



**Universität  
Zürich**<sup>UZH</sup>

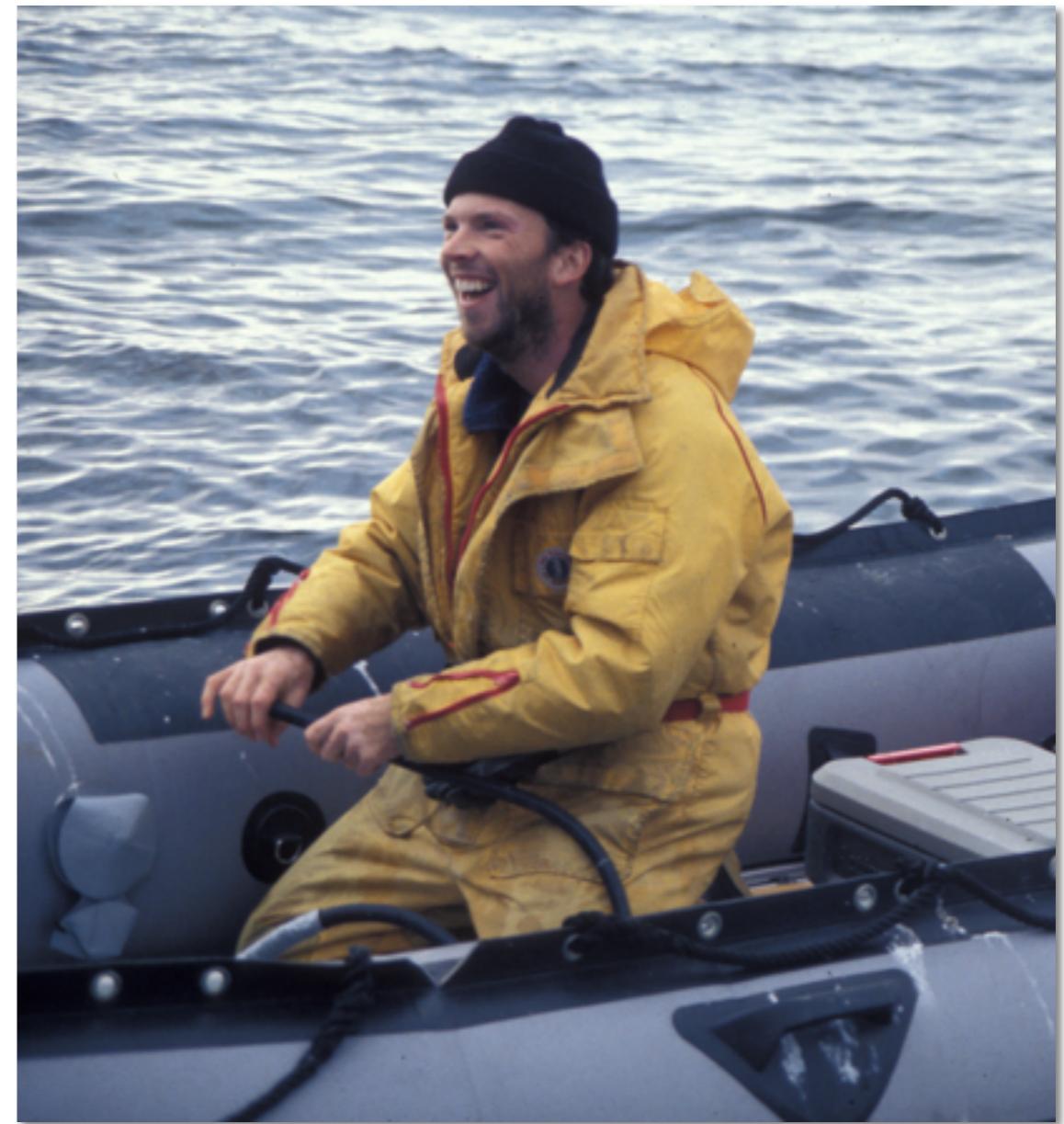
Institut für Evolutionsbiologie und Umweltwissenschaften

# The genetic footprint of Alpine ibex reintroductions and implications for population management

WISO 2012, Christine Grossen

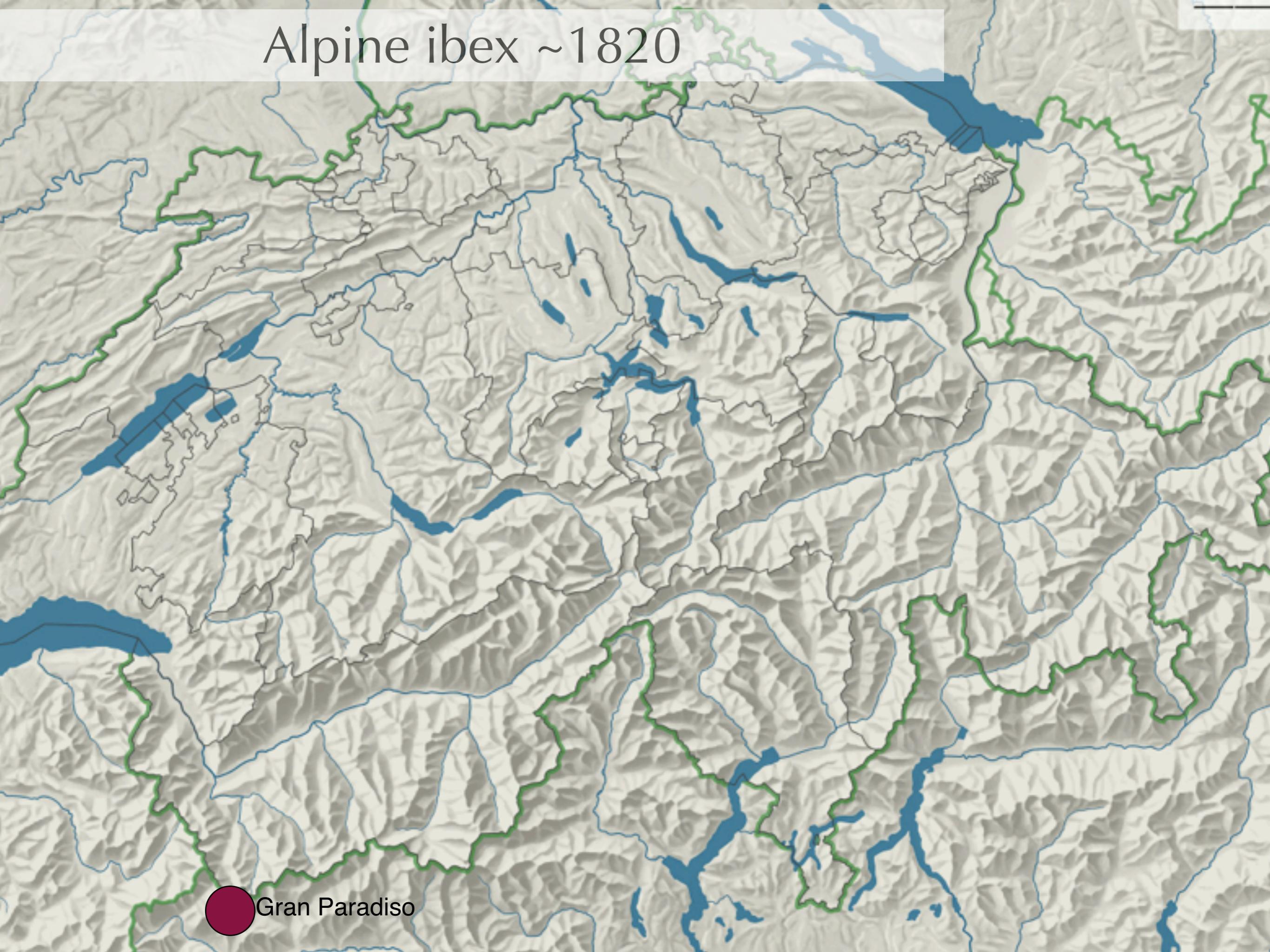


Iris Biebach



Lukas Keller

# Alpine ibex ~1820



Gran Paradiso

1906

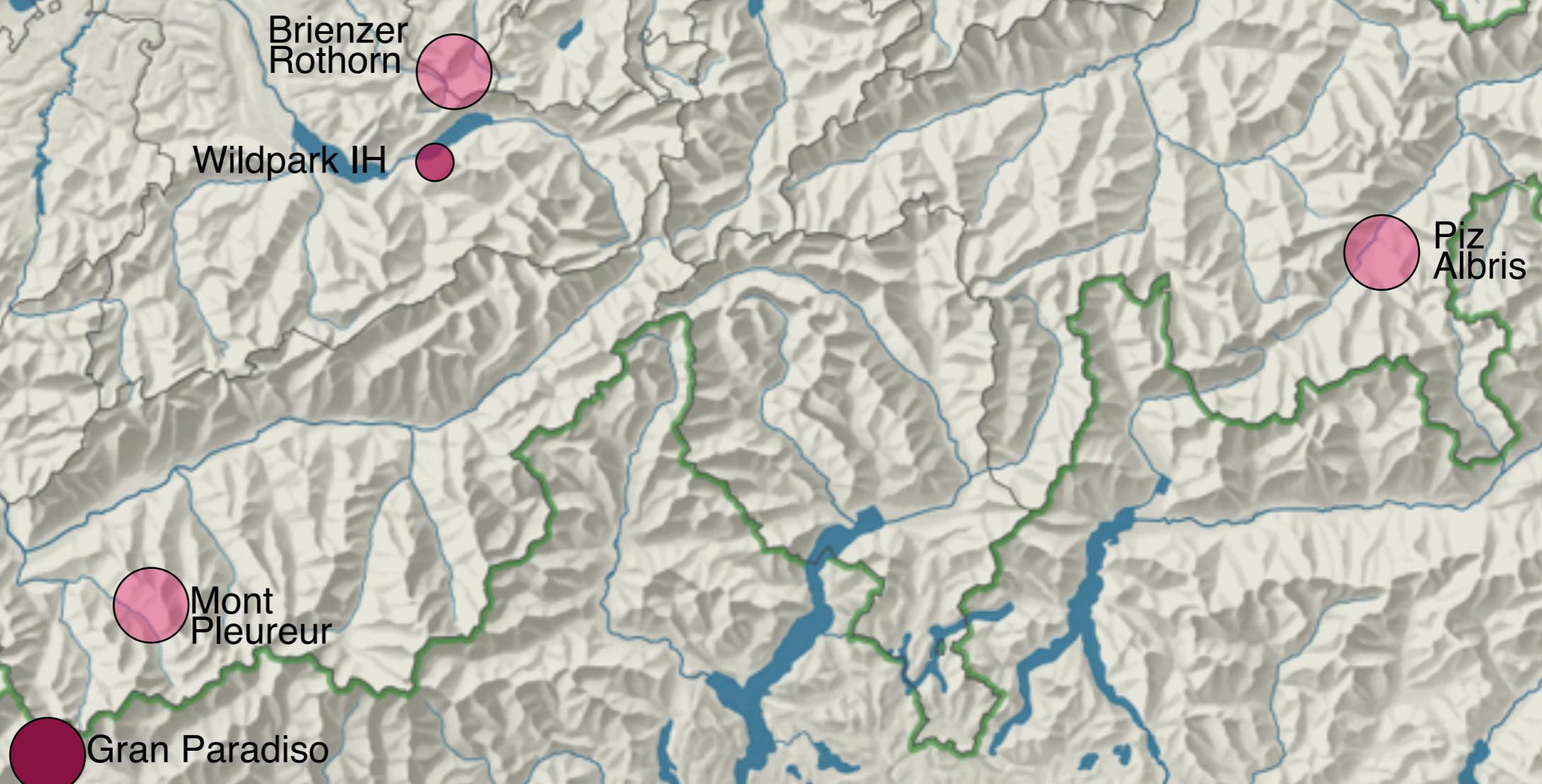


Wildpark PP

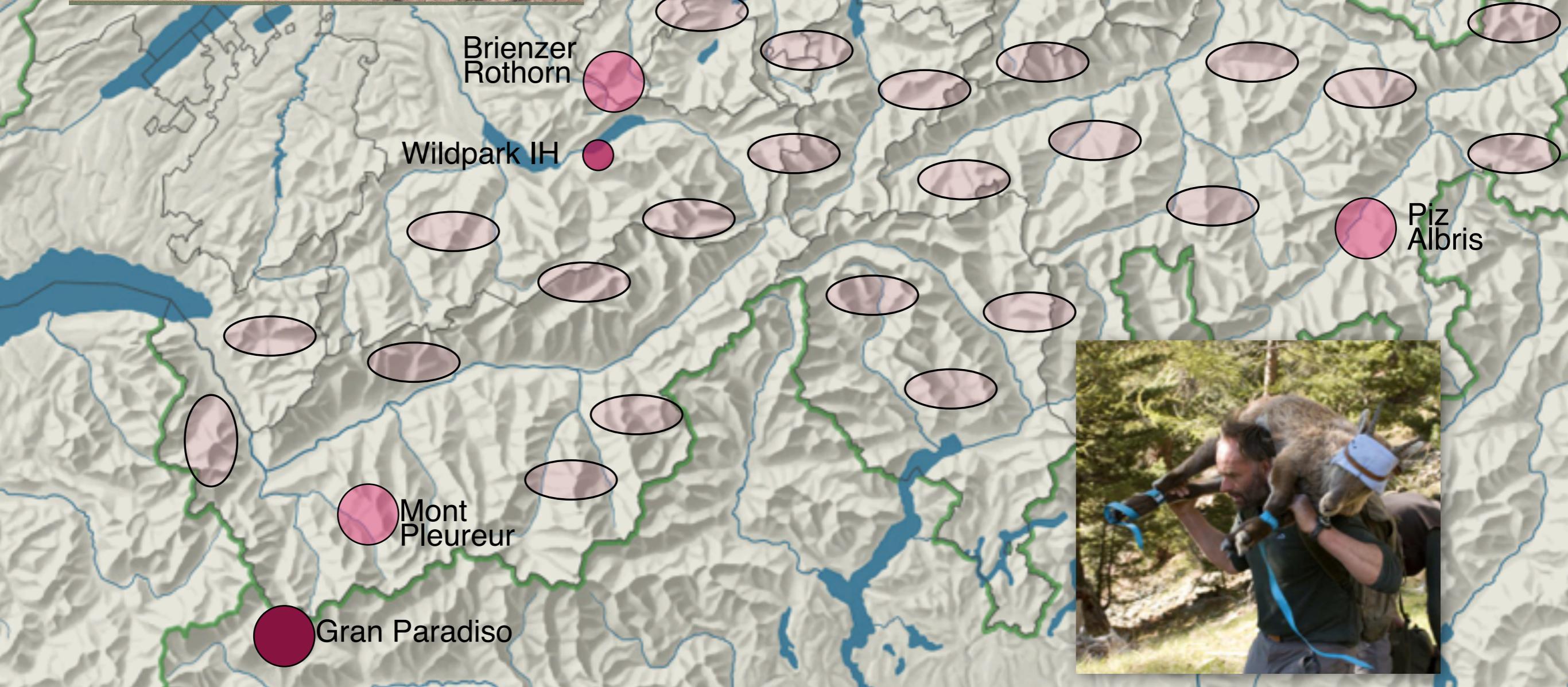
Wildpark IH

Gran Paradiso

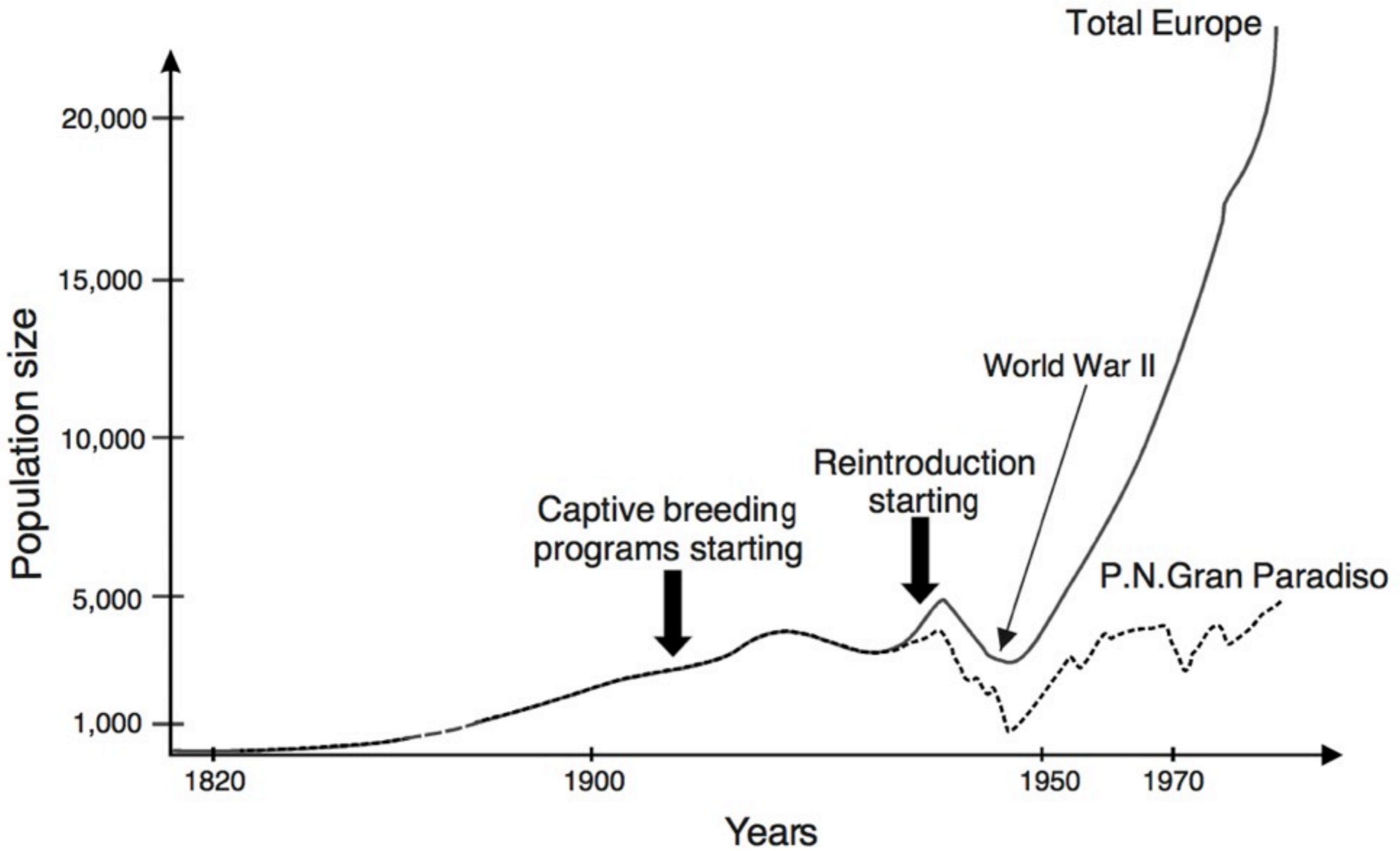
# reintroductions after 1911



# reintroductions after 1911



# Fast recovery of Alpine ibex populations

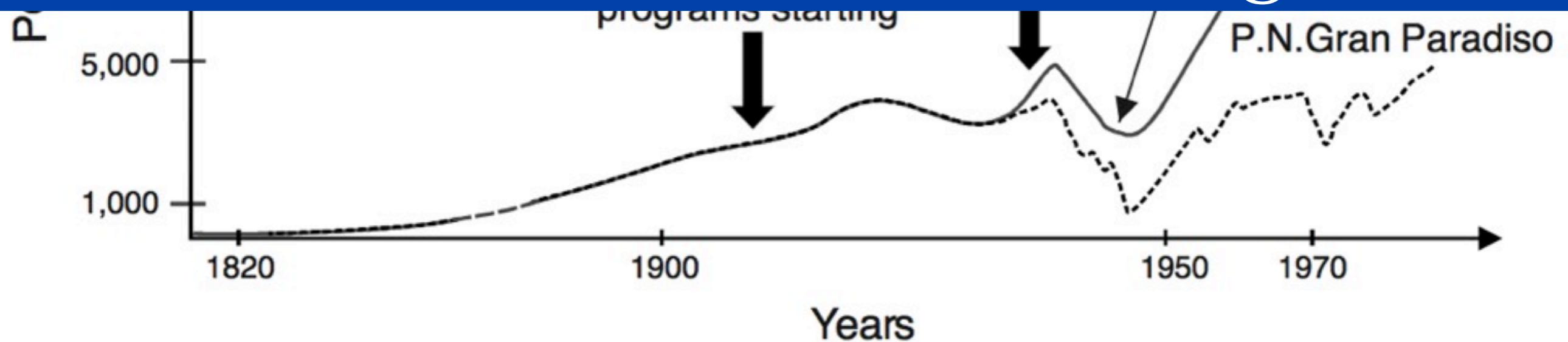


(Maudet et al. 2002, Molecular Ecology)

# Fast recovery of Alpine ibex populations



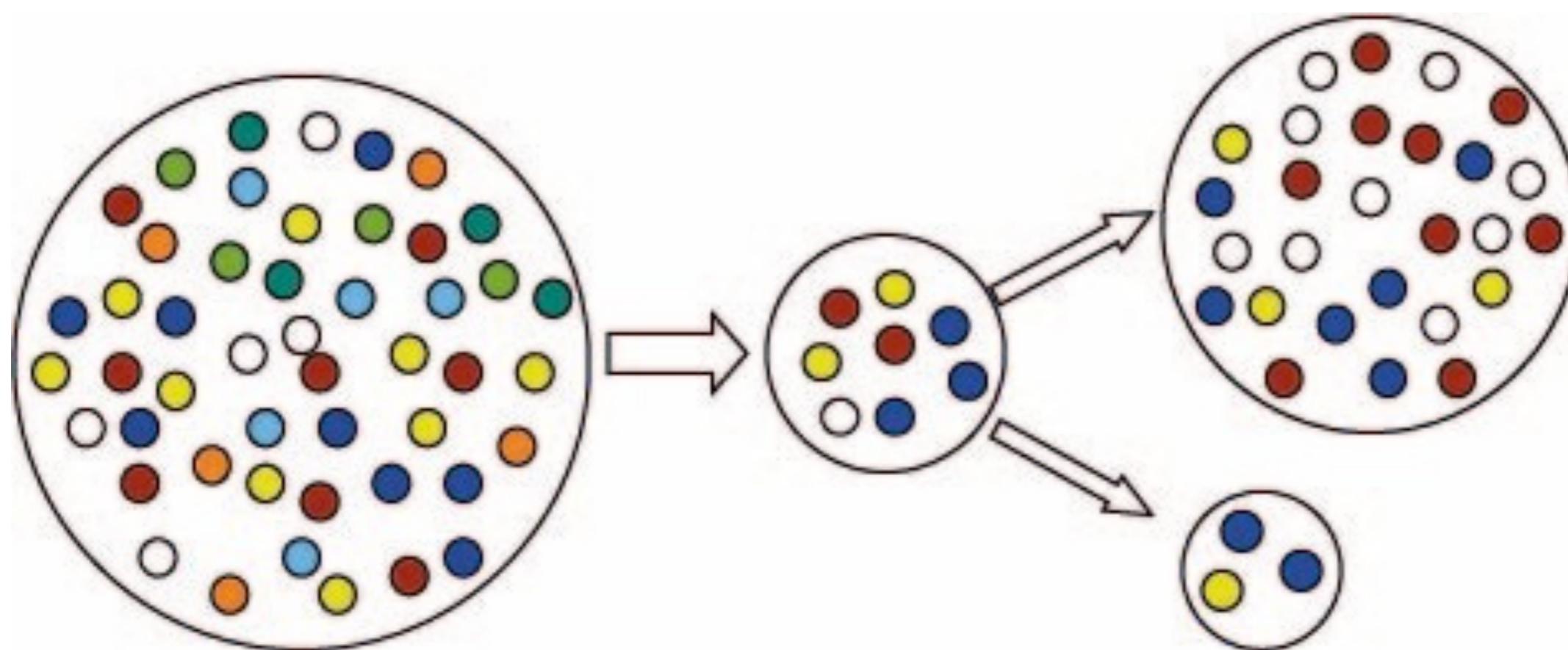
Small populations:  
Decrease of genetic diversity  
Increase of inbreeding



(Maudet et al. 2002, Molecular Ecology)

# Genetic drift: decrease of genetic diversity

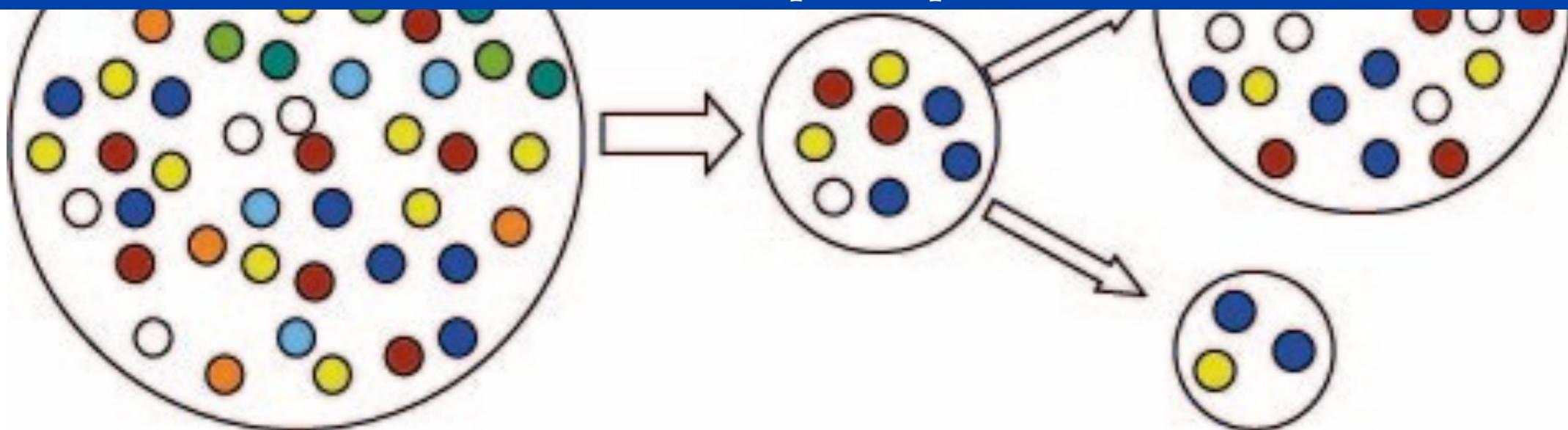
Random change in frequency of gene variants (alleles) over generations



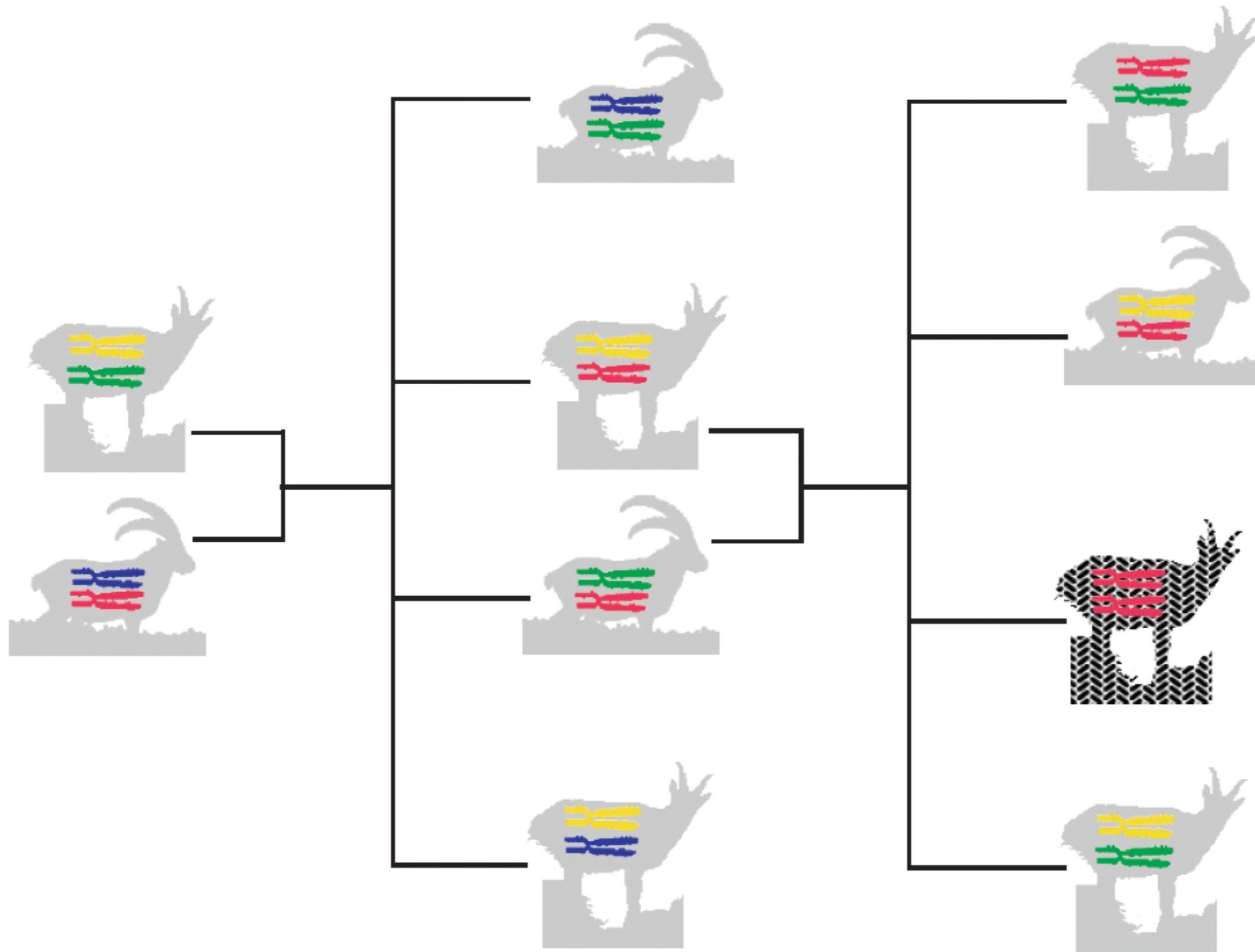
# Genetic drift: decrease of genetic diversity

Random change in frequency of gene variants (alleles) over generations

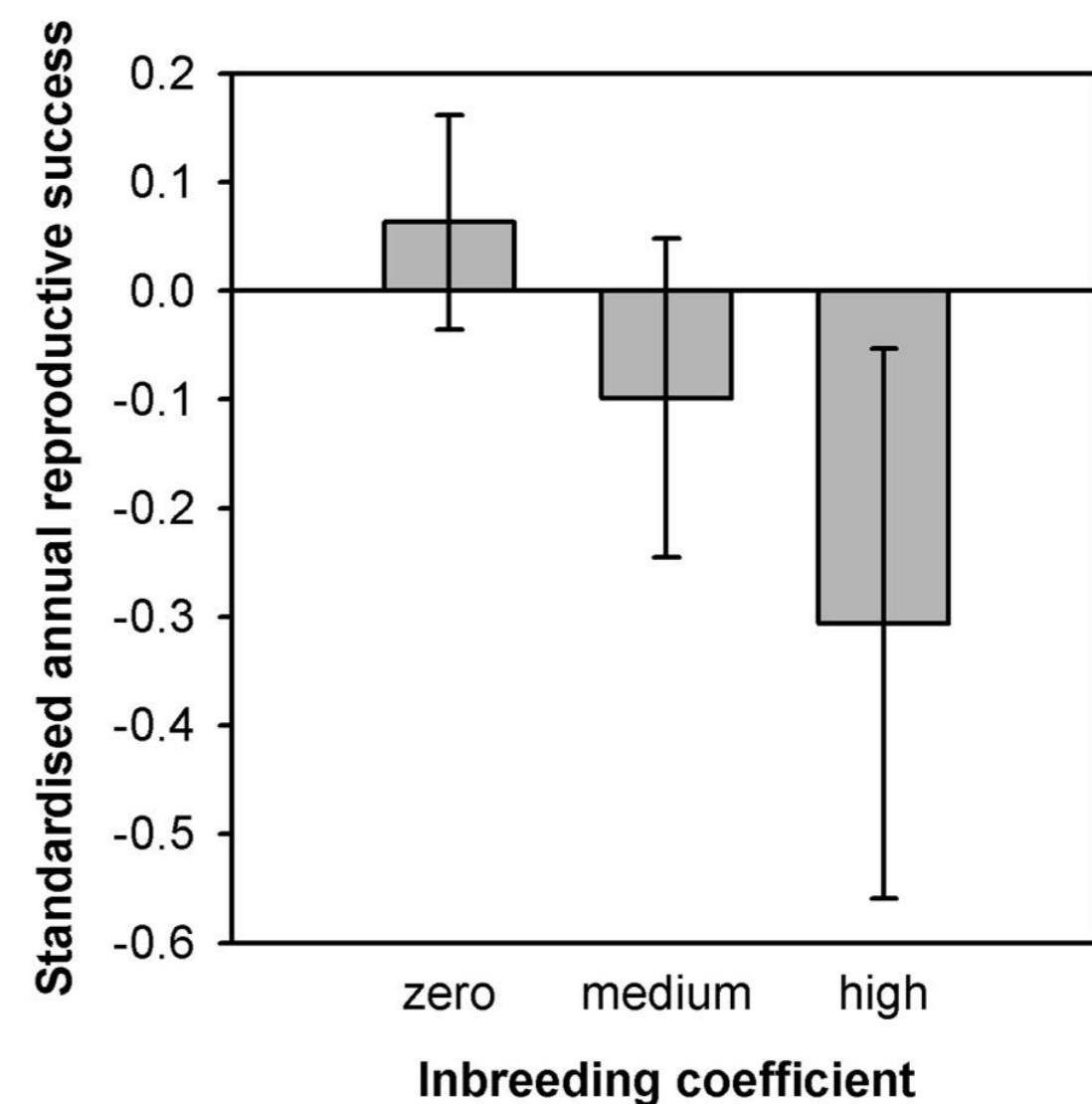
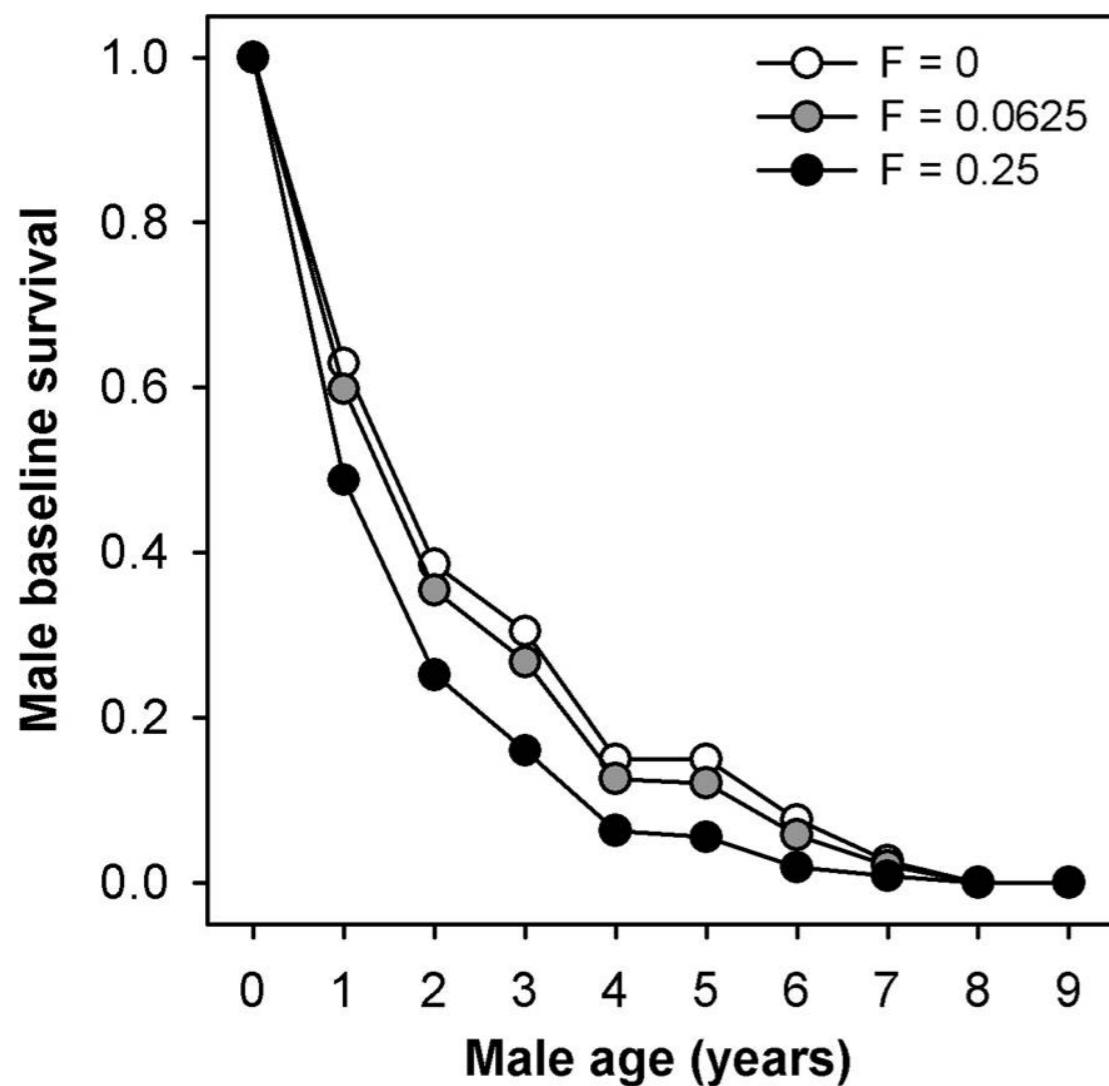
Genetic drift is strongest  
in small populations



Inbreeding = breeding between related individuals

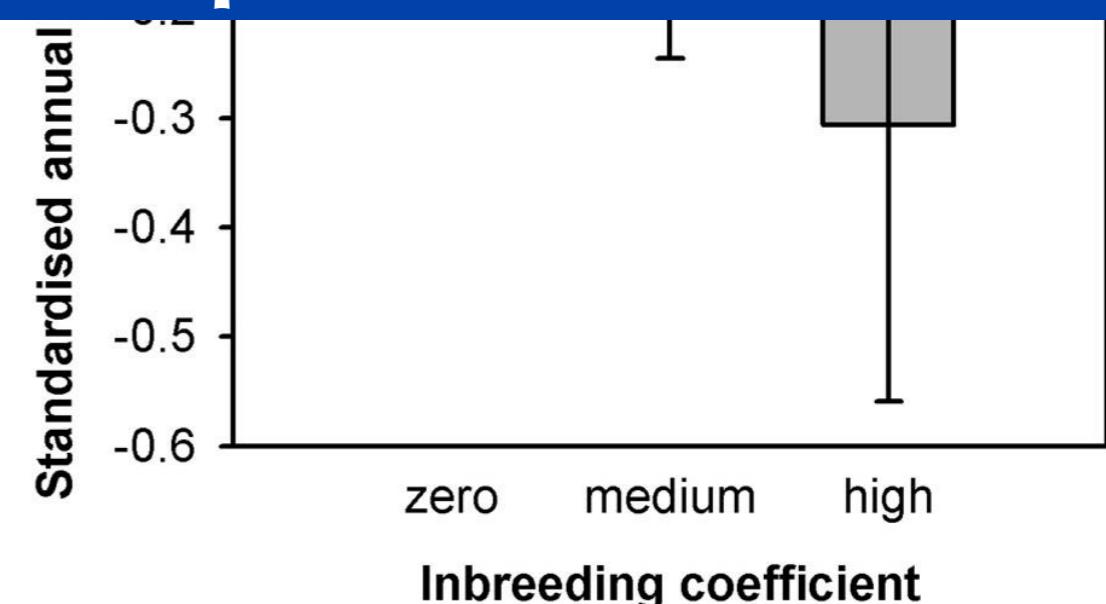
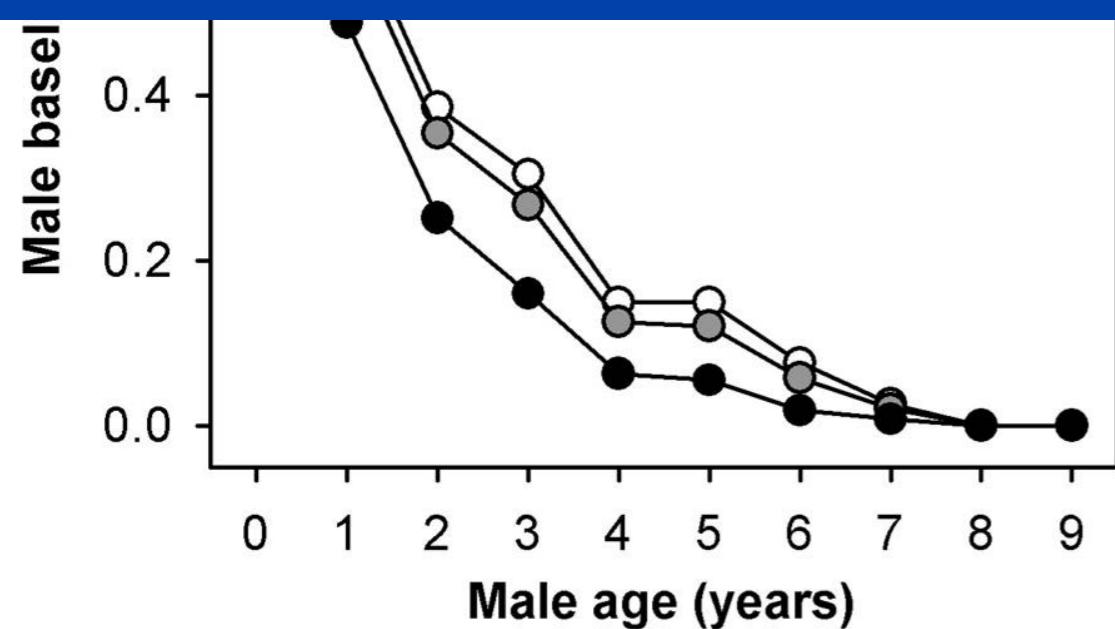
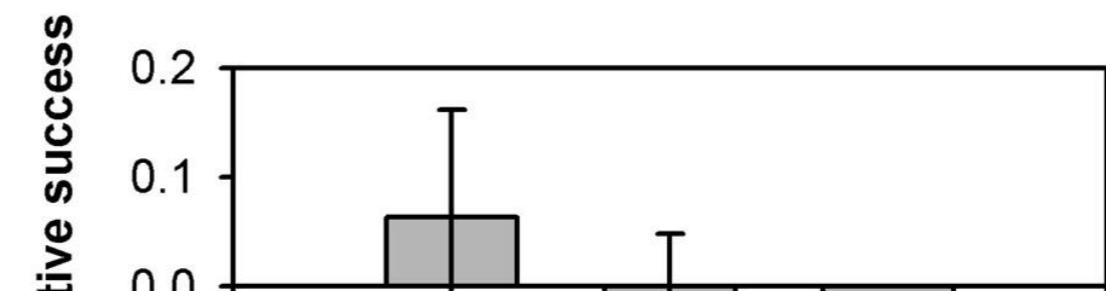


# Inbreeding: reduced survival and reproduction



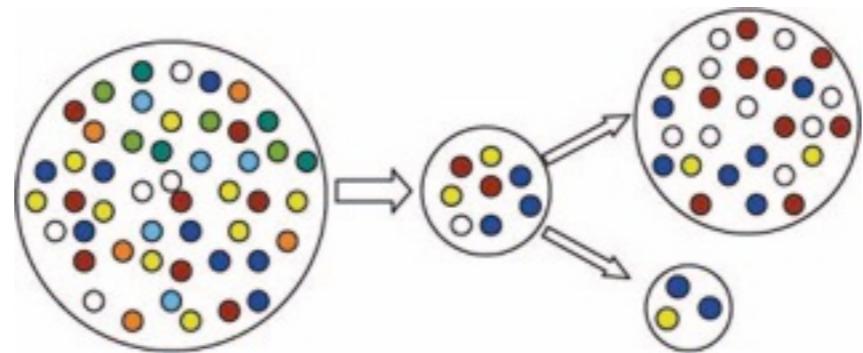
(Keller et al. 1998, Evolution)

# Inbreeding: reduced survival and reproduction

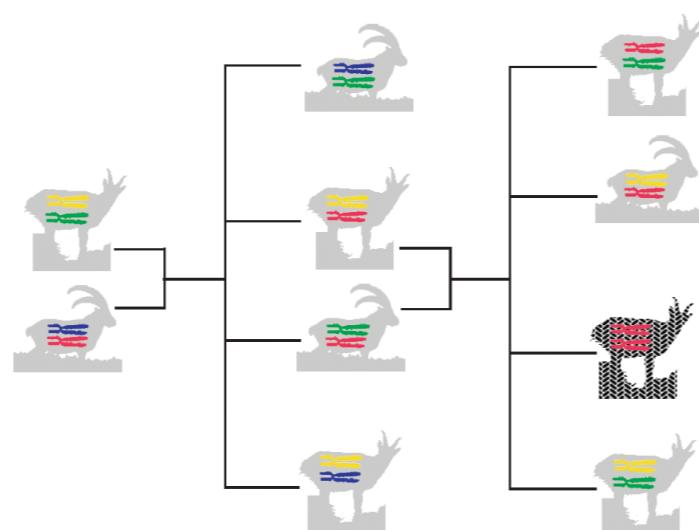


# Effects of reintroductions on genetic variability of Alpine ibex

Do we see genetic drift?



Are Alpine ibex populations inbred?

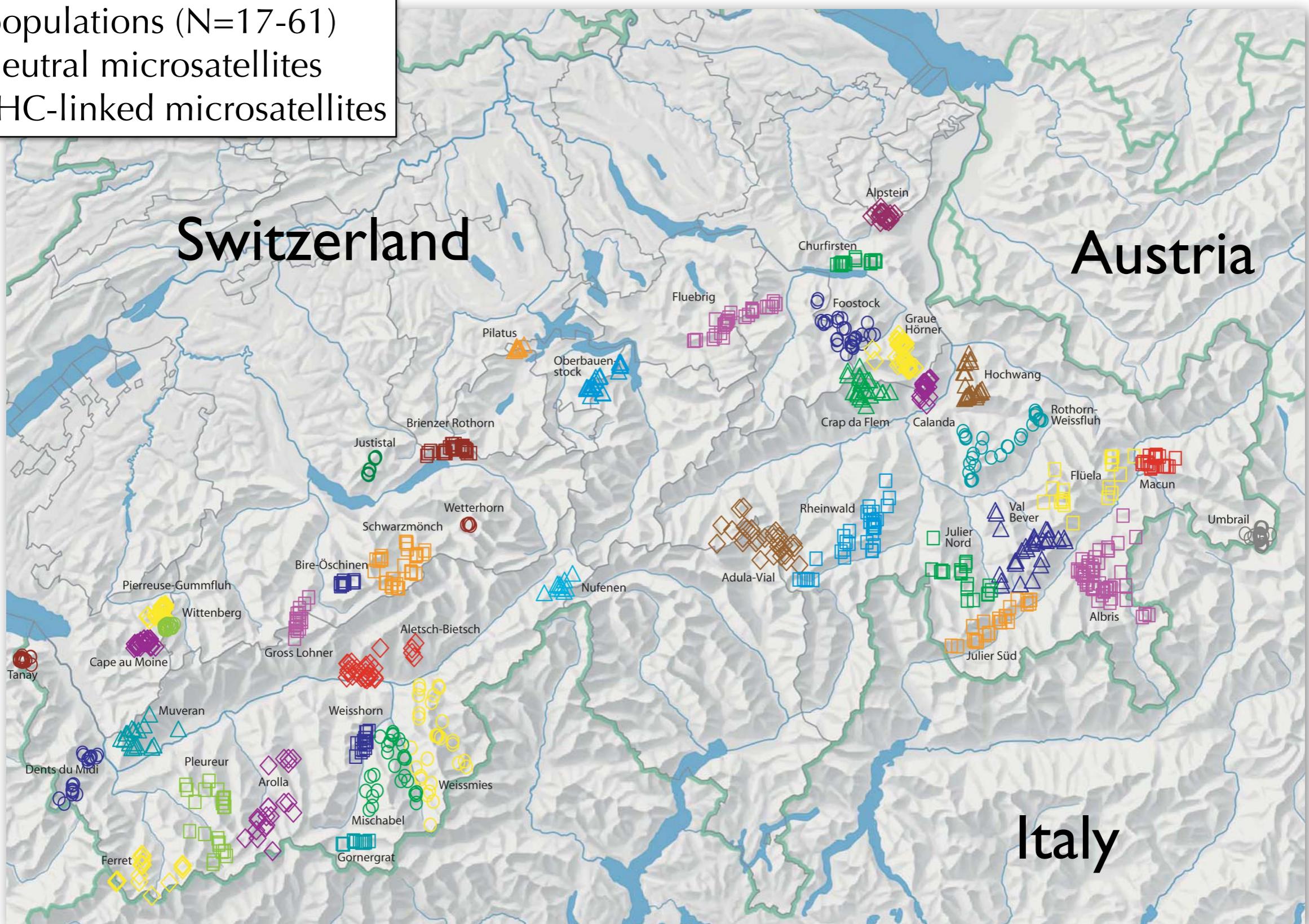


1262 samples

42 populations (N=17-61)

37 neutral microsatellites

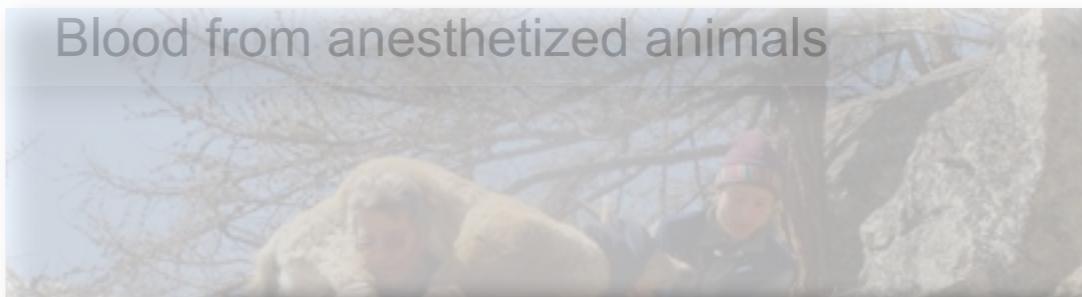
5 MHC-linked microsatellites



# Sampling



# Sampling

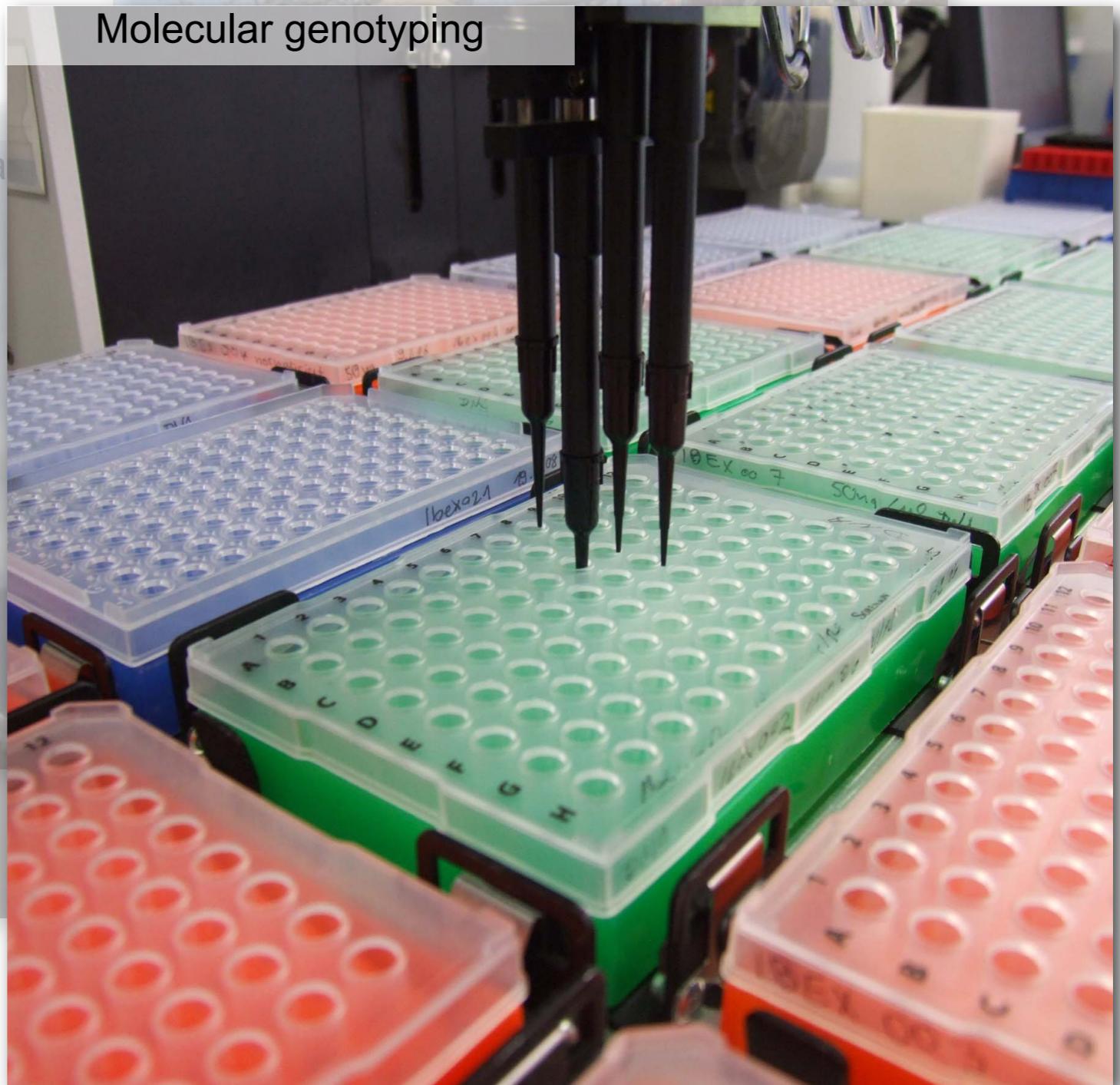


# Sampling

Blood from anesthetized animals



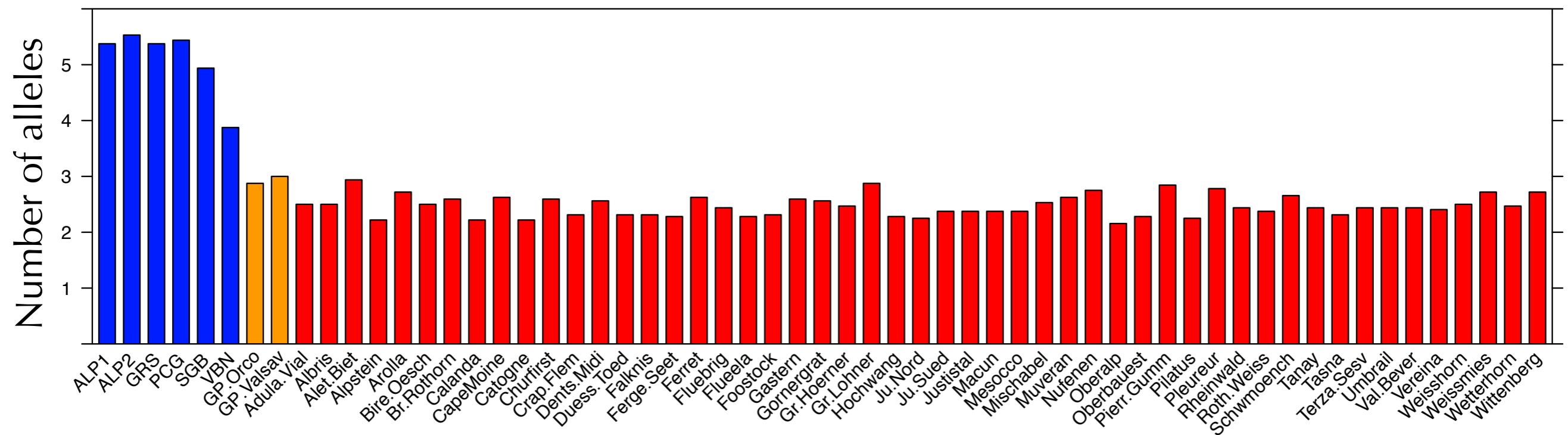
Molecular genotyping



# Genetic diversity in Alpine ibex is low

Low potential to adapt to changing environments

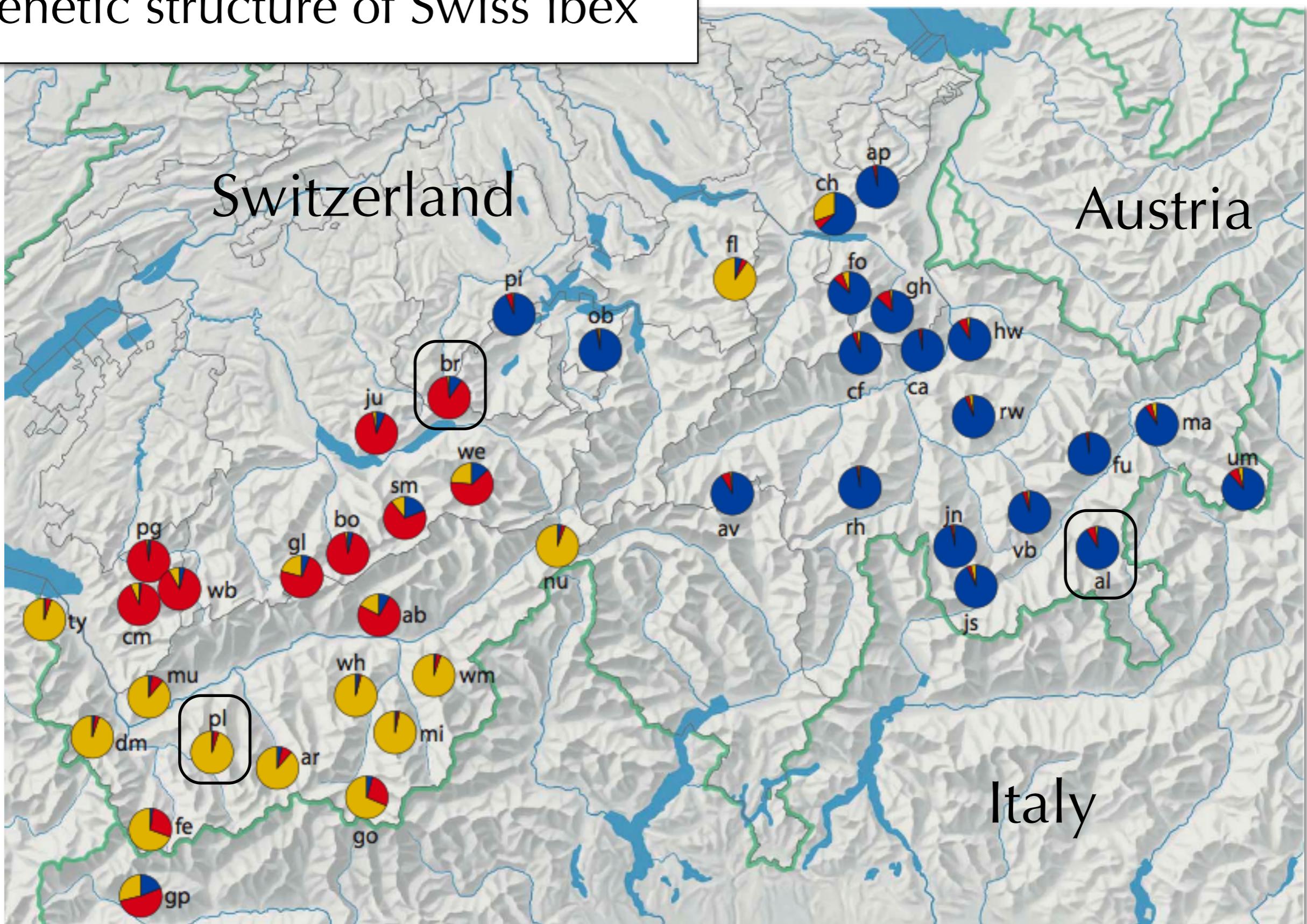
Domestic goat  
breeds



↑  
Alpine ibex  
Gran Paradiso

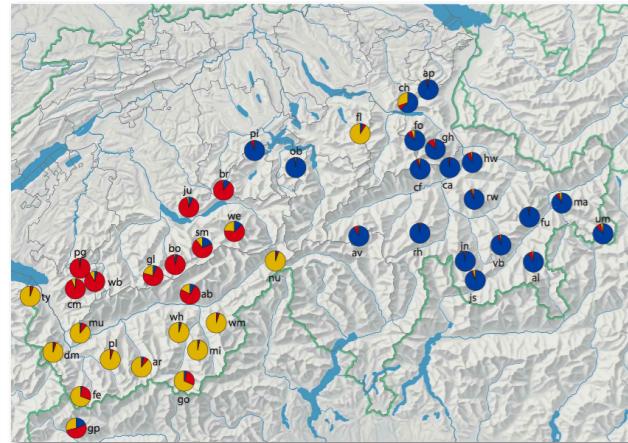
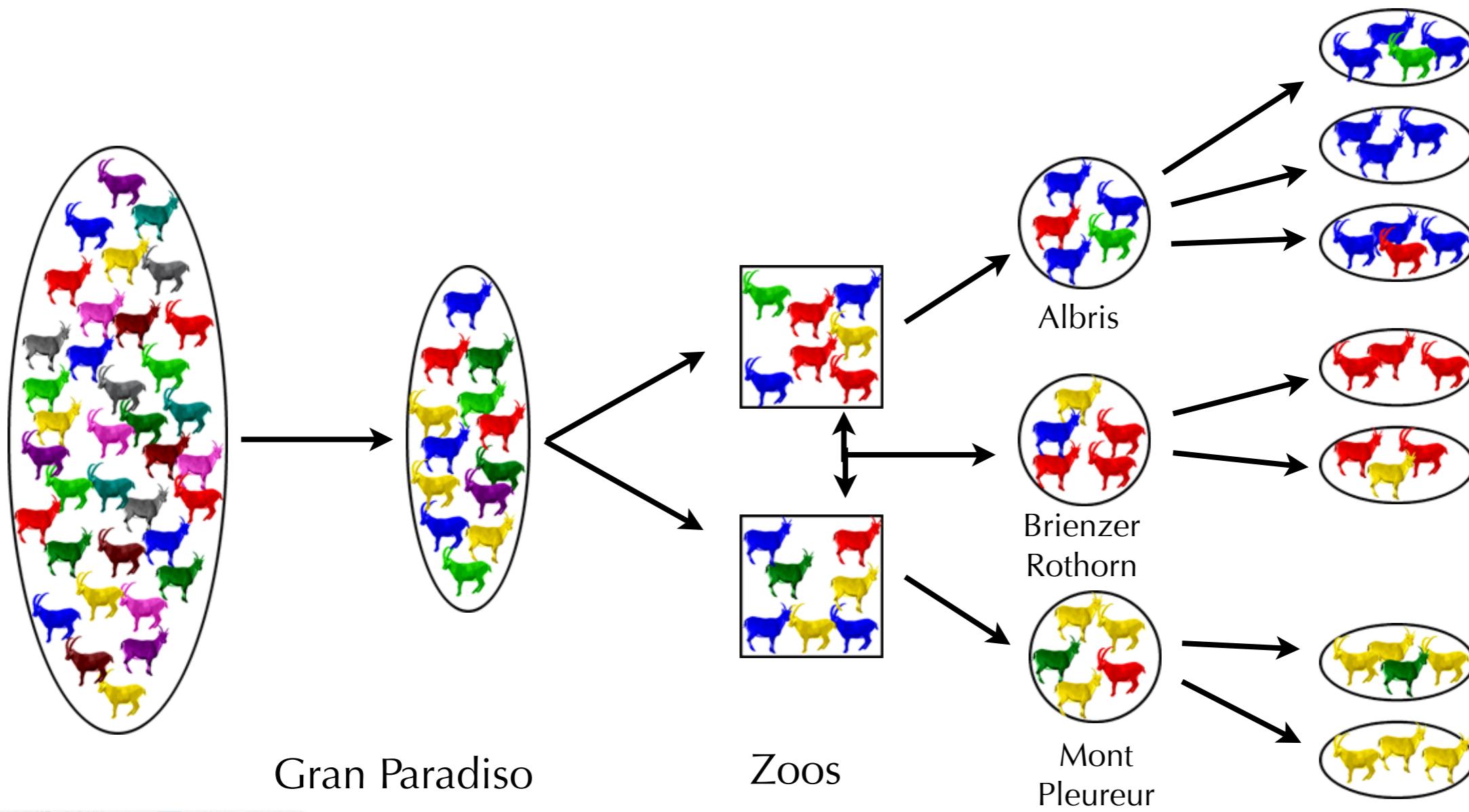
↑  
Alpine ibex  
Switzerland

# Genetic structure of Swiss ibex

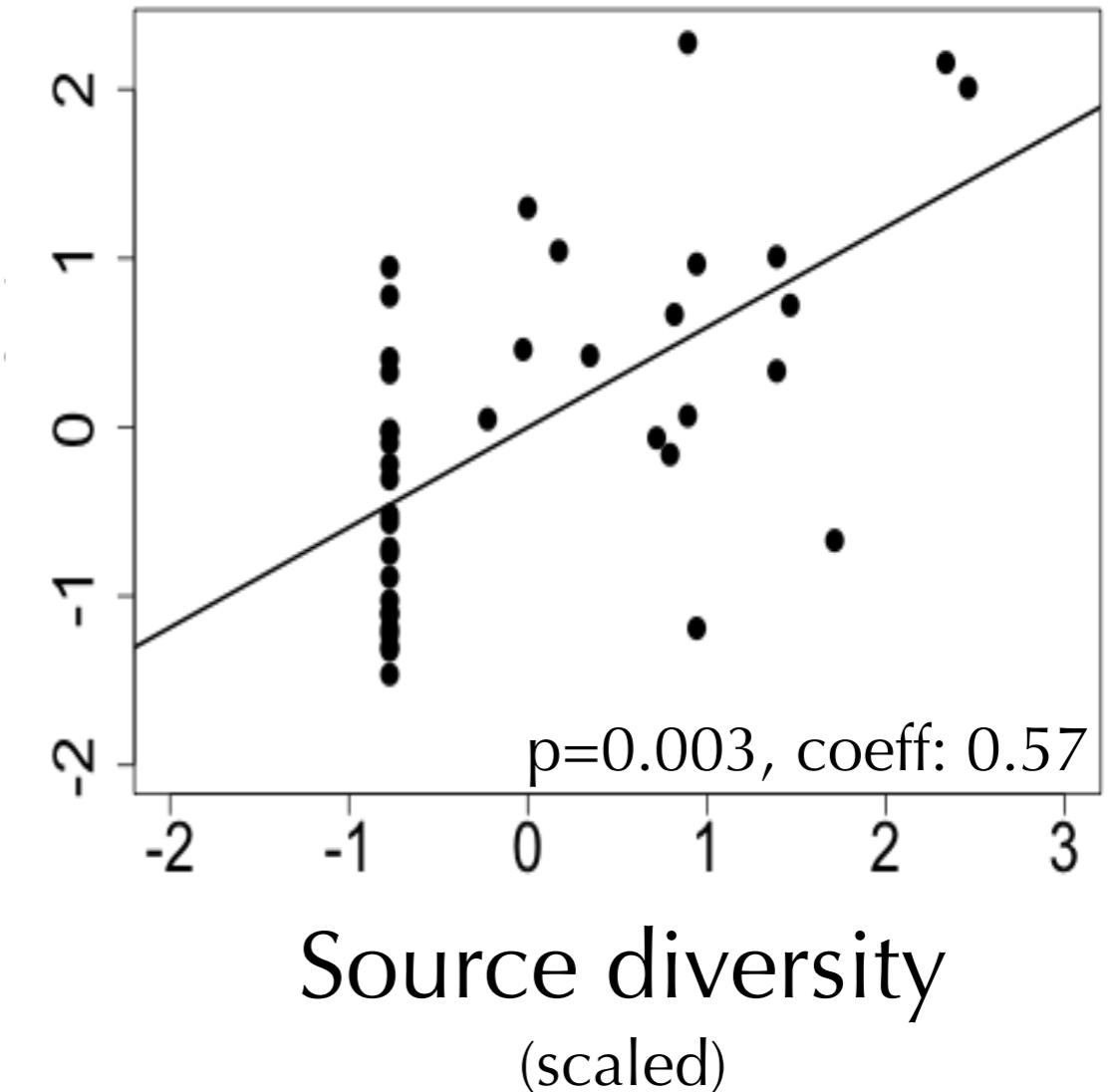
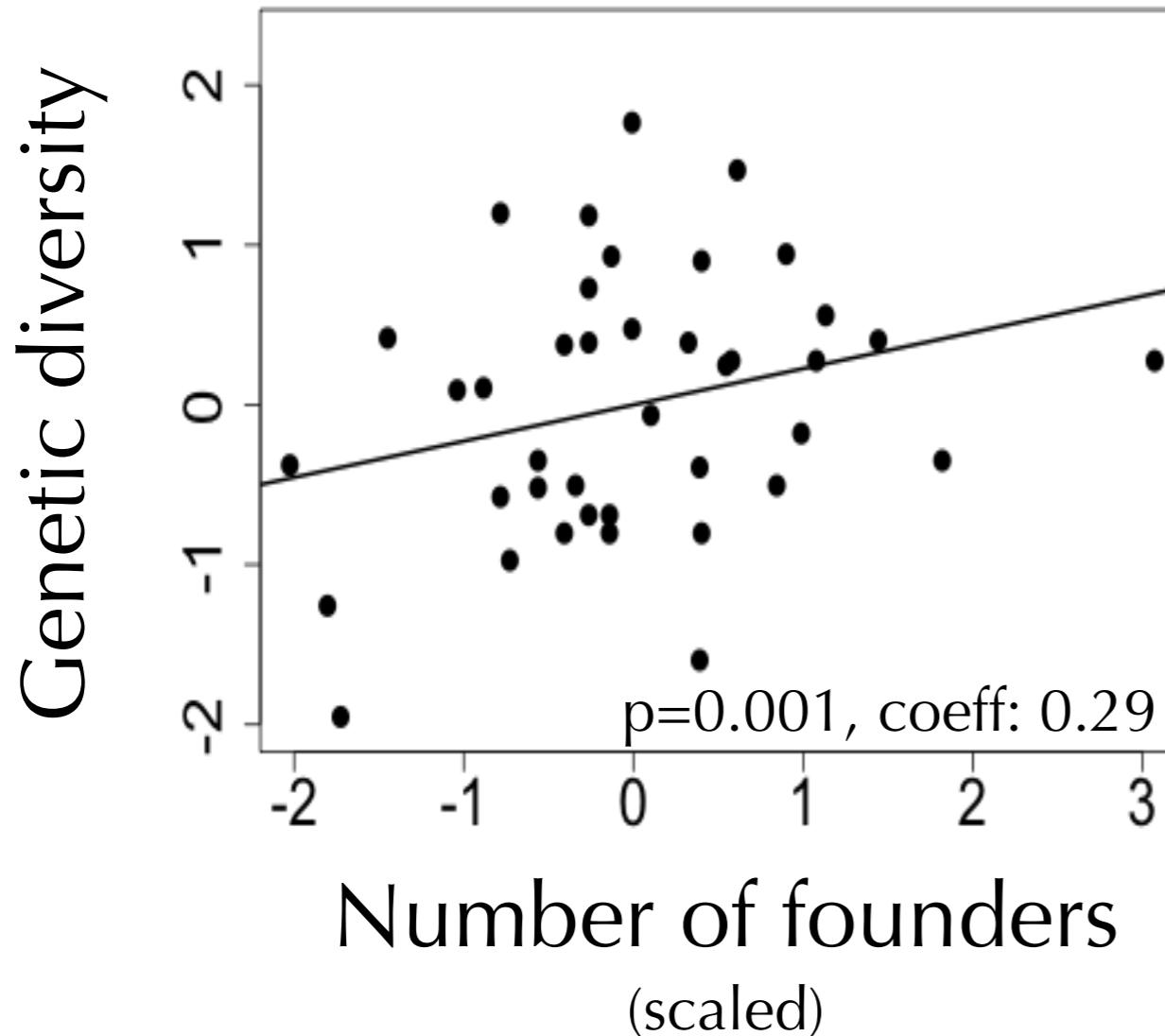


(Biebach and Keller 2009, Molecular Ecology)

# Reintroductions shaped the genetic diversity



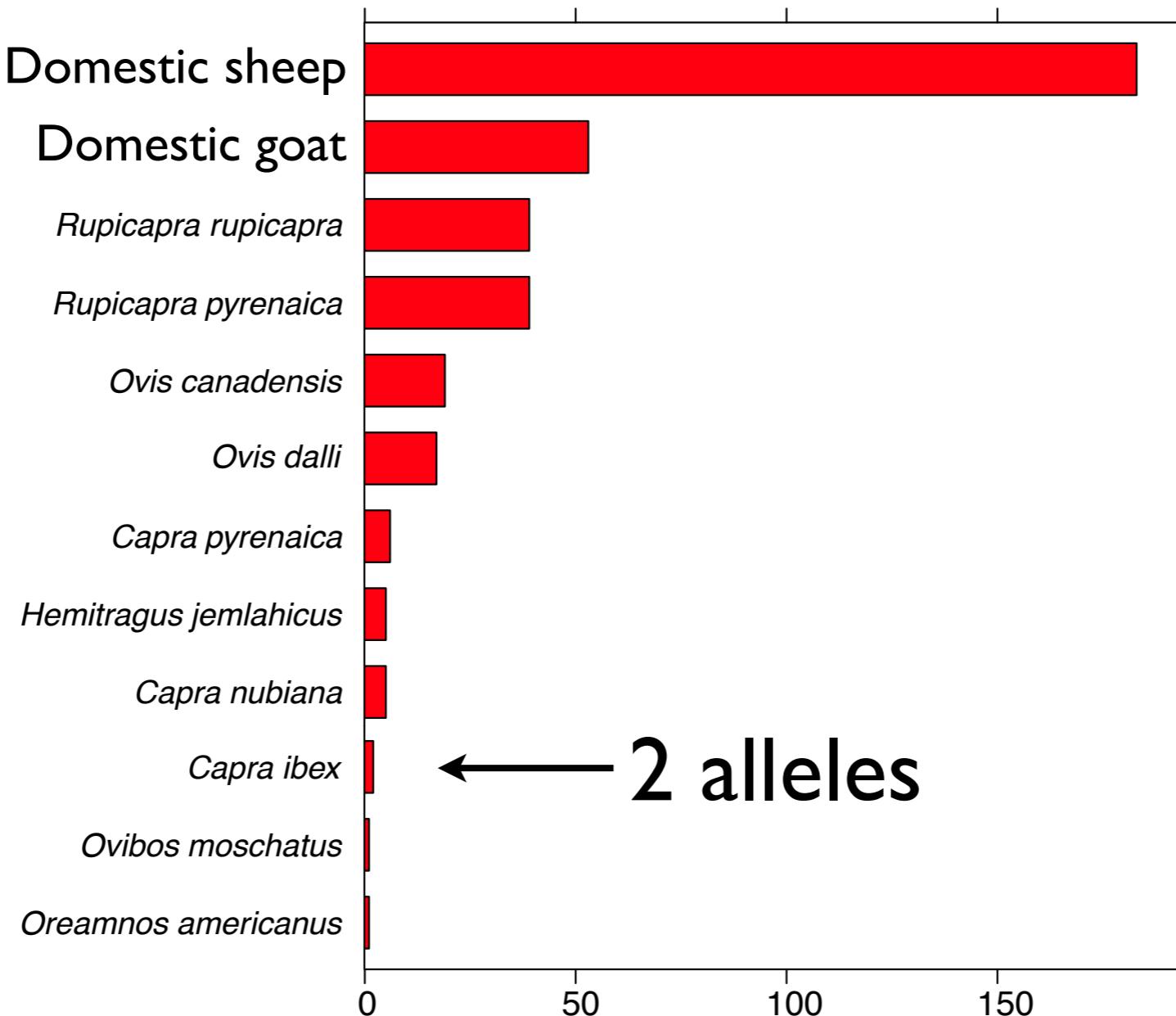
# Reintroductions shaped the genetic diversity



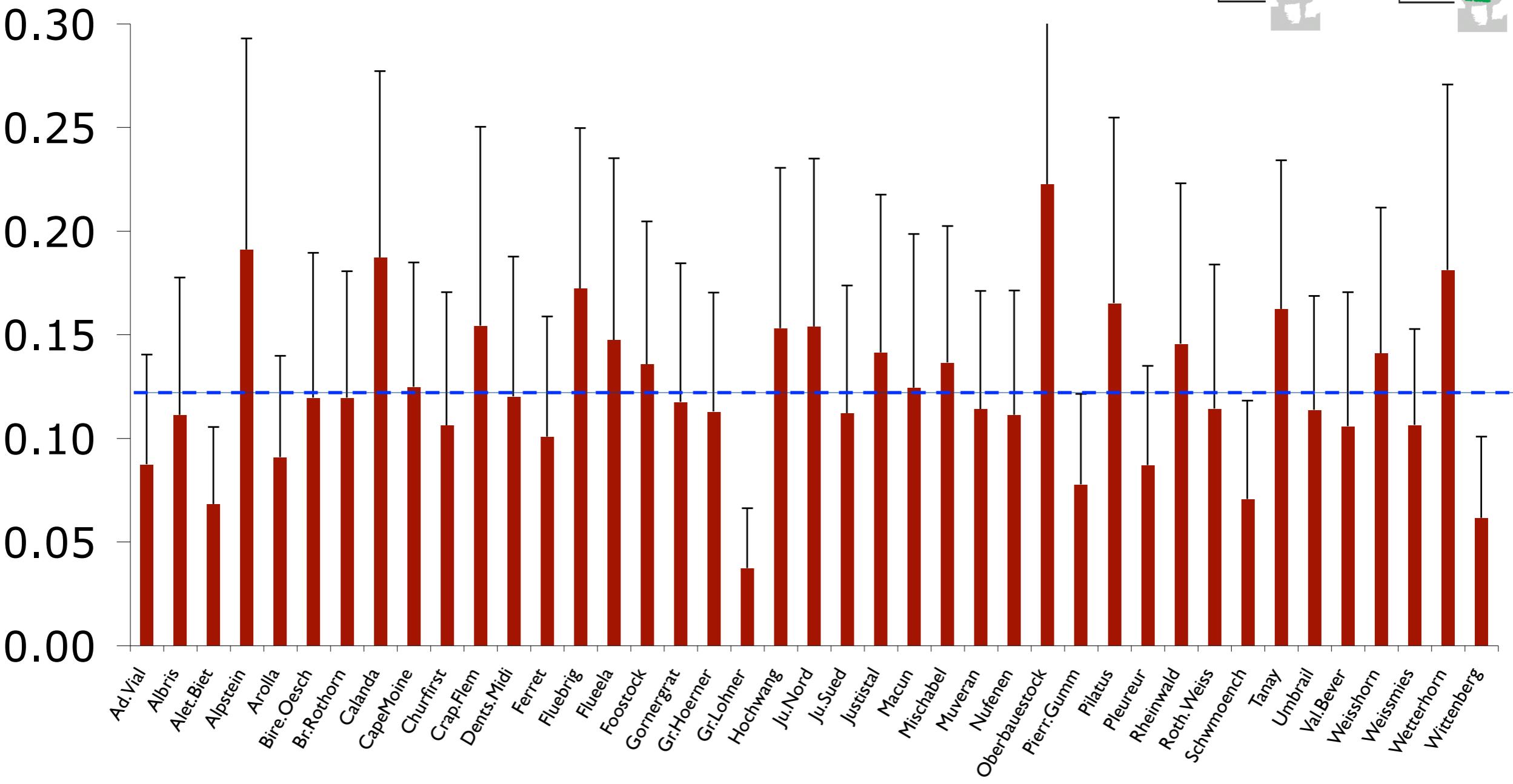
Both number of founders and number of source populations positively affected genetic diversity

Relationship between neutral and selected diversity?

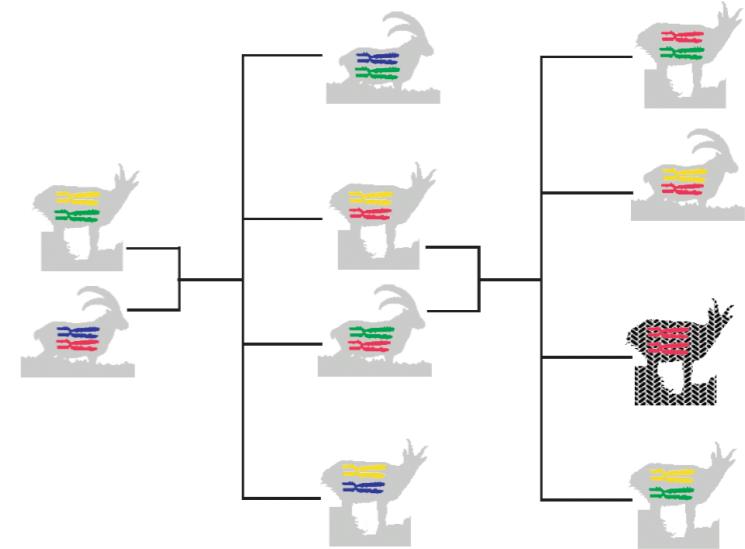
# Low diversity at the MHC (important for immune response)



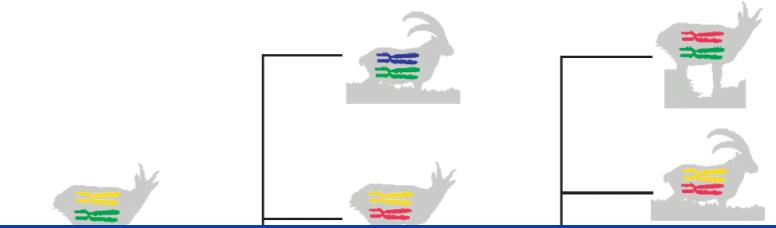
# High extent of inbreeding



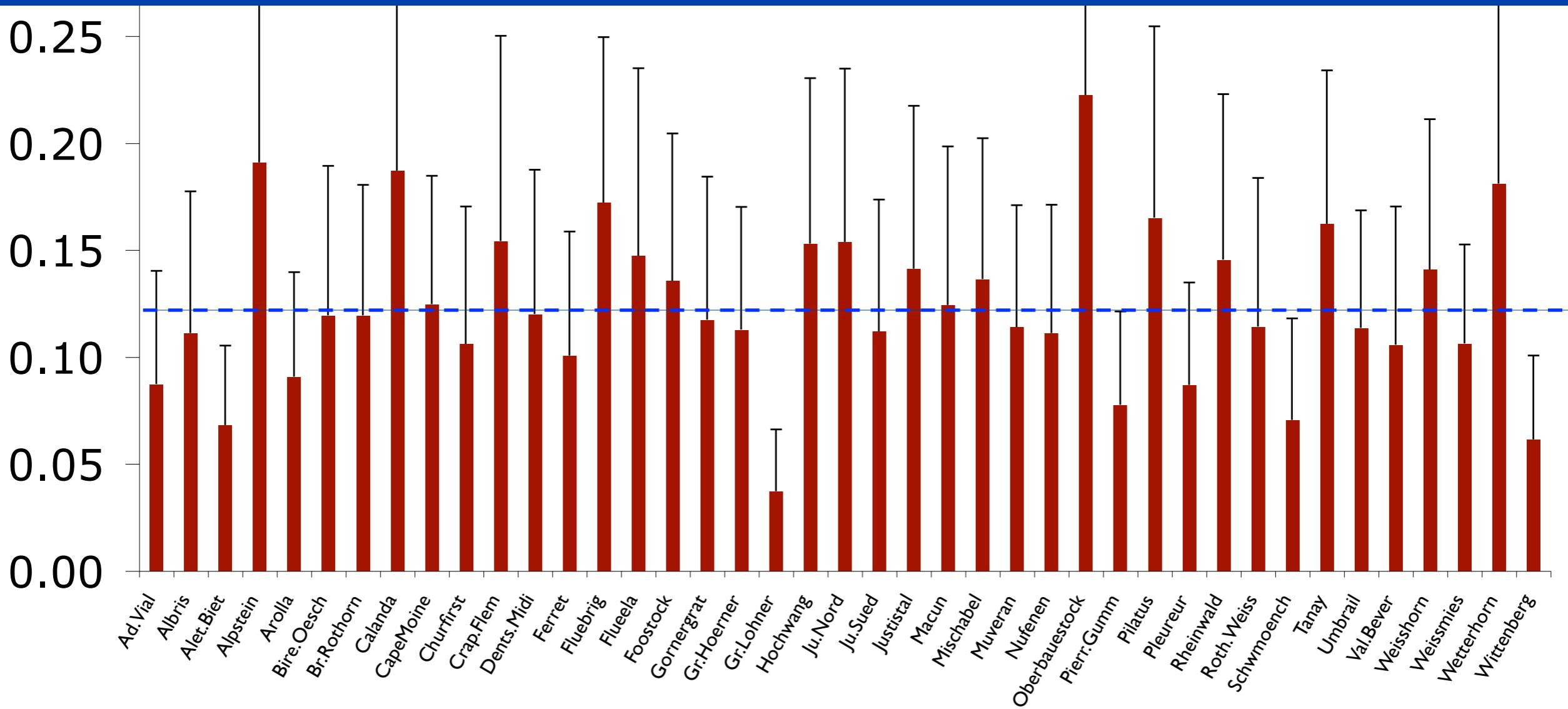
(Biebach and Keller 2010, Conservation Genetics)



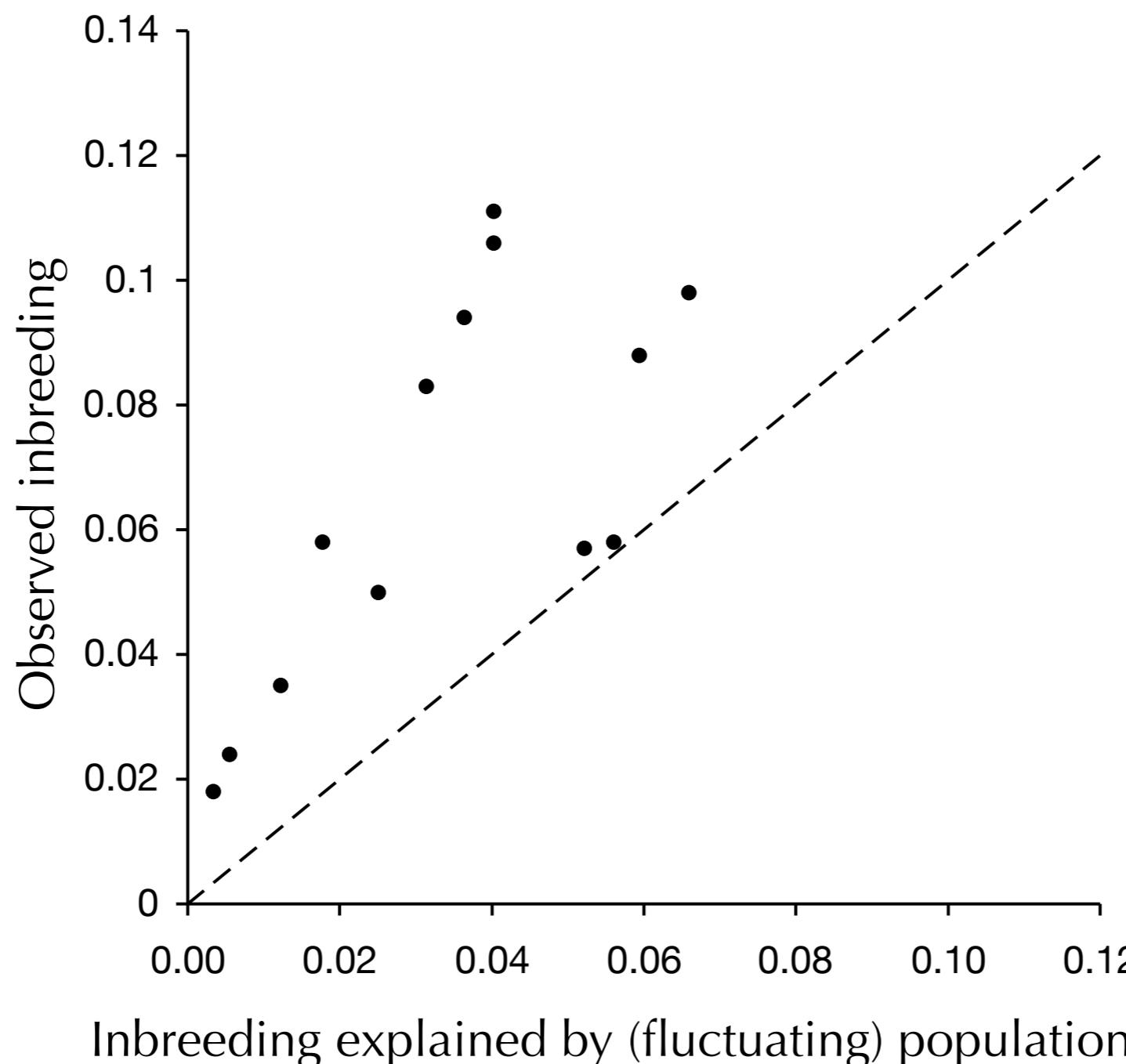
# High extent of inbreeding



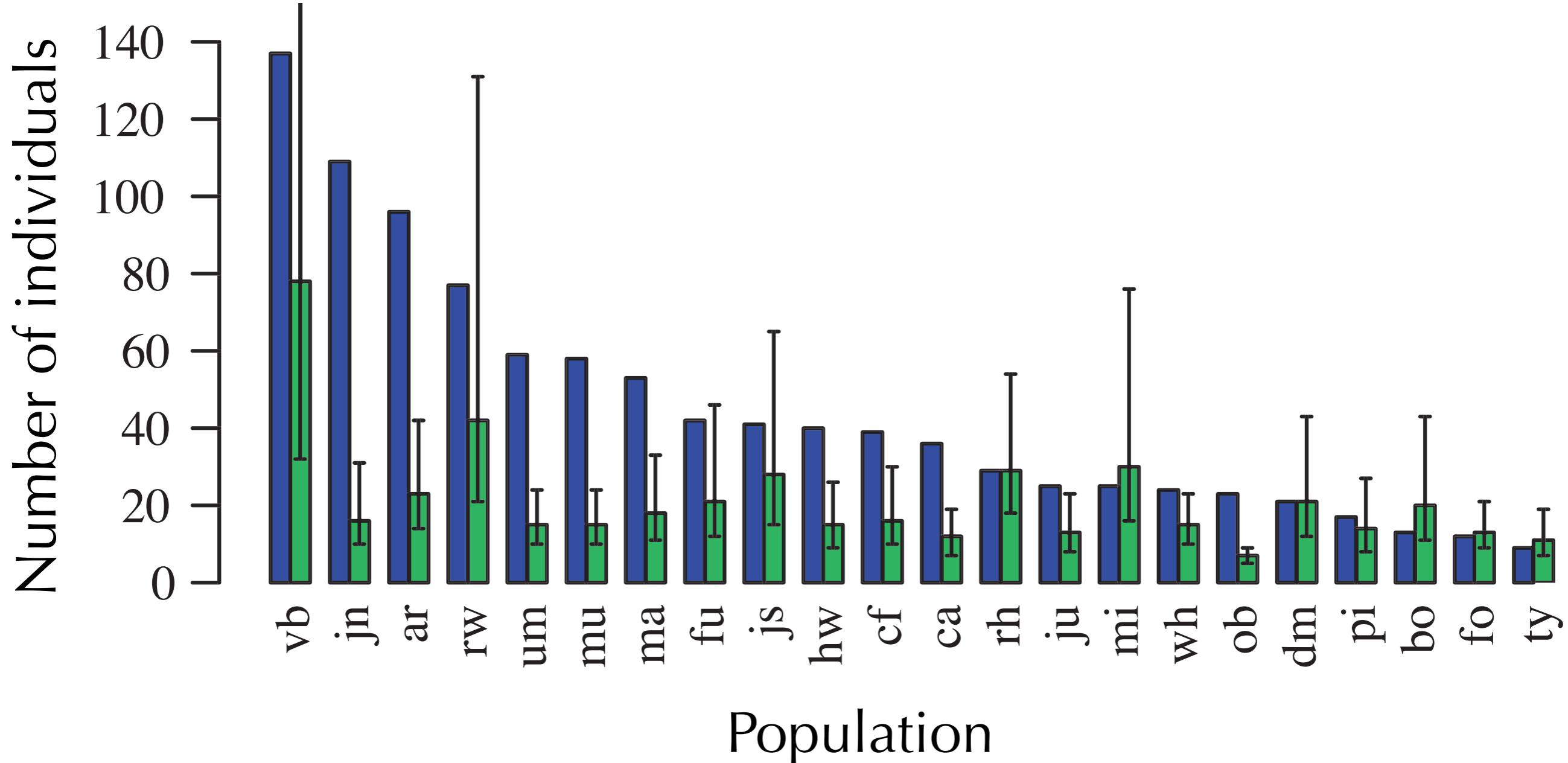
Average total inbreeding = 0.125  
(mating between half siblings!)



# Population size alone does not explain observed level of inbreeding

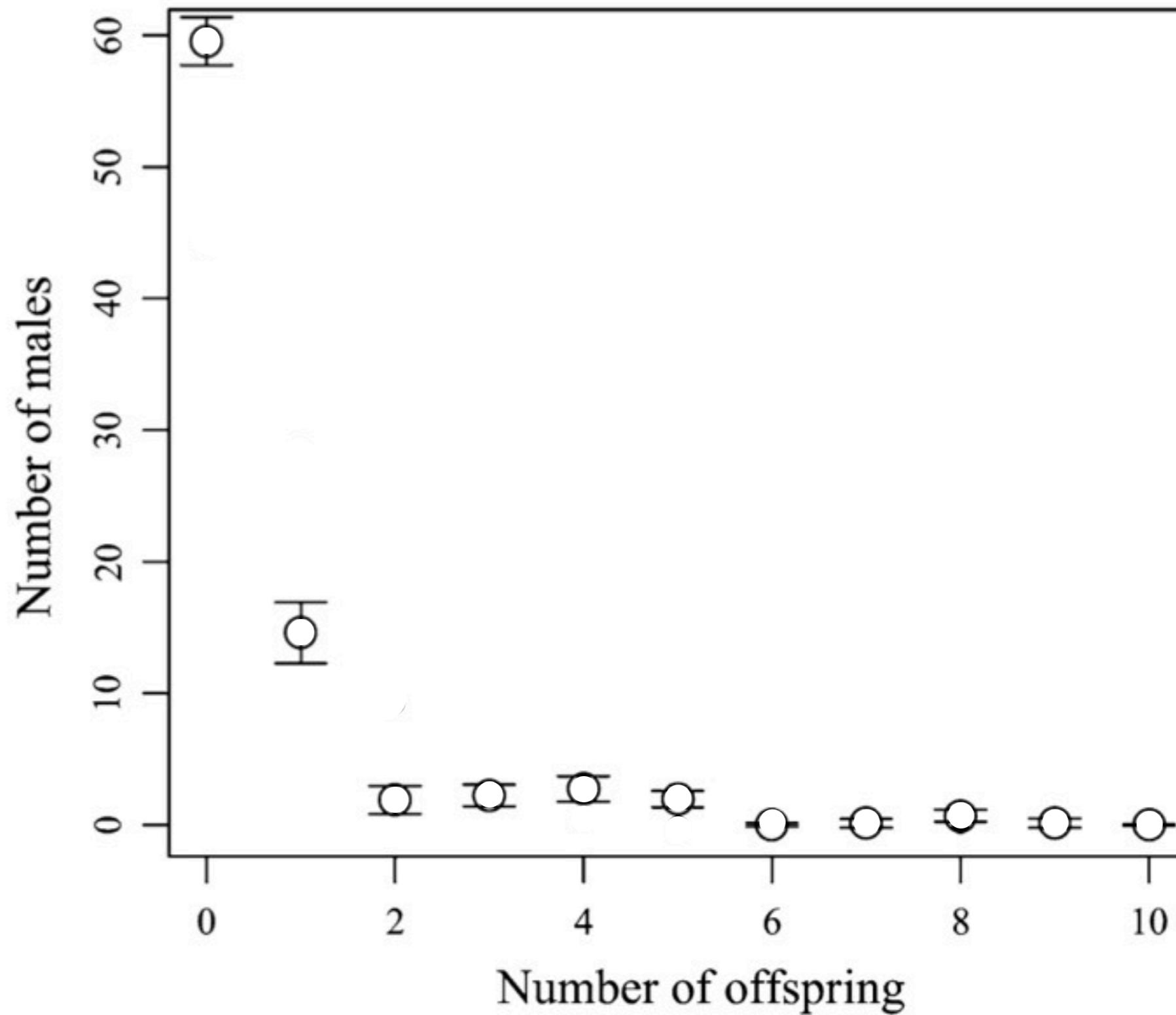


# Not every released individual is a founder



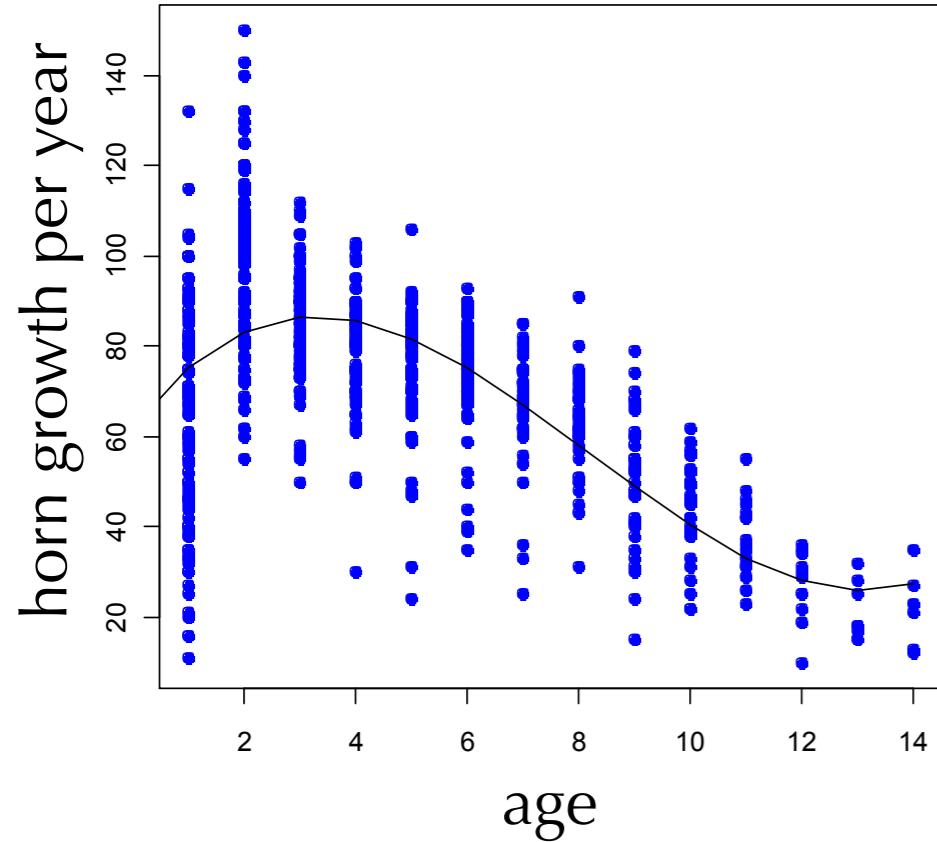
individuals released  
genetic founders

# Only a few males reproduce



(Willisch et al. 2012)

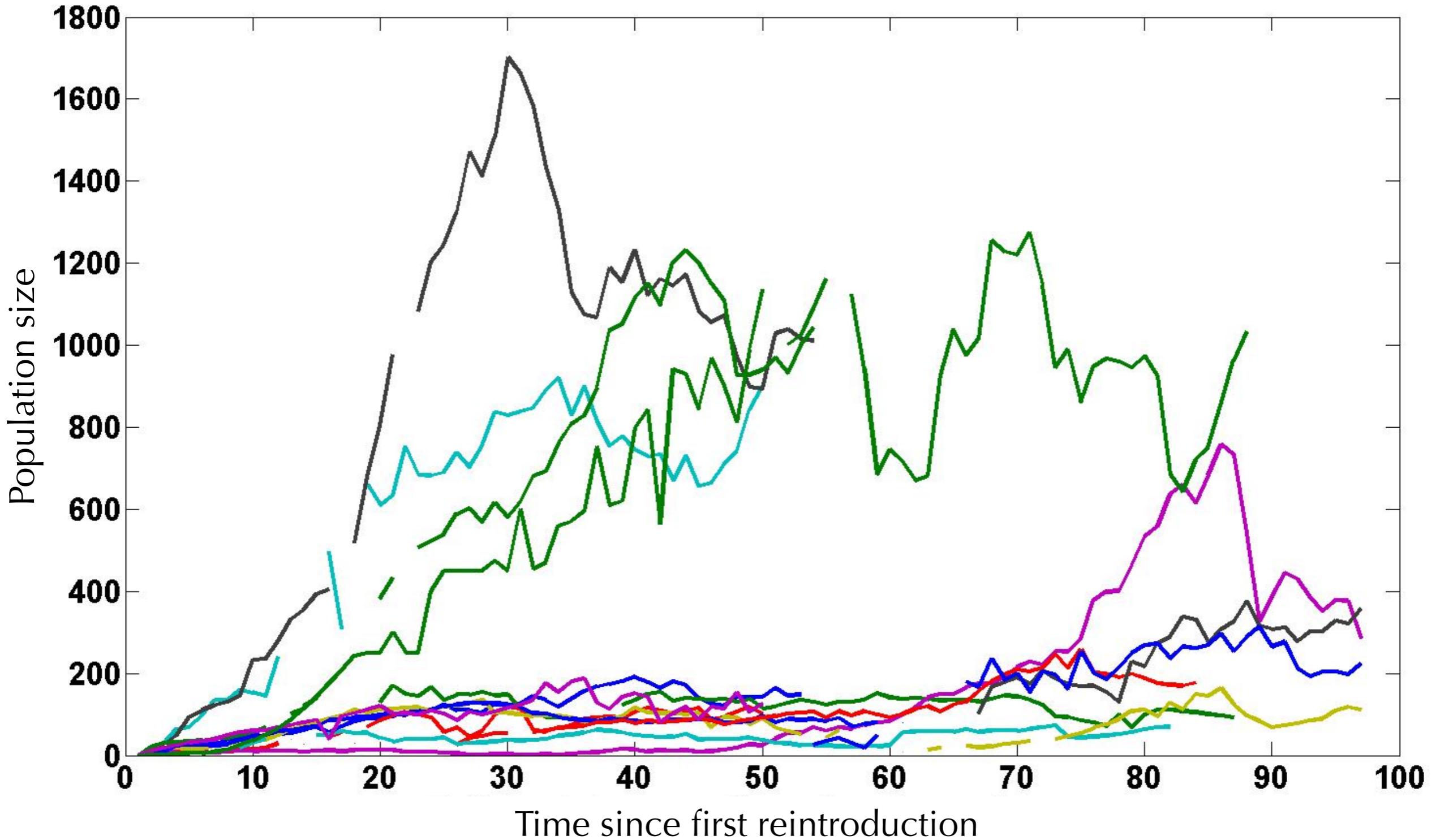
# Genetic effects on horn growth?



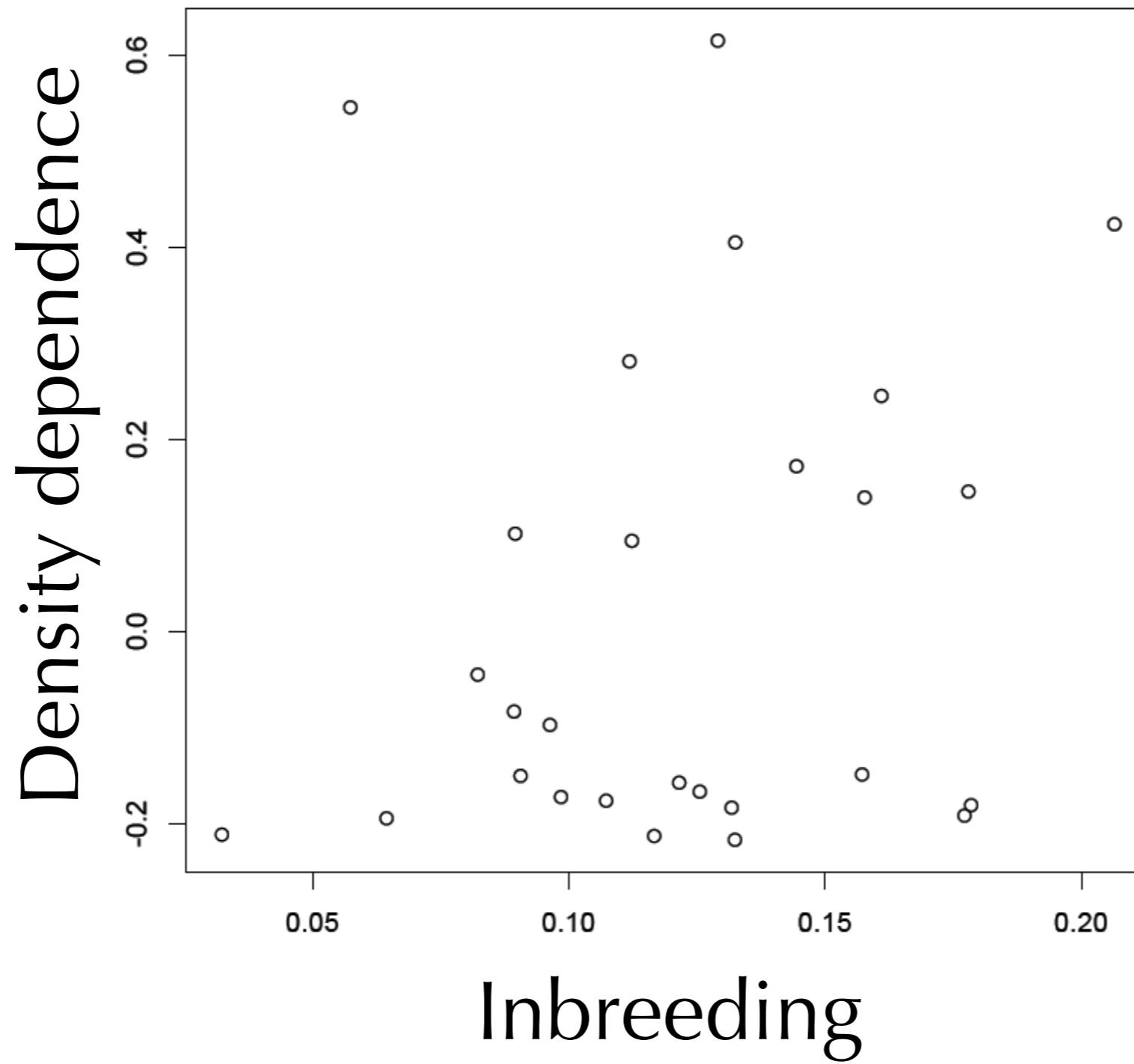
No effect of inbreeding on horn growth

Significant effect of genotype at MHC (immune gene) on horn growth of male ibex older than ~6 years.

# Population size over time



Inbred populations react stronger to changes in density

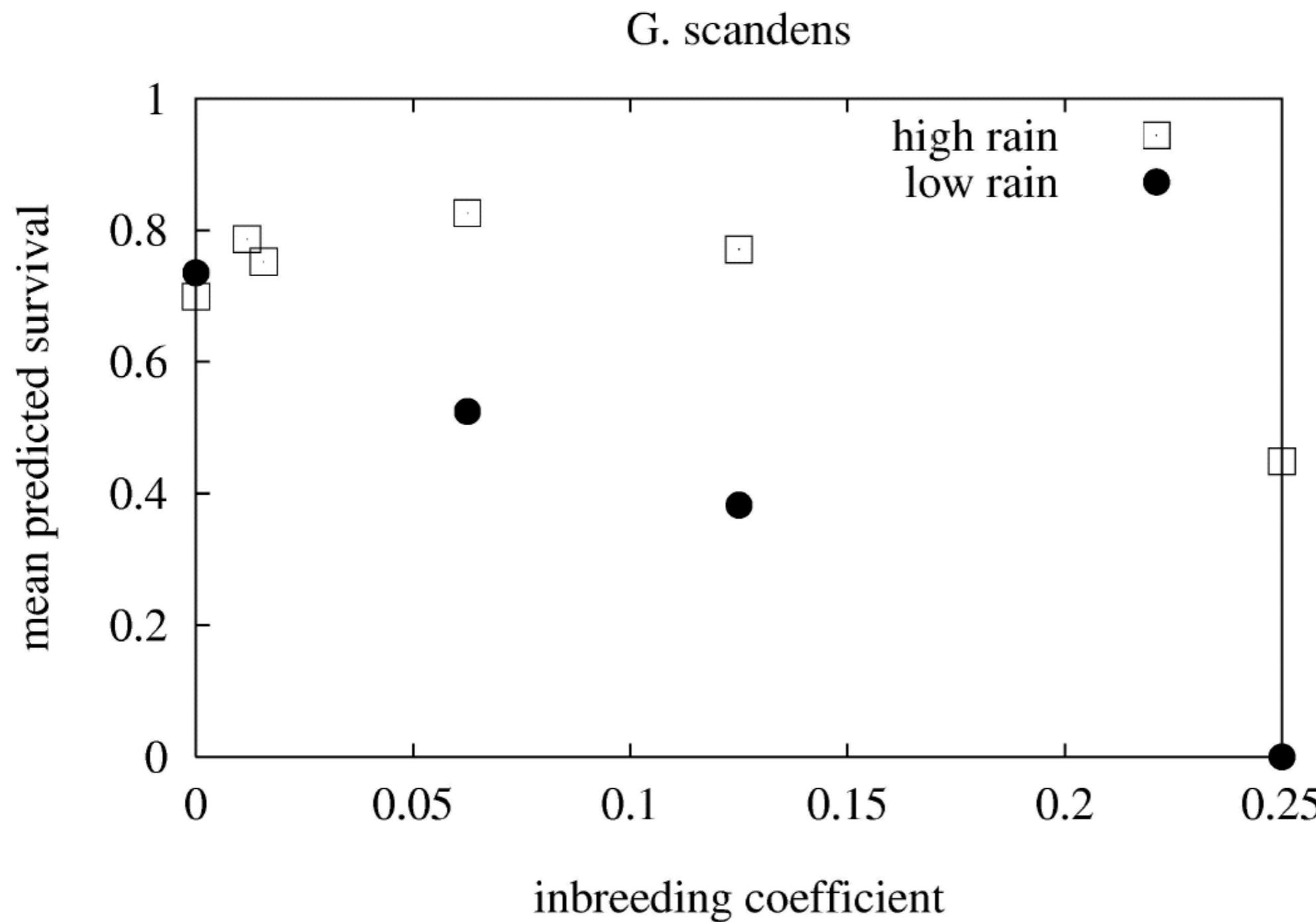


(Claudio Bozzuto)

# Inbreeding in variable environments

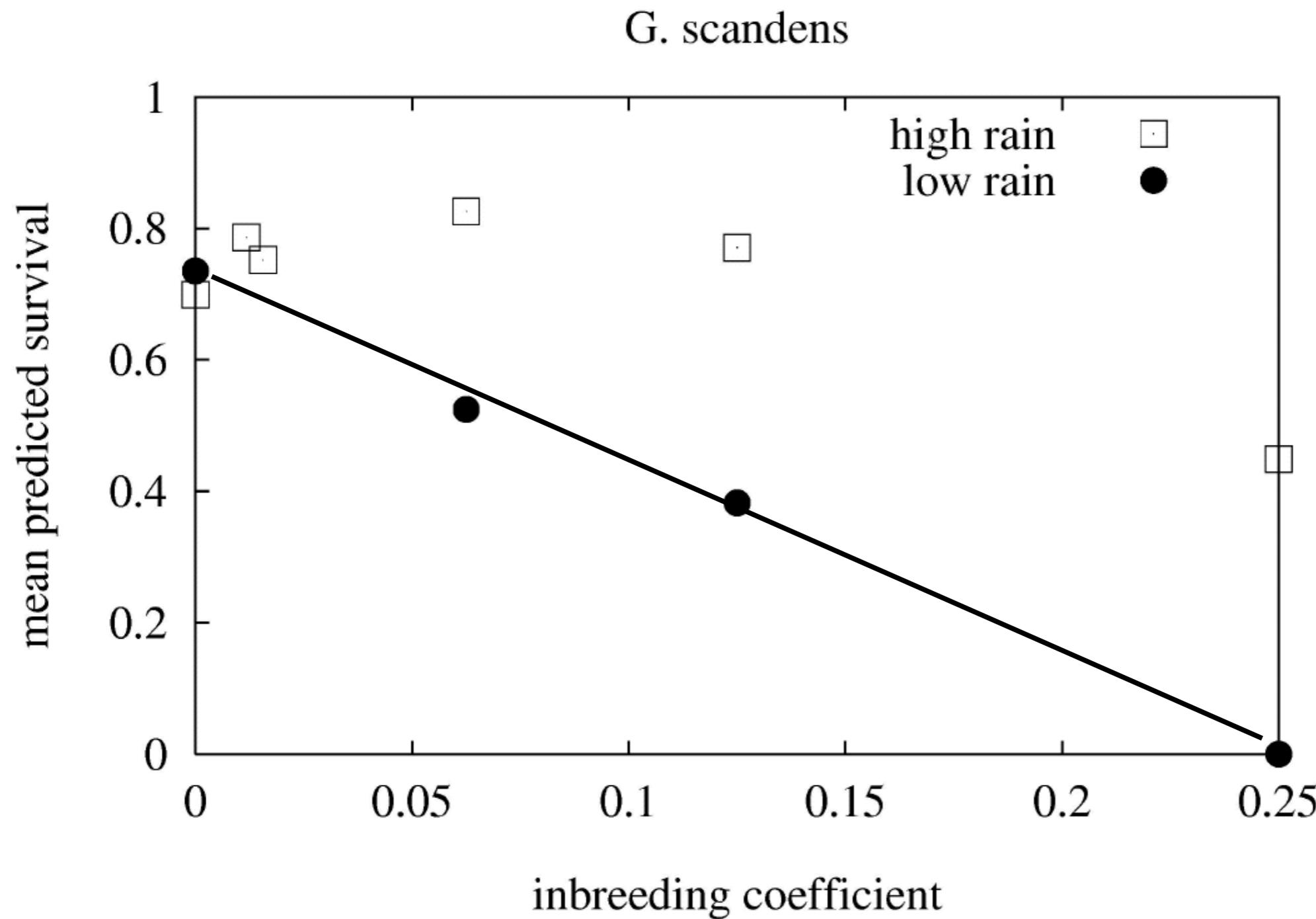


# Inbreeding in variable environments



(Keller et al. 2002,  
Evolution)

# Inbreeding in variable environments

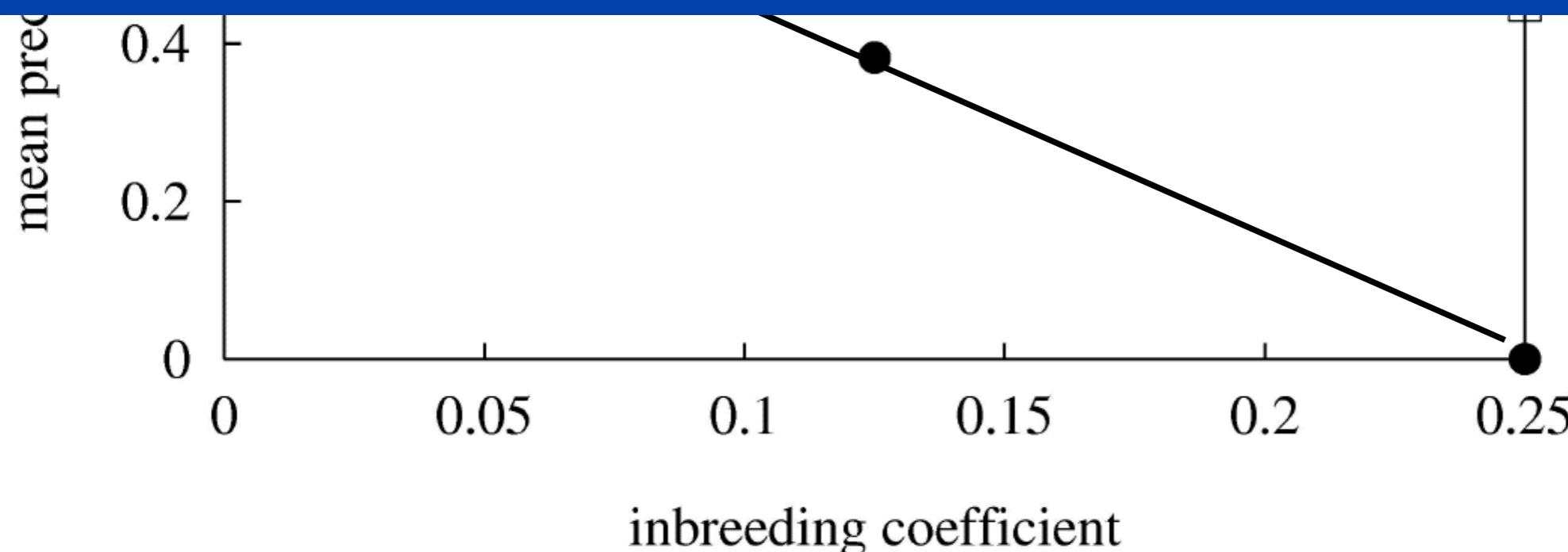


(Keller et al. 2002,  
Evolution)

# Inbreeding in variable environments

*G. scandens*

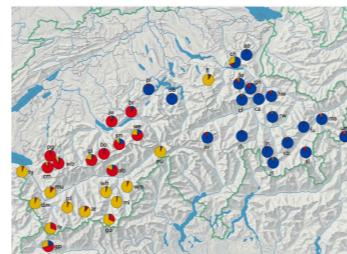
Extent of inbreeding depression  
depends on environmental  
conditions



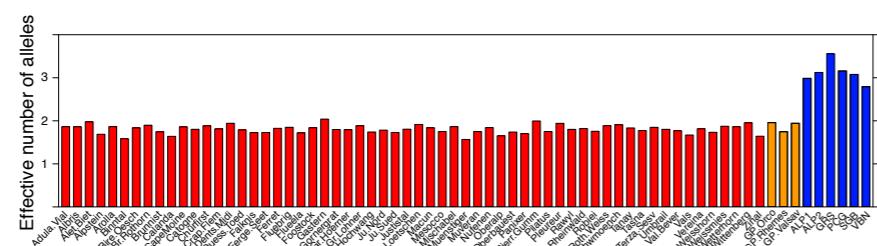
(Keller et al. 2002,  
Evolution)

# Summary

Strong genetic footprint of the reintroduction history in Swiss Alpine ibex populations



Genetic variation (also at the MHC) is low and inbreeding is high



No effect of inbreeding but significant effect of genotype at MHC on horn growth



Populations with particularly high inbreeding show stronger density dependence

# What do we learn for future translocations?

Many individuals should be released (better 100 than 10)

Translocate individuals from several different source populations

Take into account genetic relatedness among founder populations



# Thank you!

Lukas Keller  
Iris Biebach

Christian Willisch  
Anina Knauer  
Claudio Bozzuto

Game keepers and  
Jagdinspektorate

Achaz von Hardenberg  
Flurin Filli

Heinz Maag



Schweizerische Eidgenossenschaft  
Confédération suisse  
Confederazione Svizzera  
Confederaziun svizra

Bundesamt für Umwelt BAFU

