

Natural Selection

Natural selection in population genetics

Selection is differential survival and reproductive success with respect to phenotype.

- ▶ At the population level, when individuals with certain heritable phenotypes are able to survive and produce more offspring than individuals with other phenotypes, then natural selection has occurred.
- ▶ When the phenotype is determined entirely by the genotype at a single locus, we can assign particular levels of lifetime reproductive success to each genotype. In reality, phenotypes are usually affected by genotypes at multiple loci. For now, however, we will deal with the simpler single locus case.

Example of viability selection

- ▶ Alleles: A_1 and A_2
- ▶ Frequencies: $p = 0.5$ and $q = 0.5$
- ▶ Genotypes: A_1A_1 , A_1A_2 , and A_2A_2

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Zygote stage (before selection): $N = 1000$

Genotype	A_1A_1	A_1A_2	A_2A_2
Individuals	250	500	250
Frequencies	0.25	0.50	0.25

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Adult stage (after selection): $N = 700$

Genotype	A_1A_1	A_1A_2	A_2A_2
Prob. survival (λ)	1.00	0.70	0.40
Surviving to reproduce	250	350	100

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Allele counts after selection: call them p' and q'

$$\text{Total } A_1 \text{ alleles: } = (2 \times 250) + (1 \times 350) = 850$$

$$\text{Total } A_2 \text{ alleles: } = (2 \times 100) + (1 \times 350) = 550$$

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Allele frequencies after selection

$$\Pr(A_1): = p' = 850/1400 = 0.607$$

$$\Pr(A_2): = q' = 550/1400 = 0.393$$

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No longer in HWE ($N = 700$)

Genotype	A_1A_1	A_1A_2	A_2A_2
Prob. survival (λ)	1.00	0.70	0.40
Surviving to reproduce	250	350	100
Observed Frequency	250/700 0.357	350/700 0.500	100/700 0.143
Expected Frequency	p'^2 0.368	$2p'q'$ 0.477	q'^2 0.154

General Viability Selection Model (GSM)

- ▶ Mathematical treatment of HWE incorporating differential survival of genotypes (selection)
- ▶ Using the GSM, can predict changes in gene frequency from one generation to the next given specific survival (s)
- ▶ Can predict genotypic survival given change in allele frequencies

The peppered moth: *Biston betularia*

- ▶ Two forms: Light and Dark
- ▶ Light more common because it mimics lichen (black preyed upon)
- ▶ 1848-1898: Industrial Revolution
- ▶ Soot from factories turns bark from light to dark
- ▶ Dark form better camouflaged
- ▶ Melanic allele increases from 0.01 to 0.9



¹Image: Siga, CC BY-SA 4.0 (image cropped).

Peppered moth General Selection Model (GSM)

Genotypes	CC	Cc	cc
Freq.	p^2	$2pq$	q^2
Pr. Survival	λ_0	$\lambda_0 = \lambda_1$	λ_2

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Freq.	p^2	$2pq$	q^2
Pr. Survival	λ_0	$\lambda_0 = \lambda_1$	λ_2
Relative fitness	$w_0 = \frac{\lambda_0}{\lambda_0}$ 1	$w_1 = \frac{\lambda_1}{\lambda_0}$ 1	$w_2 = \frac{\lambda_2}{\lambda_0}$ $1 - s_2$

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Genotype ratios	$p^2 w_0$ p^2	$2pq w_1$ $2pq$	$q^2 w_2$ $q^2(1 - s_2)$

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Genotype ratios	$p^2 w_0$ p^2	$2pq w_1$ $2pq$	$q^2 w_2$ $q^2(1 - s_2)$
New freq.	$\frac{p^2}{\bar{w}}$	$\frac{2pq}{\bar{w}}$	$\frac{q^2(1-s_2)}{\bar{w}}$

Note mean fitness: $\bar{w} = p^2 + 2pq + q^2(1 - s_2)$

GSM adapted to different modes of inheritance and selection

Selection		AA	Aa	aa	Constraint
Directional	Dominant	$1 - s_0$	$1 - s_0$	1	$s_0 = s_1$
		1	1	$1 - s_2$	
	Codominant	1	$1 - s_1$	$1 - s_1$	$s_1 = \frac{1}{2}s_2$
		$1 - s_0$	$1 - s_1$	1	$s_1 = \frac{1}{2}s_0$
Disruptive	Het. Dis.	1	$1 - s_1$	1	
Stabilising	Het. Adv.	$1 - s_0$	1	$1 - s_2$	
Freq. Dep.		$1 + s_0 p^2$	1	$1 + s_2 q^2$	Pos.
		$1 - s_0 p^2$	1	$1 - s_2 q^2$	Neg.