

Overview

- Hardy-Weinberg
- Relative fitness
- Directional selection:
 - In a haploid
 - In a diploid
- Mean fitness of a population

From the one-minute responses

- Connect concepts to homework more tightly
- TMRCA: generation time versus calendar time? How to convert?

TMRCA

- Coalescent theory predicts TMRCA in generations
- Time in years (calendar time):
 - Need generation time of organism to relate it to the coalescent
- Time in mutations (mutational distance):
 - To convert to years, need μ in mutations/year
 - To convert to generations, need μ in mutations/generation
 - Often used when we don't know μ at all and are just looking at mutations in sequences

Hardy-Weinberg Law

In a random-mating population with allele frequencies p (for A) and q (for a), we expect:

Genotype	Frequency
AA	p^2
Aa	$2pq$
aa	q^2

- Even if this isn't true among parents, it will be true among offspring (at conception)
- Called an equilibrium because frequencies go to H-W with 1 generation of random mating

What pushes a population out of H-W?

- Reasonably often:
 - Population subdivision
 - Natural selection
 - Non-random mating
 - Undetected null alleles
- Hardly ever:
 - Mutation
 - Genetic drift (unless population is tiny)

Undetected null alleles

The experimenter presented us with this, which is not in H-W:

aa	47%
ab	31%
bb	22%

On questioning, she admitted that she really observed this:

aa	450
ab	300
bb	210
test failed	40

Undetected null alleles

aa	450
ab	300
bb	210
test failed	40

What she probably has is this:

aa + ac	450
ab	300
bb + bc	210
cc	40

but she cannot detect allele *c*. (Could these be in H-W?)

When you can test H-W and when you can't

No problem (use a χ^2 test):

<i>AA</i>	84
<i>Aa</i>	12
<i>aa</i>	4
<hr/>	
Total	100

- Calculate the allele frequencies
- Calculate expected numbers
- Compute $\chi^2 = \sum (o - e)^2 / e$
- Compare to table (with 1 degree of freedom in this case)

When you can test H-W and when you can't

Not possible:

Brown eyes (BB or Bb)	96
Blue eyes (bb)	4

- Statistician's reason: no degrees of freedom left
- Layman's reason: we'd need to assume H-W to get the allele frequencies, but if we got them with H-W we can't use them to test H-W

Relative fitness

- Assume population size is constant despite selection
- Individual gene copies are competing for a fixed number of slots
- Selection coefficient is observed/expected
- Typically normalized so that the best genotype has fitness 1, or that “wild-type” has fitness 1

Nomenclature

I will use:

- w_A for the fitness of the A genotype in a haploid
- w_{AA} for the fitness of the AA genotype in a diploid

Practice problem

$p = 0.8$, $q = 0.2$ among gametes

Genotype	Observed	Expected	Fitness	Normalized Fitness
<i>AA</i>	80			
<i>Aa</i>	18			
<i>aa</i>	2			
Total	100			

Practice problem

$p = 0.8$, $q = 0.2$ among gametes

Genotype	Observed	Expected	Fitness	Normalized Fitness
<i>AA</i>	80	64	1.25	1.0
<i>Aa</i>	18	32	0.56	0.49
<i>aa</i>	2	4	0.50	0.40
Total	100	100		

Selection in a haploid

In one generation:

$p = 0.8$, $q = 0.2$ among gametes (or in previous generation's adults)

$w_A = 1.0$, $w_a = 0.7$

Genotype	At conception	After selection	Renormalize
A	0.8	0.8	0.85
a	0.2	0.14	0.15
Total	1.0	0.94	1.0

New allele frequencies:

$p = 0.85$, $q = 0.15$

Selection over time

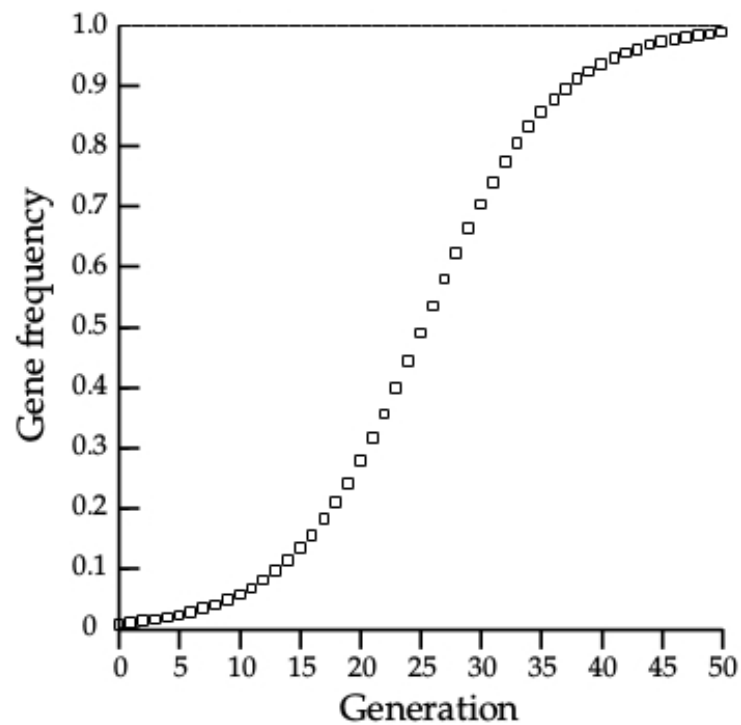


Figure 2.1: Course of gene frequency change in haploid selection with initial gene frequency $p_0 = 0.01$ and relative fitness 1.2 of the A genotype.

Selection in a diploid

$p = 0.8$, $q = 0.2$ among gametes (or in previous generation's adults)

$w_{AA} = 1.0$, $w_{Aa} = 0.9$, $w_{aa} = 0.8$

Genotype	At conception	After selection	Renormalize
AA	0.64	0.640	0.667
Aa	0.32	0.288	0.300
aa	0.04	0.032	0.033
Total	1.0	0.96	1.0

New allele frequencies:

$$p = AA + 1/2 Aa = 0.817$$

$$q = aa + 1/2 Aa = 0.183$$

The selection coefficient s

- Convenient to attach a number to these fitness differences
- Unfortunately this is done two different ways in the literature
- Haploid example:
 - Way 1: fitnesses are $1+s$ and 1
 - Way 2: fitnesses are 1 and $1-s$
 - These won't in general yield the same numeric s !
- If a study says "We estimated the selection coefficient" you will have to read the fine print to see what they did....
- I am going to use Way 2 everywhere

Specific fitness patterns

- Dominant/recessive: $1 : 1 : 1-s$
- Additive: $1 : 1-s : 1-2s$
- Multiplicative: $1 : 1-s : (1-s)^2$

Intuitively I'd expect additive to be the same as haploid. In fact, multiplicative is the same as haploid. Why?

Selection over time

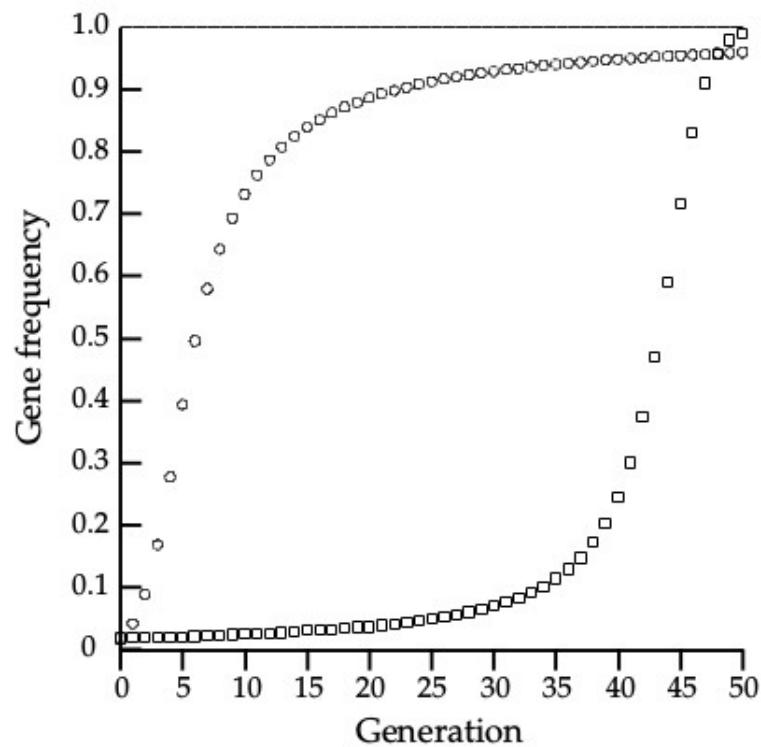


Figure 2.3: The course of gene frequency change over 50 generations when fitnesses of AA , Aa , and aa are 2.3 : 2.3 : 1 (circles) and 2.3 : 1 : 1 (squares). Initial frequency of A is 0.02.

Theory fits experiment

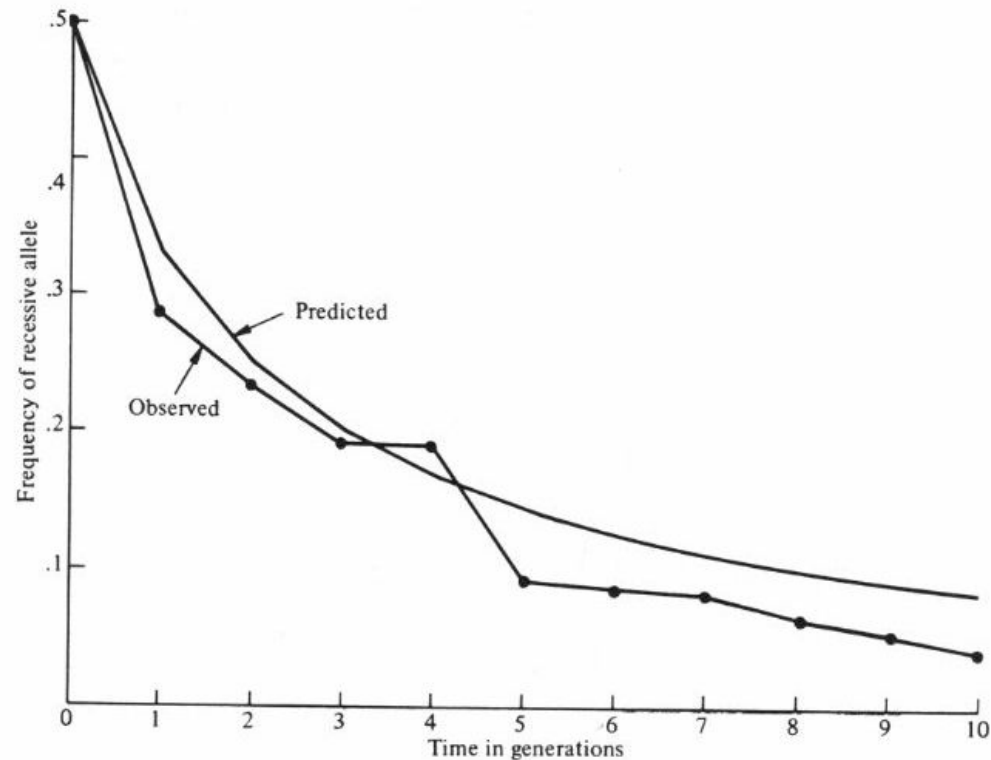
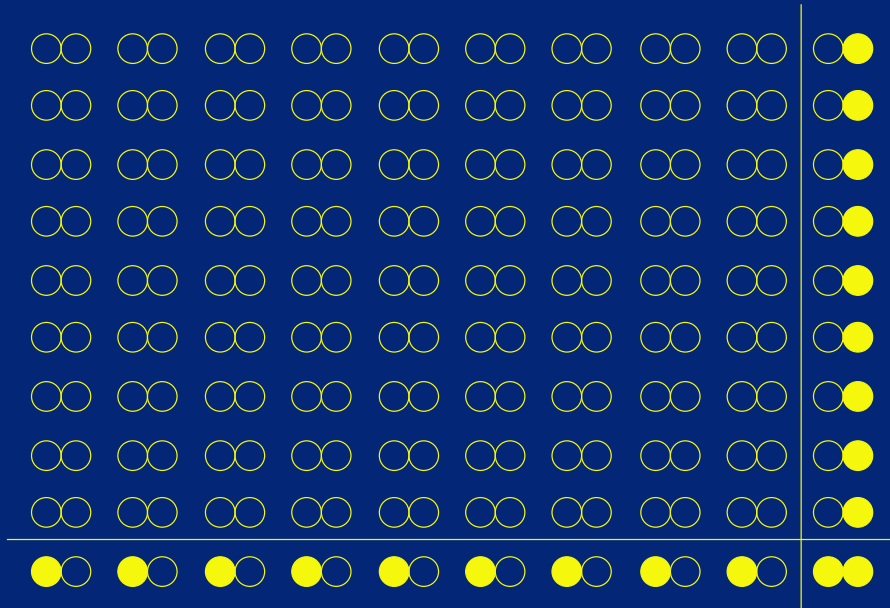


FIGURE 3.4. Experiment illustrating selection against a recessive lethal gene. The frequency of the recessive allele is on the vertical axis, time in generations is on the horizontal axis. [Data from B. Wallace (1963), The elimination of an autosomal lethal from an experimental population of *Drosophila melanogaster*, *Amer. Natur.* **97**: 65–66.]

Rare alleles occur mostly in heterozygotes



This shows a population in Hardy–Weinberg equilibrium
at gene frequencies of 0.9 A : 0.1 a

Genotype frequencies:

0.81 AA : 0.18 Aa : 0.01 aa

Note that of the 20 copies of a,

18 of them, or $18 / 20 = 0.9$ of them are in Aa genotypes

Mean fitness of a population

- Genotype fitnesses weighted by genotype frequencies (before selection):
- $W = w_{AA} \times p^2 + w_{Aa} \times 2pq + w_{aa} \times q^2$
- In the cases we have considered, this increases over time under the influence of selection

Summary

- Hardy-Weinberg gives us a prediction for the frequencies of the genotypes in a random-mating population before selection
- Relative fitness is the excess or deficit of a genotype after selection has happened
- Combine the two to predict change in allele frequencies
- In diploids, the shape of the frequency curve depends on dominance

Friday

- Overdominance (heterozygote advantage)
- Underdominance (heterozygote disadvantage)
- Local optimization misses the global optimum

One-minute responses

- Please:
 - Tear off a slip of paper
 - Give me one comment or question on something that worked, didn't work, needs elaboration, etc.