**AP Biology Hardy-Weinberg Introduction**

*Part I:* *Genetics terms review.*

Distinguish between genotype and phenotype. Give an example of each.   
 Define: Dominant allele, Recessive allele, gene pool, homozygous, heterozygous

*Part II: Demo*

Collect a cup and put 100 black beans and 100 white beans in the cup. This cup will represent the gene pool for a hypothetical population consisting of individuals with the following genotypes: 25 BB: 50 Bb: 25 bb, where B is the allele for Black fur and b is the allele for white fur.

1. With the information above in mind, What genotype is exhibited by the following bean combinations:
   1. Two blacks?
   2. A black and a white?
   3. Two whites?

2. Copy the following chart onto your paper:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Offspring # | # Black Beans Drawn (B alleles) | # White Beans Drawn (b alleles) | Offspring Genotype | Offspring Phenotype |
| 1 |  |  |  |  |
| 2 |  |  |  |  |
| 3 |  |  |  |  |
| 4 |  |  |  |  |

(continue your chart to offspring #25)

3. Once your chart is copied, draw 2 beans from your cup without looking. This is offspring 1. Record the number of black beans and/or white beans drawn, the genotype, and phenotype of the offspring.

4. Repeat step 3 until you have 25 offspring recorded.

5. There are 2 mathematical equations that scientists use when trying to model the impact of natural selection on a population's gene pool. The first equation allows scientists to determine the frequency or percent of the ***allele***s in a population's gene pool. This is the first equation: p + q=1, where p=the frequency of the dominant allele (expressed as a decimal, not percent) and q= the frequency of the recessive allele (also expressed as a decimal, not percent). It makes sense, since the percent of dominant and percent of recessive alleles in a gene pool should equal 100%. On your chart, circle the column that represents p in green and the one that represents q in red.

6. Now, let's use what we know to calculate the frequencies of p and q in our original gene pool and in that of the offspring. Copy and fill in the chart below:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | #B alleles | Total # of alleles | Value of p (expressed as a decimal) | #b alleles | Total # of alleles | Value of q (expressed as a decimal) |
| Original (Parental) Gene Pool | 100 | 200 |  | 100 | 200 |  |
| Offspring gene pool |  | 50 |  |  | 50 |  |

7. The second equation is the Hardy-Weinberg equation, which is related to the allele frequency equation, but instead, charts the frequencies of each ***genotype*** in the population. The Hardy-Weinberg equation is p2+2pq+q2=1, where p2 is the frequency of the homozygous dominant individuals, 2pq is the frequency of the heterozygous individuals, and q2 is the frequency of the homozygous recessive individuals in the population. Again, the frequencies should be expressed as decimals and should add up to 1 or 100% of the population. Let's calculate the parts of the H-W equation. Copy and fill in the chart below:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Generation | # Homozygous Black Animals | # Heterozygous Black Animals | # Homozygous White Animals | Total # of animals |
| Original (Parental) Genotypes |  |  |  |  |
| Offspring Genotypes |  |  |  |  |

a. Which column(s) would you use to calculate p2? Calculate that value now: \_\_\_\_\_

b. Which column(s) would you use to calculate 2pq? Calculate that value now: \_\_\_\_\_

c. Which column(s) would you use to calculate q2? Calculate that value now: \_\_\_\_\_

*Wrap-up:*

1. How do the two equations used here relate to each other? How are they different from one another?  
2. If you know the value of all of the frequencies in the H-W equation, could you calculate the allele frequencies? Explain. What about if you knew the allele frequencies, could you calculate the genotype frequencies? Explain.