

Frequency of **genotypes** after selection

TABLE 3.4 The frequency of genotypes before and after selection, assuming Hardy–Weinberg proportions before selection.

	<i>Genotype</i>			<i>Total</i>
	A_1A_1	A_1A_2	A_2A_2	
Relative fitness	w_{11}	w_{12}	w_{22}	—
Frequency before selection	p_0^2	$2p_0q_0$	q_0^2	1
Weighted contribution	$p_0^2w_{11}$	$2p_0q_0w_{12}$	$q_0^2w_{22}$	\bar{w}
Frequency after selection	$\frac{p_0^2w_{11}}{\bar{w}}$	$\frac{2p_0q_0w_{12}}{\bar{w}}$	$\frac{q_0^2w_{22}}{\bar{w}}$	1

Lecture Handout 8

mean fitness

Frequency is unity before and after selection

Frequency of **alleles** after selection...

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Frequency after selection	$\frac{p_0^2w_{11}}{\bar{w}}$	$\frac{2p_0q_0w_{12}}{\bar{w}}$	$\frac{q_0^2w_{22}}{\bar{w}}$	1

...depends on allele frequency before selection and relative fitness of genotypes

$$\begin{aligned}
 q_1 &= \frac{1}{2} \left(\frac{2p_0q_0w_{12}}{\bar{w}} \right) + \frac{q_0^2w_{22}}{\bar{w}} \\
 &= \frac{p_0q_0w_{12} + q_0^2w_{22}}{\bar{w}}
 \end{aligned}$$

Amount of **allele** frequency change

$$\Delta q = q_1 - q_0$$

See Hedrick page 121 for derivation:

$$\Delta q =$$

$$\frac{pq[q(w_{22} - w_{12}) - p(w_{11} - w_{12})]}{\bar{w}}$$

Amount of **allele** frequency change

$$\Delta q =$$

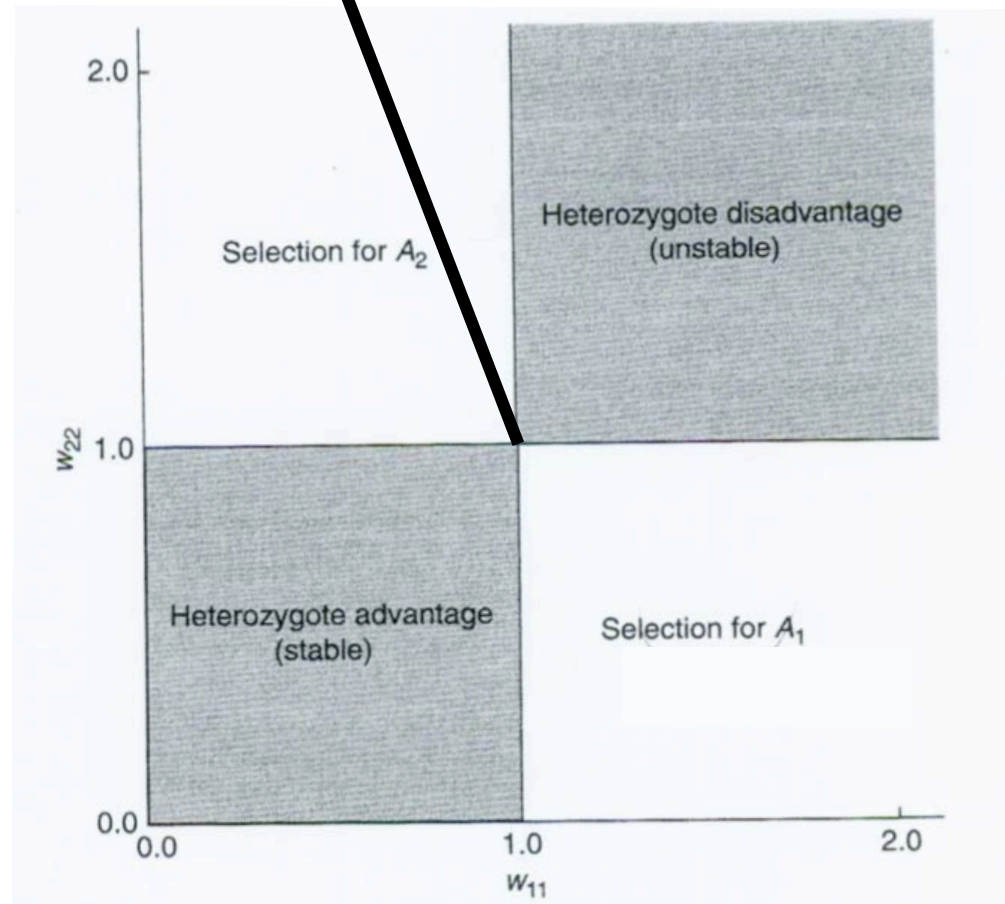
$$\frac{pq[q(w_{22} - w_{12}) - p(w_{11} - w_{12})]}{\bar{w}}$$

Fitness difference
between genotypes

Weighted by
allele frequencies

So change in allele frequency is a function of allele frequencies, mean fitness, and change in mean fitness with respect to allele frequency.

Point at which all genotypes (both homozygotes and the heterozygote) have the same relative fitness.



Two new parameters:

- Selection coefficient, s** , measures the amount of selection against a homozygote

- The level of **dominance, h** , when multiplied by **s** measures the amount of selection against the heterozygote

Specific fitness relationships

TABLE 3.5 The fitness values for the different fitness relationships examined.

	<i>Genotype</i>		
	A_1A_1	A_1A_2	A_2A_2
General fitnesses	w_{11}	w_{12}	w_{22}
(a) Recessive lethal	1	1	0
(b) Detrimental alleles			
(1) Recessive	1	1	$1 - s$
(2) Additive	1	$1 - s/2$	$1 - s$
(3) Dominant	1	$1 - s$	$1 - s$
(c) General dominance			
(1) Purifying selection	1	$1 - hs$	$1 - s$
(2) Adaptive Darwinian selection	$1 + s$	$1 + hs$	1
(d) Heterozygote advantage	$1 - s_1$	1	$1 - s_2$
(e) Heterozygote disadvantage	$1 + s_1$	1	$1 + s_2$

Lethal recessive

$$q_1 = q_0 / 1 + q_0$$

This relationship is recursive across generations:

$$q_t = q_0 / 1 + tq_0$$

Lethal recessive

TABLE 3.6 The number of generations (t) needed to reduce the allele frequency from an initial value of q_0 to q_t for a recessive lethal.

q_0	q_t	t
0.5	0.25	2
	0.1	8
	0.01	98
0.1	0.05	10
	0.01	90
	0.001	990
0.01	0.005	100
	0.001	900
	0.0001	9900

Detrimental or deleterious recessive allele

A_2A_2 is less fit by s than A_1A_1 or A_1A_2

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s is the selective disadvantage or selection coefficient of the homozygote; maximum value of $s = 1$, for a lethal homozygote

Detrimental or deleterious recessive allele

Frequency after selection:

$$q_1 = \frac{q_0(1 - sq_0)}{1 - sq_0^2}$$

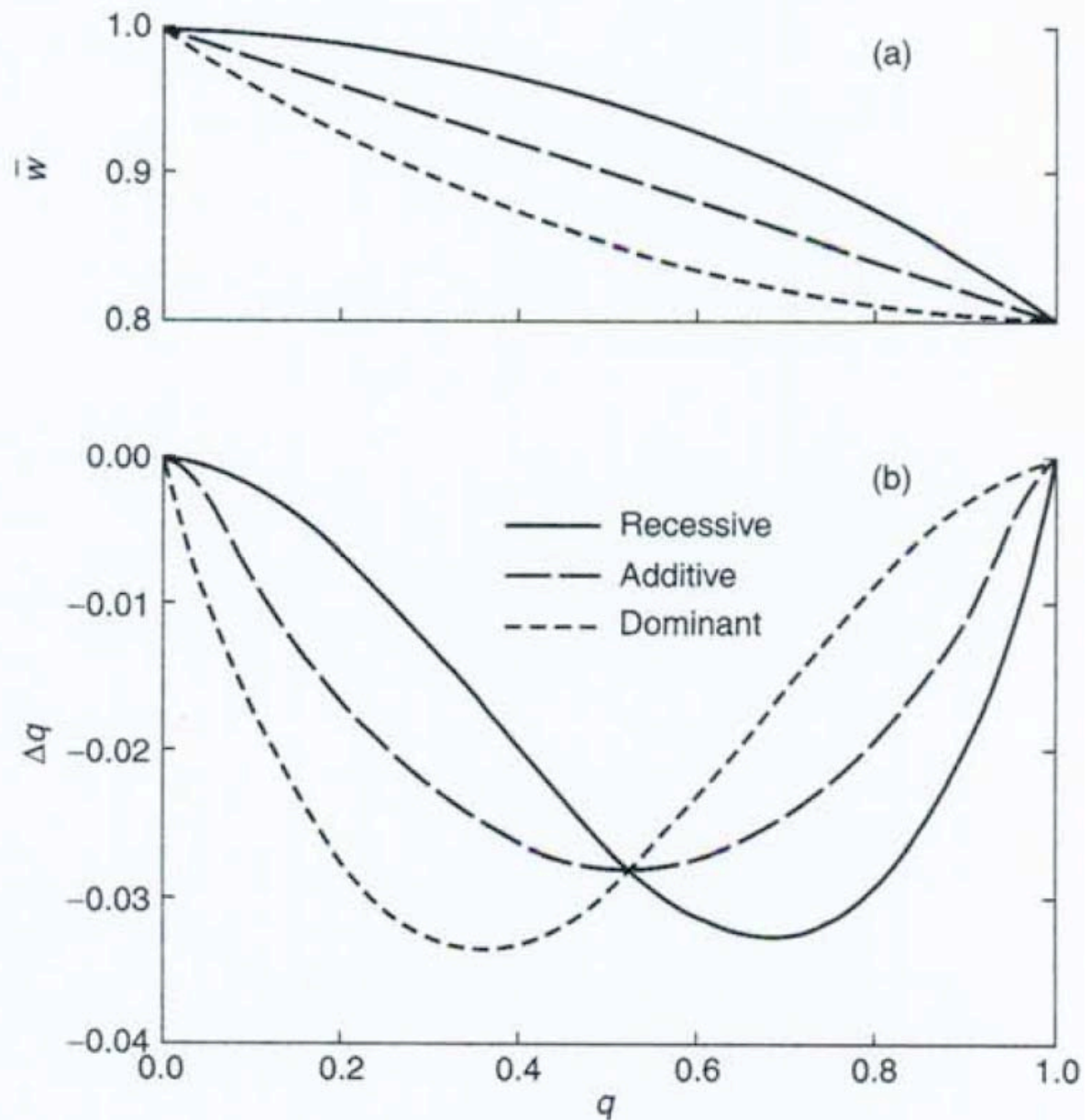
Change in frequency:

$$\Delta q = -\frac{sq^2(1 - q)}{1 - sq^2}$$

Fisher's fundamental theorem of natural selection (1930):

"The rate of increase in fitness of any organism at any time is equal to its genetic variance in fitness at that time."

Mean fitness
(top) and drop in
allele frequency
(bottom) at
different
frequencies of q
(where q is
recessive,
additive or
dominant) when
 $s = 0.2$



Specific fitness relationships

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Additivity or additive gene action: heterozygote is midway between the 2 homozygotes

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A_1A_2 is less fit by $s/2$ than A_1A_1

Additivity or additive gene action: heterozygote is midway between the 2 homozygotes

Allele frequency after selection:

$$q_1 = \frac{q_0 \left[1 - \frac{s}{2}(1 + q_0) \right]}{1 - sq_0}$$

Change in the frequency of A_2 :

$$\Delta q = -\frac{sq(1 - q)}{2(1 - sq)}$$

TABLE 3.6 The number of generations (t) needed to reduce the allele frequency from an initial value of q_0 to q_t for a recessive lethal.

q_0	q_t	t
0.5	0.25	2
	0.1	8
	0.01	98
0.1	0.05	10
	0.01	90
	0.001	990
0.01	0.005	100
	0.001	900
	0.0001	9900

Detrimental recessive alleles are shielded from selection in the heterozygous state

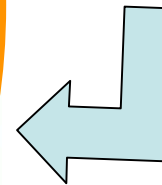
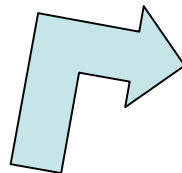


TABLE 3.7 The number of generations (t) needed to reduce the allele frequency from an initial value of q_0 to q_t for intermediate dominance (additivity) when $s = 0.1$.

q_0	q_t	t
0.9	0.5	44
	0.1	89
	0.01	136
0.5	0.25	22
	0.1	44
	0.01	92
0.1	0.05	15
	0.01	48
	0.001	194

Detrimental alleles are NOT shielded from selection in the heterozygous state under additivity



Selection example for additive allele:

Dark coat color in jaguarundi, *Herpailurus yaguarondi*, has spread at expense of wild type reddish color.



Selection example for additive allele:

Dark coat color in jaguarundi, *Herpailurus yaguarondi*, due to **indel** (insertion-deletion variant) in *MC1R* gene has spread at expense of wild type reddish color.

B	MC1R	274 (92)															324 (108)		
		V	L	E	T	A	V	M	L	L	L	E	A	G	A	L	A	G	
D.cat		GTG	<u>CTG</u>	<u>GAG</u>	ACG	GCC	GTC	ATG	CTG	CTG	<u>CTG</u>	<u>GAG</u>	GCA	GGC	GCC	<u>CTG</u>	GCC	GGC	
Jaguar-WT	G	...	A..	
Jaguar-Mel		---	---	---	---	---	AC	
Jaguarundi-Dark		---	---	---	---	---	---	---	---	A..	
Jaguarundi-Red		A..	
Dog		G..	T..	..T	.CG	
Pig	G	C..GC.	
Cattle	AC	..T	.T.	AC.	
Horse	T.	..A	A..	T..C	..A	.T.	AC.	
Human	C	..CC	..T	..ATG	.C.	

Selection against dominants

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A_1A_2 is less fit by s than A_1A_1

?

Selection against dominants

Allele frequency after selection:

$$q_1 = \frac{q_0(1 - s)}{1 - sq_0(2 - q_0)}$$

Change in the frequency of A_2 :

$$\Delta q = -\frac{sq(1 - q)^2}{1 - sq(2 - q)}$$