

Population Genetics

Contents

	Objectives	1
	Introduction	1
Activity 14.1	Calculating Frequencies	2
Activity 14.2	More Hardy-Weinberg	3
	Results Section	4

Objectives

- To be able to apply the Hardy-Weinberg equations to calculate genetic frequencies

Introduction

Unlike Mendelian genetics which deals with the absolutes of individual genotypes, population genetics concerns itself with the numbers and proportions of different alleles and genotypes within the population as a whole. Population genetics is not concerned with whether two specific individuals mate and the specific type of offspring they have, but rather with how often that type of match occurs in the population at large.

Two of the individuals that worked in this field of population genetics were Godfrey Hardy and Wilhelm Weinberg. These individuals defined the what we now term the Hardy-Weinberg law. Basically this states that if p represents the frequency of one allele and q represents the frequency of the alternative allele in a population, the frequency of the genotypes in the population can be derived from the equation $p^2 + 2pq + q^2$ provided five conditions are met. These conditions are that the population is large, that migration does not occur, that mutations do not occur, that mate selection is random with respect to these alleles, and that these alleles do not affect the reproductive outcomes of the individuals. If all of these conditions are met, evolution will not occur.

Activity 14.1 Calculating Frequencies

Open the Population Genetics lab simulation in the Genetic and Evolution section of the BiologyOne DVD. When you start this simulation, a population of 80 organisms will appear. You will note that the individuals are of two phenotypes, one dominant and one recessive. If you would like to work with a different population, click on the New Population button and a different population of 80 individuals will appear.

You are asked to calculate genotype and allele frequencies for this population. You must calculate these in the order asked since subsequent calculations rely on earlier results. Enter the frequency values asked for. If correct, you will proceed to the next calculation. If incorrect, you will have the opportunity to recalculate the value. The program checks for values out to four digits if appropriate.

To calculate these frequencies, follow the steps in order.

1. Calculate the frequency of the recessive phenotype in the population by dividing the number of individuals with the recessive phenotype by the total number of individuals in the population. This is the value of q^2 .
2. Calculate the recessive allele frequency by calculating the square root of the value in step 1. This is the value of q .
3. Calculate the dominant allele frequency by subtracting the value determined in step 3 from 1.0. This is the value for p .
4. Calculate the genotype frequencies by inserting the p and q values into the Hardy-Weinberg equation.

$$p^2 + 2pq + q^2 = 1.0$$

Simulation for Calculating Frequencies

The screenshot shows a simulation interface for calculating frequencies. On the left, a calculator is open, and the input field for 'dominant allele frequency' contains 'p = .553'. A blue 'Check Answer' button is visible below. At the bottom left is a 'New Population' button. The central area displays a population of 80 organisms, represented by brown shells, arranged in a grid. The top of the grid is labeled 'dominant phenotype' and 'recessive phenotype' under the heading 'population'. On the right, the results are displayed: 'allele frequencies' shows 'q = 0.447' and 'genotype frequencies' shows 'q^2 = 0.200'. Annotations with arrows point to the calculator, the input field, the 'Check Answer' button, and the result boxes.

'C' opens calculator

input your answer here

input dominant allele frequency
p = .553

click on button to check answer

correct answers appear here

allele frequencies
q = 0.447

genotype frequencies
q² = 0.200

Activity 14.2 **More Hardy-Weinberg**

In the Results Section is a group of 100 circles that represent the 100 individuals of a hypothetical population. The filled circles are individuals which express the recessive phenotype, the open circles are individuals with the dominant phenotype. Calculate the phenotype, allele and genotype frequencies for this population using the Hardy-Weinberg equations.

Results Section

Activity 14.1 Calculating Frequencies

Description of dominant phenotype:

Description of recessive phenotype:

Population Frequencies:

Dominant phenotype frequency:

Recessive phenotype frequency:

Dominant allele frequency:

Recessive allele frequency:

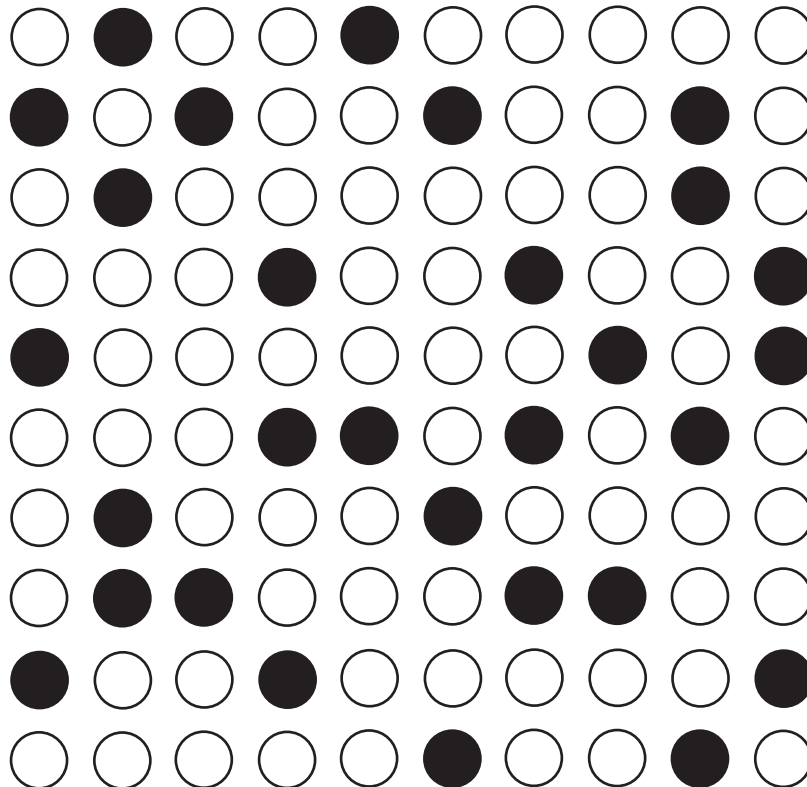
Homozygous dominant genotype frequency:

Heterozygous dominant genotype frequency:

Homozygous recessive genotype frequency:

Activity 14.2
More Hardy-Weinberg

The following circles represent the individuals in a population. Filled circles are individuals which express the recessive phenotype while open circles represent individuals with the dominant phenotype. Calculate the population's frequencies and place your answers in the spaces below.



Dominant phenotype frequency:

Recessive phenotype frequency:

Dominant allele frequency:

Recessive allele frequency:

Homozygous dominant genotype frequency:

Heterozygous dominant genotype frequency:

Homozygous recessive genotype frequency: