

Bio 112 Handout for Evolution 4

This handout contains:

- Today's iClicker Question
- Figures for today's lecture

iClicker Question #1 - after lecture

Which of the following statements are false:

- A. If the genotype frequencies of a population in nature match those expected at HWE, the population is at HWE.
- B. After one generation where all 5 conditions for HWE are met, the population will be at HWE.
- C. If a small sample of a starting population that was at HWE founds a new population, that new population will always be at HWE.
- D. More than one is false.
- E. All are true.

Beaming in your answers

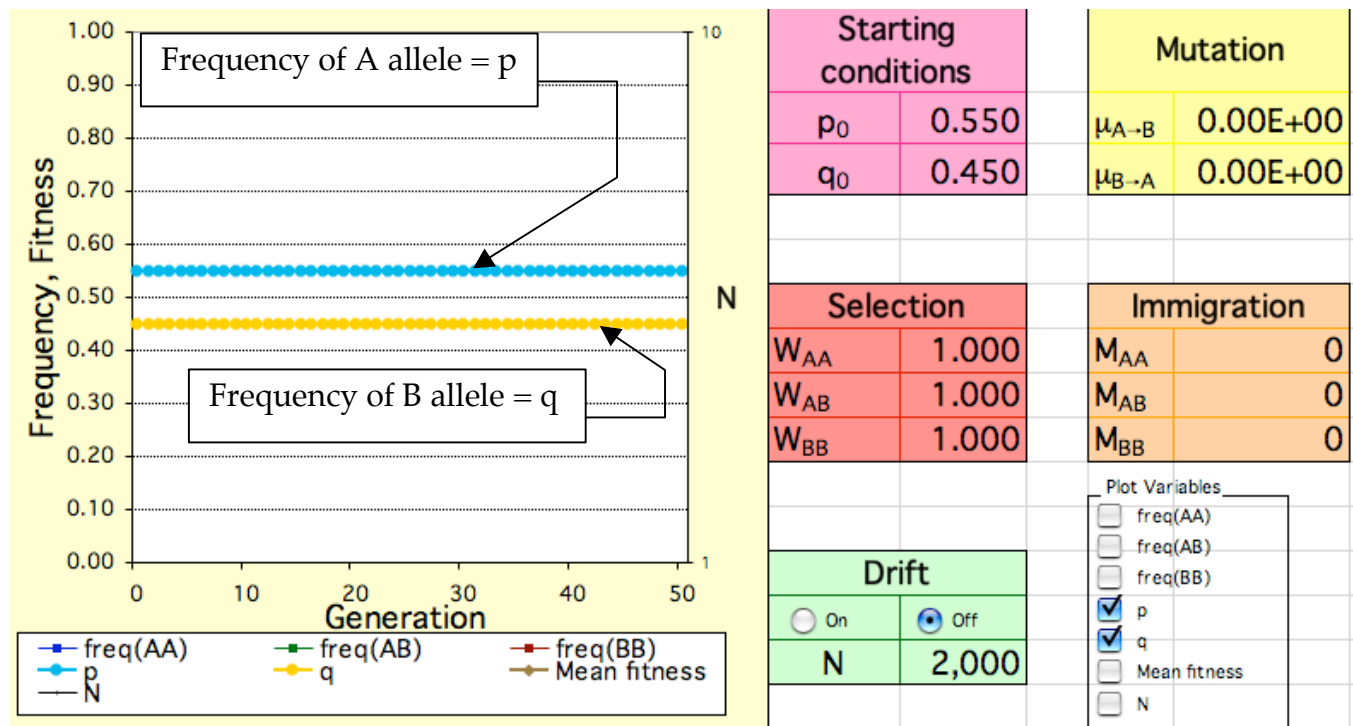
1. Figure out your answer and select the appropriate letter (A-E).
2. Turn on your iClicker by pressing the "ON/OFF" button; the blue "POWER" light should come on. If the red "LOW BATTERY" light comes on, you should replace your batteries soon.
3. Transmit your answer as follows:
 - a. Press the button corresponding to the answer you've selected (A thru E).
 - b. The "STATUS" light will flash green to indicate that your answer has been received. If the "STATUS" light flashed red, your answer was not received; you should re-send it until you get a green "STATUS" light.

Hardy-Weinberg Simulations

Deme 1.0 is a Microsoft Excel spreadsheet available on the course website.

The simplest case:

- large population (Drift OFF)
- no mutation (rates = 0)
- no migration (immigration = 0)
- random mating
- no selection (all fitnesses = 1)



Since all 5 HWE conditions hold, the population is at HWE “forever”
 - allele frequencies stay the SAME in all generations

Uses of HWE (1): Human Genetic Traits

Example: attached/detached earlobes (model for genetic disease)



Attached Earlobe



Unattached Earlobe

Are your earlobes attached or unattached? A person with attached ear lobes will have the lowest point of the ear lobe attached to the face. A person with unattached ear lobes will not have the lowest point of the ear lobe attached to the face.

<u>allele</u>	<u>contribution to phenotype</u>	<u>frequency</u>
E	unattached earlobe (dominant)	p
e	attached earlobe (recessive)	q

<u>Genotype</u>	<u>Phenotype</u>
EE	unattached
Ee	unattached
ee	attached

Q: How many people in class are carriers for the attached allele?

Assume that this trait is at HWE.

Bio 112: Hardy-Weinberg Equilibrium Examples

General Info

- Allele frequencies: the frequency of each allele (R or r, for example) in the gene pool. The symbols p and q are used to represent these frequencies.
- Genotype frequencies: the frequency of each genotype (RR, Rr, rr for example) in the population. These are always equal to the number of individuals with a particular genotype divided by the total population size. They are sometimes equal to p^2 , $2pq$, and q^2 - only when the population is at HWE.

For a particular pair of allele frequencies ($p = 0.2$ and $q = 0.8$ for example), there are many possible sets of genotype frequencies that have the same allele frequencies (actually, infinitely many). This is illustrated by the 4 example populations below; all 4 of these populations have the same allele frequencies. However, given a pair of allele frequencies, there is only one set of these genotype frequencies that are at HWE. This is illustrated by the last two populations shown below; in addition to having the same allele frequencies as the other populations, their genotype frequencies match the predictions of HWE - that the frequency of RR = p^2 (0.04 in this example), the frequency of Rr = $2pq$ (0.32 in this example), and the frequency of rr = q^2 (0.64 in this example).

Population 1

<u>Genotype</u>	<u>#</u>	<u>Genotype frequency</u>	<u>#R's contributed to gene pool</u>	<u>#r's contributed to gene pool</u>
RR	0	0	0	0
Rr	40	0.40	40	40
rr	60	0.60	0	120
<u>totals</u>			40	160

Allele frequencies

Freq. of R = $p = 40/200 = 0.2$

Freq. of r = $q = 160/200 = 0.8$

Genotype frequencies

Freq. of RR = 0, not 0.04

Freq. of Rr = 0.4, not 0.32

Freq. of rr = 0.6, not 0.64

NOT AT HWE

Population 2

<u>Genotype</u>	<u>#</u>	<u>Genotype frequency</u>	<u>#R's contributed to gene pool</u>	<u>#r's contributed to gene pool</u>
RR	400	0.20	800	0
Rr	0	0.00	0	0
rr	1600	0.80	0	3200
<u>totals</u>			800	3200

Allele frequencies

Freq. of R = $p = 800/4000 = 0.2$

Freq. of r = $q = 3200/4000 = 0.8$

Genotype frequencies

Freq. of RR = 0.2, not 0.04

Freq. of Rr = 0.0, not 0.32

Freq. of rr = 0.8, not 0.64

NOT AT HWE

Population 3

<u>Genotype</u>	<u>#</u>	<u>Genotype frequency</u>	<u>#R's contributed to gene pool</u>	<u>#r's contributed to gene pool</u>
RR	4	0.04	8	0
Rr	32	0.32	32	32
rr	64	0.64	0	128
		<u>totals</u>	40	160

Allele frequencies

Freq. of R = $p = 40/200 = 0.2$

Freq. of r = $q = 160/200 = 0.8$

Genotype frequencies

Freq. of RR = 0.04

Freq. of Rr = 0.32

Freq. of rr = 0.64

AT HWE

Population 4

<u>Genotype</u>	<u>#</u>	<u>Genotype frequency</u>	<u>#R's contributed to gene pool</u>	<u>#r's contributed to gene pool</u>
RR	12	0.04	24	0
Rr	96	0.32	96	96
rr	192	0.64	0	384
		<u>totals</u>	120	480

Allele frequencies

Freq. of R = $p = 120/600 = 0.2$

Freq. of r = $q = 480/600 = 0.8$

Genotype frequencies

Freq. of RR = 0.04

Freq. of Rr = 0.32

Freq. of rr = 0.64

AT HWE

