

Knowledge-based Learning Outcomes

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

1. Describe the meaning of and explain relationships between the following vocabulary words: gene, allele, dominant, recessive, homozygous, heterozygous, genotype, phenotype, pure-breeding, codominant, receptor, ligand, F1, F2, back-cross.
2. Describe how the frequency of an allele in a population is determined by evolutionary processes.
3. In large populations and in the absence of selection or other perturbations, predict how allele frequencies will change.
4. Explain why allele frequencies do not change much over time in large populations, in the absence of selection or other perturbations.
5. Predict that Mendelian dominance relationships will not influence how allele frequencies change over time, absent selection; avoid the confusion that dominant alleles will increase in frequency.
6. Explain why Mendelian dominance relationships will not influence how allele frequencies change over time absent selection.
7. 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 Learning Outcomes

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

1. Determine the dominance relationship between simple Mendelian autosomal traits through crosses.
2. 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.
3. Infer the Mendelian dominance relationships among traits based on simple molecular mechanisms involving a receptor.
4. 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.