Bio 112 Handout for Evolution 4

This handout contains:
• Today's iClicker Question
• Figures for today's lecture

iClicker Question #1 - <u>after</u> 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.
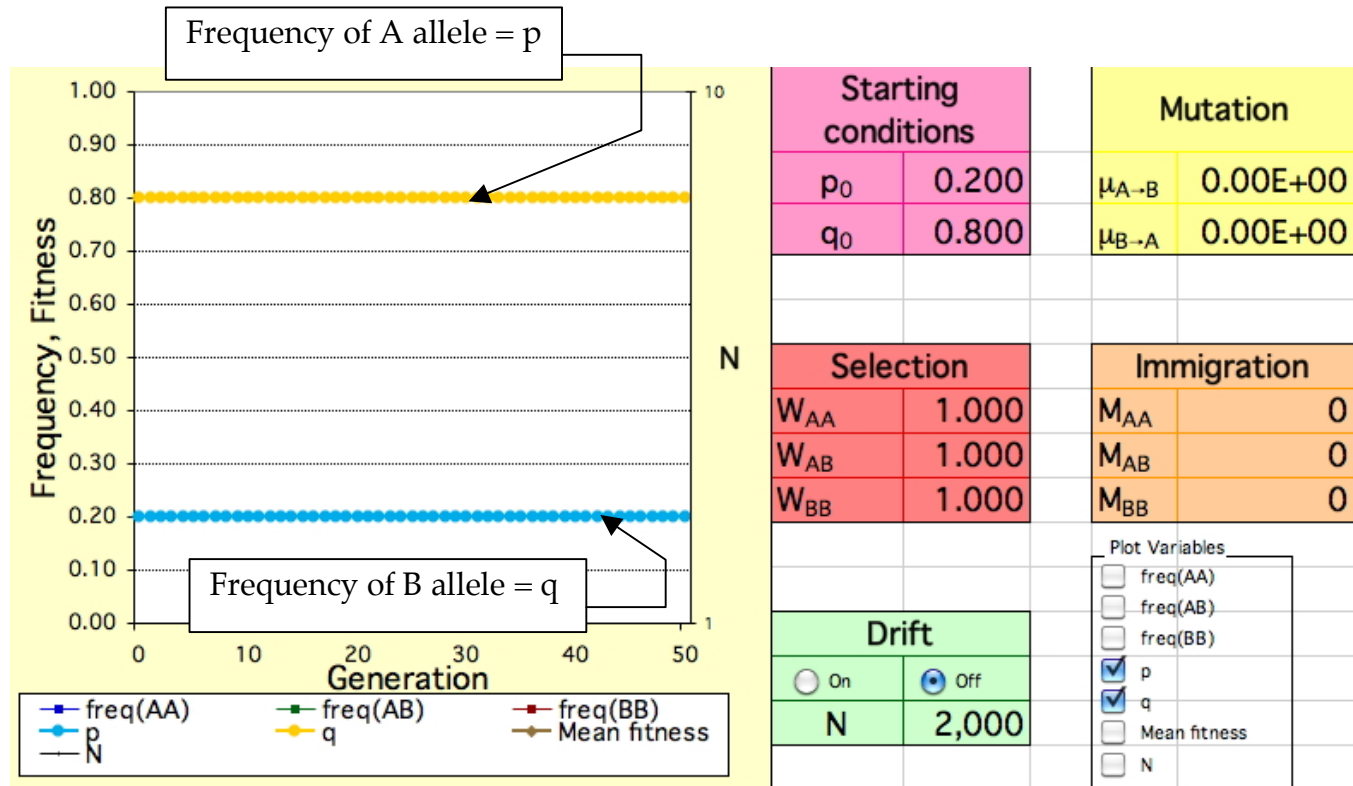E. All are true.

<u>Beaming in your answers</u>

1. Figure out your answer and select the appropriate letter (A-E).
2. Turn on your iCliker 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)

Frequency of A allele = p

Frequency of B allele = q

Starting conditions	
p_0	0.200
q_0	0.800

Mutation	
$\mu_{A \to B}$	0.00E+00
$\mu_{B \to A}$	0.00E+00

Selection	
W_{AA}	1.000
W_{AB}	1.000
W_{BB}	1.000

Immigration	
M_{AA}	0
M_{AB}	0
M_{BB}	0

Plot Variables
- ☐ freq(AA)
- ☐ freq(AB)
- ☐ freq(BB)
- ☑ p
- ☑ q
- ☐ Mean fitness
- ☐ N

Drift	
○ On ⊙ Off	
N	2,000

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

Evolution 4 - 2

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.

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

Genotype	Phenotype
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 <u>allele</u> (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 <u>genotype</u> (RR, Rr, rr for example) in the population. These are <u>always</u> equal to the number of individuals with a particular genotype divided by the total population size. They are <u>sometimes</u> 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 <u>many</u> 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 <u>the same allele frequencies</u>. However, given a pair of allele frequencies, there is <u>only one</u> 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

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

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

Evolution 4 - 4

Population 3

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

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

Evolution 4 - 6