Evolution 4

- Population Genetics II
 - Hardy-Weinberg Equilibrium
- Yadyra C see me Tim A see me

- Equilibrium
- Human genetic traits
- is a population at HWE?
- examples
- iClicker Question #1
- Labs start this week; go to HMNH ***BE PREPARED***
- no pre-lab this week; report due wk of 2/8
- go to HMNH anytime Mon-Sat 9-5 & Sun 1-5

* don't Forget "Tree Building Survey" - see link at Evolution G (due Evolution 7)

from last time: if, in parental generation, i freq of R: p = 0.2 : freq of r: 9 = 0.8

all 5 conditions hold

then the offspring will be:

× freq of RR kirds = p2 = 0.04

* freq of Rr kids = 2pq = 0.32 32 fast kids

x freq of rr kids = q2 = 0.64 64 slow kids

if 100 kids bother 4 v. fast krds

if all these kills have kilds (& all 5 conditions hold)

the allele & genotype frequencies will stay the same

in all following generations

= Hardy-weinberg equilibrium (HWE)

= NO EVOLUTION

Uses of HWE (1): Human Genetic Traits

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



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.

- large par (yes)
 - · no mutation (low rate)
 - · no migration
 - · randon mating 3 mating/ · no selection 3 surviva;

do not depend on earlobes

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

Genotype
EE unattached
unattached
ee attached

at HWE

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

Assume that this trait is at HWE.

Problem. EE, Ee have same phonotype, so can't find p^2 directly but freq (ee) = $q^2 = \frac{60 \text{ attached}}{240 \text{ total}} = 0.286$

frequency

= 9 = Jo.286 = 0.534 & Since p+ 9=1 p=1-9 = 0.466

: freg of carriers is 2pg = 2(.534)(.466) = 0.498

:. in class of 210 students, 210 x 0.498 = 104 should be

compare with reality - expect frey to be constant

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uses (8) studying wolution

Q: is population X at HWE? (not evolving)

step 1: calculate allele frequencies of x

ster 2: predict genotype freqs if x were at HWE

ster 3: compare predicted and autual

example. given genotype #



Step 1: find allele freqs (since we know all genotype freqs)

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$$2 \times AA + Aa$$

freq (A) = $p = (2 \times 2S) + 2S$
 $200 + 101$
 $2 \times aa + Aa$

freq (a) = $q = (2 \times S) + 2S$
 $2 \times aa + Aa$
 $2 \times aa + Aa$
 $3 \times aa + Aa$
 $4 \times aa + Aa$
 4

Step 2: If pop were at HWE (=) all 5 conditions hold) wed expect:

wed expect:

Step 3 observed frequencies

AA
$$p^2 = 0.140$$

AQ $2pq = 0.469$

Quantity of the prediction of the predict

observed & HWE predictions

- : Pop is not at HWE
- = must be evolving
- :. One or more of HWE assumptions is being Vio lated

Bio 112: Hardy-Weinberg Equilibrium Examples General Info

• <u>Allele frequencies</u>: 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 genotype (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 p², 2pq,
and q² - 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 = p^2 (0.04 in this example).

Population 1

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

Allele frequencies

Freq. of R = p = 40/200 = 0.2Freq. of r = q = 160/200 = 0.8Genotype 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**

different

Population 2

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

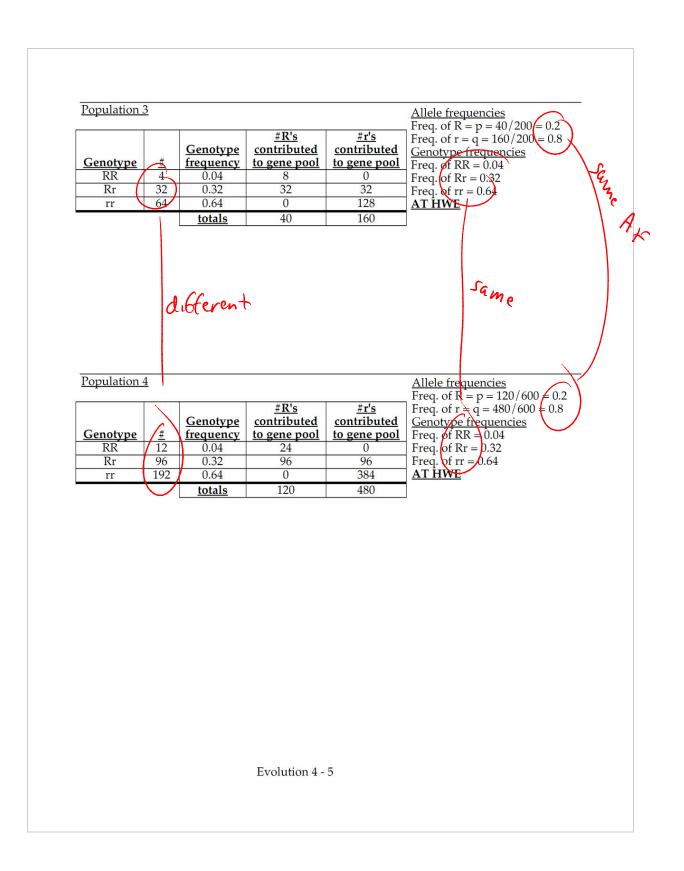
Allele frequencies

Freq. of R = p = 800/4000 = 0.2Freq. of r = q = 3200/4000 = 0.8

Genotype frequencies Freq. of RR = 0.2, not 0.04Freq. of Rr = 0.0, not 0.32Freq. of rr = 0.8, not 0.64

NOT AT HWE

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