Optional - Hardy Weinberg Practice Worksheet  – Answer Key

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**1.** As part of your graduate studies, you are studying a lab population of diploid dinoflagellates (a type of marine plankton). Spots are a dominant trait in this species; presence or absence of spots is controlled by a single gene with two alleles. There are a total of 200 individuals in this population, and 175 of these individuals have spots.

   **a.** What is the frequency of homozygous recessive individuals in this population? Show all your work. (**3 marks**)

**Total # of individuals in the population = 200**
**# Individuals with the dominant phenotype (i.e., *A/A* + *A/a* individuals) = 175**
**200 – 175 = 25 individuals with the recessive phenotype (i.e., *a/a*)**
**freq(*a/a*) = 25/200 = 0.125**

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   **b.** Assume this population is in Hardy-Weinberg equilibrium. Based on this assumption, calculate the frequency of the recessive allele in the population. Show all your work. (**2 marks**)
   *Hint*: When a population is in H-W equilibrium, if we know that freq(*a*) = *p*, then we can assume that freq(*a/a*) = $p^2$.

**freq(*a/a*) = 0.125 = $p^2$**
**$\sqrt{p^2} = p$**
**$\sqrt{0.125}$ = 0.353 = *p***

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   **c.** Still assuming the population is in H-W equilibrium, what is the frequency of the dominant allele? (**2 marks**)
   *Hint*: Because there are only two alleles in the population, that means *p* + *q* = 1.

**1 – *p* = *q***
**1 – 0.353 = 0.647 = *q***
[If you retained more that three decimal places during calculations, your answer might be closer to 0.646]

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   **d.** Using the allele frequencies you have calculated above, how many of the 200 individuals in this population should be heterozygotes? (**3 marks**)

**$p$ = 0.353; $q$ = 0.647**
**freq(*A/a*) = 2*pq* = 2 × 0.353 × 0.647 = 0.457**

**0.457 × 200 = 91.4 → round to nearest whole number = 91 individuals are heterozygotes**
[Note: If you found that the predicted number of individuals was closer to 92 than 91, you may have rounded the values from earlier calculations too much. If your final answer is going to be reported to the nearest two decimal places (e.g., 0.01), then it's a good idea to retain at least three decimal places (e.g., 0.001) while doing your calculations in order to ensure accuracy.]

**2.** After further research, you discover that homozygous dominant individuals have twice as many spots as heterozygous individuals (i.e., spots actually show incomplete dominance instead of complete dominance). Based on this information, you determine that 45 individuals in the population are heterozygotes.

  **a.** Is this population in Hardy-Weinberg equilibrium with regards to the "spot-or-no-spot" locus? (i.e., does the observed frequency of heterozygotes match the predicted frequency)? Briefly explain your reasoning. **(2 marks)**

**No, the population is not in H-W equilibrium – assuming H-W equilibrium, we predicted that 91 of the individuals were heterozygotes; instead, only 45 of the individuals are heterozygotes.**

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  **b.** Are you surprised by this result? Please explain why or why not. Your answer should make reference to the assumptions of the Hardy-Weinberg equilibrium model. **(4 marks)**

[Note: Either answer, yes or no, would be acceptable, as long as you do a good job of defending it. Also, shorter answers are okay, as long as you do a good job of supporting your position, and refer to specific evolutionary mechanisms.]

Example "Yes" answer: **Yes, I am surprised that the population is not in H-W equilibrium with regards to the spots gene. The population is relatively large (200 individuals), which, assuming that it has been about this size over multiple generations leads me to think that genetic drift due to the bottleneck effect or founder effect is probably not affecting allele frequencies. Also, it is a lab population, so I am assuming that individuals in this population are experiencing little competition over resources, and no predation – in other words, natural selection probably isn't having a strong effect on the population (and there's no reason to think that spots would be under selection). Furthermore, the lab population is probably isolated, so allele frequencies will not be influenced by individuals migrating in or out of the population. Lastly, mutation rates in the "spot" gene are probably low enough that they would not have much of an affect on allele frequencies at this locus either.**

Example "No" answer: **No, I am not surprised that the population is not in H-W equilibrium with regards to the spot gene. Any one of the five H-W equilibrium assumptions could have easily been violated. For one, we aren't told what the population size in the previous generation was – maybe the lab population used to be larger, but a bunch of individuals were removed (perhaps to run experiments). If individuals with a small number of spots (i.e., heterozygotes) were specifically removed (this could be seen as an example of selection against heterozygotes, or migration of heterozygotes out of the population), it could have caused the number of heterozygotes in the population to be lower than what we would predict under H-W equilibrium. It is also possible, but maybe less likely, that the random removal of a bunch of individuals unintentionally reduced the number of heterozygotes in the lab population (if so, this would be an example of genetic drift). Or, if individuals were recently added to the lab population from another population (i.e., one with different genotype frequencies), that could also have changed the genotype frequencies from those expected under H-W equilibrium. There may also be non-random mating in the lab population, based on spot genotype. Maybe individuals with lots of spots prefer to mate with other individuals with lots of spots, and/or individuals with no spots prefer to mate with other individuals with no spots; this could also reduce the number of heterozygotes in the population, compared to what we expect. There are many, many ways in which the assumptions of H-W equilibrium could have been violated.**

**3**. You are helping one of your friends with homework from another biology class. They are also learning about population genetics and Hardy-Weinberg equilibrium. This is the question they are working on:

"There are 200 individuals in the population: 20 are homozygous dominant (A/A), 20 are heterozygous (A/a) and 160 are homozygous recessive (a/a). Is this population in Hardy-Weinberg equilibrium with respect to Gene A?

Your friend thinks the population is in HWE. Are they correct? Explain your answer.

No, my friend is not correct. More homozygous dominant (0.10) and homozygous recessive (0.80) individuals were observed (A/A=0.10, a/a=0.80) than expected (A/A=0.02, a/a=0.72). Fewer heterozygotes (A/a) were observed (0.10) than expected (0.26). Therefore, the population is not in HWE for the A gene.

# A/A individuals = 20
# A/a individuals = 20
# a/a individuals = 160
Total # of individuals = 200

Observed allele frequencies
Observed freq(A) = $p$ = (2×20 + 20) ÷ (2×200) = 60 ÷ 400 = **0.150**
Observed freq(a) = $q$ = (2×160 + 20) ÷ (2×200) = 340 ÷ 400 = **0.850**

Predicted genotype freq based on observed allele freq
If pop' is in H-W eq:
Predicted freq(A/A) = $p^2$ = 0.150² = **0.02**
Predicted freq(A/a) = $2pq$ = 2×0.150×0.850 = **0.26**
Predicted freq(a/a) = $q^2$ = 0.850² = **0.72**

Observed genotype frequencies
Based on data provided in the question:
Observed freq(A/A) = 20/200 = **0.10**
Observed freq(A/a) = 20/200 = **0.10**
Observed freq(a/a) = 160/200 = **0.80**

Observed genotype frequencies do not match the genotype frequencies that are predicted under H-W equilibrium; therefore, the population is <u>not</u> in Hardy-Weinberg equilibrium.