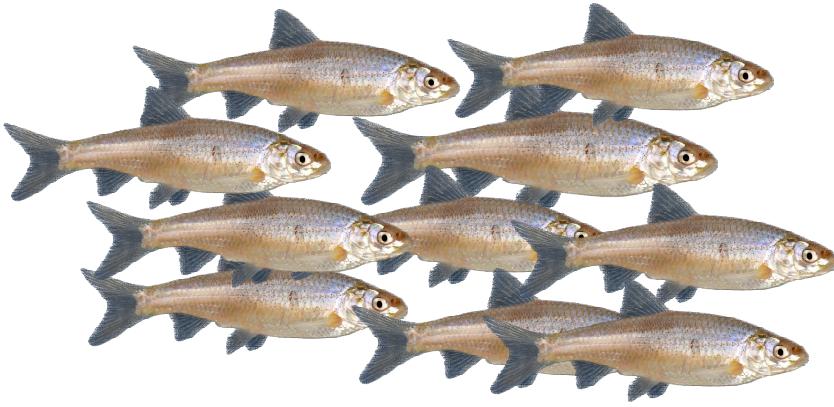


- Distribution: Rio Grande and Pecos River
- Small-bodied, short-lived
- Only member of PBS guild remaining in the Rio Grande (NM)
- Spawning associated with increases in flows/temperature (i.e., snow-melt) spring
- Abundance linked to spring flows & extent of summer drying

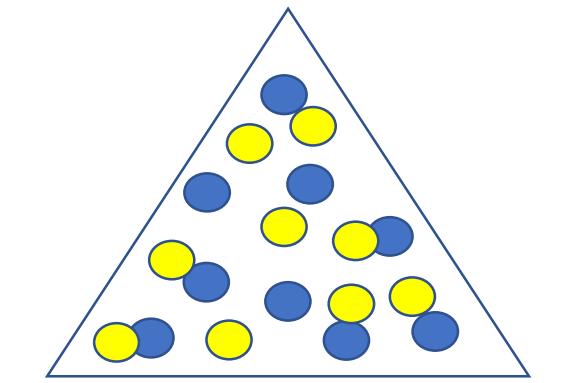


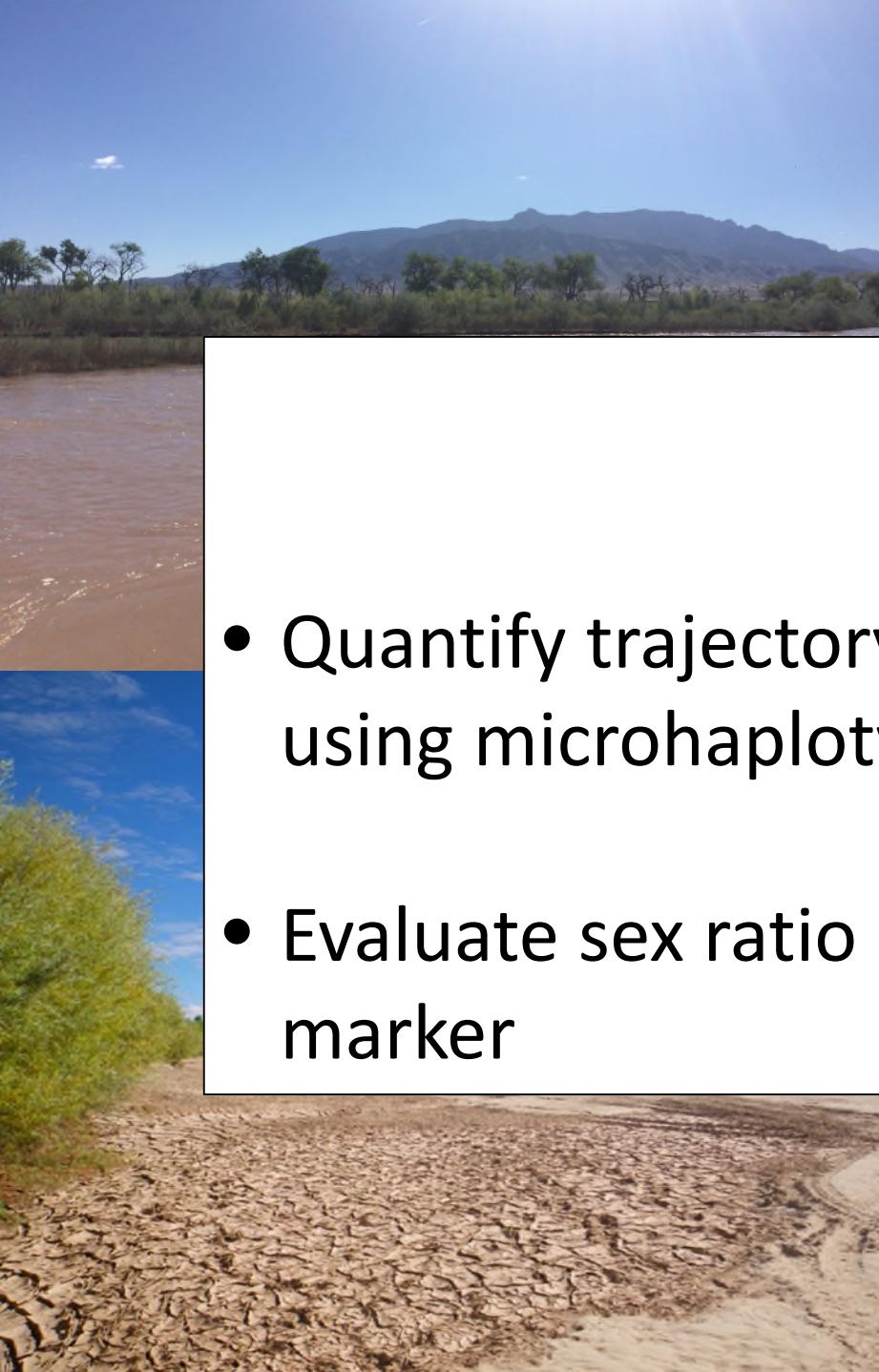
Changes in abundance from year to year & inputs from the hatchery
may change genetic characteristics of the population





Genetic drift: random change
in allele frequencies





Why conduct genetic monitoring?

Objectives

- Quantify trajectory of genetic change over past two decades using microhaplotypes (GT-seq panel)
- Evaluate sex ratio in the wild population using sex-specific marker

-
- Genetic diversity affected over contemporary time scales

Microsatellites/ MtDNA

- 1999-2022
- ~450 samples/year
- Wild (n=6,889)
- Hatchery (5,291)
- 9 loci



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Genetic monitoring and complex population dynamics: insights from a 12-year study of the Rio Grande silvery minnow

Megan J. Osborne, Evan W. Carson, Thomas F. Turner



CONTRIBUTED PAPERS | Full Access

Genetic erosion in an endangered desert fish during a megadrought despite long-term supportive breeding

Megan J. Osborne , Thomas P. Archdeacon, Charles B. Yackulic, Robert K. Dudley, Guilherme Caeiro-Dias, Thomas F. Turner

1999

2012

2015

2022

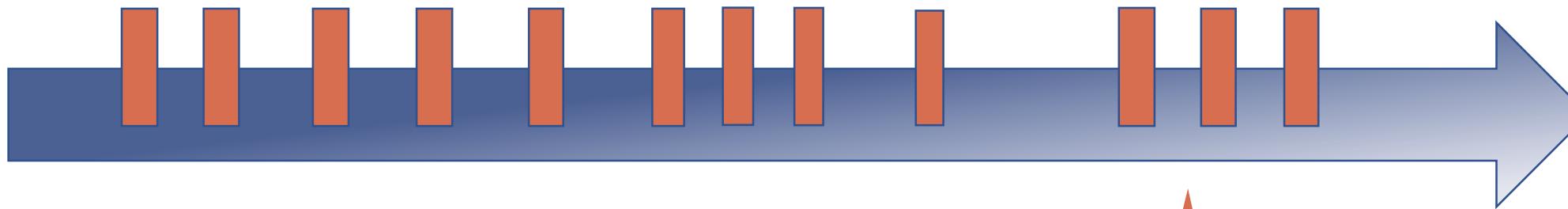
1987



Microsatellites/ MtDNA

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- Hatchery (5,291)
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1999 - - - - - 2012 2015 - - - - 2018



SNP Discovery

- Draft genome (Illumina)
- 30-40 archived samples
- Min. every 2 years (1999-2012)
- Spanning major population bottlenecks
- Microhaplotypes (3,151 loci 5,549 SNPs)
- n=366
- Mitogenomes (n=106)

MOLECULAR ECOLOGY

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Transitioning from microsatellites to SNP-based
microhaplotypes in genetic monitoring programmes: Lessons
from paired data spanning 20 years

Megan J. Osborne Guilherme Caeiro-Dias, Thomas F. Turner

Microsatellites/ MtDNA

- 1999-2022
- ~450 samples/year
- Wild (n=6,889)
- Hatchery (5,291)
- 9 loci

- ~96 samples/year
- 283 loci
- 1987, 1999-2024
- Sex-specific marker
- Chromosome-level genome assembly

Gt-Seq Panel

1999

2012

2015

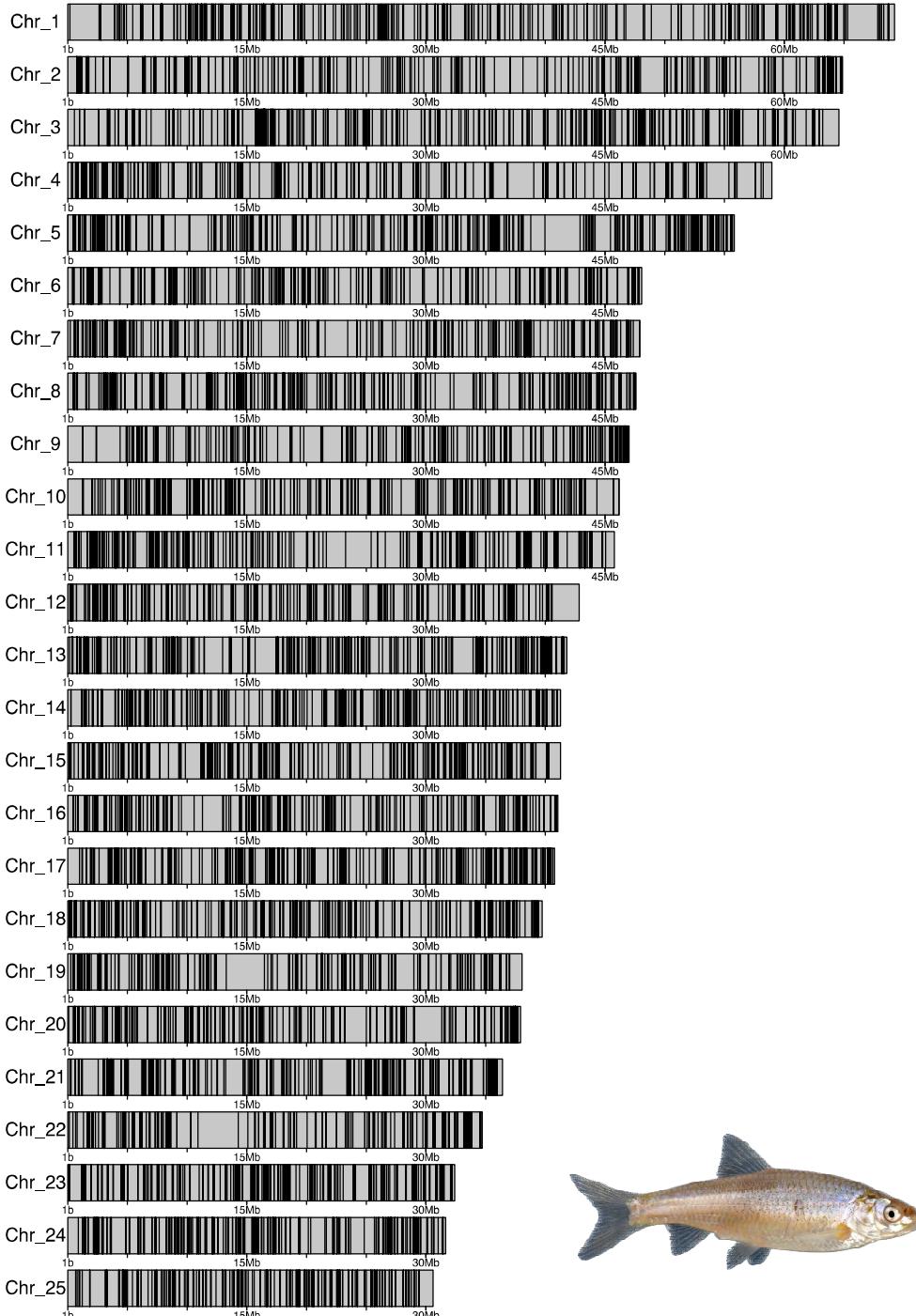
2024

1987



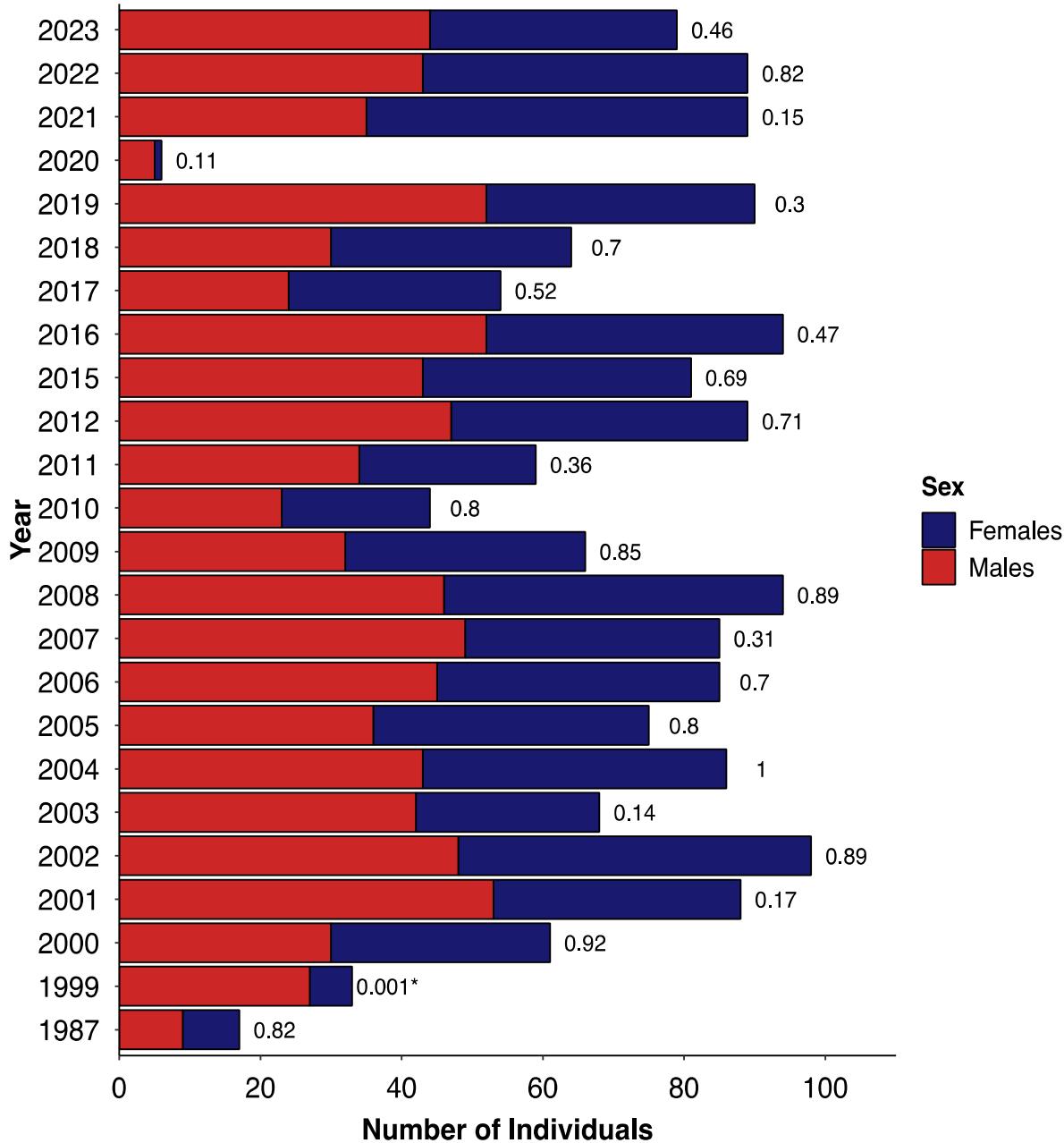
SNP Discovery

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Wild-MRG	N
1987	27
1999	-
2000	92
2001	93
2002	103
2003	86
2004	93
2005	90
2006	93
2007	94
2008	96
2009	89
2010	62
2011	78
2012	94
2013	-
2014	-
2015	93
2016	94
2017	50
2018	61
2019	93
2020	86
2021	86
2022	89
2023	93

- Unmarked fish sampled within each river reach 1987, 1999-2024
 - Angostura
 - Isleta
 - San Acacia
- Genotyped ~ 100 samples per year using **Genotyping-in-Thousands by Sequencing panel** (283 loci and 1 sex specific marker)

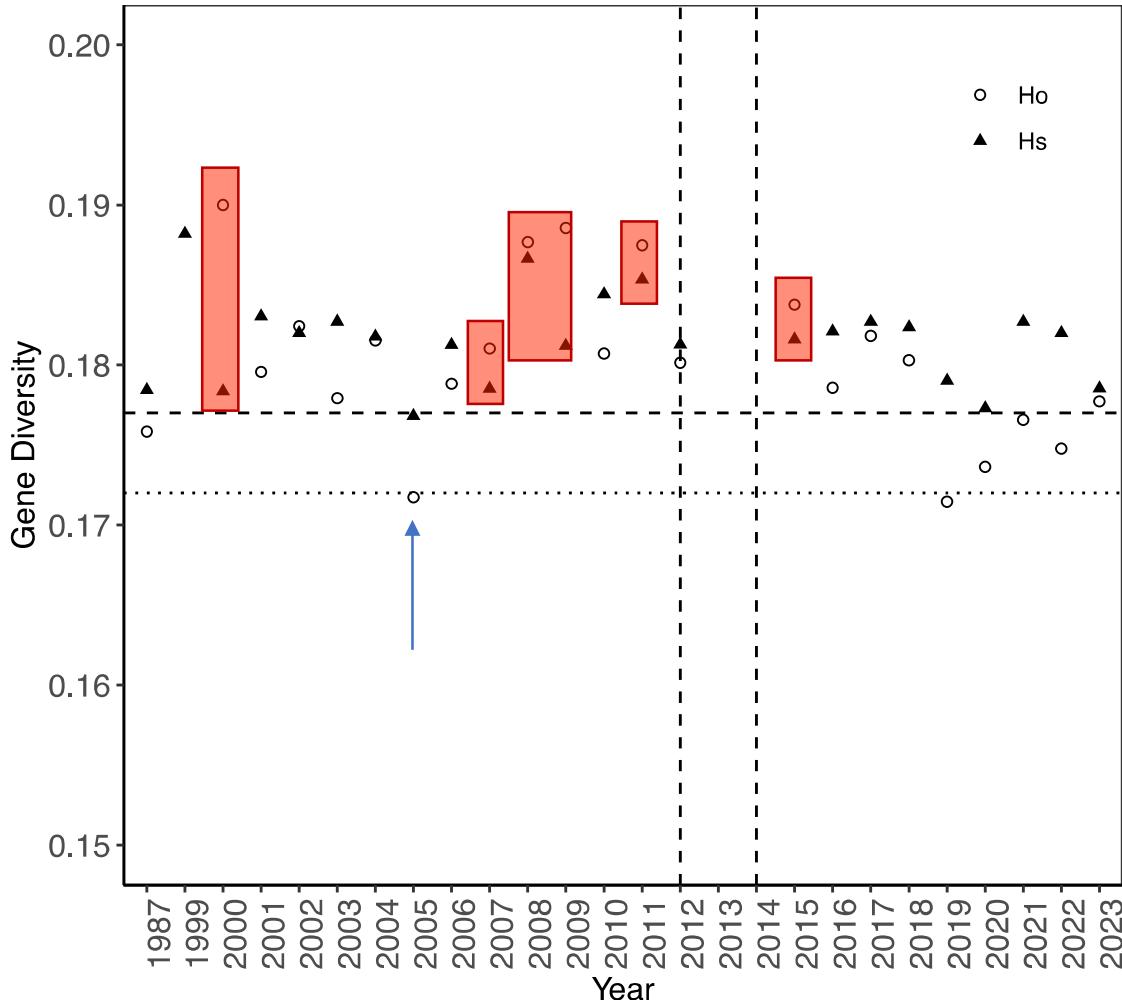


Why is the sex ratio important?

- Biased sex ratio reduces effective population size (N_e)
- Smaller N_e increases rate of genetic diversity loss
- **RGSM: Equal sex ratio**

Key point

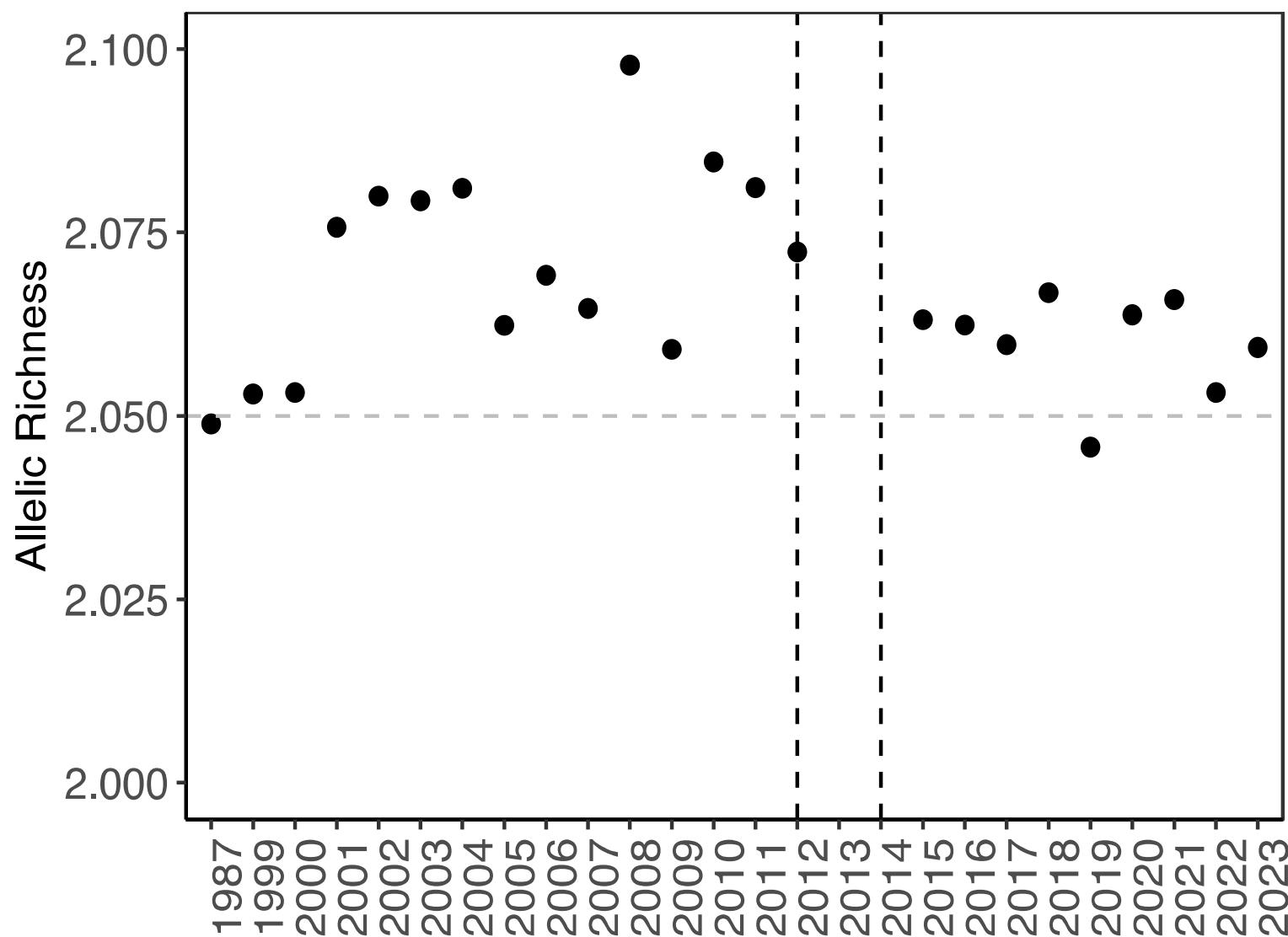
Decreases in observed heterozygosity following multiyear population bottleneck (vertical lines)



- Most values above benchmarks (horizontal lines) from 2002-2015
- Augmentation stabilized genetic diversity (H_s , H_o)-through 2018
- Significant reduction in H_o 2015-2023 compared to 2004-2012
- H_o exceeds H_s in some years: indicative of population bottlenecks

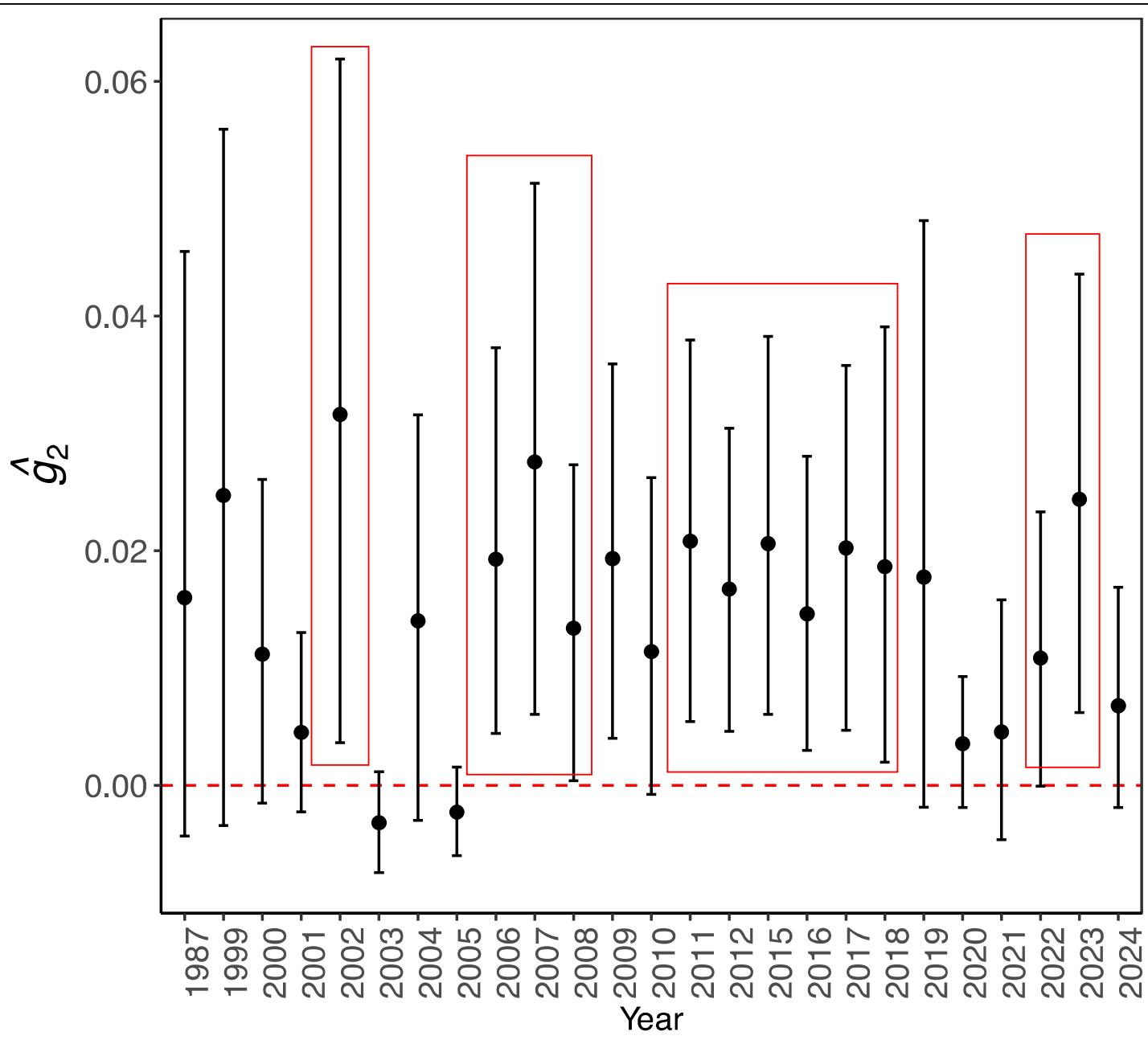
Key points

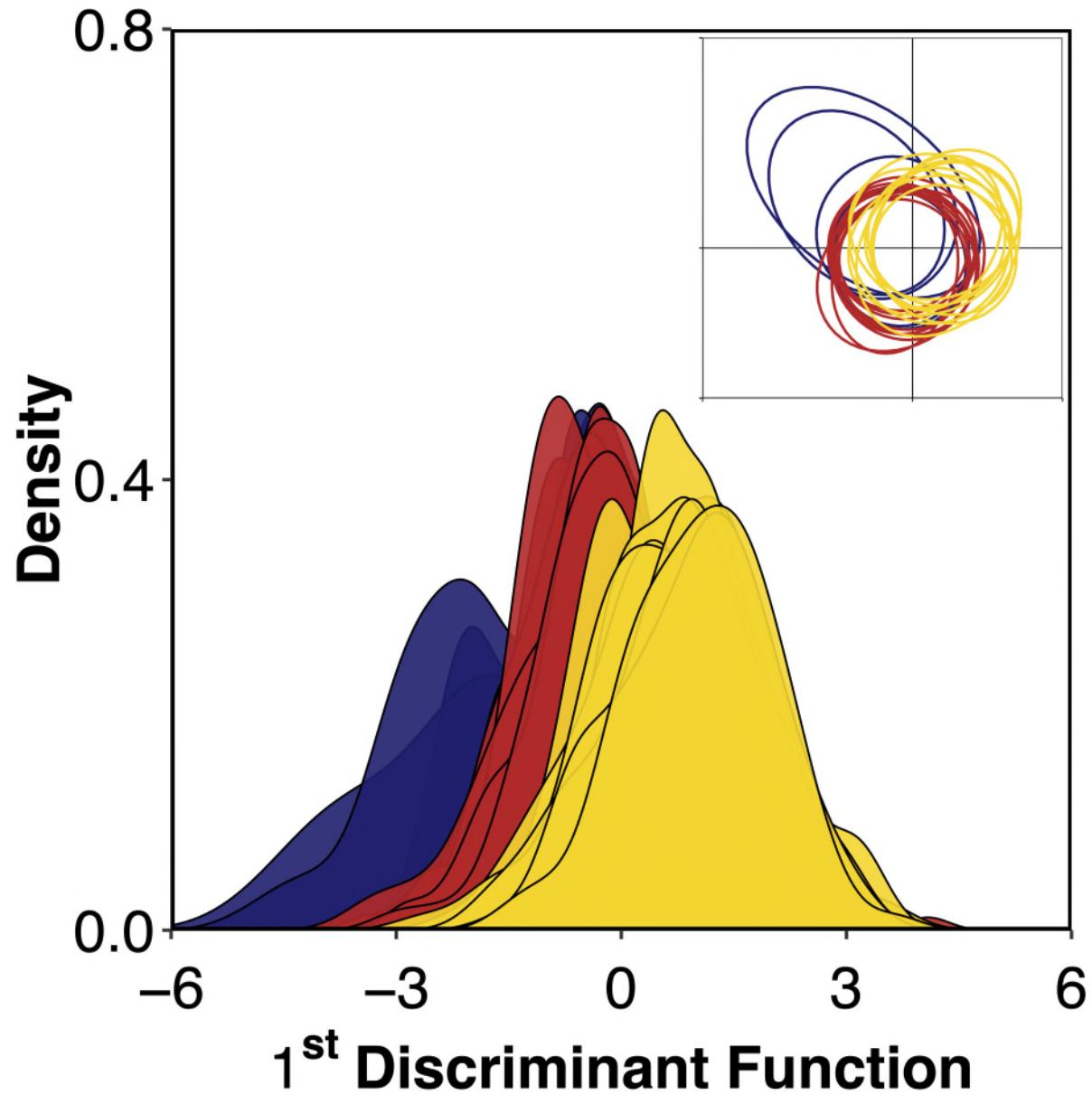
- Genetic drift associated with population bottleneck and augmentation
- Significant decrease in allelic diversity following multiyear population bottleneck (2012-2014)



Key points

- g_2 is a population parameter that summarizes the variance in inbreeding
- g_2 affected by demographic history
- 12 significant g_2 values ($g_2 > 0$) indicating variance in inbreeding



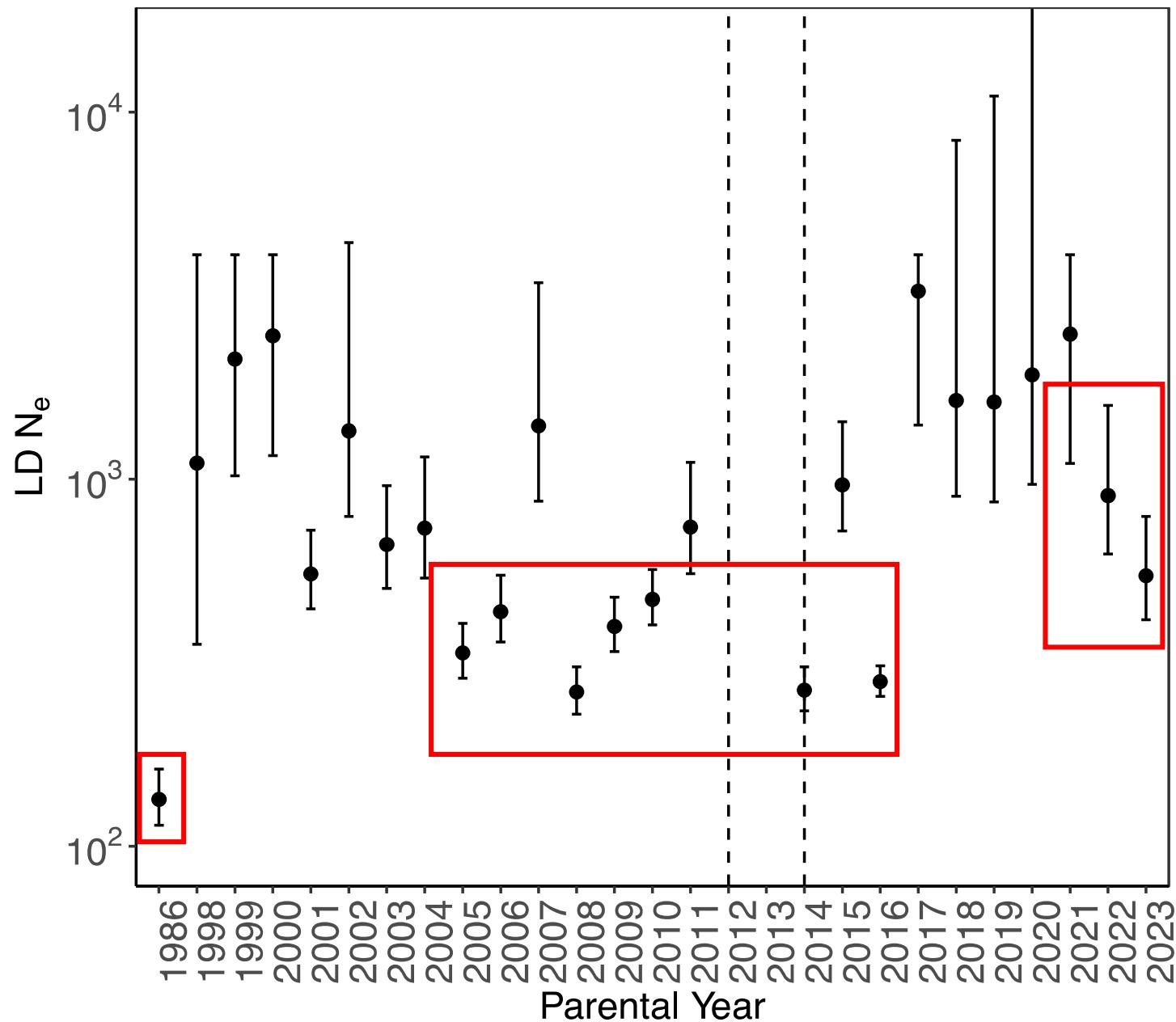


- Microhaplotypes record shifts in allele frequencies associated with population bottlenecks/augmentation
- Consistent with microsatellite data and microhaplotypes from 3,151 loci.

Why is the N_e important?

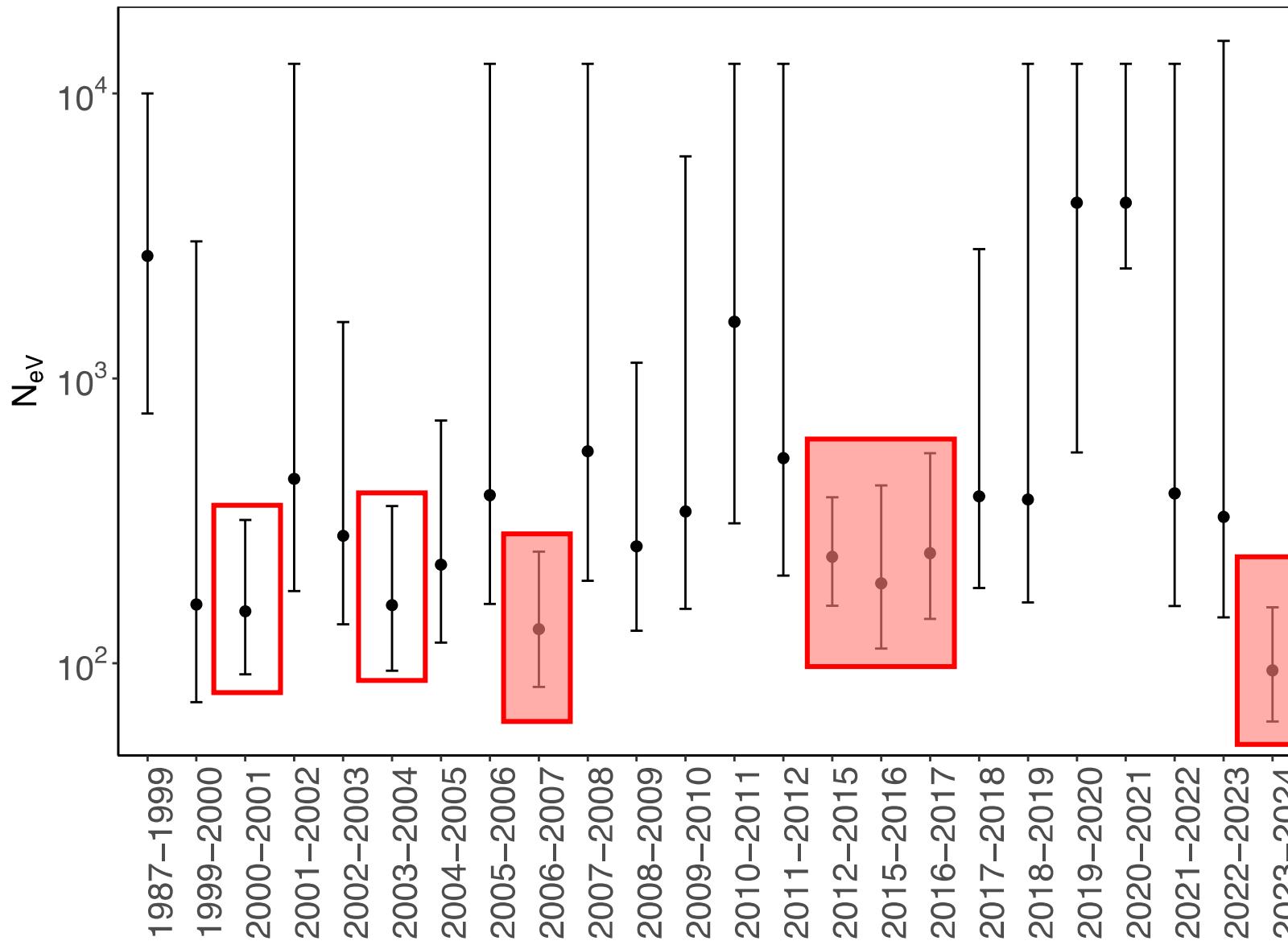
- Determines how fast genetic diversity is lost
- Small N_e – more rapid loss of diversity
- Provides insights into population demography

Effective Population Size



- Microhaplotypes detect declines associated with periods of reduced spring abundance (e.g., 2013-2015, 2023, 2024)
- Increases in $\text{LD } N_e$ 2017-2021
- **Large $\text{LD } N_e$ decline in most recent samples**
- Narrower CIs compared to estimates based on microsatellites
- Increased power of GT-seq panel

Effective Population Size



- N_{eV} - genetic drift
- Microhaplotypes detect declines associated with periods of reduced spring abundance (e.g., 2000-2001, 2003-2004) and high hatchery-origin: wild (e.g. 2006-2007, 2012-2015, 2015-2016)
- Increased genetic drift = low N_{eV}
- Increases in N_{eV} 2017-2021

GT-seq panel provides new insights & supports previous data

- Equal sex ratio in wild population
- Reduction in allelic diversity and observed heterozygosity in recent years
- Identifies periods of reduced N_e and temporary increases in a population-level inbreeding
- Microhaplotypes record shifts in allele frequencies associated with population bottlenecks & augmentation



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