BIOL3110 Genetic Rescue

Genetics & Population size

Population size & genetic dynamics:

SMALL $\quad$ N_e $\quad$ LARGE
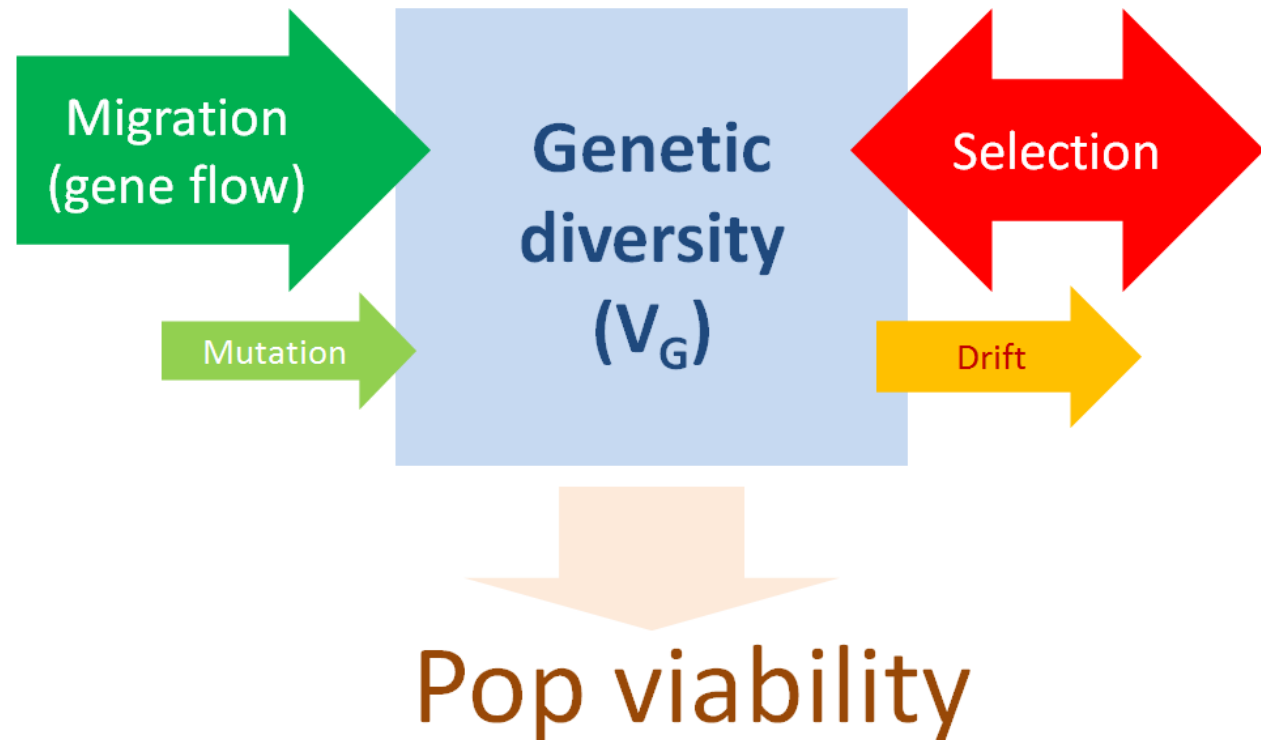
Drift

Selection

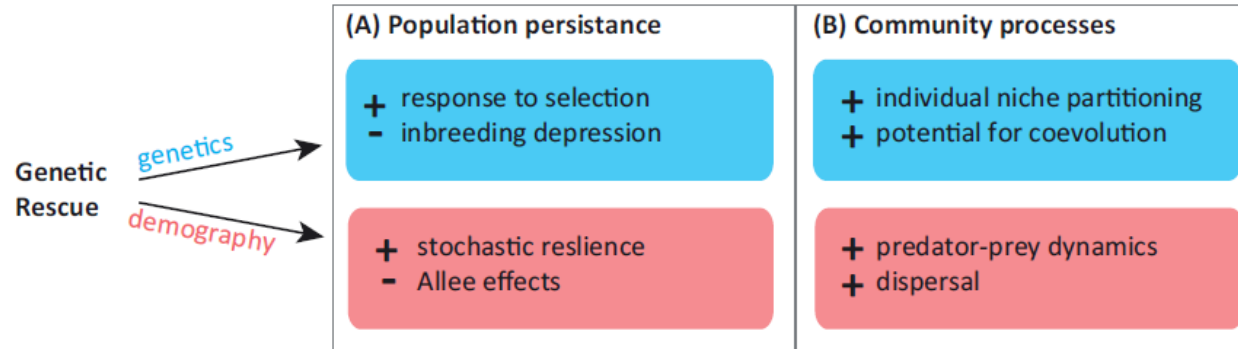Migration
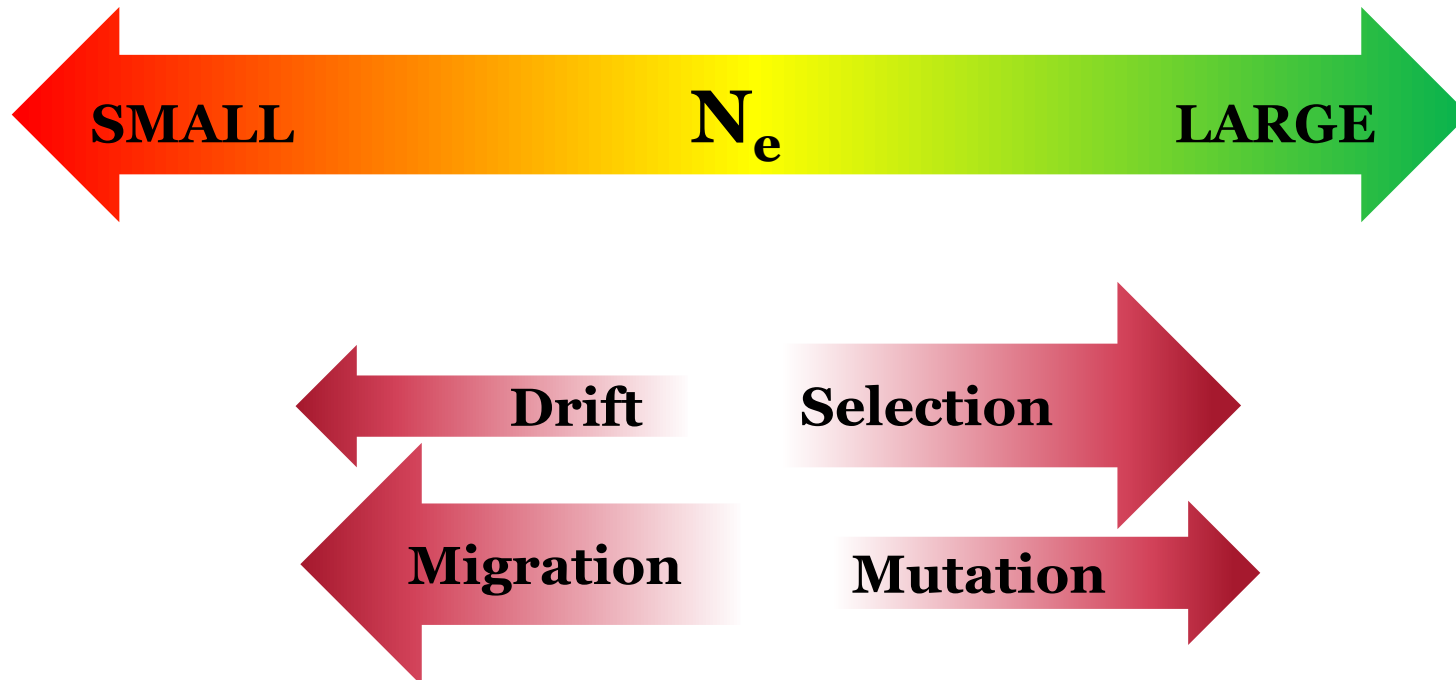
Mutation

Genetics & Population size

SUMMARY II

V_G **balanced** between selection, drift, migration & mutation;

Balance more **stable** with $> N$

Accumulated negative mutations revealed by small N.

Migration (gene flow)

Mutation

Genetic diversity (V_G)

Selection

Drift

Pop viability

3

Figure I. The benefits of genetic rescue include an increase in genetic diversity and an increase in abundance of individuals. Positive effects of genetic rescue on population persistance (A) can propagate to influence community processes (B).
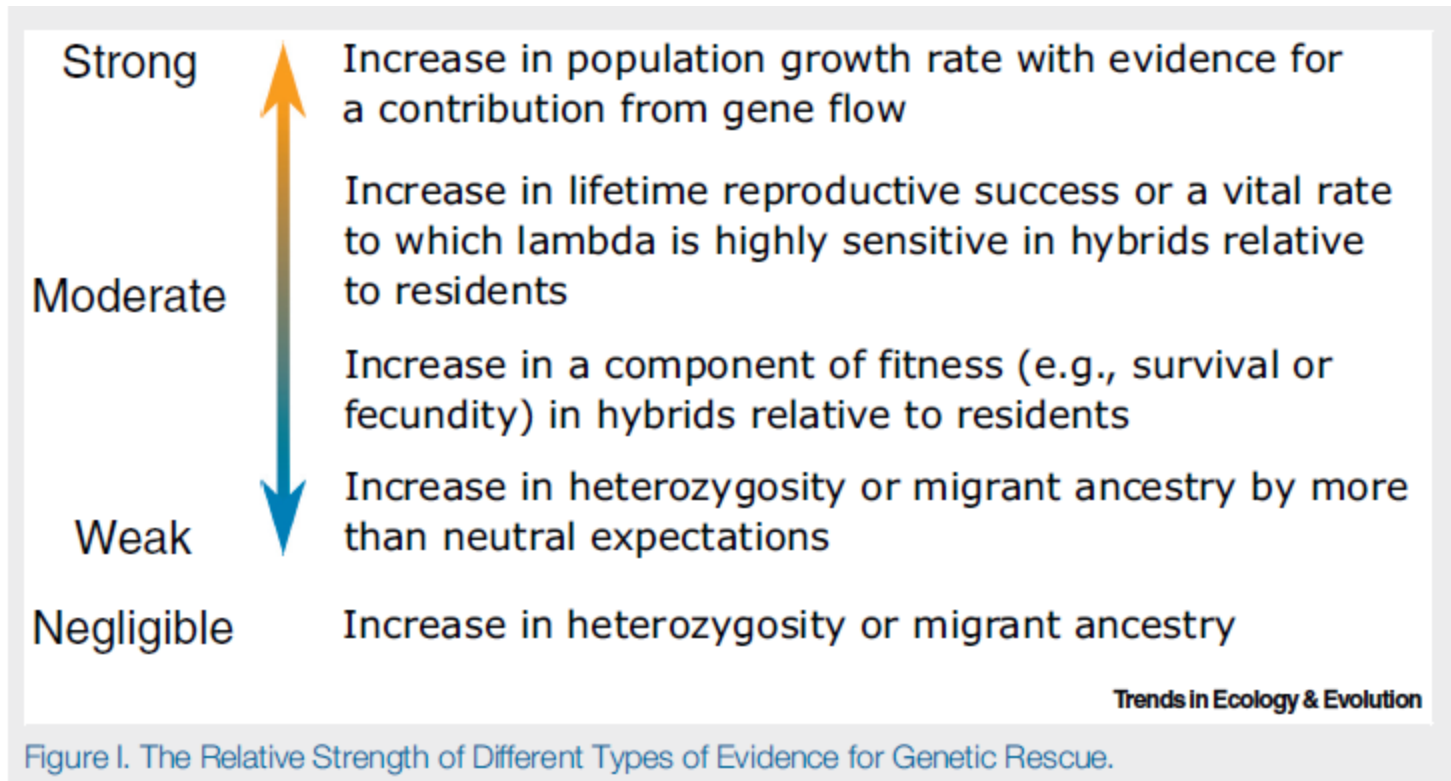
Whitely et al. TREE 2015

Trophic cascade

Evidence for the benefits of genetic rescue

Strength	Evidence
Strong	Increase in population growth rate with evidence for a contribution from gene flow
Moderate	Increase in lifetime reproductive success or a vital rate to which lambda is highly sensitive in hybrids relative to residents
	Increase in a component of fitness (e.g., survival or fecundity) in hybrids relative to residents
Weak	Increase in heterozygosity or migrant ancestry by more than neutral expectations
Negligible	Increase in heterozygosity or migrant ancestry

Trends in Ecology & Evolution

Figure I. The Relative Strength of Different Types of Evidence for Genetic Rescue.

Bell et al. 2019 TREE
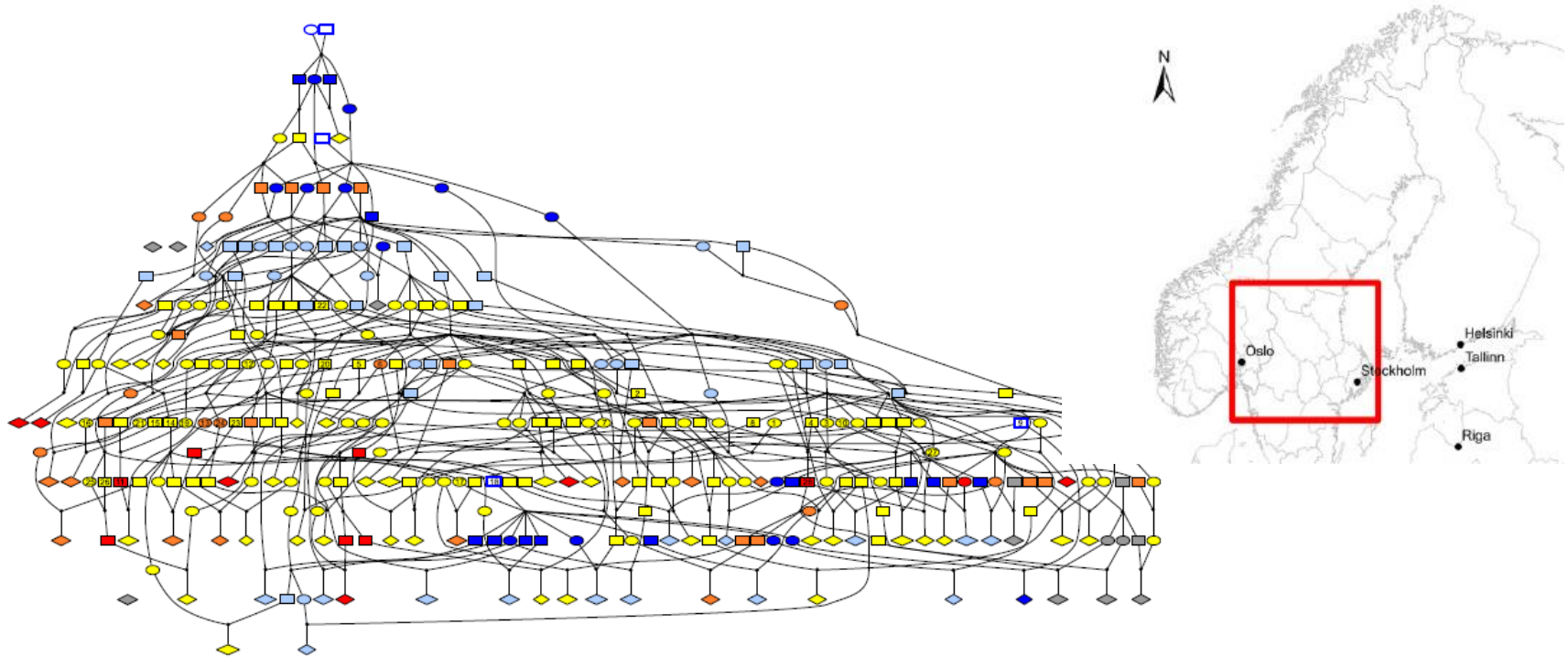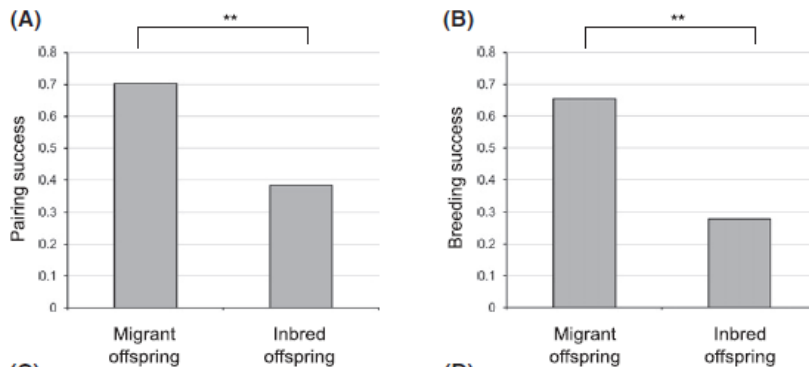
Scandinavian Wolves

Fig. 1 Pedigree of breeding Scandinavian wolves from 1983 to 2012. Ellipses are females, rectangles are males, and diamonds represent litters where no offspring has yet entered the breeding population. The colours represent the inbreeding coefficient f of the individuals and litters (dark blue: $0 \leq f < 0.1$, light blue: $0.1 \leq f < 0.2$, yellow: $0.2 \leq f < 0.3$, orange: $0.3 \leq f < 0.4$, red: $0.4 \leq f < 0.5$, grey: unknown f). Founders, assumed to be nonrelated and thus their offspring $f = 0$, are nonfilled symbols with a blue frame. The pedigree also contains the identity (numbers) of the 28 wolves (Table S3, Supporting information) included in the 14 target pairs.

Kesson et al. 2016 Mol Ecol.

Migrant wolves more successful
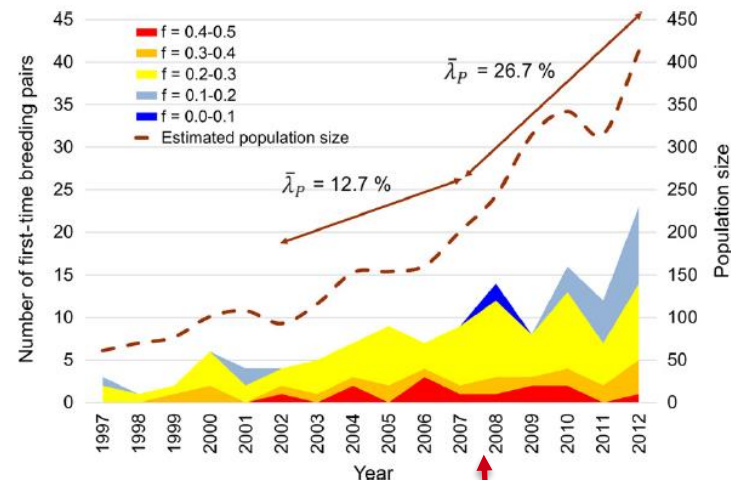

Kesson et al. 2016 Mol Ecol.

Fig. 4 Annual population size and inbreeding levels of first-time breeding pairs in the Scandinavian wolf population from 1997 to 2012. Population size is the mean census size using yearly direct count estimates from the combination of snow tracking and DNA analysis carried out within the framework of the Scandinavian wolf monitoring programme. Inbreeding levels refer to the inbreeding coefficients of the offspring in litters to first-time breeding pairs. The angles of the arrows represent the average annual population growth rate ($\bar{\lambda}_p$) before and after 2008, when the two immigrants started to breed. The population growth rate is corrected each year for the number of legally shot wolves (see Materials and methods).
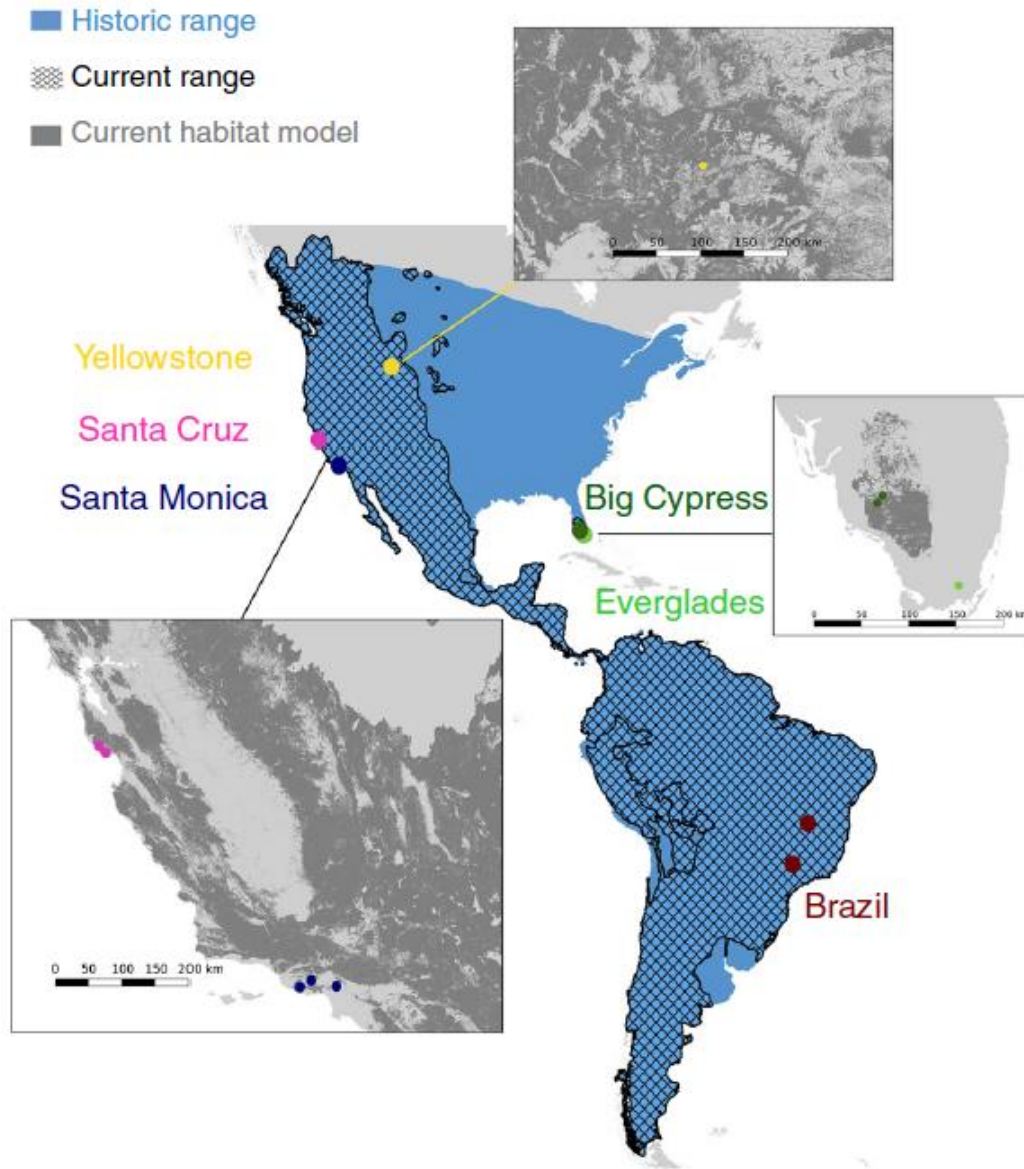
Big Horn Sheep
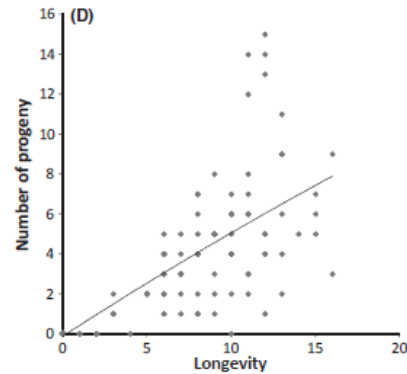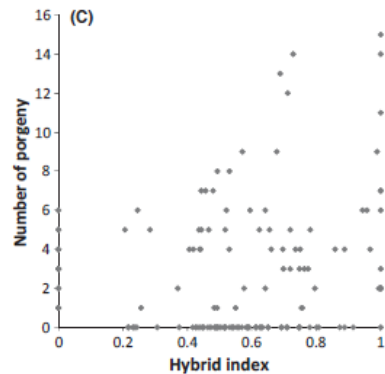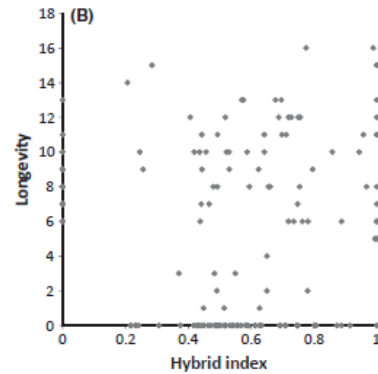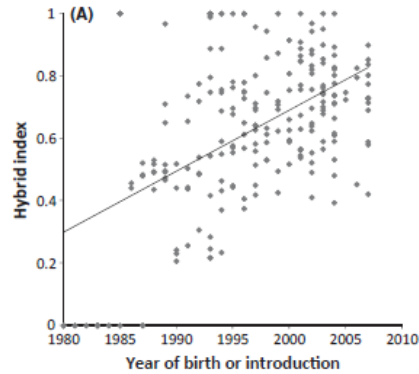
Big Horn Sheep – fitness benefits of admixture
Miller et al. Mol Ecol 2012

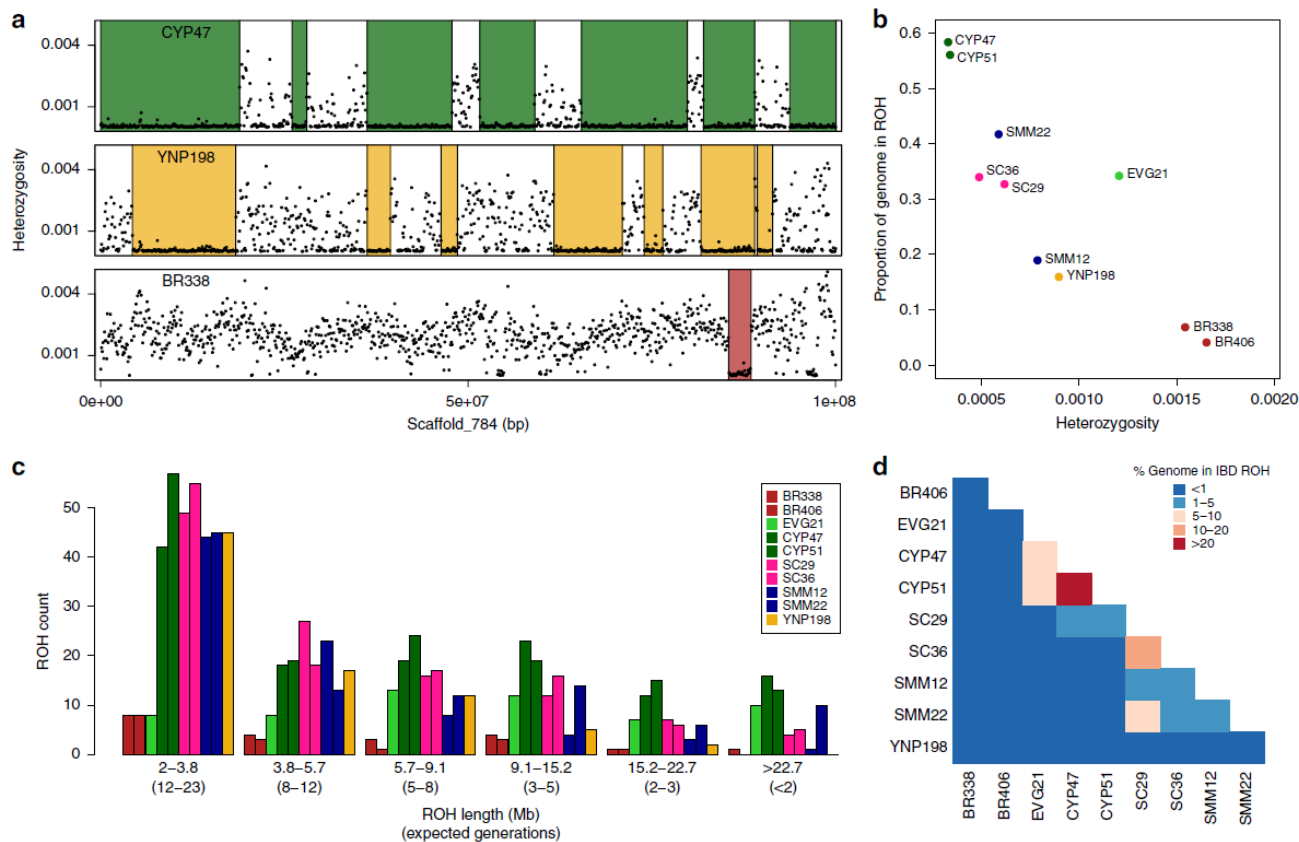# Florida Puma

Saremi et al. 2019 Nat Com

Fig. 4 Heterozygosity and runs of homozygosity. **a** Sliding window heterozygosity (black dots) and called ROH (colored boxes) across a single scaffold for three pumas from three different populations (Big Cypress, Yellowstone, and Brazil). Plots for all pumas are provided as Supplementary Fig. 12. **b** Average genome-wide heterozygosity versus the proportion of the genome in ROH for the ten pumas sequenced. **c** Distribution of lengths of ROH. The length in Mb is indicated, as is the associated expected number of generations since the individual's maternal and paternal lineages shared a common ancestor. **d** Heat map showing the percent of the genomes that are in ROH that are shared IBD between pairs of pumas (Supplementary Table 6)
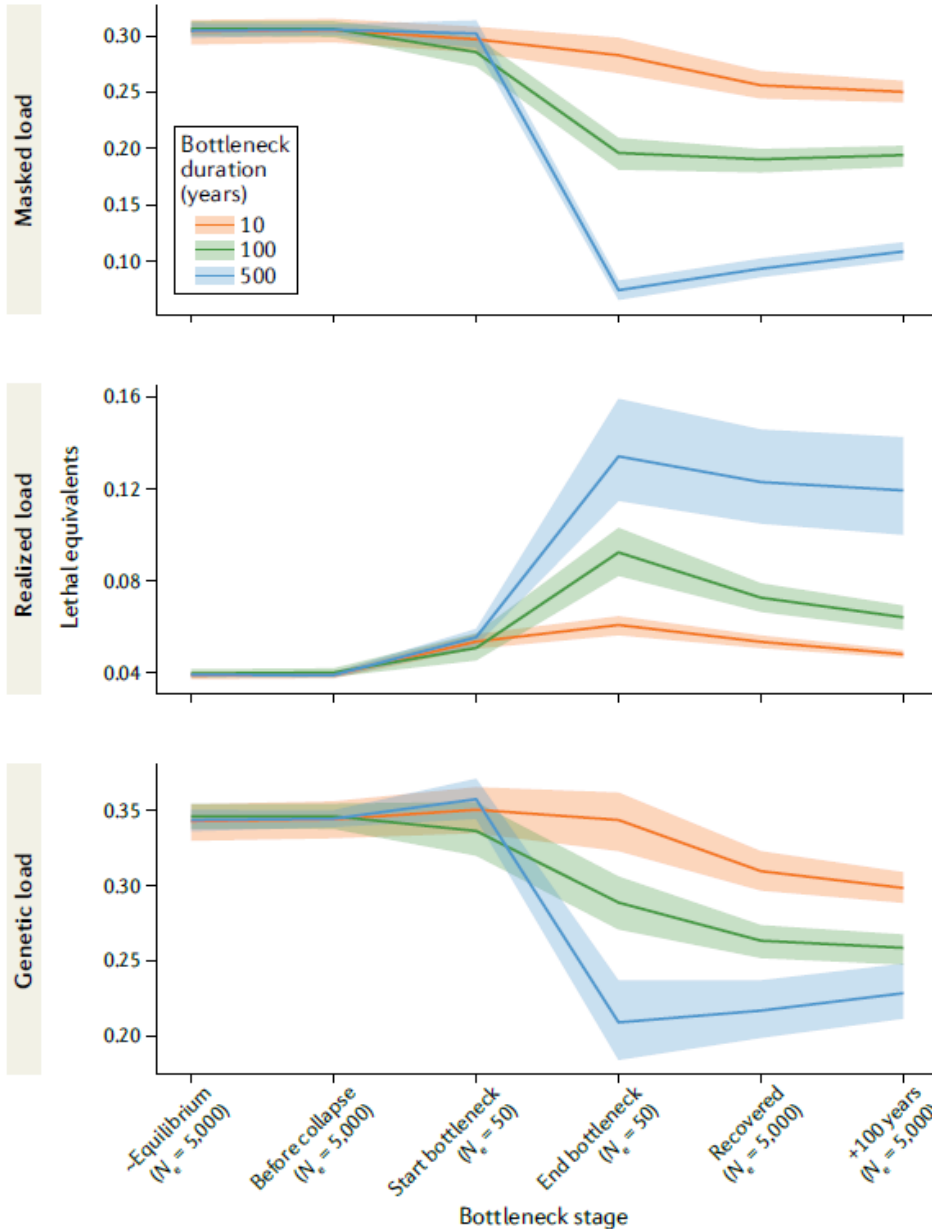
Inbreeding can occur very quickly
even after genetic rescue – requires ongoing management

Realized 'genetic load' increases with decreasing Ne

Bertorelle et al. Nat Rev 2021
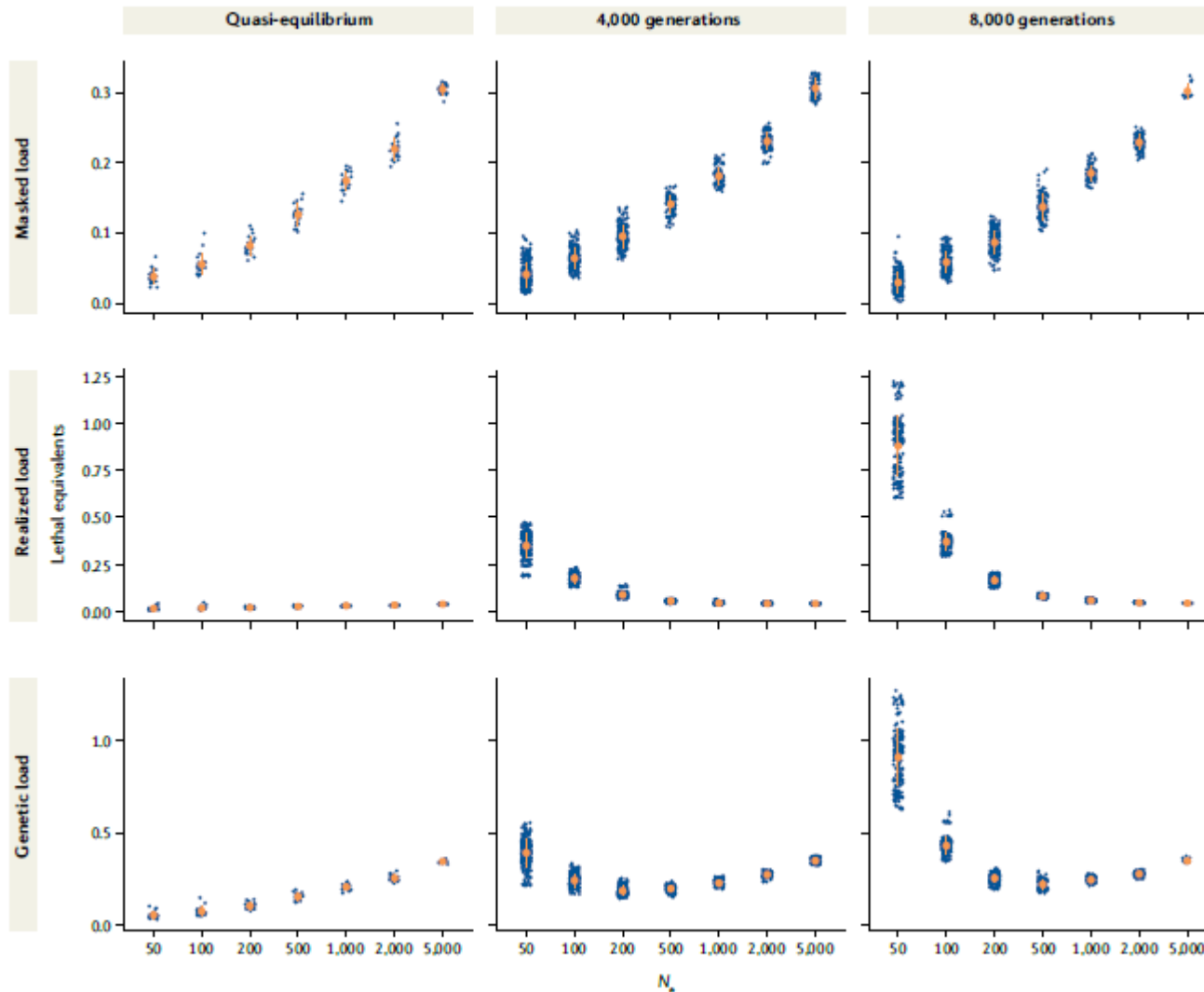
Based on forward simulations

The length of the demographic bottleneck is important

Bertorelle et al. Nat Rev 2021

Robinson et al 2022 Science

MACQUARIE

Vaquita – critically endangered

'Purging can remove some
very deleterious alleles from
small populations,
but that is only a small part of
the genomic architecture of fitness.'
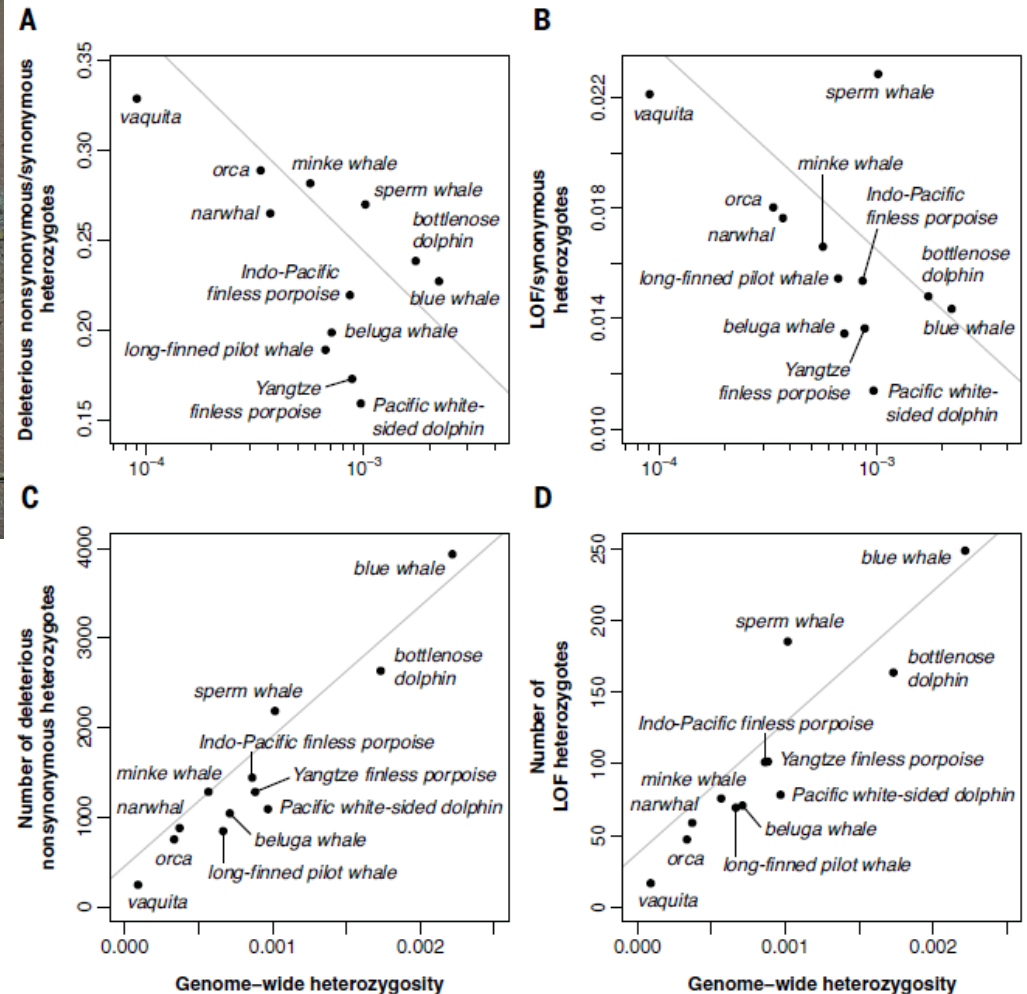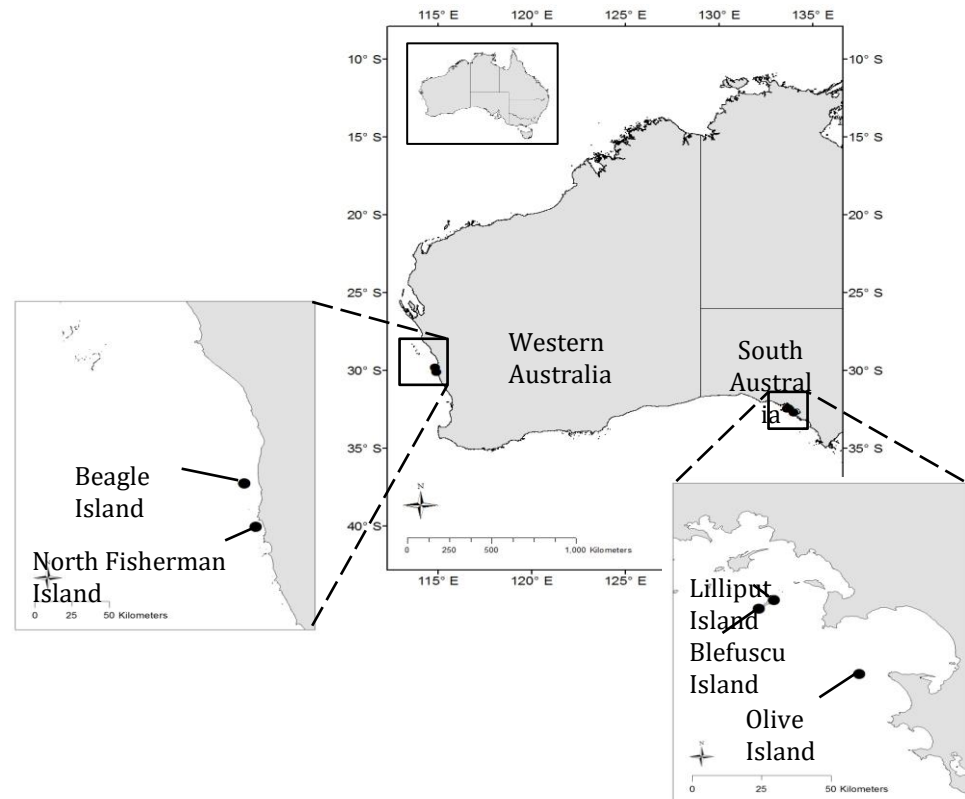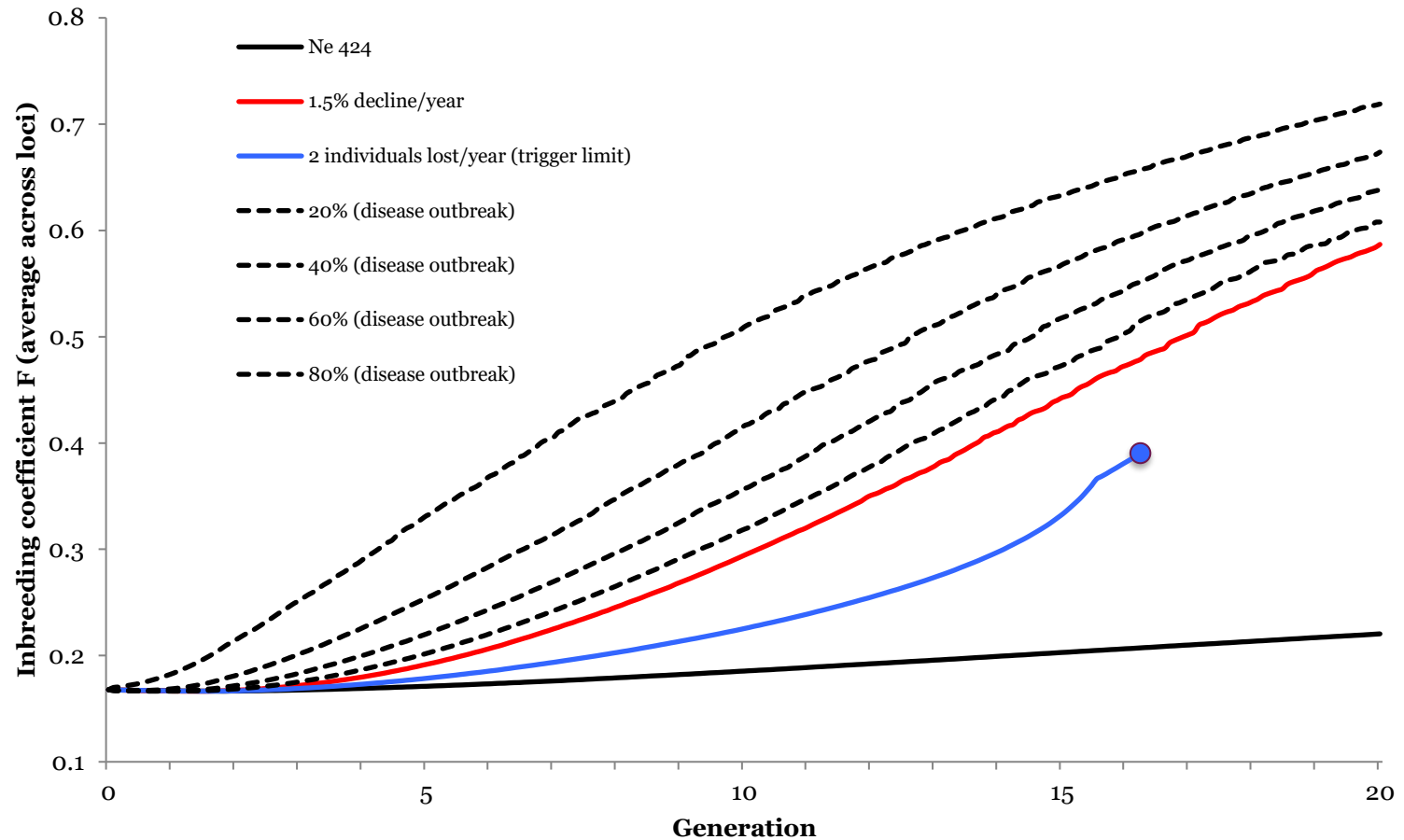
Sunnucks & Gruber, Science 2022

Fig. 2. Deleterious variation in vaquitas and other cetaceans. (A and **B)** Ratios of deleterious nonsynonymous (A) and LOF (B) heterozygotes to synonymous heterozygotes are significantly negatively correlated with genome-wide heterozygosity (per base pair, log-scaled). (**C** and **D)** Total numbers of deleterious nonsynonymous (C) and LOF (D) heterozygotes per genome are significantly positively correlated with genome-wide heterozygosity (per base pair). Gray lines show phylogeny-corrected regressions [excluding the Indo-Pacific finless porpoise (5)].

Australian Sea lion – evaluating the risk

Beagle Island

North Fisherman Island

Western Australia

South Australia

Lilliput Island
Blefuscu Island
Olive Island

Predicting the consequences of future events

Next Lecture: metagenomics