

Population Genomics 101: Population Structure, Selection, and Mutation Load



Alexander Ochoa | GDW 2023

Genomic Flatlining in the Endangered Island Fox

Jacqueline A. Robinson,¹ Diego Ortega-Del Vecchio,² Zhenxin Fan,³ Bernard Y. Kim,¹ Bridgett M. vonHoldt,⁴ Clare D. Marsden,¹ Kirk E. Lohmueller,^{1,2,5,6} and Robert K. Wayne^{1,6,*}

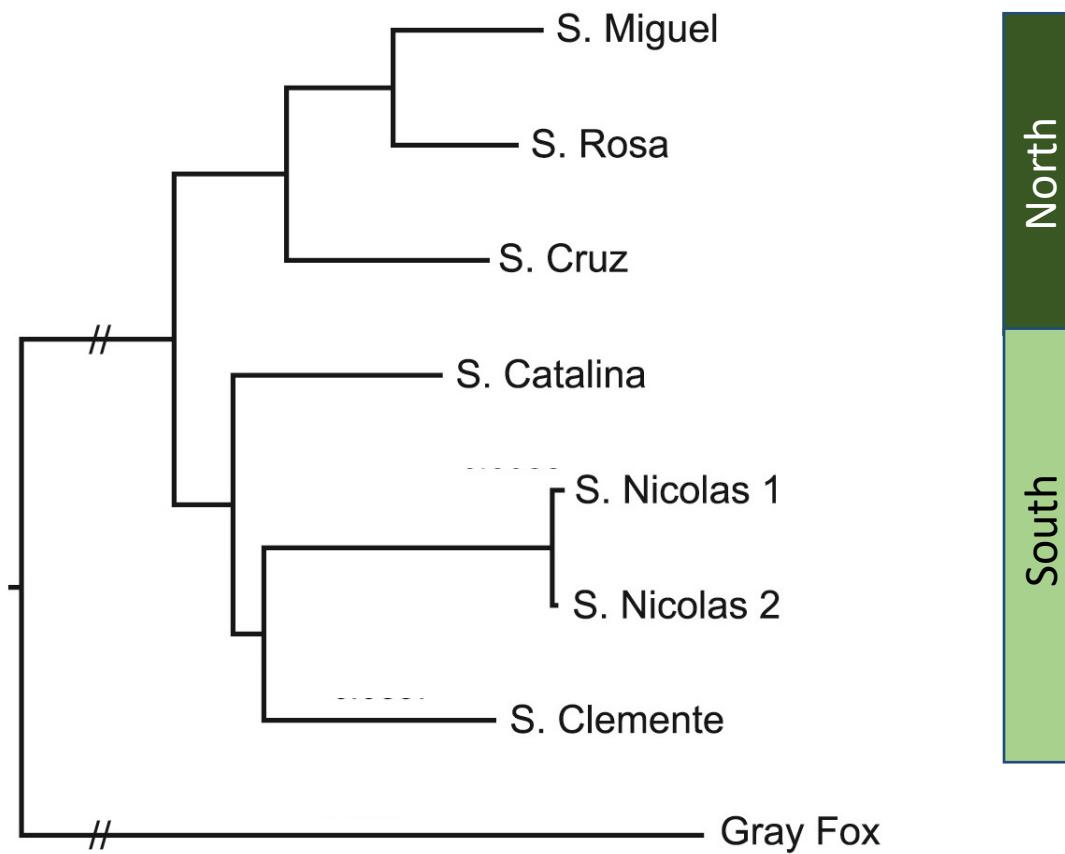
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²Interdepartmental Program in Bioinformatics, University of California, Los Angeles, Los Angeles, CA 90095, USA

³Key Laboratory of Bioresources and Ecoenvironment (Ministry of Education), College of Life Sciences, Sichuan University, Chengdu 610064, People's Republic of China

⁴Department of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ 08544, USA

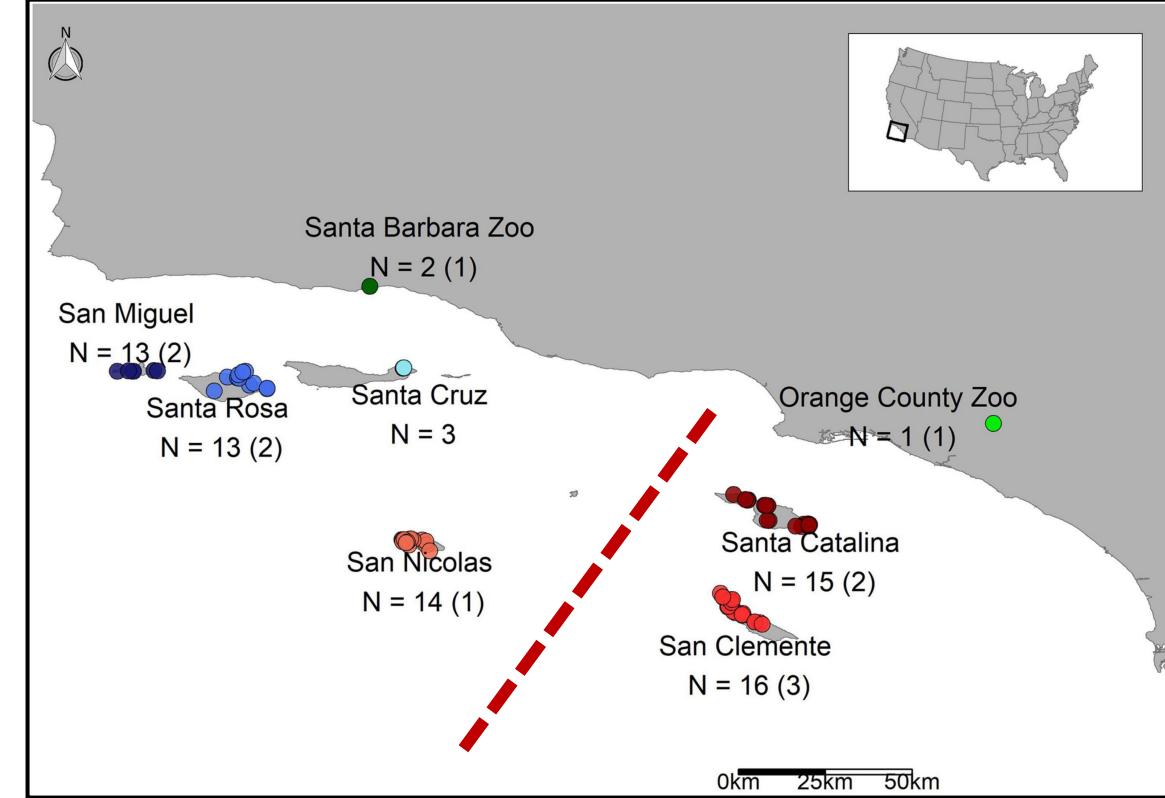
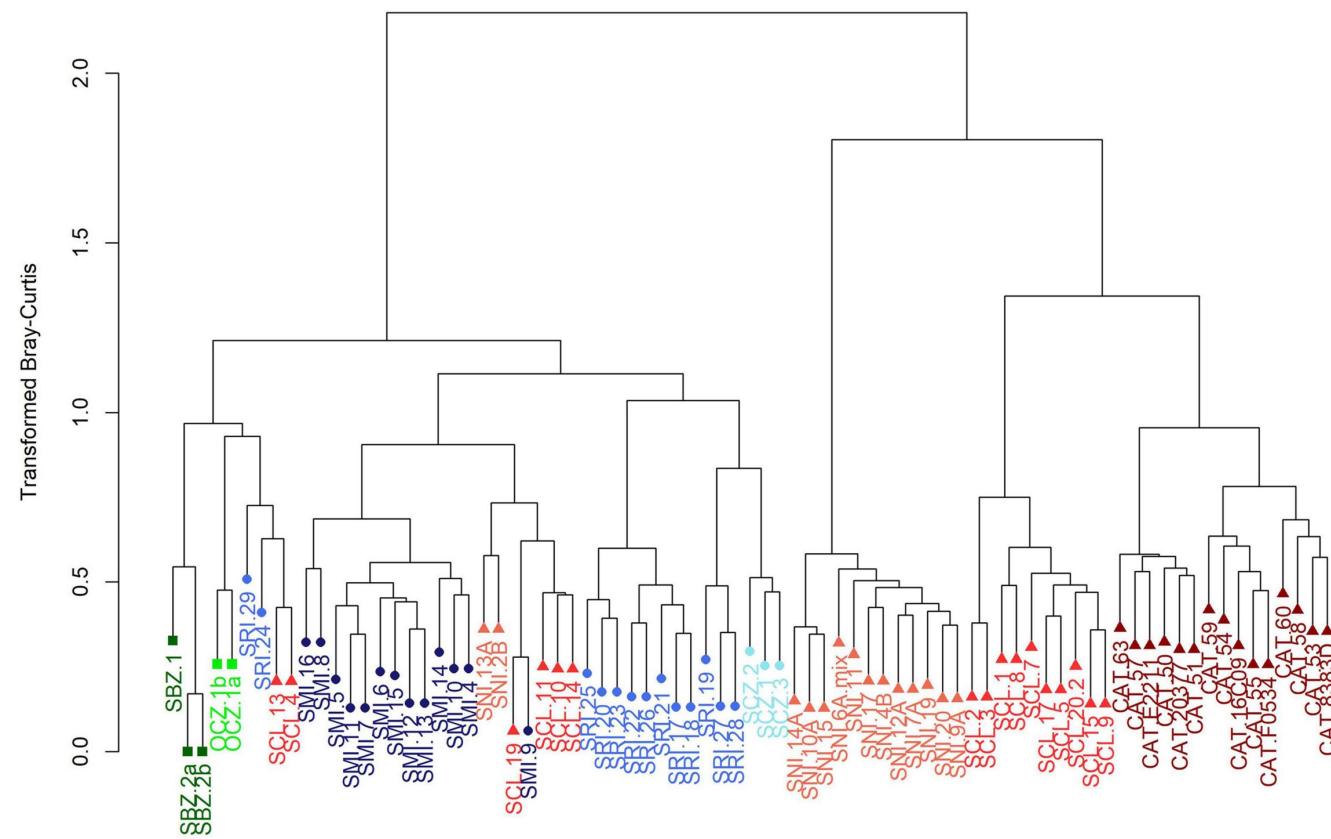
⁵Department of Human Genetics, David Geffen School of Medicine, University of California, Los Angeles, Los Angeles, CA 90095, USA



Effect of Geography and Captivity on Scat Bacterial Communities in the Imperiled Channel Island Fox

Nicole E. Adams^{*†}, Madeleine A. Becker[†] and Suzanne Edmands

Department of Biological Sciences, University of Southern California, Los Angeles, CA, United States

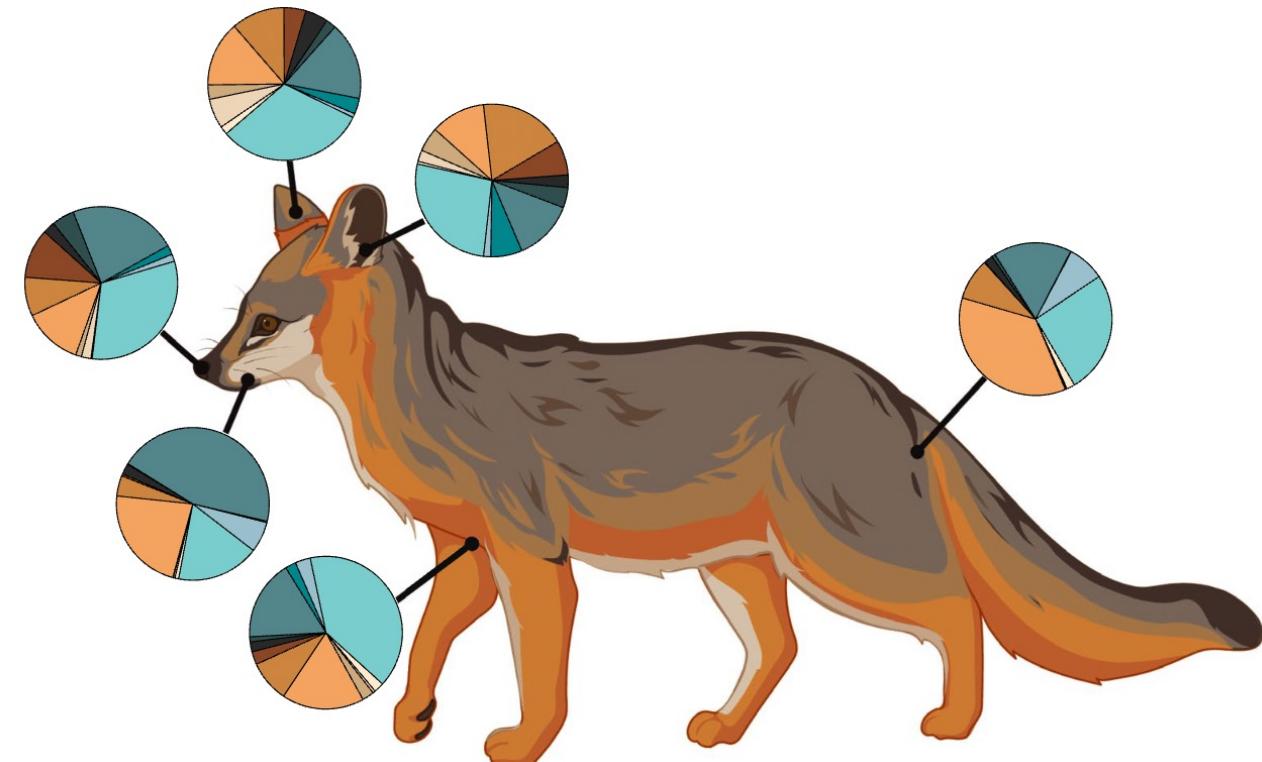
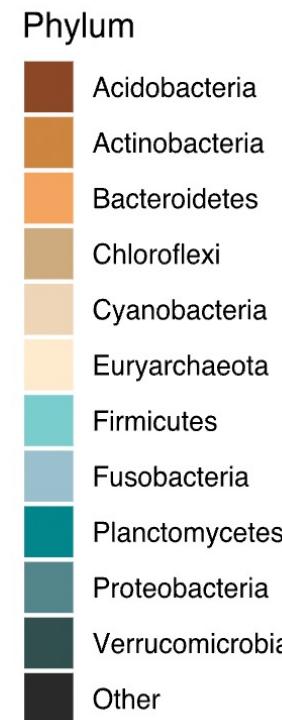


¹Department of Ecology & Evolutionary Biology, Princeton University, Princeton, NJ, USA

²Catalina Island Conservancy, Avalon, CA, USA

Ear mite infection is associated with altered microbial communities in genetically depauperate Santa Catalina Island foxes (*Urocyon littoralis catalinae*)

Alexandra L. DeCandia¹  | Lara J. Brenner² | Julie L. King² | Bridgett M. vonHoldt¹ 

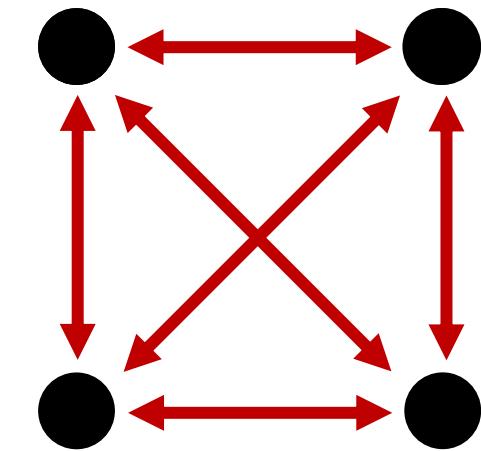
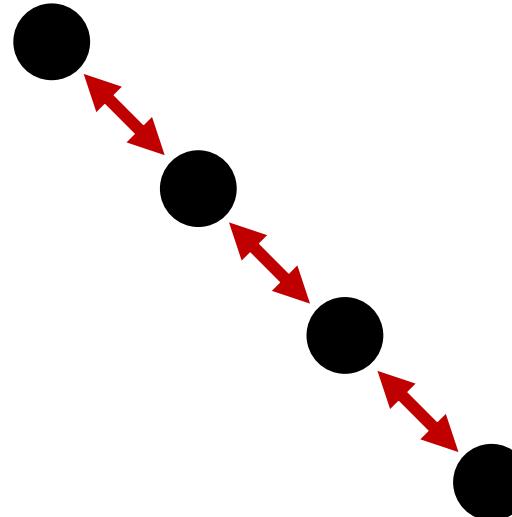
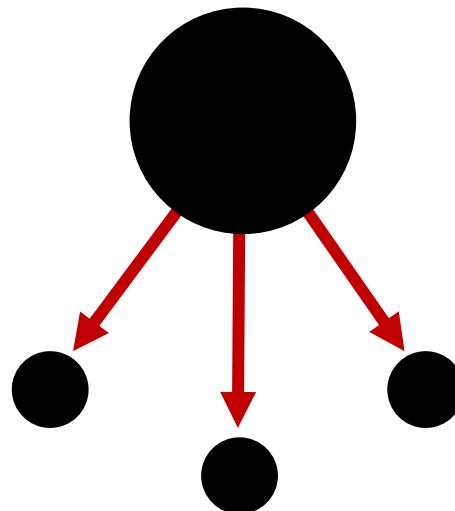


Population Structure

- Differences in genetic variation between populations
- Population structure arises primarily as a function of the amount of **gene flow** (or the lack thereof) between populations

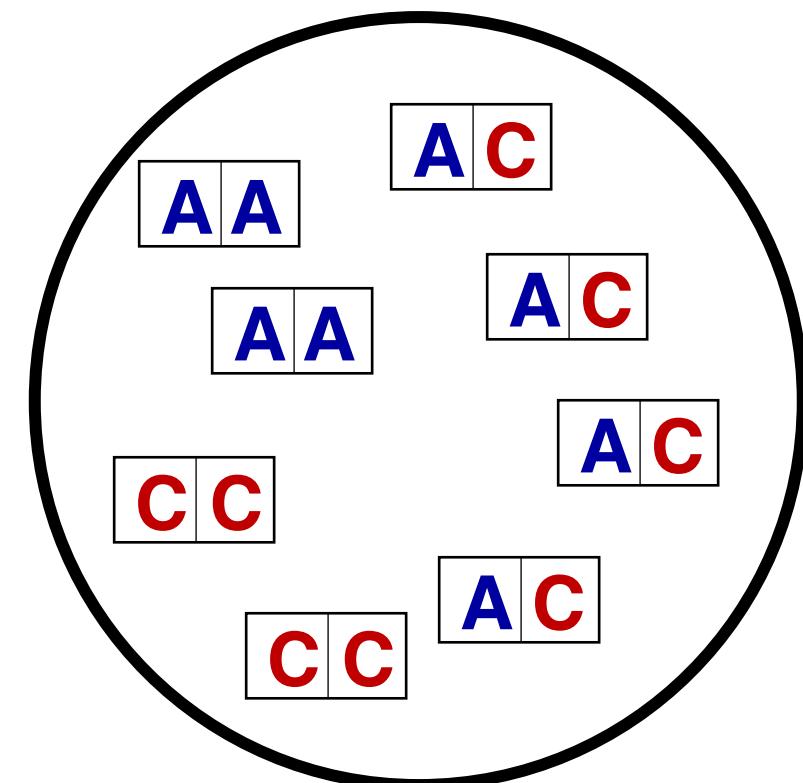
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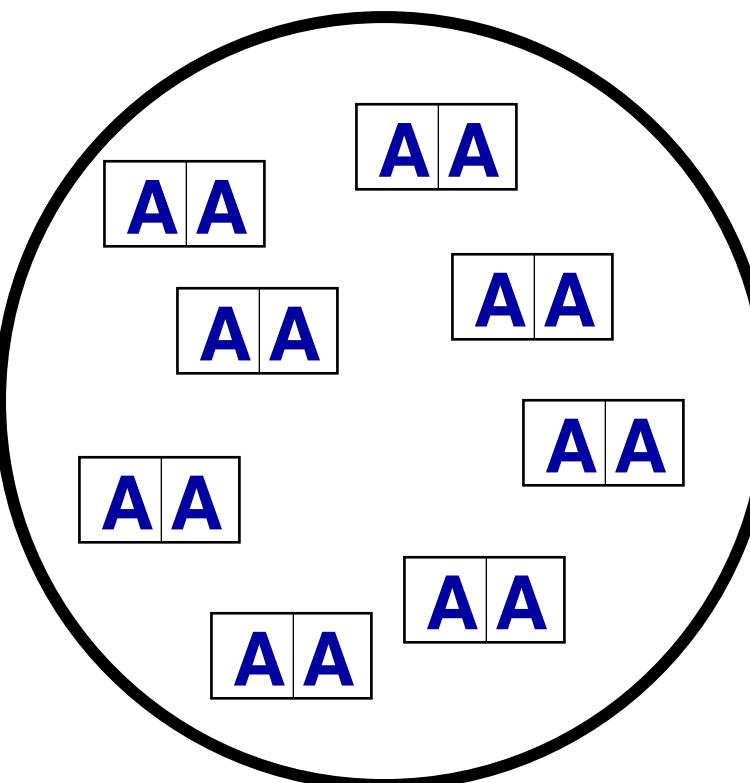
Population Structure (F_{ST})

Freq A (p) = 0.5
Freq C (q) = 0.5



Population 1

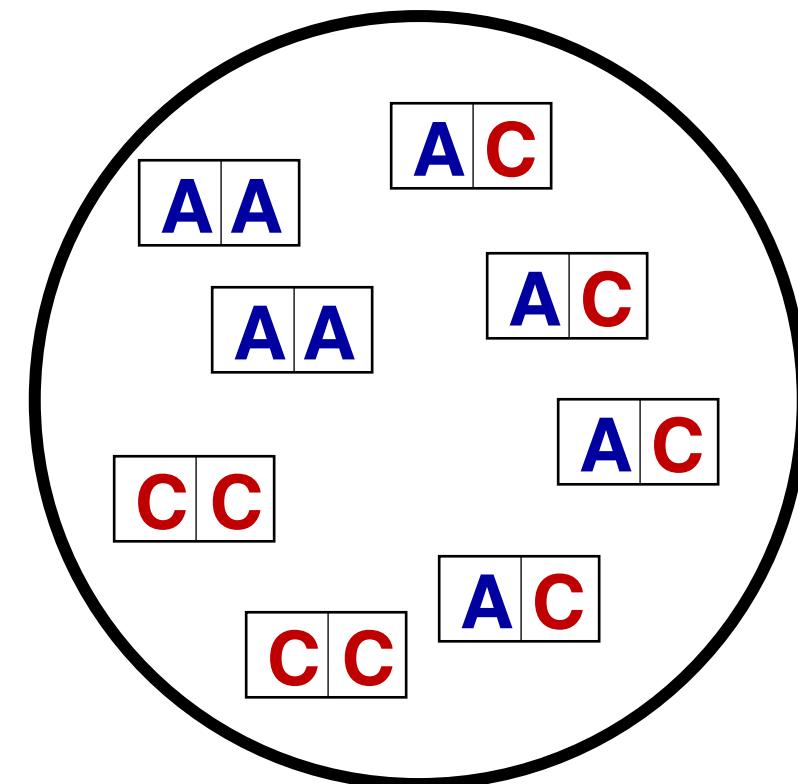
Freq A (p) = 1
Freq C (q) = 0



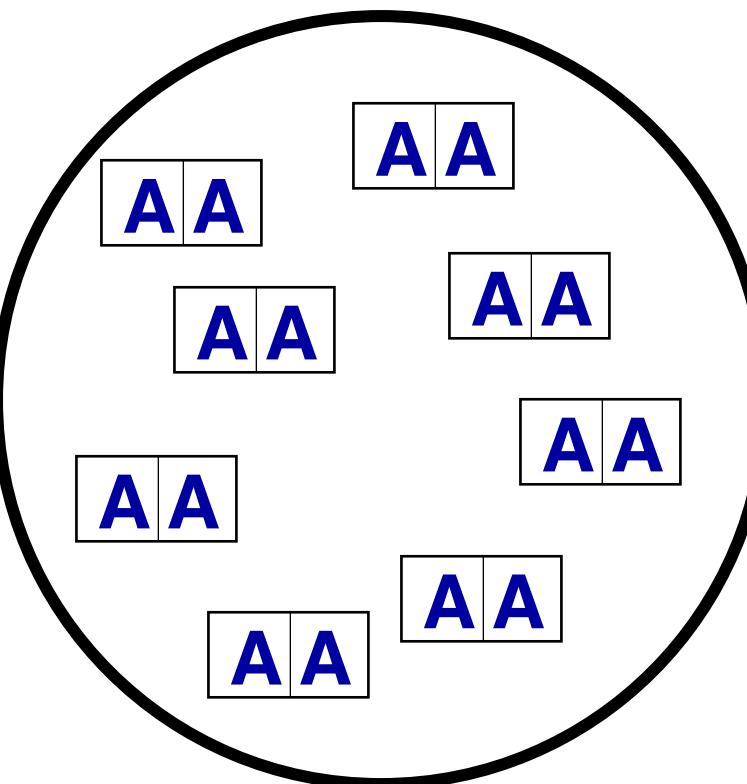
Population 2

Population Structure (F_{ST})

Freq A (p) = 0.5
Freq C (q) = 0.5



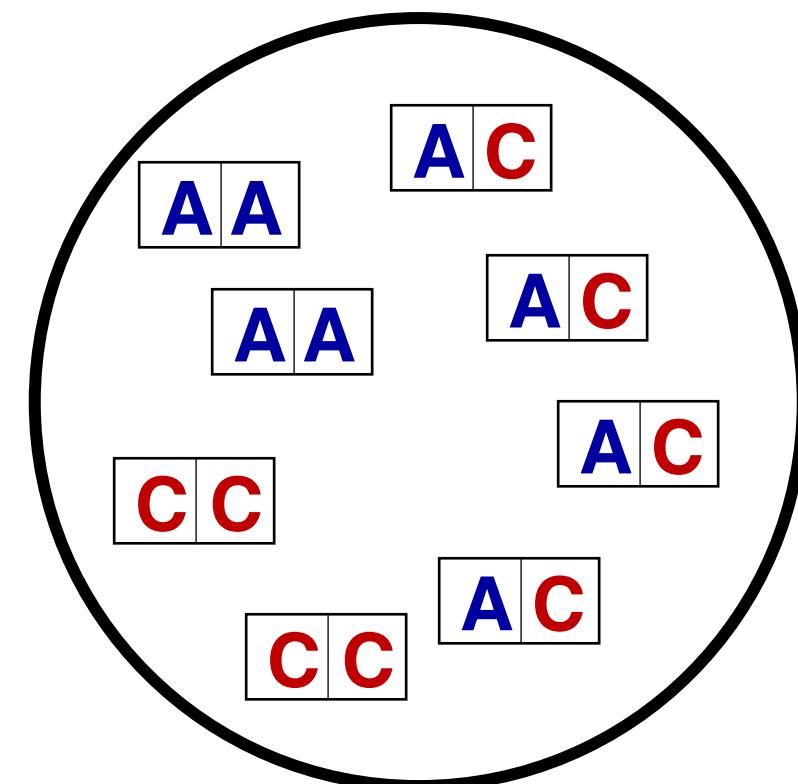
Freq A (p) = 1
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$$2pq \text{ (Pop1)} = 2 \times 0.5 \times 0.5 = 0.5$$
$$2pq \text{ (Pop2)} = 2 \times 1 \times 0 = 0$$
$$\text{AVG } (H_s) = 0.25$$

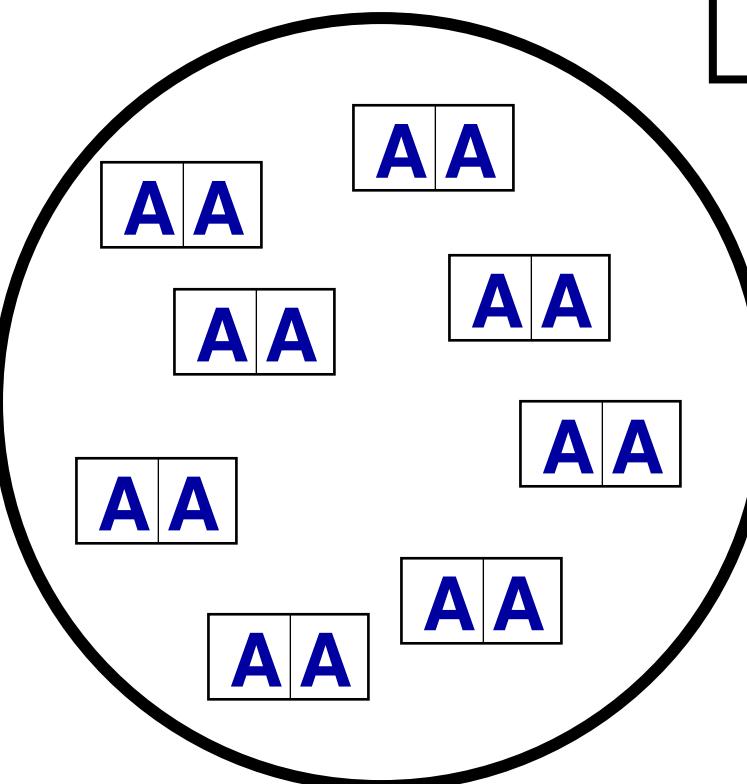
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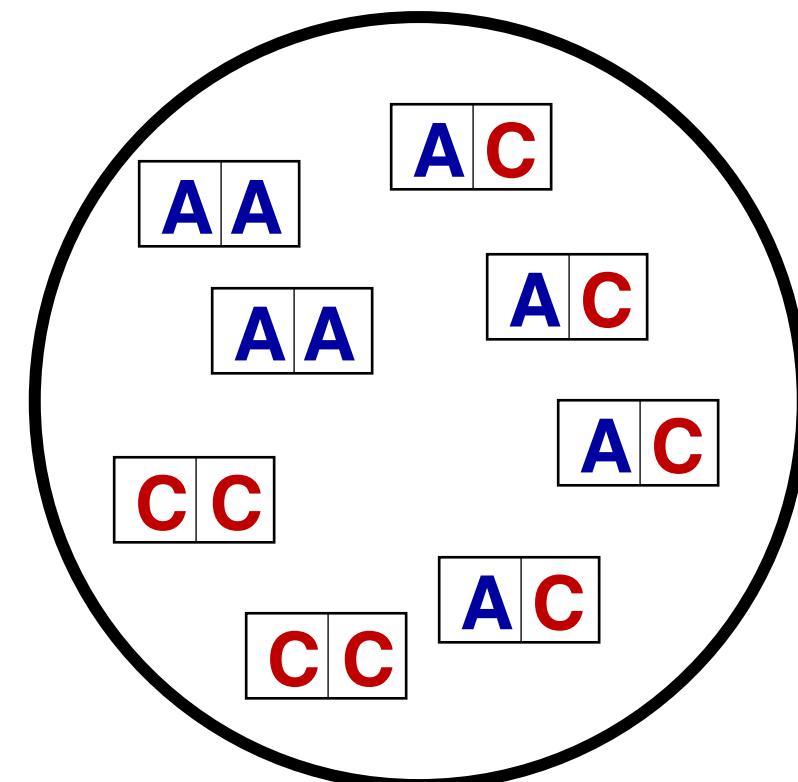
$$2pq \text{ (Pop2)} = 2 \times 1 \times 0 = 0$$

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$$2\bar{pq} \text{ (} H_T \text{)} = 2 \times 0.75 \times 0.25 = 0.375$$

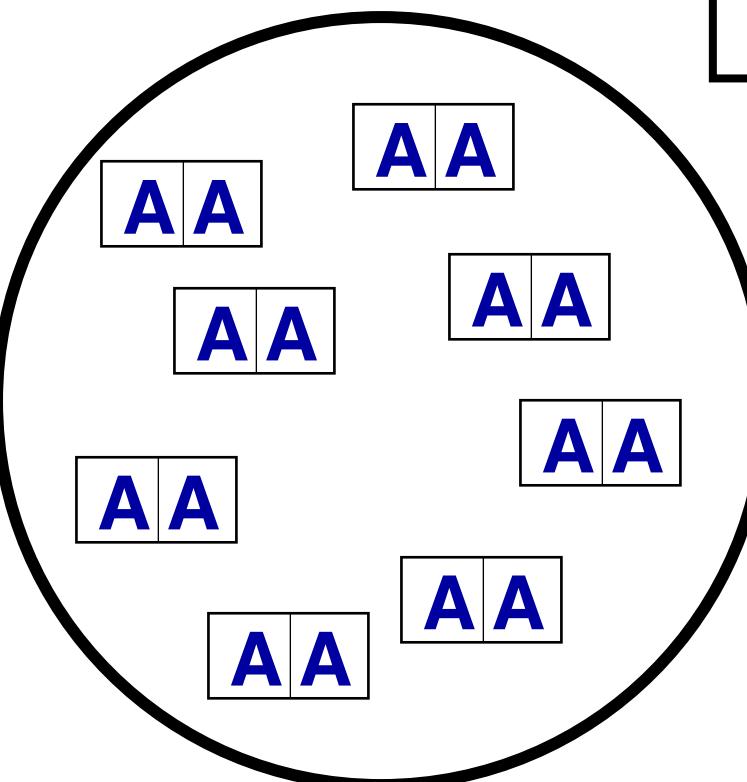
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Population 2

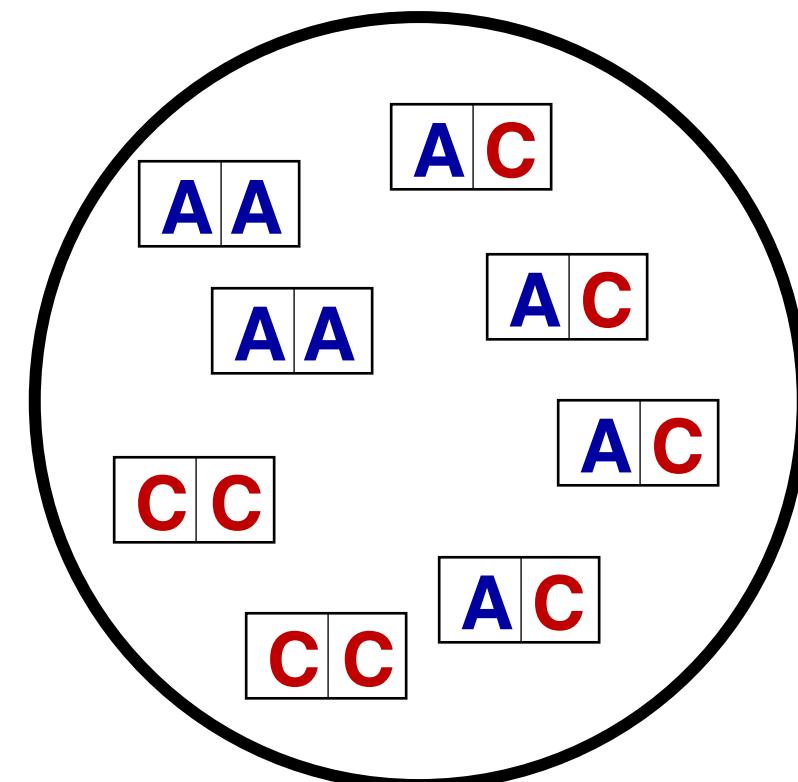
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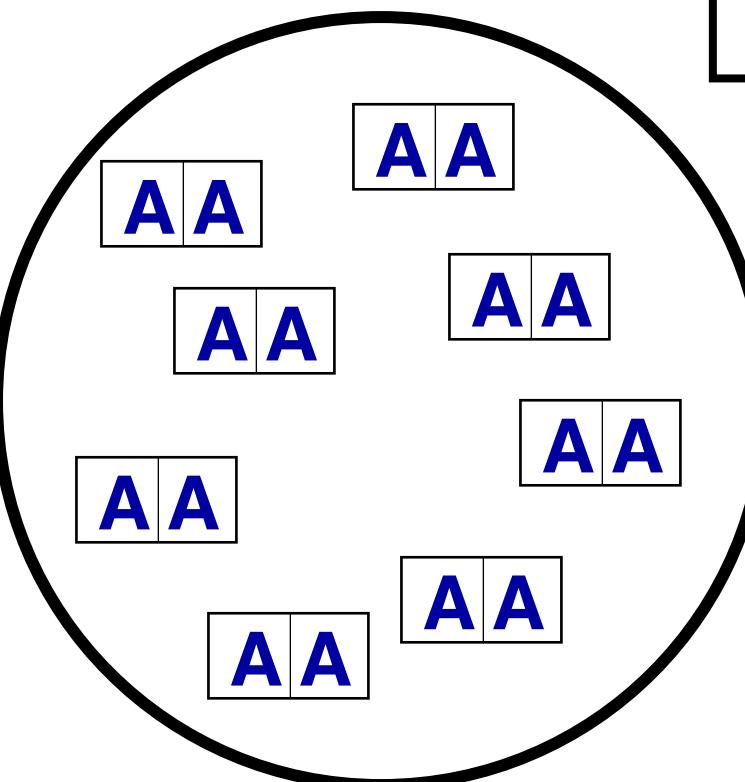
$$F_{ST} = 1 - \frac{H_s}{H_T} = 0.33$$

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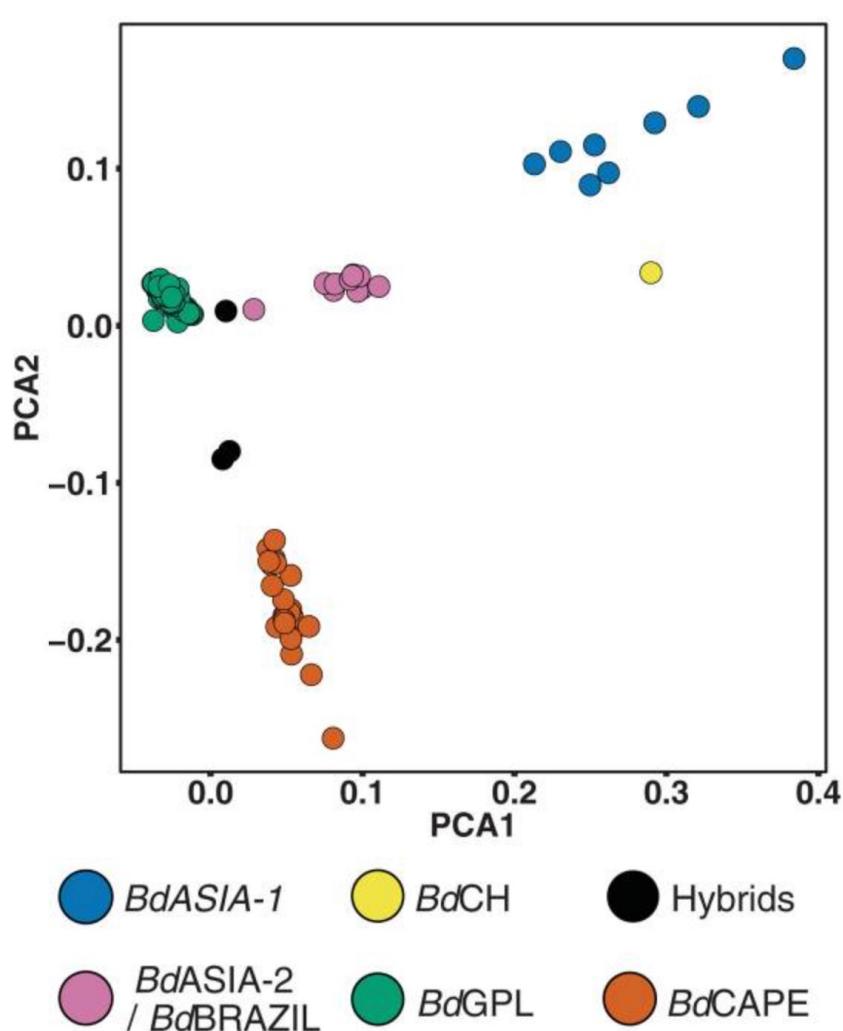
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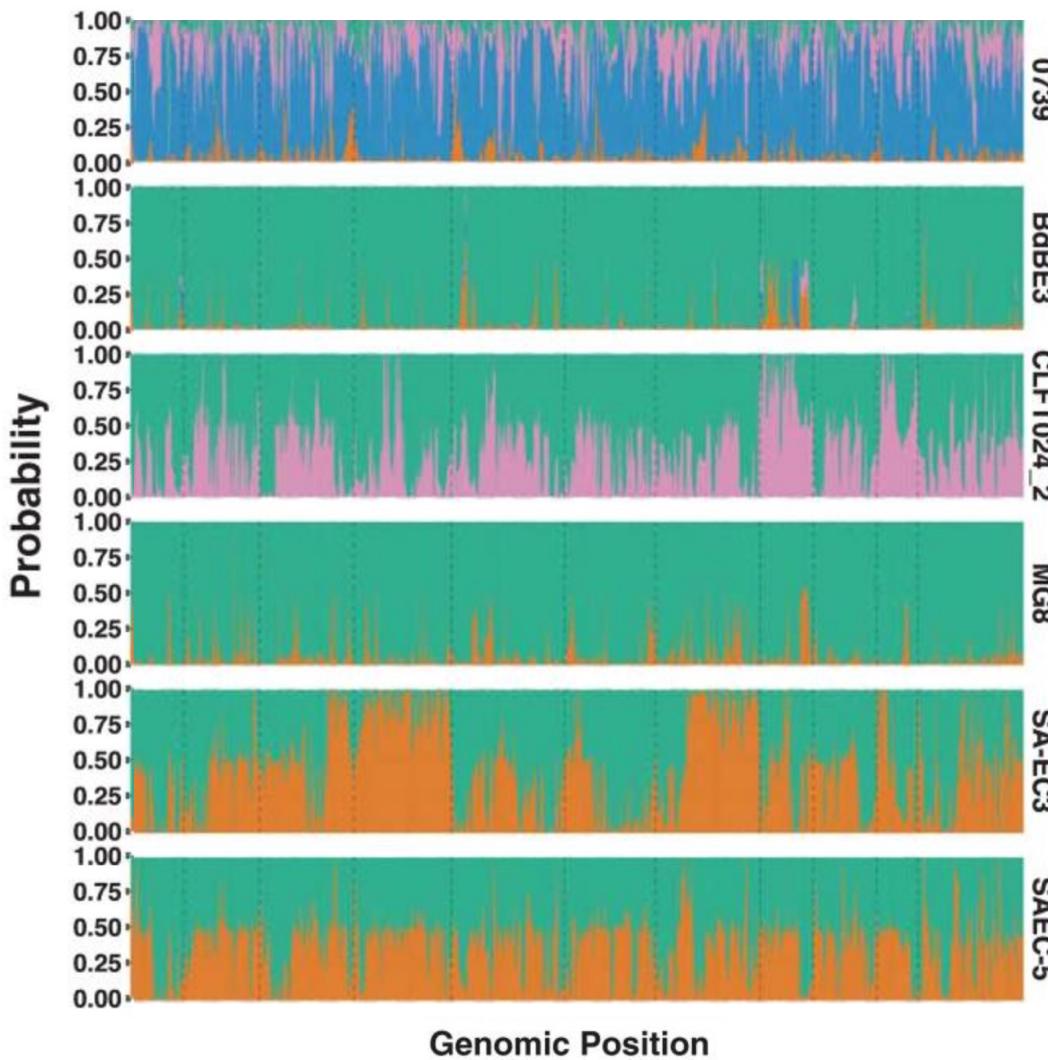
$$F_{ST} = 1 - \frac{H_s}{H_T} = 0.33$$

Average decrease of 33% in the expected heterozygosity due primarily to gene flow barriers

Population Structure (Principal Component Analysis)



Population Structure (Assignment and Admixture)



O'Hanlon et al., 2018

Selection

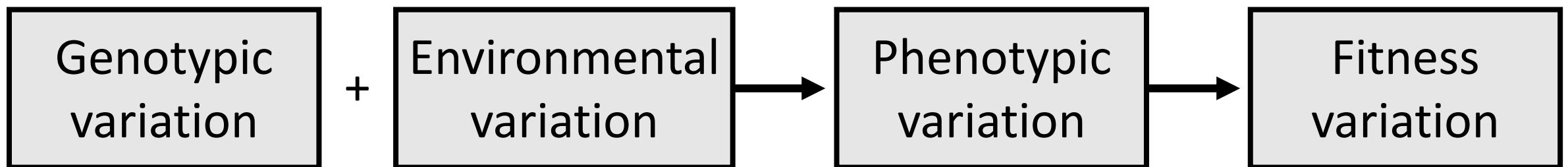
- Non-random differential survival and reproduction of individuals (i.e., fitness)
- Acts on the phenotype and—by extension—on the genotype

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Measures of Genetic Variation (Tajima's D)

Large Population

Sample_1 **A A A A C A A A A A A**
Sample_1 **A C A A A C A A A A A A**
Sample_2 **A A A C A A A A A A C**
Sample_2 **A A A A A C A A A A A A**
Sample_3 **A A A A A A C A A A A A**
Sample_3 **A A A C A A A C A A A A A**
Sample_4 **C A A A A C A A A A A A**
Sample_4 **A A A A C A A A A A A A A A**
Sample_5 **A A C A A A A A A A A A A A A**
Sample_5 **A A C A A A A A A A A C A A A A A A**



$$D < 0$$

Demographic Expansion

Small Population

Sample_1 **A A A C A A A C A A A A A A**
Sample_1 **A A A C A A A C A A A C A A A A A A**
Sample_2 **A A A C A A A C A A A C A A A A A A**
Sample_2 **A A A C A A A C A A A C A A A A A A**
Sample_3 **A A A C A A A C A A A C A A A A A A**
Sample_3 **A A A C A A A C A A A C A A A A A A A A A A A A**
Sample_4 **A A A C A A A C A A A C A A A A A A A A A A A A**
Sample_4 **A A A C A A A C A A A C A A A A A A A A A A A A**
Sample_5 **A A A C A A A C A A A C A A A A A A A A A A A A A A A A A A**
Sample_5 **A A A C A A A C A A A C A A A A A A A A A A A A A A A A A A**



$$D > 0$$

Demographic Decline

Measures of Genetic Variation (Tajima's D)

Large Population

Sample_1	A A A A C A A A A A
Sample_1	A C A A A C A A A A
Sample_2	A A A C A A A A A C
Sample_2	A A A A A C A A A A
Sample_3	A A A A A A C A A A
Sample_3	A A A C A A A C A A
Sample_4	C A A A A C A A A A
Sample_4	A A A A C A A A A A A
Sample_5	A A C A A A A A A A A
Sample_5	A A C A A A A A C A

$$D < 0$$

Positive/Negative Selection

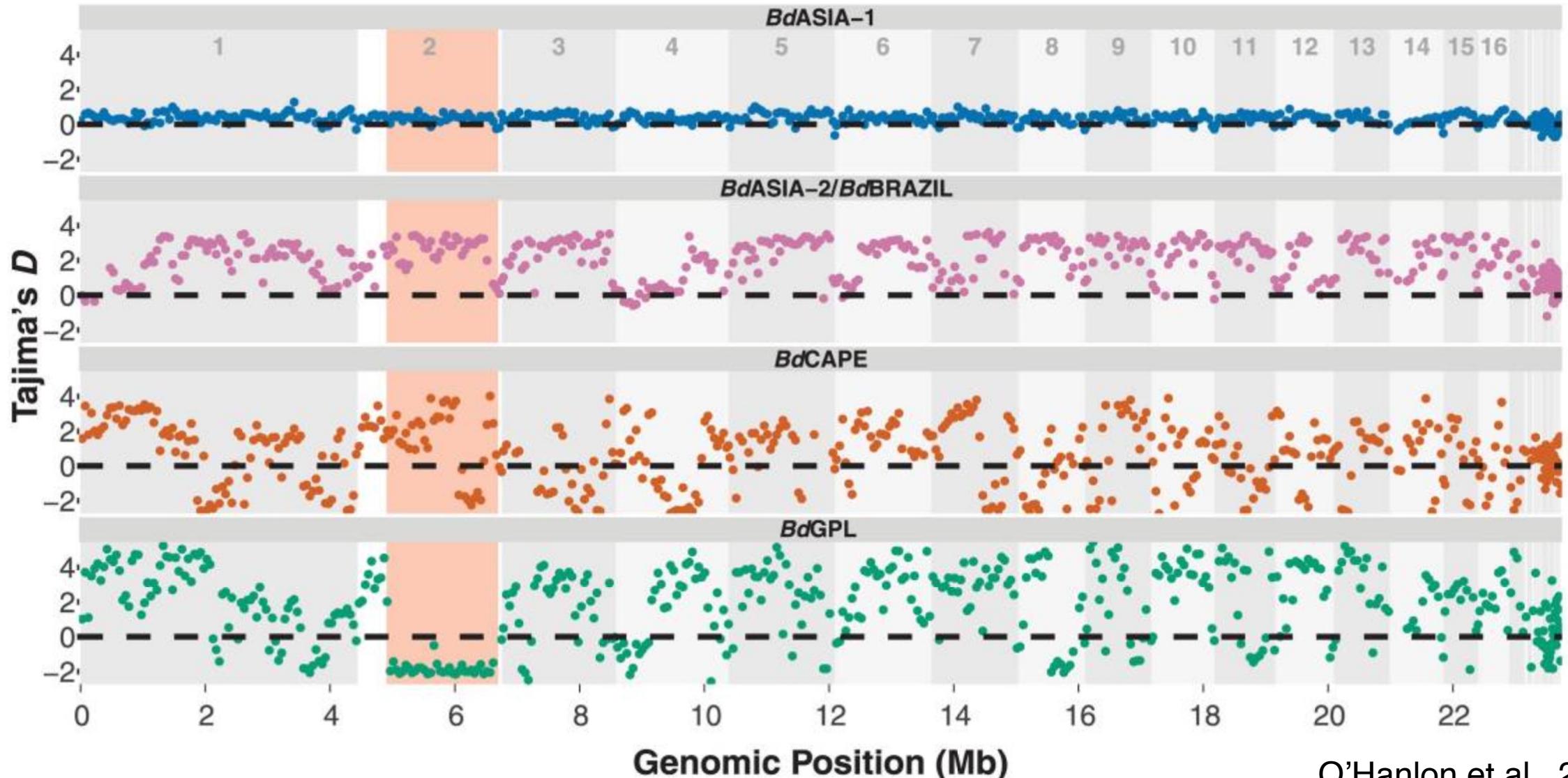
Small Population

Sample_1	A A A C A A A C A A
Sample_1	A A A C A A A C A A
Sample_2	A A A C A A A C A A
Sample_2	A A A C A A A C A A
Sample_3	A A A C A A A C A A
Sample_3	A A A C A A A A A A A
Sample_4	A A A C A A A A A A A
Sample_4	A A A C A A A A A A A
Sample_5	A A A C A A A A A A A
Sample_5	A A A C A A A A A A A

$$D > 0$$

Balancing Selection

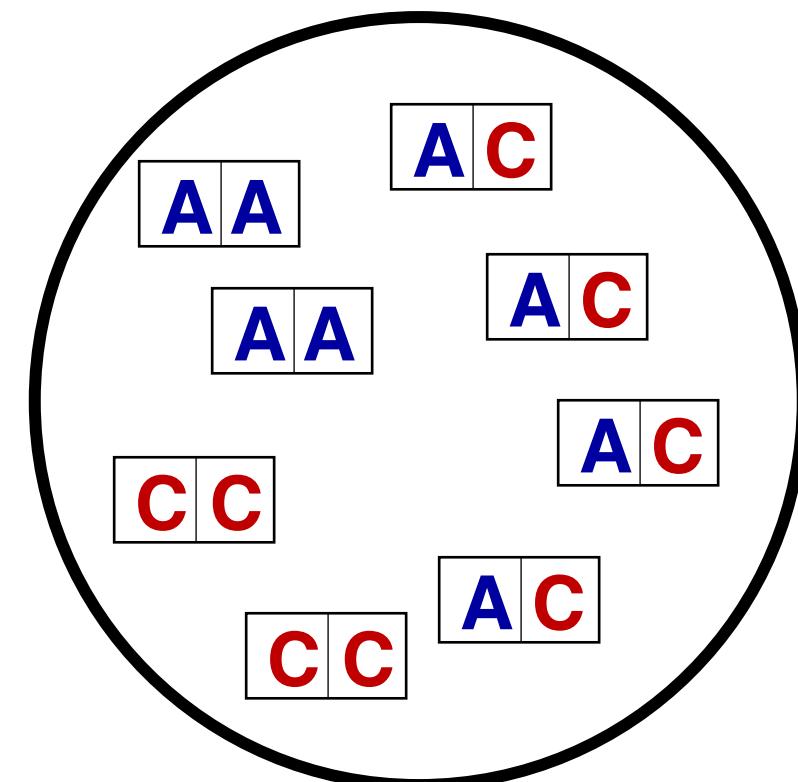
Selection (Tajima's D)



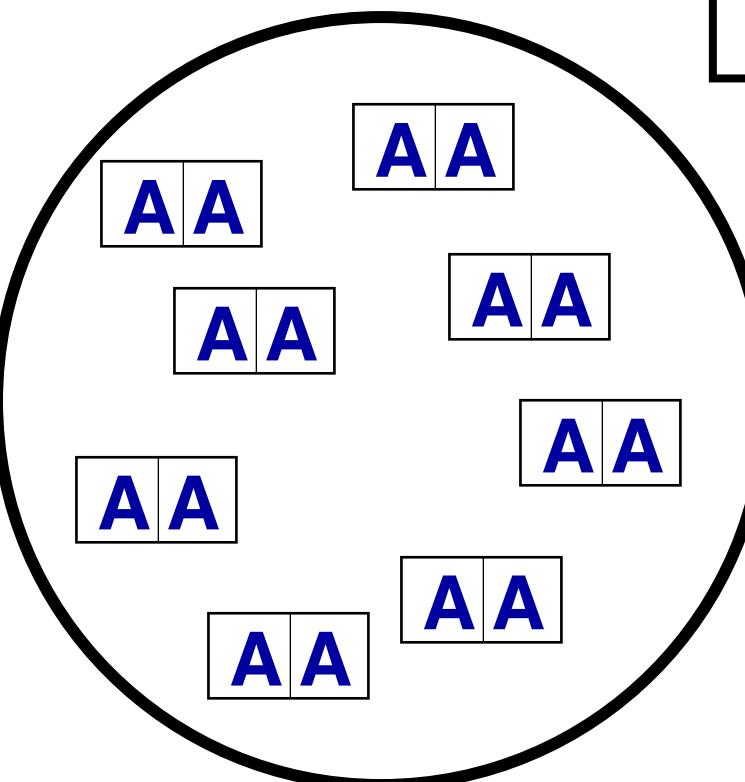
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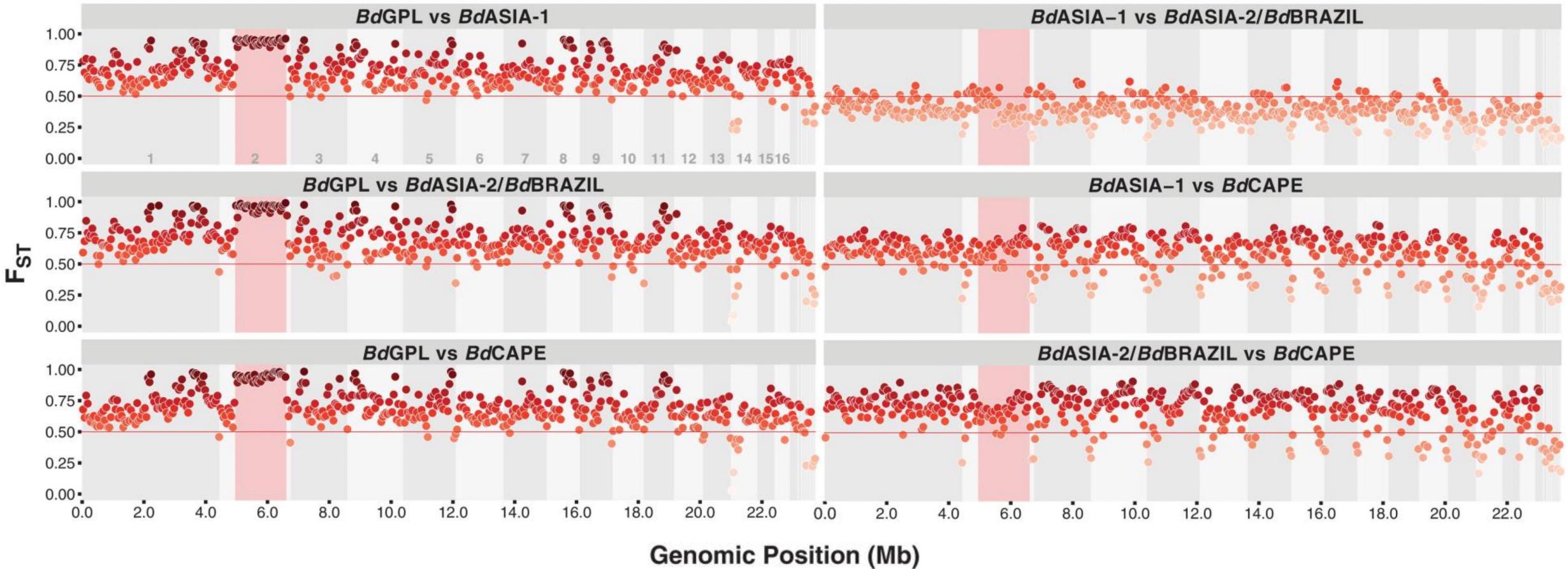
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Average decrease of 33% in the expected heterozygosity due primarily to gene flow barriers

Selection (F_{ST})



Selection (**Nonsynonymous** / **Synonymous** Substitutions)

TCCGATATATTGGCAACCCGACAAA
S D I W Q P D K

TCAGATCTATGGCAGCCCCACAAA
S D L W Q P R K

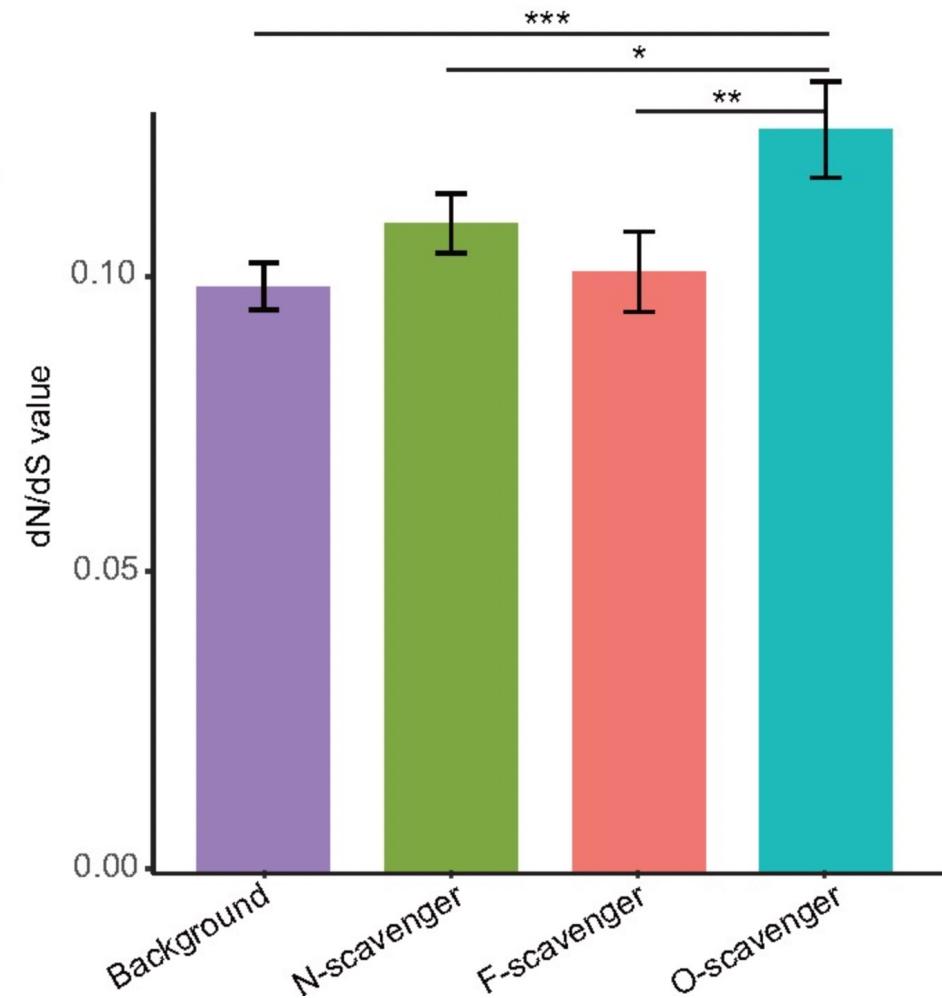
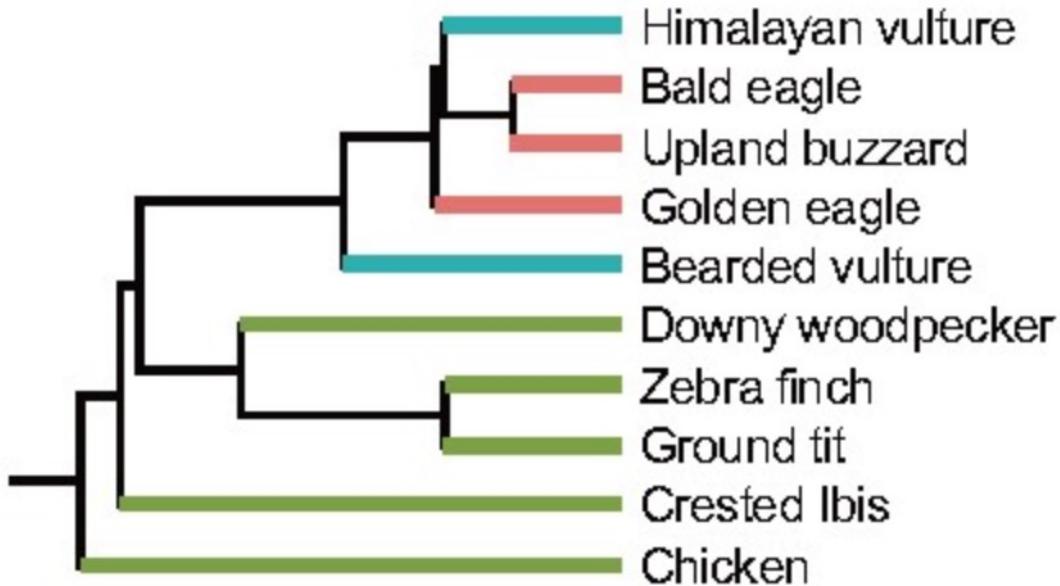
Selection (dN/dS)



Vulture Genomes Reveal Molecular Adaptations Underlying Obligate Scavenging and Low Levels of Genetic Diversity

Dahu Zou,¹ Shilin Tian,¹ Tongzuo Zhang,² Nima Zhuoma,³ Guosheng Wu,⁴ Muyang Wang,⁵ Lu Dong,⁶ Stephen J. Rossiter,⁷ and Huabin Zhao ^{ID*,1,3}

- Background
- Non-scavenger
- Facultative scavenger
- Obligate scavenger



Mutation Load

- Proportion of deleterious alleles and genotypes carrying these alleles at the genome-wide level

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Radical / Conservative substitution

ATT	<u>GAC</u>	TATTCC	<u>TGT</u>	TGGTTT	<u>GAA</u>	CCAGGC	<u>AGA</u>			
I	<u>D⁻</u>	Y	S	<u>C^N</u>	W	F	<u>E⁻</u>	P	G	<u>R⁺</u>

ATT	<u>CAC</u>	TACTCC	<u>GGT</u>	TGGTTTC	<u>GCA</u>	CCAGGA	<u>AAA</u>			
I	<u>R⁺</u>	Y	S	<u>G^N</u>	W	F	<u>A^N</u>	P	G	<u>K⁺</u>

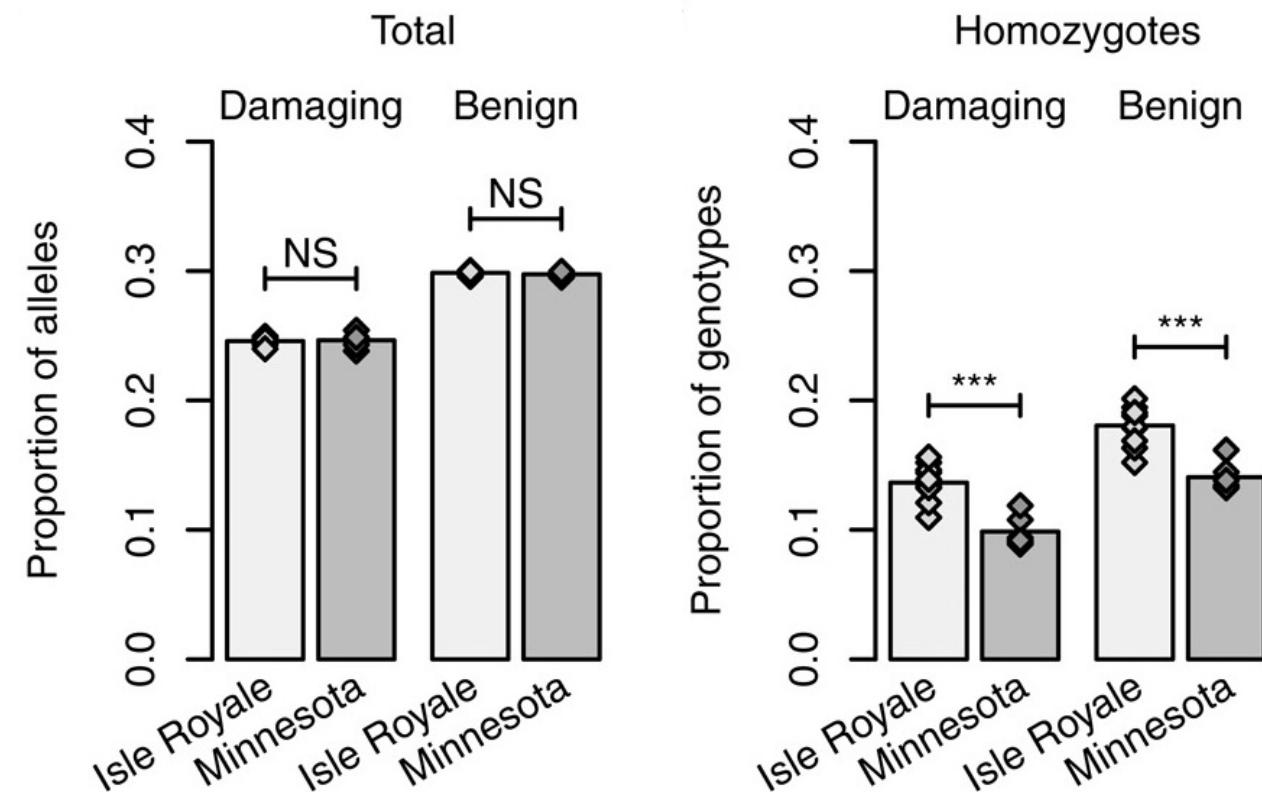
- + positive
- negative
- N neutral

Mutation Load

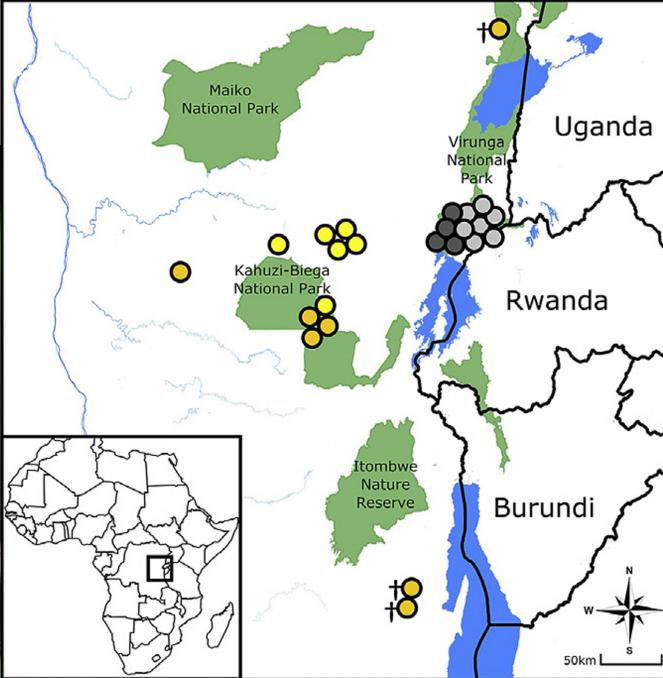


Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction

Jacqueline A. Robinson^{1*†}, Jannikke Räikkönen², Leah M. Vucetich³, John A. Vucetich³, Rolf O. Peterson³, Kirk E. Lohmueller^{1,4,5‡}, Robert K. Wayne^{1‡}



Mutation Load

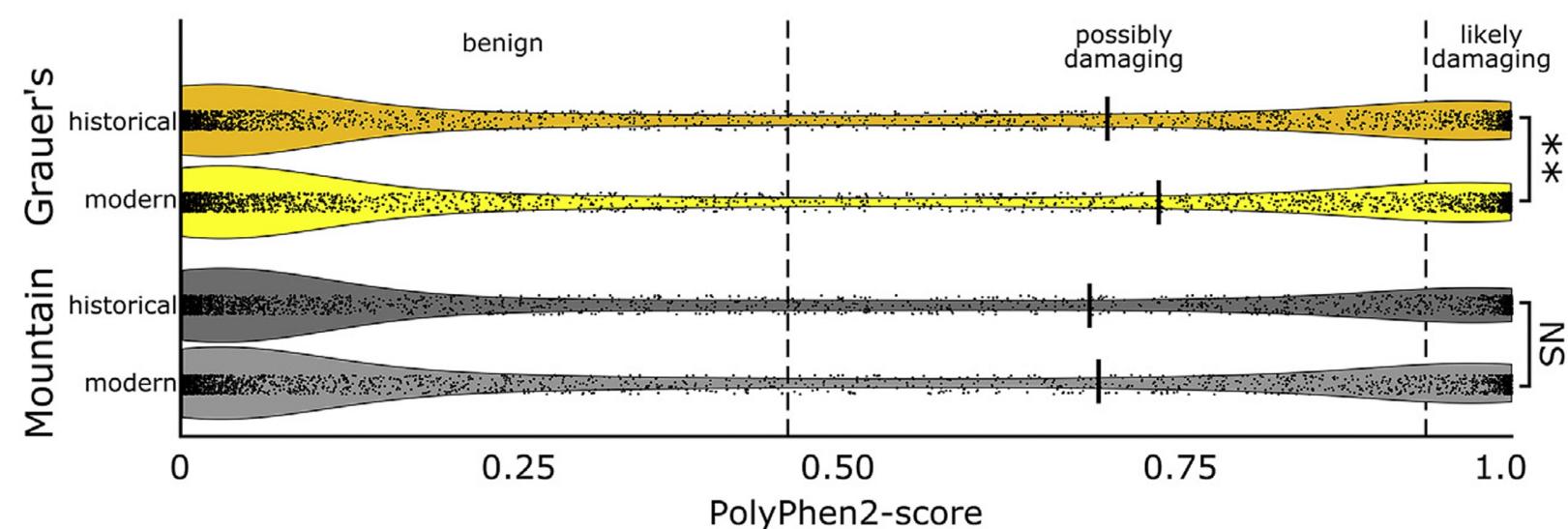
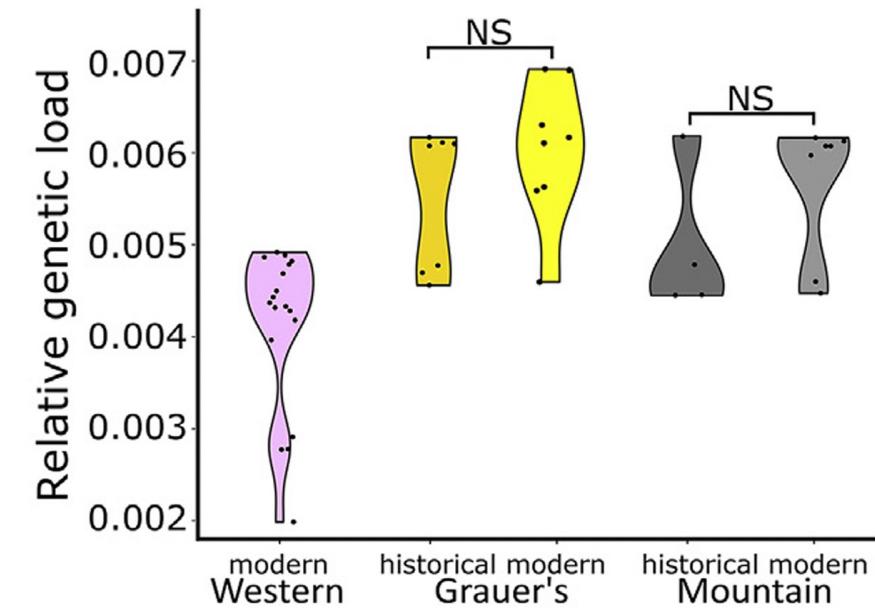


Current Biology

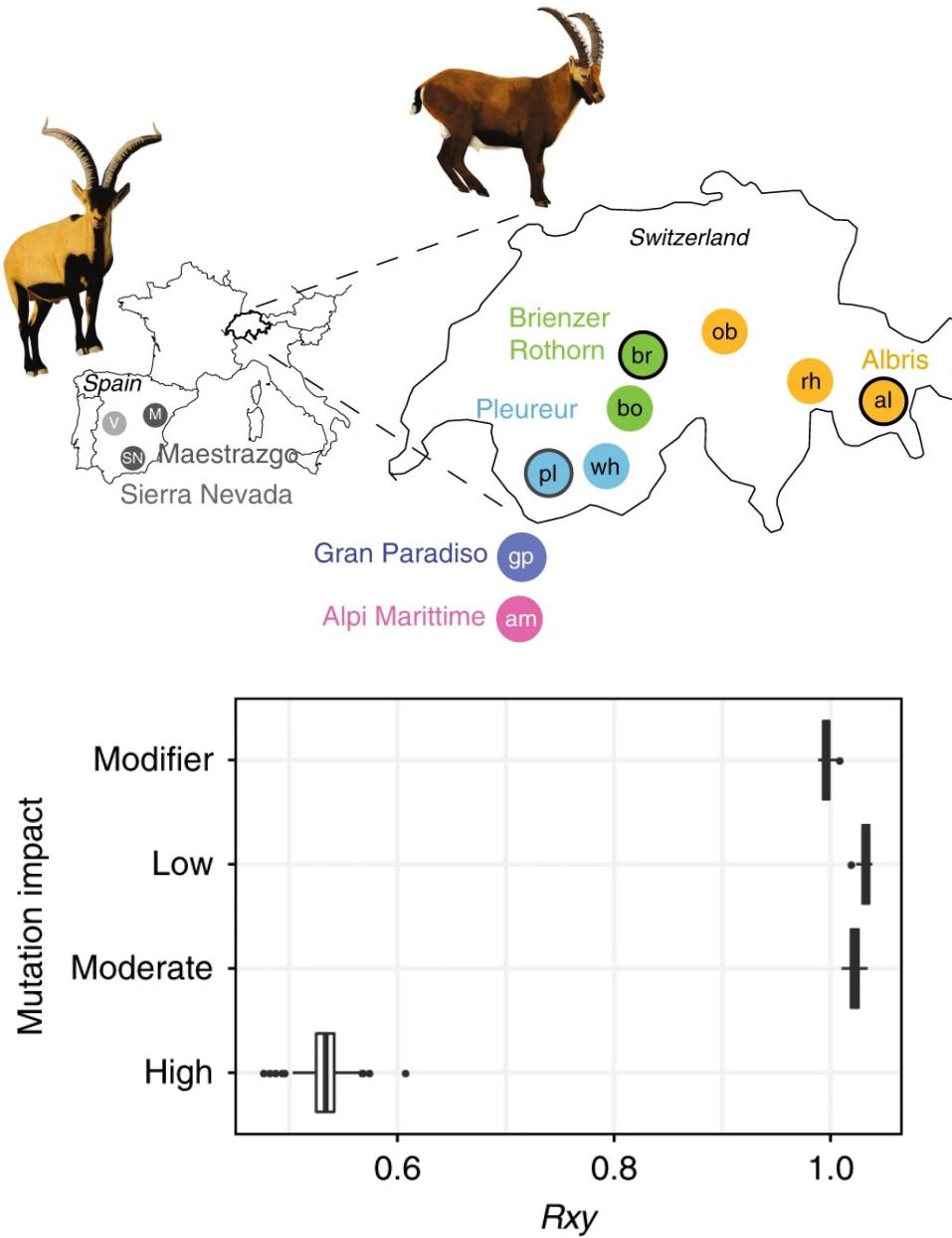
Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas

Authors

Tom van der Valk,
David Díez-del-Molino,
Tomas Marques-Bonet,
Katerina Guschanski, Love Dalén



Mutation Load



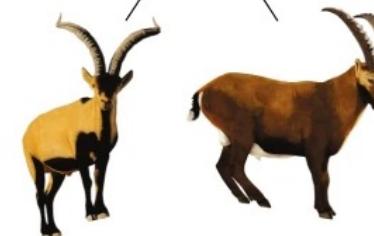
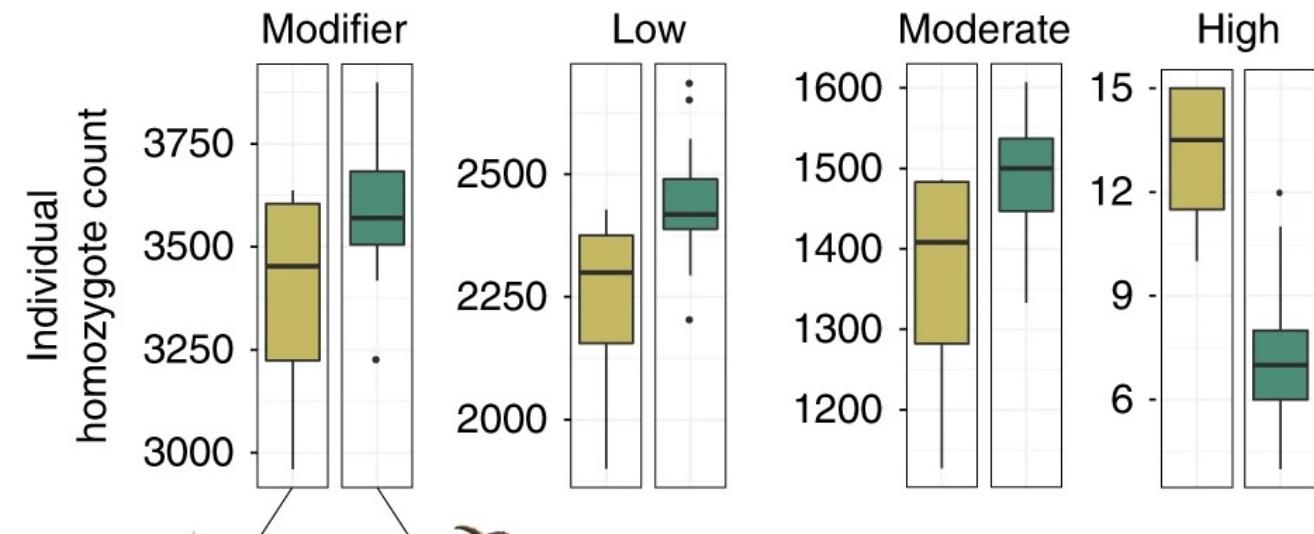
ARTICLE

<https://doi.org/10.1038/s41467-020-14803-1>

OPEN

Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex

Christine Grossen¹ , Frédéric Guillaume¹, Lukas F. Keller^{1,2} & Daniel Croll³



Mutation Load

MOLECULAR ECOLOGY

Molecular Ecology (2016) 25, 1429–1448

doi: 10.1111/mec.13559

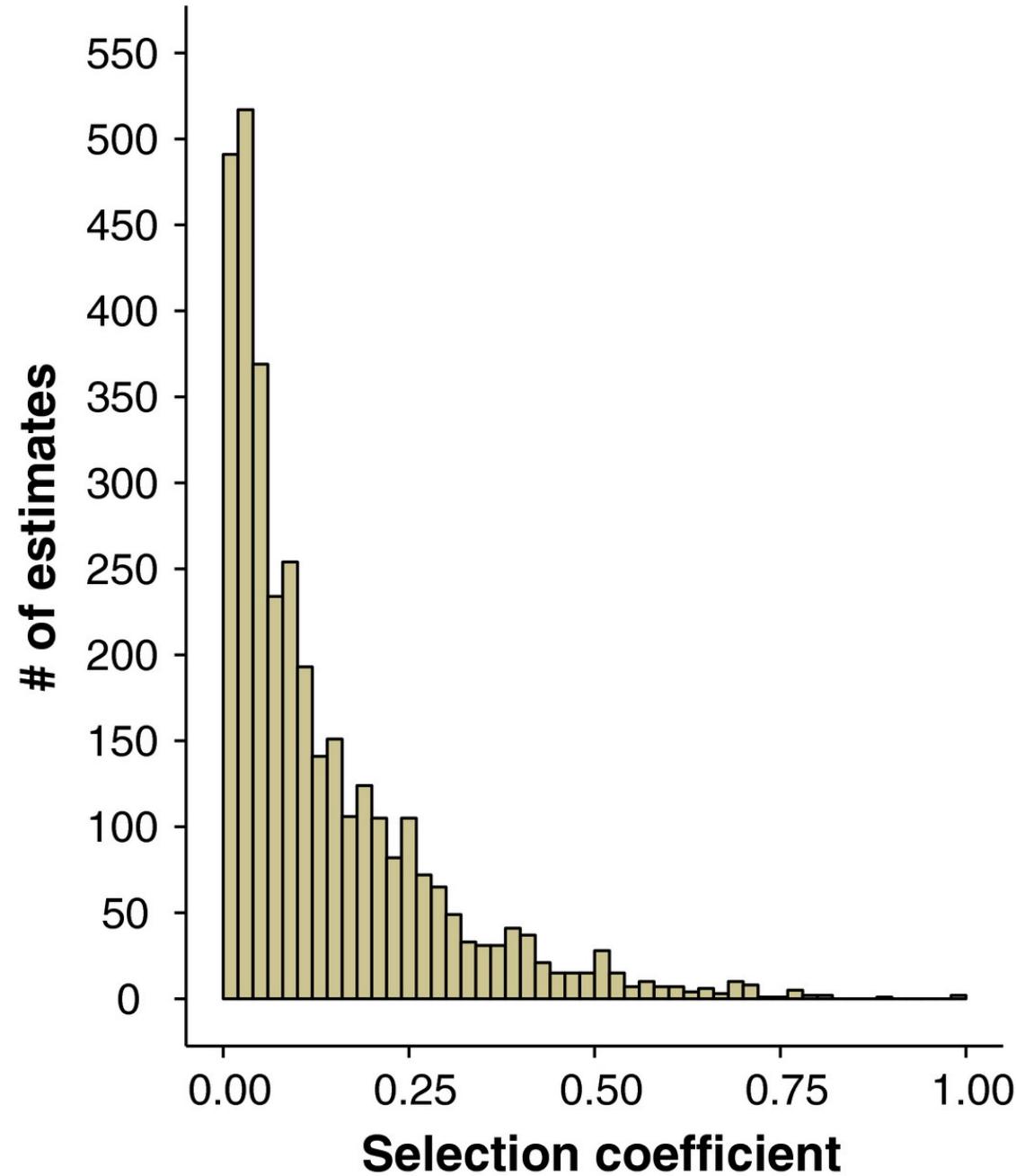
INVITED REVIEWS AND SYNTHESES

The genetic consequences of selection in natural populations

TIMOTHY J. THURMAN*† and ROWAN D. H. BARRETT*

*Redpath Museum and Department of Biology, McGill University, Sherbrooke Street West, Montreal, Quebec, Canada H3A 1B1,

†Smithsonian Tropical Research Institute, Panamá, Panamá



Mutation Load

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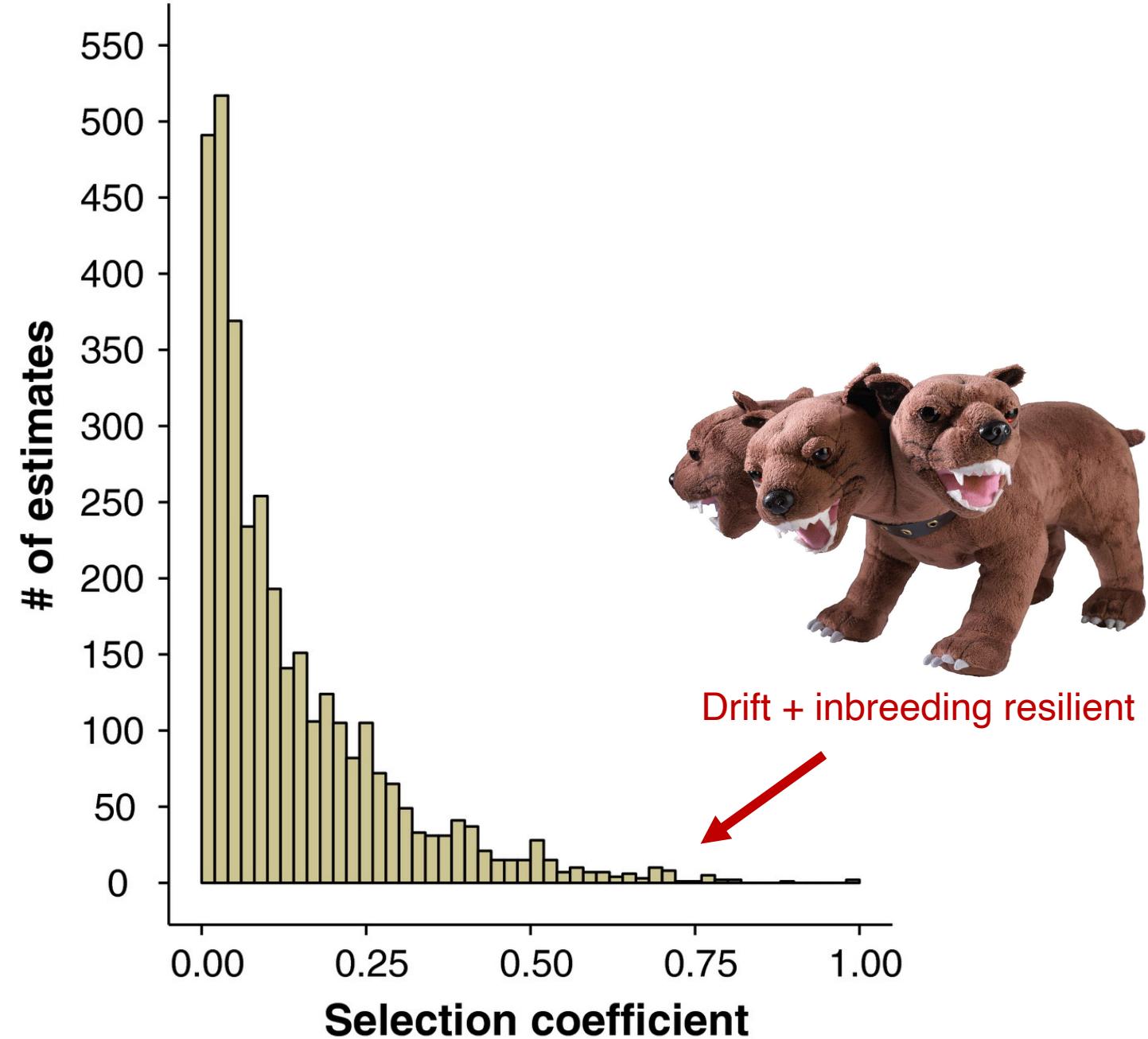
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Drift + inbreeding resilient

Mutation Load

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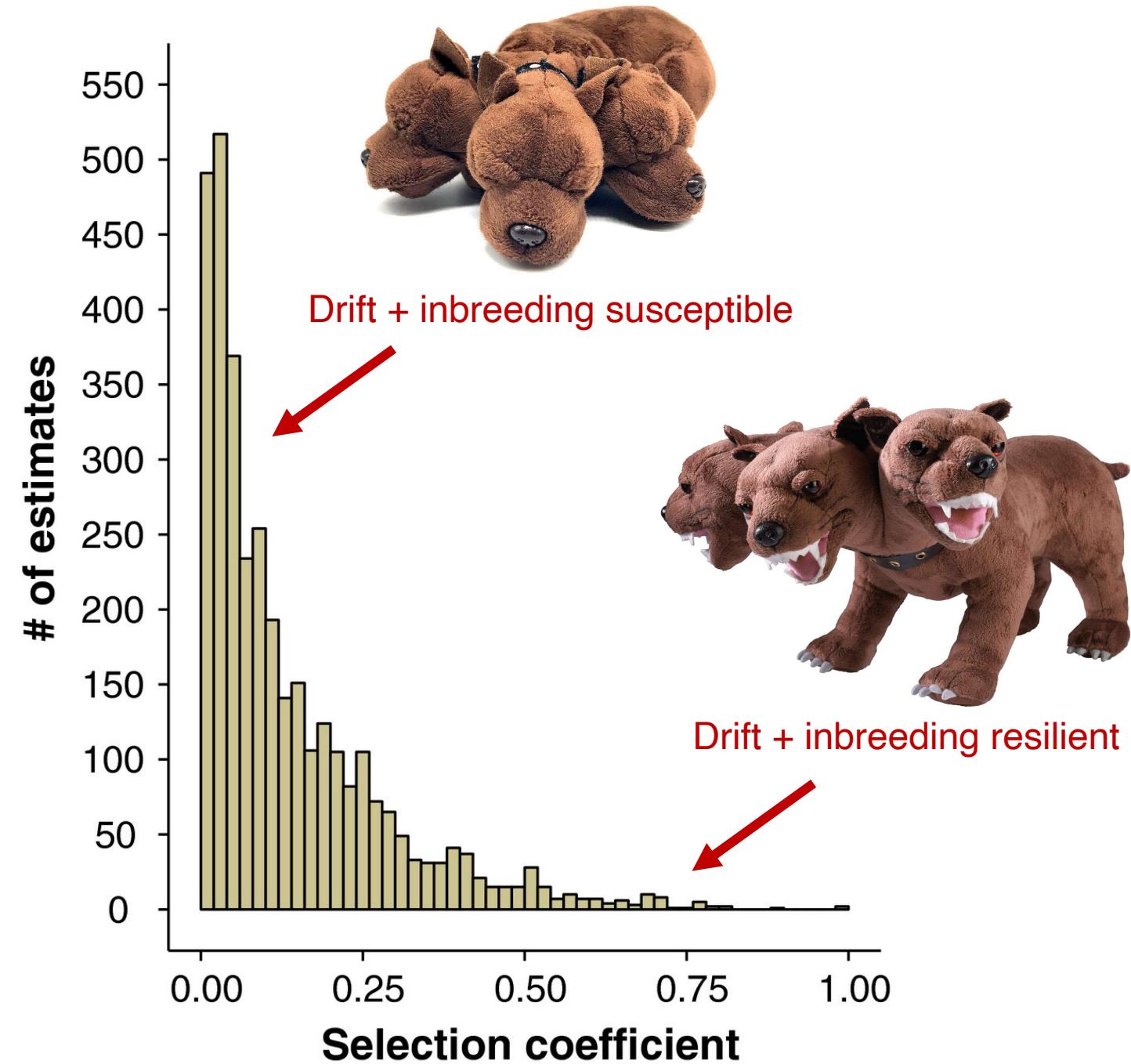
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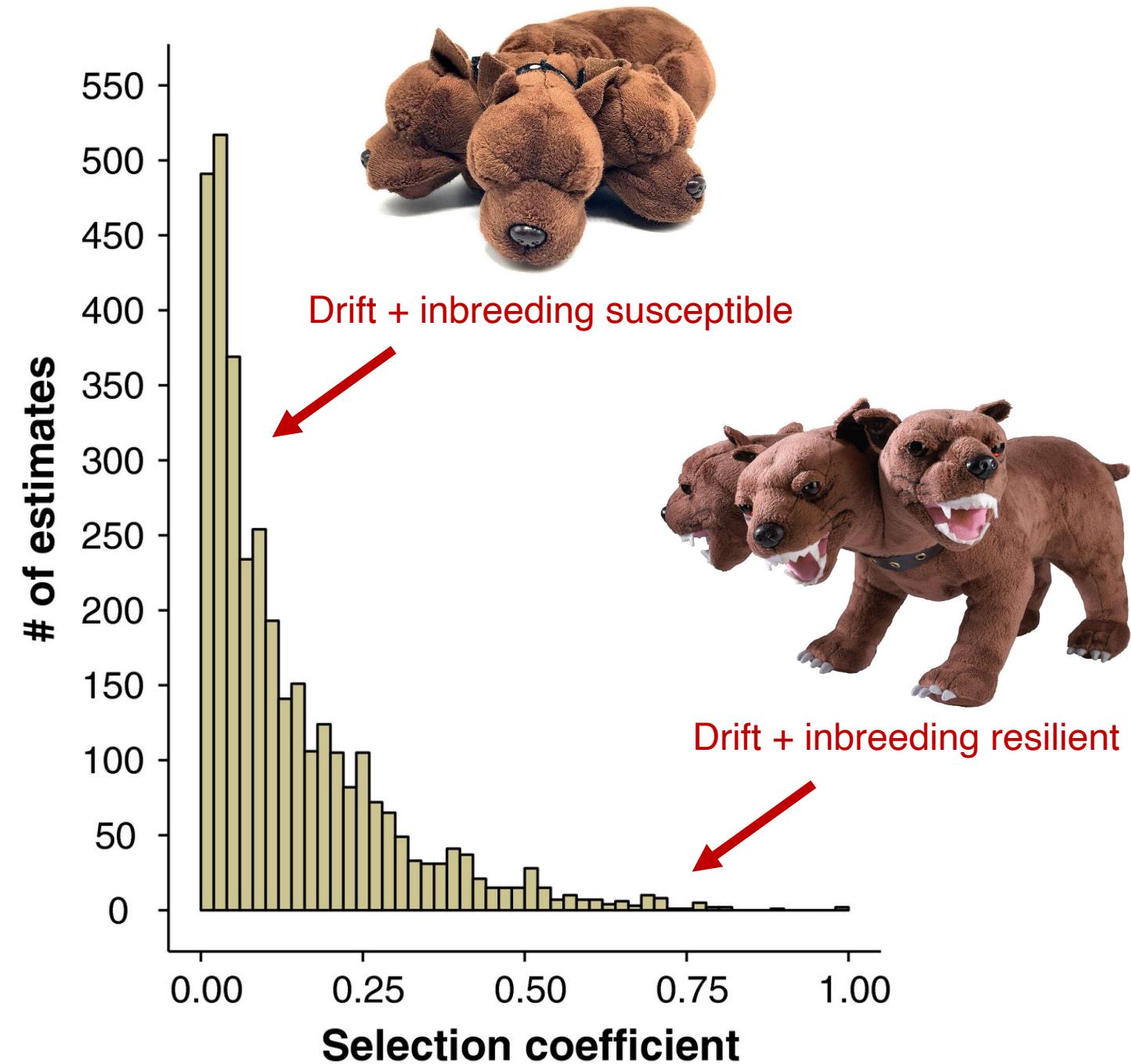
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Mutation Load



American Genetic Association

Journal of Heredity

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Advance access publication 5 August 2022
Original Article



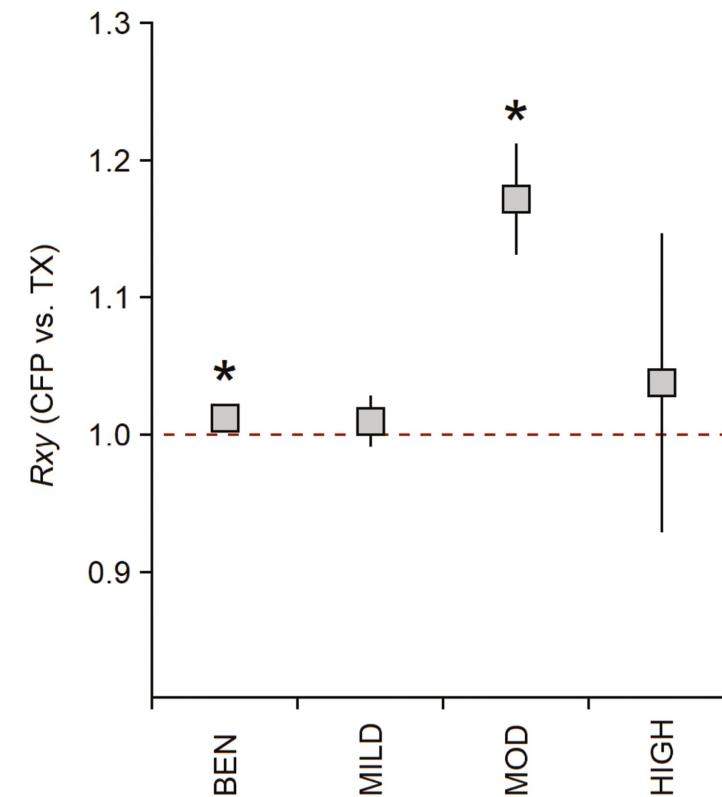
American
Genetic
Association

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Original Article

Give and Take: Effects of Genetic Admixture on Mutation Load in Endangered Florida Panthers

Alexander Ochoa^{1, ID}, David P. Onorato^{2, ID}, Melody E. Roelke-Parker^{3, ID}, Melanie Culver^{4, ID}, Robert R. Fitak^{1, ID}



Final Thoughts

- In small populations drift could erode deleterious variation, while inbreeding may expose a mosaic of deleterious traits that could be purged by selection
- Is the risk worth it?

