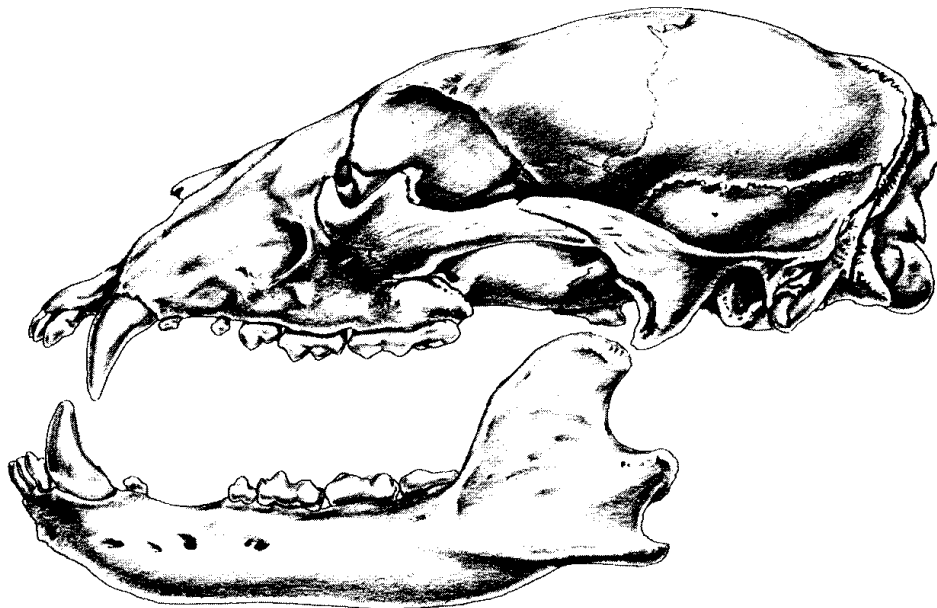


Genetic Diversity Issues for the Yellowstone Grizzly Bear

Craig Miller and Lisette Waits







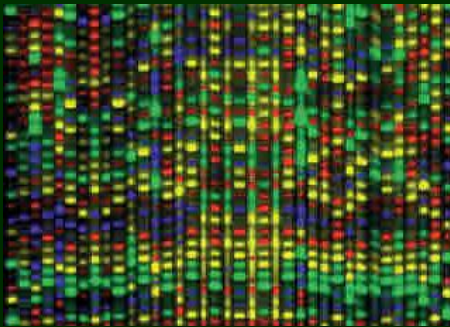
Current and
Historic Range
Of the Grizzly Bear
(*Ursus arctos*)

British
Columbia

“...the FWS has failed to meet its obligation under the ESA to incorporate into the Grizzly Bear Recovery Plan objective, measurable criteria addressing genetic isolation.” (Federal Court decision 1995)



Are levels of genetic diversity in YE grizzly bears significantly lower than other brown bear populations?

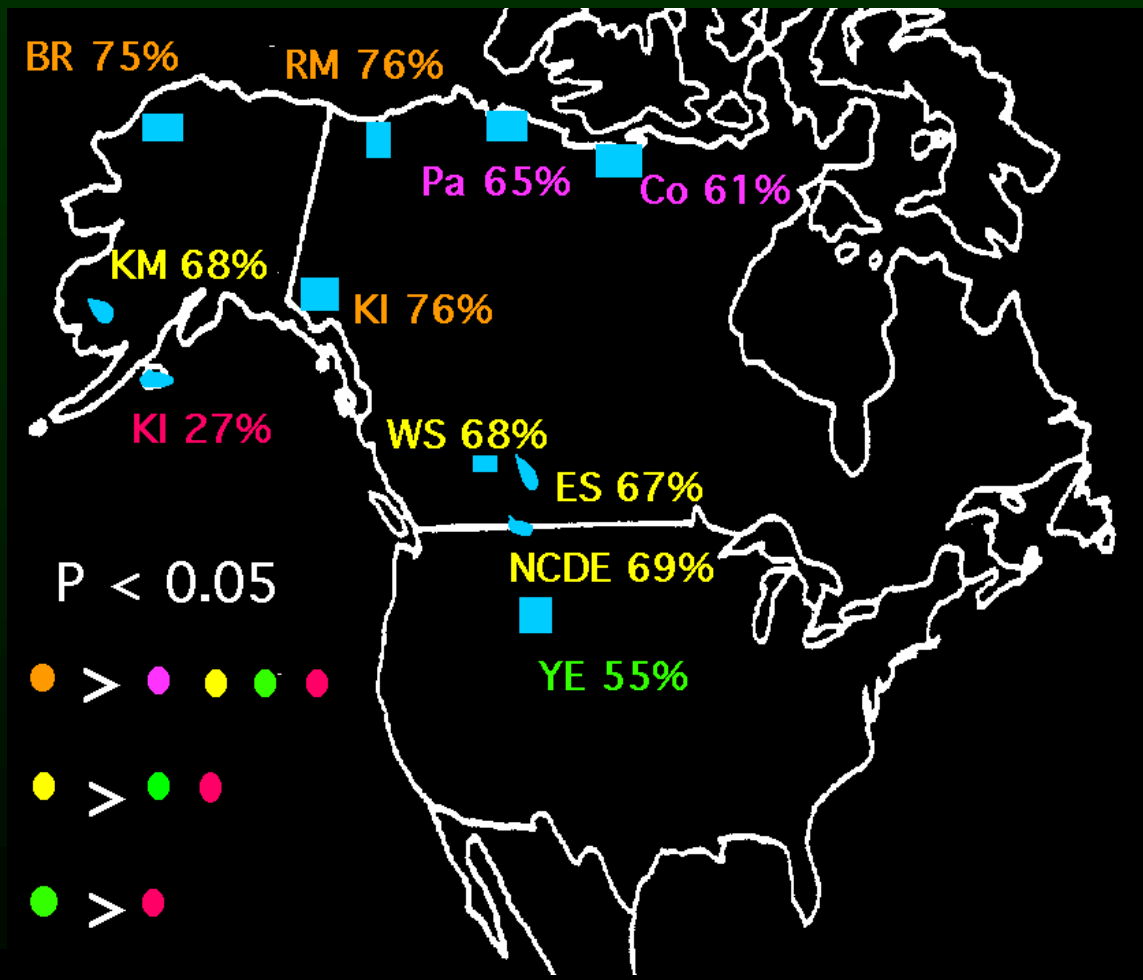


Methods

- Sample > 20 individuals from brown bear populations across North America
- Collect genotype data from 8 nuclear DNA microsatellite loci
- Compare #alleles/locus and heterozygosity

Microsatellite Heterozygosity in Modern NA Brown Bears

(8 loci, mean 2n=124)




Paetkau et al. 1998
ConBio

Current Diversity in Yellowstone vs. NCDE

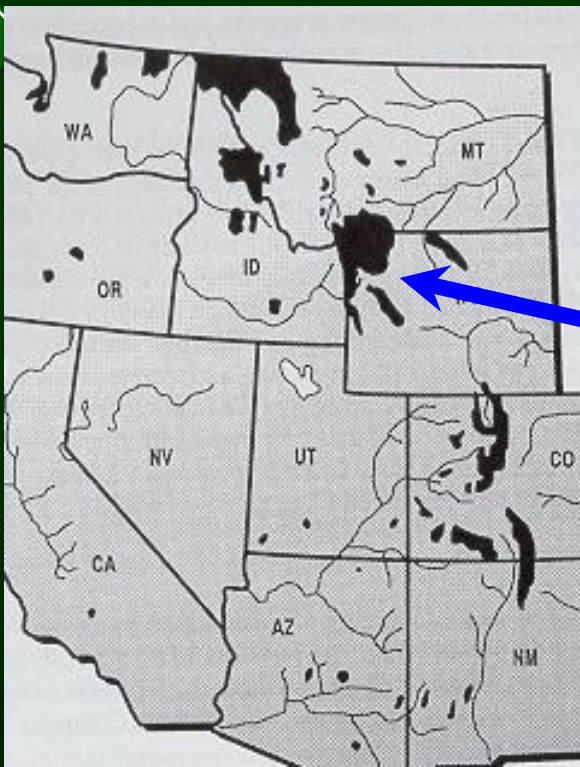
	Heterozygosity (Diversity)		
	Allozymes ¹	Micro-satellites ²	mtDNA ³
Yellowstone (YE)	0.008	0.557	0.24
NCDE	0.014	0.694	0.61
YE / NCDE	57%	80%	39%

¹ Allendorf pers. com.; ² Paetkau et al. (1998); ³ Waits et al. (1998)

Questions

- 
- Has genetic variation been lost in Yellowstone? If so how much and when?
 - What has the effective population size (N_e) been over the last century?
 - What is the ratio of N_e / N ? What does this imply about the current N_e ?
 - What is the likely future trajectory of genetic diversity in the population assuming continued isolation compared to various levels of gene flow from other populations?
 - What are the implications for conservation and management?

Yellowstone



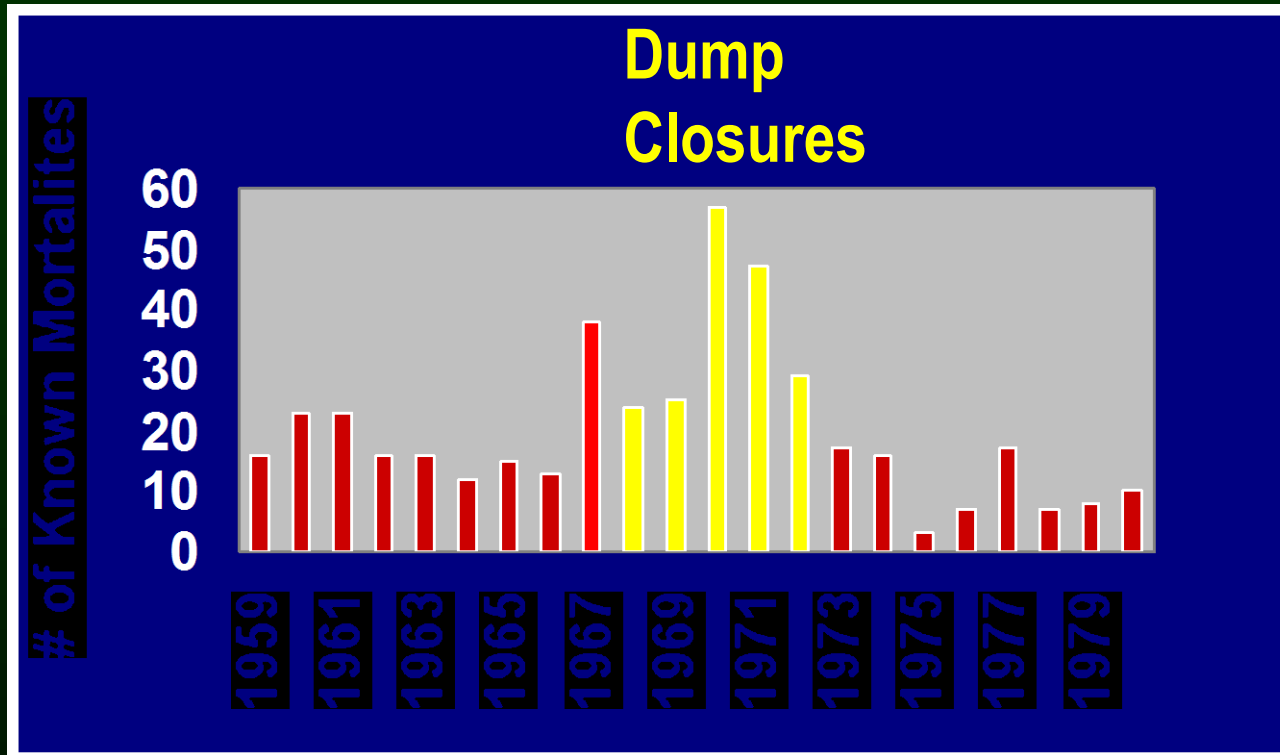
Isolated by 1920

Dump feeding began
in late 1800's



photo by E.W. Hunter (Montana Historical Society)

Known Mortalities in Yellowstone Ecosystem, 1959-1980

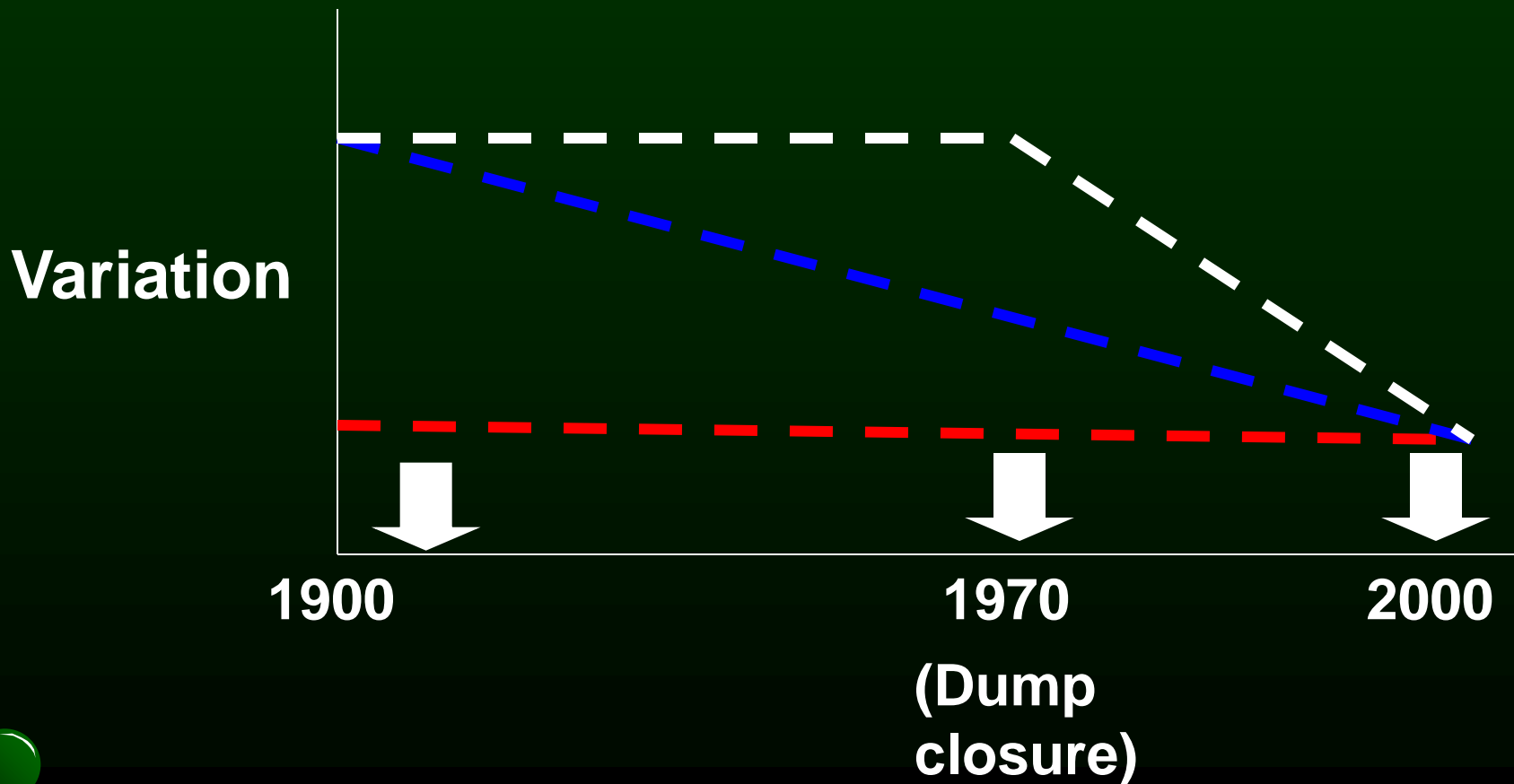


of known mortalities 1961-1966: **95**

1967-1972: **220**

Estimate of mean population size 1959-1970: **312** (Craighead et al. 1995)

Experimental Design to Resolve Competing Hypotheses



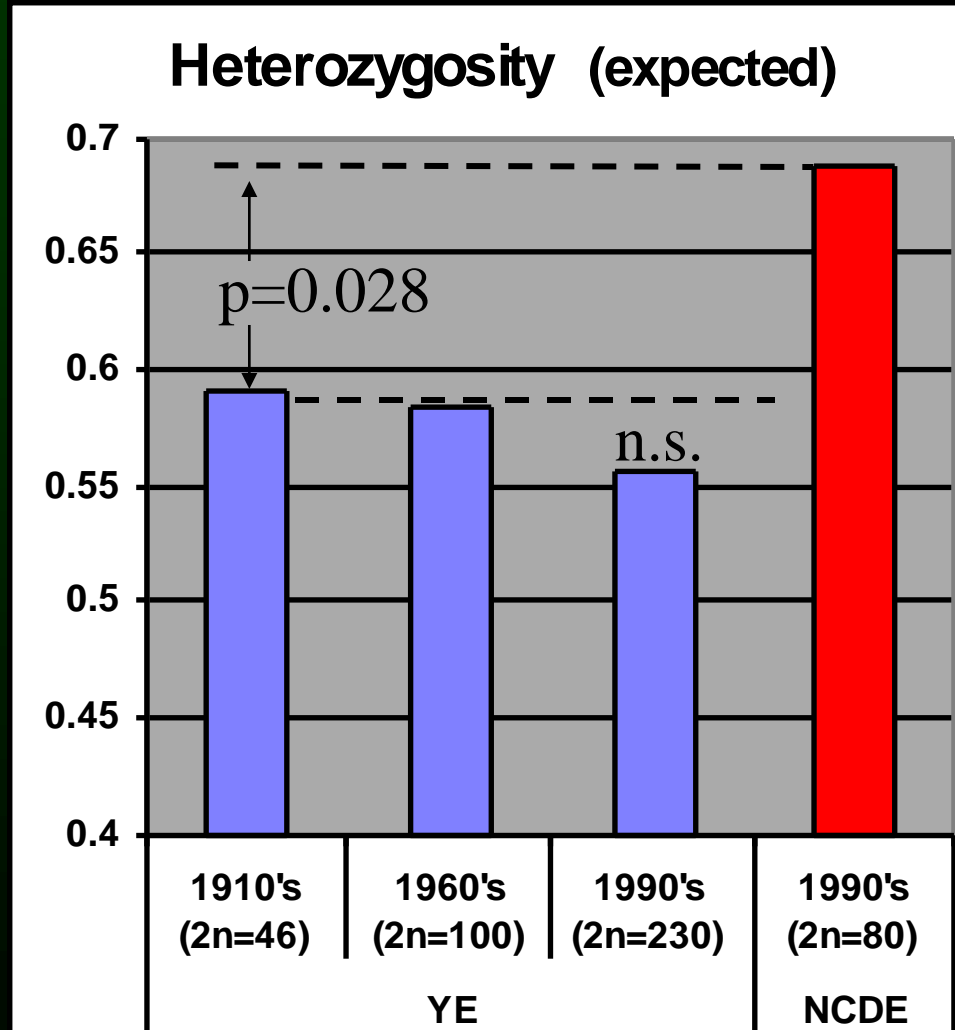
Methods



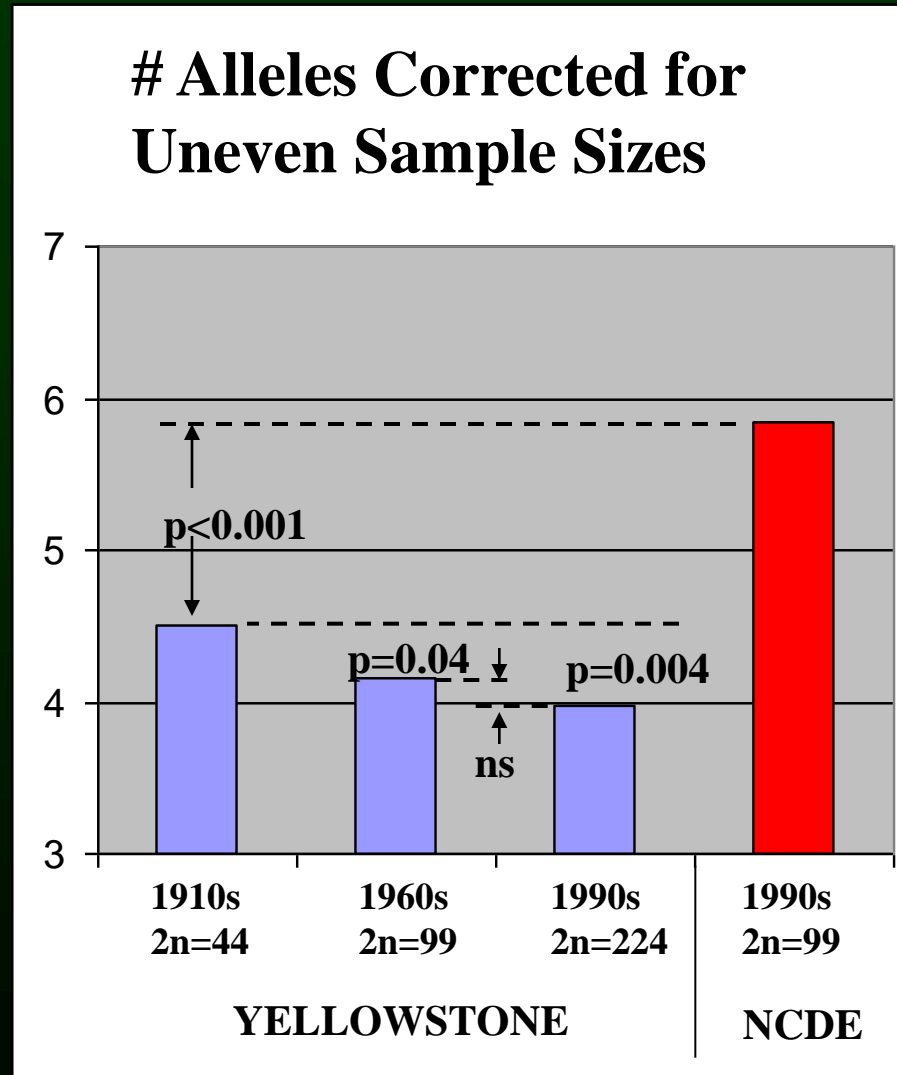
- Used museum specimens as source of DNA
- Genotyped 8 microsatellite loci
- Sample sizes:

1912-1920	N=38
1960-1972	N=72
1992-1999	N=136
- Analysis excludes unreplicated historic genotypes and mean # of PCRs/sample/locus = 3.5
- Compare 1910's, 1960's and 1990's populations for heterozygosity, # of alleles / locus

Results: Heterozygosity



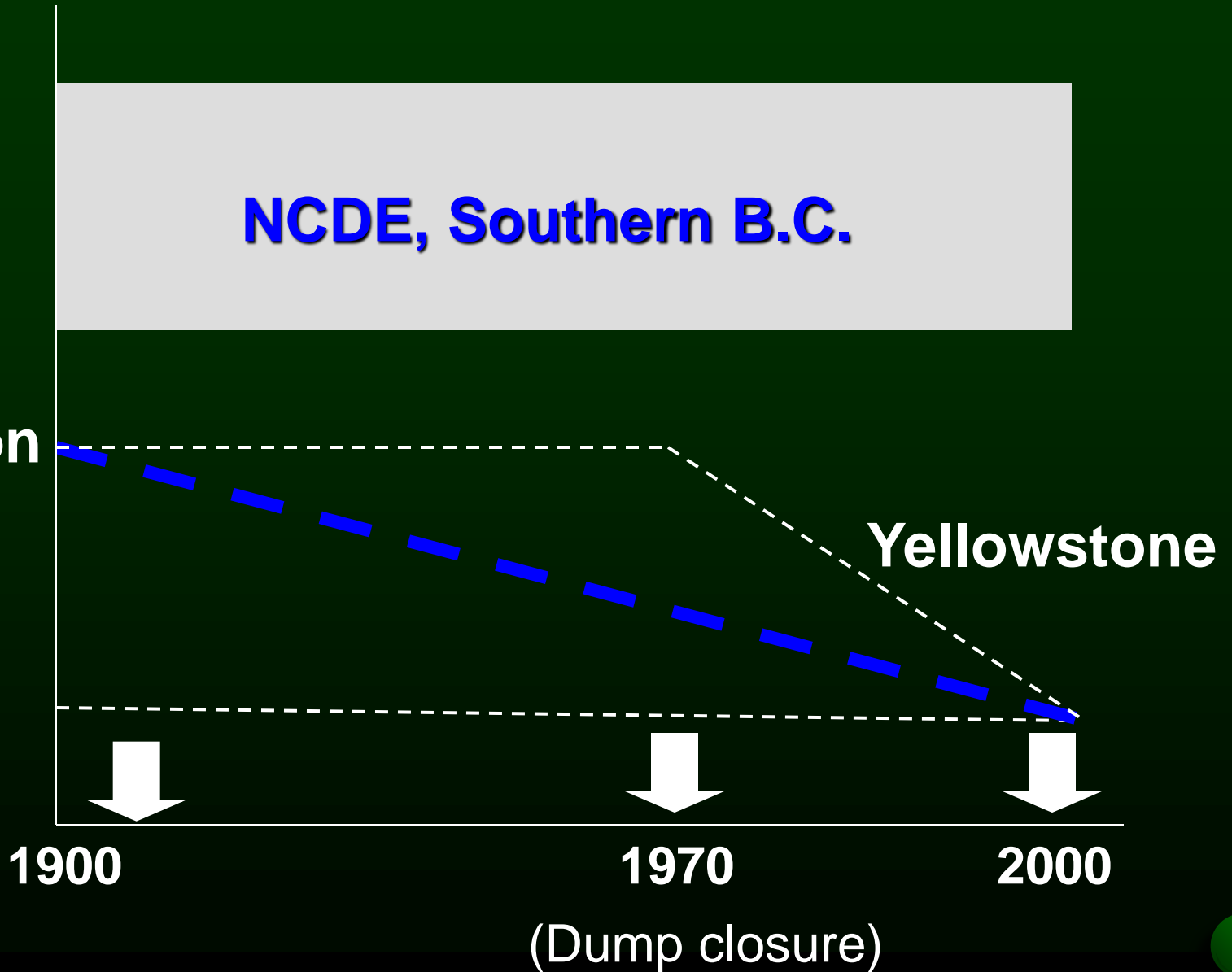
Results: Allelic Diversity



Conclusion

NCDE, Southern B.C.

Variation



Questions



□ Has genetic variation been lost in Yellowstone? If so how much and when?

Past

□ What has the effective population size (N_e) been over the last century?

Present

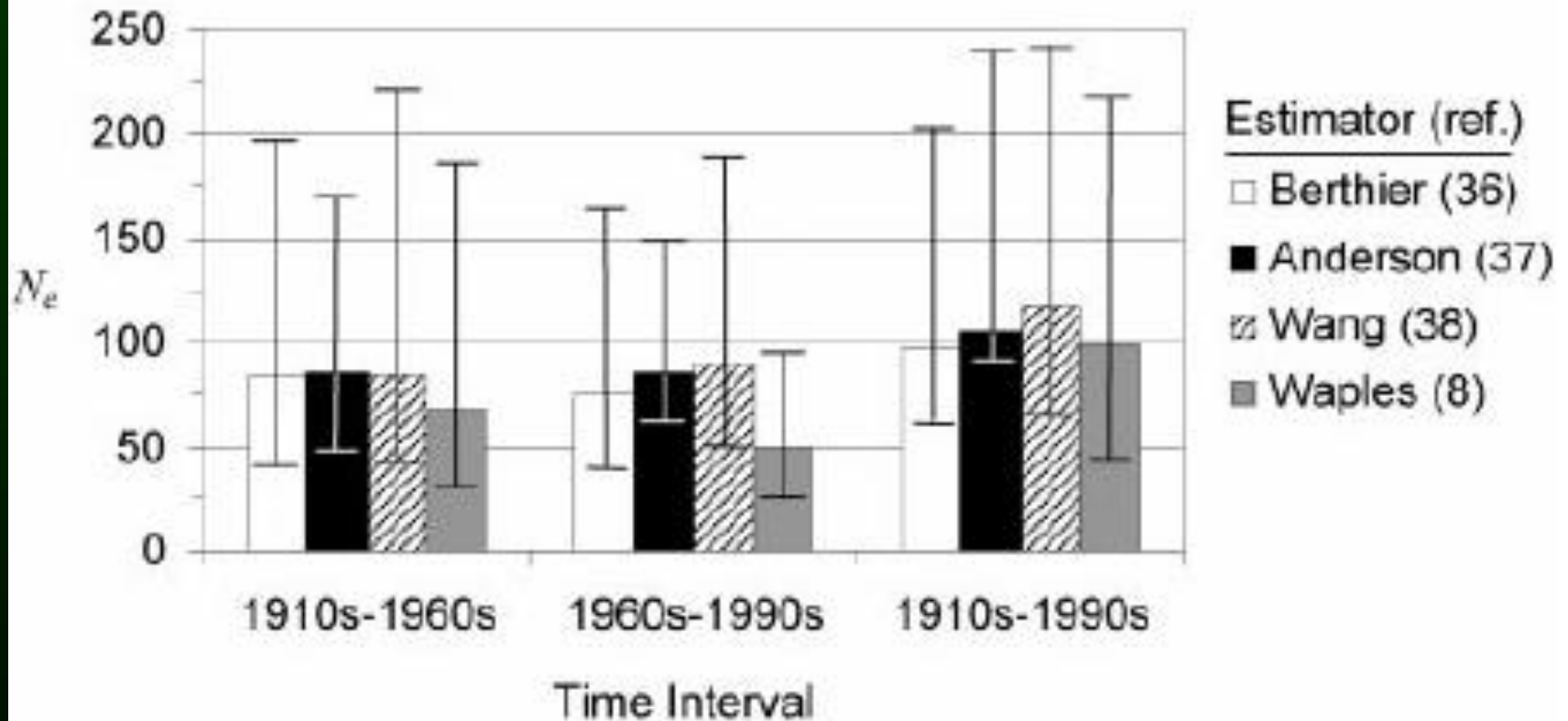
□ What is the ratio of N_e / N ? What does this imply about the current N_e ?

Future

□ What is the likely future trajectory of genetic diversity in the population assuming continued isolation compared to various levels of gene flow from other populations?

□ What management strategies follow from these findings?

Results

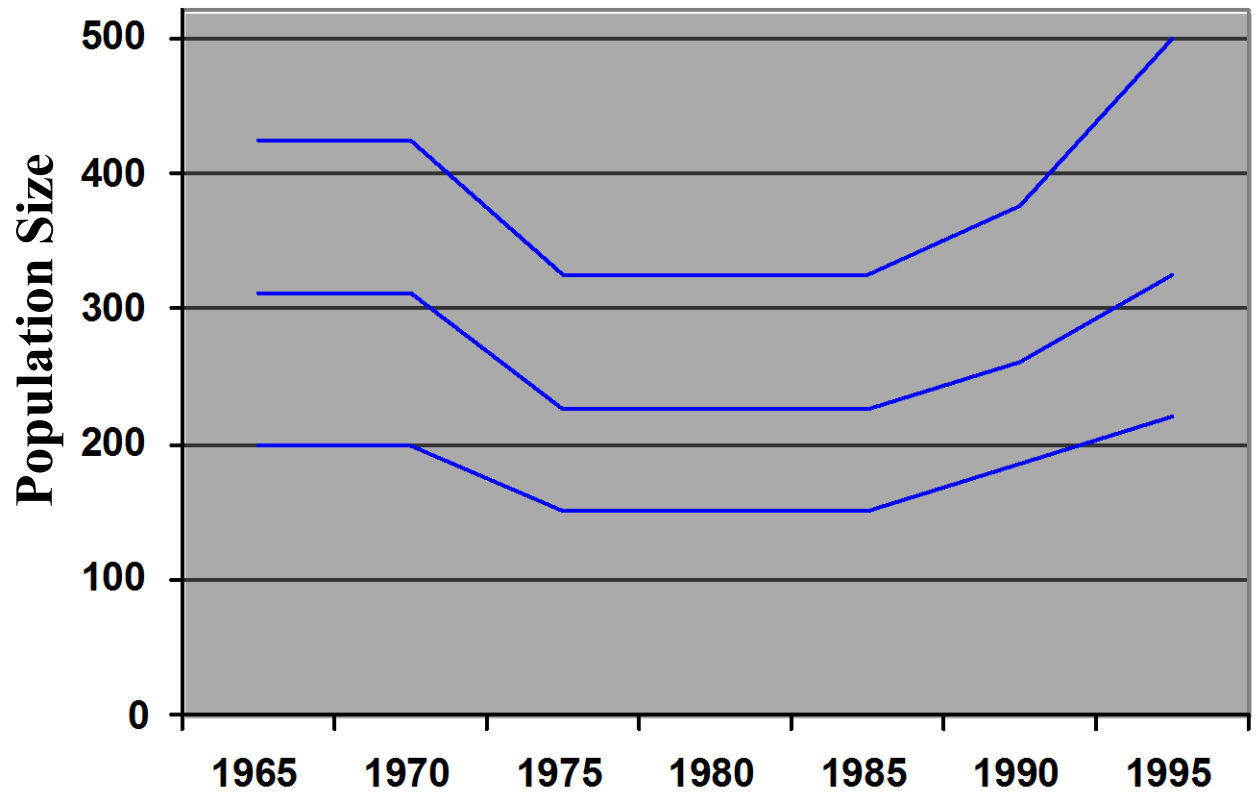


✓ N_e (harmonic)

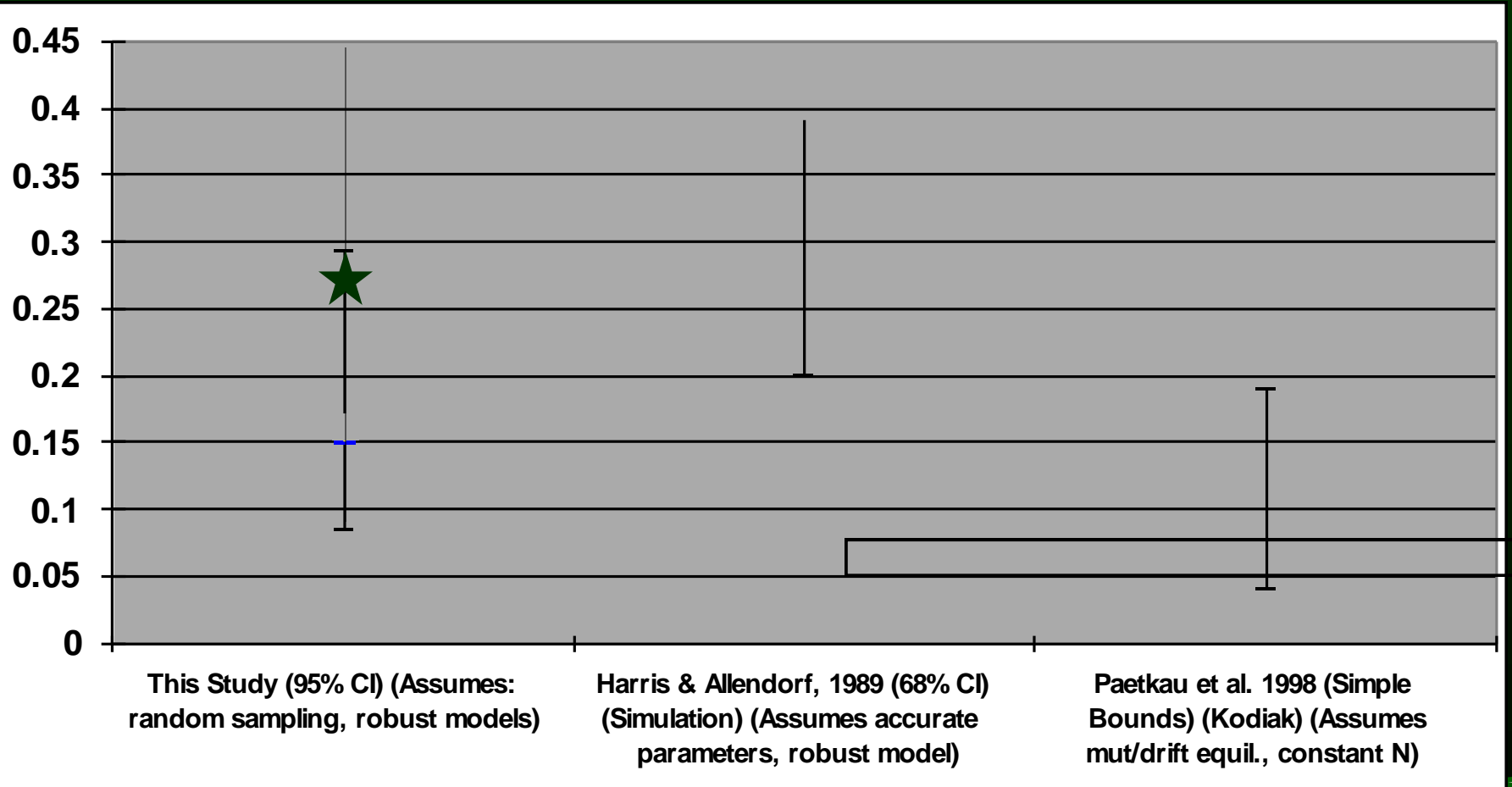
N (harmonic)

Population Size in Yellowstone 1965- 1995

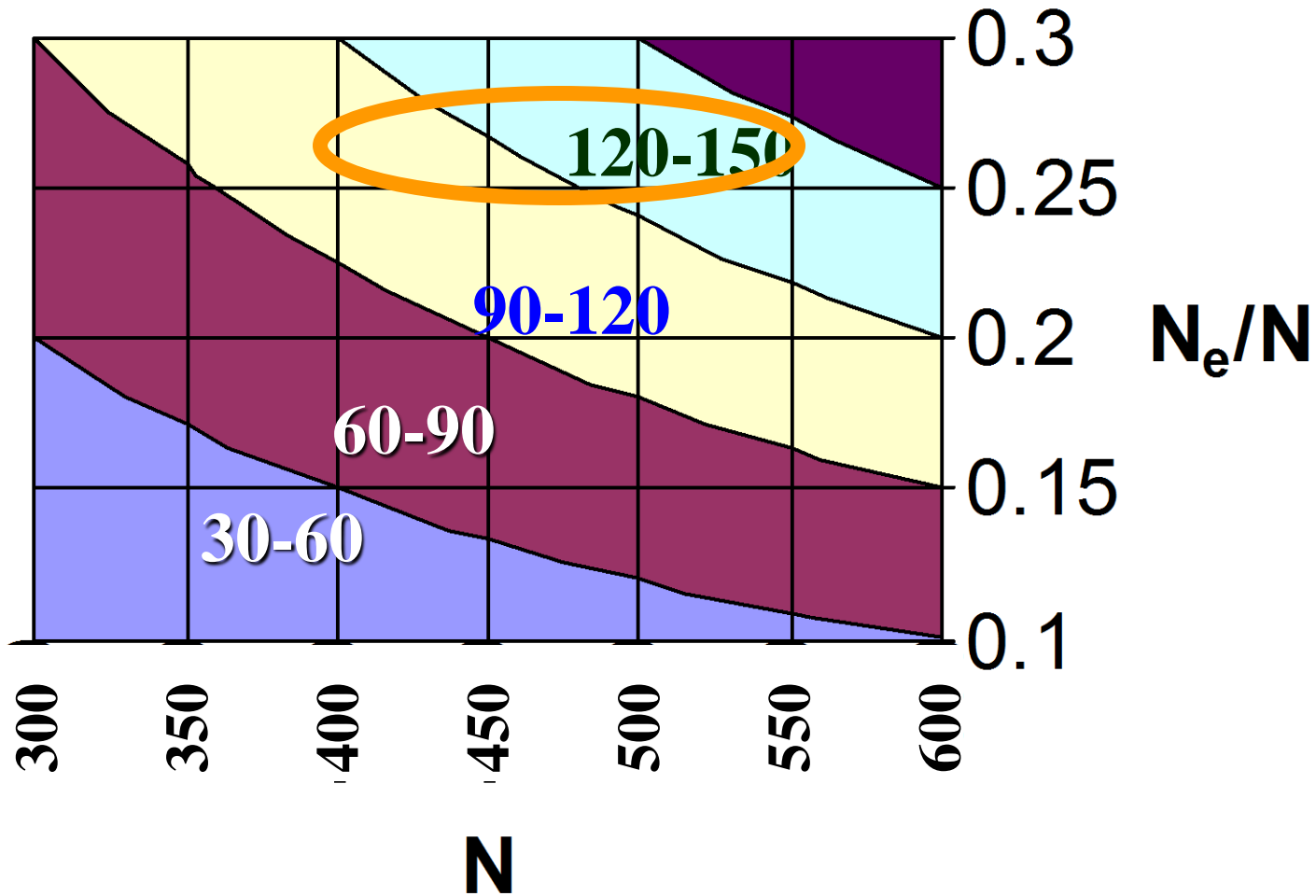
(based on estimates in the literature)



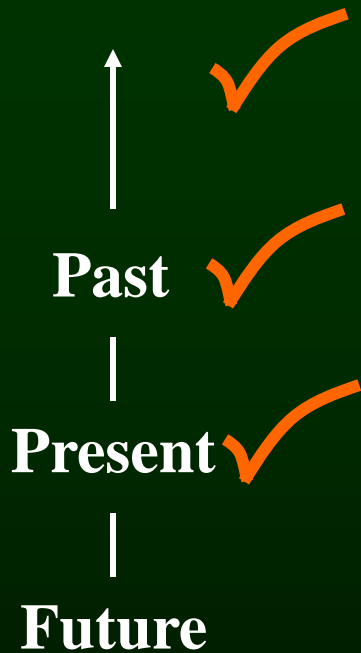
Estimation of N_e / N ratio in Brown Bears



Current N_e as a function of current N & N_e/N



Questions



- What is the likely future trajectory of genetic diversity in the population assuming continued isolation compared to various levels of gene flow from another population?
- What management strategies follow from the findings?

Projecting Variation in Yellowstone into the Future

- Developed analytic theory and used simulations to predict H_E and allelic diversity in the near future as a function of N_e , migration rate and allele frequencies in source & recipient populations

$$H_{S(t)} \approx H_{S(0)} \left(1 - \frac{1}{2N} - 2m\right)^t + 2mH_{ST(0)} \left(1 - \frac{1}{2N} - 2m\right)^{t-1} + 2mH_{ST(1)} \left(1 - \frac{1}{2N} - 2m\right)^{t-2} + \dots$$
$$+ 2mH_{ST(t-2)} \left(1 - \frac{1}{2N} - 2m\right) + 2mH_{ST(t-1)}$$

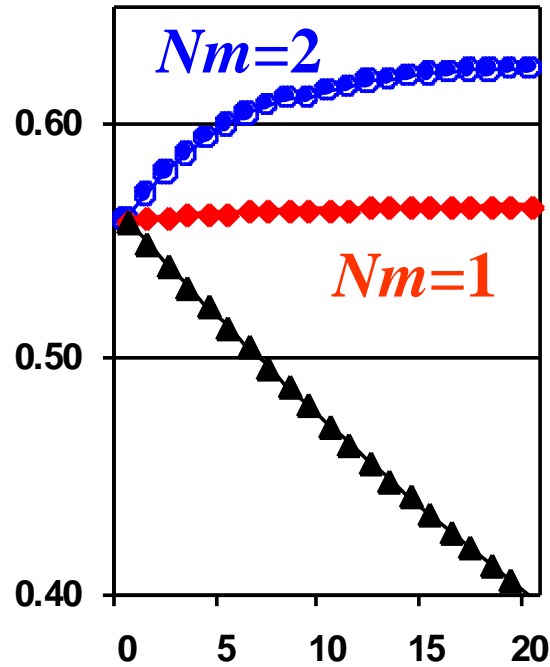
- Assumed island-continent model

projecting variation cont.

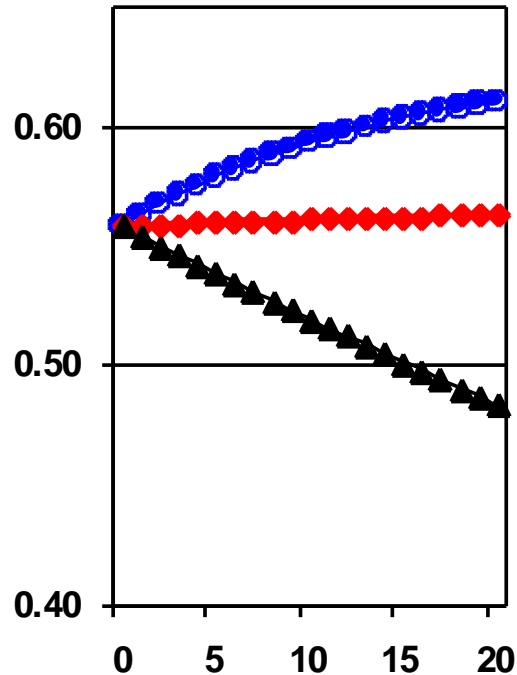
- Parameterized model with empirical allele frequencies from YE and NCDE populations
- Considered N_e over next 20 generations of 30, 70 and 125.
- Assumed NCDE as source (ie. continent)
- Considered migration rate (Nm) between 0-2 per generation (10 years)
- Considered initiating gene flow now (ie. via transplantation) and 5 or 10 generations from now (natural or transplantation)

Heterozygosity

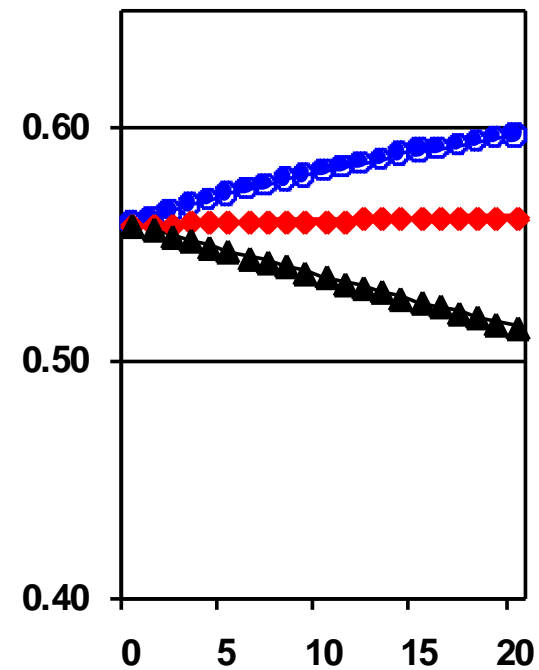
$N_e = 30$



$N_e = 70$



$N_e = 125$

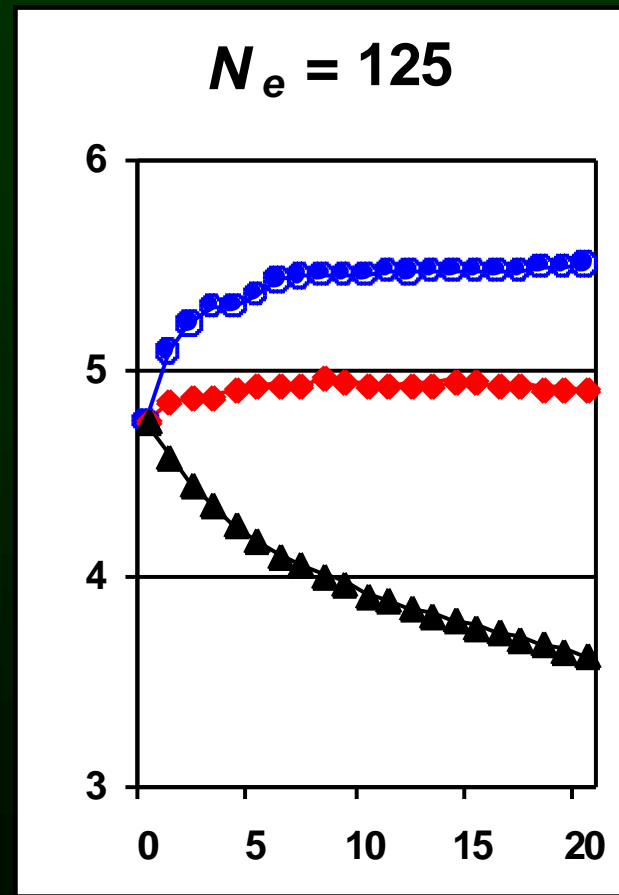
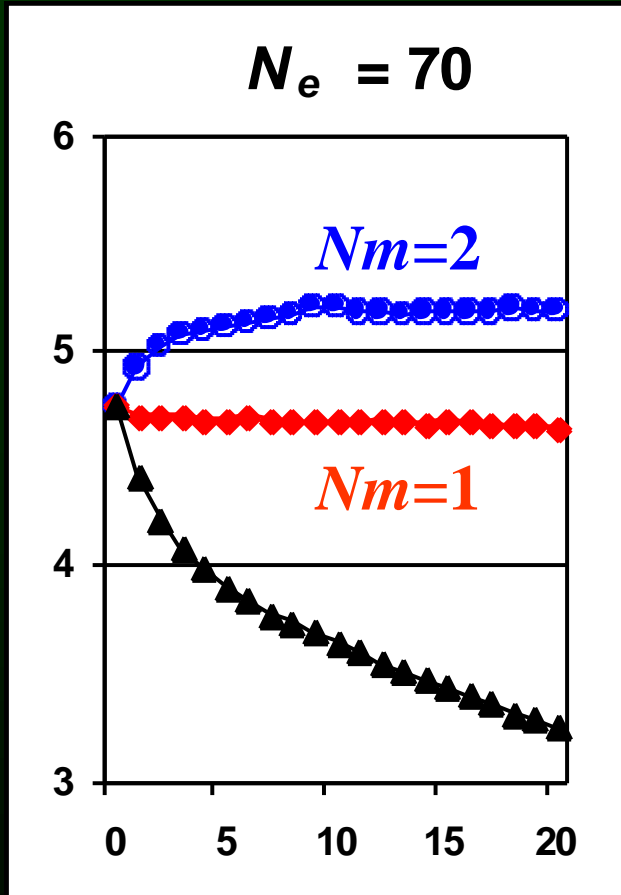


Generation

H_s

Allelic Diversity

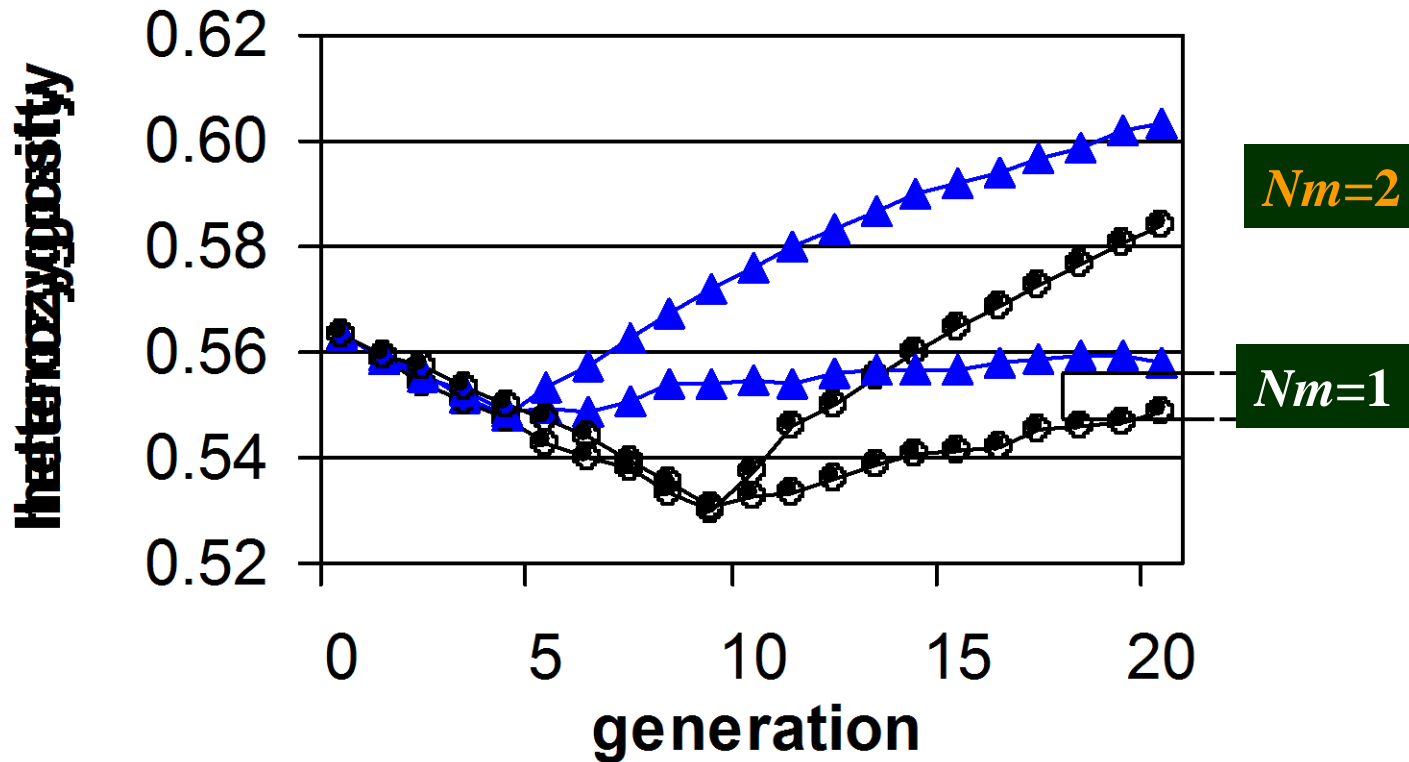
Alleles / Locus



Generation

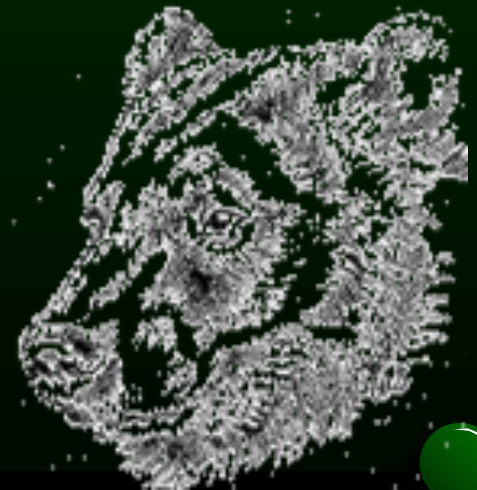
What if gene flow is delayed?

Projected Heterozygosity in Yellowstone
when Gene Flow from NCDE is delayed
5 (▲) or 10 (●) Generations ($N_e=70$)



Conclusions & Management Recommendations

- Diversity has declined across the century and will continue to decline in isolation.
- Long-term viability - at least maintain variation at its current level.
- One or two (effective) migrants per generation is sufficient to accomplish this goal.
- Best guess is that N_e is currently near or > 100 .



recommendations continued

- Gene flow: (1) translocation: immediate or delayed. (2) natural dispersal: delayed or not at all.
- Current efforts should focus on enhancing natural linkage to YE.
- If natural gene flow is not documented within several generations, translocation from NCDE or SW Canada should be conducted.
- Any translocated bears should be monitored for reproductive success. Suggests female transplants.



Acknowledgements

□ The following collections and associated curators:

- Smithsonian
- Washington State University
- University of Montana
- Montana Dept. of Fish, Wildlife and Parks
- UC Berkeley Museum of Vertebrate Zoology
- California Academy of Sciences
- University of Kansas Museum of Natural History
- University of British Columbia
- Denver Museum of Natural History
- University of Kansas Museum of Natl. History
- American Museum of Natural History
- Academy of Natural Sciences
- Field Museum of Natural History
- Glacier National Park



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□ National Science Foundation and EPSCOR