Genetic diversity, gene flow, and effective population size of the Selkirk and Cabinet-Yaak grizzly bear populations

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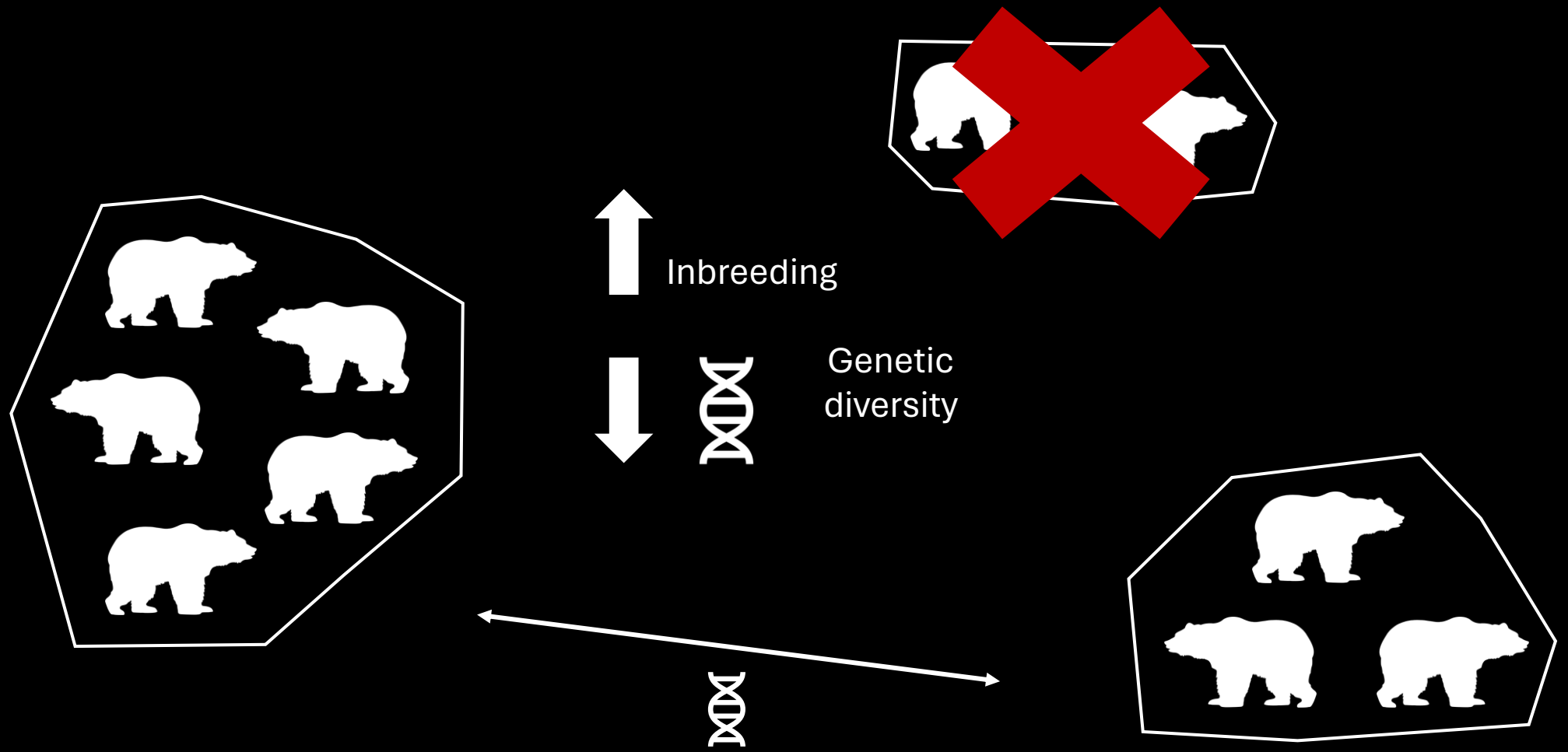
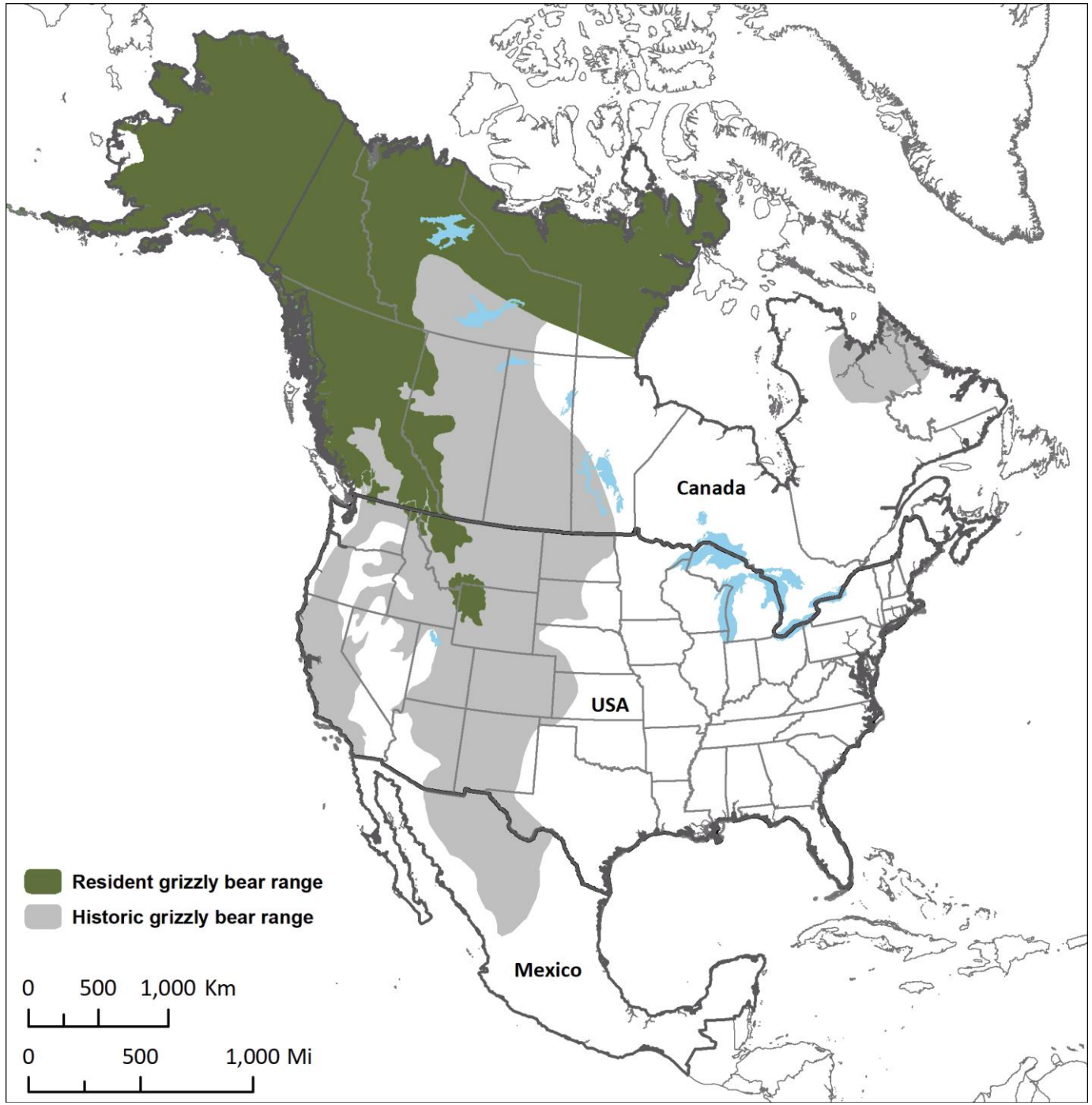
IGBC S/CY Subcommittee Meeting
May 8, 2024

Fragmentation

Fragmentation




Canada
USA
Mexico
Resident grizzly bear range
Historic grizzly bear range
0 500 1,000 Km
0 500 1,000 Mi

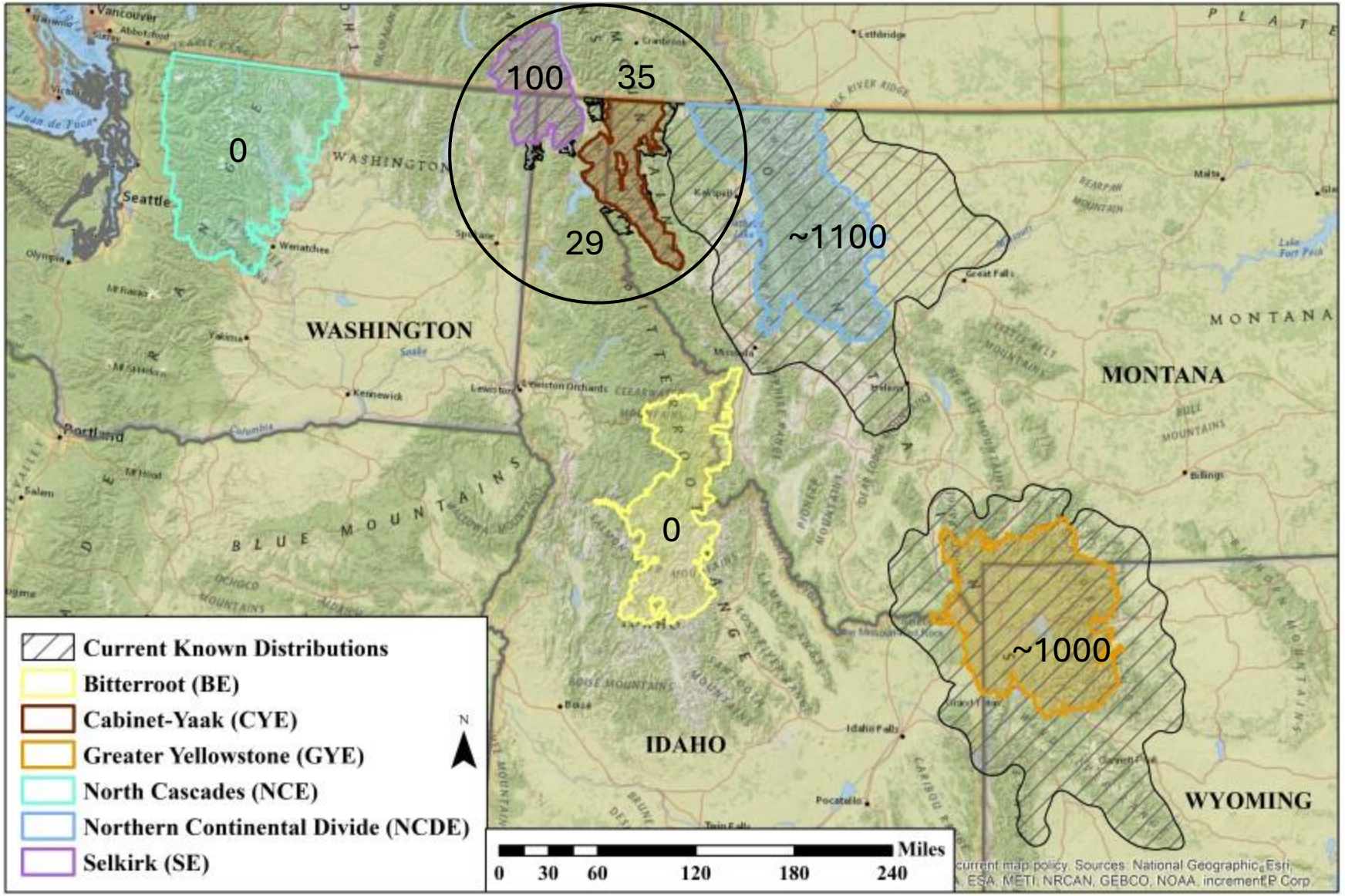
NATIONAL

Judge Restores Grizzly Bears' Protections As Endangered Species

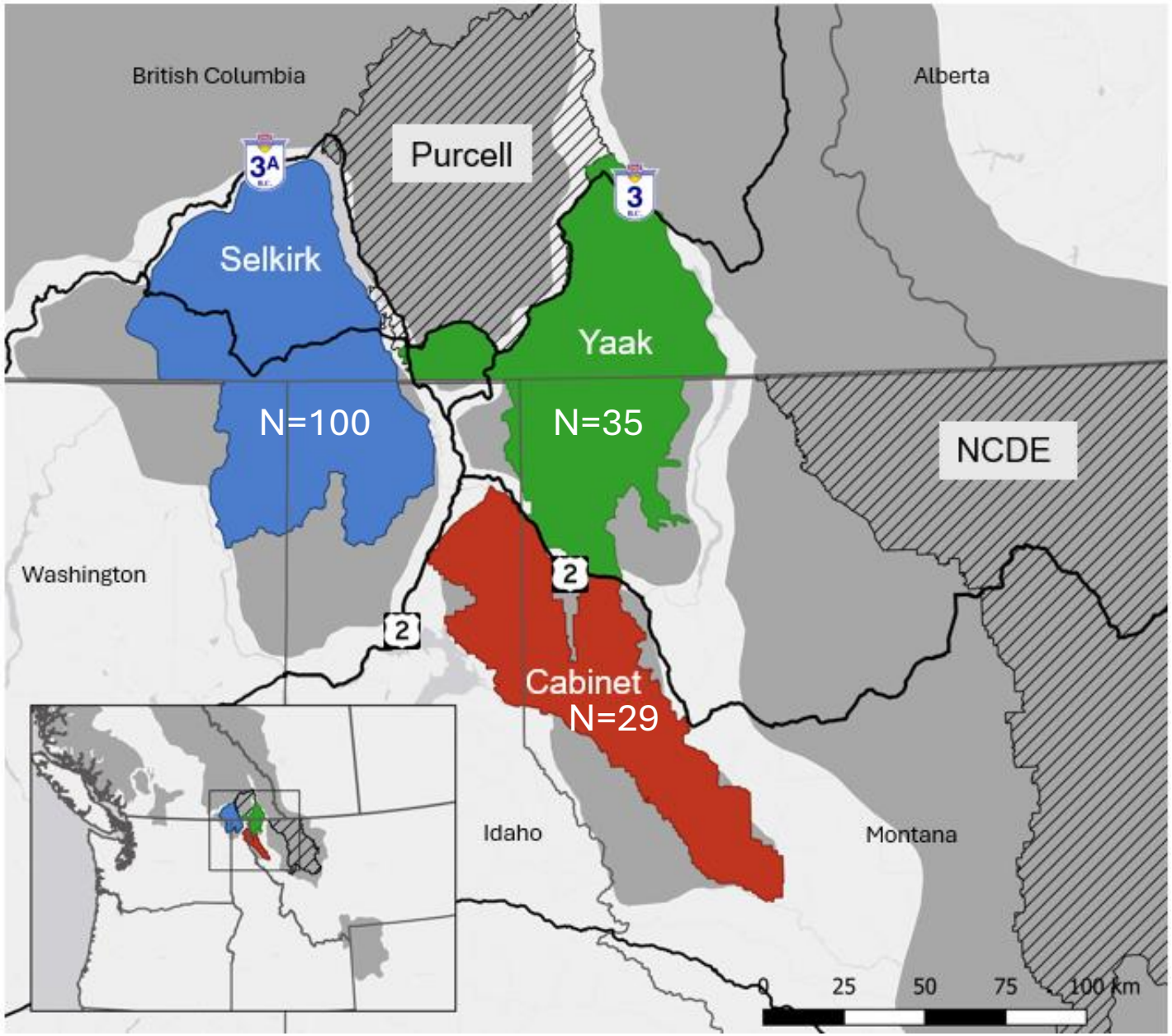
SEPTEMBER 24, 2018 · 10:20 PM ET

By Nate Hegyi

Grizzly Bear Recovery Zones and Distributions



Map: USFWS 2018
Costello et al. 2022, van Manen et al. 2023


British Columbia
Alberta
Purcell
3A
3
Selkirk
Yaak
N=100
N=35
NCDE
Washington
2
2
Cabinet
N=29
Idaho
Montana
0
25
50
75
100 km

History of Fragmentation

- Selkirk – completely isolated for multiple generations
- Cabinet – history of isolation and extremely low population size in 1980s-90s
- Yaak – no female movements

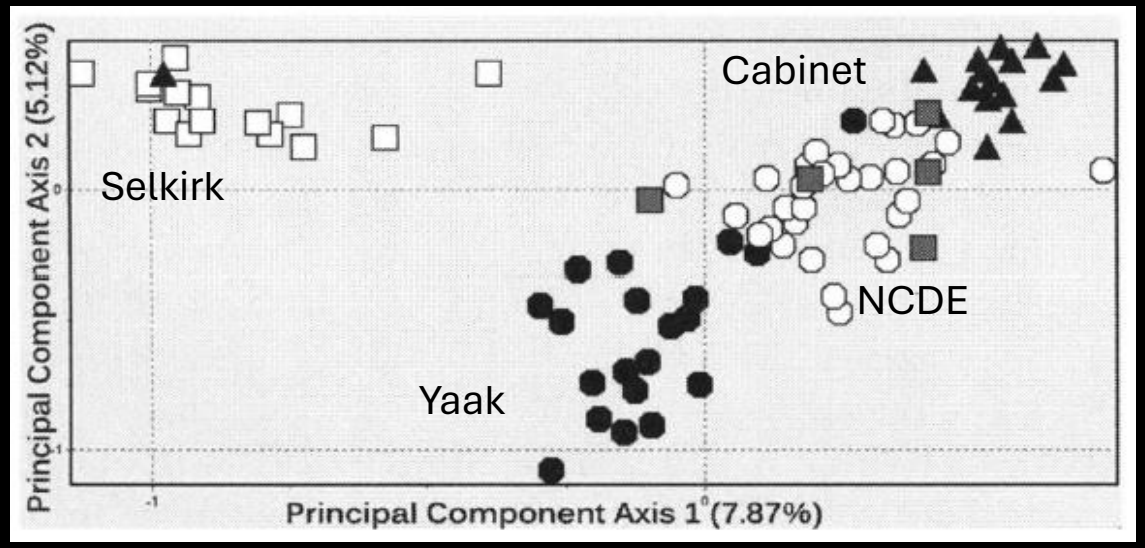
Genetic analysis reveals demographic fragmentation of grizzly bears yielding vulnerably small populations

Michael F. Proctor[1,*], Bruce N. McLellan[2], Curtis Strobeck[3] and Robert M. R. Barclay[1]

Proctor et al. 2005, Proctor et al. 2018, Kasworm et al. 2023

Effects of Fragmentation

- Selkirk: lowest genetic diversity in North America
- Cabinet population is inbred

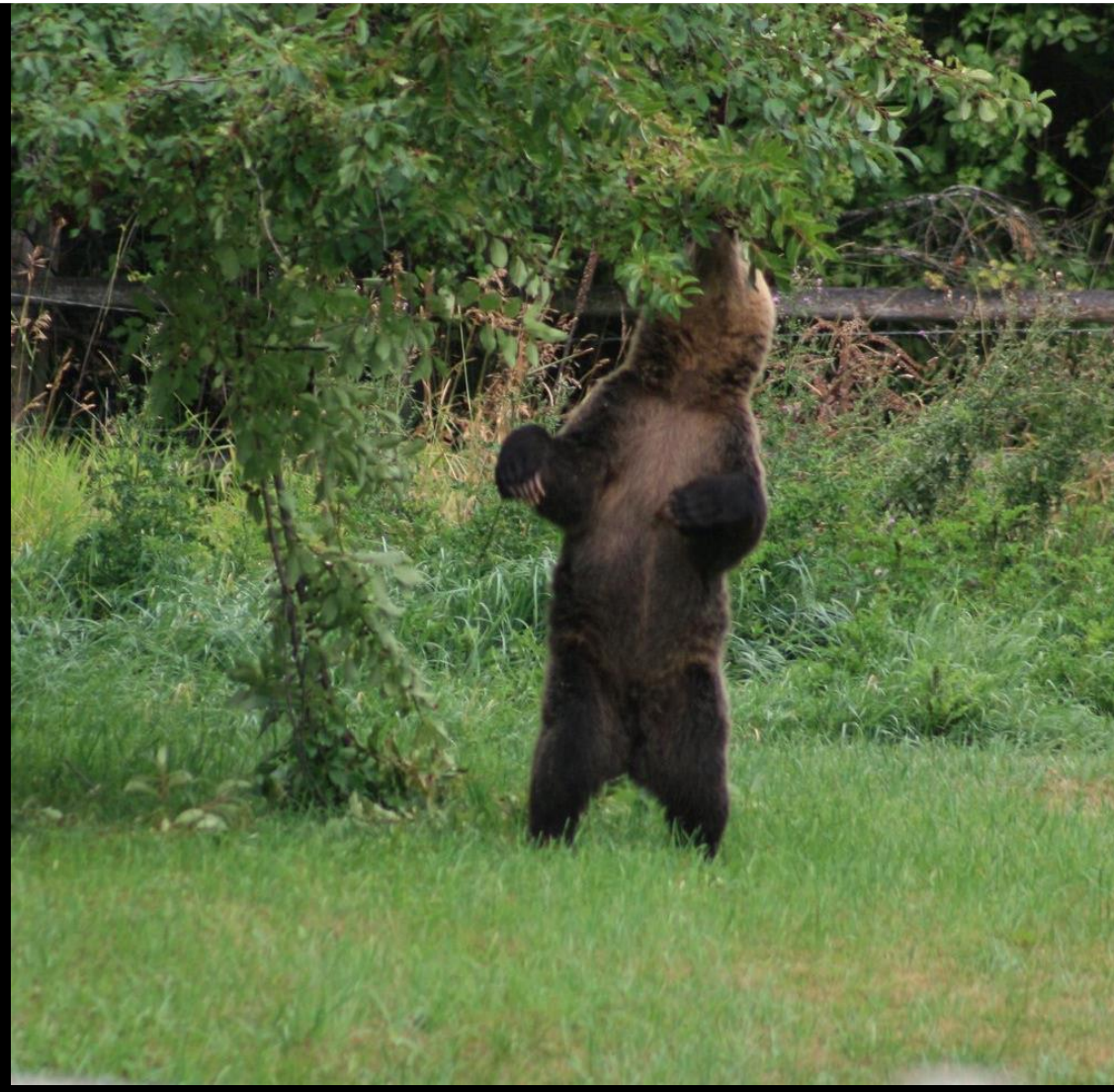


Proctor et al. 2012, Kendall et al. 2016

Movements and Gene Flow

- Management actions
  - Conflict prevention
  - Land purchases
- Around 2006, movements and gene flow increased
  - Movement=migration
  - Reproduction=gene flow
- Gene flow in Selkirk and Yaak only

Proctor et al. 2022



Cabinet Augmentation

22 bears translocated from NCDE since 1990

Need for Project

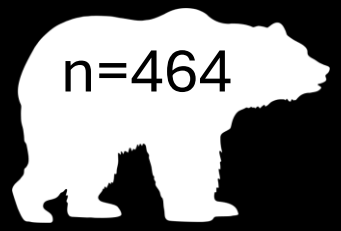
"Long-term survival of these small, threatened subpopulations will depend on successful management that reconnects them with a larger adjacent regional subpopulation" – Proctor et al. 2015

Chapter I Objectives

i. Determine how migration and augmentation are affecting genetic diversity

ii. Estimate effective population size

Dataset

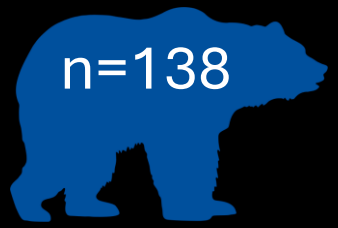


21 microsatellite loci

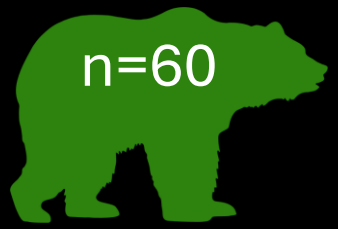
Methods

Genetic diversity

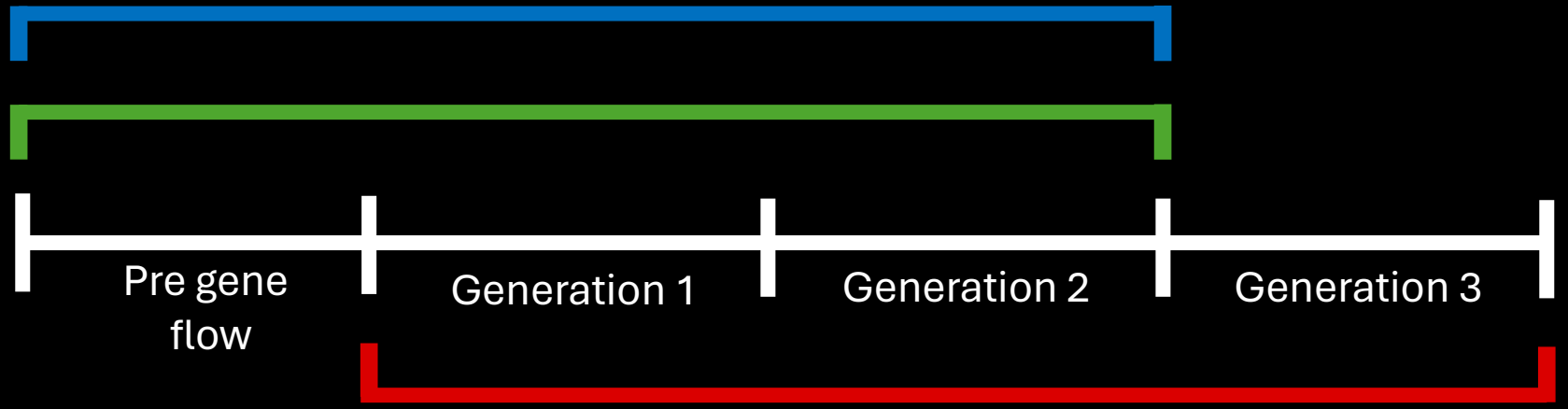
Selkirk



Yaak



Cabinet



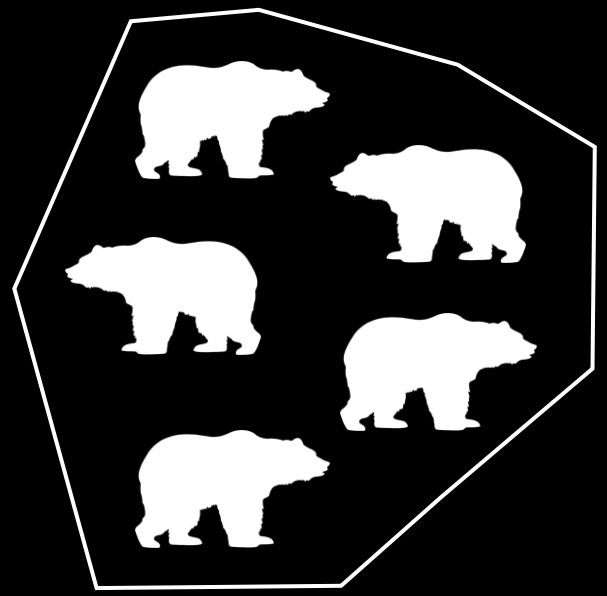
Methods

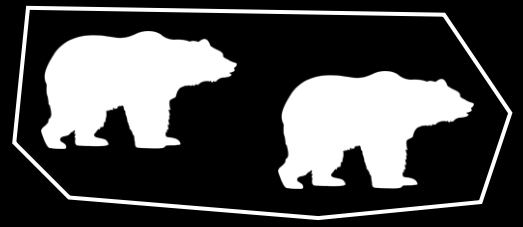
Genetic diversity

- Observed & expected heterozygosity: common diversity metrics
- Allelic richness: number of variants at a particular gene
- Pairwise relatedness: average genetic similarity between two individuals in a population
- Two-sided t-test

Methods

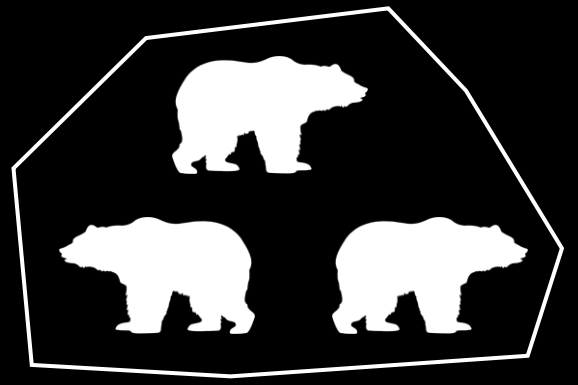
Effective population size





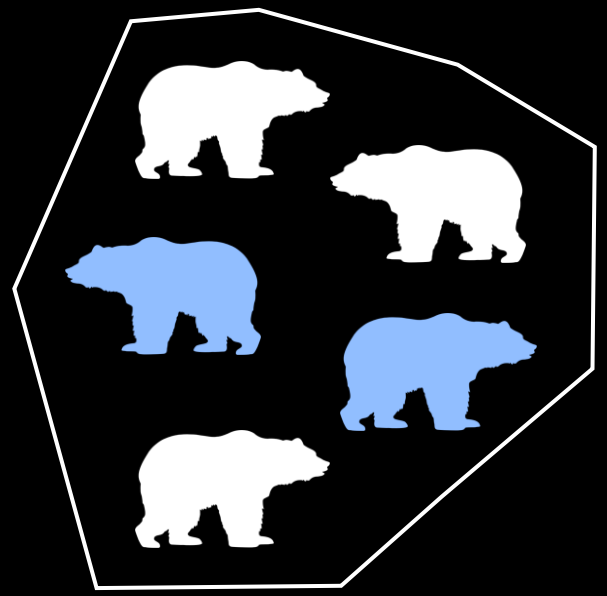
N: ecological processes

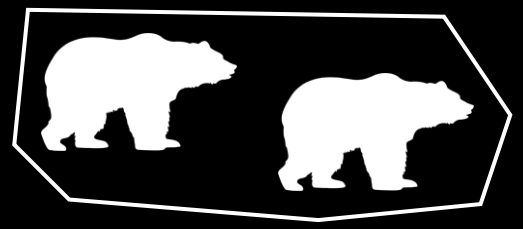
- Population growth
- Competition
- Density dependence



Methods

Effective population size

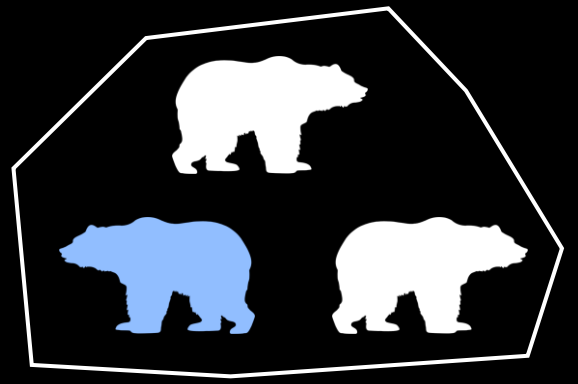




N_e: evolutionary processes

- Genetic drift
- Inbreeding

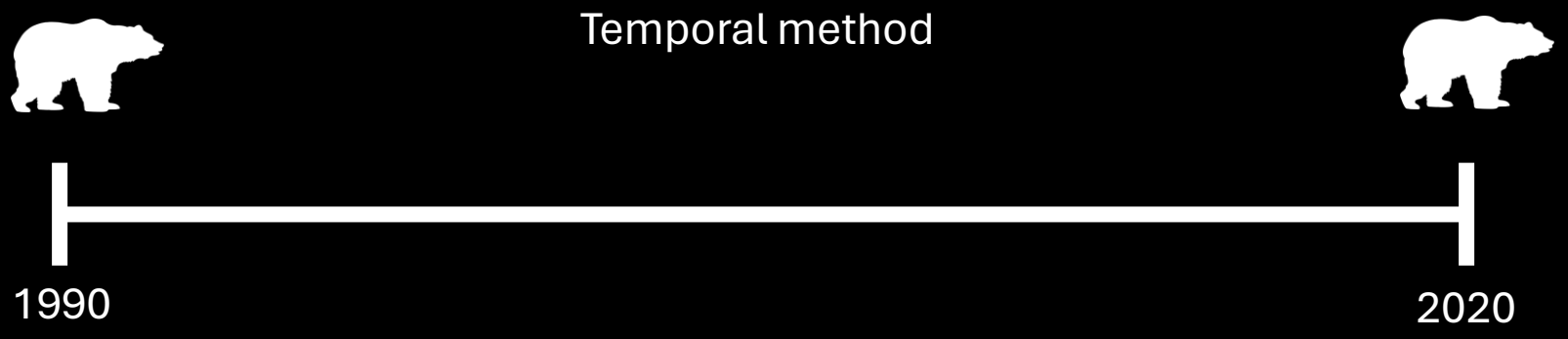
50/500 rule

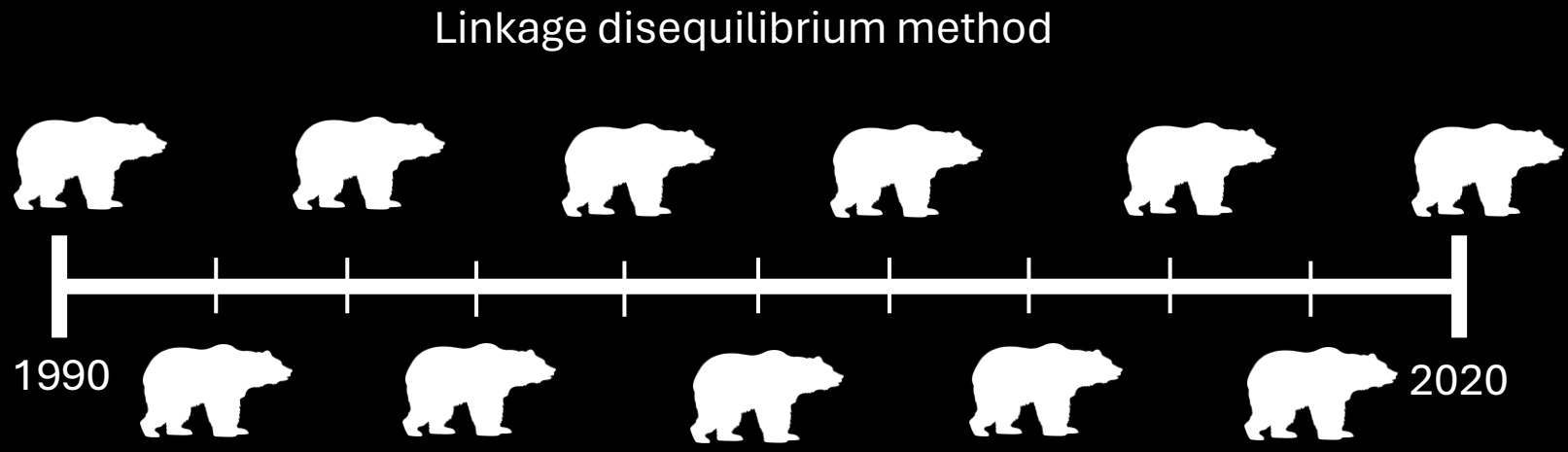


Waples 2022

Methods

Effective population size



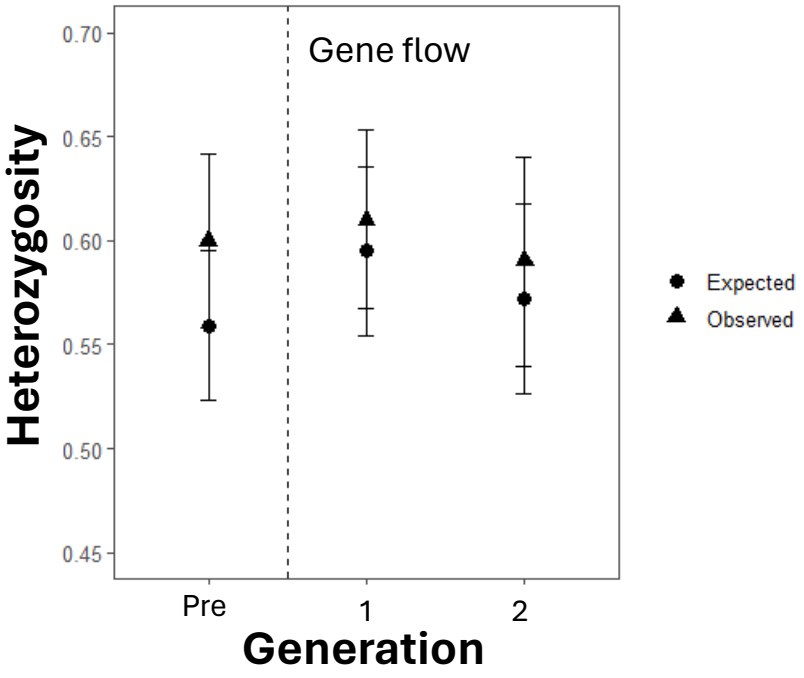


Kamath et al. 2015

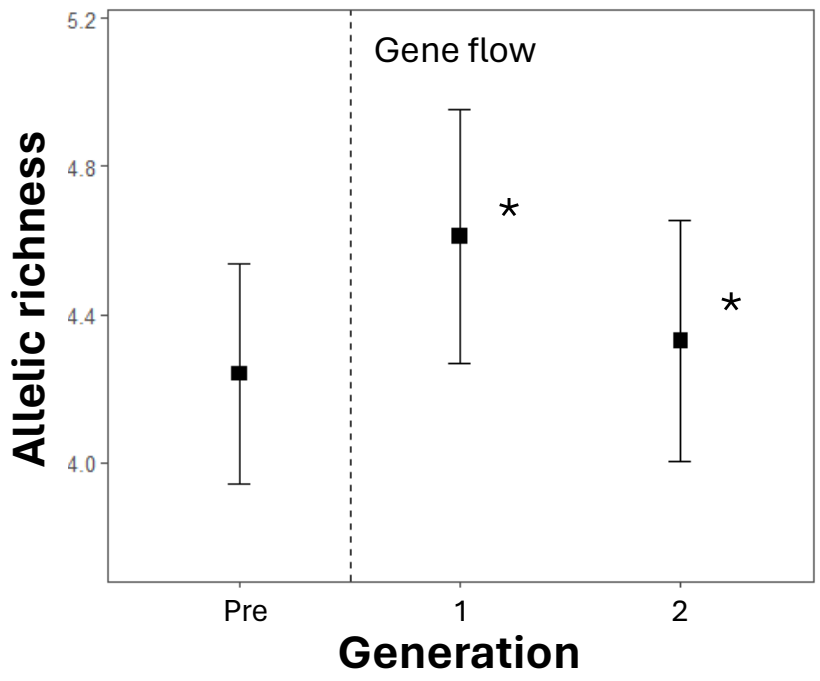
Results

Selkirk genetic diversity

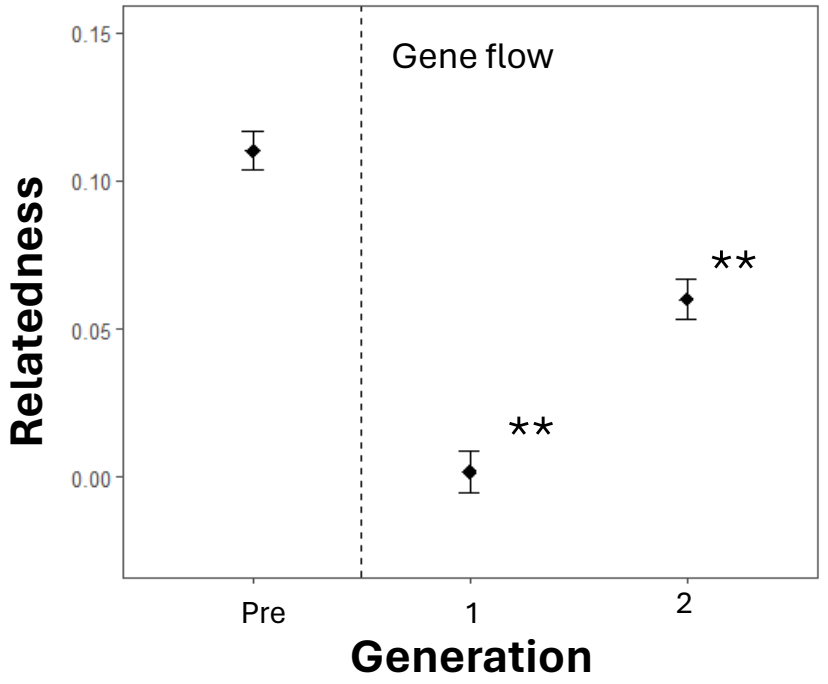
Heterozygosity



Allelic richness



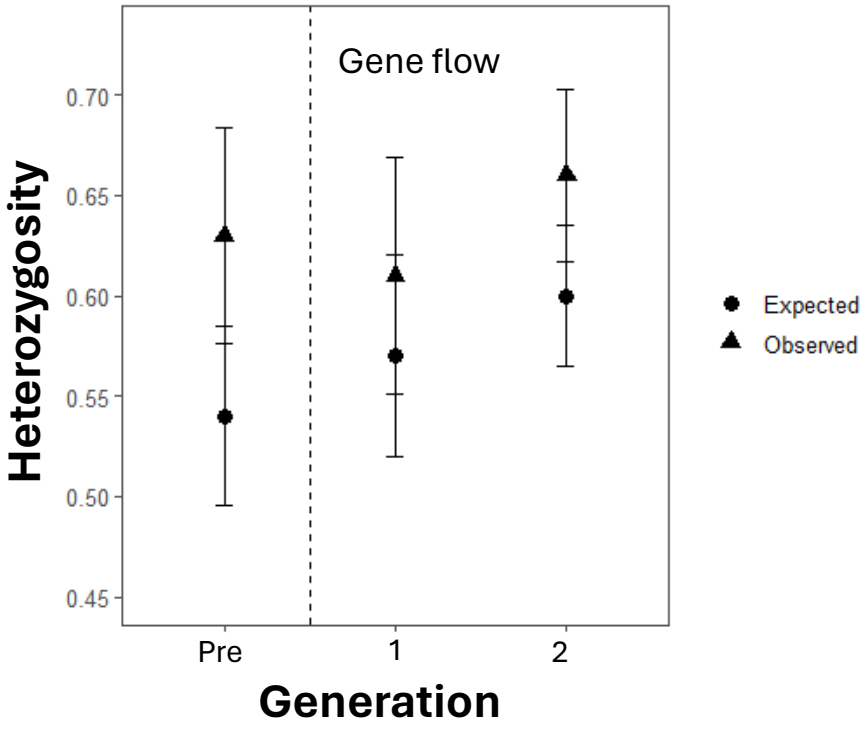
Relatedness



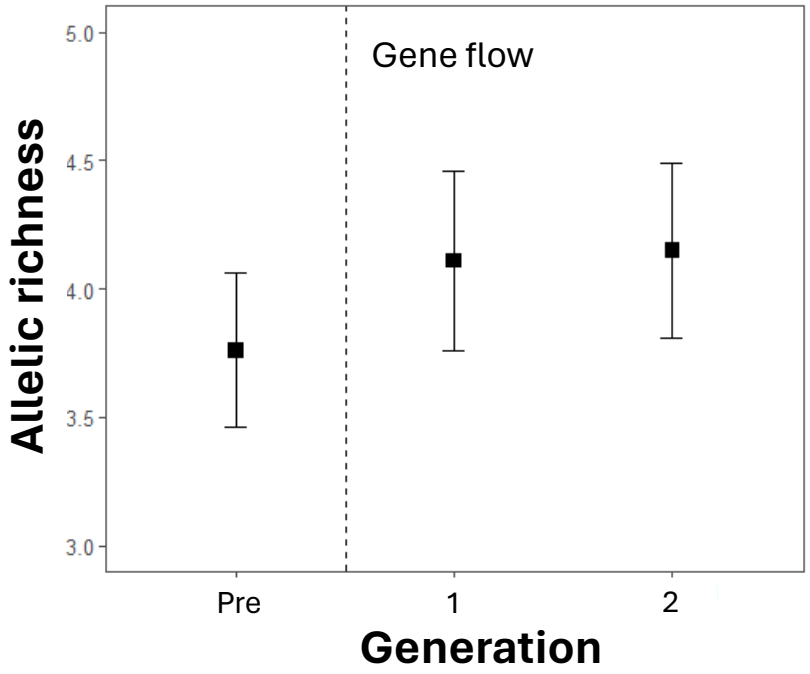
Results

Yaak genetic diversity

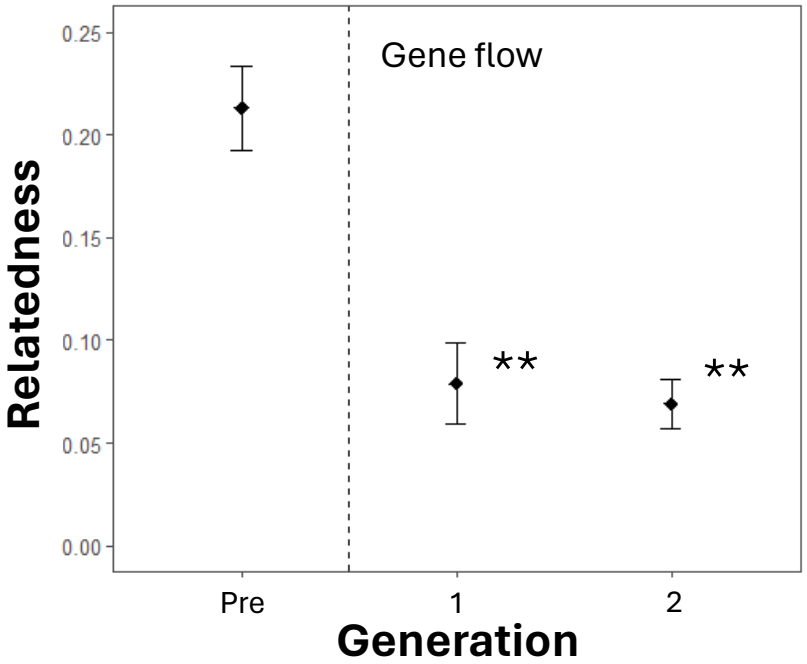
Heterozygosity



Allelic richness



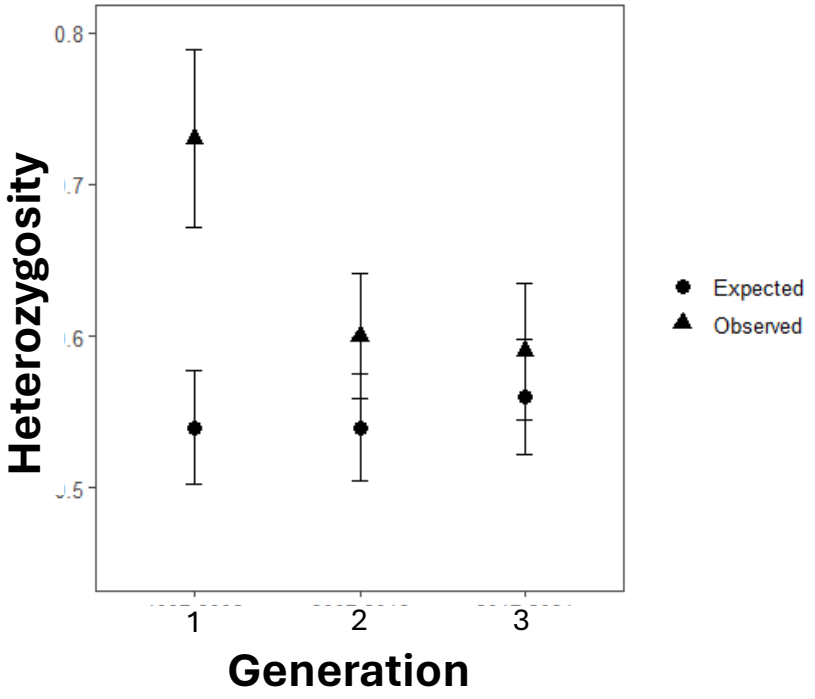
Relatedness



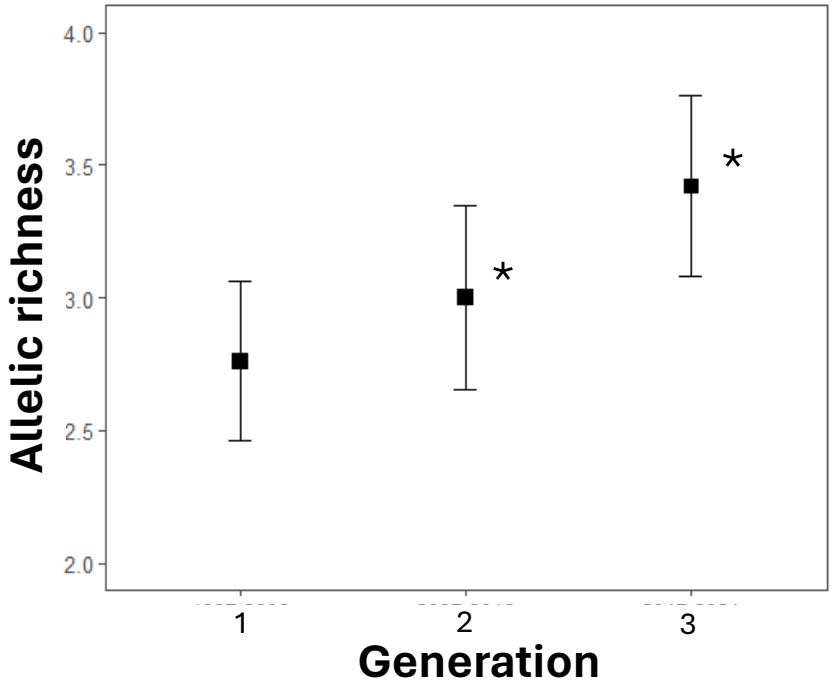
Results

Cabinet genetic diversity

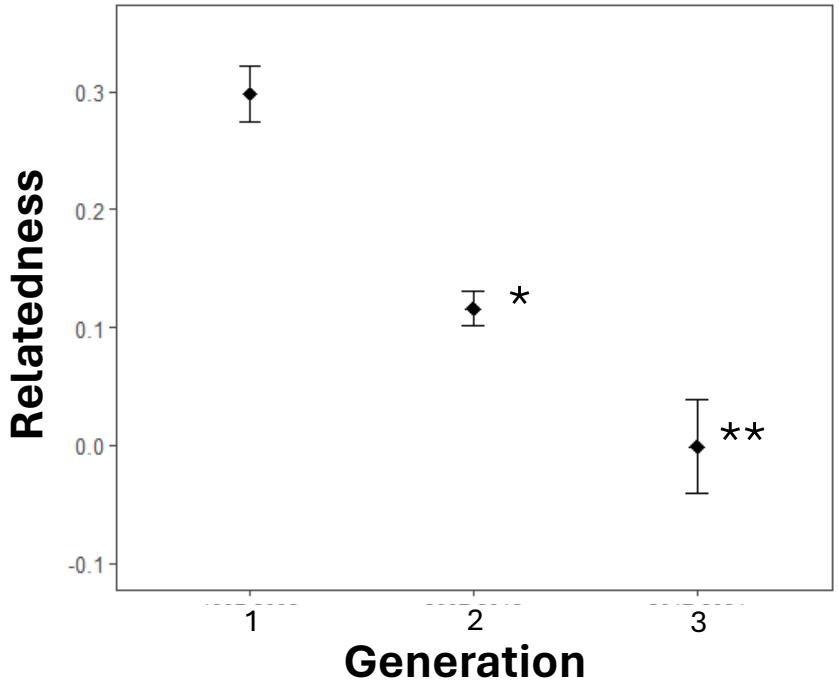
Heterozygosity



Allelic richness



Relatedness



Results

Genetic diversity

- **Selkirk**
  - Heterozygosity: NC
  - Allelic richness: ↑
  - Relatedness: ↓

Results

Genetic diversity

- **Selkirk**
  - Heterozygosity: NC
  - Allelic richness: ↑
  - Relatedness: ↓
- **Yaak**
  - Heterozygosity: NC
  - Allelic richness: NC
  - Relatedness: ↓

Results

Genetic diversity

- **Selkirk**
  - Heterozygosity: NC
  - Allelic richness: ↑
  - Relatedness: ↓
- **Yaak**
  - Heterozygosity: NC
  - Allelic richness: NC
  - Relatedness: ↓
- **Cabinet**
  - Heterozygosity: NC
  - Allelic richness: ↑
  - Relatedness: ↓

Results

Effective population size

	Selkirk
Temporal	15.8
Linkage disequilibrium	15.2
N_e/N_c	0.15-0.16

Results

Effective population size

	Selkirk	Yaak
Temporal	15.8	17.5
Linkage disequilibrium	15.2	15.4
N_e/N_c	0.15-0.16	0.44-0.50

Results

Effective population size

	Selkirk	Yaak	Cabinet
Temporal	15.8	17.5	8.9
Linkage disequilibrium	15.2	15.4	5.6
N_e/N_c	0.15-0.16	0.44-0.50	0.19-0.31

50/500 rule

Synthesis

Chapter I

- Gene flow from migration and augmentation is maintaining or increasing genetic diversity

- Ne/Nc ratios are comparable to other populations
  - GYE: 0.42-0.66

BUT…

- Effective population sizes are small

Management Implications

- Management actions to improve connectivity are working
- Genetic diversity and effective population size baseline for future monitoring

Proctor et al. 2018

Future Work

- Continued genetic monitoring
- Cabinet gene flow
- Genomic markers

Acknowledgements

- Advisor: Lisette Waits
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- Michael Proctor
- Waits Lab
- Field technicians and agency collaborators

Questions?