

AP Biology Laboratory 8

Population Genetics and Evolution

Objectives

- Estimate the frequency of alleles in a population using Hardy-Weinberg equations.
- Demonstrate that allele frequencies can change in a population over time.

Background

In the early 1900s, many biologists attempted to explain evolution in terms of the emerging science of genetics. Because the F_2 of monohybrid cross show a 3:1 ratio of dominant to recessive phenotypes many assumed that populations would evolve toward similar ratios of phenotypes. Two mathematicians, Godfrey Hardy and Wilhelm Weinberg, realized that the frequency of alleles in a population was independent of the alleles' inheritance pattern from parents to offspring. They postulated an ideal breeding population with the following properties:

1. Population size is infinite, or very large.
2. Mating is random. Mating pairs show no preference for one phenotype over another.
3. There is no mutation.
4. There is no exchange with other populations. No immigration or emigration occurs.
5. There is no selection for one phenotype over another. All phenotypes have an equal chance of reproducing.

If these conditions are met, the population's allele and genotype frequencies will remain statistically constant over time, a condition referred to as Hardy-Weinberg equilibrium. If we determine the frequency of a pair of alleles in a population, we can sample that population over several generations to determine if the frequency changes. If it does, we know that the population is evolving with respect to that pair of alleles.

Hardy and Weinberg developed mathematical formulas for estimating the frequencies of alleles in populations. Consider the following data on Rh blood type for a hypothetical human population of 6000:

Results of Testing for Human Rh Blood Type

Blood Type	Number of People
Rh+	4680
Rh-	1320
Total	6000

Assume that Rh blood type is inherited through two alleles: D , a dominant allele for Rh+ blood type, and d , a recessive allele for Rh- blood type.

Using Hardy-Weinberg equations, let

p = frequency of the dominant allele (D)

q = frequency of the recessive allele (d)

Each person is either Rh+ or Rh-, therefore,

$$p + q = 1 \text{ or } 100\% \text{ of the population.}$$

Since humans are diploid, individuals may be homozygous dominant (DD), heterozygous (Dd) or homozygous recessive (dd). The basic equation must be expanded to represent all the genotype frequencies. Thus,

$$(p + q)(p + q) = 1$$

Population Genetics Lab Answers Kim Foglia

Thomas Nagylaki



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Cumulated Index Medicus ,1989 *Agrindex* ,1995 **Population Genetics** Ching Chun Li,1958 **Introduction to Theoretical Population Genetics** Thomas Nagylaki,1992 This book covers those areas of theoretical population genetics that can be investigated rigorously by elementary mathematical methods An attempt has been made to formulate the various models fairly generally and to state the biological assumptions quite explicitly The choice and treatment of topics should enable the reader to understand and evaluate detailed analyses of many specific models and applications in the literature The material suffices for a one year course and is almost entirely self contained The little basic genetics needed for understanding it is presented in the text Calculus and linear algebra are used freely Previous exposure to elementary probability theory would be helpful The major mathematical theme of the book is the dynamical analysis of recursion relations Many exact and approximate techniques for investigating linear and nonlinear recursion relations in one dimension and in several dimensions are developed and applied The problems are an essential part of this book Although some of them ask the reader merely to supply details of derivations in the text many illuminate, rigorize or extend these derivations Some of the results in the problems are useful and important They vary in difficulty the harder ones offer a challenge even to good students Page 4 de la couverture

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