HARDY-WEINBERG: WORKSHEET ACTIVITY

1. Observations: How many individuals are there for each genotype?

A1/A1: 28 individuals A1/A2: 79 individuals A2/A2: 15 individuals

2. Based on this information, what is the <u>total number</u> of each of our 2 alleles (i.e., A1 and A2) in the population?

If we have 122 individuals total, we have 122×2 alleles = 244 alleles total in this population (" \times 2" because each person is diploid).

For *A1*: 56 + 79 = 135 *A1* alleles

- 28 A1/A1 individuals
 - 2 × 28 A1 alleles = 56 A1 alleles in the homozygous individual
- 79 *A1/A2* individuals
 - 79 A1 alleles in the heterozygous individuals

For A2: 30 + 79 = 109 A2 alleles

- 15 A2/A2 individuals
 - 2 × 15 A2 alleles = 30 A2 alleles in the homozygous individual
- 79 *A1/A2* individuals
 - 79 A2 alleles in the heterozygous individuals
- 3. What is the <u>frequency</u> of each of our 2 alleles (i.e., A1 and A2) in the population? Fill out the table below, assigning one of the alleles to "p", and the other allele to "q".

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Alleles	Frequency		
р	(If we assign "p" to A1, p = 0.55:) A1: 135/244 = 0.55 (rounded)		
q	(If we assign "q" to A2, p = 0.45:) A1: 109/244 = 0.45 (rounded)		
Check: p + q = 1?	0.55 + 0.45 = 1 (confirms that we did our math correctly!)		

4. Based on the allele frequencies you calculated above (and assuming that mating is random with respect to these alleles), what is the <u>expected</u> frequency of each genotype (i.e., A1/A1, A1/A2, and A2/A2)? Check your calculations by confirming that $p^2 + 2pq + q^2 = 1$.

$$p^2$$
 (A1/A1) = 0.55 *0.55 = 0.3025
2pq (A1/A2) = 2 × 0.45 *0.55 = 0.495
 q^2 (A2/A2) = 0.45 *0.45 = 0.2025

Check: 0.3025 + 0.495 + 0.2025 = 1 (confirms that we did our math correctly)

5. Now go back to your original observations. What is the **observed** <u>frequency</u> of each genotype (i.e., A1/A1, A1/A2, and A2/A2) in the population? Check your calculations by confirming that $p^2 + 2pq + q^2 = 1$. A1/A1 = 28 people/122 total = 0.23 (rounded)

A1/A2 = 79 people/122 total = 0.65 (rounded)

A2/A2 = 15 people/122 total = 0.12 (rounded)

Check: 0.23 + 0.12 + 0.65 = 1 (confirms that we did our math correctly) Continued on the next page...

6. **Is our population in Hardy-Weinberg equilibrium?** Justify your response by comparing your predictions to the observations.

Genotype	Expected frequency	Observed frequency
A1/A1	0.3025	> 0.23 -> fewer than expected
A1/A2	0.495	< 0.65 → more than expected
A2/A2	0.20	> 0.12 → fewer than expected

No, we are not in Hardy-Weinberg equilibrium because the observed genotype frequencies are very different from the expected; we observe fewer homozygous individuals and more heterozygotes than expected.

7. If the population is *not* in Hardy-Weinberg equilibrium, can you come up with a possible explanation for why it isn't? *Note*: Your explanation should fit with your observations. We observed that there are more heterozygotes than expected, and fewer homozygotes than expected.

Possible explanations:

- 1. Mating is non-random; A1/A1 individuals don't like mating with other A1/A1 individuals, and A2/A2 individuals don't like mating with other A2/A2 individuals.
- 2. Natural selection is occurring; homozygotes have lower fitness than heterozygotes
- 3. Genetic drift is occurring; due to random sampling we happen to have a disproportionately large number of heterozygotes
- 4. Gene flow is occurring; homozygotes are leaving the population, or heterozygotes are entering it
- 5. ...Mutation is not a very likely explanation; it's unlikely that random mutations have created an excess of heterozygotes in the population
- 8. Is it possible to make a definite statement about whether or not our population is evolving? Hint: What are the assumptions of the Hardy-Weinberg equilibrium model?
 - If our observations do not match the predictions made by the model, it suggests that one or more of the assumptions have not been met.
 - ...Are there any assumptions that might not be met, even if allele frequencies are staying the same between generations (i.e., even if evolution is *not* occurring)?

We can't know for sure if the population is evolving; it might just be that mating is non-random (non-random mating could result in more A1/A2 individuals than expected, if homozygotes avoid mating with their own genotype). However, if mating is random, that means one of the other assumptions of Hardy-Weinberg equilibrium has been violated (e.g., natural selection, genetic drift, migration (gene flow), or mutation). If one of these other assumptions has been violated, it means the genotype frequencies in the previous generation probably didn't match up with the "expected" genotype frequencies we have calculated using p^2 , 2pq, and q^2 (i.e., we have no way of knowing what they were, we can't calculate them). ...If the genotype frequencies were something else, it's possible that the allele frequencies in the previous generation were also something else... which means evolution could have occurred between the generations.