Here is a population in HW equilibrium. This population of Harlequin ladybirds have two alleles in one gene that determine spot patterns. The black-with-spots allele (B) is dominant over the red-with-spots allele (b).

36 x

Black with red spots

x 64

Red with black spots

In population genetics, there is a concept called Hardy-Weinberg Equilibrium.

<u>If a population is in HW Equilibrium:</u>

- The population must have two different alleles of a gene being studied. The gene must be an autosomal trait and the organisms must be diploid, sexually reproducing organisms.
- The population has allele frequencies that do not change from one generation to the next generation.
- The population is considered to be non-evolving.
- Because allele frequencies do not change, scientists can calculate the number of each genotype and phenotype in a population, given p and q.

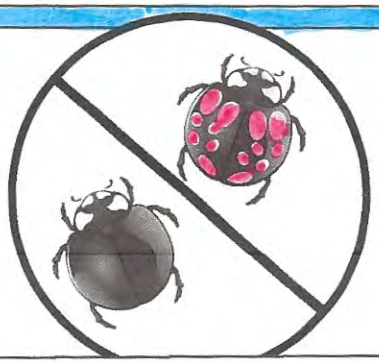
Use the formulas in the chart below to calculate all the statistics for the ladybug population.

<u>Population Statistic</u>	<u>Formula</u>	<u>Calculate</u>
Dominant allele frequency	p	1-0.8 = 0.2
Recessive allele frequency	q	square root (.64)
BB genotype frequency	p^2	0.2 · 2 = 0.04
Bb genotype frequency	2pq	2 (0.2) (0.8) = 0.32
bb genotype frequency	q^2	64/100 = 0.64
Black with red spots frequency	$p^2 + 2pq$	0.36
Red with black spots frequency	q^2	0.64

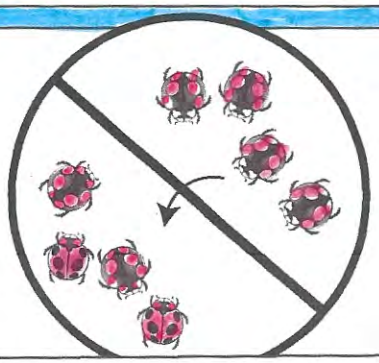
IMPORTANT NOTE: If the population is not in HW equilibrium, you cannot use these formulas to figure out each genotype and phenotype frequency for a population.

Name: _____

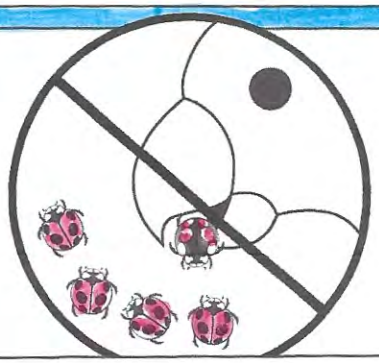
Hardy-Weinberg Equilibrium



No mutations
No introduction of new alleles or changes from B to b



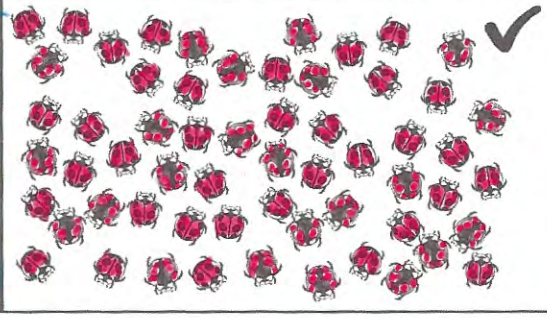
No migration/gene flow from another population of ladybugs



No natural selection
Neither phenotype has an advantage over the other.

Name: _____

A Population in HW Equilibrium Must Have:



A large or "infinite" size to prevent genetic drift, which causes allele frequencies to change due to random chance.

Individuals that mate randomly
Nonrandom mating doesn't change allele frequencies but it can create genotype frequency differences and lead to genetic drift.