

Lab-wide Learning Outcomes for Mendelian Pigs

Knowledge-Based Outcomes

Upon completion of *Mendelian Pigs*, students should be able to:

1. Describe the meaning of and explain relationships among the following terms: gene, allele, dominant, recessive, homozygous, heterozygous, genotype, phenotype, pure-breeding, codominant, receptor, F_1 , F_2 , back-cross.
2. Explain why allele frequencies in populations do not follow the same proportions as those predicted using a Punnett square for a cross between individuals.

Skills-Based Outcomes

Upon completion of *Mendelian Pigs*, students should be able to:

1. Predict the genotypes, phenotypes, and their frequencies resulting from crosses between individuals with single-locus traits that show dominant, recessive, and co-dominant phenotypes using a Punnett square.

Mendelian Pigs, Part 1: Breed Your Bacon

Knowledge-Based Outcomes

Upon completion of *Part 1: Breed Your Bacon*, students should be able to:

1. Explain the relationship between genes and alleles.
2. Using the concepts of genotype and phenotype, describe a hypothetical genetic system that involves one dominant and one recessive allele.
3. Define "pure-breeding" for a genetically determined trait, and describe F_1 and F_2 generations.

Skills-Based Outcomes

Upon completion of *Part 1: Breed Your Bacon*, students should be able to:

1. Determine the dominance relationship between simple Mendelian traits through crosses.

Mendelian Pigs, Part 2: Pigmented Pigs

Knowledge-Based Outcomes

Upon completion of *Part 2: Pigmented Pigs*, students should be able to:

1. Explain in general how different alleles for the melanocortin 1 receptor (MC1R) produce different coat colors in pigs.

Skills-Based Outcomes

Upon completion of *Part 2: Pigmented Pigs*, students should be able to:

1. Infer the Mendelian dominance relationships among traits based on simple molecular mechanisms involving a receptor (for example, MC1R).

Mendelian Pigs, Part 3: Going Hog Wild

Knowledge-Based Outcomes

Upon completion of *Part 3: Going Hog Wild*, students should be able to:

1. Describe how the frequency of an allele in a population is determined by evolutionary processes.
2. In large populations and in the absence of selection or other perturbations, predict how allele frequencies will change.
3. Predict that Mendelian dominance relationships will not influence how allele frequencies change over time, absent selection. In other words, avoid the confusion that dominant alleles will increase in frequency.
4. Explain why Mendelian dominance relationships will not influence how allele frequencies change over time, absent selection.
5. Predict how Mendelian dominance relationships for alleles under selection may influence changes in their allele frequencies over time, avoiding the misconception that dominance is related to a selective advantage.

Skills-Based Outcomes

Upon completion of *Part 3: Going Hog Wild*, students should be able to:

1. Assuming Hardy-Weinberg assumptions apply, use the Hardy-Weinberg equation to calculate expected numbers (or proportions) of each genotype at a locus with two alleles, given allele frequencies.