

# Genetic Rescue in Headwater Trout

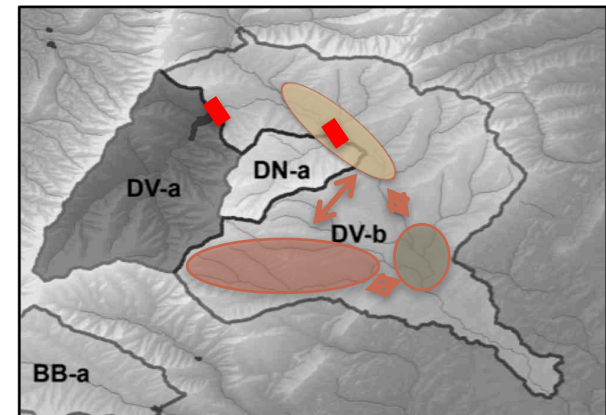
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Wildlife Biology Program  
Montana Conservation Genomics Lab  
University of Montana



# Conservation Prioritization

- Which population(s) do we conserve?
  - Intact metapopulations
    - Maintain ‘portfolio effect’
  - Restore connectivity to small isolated populations when possible
    - If restoration of natural connectivity is not feasible, should we assist gene flow?

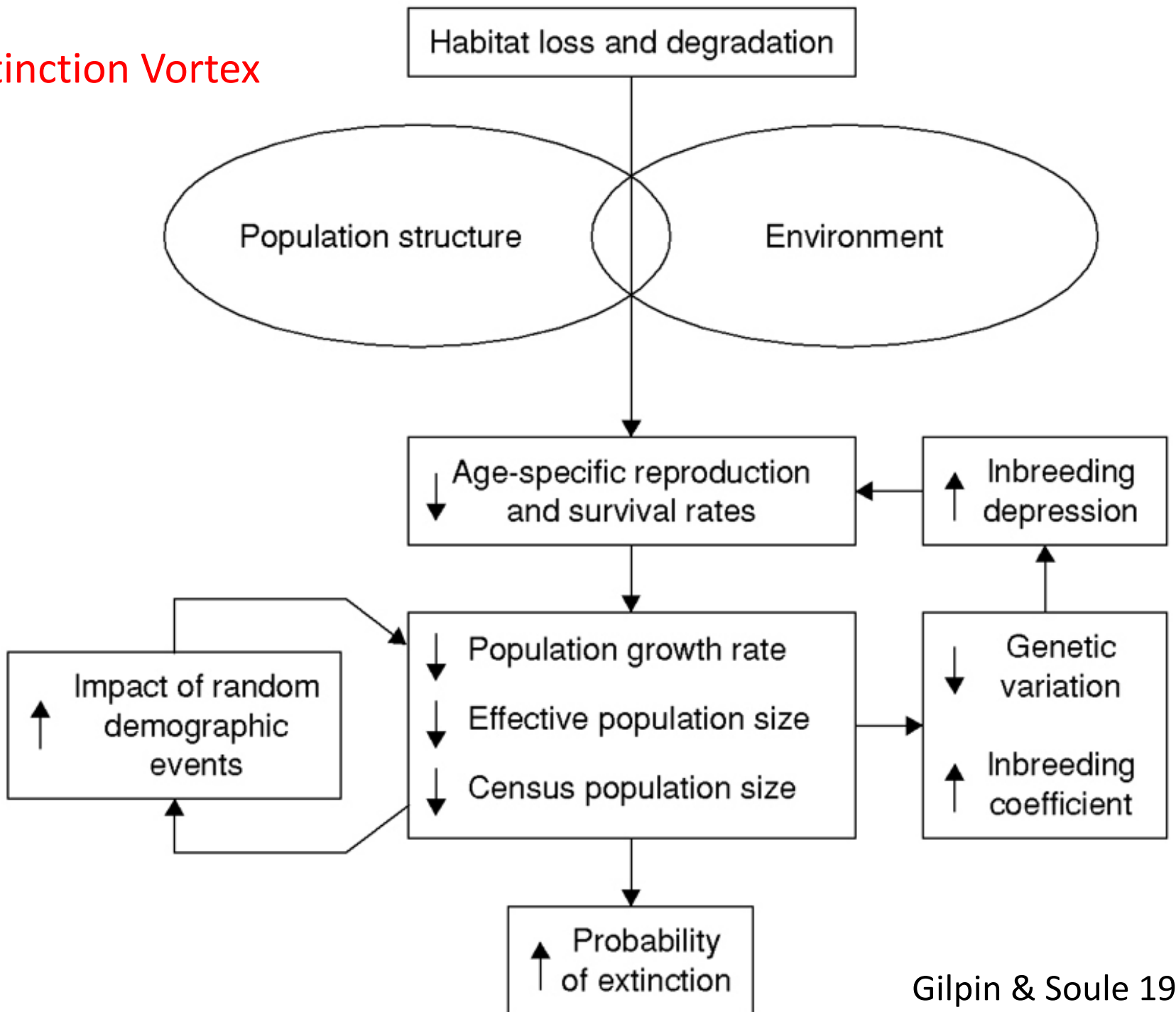


# Genetic Rescue

- Definition: a decrease in population extinction probability owing to gene flow, best measured as an
- increase in population growth rates
  - Requires a small amount of gene flow into a small, inbred population (< 10 individuals)
  - Goal is to boost population growth rate, increase in genetic variation and adaptive potential is an additional benefit
  - Primary risk: outbreeding depression



# Extinction Vortex







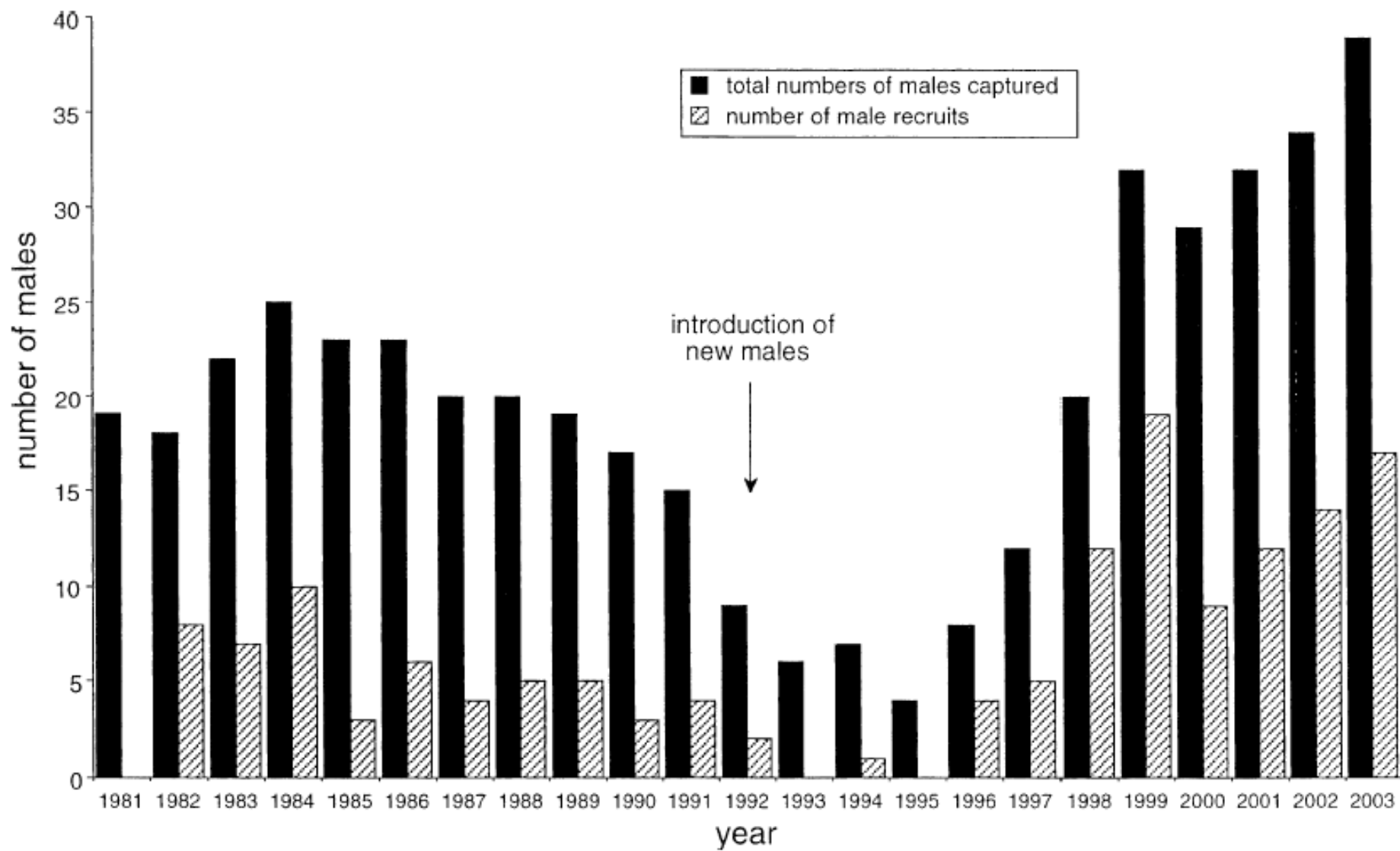


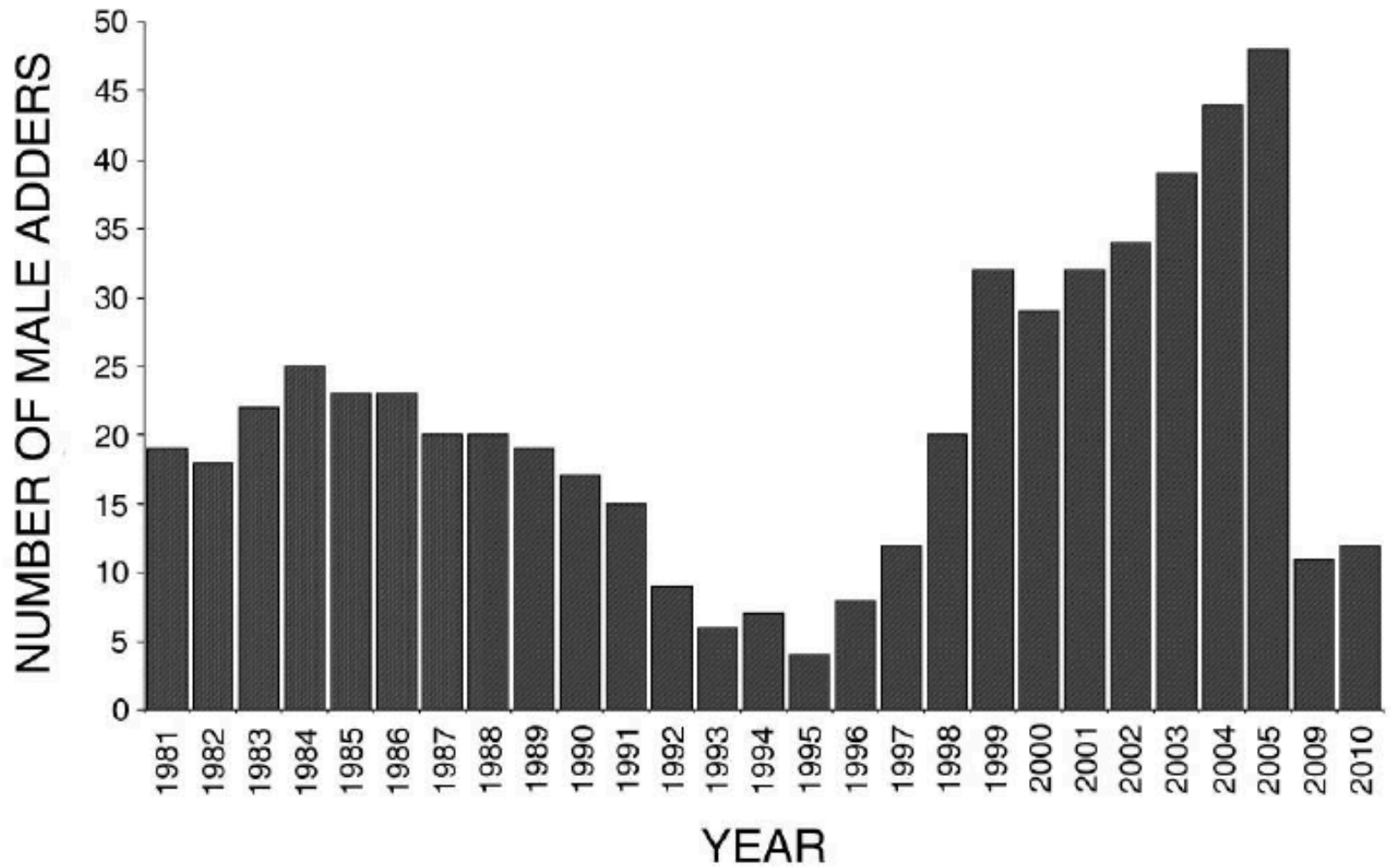
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Conservation biology

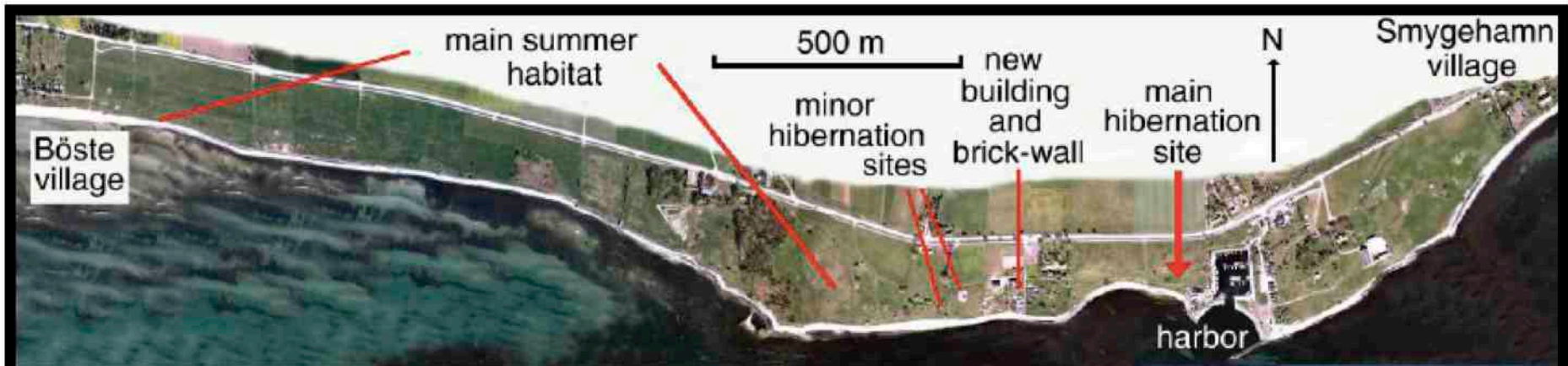
# Restoration of an inbred adder population







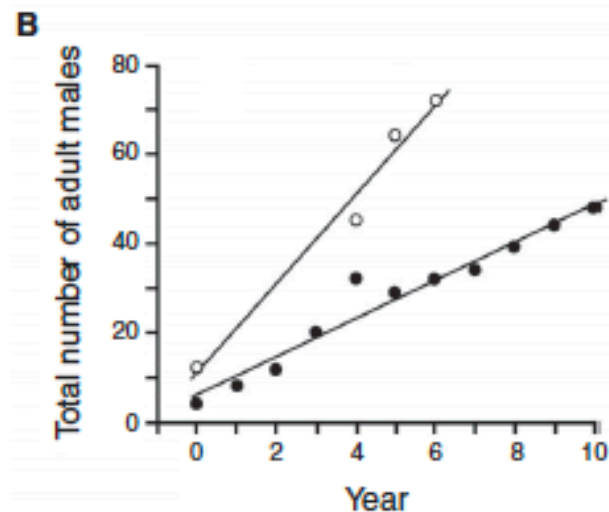
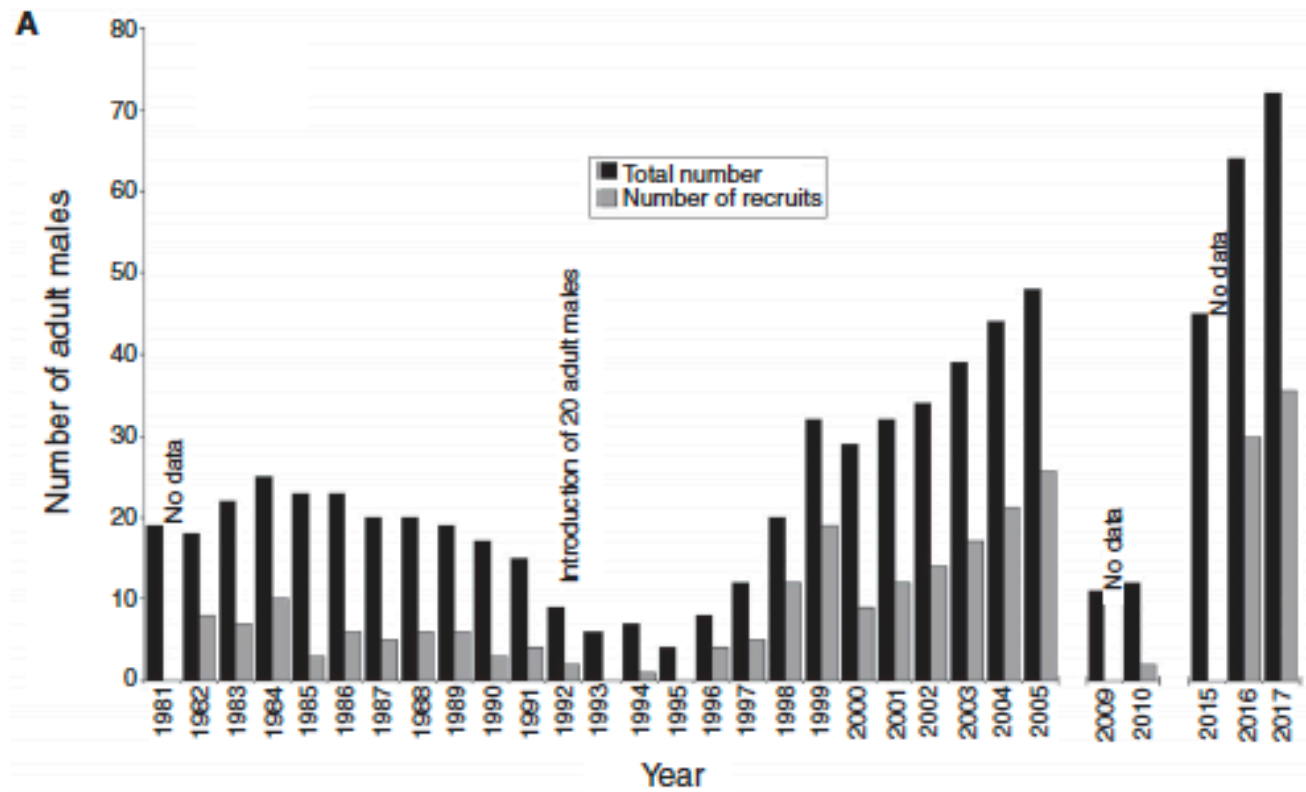




## Correspondence

# Genetic rescue restores long-term viability of an isolated population of adders (*Vipera berus*)

Thomas Madsen<sup>1,2,\*</sup>, Jon Loman<sup>3,6</sup>,  
Lewis Anderberg<sup>4</sup>, Håkan Anderberg<sup>4</sup>,  
Arthur Georges<sup>5</sup>, and Beata Ujvari<sup>2</sup>



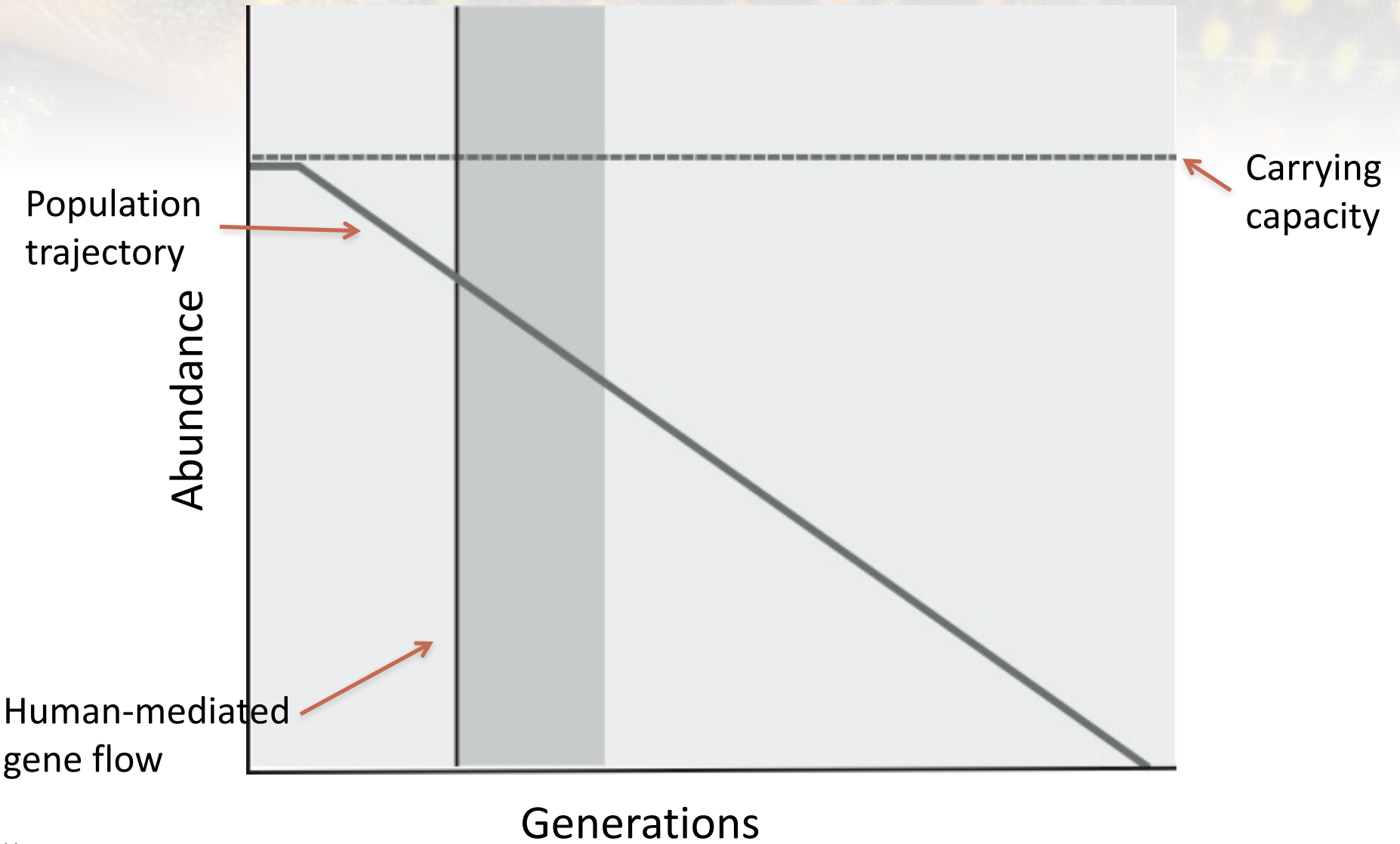
**C**

Year	$H_{obs}$	$H_{exp}$
1991–92	0.181	0.170
2005	0.244	0.237
2017	0.243	0.241

**D**

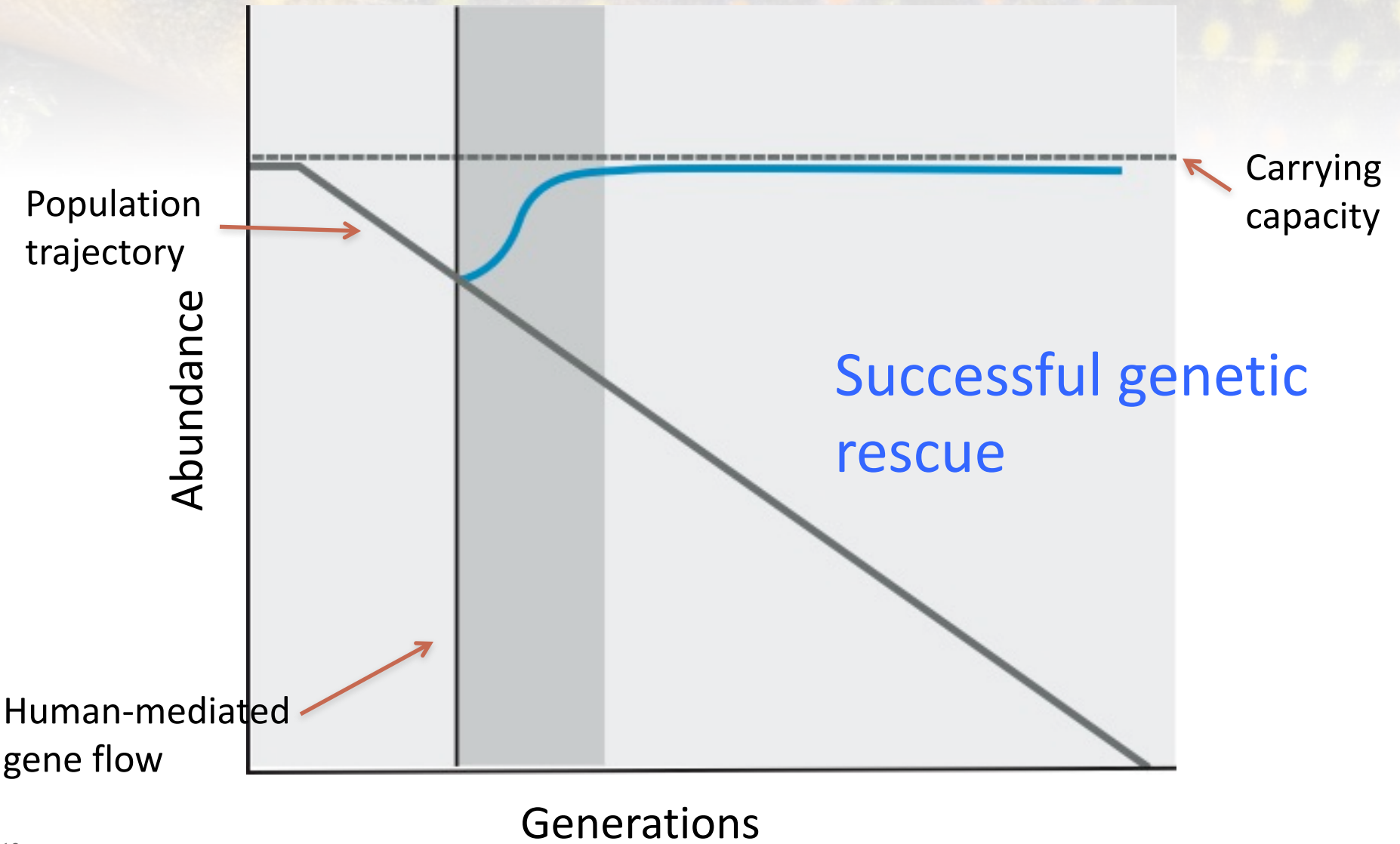
Year	$\Delta H$	p
1991–92 vs 2005	0.066	<0.0001
1991–92 vs 2017	0.070	<0.0001
2005 vs 2017	-0.004	0.0008

Duration of most studies

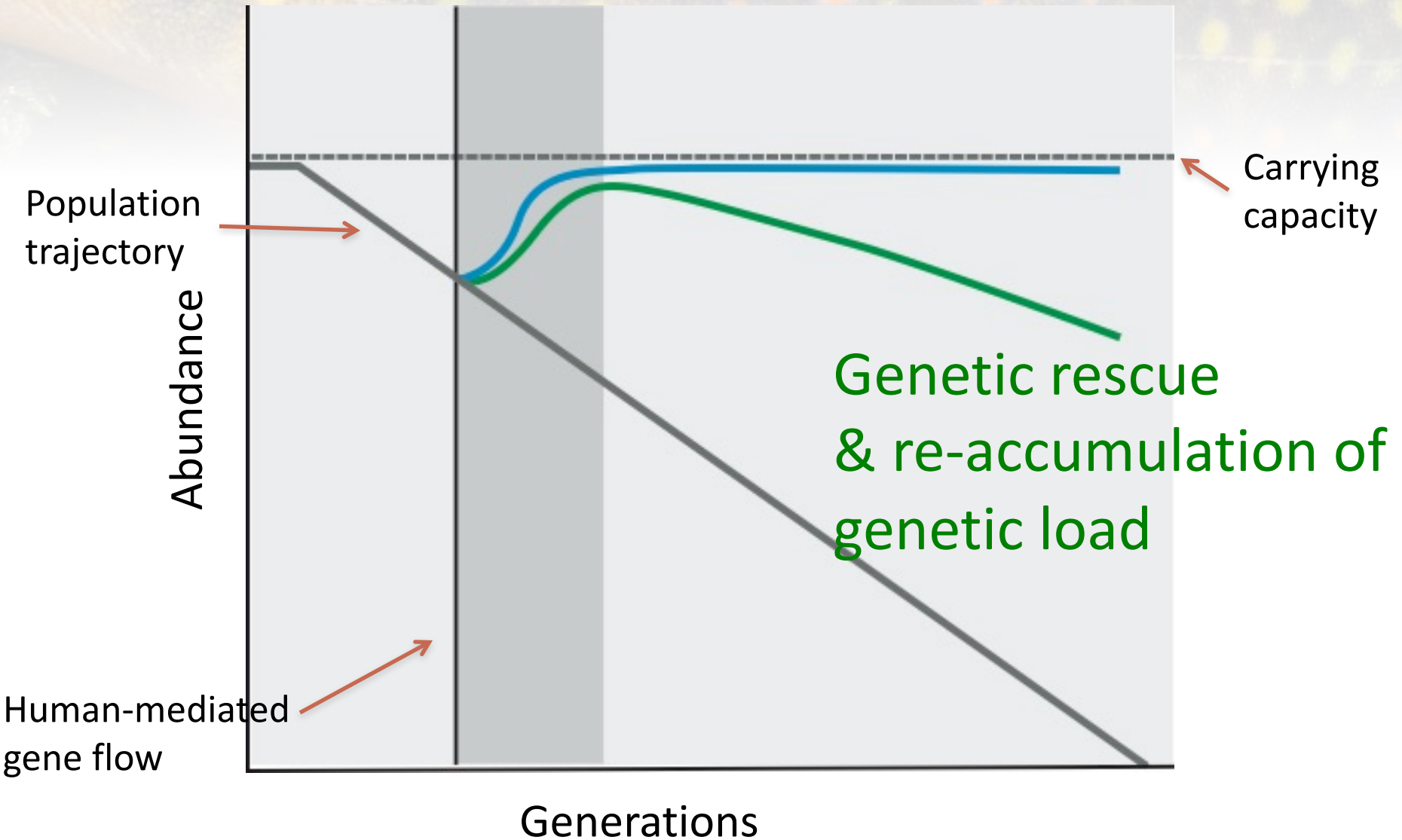




Duration of most studies



Duration of most studies



Carrying capacity

Population trajectory

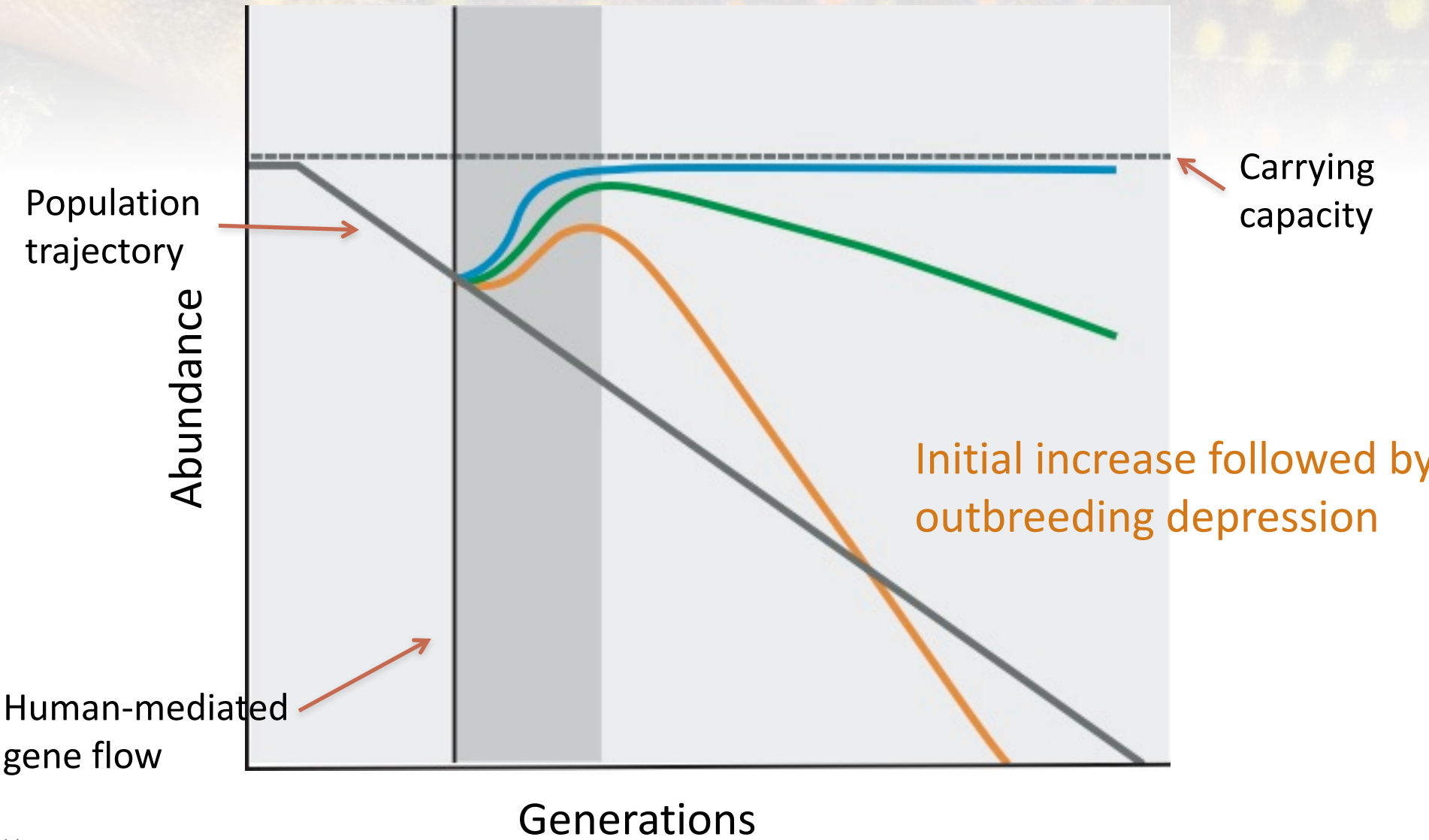
Abundance

Genetic rescue & re-accumulation of genetic load

Human-mediated gene flow

Generations

Duration of most studies





# Emerging Patterns

Review

CellPress

## Genetic rescue to the rescue

Andrew R. Whiteley<sup>1\*</sup>, Sarah W. Fitzpatrick<sup>2\*</sup>, W. Chris Funk<sup>2,3</sup>  
David A. Tallmon<sup>4\*</sup>

<sup>1</sup>Department of Environmental Conservation, University of Massachusetts Amherst, Amherst, MA  
<sup>2</sup>Department of Biology, Colorado State University, Fort Collins, CO 80523, USA  
<sup>3</sup>Graduate Degree Program in Ecology, Colorado State University, Fort Collins, CO 80523, USA  
<sup>4</sup>Department of Biology and Marine Biology, University of Alaska Southeast, Juneau, AK 99801,

Trends in Ecology & Evolution

CellPress  
REVIEWS

Opinion

The Exciting Potential and Remaining  
Uncertainties of Genetic Rescue

Donovan A. Bell,<sup>1,2\*</sup> Zachary L. Robinson,<sup>1,7</sup> W. Chris Funk,<sup>2</sup> Sarah W. Fitzpatrick,<sup>3,4</sup> Fred W. Allendorf,<sup>5</sup>  
David A. Tallmon,<sup>6</sup> and Andrew R. Whiteley<sup>1</sup>

- Evidence strongly supports that re-establishing gene flow among relatively recently connected populations will increase fitness
- Risks occur with strong genetic divergence or when life-history/phenological differences large
- Clear need for more aggressive **replicated tests** and use of GR
- Genomics might help identify source populations or individuals (we aren't there yet)
  - Maximize alleviation of inbreeding depression
  - Minimize risk of outbreeding depression

Whiteley et al. 2015, Bell et al. 2019

# New Paradigm?

- **Call for flipping the script** (Frankham et al. 2017, Ralls et al. 2018)
  - Acknowledges the cost of doing nothing
  - Argues that managed gene flow should be the default consideration
- We agree that more widespread restoration of gene flow is likely called for, but we recommend a more tempered approach, especially in taxa known for local adaptation

# Headwater Trout

- Many inbred and isolated populations
- Managing for isolation to keep non-native species out at times
- But, we also know salmonids are often locally adapted
  - Taxa for which concerns about outbreeding depression justified?



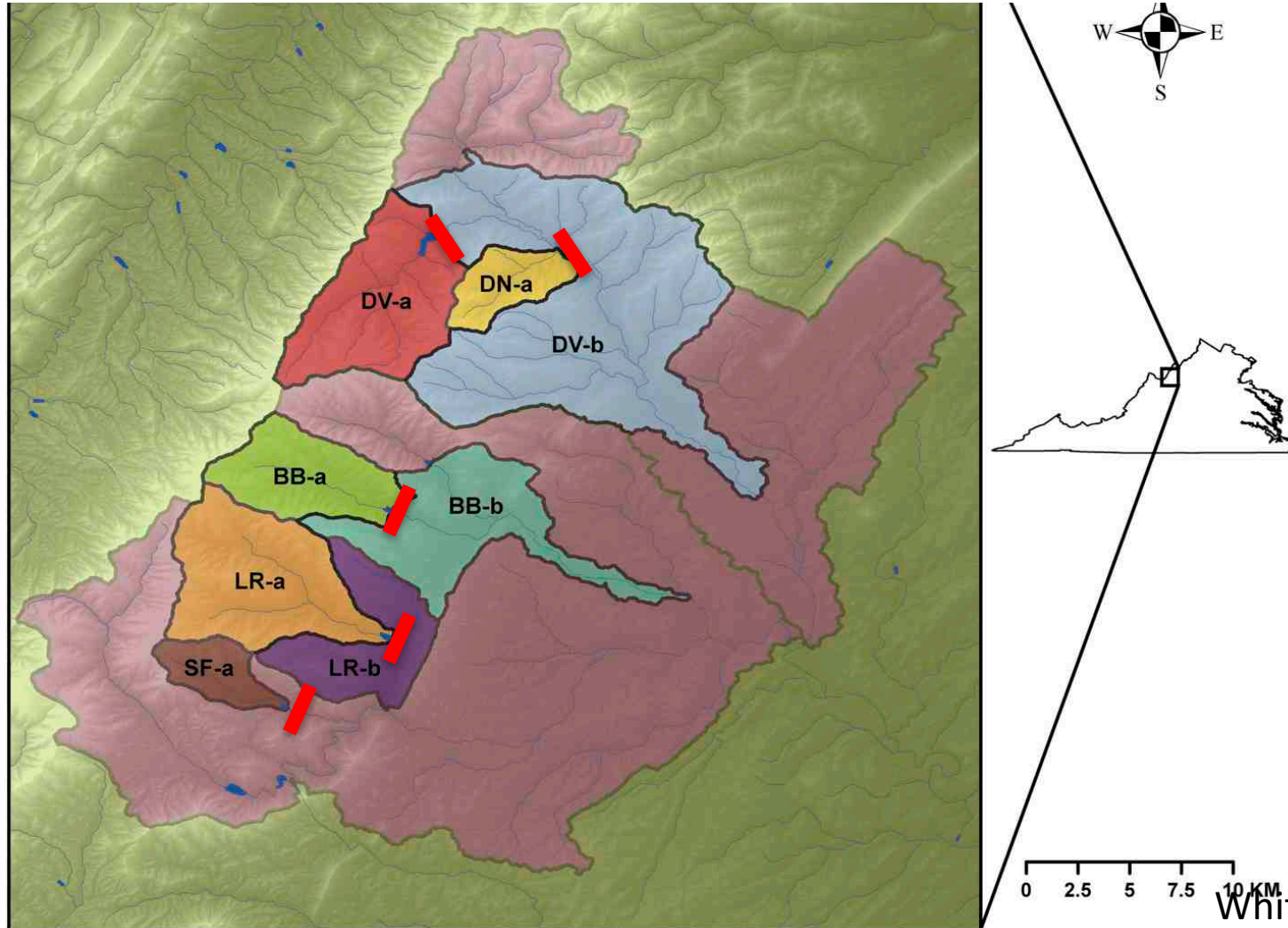
- 
- Data from replicated experiments
  - Brook trout in Virginia
    - Initiated in 2011
  - Westslope cutthroat trout in Montana
    - Initiated in 2017

# Test in Virginia Brook Trout

- We conducted a replicated GR experiment in natural brook trout populations
  - 4 isolated recipient sites
  - 1 isolated control site

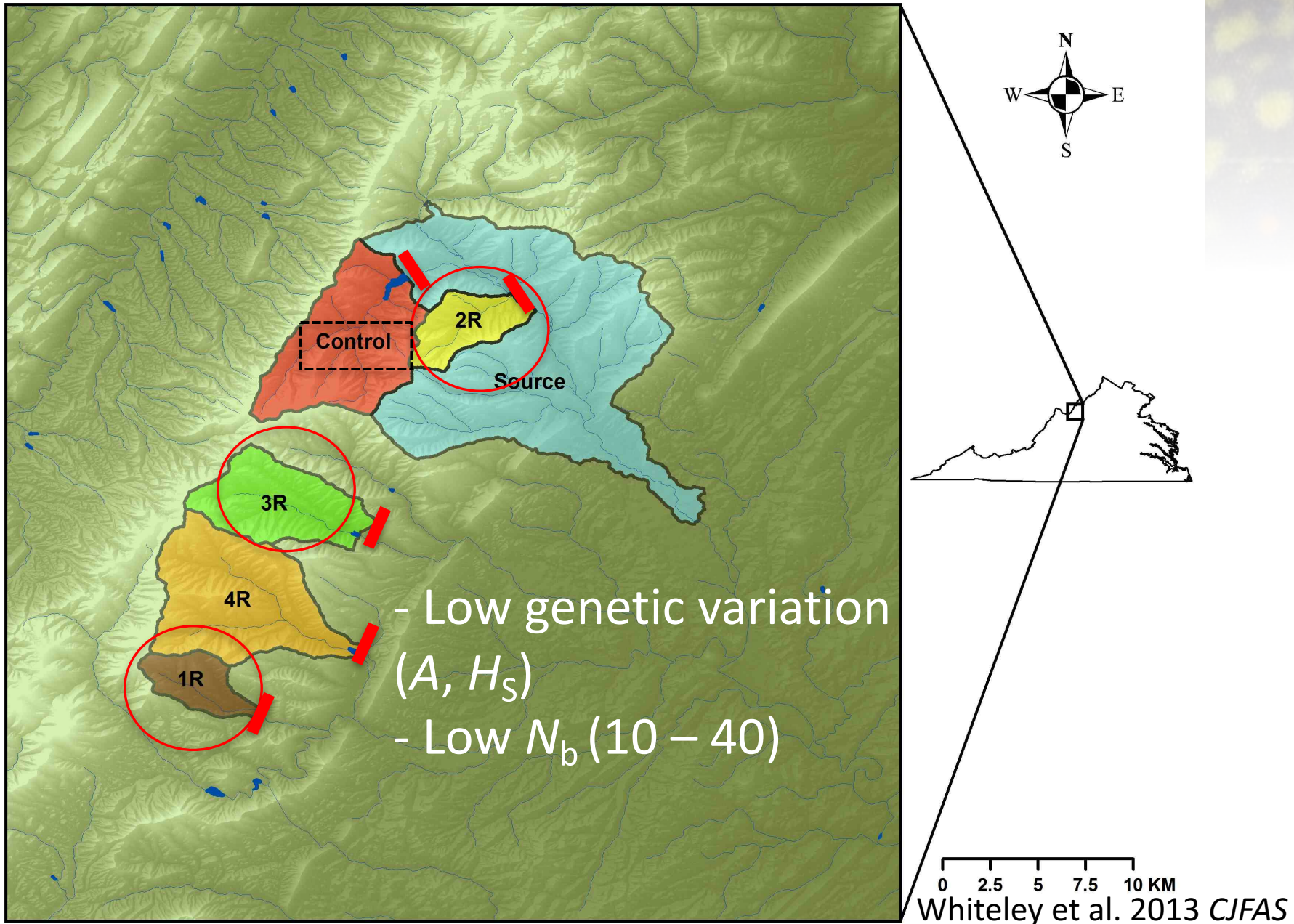
# Fragmentation and patch size shape genetic structure of brook trout populations

Andrew R. Whiteley, Jason A. Coombs, Mark Hudy, Zachary Robinson, Amanda R. Colton, Keith H. Nislow, and Benjamin H. Letcher

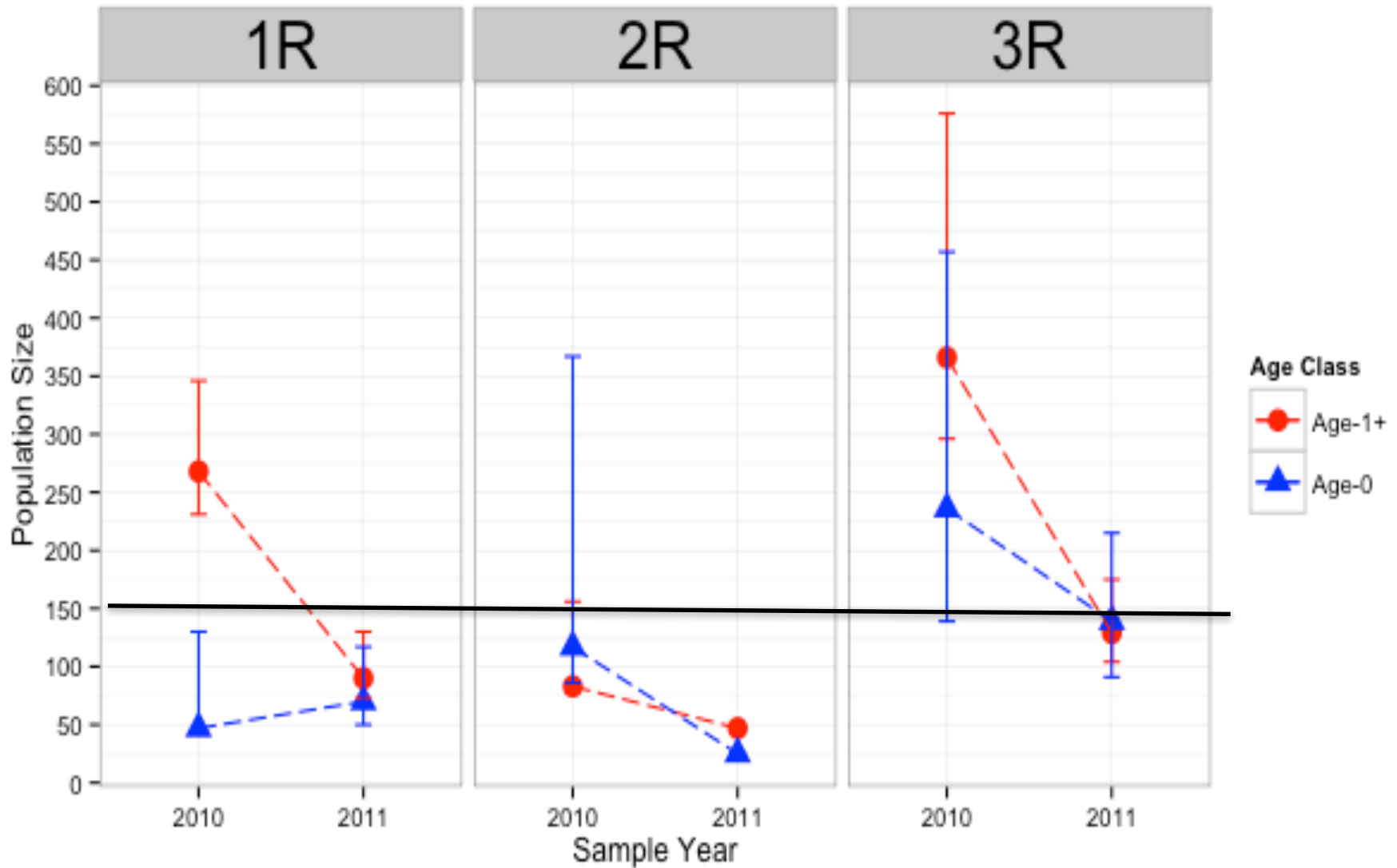




# Five Above-Dam Headwater Streams

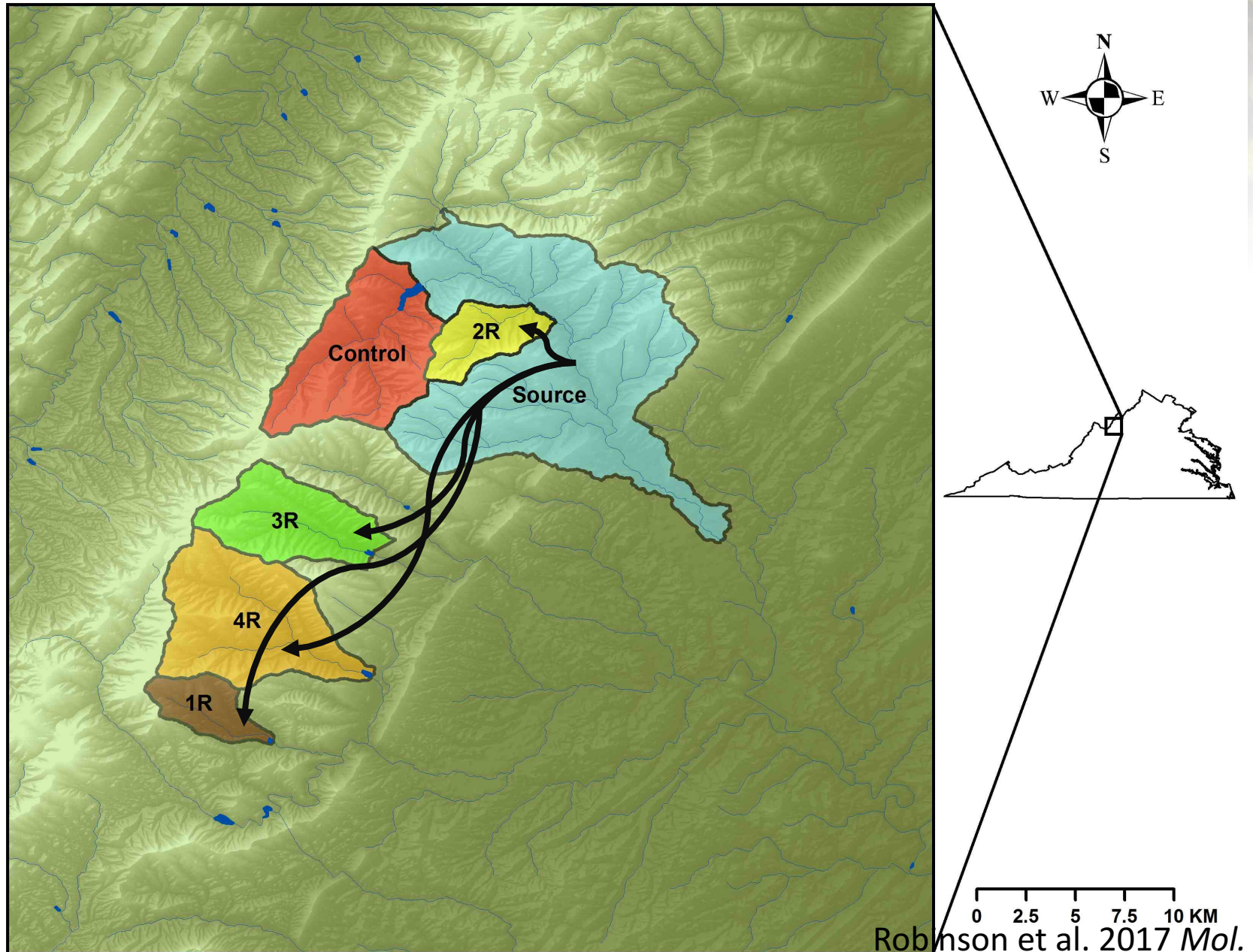


# Abundance 2010-2011





# GR-motivated Translocations 2011





# Experimental Design

- **Source**

- Downstream large patch
- Moved 5 males, 5 females in the autumn
  - Same for every site
- Transported with aerated backpack tanks
  - Same day as capture

- **Translocation**

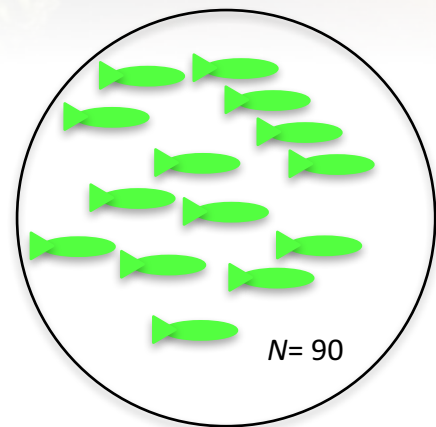
- Released at multiple nearby locations
- Removed 5 males and 5 females
  - To control for demographic effects



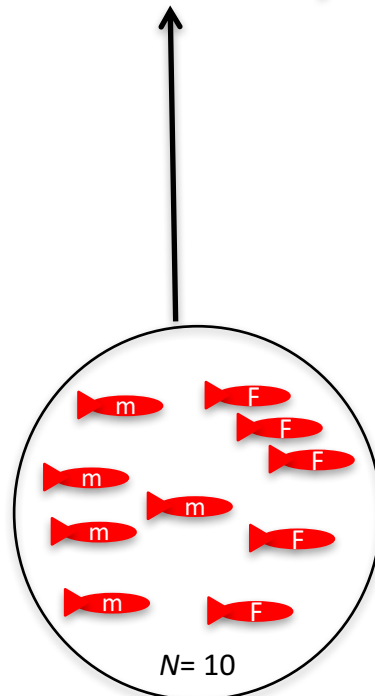
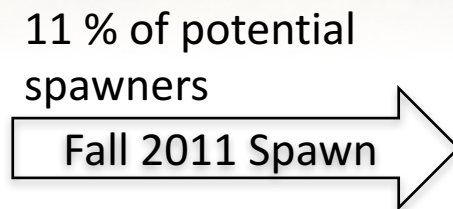
# Parentage Assignment for 2012 Offspring

- $F_1$  Offspring in 2012
  - 2 resident parents (RR)
  - 2 transplant parents (TT)
  - Resident x Transplant Hybrid (RT)

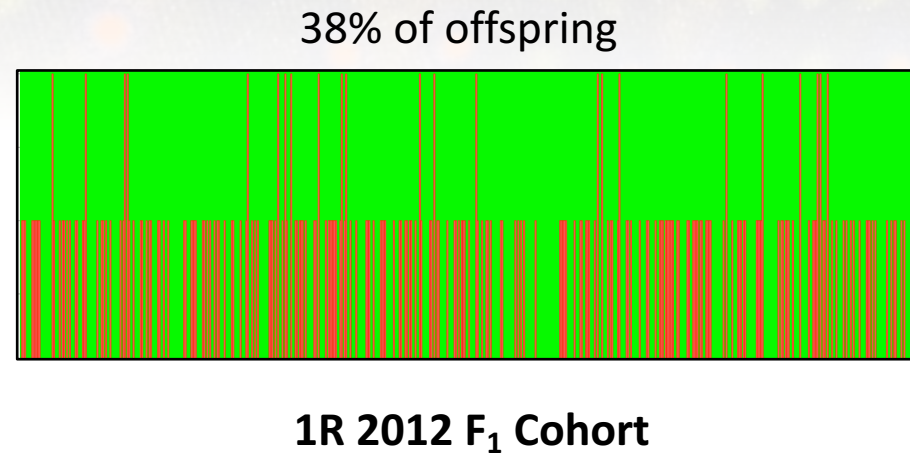
# Site 1R



Resident  $\geq$  Age 1



Transplants



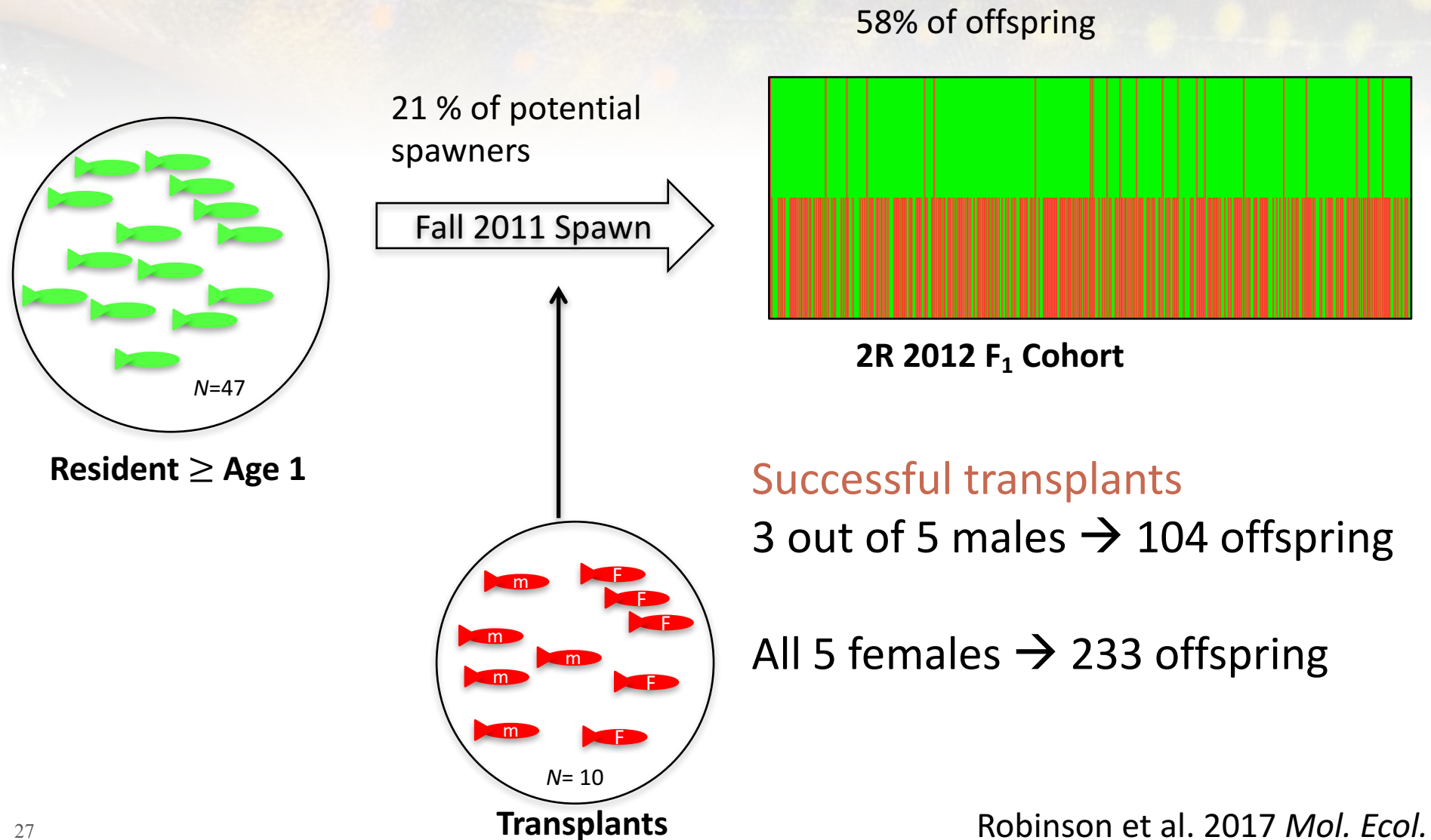
Successful transplants

4 out of 5 males  $\rightarrow$  89 offspring

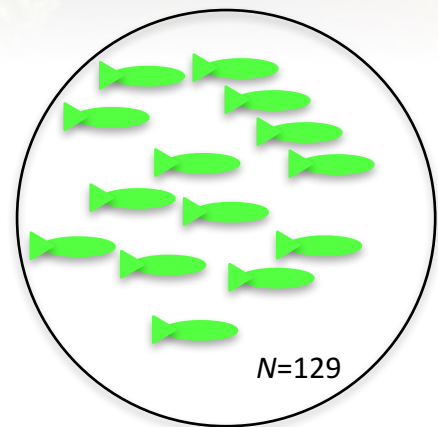
4 out of 5 females  $\rightarrow$  169 offspring



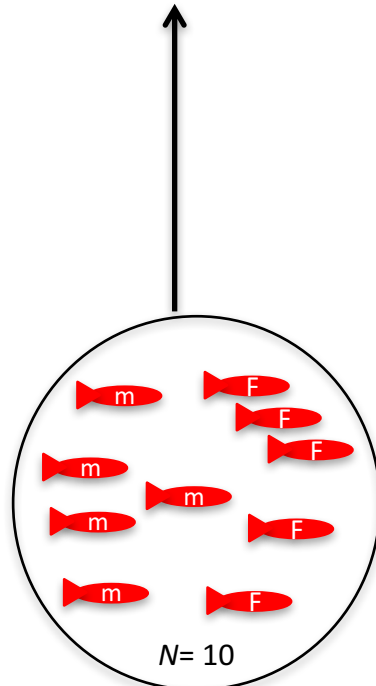
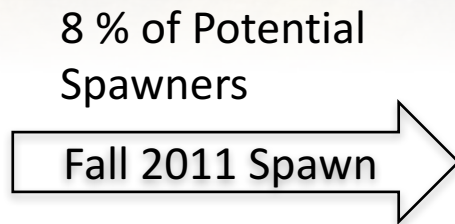
# Site 2R



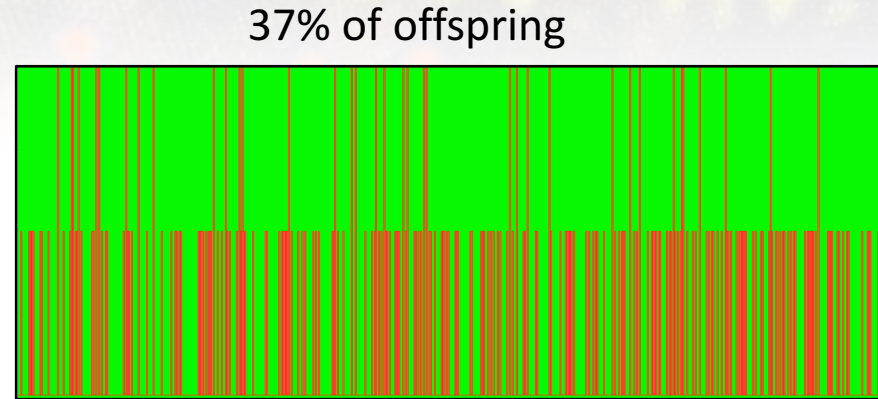
# Site 3R



Resident  $\geq$  Age 1



Transplants



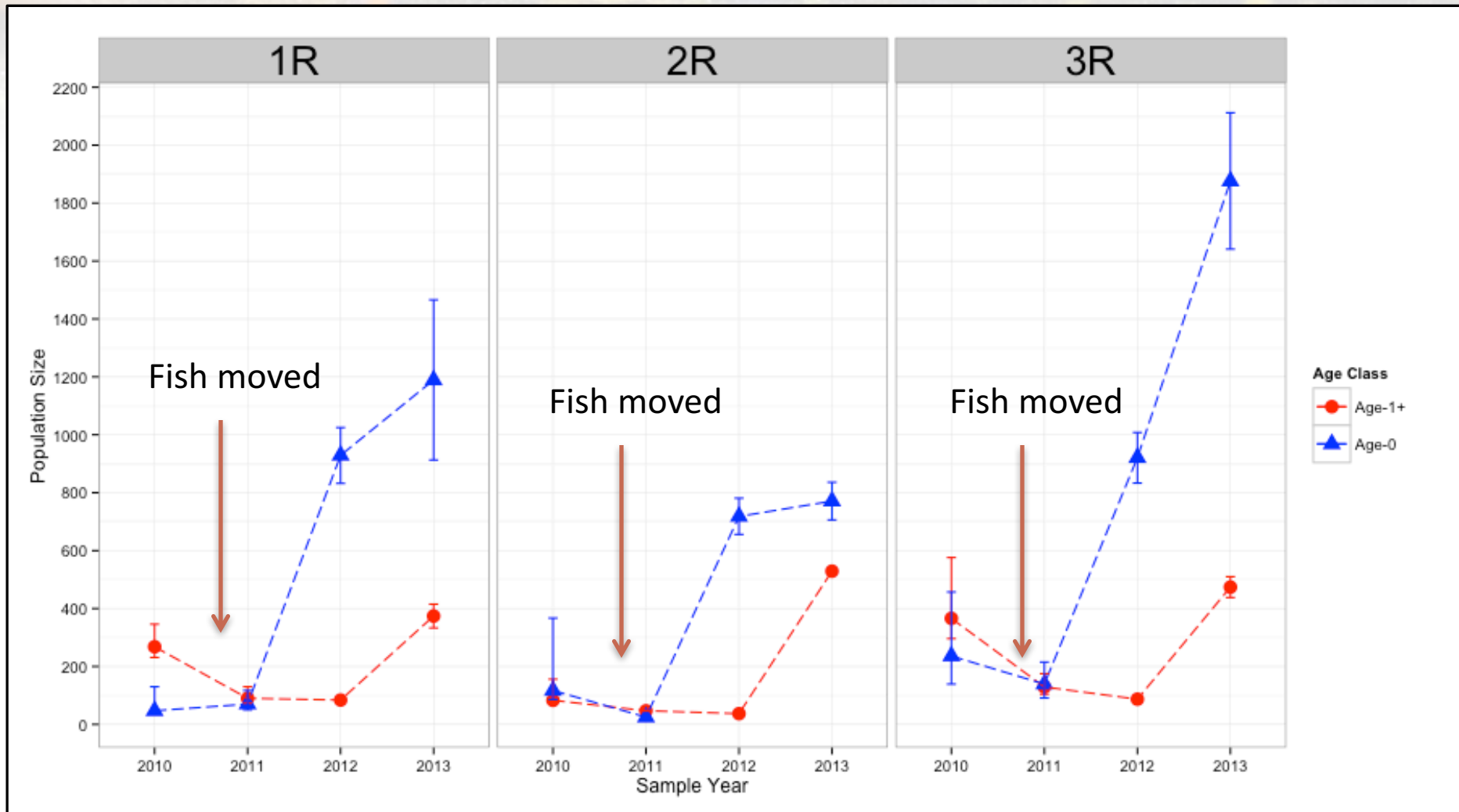
3R 2012 F<sub>1</sub> Cohort

Successful transplants

3 out of 5 males  $\rightarrow$  158 offspring

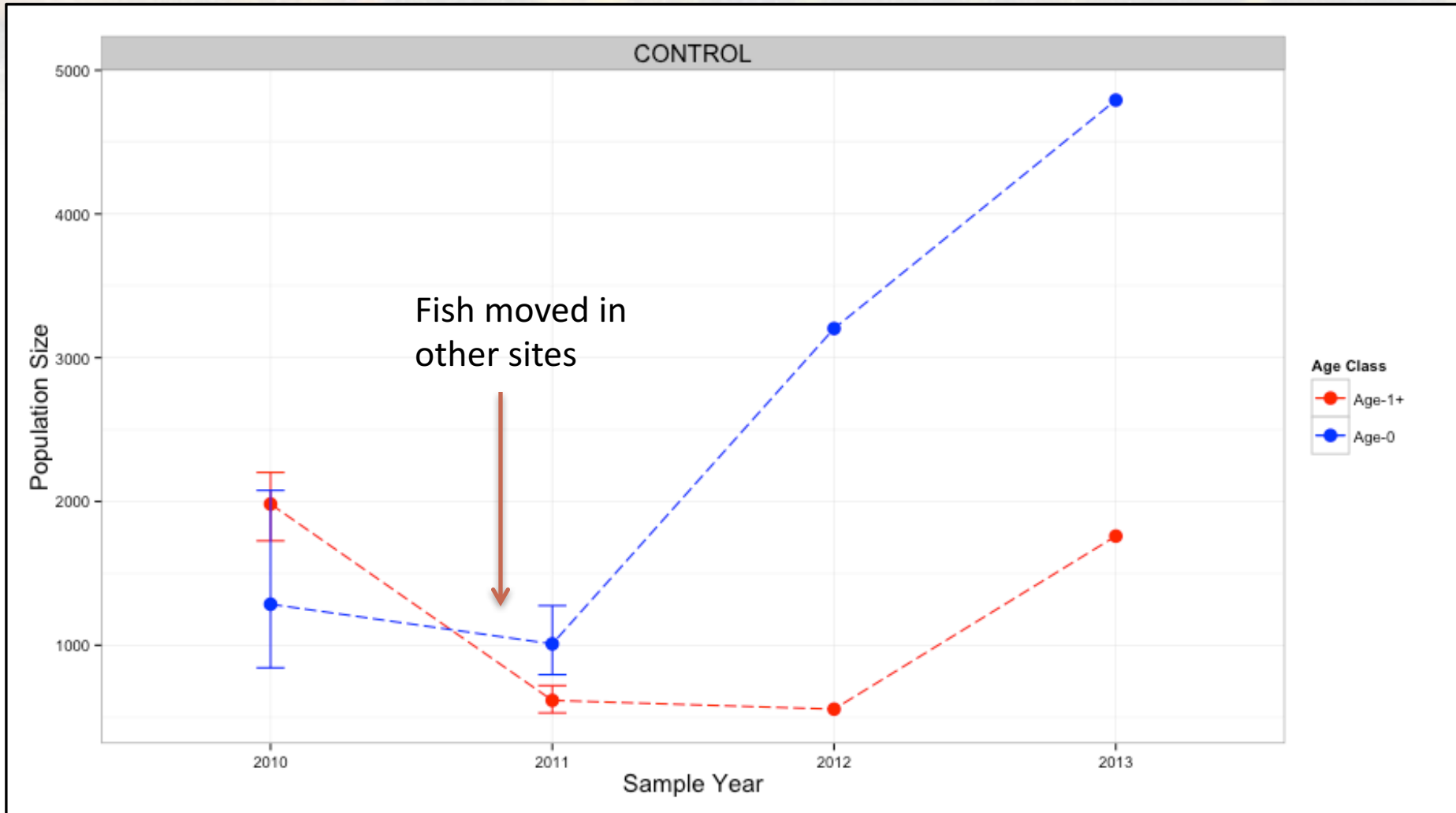
All 5 females  $\rightarrow$  115 offspring

# Population Size 2010-2013

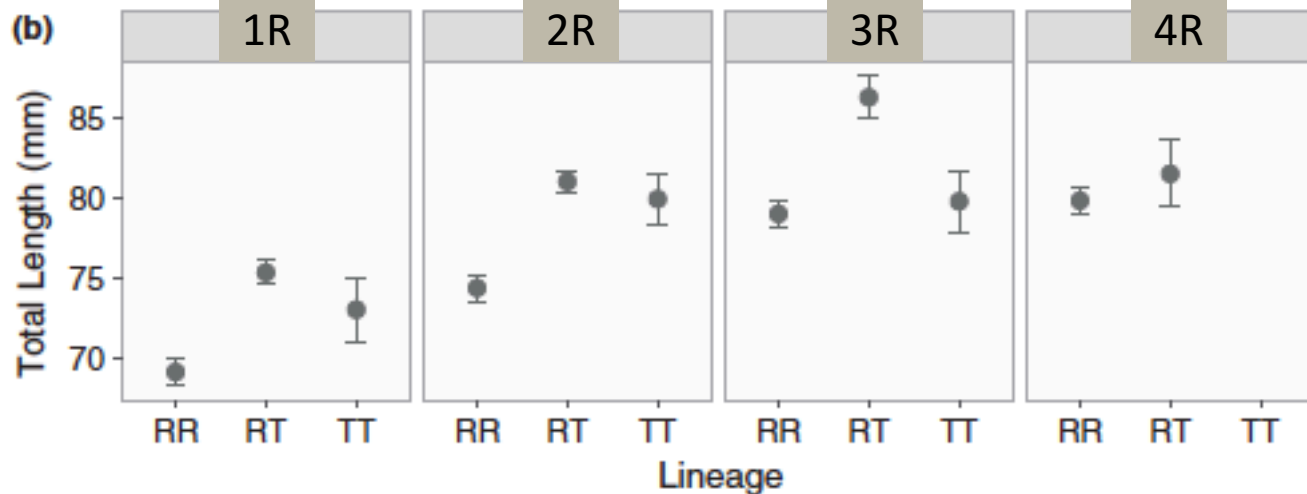
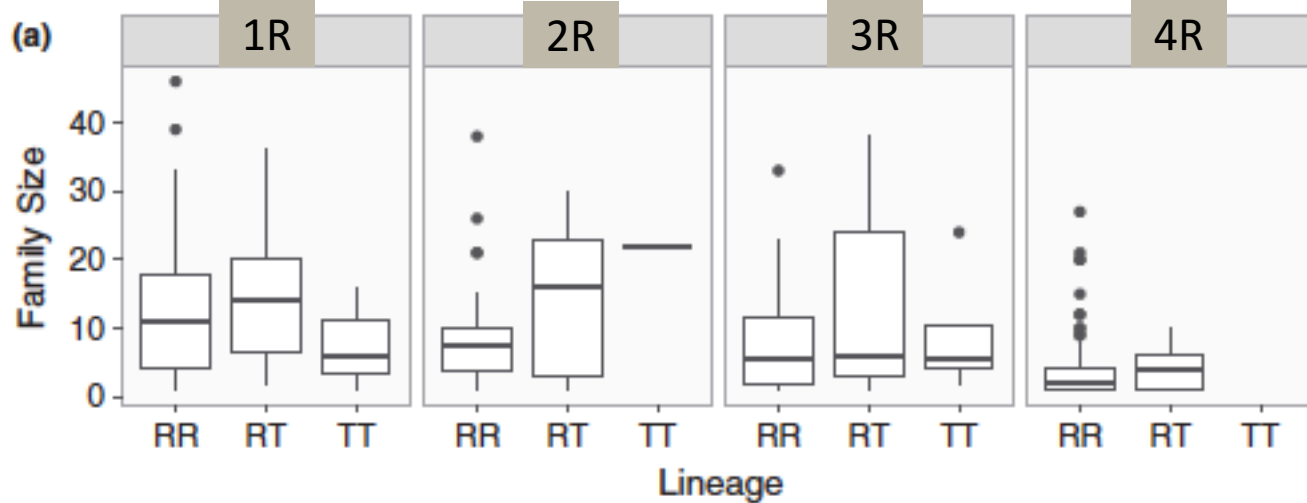




# Control



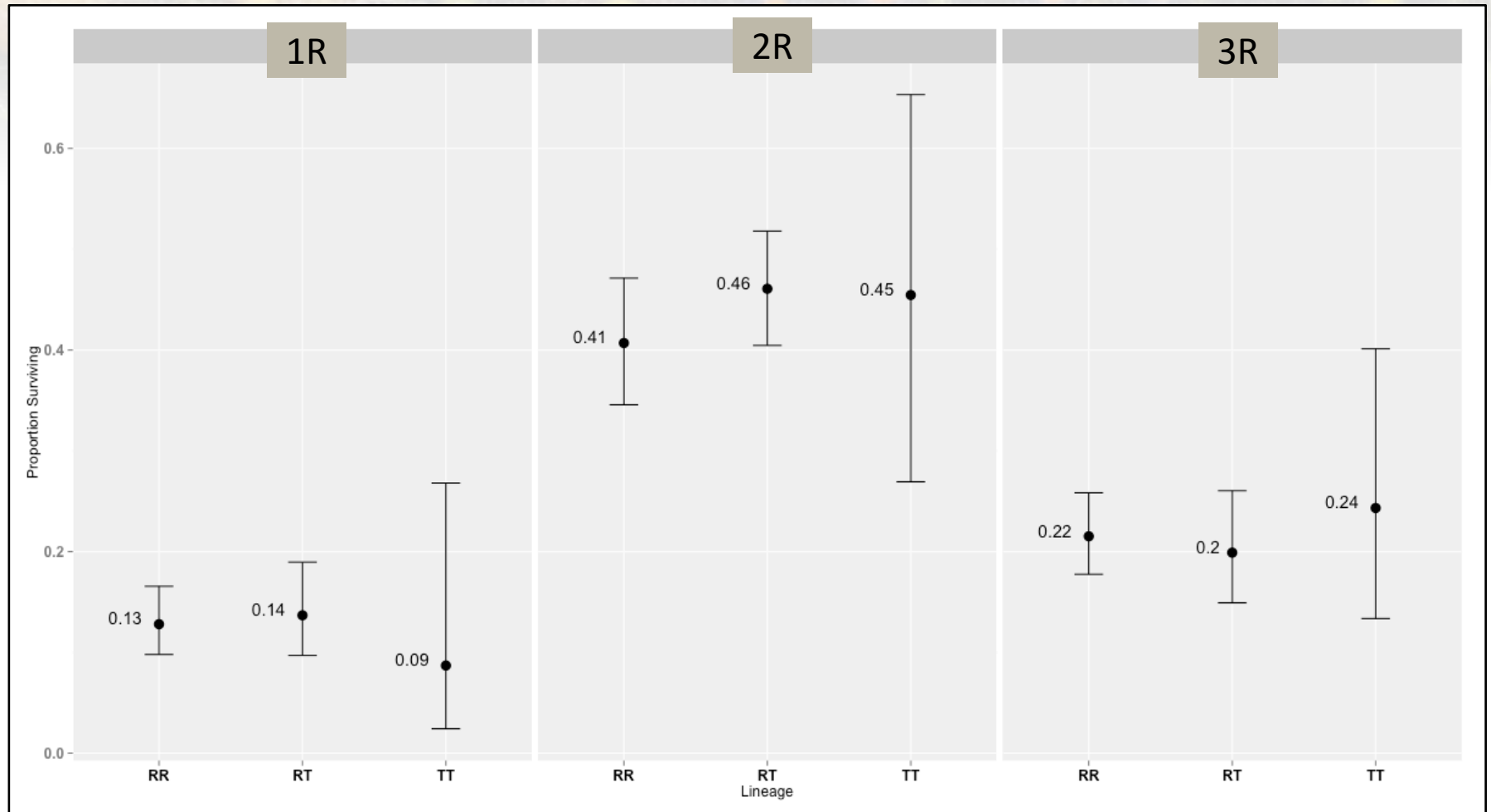
# Family size or Body Size Differences? 2012 Age-0



Robinson et al. 2017 *Mol. Ecol.*

Transplant adults not significantly larger than residents

# Survival 2012 to 2013

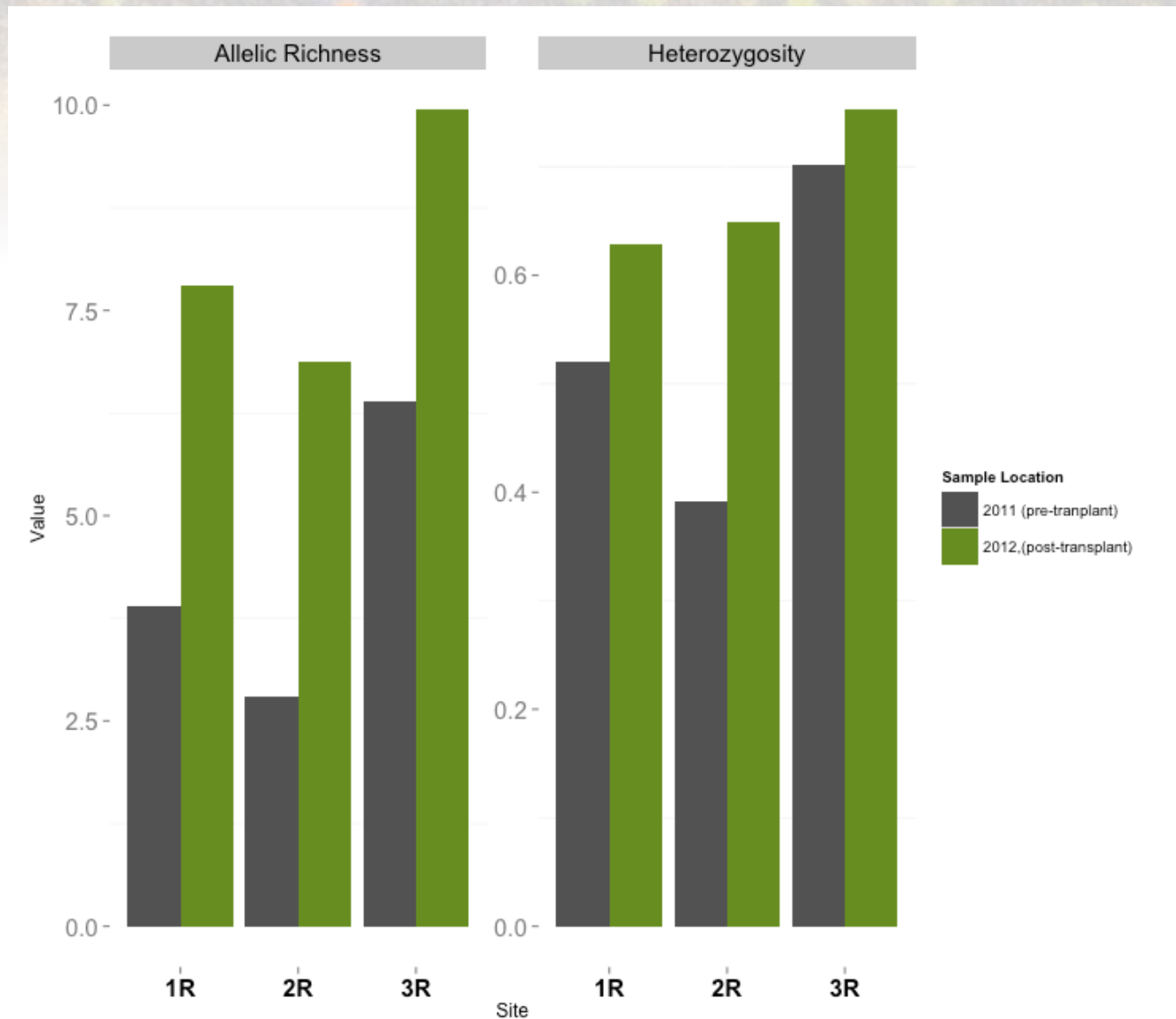


Note: Benign environmental conditions

Robinson et al. 2017 *Mol. Ecol.*

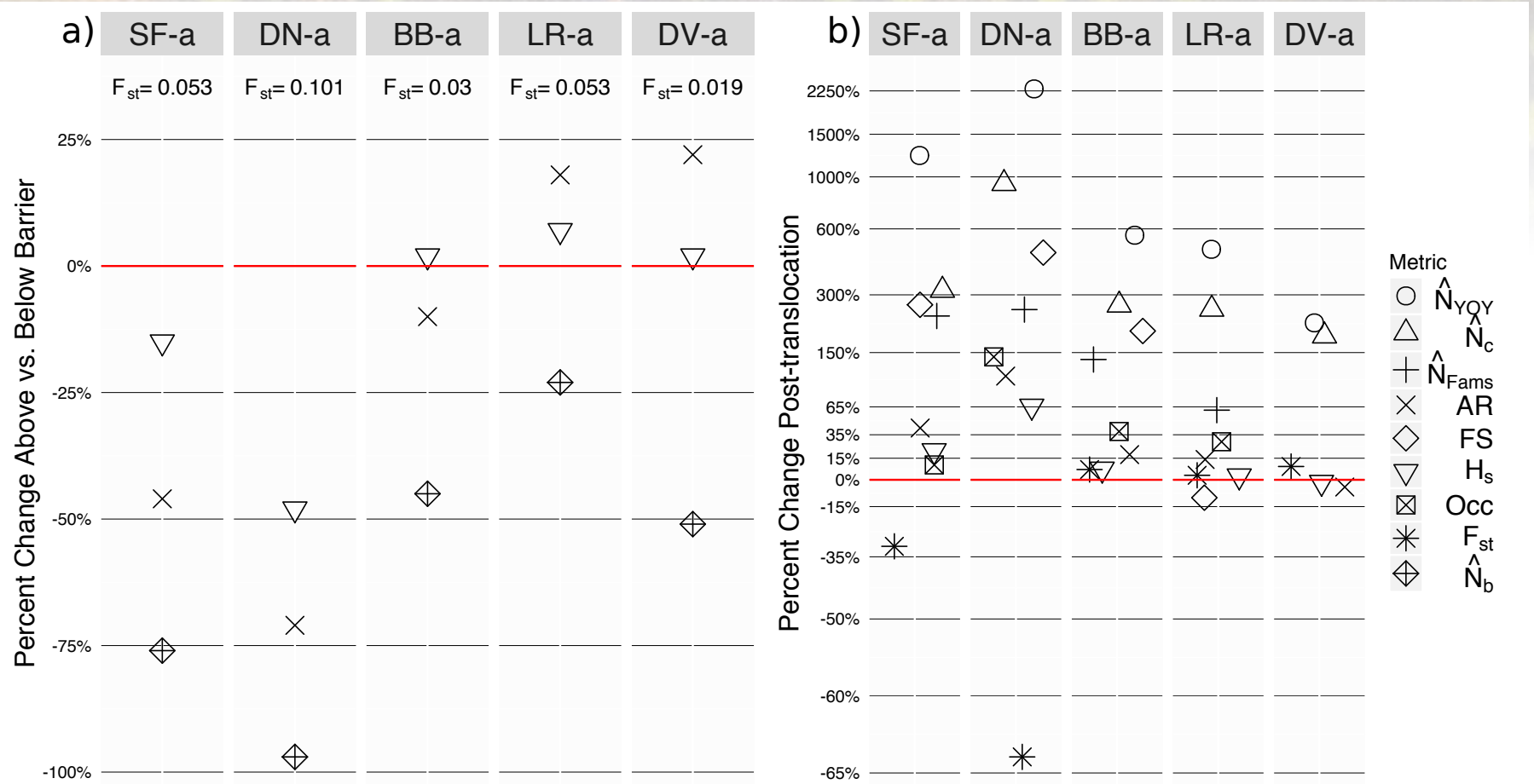


# Response in Genetic Variation

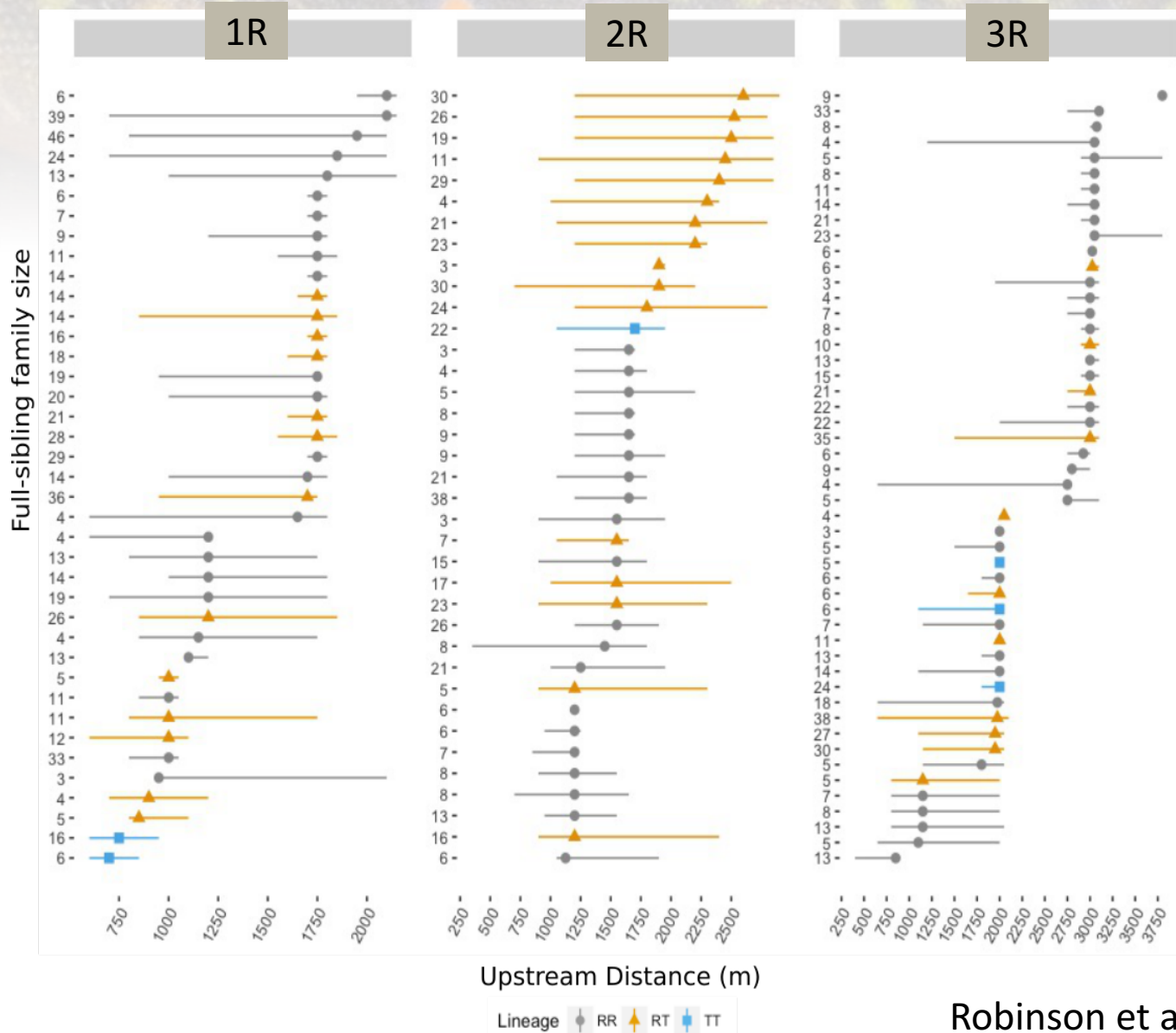


# Before

# After



# Habitat Use





# Summary of the $F_1$

- Disproportionately high transplant reproductive success
- Body size and growth differences
  - Consistent with heterosis
- YOY body size differences could translate to positive demographic effects
- No survival differences, but they could have occurred later
- Large gains in genetic variation

# Continued Analysis

- Outbreeding depression could still occur
  - $F_2$  and beyond
  - Pedigree reconstruction for  $F_2$  with SNPs
- Continued estimates of reproductive success and survival for the  $F_1$  and  $F_2$

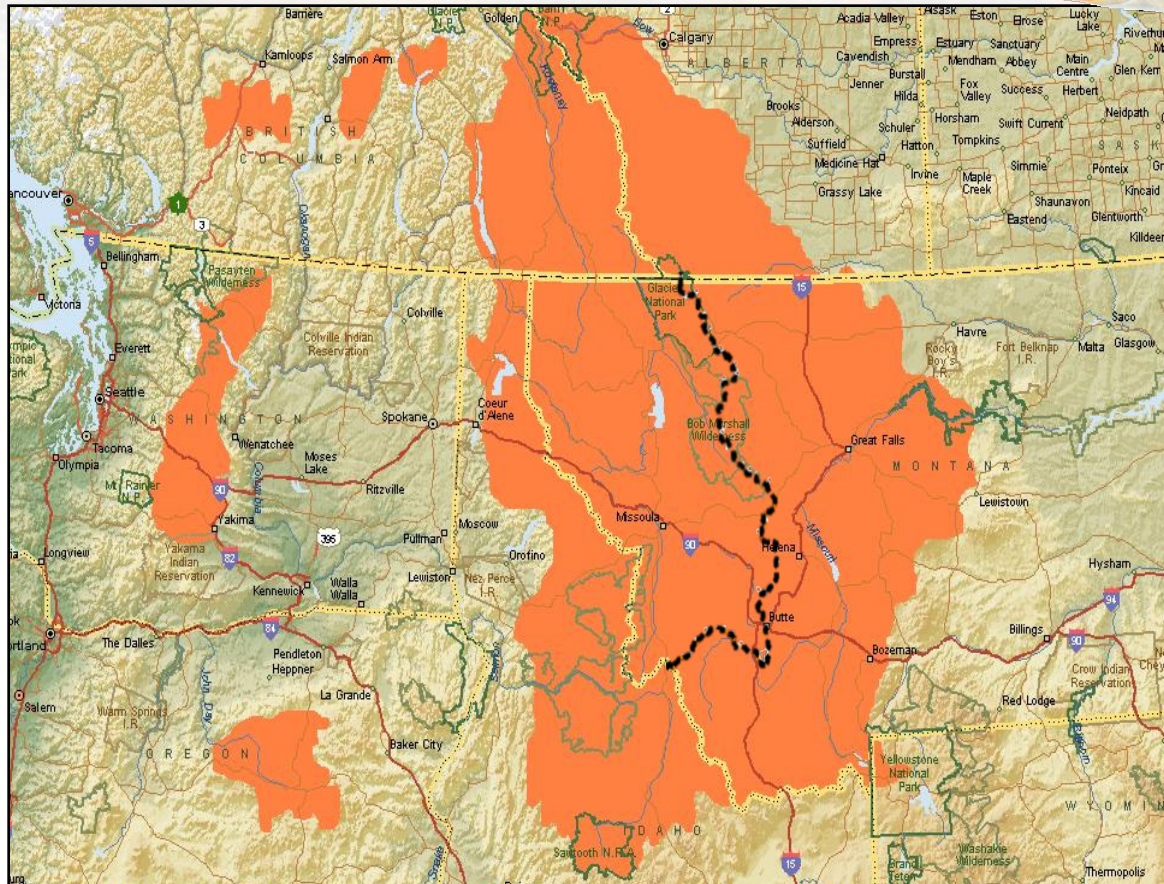


# Analysis from 2011 – 2018

- Build a pedigree through F2, hopefully F3 to examine fitness effects of admixture
- New GTSeq panel (work by Zak Robinson)
  - Based on discovery data set led by Mariah Meek's lab
  - 244 SNPS
    - 201 'microhaps' or 'microhaplotypes'
      - Multiple nearby SNPs scored as a single locus
      - Makes SNPs more like microsatellites
      - Mean heterozygosity of microhaps = 0.401
        - » Up to 6 alleles at a locus (59% of microhap loci have 3 alleles)
      - 5 sex markers included

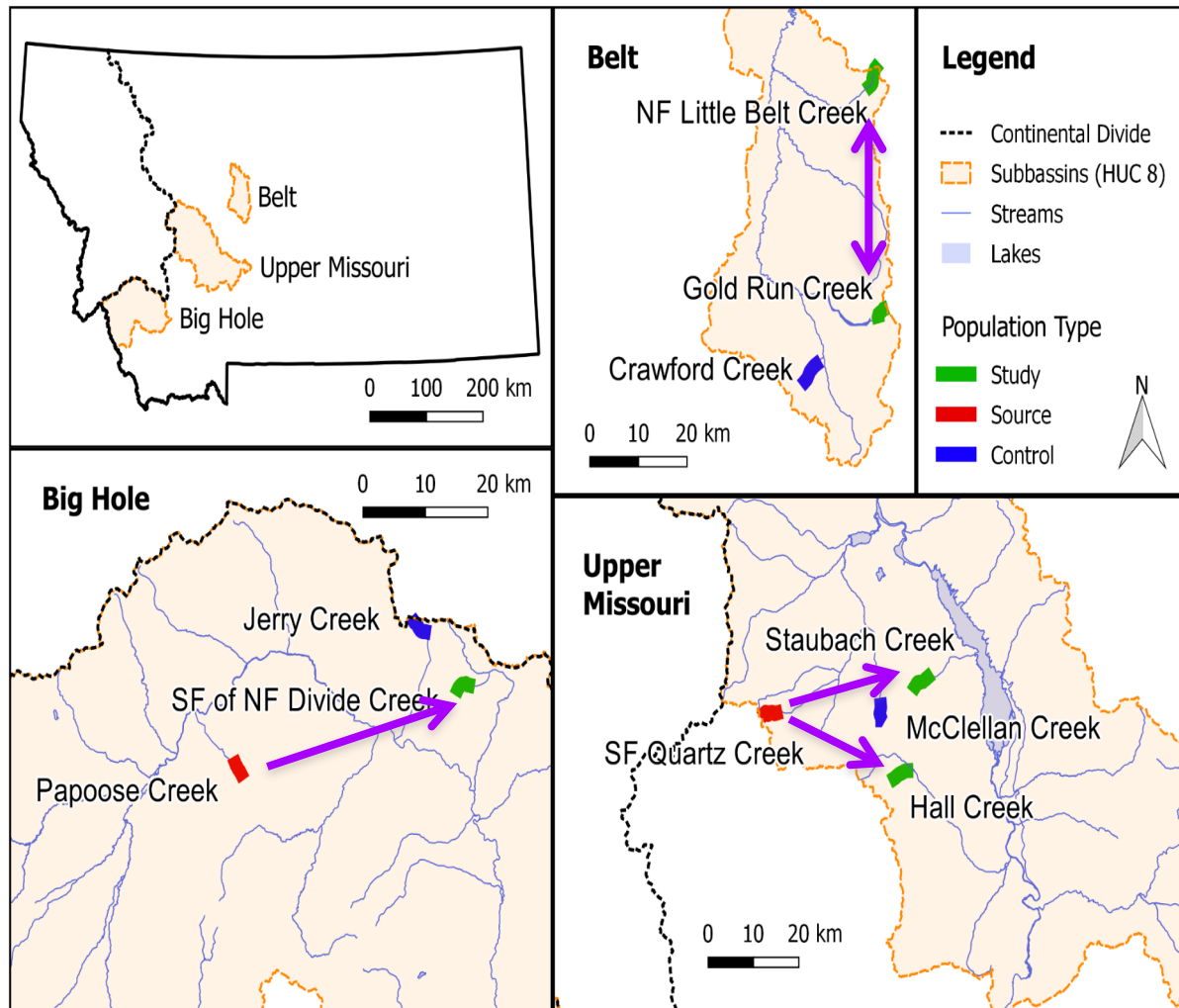


# Test in Westslope Cutthroat Trout



- Few non-hybridized populations remain east of the Continental Divide
- Manage for isolation to avoid:
  - Hybridization with rainbow trout
  - Brook trout competition, replacement

# Study streams and translocations



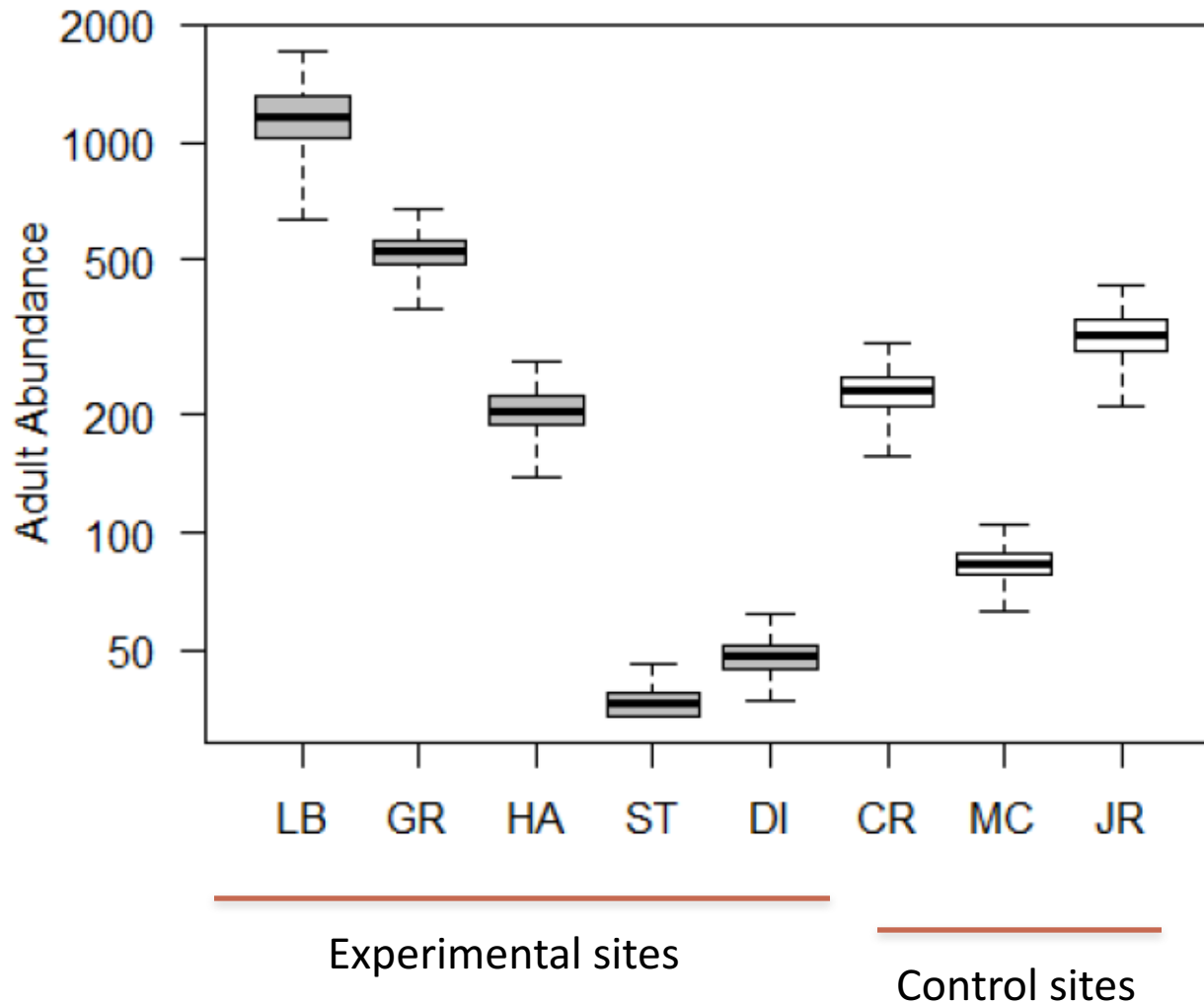
- Transplant 6 or 8 adults
  - Within basins (Big Hole, Upper Missouri, Belt)
  - Removed adults from recipient sites

- Low genetic variation:
  - Average  $H_E$  of selected = 0.024
  - Average eastside  $H_E$  = 0.038
  - Average westside  $H_E$  = 0.106

- Disease testing
- Limited habitat (~3 km of stream)
  - Isolated
  - Allows monitoring entire pop.



# Population abundance

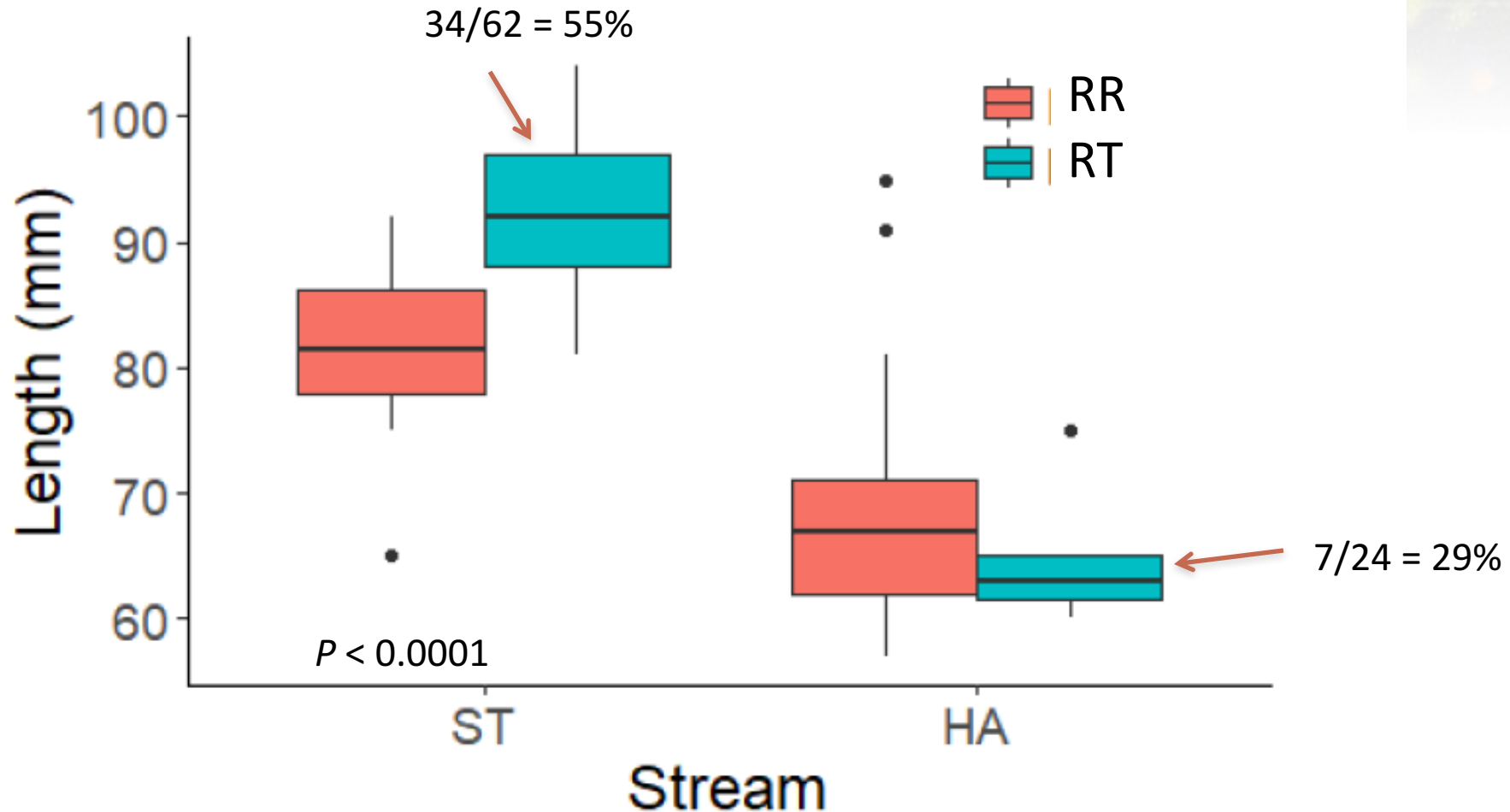


Age-2 and older  
Summer 2017

Age-1 abundance  
increased in 3 of 4  
experimental sites  
In 2018 (translocations  
occurred in Spring 2017)



# Offspring size at age-1 (2017 year-class captured in 2018)



- We have sampled annually through 2021
  - Build a pedigree with a combined approach of GTSeq and RAD-Capture
  - Hopefully we will have results through 2021 within a year

- Divergence between transplants and recipient population continuum



Decades  
 - Reconnect following recent fragmentation

~ Thousands of years  
 - Gene flow between long-isolated major genetic assemblages

Low likelihood of outbreeding depression (OD)      higher likelihood of OD



# Acknowledgments

## Collaborators

### *Montana (WCT)*

Gordon Luikart, Steve Amish, Seth Smith, **U. Montana**

Ryan Kovach, Lee Nelson, **FWP**

Jim Olsen, Dave Moser, Jason Mullen, Katie Webster - **FWP**

### *Virginia (brook trout)*

Zachary Robinson, **U. Montana**

Keith H. Nislow, Jason Coombs, **USFS Northern Research Station**

Ben Letcher, Matt O'Donnell, Todd Dubreuil, **USGS, Conte Lab**

Mark Hudy, **USFS and USGS**

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