

CHAPTER 19	Investigation 19.B: Testing the Hardy-Weinberg Principle	BLM 19.1.8
HANDOUT		
Question: What processes affect the genetic equilibrium of a population?		

Part 1: Demonstrating Genetic Equilibrium

Hypothesis

Make a hypothesis about the effects of random mating on allele and genotype frequencies in a population over time.

Prediction

In a model simulation using 80 beads, the proportion of corresponding alleles in a population undergoing random mating are $\frac{48}{80}$ for D , the dominant allele, and $\frac{32}{80}$ for L , the recessive allele.

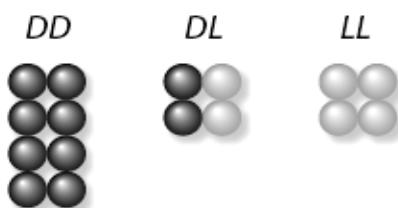
Calculate the allele frequencies for L and D . Use the Hardy-Weinberg equation to predict the expected frequency of each genotype DD , DL , and LL . Then predict the allele and genotype frequencies for future generations.

Materials

- 2 paper cups (or similar containers)
- 48 dark-coloured beads
- 32 light-coloured beads

Procedure

1. Label one paper cup “male gene pool” and the other paper cup “female gene pool.” Put 24 dark-coloured (*D*) and 16 light-coloured (*L*) beads in each cup. The beads represent the alleles for a specific trait.
2. Gently shake the cups to mix the beads. To simulate random mating, without looking, select one bead (allele) from each cup. Place the pair of beads (the genotype of the offspring) on the table. Repeat this process, lining up the genotypes (*DD*, *DL*, and *LL*) in separate columns until you have used all the beads.



3. In the following table, record the number of offspring with each genotype for this generation.

Number of Each Genotype in a Population Undergoing Random Mating (individual data)

Generation	Number of DD	Number of DL	Number of LL	Total # of individuals

4. To establish the gene pool for the next generation, assume that half the population in each column of beads is male and the other half is female. Place the beads representing the male genotypes in the male gene pool and the beads representing the female genotypes in the female gene pool. Remember that genotypes are made up of two alleles, so each male and female must contribute two beads to the gene pool. (You should end up with an equal number of alleles in each gene pool. If there is an odd number of genotypes in a column, assume that the last genotype belongs to a male. The next time this happens, assume that the last genotype belongs to a female. Switch from male to female every time there is an odd number of genotypes in a column.)
5. Repeat steps 3 to 5 three more times to obtain data for a total of four generations.
6. Pool your data with the data obtained by the rest of the class and record the class data in the following table.

Number of Each Genotype in a Population Undergoing Random Mating (class data)

Generation	Number of DD	Number of DL	Number of LL	Total # of individuals

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Part 2: Testing for Genetic Equilibrium

Hypothesis

Make a hypothesis about the effects of a recessive lethal allele on allele frequencies and genotype frequencies in a population over time.

Prediction

The proportions of corresponding alleles in a population are $\frac{48}{80}$ for D (the dominant allele for a healthy phenotype) and $\frac{32}{80}$ for L (the recessive lethal allele). Calculate the allele frequencies for L and D . Use the Hardy-Weinberg equation to predict the expected frequency of each genotype DD , DL , and LL . Then predict the allele and genotype frequencies for future generations.

Materials

- 3 paper cups (or similar containers)
- 48 dark-coloured beads
- 32 light-coloured beads

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Procedure

- Complete steps 2 to 4 as described in Part 1. Record your data in the following table.

Number of Each Genotype in a Population with a Lethal Allele, L (individual data)

Generation	Number of DD	Number of DL	Number of LL	Total # of individuals

- Assume that the light bead (L) is the recessive lethal allele. Therefore, none of the organisms with the LL genotype will survive to reproduce. Remove the LL genotypes from the population on the table, and place them in a separate cup. You now have two columns of beads on the table: DD and DL .
- Complete step 5 as described in Part 1.
- Repeat steps 2 to 4 three more times to obtain data for a total of four generations.
- Pool your data with the data obtained by the rest of the class and record the class data in the table below.

Number of Each Genotype in a Population with a Lethal Allele, L (class data)

Generation	Number of DD	Number of DL	Number of LL	Total # of individuals

Analysis

- Use the class data from Part 1 to graph the genotype frequencies over four generations. Compare your results with your prediction.
 - Use the class data from Part 1 to determine the allele frequencies for the fourth generation. **Hint:** Use the Hardy-Weinberg equation and the equation $p + q = 1.00$.) Compare your results with your prediction.

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2. a) Use the class data from Part 2 to graph the genotype frequencies over four generations. Compare your results with your prediction.

- b) Use the class data from Part 2 to determine the allele frequencies for the fourth generation. Compare your results with your prediction.

- c) What happened to the total number of alleles in the population over the course of the investigation? Did this affect the results of the investigation? Explain your answer.

3. Explain why data from the whole class were pooled.
4. In reality, each individual contributes one allele to the next generation. Identify any false assumptions that were made when choosing alleles in this investigation.

Conclusions

5. Account for the allele and genotype frequencies observed over time in Part 1. Were the conditions of the Hardy-Weinberg principle met in this population? Explain your answer.

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6. Account for the allele and genotype frequencies observed over time in Part 2. Were the conditions of the Hardy-Weinberg principle met in this population? Explain your answer.