AP BIOLOGY · UNIT 5 · TOPIC 5.3

Mendelian Genetics

Learning objective 5.3.A Explain the inheritance of traits using Mendel's laws.

Name: Date: Period:

Use the tool **Where the Ratio Comes From**. Each Part names the tab it uses. The tool uses abstract alleles **A/a** and **B/b**; the questions here attach them to Mendel's peas, where **A** = round seed, **a** = wrinkled seed, **B** = yellow seed and **b** = green seed.

Part 1 · Build the squares yourself

Open **Build the square**. For each cross in the table, write the four boxes of the Punnett square and the two ratios first. Then set Parent 1 and Parent 2 in the tool to check them.

Cross	The four boxes	Genotype ratio (AA:Aa:aa)	Phenotype ratio (round:wrinkled)
Aa × Aa			
AA × aa			
Aa × aa			
aa × aa			
Aa × AA			

1. Explain why the genotype ratio of the offspring of Aa × Aa is 1:2:1 and not 1:1:1.

2. In the Part 1 table, the crosses AA × aa and Aa × AA give the same phenotype ratio but different genotype ratios. Explain why the phenotype ratio cannot distinguish these two crosses.

Part 2 · The test cross

A pea plant has round seeds, so it is either **AA** or **Aa**, and its phenotype does not show which. On Build the square, set Parent 1 to each possible genotype of the plant, cross it with aa and then with AA, and record the phenotype ratios.

Unknown parent	Crossed with aa	Crossed with AA
AA		
Aa		
Does this cross identify the unknown?		

3. (a) Identify the partner, aa or AA, that should be crossed with the round-seeded plant to determine its genotype.

(b) Explain why a cross with the other partner cannot determine the genotype of the round-seeded plant.

4. The round-seeded plant is crossed with aa and produces 20 offspring, all with round seeds.
(a) Identify the most likely genotype of the round-seeded plant.

(b) Explain why this result does not prove that the plant has this genotype.

Part 3 · Two genes at once

Switch to **Two genes at once**. Both parents are **AaBb**, so they have round yellow seeds. The class buttons name each class by gene: dominant for A means round, recessive for A means wrinkled, dominant for B means yellow and recessive for B means green. Click each class button and record the Boxes in that class readout. In the First gene and Second gene columns, record the probability of each trait, and in the Product column, multiply them.

Phenotype	Boxes counted	First gene	Second gene	Product
Round, yellow				
Round, green				
Wrinkled, yellow				
Wrinkled, green				

5. Explain why the 9:3:3:1 phenotype ratio from AaBb × AaBb is the product of two 3:1 ratios.

6. Without drawing a Punnett square, calculate the probability that an offspring of AaBb × AaBb has round green seeds. Show your work.

Part 4 · Testing the prediction

Switch to **Does it fit?** Click each dataset and record its χ^2, degrees of freedom, critical value and decision. Question 7 asks you to check the first dataset's χ^2 by hand. **$\chi^2 = \Sigma\ (O - E)^2 / E$**, and degrees of freedom is the number of classes minus one.

Dataset	χ^2	df	Critical value	Reject or not?
A 3:1 cross that fits				
A 3:1 cross that is off but survives				
A 3:1 cross that fails				
A 9:3:3:1 cross that fits				
A dihybrid cross that fails				

7. (a) State the null hypothesis for a chi-square goodness-of-fit test on the offspring of a genetic cross.

(b) For the dataset "A 3:1 cross that fits," calculate χ^2 from the Observed and Expected columns in the tool's table. Show your work.

8. For the dataset "A 3:1 cross that fails," the chi-square value is greater than the critical value.
(a) Describe the conclusion that can be drawn about the null hypothesis.

(b) Explain why this result does not identify the cause of the difference between the observed and expected counts.

9. On the Does it fit? tab, the section Why sample size still matters compares the same proportions of offspring (68 : 32) counted in a sample of 100 and in a sample of 1000.

(a) Explain why the number of offspring does not affect the degrees of freedom.

(b) Explain why the number of offspring affects the chi-square value.

What the model simplifies

Every cross here assumes complete dominance, two alleles per gene, genes on different chromosomes, and equal survival of all genotypes. Topic 5.4 removes the first two of those assumptions, and linked genes break the third.

The tool uses abstract alleles A/a and B/b; the handout attaches them to Mendel's pea traits. The counting is identical either way, and the abstraction is deliberate: a ratio derived from letters transfers to any trait.

A Punnett square gives probabilities, not predictions about a particular family. Four offspring from an Aa × Aa cross are not guaranteed to be three round and one wrinkled, any more than four coin tosses are guaranteed to be two heads and two tails.

The chi-square critical values are those for $p = 0.05$, the threshold the AP course uses. That choice is a convention, not a property of the data: a departure significant at $p = 0.05$ may not be at $p = 0.01$.

Mendel's dihybrid figures (315, 108, 101, 32) are his published counts. The other datasets are constructed so that the arithmetic is checkable and so that a rejected result can be shown as well as an accepted one.