12 | MENDEL'S EXPERIMENTS AND HEREDITY

Figure 12.1 Experimenting with thousands of garden peas, Mendel uncovered the fundamentals of genetics. (credit: modification of work by Jerry Kirkhart)

Chapter Outline

Introduction

During the 19th century, long before chromosomes or genes had been identified, Johann Gregor Mendel set the framework for genetics by studying a simple biological system, the garden pea. He conducted methodical, quantitative analyses using large sample sizes. Mendel’s work laid the foundation for the fundamental principles of heredity. We now know that genes, carried on chromosomes, are the basic functional units of heredity with the capacity to be replicated, expressed, repressed, modified and mutated. Today, the postulates put forth by Mendel form the basis of classical, or Mendelian, genetics. Genes do not all obey the tenets of Mendelian genetics, but Mendel’s experiments serve as an excellent starting point for thinking about inheritance.

An understanding of genetic inheritance enables scientists to study and explain complex phenomena. For example, scientists studied the remains of 84 ancient dogs from North and South America. They found that some of the dogs had greater genetic diversity, indicating that these dogs might have interbred with American wolves. Other dogs in their sample had low diversity, indicating that ancient humans were purposely breeding dogs. The study also found that dogs migrated to the Americas with humans only about 10,000 years ago. You can read more about this fascinating story **here (http://openstaxcollege.org/l/32dogs)** .

12.1 | Mendel's Experiments and the Laws of Probability

In this section, you will explore the following questions:

- Why was Mendel's experimental work so successful?
- How do the sum and product rules of probability predict the outcomes of monohybrid crosses involving dominant and recessive alleles?

Connection for AP® Courses

Genetics is the science of heredity. Austrian monk Gregor Mendel set the framework for genetics long before chromosomes or genes had been identified, at a time when meiosis was not well understood. Working with garden peas, Mendel found that crosses between true-breading parents (P) that differed in one trait (e.g., color: green peas versus yellow peas) produced first generation (F1) offspring that all expressed the trait of one parent (e.g., all green or all yellow). Mendel used the term dominant to refer to the trait that was observed, and recessive to denote that non-expressed trait, or the trait that had "disappeared" in this first generation. When the F1 offspring were crossed with each other, the F2 offspring exhibited both traits in a 3:1 ratio. Other crosses (e.g., height: tall plants versus short plants) generated the same 3:1 ratio (in this example, tall to short) in the F2 offspring. By mathematically examining sample sizes, Mendel showed that genetic crosses behaved according to the laws of probability, and that the traits were inherited as independent events. In other words, Mendel used statistical methods to build his model of inheritance.

As you have likely noticed, the AP Biology course emphasizes the application of mathematics. Two rules of probability can be used to find the expected proportions of different traits in offspring from different crosses. To find the probability of two or more independent events (events where the outcome of one event has no influence on the outcome of the other event) occurring together, apply the product rule and *multiply* the probabilities of the individual events. To find the probability that one of two or more events occur, apply the sum rule and *add* their probabilities together.

The content presented in this section supports the learning objectives outlined in Big Idea 3 of the AP® Biology Curriculum Framework. The AP® learning objectives merge essential knowledge content with one or more of the seven science practices. These objectives provide a transparent foundation for the AP® Biology course, along with inquiry-based laboratory experiences, instructional activities, and AP® exam questions.

Big Idea 3	Living systems store, retrieve, transmit and respond to information essential to life processes.
Enduring Understanding 3.A	Heritable information provides for continuity of life.
Essential Knowledge	**3.A.3** The chromosomal basis of inheritance proposed by Mendel provides an understanding of the pattern of passage of genes from parent to offspring.
Science Practice	**3.1** The student can pose scientific questions.
Learning Objective	**3.13** The student is able to pose questions about ethical, social, or medical issues surrounding human genetic disorders.
Essential Knowledge	**3.A.3** The chromosomal basis of inheritance proposed by Mendel provides an understanding of the pattern of passage of genes from parent to offspring.
Science Practice	**2.2** The student can apply mathematical routines to quantities that describe natural phenomena.
Learning Objective	**3.14** The student is able to apply mathematical routines to determine Mendelian patterns of inheritance provided by data sets.

Figure 12.2 Johann Gregor Mendel is considered the father of genetics.

Johann Gregor Mendel (1822–1884) (**Figure 12.2**) was a lifelong learner, teacher, scientist, and man of faith. As a young adult, he joined the Augustinian Abbey of St. Thomas in Brno in what is now the Czech Republic. Supported by the monastery, he taught physics, botany, and natural science courses at the secondary and university levels. In 1856, he began a decade-long research pursuit involving inheritance patterns in honeybees and plants, ultimately settling on pea plants as his primary **model system** (a system with convenient characteristics used to study a specific biological phenomenon to be applied to other systems). In 1865, Mendel presented the results of his experiments with nearly 30,000 pea plants to the local Natural History Society. He demonstrated that traits are transmitted faithfully from parents to offspring independently of other traits and in dominant and recessive patterns. In 1866, he published his work, *Experiments in Plant Hybridization*,[1] in the proceedings of the Natural History Society of Brünn.

Mendel's work went virtually unnoticed by the scientific community that believed, incorrectly, that the process of inheritance involved a blending of parental traits that produced an intermediate physical appearance in offspring; this hypothetical process appeared to be correct because of what we know now as continuous variation. **Continuous variation** results from the action of many genes to determine a characteristic like human height. Offspring appear to be a "blend" of their parents' traits when we look at characteristics that exhibit continuous variation. The **blending theory of inheritance** asserted that the original parental traits were lost or absorbed by the blending in the offspring, but we now know that this is not the case. Mendel was the first researcher to see it. Instead of continuous characteristics, Mendel worked with traits that were inherited in distinct classes (specifically, violet versus white flowers); this is referred to as **discontinuous variation**. Mendel's choice of these kinds of traits allowed him to see experimentally that the traits were not blended in the offspring, nor were they absorbed, but rather that they kept their distinctness and could be passed on. In 1868, Mendel became abbot of the monastery and exchanged his scientific pursuits for his pastoral duties. He was not recognized for his extraordinary scientific contributions during his lifetime. In fact, it was not until 1900 that his work was rediscovered, reproduced, and revitalized by scientists on the brink of discovering the chromosomal basis of heredity.

Mendel's Model System

Mendel's seminal work was accomplished using the garden pea, *Pisum sativum*, to study inheritance. This species naturally self-fertilizes, such that pollen encounters ova within individual flowers. The flower petals remain sealed tightly until after pollination, preventing pollination from other plants. The result is highly inbred, or "true-breeding," pea plants. These are plants that always produce offspring that look like the parent. By experimenting with true-breeding pea plants, Mendel avoided the appearance of unexpected traits in offspring that might occur if the plants were not true breeding. The garden pea also grows to maturity within one season, meaning that several generations could be evaluated over a relatively short time. Finally, large quantities of garden peas could be cultivated simultaneously, allowing Mendel to conclude that his results did not come about simply by chance.

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1. Johann Gregor Mendel, *Versuche über Pflanzenhybriden Verhandlungen des naturforschenden Vereines in Brünn, Bd. IV für das Jahr*, 1865 Abhandlungen, 3–47. [go here for the English translation **here (http://openstaxcollege.org/l/32mendelPlain)**]

Mendelian Crosses

Mendel performed **hybridizations**, which involve mating two true-breeding individuals that have different traits. In the pea, which is naturally self-pollinating, this is done by manually transferring pollen from the anther of a mature pea plant of one variety to the stigma of a separate mature pea plant of the second variety. In plants, pollen carries the male gametes (sperm) to the stigma, a sticky organ that traps pollen and allows the sperm to move down the pistil to the female gametes (ova) below. To prevent the pea plant that was receiving pollen from self-fertilizing and confounding his results, Mendel painstakingly removed all of the anthers from the plant's flowers before they had a chance to mature.

Plants used in first-generation crosses were called $\mathbf{P_0}$, or parental generation one, plants (**Figure 12.3**). Mendel collected the seeds belonging to the P_0 plants that resulted from each cross and grew them the following season. These offspring were called the $\mathbf{F_1}$, or the first filial (*filial* = offspring, daughter or son), generation. Once Mendel examined the characteristics in the F_1 generation of plants, he allowed them to self-fertilize naturally. He then collected and grew the seeds from the F_1 plants to produce the $\mathbf{F_2}$, or second filial, generation. Mendel's experiments extended beyond the F_2 generation to the F_3 and F_4 generations, and so on, but it was the ratio of characteristics in the P_0–F_1–F_2 generations that were the most intriguing and became the basis for Mendel's postulates.

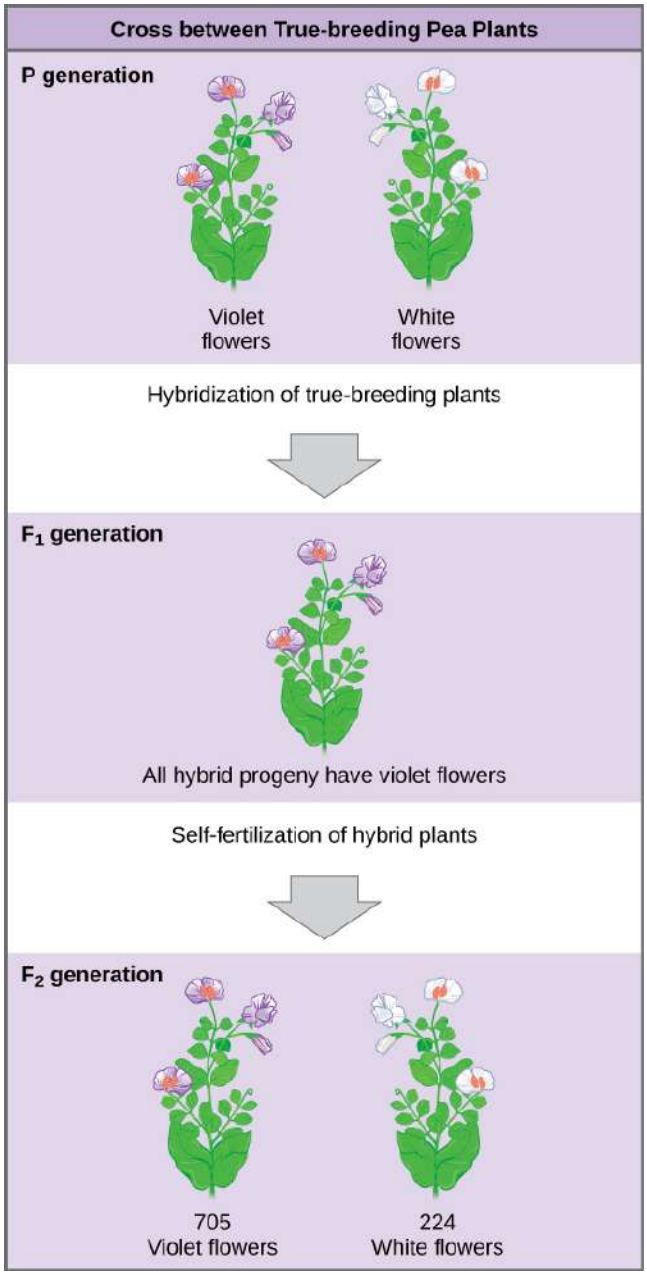


Figure 12.3 In one of his experiments on inheritance patterns, Mendel crossed plants that were true-breeding for violet flower color with plants true-breeding for white flower color (the P generation). The resulting hybrids in the F_1 generation all had violet flowers. In the F_2 generation, approximately three quarters of the plants had violet flowers, and one quarter had white flowers.

Garden Pea Characteristics Revealed the Basics of Heredity

In his 1865 publication, Mendel reported the results of his crosses involving seven different characteristics, each with two contrasting traits. A **trait** is defined as a variation in the physical appearance of a heritable characteristic. The characteristics included plant height, seed texture, seed color, flower color, pea pod size, pea pod color, and flower position. For the characteristic of flower color, for example, the two contrasting traits were white versus violet. To fully examine each characteristic, Mendel generated large numbers of F_1 and F_2 plants, reporting results from 19,959 F_2 plants alone. His findings were consistent.

What results did Mendel find in his crosses for flower color? First, Mendel confirmed that he had plants that bred true for white or violet flower color. Regardless of how many generations Mendel examined, all self-crossed offspring of parents with white flowers had white flowers, and all self-crossed offspring of parents with violet flowers had violet flowers. In addition, Mendel confirmed that, other than flower color, the pea plants were physically identical.

Once these validations were complete, Mendel applied the pollen from a plant with violet flowers to the stigma of a plant with white flowers. After gathering and sowing the seeds that resulted from this cross, Mendel found that 100 percent of the F_1 hybrid generation had violet flowers. Conventional wisdom at that time would have predicted the hybrid flowers to be pale violet or for hybrid plants to have equal numbers of white and violet flowers. In other words, the contrasting parental traits were expected to blend in the offspring. Instead, Mendel's results demonstrated that the white flower trait in the F_1 generation had completely disappeared.

Importantly, Mendel did not stop his experimentation there. He allowed the F_1 plants to self-fertilize and found that, of F_2-generation plants, 705 had violet flowers and 224 had white flowers. This was a ratio of 3.15 violet flowers per one white flower, or approximately 3:1. When Mendel transferred pollen from a plant with violet flowers to the stigma of a plant with white flowers and vice versa, he obtained about the same ratio regardless of which parent, male or female, contributed which trait. This is called a **reciprocal cross**—a paired cross in which the respective traits of the male and female in one cross become the respective traits of the female and male in the other cross. For the other six characteristics Mendel examined, the F_1 and F_2 generations behaved in the same way as they had for flower color. One of the two traits would disappear completely from the F_1 generation only to reappear in the F_2 generation at a ratio of approximately 3:1 (Table 12.1).

The Results of Mendel's Garden Pea Hybridizations

Characteristic	Contrasting P_0 Traits	F_1 Offspring Traits	F_2 Offspring Traits	F_2 Trait Ratios
Flower color	Violet vs. white	100 percent violet	705 violet 224 white	3.15:1
Flower position	Axial vs. terminal	100 percent axial	651 axial 207 terminal	3.14:1
Plant height	Tall vs. dwarf	100 percent tall	787 tall 277 dwarf	2.84:1
Seed texture	Round vs. wrinkled	100 percent round	5,474 round 1,850 wrinkled	2.96:1
Seed color	Yellow vs. green	100 percent yellow	6,022 yellow 2,001 green	3.01:1
Pea pod texture	Inflated vs. constricted	100 percent inflated	882 inflated 299 constricted	2.95:1
Pea pod color	Green vs. yellow	100 percent green	428 green 152 yellow	2.82:1

Table 12.1

Upon compiling his results for many thousands of plants, Mendel concluded that the characteristics could be divided into expressed and latent traits. He called these, respectively, dominant and recessive traits. **Dominant traits** are those that are inherited unchanged in a hybridization. **Recessive traits** become latent, or disappear, in the offspring of a hybridization. The recessive trait does, however, reappear in the progeny of the hybrid offspring. An example of a dominant trait is the violet-flower trait. For this same characteristic (flower color), white-colored flowers are a recessive trait. The fact that the recessive trait reappeared in the F_2 generation meant that the traits remained separate (not blended) in the plants of the F_1 generation. Mendel also proposed that plants possessed two copies of the trait for the flower-color characteristic, and that each parent transmitted one of its two copies to its offspring, where they came together. Moreover, the physical observation of a dominant trait could mean that the genetic composition of the organism included two dominant versions of the characteristic or that it included one dominant and one recessive version. Conversely, the observation of a recessive trait meant that the organism lacked any dominant versions of this characteristic.

So why did Mendel repeatedly obtain 3:1 ratios in his crosses? To understand how Mendel deduced the basic mechanisms of inheritance that lead to such ratios, we must first review the laws of probability.

science practices CONNECTION for AP® Courses

Think About It

Students are performing a cross involving seed color in garden pea plants. Yellow seed color is dominant to green seed color. What F1 offspring would be expected when cross true-breeding plants with green seeds with true-breading plants with yellow seeds? Express the answer(s) as percentage.

Probability Basics

Probabilities are mathematical measures of likelihood. The empirical probability of an event is calculated by dividing the number of times the event occurs by the total number of opportunities for the event to occur. It is also possible to calculate theoretical probabilities by dividing the number of times that an event is expected to occur by the number of times that it could occur. Empirical probabilities come from observations, like those of Mendel. Theoretical probabilities come from knowing how the events are produced and assuming that the probabilities of individual outcomes are equal. A probability of one for some event indicates that it is guaranteed to occur, whereas a probability of zero indicates that it is guaranteed not to occur. An example of a genetic event is a round seed produced by a pea plant. In his experiment, Mendel demonstrated that the probability of the event "round seed" occurring was one in the F_1 offspring of true-breeding parents, one of which has round seeds and one of which has wrinkled seeds. When the F_1 plants were subsequently self-crossed, the probability of any given F_2 offspring having round seeds was now three out of four. In other words, in a large population of F_2 offspring chosen at random, 75 percent were expected to have round seeds, whereas 25 percent were expected to have wrinkled seeds. Using large numbers of crosses, Mendel was able to calculate probabilities and use these to predict the outcomes of other crosses.

The Product Rule and Sum Rule

Mendel demonstrated that the pea-plant characteristics he studied were transmitted as discrete units from parent to offspring. As will be discussed, Mendel also determined that different characteristics, like seed color and seed texture, were transmitted independently of one another and could be considered in separate probability analyses. For instance, performing a cross between a plant with green, wrinkled seeds and a plant with yellow, round seeds still produced offspring that had a 3:1 ratio of green:yellow seeds (ignoring seed texture) and a 3:1 ratio of round:wrinkled seeds (ignoring seed color). The characteristics of color and texture did not influence each other.

The **product rule** of probability can be applied to this phenomenon of the independent transmission of characteristics. The product rule states that the probability of two independent events occurring together can be calculated by multiplying the individual probabilities of each event occurring alone. To demonstrate the product rule, imagine that you are rolling a six-sided die (D) and flipping a penny (P) at the same time. The die may roll any number from 1–6 ($D_{\#}$), whereas the penny may turn up heads (P_H) or tails (P_T). The outcome of rolling the die has no effect on the outcome of flipping the penny and vice versa. There are 12 possible outcomes of this action (Table 12.2), and each event is expected to occur with equal probability.

Twelve Equally Likely Outcomes of Rolling a Die and Flipping a Penny

Rolling Die	Flipping Penny
D_1	P_H
D_1	P_T
D_2	P_H
D_2	P_T
D_3	P_H

Table 12.2

Twelve Equally Likely Outcomes of Rolling a Die and Flipping a Penny

Rolling Die	Flipping Penny
D_3	P_T
D_4	P_H
D_4	P_T
D_5	P_H
D_5	P_T
D_6	P_H
D_6	P_T

Table 12.2

Of the 12 possible outcomes, the die has a 2/12 (or 1/6) probability of rolling a two, and the penny has a 6/12 (or 1/2) probability of coming up heads. By the product rule, the probability that you will obtain the combined outcome 2 and heads is: (D_2) x (P_H) = (1/6) x (1/2) or 1/12 (**Table 12.3**). Notice the word "and" in the description of the probability. The "and" is a signal to apply the product rule. For example, consider how the product rule is applied to the dihybrid cross: the probability of having both dominant traits in the F_2 progeny is the product of the probabilities of having the dominant trait for each characteristic, as shown here:

$$\frac{3}{4} \times \frac{3}{4} = \frac{9}{16}$$

On the other hand, the **sum rule** of probability is applied when considering two mutually exclusive outcomes that can come about by more than one pathway. The sum rule states that the probability of the occurrence of one event or the other event, of two mutually exclusive events, is the sum of their individual probabilities. Notice the word "or" in the description of the probability. The "or" indicates that you should apply the sum rule. In this case, let's imagine you are flipping a penny (P) and a quarter (Q). What is the probability of one coin coming up heads and one coin coming up tails? This outcome can be achieved by two cases: the penny may be heads (P_H) and the quarter may be tails (Q_T), or the quarter may be heads (Q_H) and the penny may be tails (P_T). Either case fulfills the outcome. By the sum rule, we calculate the probability of obtaining one head and one tail as $[(P_H) \times (Q_T)] + [(Q_H) \times (P_T)] = [(1/2) \times (1/2)] + [(1/2) \times (1/2)] = 1/2$ (**Table 12.3**). You should also notice that we used the product rule to calculate the probability of P_H and Q_T, and also the probability of P_T and Q_H, before we summed them. Again, the sum rule can be applied to show the probability of having just one dominant trait in the F_2 generation of a dihybrid cross:

$$\frac{3}{16} + \frac{3}{4} = \frac{15}{16}$$

The Product Rule and Sum Rule

Product Rule	Sum Rule
For independent events A and B, the probability (P) of them both occurring (A *and* B) is $(P_A \times P_B)$	For mutually exclusive events A and B, the probability (P) that at least one occurs (A *or* B) is $(P_A + P_B)$

Table 12.3

To use probability laws in practice, it is necessary to work with large sample sizes because small sample sizes are prone to deviations caused by chance. The large quantities of pea plants that Mendel examined allowed him calculate the probabilities of the traits appearing in his F_2 generation. As you will learn, this discovery meant that when parental traits were known, the offspring's traits could be predicted accurately even before fertilization.

12.2 | Characteristics and Traits

In this section, you will explore the following questions:

- What is the relationship between genotypes and phenotypes in dominant and recessive gene systems?
- How can a Punnett square be used to calculate expected proportions of genotypes and phenotypes in a monohybrid cross?
- How do phenomena such as incomplete dominance, codominance, recessive lethals, multiple alleles, and sex linkage explain deviations from Mendel's model of inheritance?

Connection for AP® Courses

The characteristics that Mendel evaluated in his pea plants were each expressed as one of two versions, or traits (e.g., green peas versus yellow peas). As we will explore in more detail in later chapters, the physical expression of characteristics is accomplished through the expression of genes (sequences of DNA), carried on chromosomes. The genetic makeup of peas consists of two similar, or homologous (remember this term from Chapter 11), copies of each chromosome, one from each parent. Through meiosis, diploid organisms utilize meiosis to produce haploid ($1n$) gametes that participate in fertilization. For cases in which a single gene controls a single characteristic, such as pea color, a diploid organism has genetic copies that may or may not encode the same version of the characteristic. These gene variations (e.g., green peas versus yellow peas) are called alleles.

Different alleles for a given gene in a diploid organism interact to express physical characteristics such as pea color in plants or hairline appearance in humans. The observable traits of an organism are referred to as its phenotype. The organism's underlying genetic makeup, i.e., the combination of alleles, is called its genotype. When diploid organisms carry the same alleles for a given trait, they are said to be homozygous for the genotype; when they carry different alleles, they are said to be heterozygous. For a gene whose expression is Mendelian (Section 12.1), homozygous dominant and heterozygous organisms will look identical; that is, they will have different genotypes but the same phenotype. The recessive allele will only be observed in homozygous recessive individuals.

However, alleles do not always behave in dominant and recessive patterns. In other words, there are exceptions to Mendel's model of inheritance. For example, incomplete dominance describes situation in which the heterozygote exhibits a phenotype that is intermediate between the homozygous phenotypes (e.g., a pink-flowered offspring is produced from a cross between a red-flowered parent and a white-flowered parent). Codominance describes the simultaneous expression of both of the alleles in the heterozygote (e.g., human blood types). It is also common for more than two alleles of a gene to exist in a population (e.g., variations in sizes of pumpkins). In humans, as in many animals and some plants, females have two X chromosomes, and males have one X chromosome and one Y chromosome. Genes on the X chromosome are X-linked, and males inherit and express only one allele for the gene (e.g., hemophilia, color-blindness). Some alleles can also be lethal, so their phenotype will never be observed.

Many human genetic disorders, including albinism, cystic fibrosis, and Huntington's disease can be explained on the basis of simple Mendelian inheritance patterns created by pedigree analysis. (In later Chapters we will learn how DNA analysis can be used to diagnose genetic disorders). Punnett squares are useful tools that apply the rules of probability and meiosis to predict the possible outcomes of genetic crosses. Test crosses are done to determine whether or not an individual is homozygous or heterozygous by crossing the individual with a homozygous recessive.

Information presented and the examples highlighted in the section support concepts outlined in Big Idea 3 of the AP® Biology Curriculum Framework. The learning objectives (LO) listed in the Curriculum Framework provide a transparent foundation for the AP® Biology course, an inquiry-based laboratory experience, instructional activities, and AP® exam questions. A learning objective merges required content with one or more of the seven science practices (SP).

Big Idea 3	Living systems store, retrieve, transmit and respond to information essential to life processes.
Enduring Understanding 3.A	Heritable information provides for continuity of life.

Essential Knowledge	**3.A.3** The chromosomal basis of inheritance proposed by Mendel provides an understanding of the pattern of passage of genes from parent to offspring.
Science Practice	**1.1** The student can create representations and models of natural or man-made phenomena and systems in the domain.
Science Practice	**7.2** The student can connect concepts in and across domain(s) to generalize or extrapolate in and/or across enduring understandings and/or big ideas.
Learning Objective	**3.12** The student is able to construct a representation (e.g., Punnett square) that connects the process of meiosis to the passage of traits from parent to offspring.
Essential Knowledge	**3.A.3** The chromosomal basis of inheritance proposed by Mendel provides an understanding of the pattern of passage of genes from parent to offspring.
Science Practice	**3.1** The student can pose scientific questions.
Learning Objective	**3.13** The student is able to pose questions about ethical, social or medical issues surrounding human genetic disorders.
Essential Knowledge	**3.A.3** The chromosomal basis of inheritance proposed by Mendel provides an understanding of the pattern of passage of genes from parent to offspring.
Science Practice	**2.2** The student can apply mathematical routines to quantities that describe natural phenomena.
Learning Objective	**3.14** The student is able to apply mathematical routines to determine Mendelian patterns of inheritance provided by data sets.
Essential Knowledge	**3.A.4** The inheritance patterns of many traits cannot be explained by simple Mendelian genetics.
Science Practice	**6.5** The student can evaluate alternative scientific explanations.
Learning Objective	**3.15** The student is able to explain deviations from Mendel's model of the inheritance of traits.
Essential Knowledge	**3.A.4** The inheritance patterns of many traits cannot be explained by simple Mendelian genetics.
Science Practice	**6.3** The student can articulate the reasons that scientific explanations and theories are refined or replaced.
Learning Objective	**3.16** The student is able to explain how the inheritance pattern of many traits cannot be accounted for by Mendelian genetics.
Essential Knowledge	**3.A.4** The inheritance patterns of many traits cannot be explained by simple Mendelian genetics.
Science Practice	**1.2** The student can describe representations and models of natural or man-made phenomena and systems in the domain.
Learning Objective	**3.17** The student is able to describe representations of an appropriate example of inheritance patterns that cannot be explained by Mendel's model of the inheritance of traits.

The Science Practice Challenge Questions contain additional test questions for this section that will help you prepare for the AP exam. These questions address the following standards:
[APLO 3.12][APLO 3.14][APLO 3.16][APLO 3.11][APLO 3.13][APLO 3.17]

The seven characteristics that Mendel evaluated in his pea plants were each expressed as one of two versions, or traits. The physical expression of characteristics is accomplished through the expression of genes carried on chromosomes. The genetic makeup of peas consists of two similar or homologous copies of each chromosome, one from each parent. Each pair of homologous chromosomes has the same linear order of genes. In other words, peas are diploid organisms in that they have two copies of each chromosome. The same is true for many other plants and for virtually all animals. Diploid organisms utilize meiosis to produce haploid gametes, which contain one copy of each homologous chromosome that unite

at fertilization to create a diploid zygote.

For cases in which a single gene controls a single characteristic, a diploid organism has two genetic copies that may or may not encode the same version of that characteristic. Gene variants that arise by mutation and exist at the same relative locations on homologous chromosomes are called **alleles**. Mendel examined the inheritance of genes with just two allele forms, but it is common to encounter more than two alleles for any given gene in a natural population.

Phenotypes and Genotypes

Two alleles for a given gene in a diploid organism are expressed and interact to produce physical characteristics. The observable traits expressed by an organism are referred to as its **phenotype**. An organism's underlying genetic makeup, consisting of both physically visible and non-expressed alleles, is called its **genotype**. Mendel's hybridization experiments demonstrate the difference between phenotype and genotype. When true-breeding plants in which one parent had yellow pods and one had green pods were cross-fertilized, all of the F_1 hybrid offspring had yellow pods. That is, the hybrid offspring were phenotypically identical to the true-breeding parent with yellow pods. However, we know that the allele donated by the parent with green pods was not simply lost because it reappeared in some of the F_2 offspring. Therefore, the F_1 plants must have been genotypically different from the parent with yellow pods.

The P_1 plants that Mendel used in his experiments were each homozygous for the trait he was studying. Diploid organisms that are **homozygous** at a given gene, or locus, have two identical alleles for that gene on their homologous chromosomes. Mendel's parental pea plants always bred true because both of the gametes produced carried the same trait. When P_1 plants with contrasting traits were cross-fertilized, all of the offspring were **heterozygous** for the contrasting trait, meaning that their genotype reflected that they had different alleles for the gene being examined.

Dominant and Recessive Alleles

Our discussion of homozygous and heterozygous organisms brings us to why the F_1 heterozygous offspring were identical to one of the parents, rather than expressing both alleles. In all seven pea-plant characteristics, one of the two contrasting alleles was dominant, and the other was recessive. Mendel called the dominant allele the expressed unit factor; the recessive allele was referred to as the latent unit factor. We now know that these so-called unit factors are actually genes on homologous chromosome pairs. For a gene that is expressed in a dominant and recessive pattern, homozygous dominant and heterozygous organisms will look identical (that is, they will have different genotypes but the same phenotype). The recessive allele will only be observed in homozygous recessive individuals (**Table 12.4**).

Human Inheritance in Dominant and Recessive Patterns

Dominant Traits	Recessive Traits
Achondroplasia	Albinism
Brachydactyly	Cystic fibrosis
Huntington's disease	Duchenne muscular dystrophy
Marfan syndrome	Galactosemia
Neurofibromatosis	Phenylketonuria
Widow's peak	Sickle-cell anemia
Wooly hair	Tay-Sachs disease

Table 12.4 This is a table of human inheritance traits and categorizes dominate versus recessive patterns.

Several conventions exist for referring to genes and alleles. For the purposes of this chapter, we will abbreviate genes using the first letter of the gene's corresponding dominant trait. For example, violet is the dominant trait for a pea plant's flower color, so the flower-color gene would be abbreviated as *V* (note that it is customary to italicize gene designations). Furthermore, we will use uppercase and lowercase letters to represent dominant and recessive alleles, respectively. Therefore, we would refer to the genotype of a homozygous dominant pea plant with violet flowers as *VV*, a homozygous recessive pea plant with white flowers as *vv*, and a heterozygous pea plant with violet flowers as *Vv*.

The Punnett Square Approach for a Monohybrid Cross

When fertilization occurs between two true-breeding parents that differ in only one characteristic, the process is called a

monohybrid cross, and the resulting offspring are monohybrids. Mendel performed seven monohybrid crosses involving contrasting traits for each characteristic. On the basis of his results in F_1 and F_2 generations, Mendel postulated that each parent in the monohybrid cross contributed one of two paired unit factors to each offspring, and every possible combination of unit factors was equally likely.

To demonstrate a monohybrid cross, consider the case of true-breeding pea plants with yellow versus green pea seeds. The dominant seed color is yellow; therefore, the parental genotypes were *YY* for the plants with yellow seeds and *yy* for the plants with green seeds, respectively. A **Punnett square**, devised by the British geneticist Reginald Punnett, can be drawn that applies the rules of probability to predict the possible outcomes of a genetic cross or mating and their expected frequencies. To prepare a Punnett square, all possible combinations of the parental alleles are listed along the top (for one parent) and side (for the other parent) of a grid, representing their meiotic segregation into haploid gametes. Then the combinations of egg and sperm are made in the boxes in the table to show which alleles are combining. Each box then represents the diploid genotype of a zygote, or fertilized egg, that could result from this mating. Because each possibility is equally likely, genotypic ratios can be determined from a Punnett square. If the pattern of inheritance (dominant or recessive) is known, the phenotypic ratios can be inferred as well. For a monohybrid cross of two true-breeding parents, each parent contributes one type of allele. In this case, only one genotype is possible. All offspring are *Yy* and have yellow seeds (Figure 12.4).

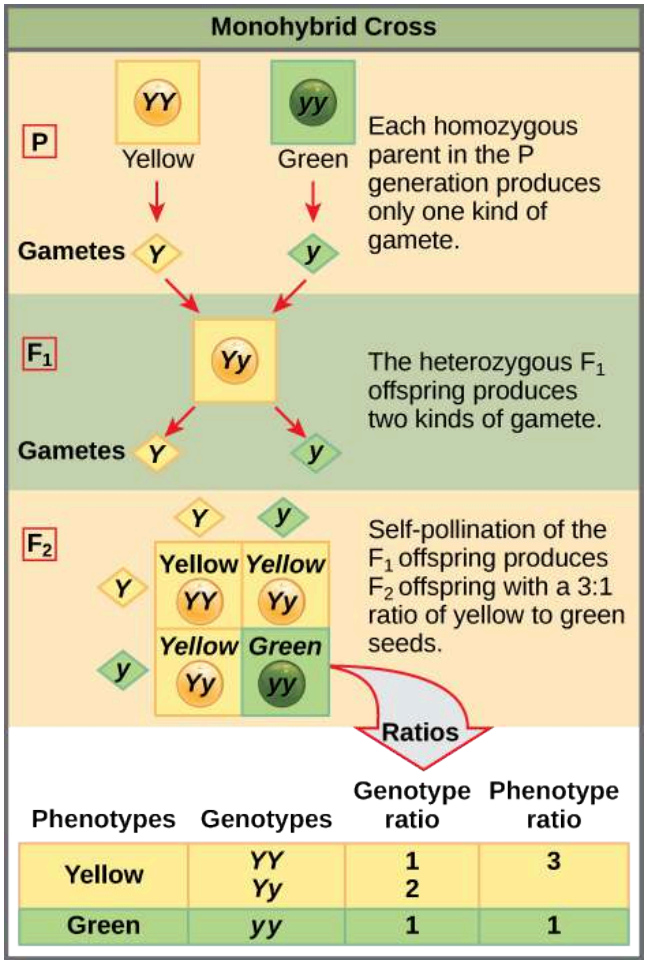


Figure 12.4 In the P generation, pea plants that are true-breeding for the dominant yellow phenotype are crossed with plants with the recessive green phenotype. This cross produces F_1 heterozygotes with a yellow phenotype. Punnett square analysis can be used to predict the genotypes of the F_2 generation.

A self-cross of one of the *Yy* heterozygous offspring can be represented in a 2 × 2 Punnett square because each parent can donate one of two different alleles. Therefore, the offspring can potentially have one of four allele combinations: *YY*, *Yy*, *yY*, or *yy* (Figure 12.4). Notice that there are two ways to obtain the *Yy* genotype: a *Y* from the egg and a *y* from the sperm, or a *y* from the egg and a *Y* from the sperm. Both of these possibilities must be counted. Recall that Mendel's pea-plant characteristics behaved in the same way in reciprocal crosses. Therefore, the two possible heterozygous combinations produce offspring that are genotypically and phenotypically identical despite their dominant and recessive alleles deriving

from different parents. They are grouped together. Because fertilization is a random event, we expect each combination to be equally likely and for the offspring to exhibit a ratio of *YY*:*Yy*:*yy* genotypes of 1:2:1 (**Figure 12.4**). Furthermore, because the *YY* and *Yy* offspring have yellow seeds and are phenotypically identical, applying the sum rule of probability, we expect the offspring to exhibit a phenotypic ratio of 3 yellow:1 green. Indeed, working with large sample sizes, Mendel observed approximately this ratio in every F_2 generation resulting from crosses for individual traits.

Mendel validated these results by performing an F_3 cross in which he self-crossed the dominant- and recessive-expressing F_2 plants. When he self-crossed the plants expressing green seeds, all of the offspring had green seeds, confirming that all green seeds had homozygous genotypes of *yy*. When he self-crossed the F_2 plants expressing yellow seeds, he found that one-third of the plants bred true, and two-thirds of the plants segregated at a 3:1 ratio of yellow:green seeds. In this case, the true-breeding plants had homozygous (*YY*) genotypes, whereas the segregating plants corresponded to the heterozygous (*Yy*) genotype. When these plants self-fertilized, the outcome was just like the F_1 self-fertilizing cross.

The Test Cross Distinguishes the Dominant Phenotype

Beyond predicting the offspring of a cross between known homozygous or heterozygous parents, Mendel also developed a way to determine whether an organism that expressed a dominant trait was a heterozygote or a homozygote. Called the **test cross**, this technique is still used by plant and animal breeders. In a test cross, the dominant-expressing organism is crossed with an organism that is homozygous recessive for the same characteristic. If the dominant-expressing organism is a homozygote, then all F_1 offspring will be heterozygotes expressing the dominant trait (**Figure 12.5**). Alternatively, if the dominant expressing organism is a heterozygote, the F_1 offspring will exhibit a 1:1 ratio of heterozygotes and recessive homozygotes (**Figure 12.5**). The test cross further validates Mendel’s postulate that pairs of unit factors segregate equally.

visual CONNECTION

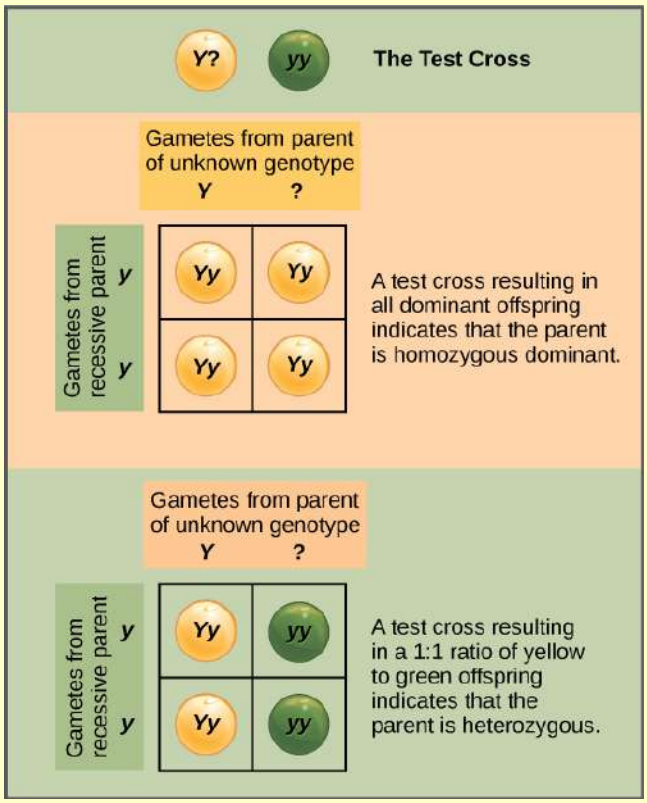


Figure 12.5 A test cross can be performed to determine whether an organism expressing a dominant trait is a homozygote or a heterozygote.

In pea plants, round peas (R) are dominant to wrinkled peas (r).You do a test cross between a pea plant with wrinkled peas (genotype rr) and a plant of unknown genotype that has round peas. You end up with three plants, all which have round peas. From this data, can you tell if the round pea parent plant is homozygous dominant or heterozygous? If the round pea parent plant is heterozygous, what is the probability that a random sample of 3 progeny peas will all be round?

a. The data set is too small to predict the genotype of the round pea plant. Assuming that the unknown parent is heterozygous, the probability of having only round pea plants from a random sample of 3 progeny will be $\frac{1}{8}$.

b. The genotype of the unknown round pea plant is Rr. Assuming that the unknown parent is heterozygous, then the probability of having only round pea plants from a random sample of 3 progeny will be $\frac{1}{4}$.

c. The genotype of the unknown round pea plant is Rr. Assuming that the unknown parent is heterozygous, the probability of having only round pea plants from a random sample of 3 progeny will be $\frac{1}{2}$.

d. The data set is too small to predict the genotype of the round pea plant. The probability of having only round pea plants from a random sample of 3 progeny will be $\frac{1}{6}$.

Many human diseases are genetically inherited. A healthy person in a family in which some members suffer from a recessive genetic disorder may want to know if he or she has the disease-causing gene and what risk exists of passing the disorder on to his or her offspring. Of course, doing a test cross in humans is unethical and impractical. Instead, geneticists use **pedigree**

analysis to study the inheritance pattern of human genetic diseases (**Figure 12.6**).

visual CONNECTION

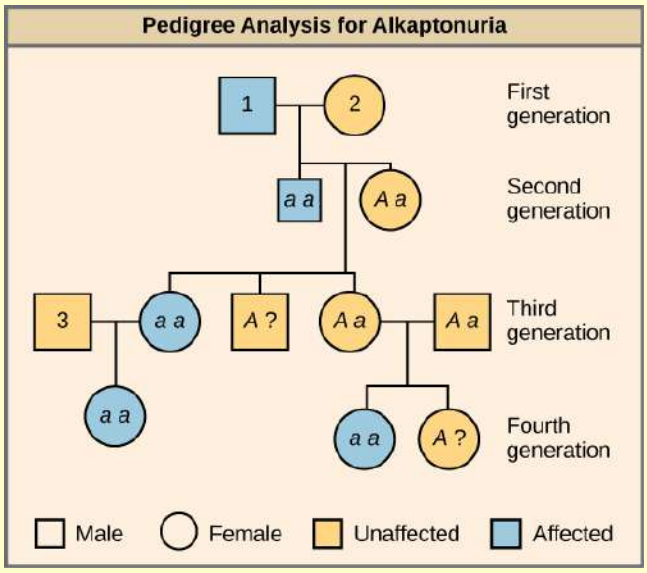
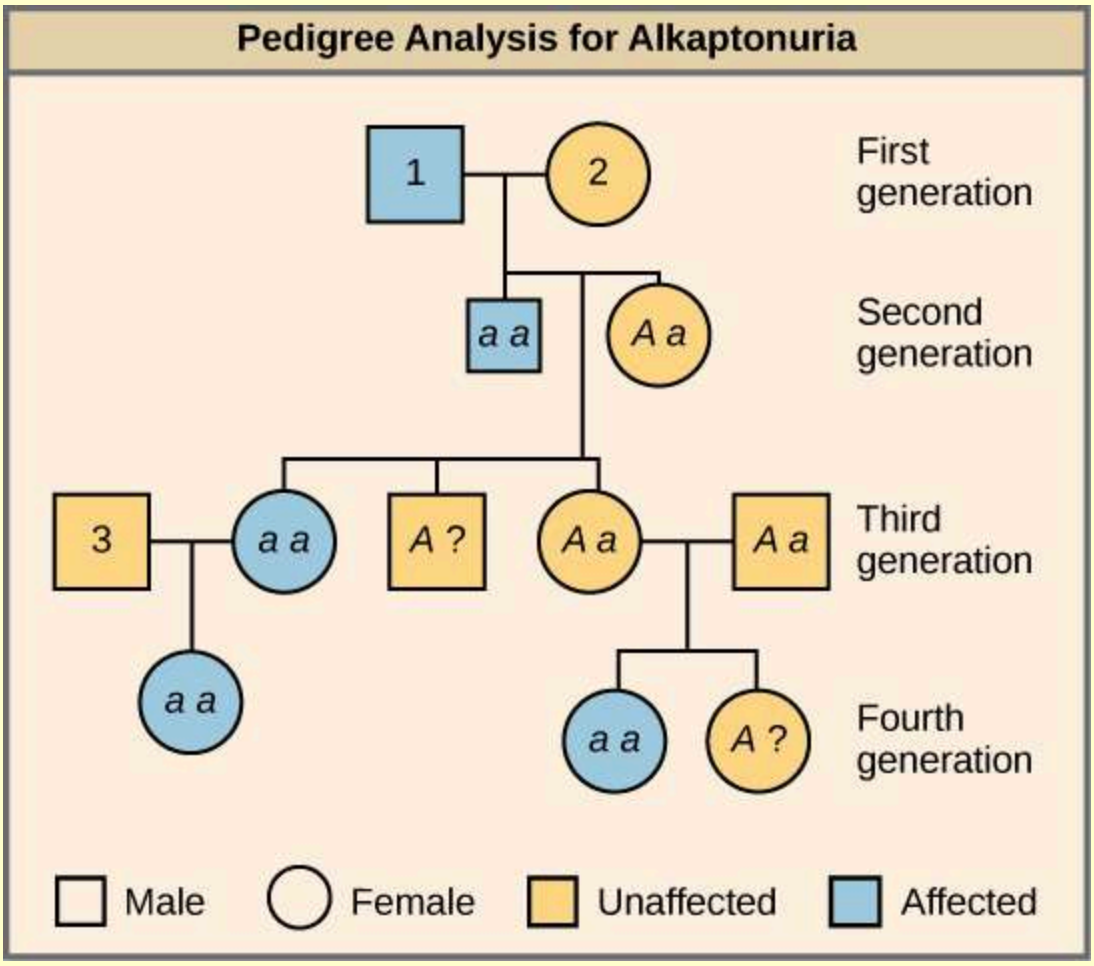


Figure 12.6 Alkaptonuria is a recessive genetic disorder in which two amino acids, phenylalanine and tyrosine, are not properly metabolized. Affected individuals may have darkened skin and brown urine, and may suffer joint damage and other complications. In this pedigree, individuals with the disorder are indicated in blue and have the genotype *aa*. Unaffected individuals are indicated in yellow and have the genotype *AA* or *Aa*. Note that it is often possible to determine a person's genotype from the genotype of their offspring. For example, if neither parent has the disorder but their child does, they must be heterozygous. Two individuals on the pedigree have an unaffected phenotype but unknown genotype. Because they do not have the disorder, they must have at least one normal allele, so their genotype gets the "*A?*" designation.



Using the pedigree above, what are the genotypes of the individuals labeled 1, 2 and 3?

a. 1- aa , 2-AA, 3- AA
b. 1-aa, 2-Aa, 3- Aa
c. 1-aa, 2-Aa, 3-AA
d. 1-Aa, 2-Aa, 3-Aa

Alternatives to Dominance and Recessiveness

Mendel's experiments with pea plants suggested that: (1) two "units" or alleles exist for every gene; (2) alleles maintain their integrity in each generation (no blending); and (3) in the presence of the dominant allele, the recessive allele is hidden and makes no contribution to the phenotype. Therefore, recessive alleles can be "carried" and not expressed by individuals. Such heterozygous individuals are sometimes referred to as "carriers." Further genetic studies in other plants and animals have shown that much more complexity exists, but that the fundamental principles of Mendelian genetics still hold true. In the sections to follow, we consider some of the extensions of Mendelism. If Mendel had chosen an experimental system that exhibited these genetic complexities, it's possible that he would not have understood what his results meant.

Incomplete Dominance

Mendel's results, that traits are inherited as dominant and recessive pairs, contradicted the view at that time that offspring exhibited a blend of their parents' traits. However, the heterozygote phenotype occasionally does appear to be intermediate between the two parents. For example, in the snapdragon, *Antirrhinum majus* (**Figure 12.7**), a cross between a homozygous parent with white flowers (C^WC^W) and a homozygous parent with red flowers (C^RC^R) will produce offspring with pink flowers (C^RC^W). (Note that different genotypic abbreviations are used for Mendelian extensions to distinguish these patterns from simple dominance and recessiveness.) This pattern of inheritance is described as **incomplete dominance**, denoting

the expression of two contrasting alleles such that the individual displays an intermediate phenotype. The allele for red flowers is incompletely dominant over the allele for white flowers. However, the results of a heterozygote self-cross can still be predicted, just as with Mendelian dominant and recessive crosses. In this case, the genotypic ratio would be 1 C^RC^R:2 C^RC^W:1 C^WC^W, and the phenotypic ratio would be 1:2:1 for red:pink:white.

Figure 12.7 These pink flowers of a heterozygote snapdragon result from incomplete dominance. (credit: "storebukkebruse"/Flickr)

Codominance

A variation on incomplete dominance is **codominance**, in which both alleles for the same characteristic are simultaneously expressed in the heterozygote. An example of codominance is the MN blood groups of humans. The M and N alleles are expressed in the form of an M or N antigen present on the surface of red blood cells. Homozygotes (L^ML^M and L^NL^N) express either the M or the N allele, and heterozygotes (L^ML^N) express both alleles equally. In a self-cross between heterozygotes expressing a codominant trait, the three possible offspring genotypes are phenotypically distinct. However, the 1:2:1 genotypic ratio characteristic of a Mendelian monohybrid cross still applies.

Multiple Alleles

Mendel implied that only two alleles, one dominant and one recessive, could exist for a given gene. We now know that this is an oversimplification. Although individual humans (and all diploid organisms) can only have two alleles for a given gene, multiple alleles may exist at the population level such that many combinations of two alleles are observed. Note that when many alleles exist for the same gene, the convention is to denote the most common phenotype or genotype among wild animals as the **wild type** (often abbreviated "+"); this is considered the standard or norm. All other phenotypes or genotypes are considered **variants** of this standard, meaning that they deviate from the wild type. The variant may be recessive or dominant to the wild-type allele.

An example of multiple alleles is coat color in rabbits (**Figure 12.8**). Here, four alleles exist for the *c* gene. The wild-type version, C^+C^+, is expressed as brown fur. The chinchilla phenotype, $c^{ch}c^{ch}$, is expressed as black-tipped white fur. The Himalayan phenotype, c^hc^h, has black fur on the extremities and white fur elsewhere. Finally, the albino, or "colorless" phenotype, *cc*, is expressed as white fur. In cases of multiple alleles, dominance hierarchies can exist. In this case, the wild-type allele is dominant over all the others, chinchilla is incompletely dominant over Himalayan and albino, and Himalayan is dominant over albino. This hierarchy, or allelic series, was revealed by observing the phenotypes of each possible heterozygote offspring.

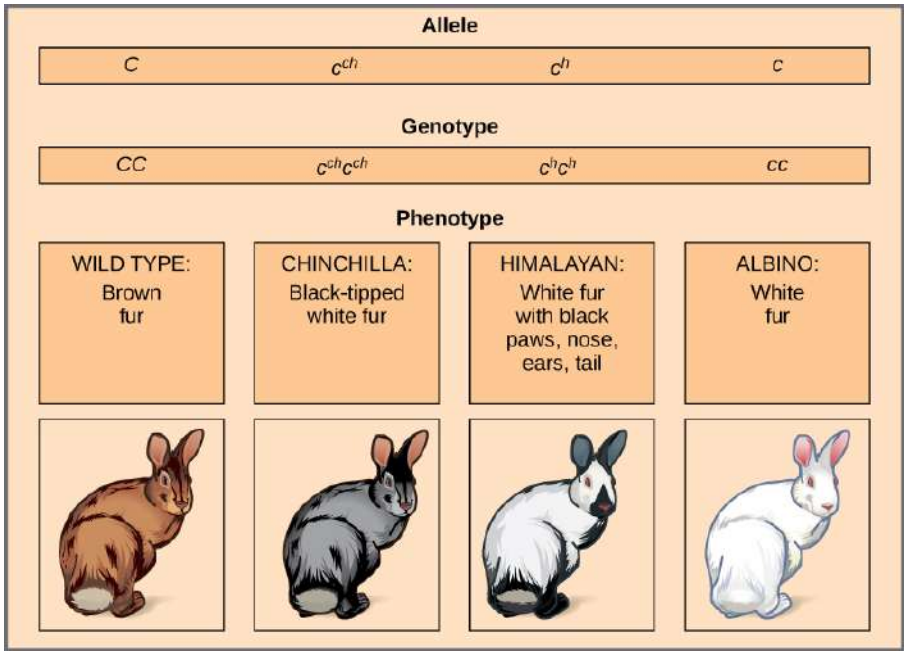


Figure 12.8 Four different alleles exist for the rabbit coat color (*C*) gene.

The complete dominance of a wild-type phenotype over all other mutants often occurs as an effect of "dosage" of a specific gene product, such that the wild-type allele supplies the correct amount of gene product whereas the mutant alleles cannot. For the allelic series in rabbits, the wild-type allele may supply a given dosage of fur pigment, whereas the mutants supply a lesser dosage or none at all. Interestingly, the Himalayan phenotype is the result of an allele that produces a temperature-sensitive gene product that only produces pigment in the cooler extremities of the rabbit's body.

Alternatively, one mutant allele can be dominant over all other phenotypes, including the wild type. This may occur when the mutant allele somehow interferes with the genetic message so that even a heterozygote with one wild-type allele copy expresses the mutant phenotype. One way in which the mutant allele can interfere is by enhancing the function of the wild-type gene product or changing its distribution in the body. One example of this is the *Antennapedia* mutation in *Drosophila* (**Figure 12.9**). In this case, the mutant allele expands the distribution of the gene product, and as a result, the *Antennapedia* heterozygote develops legs on its head where its antennae should be.

Figure 12.9 As seen in comparing the wild-type *Drosophila* (left) and the *Antennapedia* mutant (right), the *Antennapedia* mutant has legs on its head in place of antennae.

evolution CONNECTION

Multiple Alleles Confer Drug Resistance in the Malaria Parasite

Malaria is a parasitic disease in humans that is transmitted by infected female mosquitoes, including *Anopheles gambiae* (**Figure 12.10a**), and is characterized by cyclic high fevers, chills, flu-like symptoms, and severe anemia. *Plasmodium falciparum* and *P. vivax* are the most common causative agents of malaria, and *P. falciparum* is the most deadly (**Figure 12.10b**). When promptly and correctly treated, *P. falciparum* malaria has a mortality rate of 0.1 percent. However, in some parts of the world, the parasite has evolved resistance to commonly used malaria treatments, so the most effective malarial treatments can vary by geographic region.

(a) (b)

Figure 12.10 The (a) *Anopheles gambiae*, or African malaria mosquito, acts as a vector in the transmission to humans of the malaria-causing parasite (b) *Plasmodium falciparum*, here visualized using false-color transmission electron microscopy. (credit a: James D. Gathany; credit b: Ute Frevert; false color by Margaret Shear; scale-bar data from Matt Russell)

In Southeast Asia, Africa, and South America, *P. falciparum* has developed resistance to the anti-malarial drugs chloroquine, mefloquine, and sulfadoxine-pyrimethamine. *P. falciparum*, which is haploid during the life stage in which it is infectious to humans, has evolved multiple drug-resistant mutant alleles of the *dhps* gene. Varying degrees of sulfadoxine resistance are associated with each of these alleles. Being haploid, *P. falciparum* needs only one drug-resistant allele to express this trait.

In Southeast Asia, different sulfadoxine-resistant alleles of the *dhps* gene are localized to different geographic regions. This is a common evolutionary phenomenon that occurs because drug-resistant mutants arise in a population and interbreed with other *P. falciparum* isolates in close proximity. Sulfadoxine-resistant parasites cause considerable human hardship in regions where this drug is widely used as an over-the-counter malaria remedy. As is common with pathogens that multiply to large numbers within an infection cycle, *P. falciparum* evolves relatively rapidly (over a decade or so) in response to the selective pressure of commonly used anti-malarial drugs. For this reason, scientists must constantly work to develop new drugs or drug combinations to combat the worldwide malaria burden.[2]

According to this passage, why does *P. falciparum* only need one drug-resistant dhps allele to express the drug resistance trait?

a. The drug-resistant dhps allele is co-dominant with the wild type allele.
b. Only one dhps allele is present during all stages of the *P. falciparum* life cycle.
c. Only one dhps allele is present when *P. falciparum* is infectious.
d. The drug-resistant dhps allele prevents the wild type allele from being expressed.

2.
Sumiti Vinayak, et al., "Origin and Evolution of Sulfadoxine Resistant *Plasmodium falciparum*," *Public Library of Science Pathogens* 6, no. 3 (2010): e1000830, doi:10.1371/journal.ppat.1000830.

X-Linked Traits

In humans, as well as in many other animals and some plants, the sex of the individual is determined by sex chromosomes. The sex chromosomes are one pair of non-homologous chromosomes. Until now, we have only considered inheritance patterns among non-sex chromosomes, or **autosomes**. In addition to 22 homologous pairs of autosomes, human females have a homologous pair of X chromosomes, whereas human males have an XY chromosome pair. Although the Y chromosome contains a small region of similarity to the X chromosome so that they can pair during meiosis, the Y chromosome is much shorter and contains many fewer genes. When a gene being examined is present on the X chromosome, but not on the Y chromosome, it is said to be **X-linked**.

Eye color in *Drosophila* was one of the first X-linked traits to be identified. Thomas Hunt Morgan mapped this trait to the X chromosome in 1910. Like humans, *Drosophila* males have an XY chromosome pair, and females are XX. In flies, the wild-type eye color is red (X^W) and it is dominant to white eye color (X^w) (**Figure 12.11**). Because of the location of the eye-color gene, reciprocal crosses do not produce the same offspring ratios. Males are said to be **hemizygous**, because they have only one allele for any X-linked characteristic. Hemizygosity makes the descriptions of dominance and recessiveness irrelevant for XY males. *Drosophila* males lack a second allele copy on the Y chromosome; that is, their genotype can only be X^WY or X^wY. In contrast, females have two allele copies of this gene and can be X^WX^W, X^WX^w, or X^wX^w.

Figure 12.11 In *Drosophila*, several genes determine eye color. The genes for white and vermilion eye colors are located on the X chromosome. Others are located on the autosomes. Clockwise from top left are brown, cinnabar, sepia, vermilion, white, and red. Red eye color is wild-type and is dominant to white eye color.

In an X-linked cross, the genotypes of F_1 and F_2 offspring depend on whether the recessive trait was expressed by the male or the female in the P_1 generation. With regard to *Drosophila* eye color, when the P_1 male expresses the white-eye phenotype and the female is homozygous red-eyed, all members of the F_1 generation exhibit red eyes (**Figure 12.12**). The F_1 females are heterozygous (X^WX^w), and the males are all X^WY, having received their X chromosome from the homozygous dominant P_1 female and their Y chromosome from the P_1 male. A subsequent cross between the X^WX^w female and the X^WY male would produce only red-eyed females (with X^WX^W or X^WX^w genotypes) and both red- and white-eyed males (with X^WY or X^wY genotypes). Now, consider a cross between a homozygous white-eyed female and a male with red eyes. The F_1 generation would exhibit only heterozygous red-eyed females (X^WX^w) and only white-eyed males (X^wY). Half of the F_2 females would be red-eyed (X^WX^w) and half would be white-eyed (X^wX^w). Similarly, half of the F_2 males would be red-eyed (X^WY) and half would be white-eyed (X^wY).

visual CONNECTION

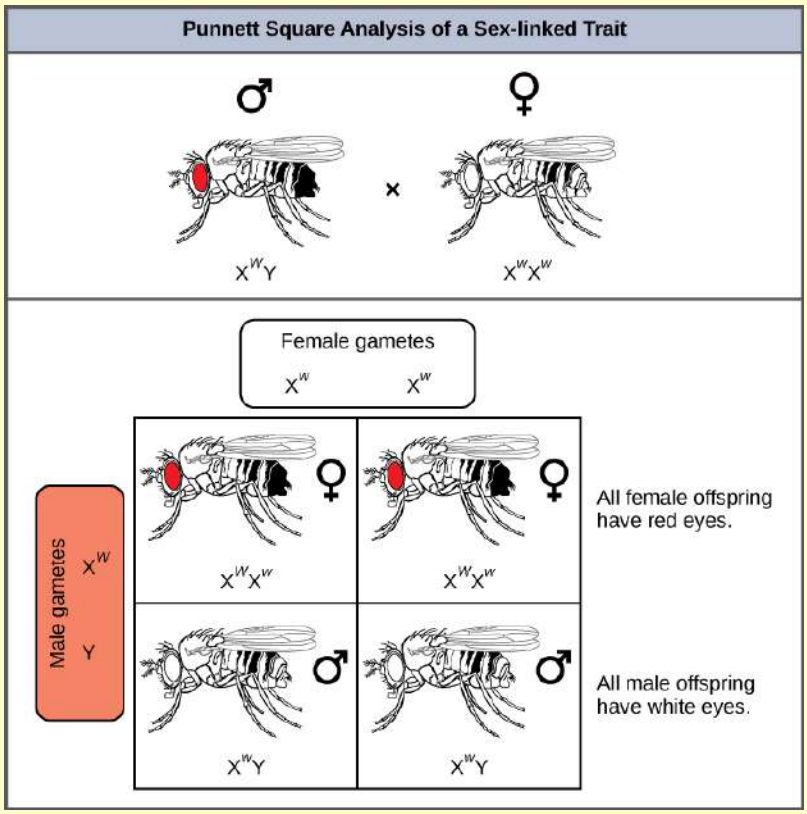


Figure 12.12 Punnett square analysis is used to determine the ratio of offspring from a cross between a red-eyed male fruit fly and a white-eyed female fruit fly.

What ratio of offspring would result from a cross between a white-eyed male fruit fly and a female fruit fly that is heterozygous for red eye color?

a. 25% of the offspring are males and hemizygous dominant with red eyes and 25% are male and hemizygous recessive with white eyes. 25% are female and heterozygous with red eyes and 25% are females and homozygous recessive with white eyes.

b. 50% of the offspring are male and hemizygous dominant with red eyes and 50% are male hemizygous recessive with white eyes. 50% are female and heterozygous with red eyes and 50% are female and homozygous recessive with white eyes.

c. 25% of the males are hemizygous dominant with red eyes and 50% of the male are hemizygous recessive with white eyes. 25% females are heterozygous with red eyes and 50% of the females are homozygous with white eyes.

d. 50% of the males are hemizygous dominant with red eyes and 25% of the male are hemizygous recessive with white eyes. 50% females are heterozygous with red eyes and 25% of the females are homozygous recessive with white eyes

Discoveries in fruit fly genetics can be applied to human genetics. When a female parent is homozygous for a recessive X-linked trait, she will pass the trait on to 100 percent of her offspring. Her male offspring are, therefore, destined to express the trait, as they will inherit their father's Y chromosome. In humans, the alleles for certain conditions (some forms of color blindness, hemophilia, and muscular dystrophy) are X-linked. Females who are heterozygous for these diseases are said to be carriers and may not exhibit any phenotypic effects. These females will pass the disease to half of their sons and will pass

carrier status to half of their daughters; therefore, recessive X-linked traits appear more frequently in males than females.

In some groups of organisms with sex chromosomes, the sex with the non-homologous sex chromosomes is the female rather than the male. This is the case for all birds. In this case, sex-linked traits will be more likely to appear in the female, in which they are hemizygous.

Human Sex-linked Disorders

Sex-linkage studies in Morgan's laboratory provided the fundamentals for understanding X-linked recessive disorders in humans, which include red-green color blindness, and Types A and B hemophilia. Because human males need to inherit only one recessive mutant X allele to be affected, X-linked disorders are disproportionately observed in males. Females must inherit recessive X-linked alleles from both of their parents in order to express the trait. When they inherit one recessive X-linked mutant allele and one dominant X-linked wild-type allele, they are carriers of the trait and are typically unaffected. Carrier females can manifest mild forms of the trait due to the inactivation of the dominant allele located on one of the X chromosomes. However, female carriers can contribute the trait to their sons, resulting in the son exhibiting the trait, or they can contribute the recessive allele to their daughters, resulting in the daughters being carriers of the trait (**Figure 12.13**). Although some Y-linked recessive disorders exist, typically they are associated with infertility in males and are therefore not transmitted to subsequent generations.

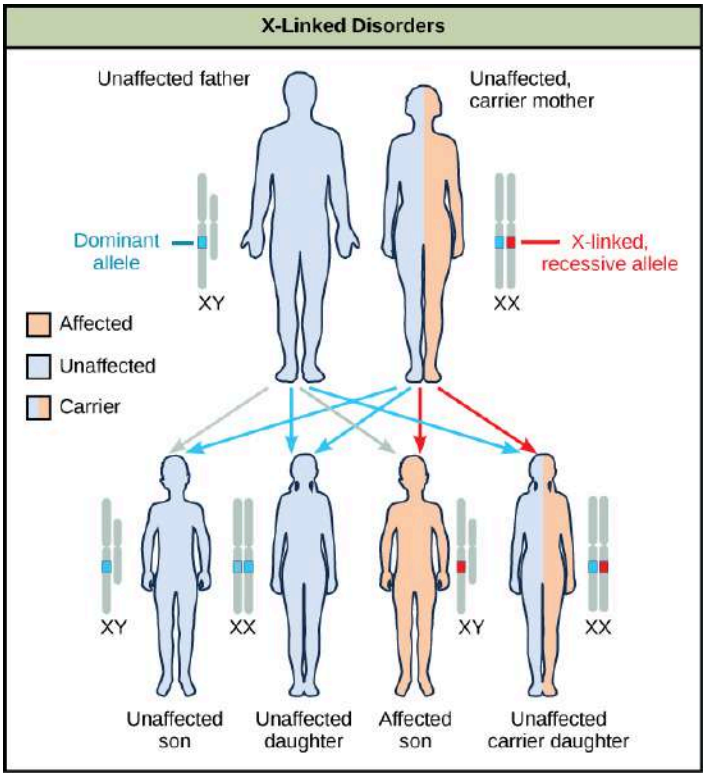


Figure 12.13 The son of a woman who is a carrier of a recessive X-linked disorder will have a 50 percent chance of being affected. A daughter will not be affected, but she will have a 50 percent chance of being a carrier like her mother.

Watch **this video (http://openstaxcollege.org/l/sex-linked_trts)** to learn more about sex-linked traits.

The most common form of hemophilia affects 1 out of every 5,000 male births worldwide, but the condition is much rarer in females. Explain why this is the case.

a. Females need two mutated X chromosomes to be hemophilic.

b. Females need one mutated X chromosome to be hemophilic.

c. Females do not inherit mutated X chromosomes.

d. Females need two mutated X chromosomes to not be hemophilic.

Lethality

A large proportion of genes in an individual's genome are essential for survival. Occasionally, a nonfunctional allele for an essential gene can arise by mutation and be transmitted in a population as long as individuals with this allele also have a wild-type, functional copy. The wild-type allele functions at a capacity sufficient to sustain life and is therefore considered to be dominant over the nonfunctional allele. However, consider two heterozygous parents that have a genotype of wild-type/nonfunctional mutant for a hypothetical essential gene. In one quarter of their offspring, we would expect to observe individuals that are homozygous recessive for the nonfunctional allele. Because the gene is essential, these individuals might fail to develop past fertilization, die *in utero*, or die later in life, depending on what life stage requires this gene. An inheritance pattern in which an allele is only lethal in the homozygous form and in which the heterozygote may be normal or have some altered non-lethal phenotype is referred to as **recessive lethal**.

For crosses between heterozygous individuals with a recessive lethal allele that causes death before birth when homozygous, only wild-type homozygotes and heterozygotes would be observed. The genotypic ratio would therefore be 2:1. In other instances, the recessive lethal allele might also exhibit a dominant (but not lethal) phenotype in the heterozygote. For instance, the recessive lethal *Curly* allele in *Drosophila* affects wing shape in the heterozygote form but is lethal in the homozygote.

A single copy of the wild-type allele is not always sufficient for normal functioning or even survival. The **dominant lethal** inheritance pattern is one in which an allele is lethal both in the homozygote and the heterozygote; this allele can only be transmitted if the lethality phenotype occurs after reproductive age. Individuals with mutations that result in dominant lethal alleles fail to survive even in the heterozygote form. Dominant lethal alleles are very rare because, as you might expect, the allele only lasts one generation and is not transmitted. However, just as the recessive lethal allele might not immediately manifest the phenotype of death, dominant lethal alleles also might not be expressed until adulthood. Once the individual reaches reproductive age, the allele may be unknowingly passed on, resulting in a delayed death in both generations. An example of this in humans is Huntington's disease, in which the nervous system gradually wastes away (**Figure 12.14**). People who are heterozygous for the dominant Huntington allele (*Hh*) will inevitably develop the fatal disease. However, the onset of Huntington's disease may not occur until age 40, at which point the afflicted persons may have already passed the allele to 50 percent of their offspring.

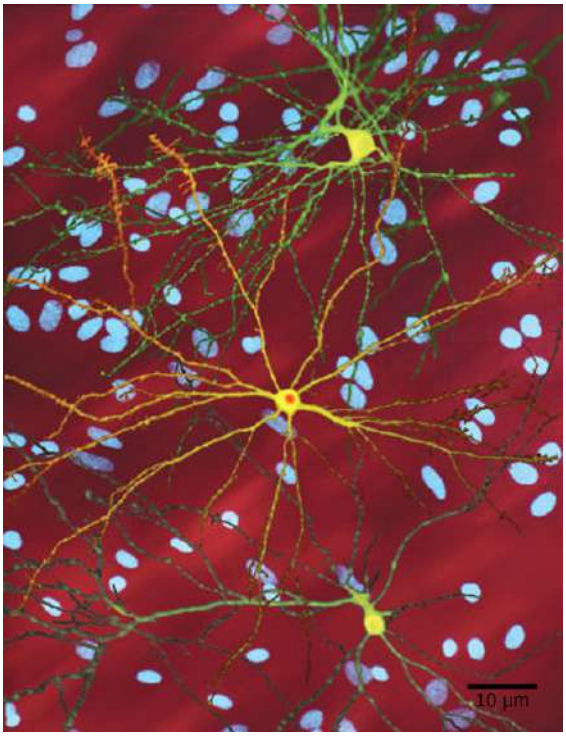


Figure 12.14 The neuron in the center of this micrograph (yellow) has nuclear inclusions characteristic of Huntington's disease (orange area in the center of the neuron). Huntington's disease occurs when an abnormal dominant allele for the Huntington gene is present. (credit: Dr. Steven Finkbeiner, Gladstone Institute of Neurological Disease, The Taube-Koret Center for Huntington's Disease Research, and the University of California San Francisco/Wikimedia)

science practices CONNECTION for AP® Courses

Activity

This section includes descriptions of genetically-inherited human diseases, such as sickle cell anemia, alkaptonuria, hemophilia, color blindness and Huntington's disease. One issue surrounding genetic disorders is the right to privacy. Can you think of other examples of ethical, social, or medical issue surrounding human genetic disorders?

Lab Investigation

Investigate inheritance patterns in an organism of choice, such as Wisconsin Fast Plants or *Drosophila melanogaster*, by performing several genetic crosses and comparing expected and observed phenotypic ratios. Virtual labs exploring Mendelian inheritance patterns are also available online.

Think About It

- In pea plants, round peas (*R*) are dominant to wrinkles peas (*r*) (**Figure 12.5**). You do a test cross between a pea plant with wrinkled peas (genotype *rr*) and a plant of unknown genotype that has round peas (genotype either *RR* or *Rr*). You end up with three offspring plants, all which have round peas. Based on the phenotype of the offspring plants, can you deduce the genotype of the round pea parent plant? If the round pea parent plant is heterozygous, calculate the probability that a random sample of 3 progeny peas will all be round.
- Can a human male be a carrier of red-green color blindness? Justify your answer.
- In pea plants, violet flowers (*V*) are dominant to white flowers (*v*). What are the possible genotypes and phenotypes for a cross between *Vv* and *vv* pea plants? Use a Punnett square to show all work.

12.3 | Laws of Inheritance

In this section, you will explore the following questions:

- What is the relationship between Mendel's law of segregation and independent assortment in terms of genetics and the events of meiosis?
- How can the forked-lined method and probability rules be used to calculate the probability of genotypes and phenotypes from multiple gene crosses?
- How do linkage, cross-over, epistasis, and recombination violate Mendel's laws of inheritance?

Connection for AP® Courses

As was described previously, Mendel proposed that genes are inherited as pairs of alleles that behave in a dominant and recessive pattern. During meiosis, alleles segregate, or separate, such that each gamete is equally likely to receive either one of the two alleles present in the diploid individual. Mendel called this phenomenon the law of segregation, which can be demonstrated in a monohybrid cross. In addition, genes carried on different chromosomes sort into gametes independently of one another. This is Mendel's law of independent assortment. This law can be demonstrated in a dihybrid cross involving two different traits located on different chromosomes. Punnett squares can be used to predict genotypes and phenotypes of offspring involving one or two genes.

Although chromosomes sort independently into gametes during meiosis, Mendel's law of independent assortment refers to genes, not chromosomes. In humans, single chromosomes may carry more than 1,000 genes. Genes located close together on the same chromosome are said to be linked genes. When genes are located in close proximity on the same chromosome, their alleles tend to be inherited together unless recombination occurs. This results in offspring ratios that violate Mendel's law of independent assortment. Genes that are located far apart on the same chromosome are likely to assort independently. The rules of probability can help to sort this out (pun intended). The law states that alleles of different genes assort independently of one another during gamete formation.

Information presented and the examples highlighted in the section support concepts outlined in Big Idea 3 of the AP® Biology Curriculum Framework. The Learning Objectives listed in the Curriculum Framework provide a transparent foundation for the AP® Biology course, an inquiry-based laboratory experience, instructional activities, and AP® exam questions. A learning objective merges required content with one or more of the seven Science Practices.

Big Idea 3	Living systems store, retrieve, transmit and respond to information essential to life processes.
Enduring Understanding 3.A	Heritable information provides for continuity of life.
Essential Knowledge	**3.A.3** The chromosomal basis of inheritance provides an understanding of the pattern of passage (transmission) of genes from parent to offspring.
Science Practice	**2.2** The student can apply mathematical routines to quantities that describe natural phenomena.
Learning Objective	**3.14** The student is able to apply mathematical routines to determine Mendelian patterns of inheritance provided by data.
Essential Knowledge	**3.A.4** The inheritance pattern of many traits cannot be explained by simple Mendelian genetics.
Science Practice	**6.5** The student can evaluate alternative scientific explanations.
Learning Objective	**3.15** The student is able to explain deviations from Mendel's model of the inheritance of traits.

Essential Knowledge	**3.A.4** The inheritance pattern of many traits cannot be explained by simple Mendelian genetics.
Science Practice	**6.3** The student can articulate the reasons that scientific explanations and theories are refined or replaced.
Learning Objective	**3.16** The student is able to explain how the inheritance patterns of many traits cannot be accounted for by Mendelian genetics.
Essential Knowledge	**3.A.4** The inheritance pattern of many traits cannot be explained by simple Mendelian genetics.
Science Practice	**1.2** The student can describe representations and models of natural or man-made phenomena and systems in the domain.
Learning Objective	**3.17** The student is able to describe representations of an appropriate example of inheritance patterns that cannot be explained by Mendel's model of the inheritance of traits.

The Science Practice Challenge Questions contain additional test questions for this section that will help you prepare for the AP exam. These questions address the following standards:
[APLO 3.11][APLO 3.15][APLO 3.14][APLO 3.17][APLO 3.12]

Mendel generalized the results of his pea-plant experiments into four postulates, some of which are sometimes called "laws," that describe the basis of dominant and recessive inheritance in diploid organisms. As you have learned, more complex extensions of Mendelism exist that do not exhibit the same F_2 phenotypic ratios (3:1). Nevertheless, these laws summarize the basics of classical genetics.

Pairs of Unit Factors, or Genes

Mendel proposed first that paired unit factors of heredity were transmitted faithfully from generation to generation by the dissociation and reassociation of paired factors during gametogenesis and fertilization, respectively. After he crossed peas with contrasting traits and found that the recessive trait resurfaced in the F_2 generation, Mendel deduced that hereditary factors must be inherited as discrete units. This finding contradicted the belief at that time that parental traits were blended in the offspring.

Alleles Can Be Dominant or Recessive

Mendel's **law of dominance** states that in a heterozygote, one trait will conceal the presence of another trait for the same characteristic. Rather than both alleles contributing to a phenotype, the dominant allele will be expressed exclusively. The recessive allele will remain "latent" but will be transmitted to offspring by the same manner in which the dominant allele is transmitted. The recessive trait will only be expressed by offspring that have two copies of this allele (**Figure 12.15**), and these offspring will breed true when self-crossed.

Since Mendel's experiments with pea plants, other researchers have found that the law of dominance does not always hold true. Instead, several different patterns of inheritance have been found to exist.

Figure 12.15 The child in the photo expresses albinism, a recessive trait.

Equal Segregation of Alleles

Observing that true-breeding pea plants with contrasting traits gave rise to F_1 generations that all expressed the dominant trait and F_2 generations that expressed the dominant and recessive traits in a 3:1 ratio, Mendel proposed the **law of segregation**. This law states that paired unit factors (genes) must segregate equally into gametes such that offspring have an equal likelihood of inheriting either factor. For the F_2 generation of a monohybrid cross, the following three possible combinations of genotypes could result: homozygous dominant, heterozygous, or homozygous recessive. Because heterozygotes could arise from two different pathways (receiving one dominant and one recessive allele from either parent), and because heterozygotes and homozygous dominant individuals are phenotypically identical, the law supports Mendel's observed 3:1 phenotypic ratio. The equal segregation of alleles is the reason we can apply the Punnett square to accurately predict the offspring of parents with known genotypes. The physical basis of Mendel's law of segregation is the first division of meiosis, in which the homologous chromosomes with their different versions of each gene are segregated into daughter nuclei. The role of the meiotic segregation of chromosomes in sexual reproduction was not understood by the scientific community during Mendel's lifetime.

Independent Assortment

Mendel's **law of independent assortment** states that genes do not influence each other with regard to the sorting of alleles into gametes, and every possible combination of alleles for every gene is equally likely to occur. The independent assortment of genes can be illustrated by the **dihybrid** cross, a cross between two true-breeding parents that express different traits for two characteristics. Consider the characteristics of seed color and seed texture for two pea plants, one that has green, wrinkled seeds (*yyrr*) and another that has yellow, round seeds (*YYRR*). Because each parent is homozygous, the law of segregation indicates that the gametes for the green/wrinkled plant all are *yr*, and the gametes for the yellow/round plant are all *YR*. Therefore, the F_1 generation of offspring all are *YyRr* (**Figure 12.16**).

visual CONNECTION

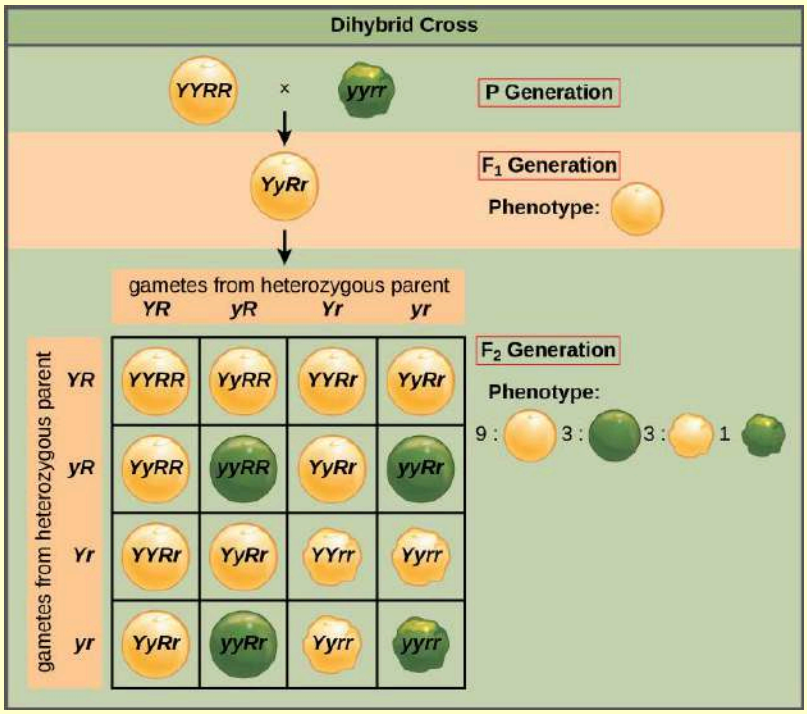


Figure 12.16 This dihybrid cross of pea plants involves the genes for seed color and texture.

In pea plants, purple flowers (P) are dominant to white flowers (p) and yellow peas (Y) are dominant to green peas (y). What are the possible genotypes and phenotypes for a cross between PpYY and ppYy pea plants? What is the minimum number of squares that you need to do a Punnett square analysis of this cross?

a. ppYY, Ppyy, ppYY, ppyy yielding white flowers with yellow peas, purple flowers with yellow peas, and white flowers with green peas. You can find this with a 3×3 Punnett square.

b. PPYY, PpYy, ppYY, ppyy yielding purple flowers with yellow peas, white flowers with yellow peas, and white flowers with green peas. You can find this with a 2×2 Punnett square.

c. Ppyy, PpYy, ppYY, ppyy yielding purple flowers with green peas, purple flowers with yellow peas, white flowers with yellow peas, and white flowers with green peas. You can find this with a 3×3 Punnett square.

d. PpYY, PpYy, ppYY, ppYy yielding purple flowers with yellow peas, and white flowers with yellow peas. You can find this with a 2×2 Punnett square.

For the F2 generation, the law of segregation requires that each gamete receive either an *R* allele or an *r* allele along with either a *Y* allele or a *y* allele. The law of independent assortment states that a gamete into which an *r* allele sorted would be equally likely to contain either a *Y* allele or a *y* allele. Thus, there are four equally likely gametes that can be formed when the *YyRr* heterozygote is self-crossed, as follows: *YR*, *Yr*, *yR*, and *yr*. Arranging these gametes along the top and left of a 4 × 4 Punnett square (**Figure 12.16**) gives us 16 equally likely genotypic combinations. From these genotypes, we infer a phenotypic ratio of 9 round/yellow:3 round/green:3 wrinkled/yellow:1 wrinkled/green (**Figure 12.16**). These are the offspring ratios we would expect, assuming we performed the crosses with a large enough sample size.

Because of independent assortment and dominance, the 9:3:3:1 dihybrid phenotypic ratio can be collapsed into two 3:1 ratios, characteristic of any monohybrid cross that follows a dominant and recessive pattern. Ignoring seed color and considering only seed texture in the above dihybrid cross, we would expect that three quarters of the F_2 generation offspring would be round, and one quarter would be wrinkled. Similarly, isolating only seed color, we would assume that three quarters of the F_2 offspring would be yellow and one quarter would be green. The sorting of alleles for texture and color are independent events, so we can apply the product rule. Therefore, the proportion of round and yellow F_2 offspring is

expected to be (3/4) × (3/4) = 9/16, and the proportion of wrinkled and green offspring is expected to be (1/4) × (1/4) = 1/16. These proportions are identical to those obtained using a Punnett square. Round, green and wrinkled, yellow offspring can also be calculated using the product rule, as each of these genotypes includes one dominant and one recessive phenotype. Therefore, the proportion of each is calculated as (3/4) × (1/4) = 3/16.

The law of independent assortment also indicates that a cross between yellow, wrinkled (*YYrr*) and green, round (*yyRR*) parents would yield the same F_1 and F_2 offspring as in the *YYRR* x *yyrr* cross.

The physical basis for the law of independent assortment also lies in meiosis I, in which the different homologous pairs line up in random orientations. Each gamete can contain any combination of paternal and maternal chromosomes (and therefore the genes on them) because the orientation of tetrads on the metaphase plane is random.

Forked-Line Method

When more than two genes are being considered, the Punnett-square method becomes unwieldy. For instance, examining a cross involving four genes would require a 16 × 16 grid containing 256 boxes. It would be extremely cumbersome to manually enter each genotype. For more complex crosses, the forked-line and probability methods are preferred.

To prepare a forked-line diagram for a cross between F_1 heterozygotes resulting from a cross between *AABBCC* and *aabbcc* parents, we first create rows equal to the number of genes being considered, and then segregate the alleles in each row on forked lines according to the probabilities for individual monohybrid crosses (**Figure 12.17**). We then multiply the values along each forked path to obtain the F_2 offspring probabilities. Note that this process is a diagrammatic version of the product rule. The values along each forked pathway can be multiplied because each gene assorts independently. For a trihybrid cross, the F_2 phenotypic ratio is 27:9:9:9:3:3:3:1.

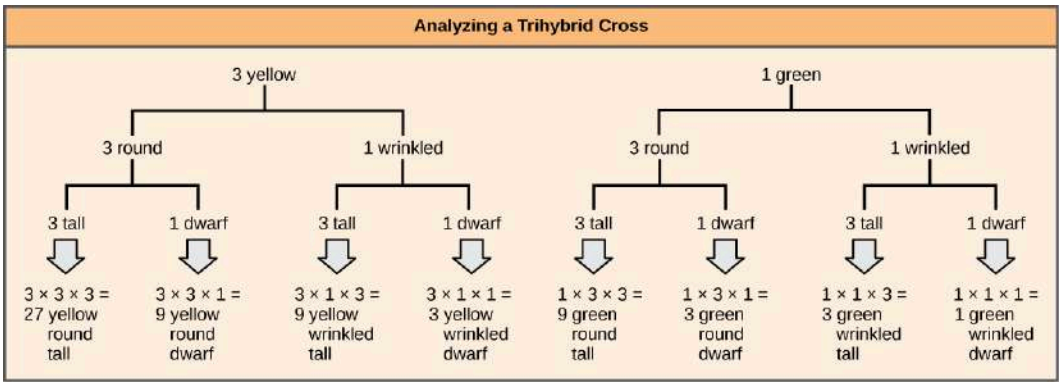


Figure 12.17 The forked-line method can be used to analyze a trihybrid cross. Here, the probability for color in the F_2 generation occupies the top row (3 yellow:1 green). The probability for shape occupies the second row (3 round:1 wrinked), and the probability for height occupies the third row (3 tall:1 dwarf). The probability for each possible combination of traits is calculated by multiplying the probability for each individual trait. Thus, the probability of F_2 offspring having yellow, round, and tall traits is 3 × 3 × 3, or 27.

Probability Method

While the forked-line method is a diagrammatic approach to keeping track of probabilities in a cross, the probability method gives the proportions of offspring expected to exhibit each phenotype (or genotype) without the added visual assistance. Both methods make use of the product rule and consider the alleles for each gene separately. Earlier, we examined the phenotypic proportions for a trihybrid cross using the forked-line method; now we will use the probability method to examine the genotypic proportions for a cross with even more genes.

For a trihybrid cross, writing out the forked-line method is tedious, albeit not as tedious as using the Punnett-square method. To fully demonstrate the power of the probability method, however, we can consider specific genetic calculations. For instance, for a tetrahybrid cross between individuals that are heterozygotes for all four genes, and in which all four genes are sorting independently and in a dominant and recessive pattern, what proportion of the offspring will be expected to be homozygous recessive for all four alleles? Rather than writing out every possible genotype, we can use the probability method. We know that for each gene, the fraction of homozygous recessive offspring will be 1/4. Therefore, multiplying this fraction for each of the four genes, (1/4) × (1/4) × (1/4) × (1/4), we determine that 1/256 of the offspring will be quadruply homozygous recessive.

For the same tetrahybrid cross, what is the expected proportion of offspring that have the dominant phenotype at all four loci? We can answer this question using phenotypic proportions, but let's do it the hard way—using genotypic proportions. The question asks for the proportion of offspring that are 1) homozygous dominant at *A* or heterozygous at *A*, and 2) homozygous at *B* or heterozygous at *B*, and so on. Noting the "or" and "and" in each circumstance makes clear where to

apply the sum and product rules. The probability of a homozygous dominant at *A* is 1/4 and the probability of a heterozygote at *A* is 1/2. The probability of the homozygote or the heterozygote is 1/4 + 1/2 = 3/4 using the sum rule. The same probability can be obtained in the same way for each of the other genes, so that the probability of a dominant phenotype at *A* and *B* and *C* and *D* is, using the product rule, equal to 3/4 × 3/4 × 3/4 × 3/4, or 27/64. If you are ever unsure about how to combine probabilities, returning to the forked-line method should make it clear.

Rules for Multihybrid Fertilization

Predicting the genotypes and phenotypes of offspring from given crosses is the best way to test your knowledge of Mendelian genetics. Given a multihybrid cross that obeys independent assortment and follows a dominant and recessive pattern, several generalized rules exist; you can use these rules to check your results as you work through genetics calculations (**Table 12.5**). To apply these rules, first you must determine *n*, the number of heterozygous gene pairs (the number of genes segregating two alleles each). For example, a cross between *AaBb* and *AaBb* heterozygotes has an *n* of 2. In contrast, a cross between *AABb* and *AABb* has an *n* of 1 because *A* is not heterozygous.

General Rules for Multihybrid Crosses

General Rule	Number of Heterozygous Gene Pairs
Number of different F_1 gametes	2^n
Number of different F_2 genotypes	3^n
Given dominant and recessive inheritance, the number of different F_2 phenotypes	2^n

Table 12.5

Linked Genes Violate the Law of Independent Assortment

Although all of Mendel’s pea characteristics behaved according to the law of independent assortment, we now know that some allele combinations are not inherited independently of each other. Genes that are located on separate non-homologous chromosomes will always sort independently. However, each chromosome contains hundreds or thousands of genes, organized linearly on chromosomes like beads on a string. The segregation of alleles into gametes can be influenced by **linkage**, in which genes that are located physically close to each other on the same chromosome are more likely to be inherited as a pair. However, because of the process of recombination, or “crossover,” it is possible for two genes on the same chromosome to behave independently, or as if they are not linked. To understand this, let’s consider the biological basis of gene linkage and recombination.

Homologous chromosomes possess the same genes in the same linear order. The alleles may differ on homologous chromosome pairs, but the genes to which they correspond do not. In preparation for the first division of meiosis, homologous chromosomes replicate and synapse. Like genes on the homologs align with each other. At this stage, segments of homologous chromosomes exchange linear segments of genetic material (**Figure 12.18**). This process is called recombination, or crossover, and it is a common genetic process. Because the genes are aligned during recombination, the gene order is not altered. Instead, the result of recombination is that maternal and paternal alleles are combined onto the same chromosome. Across a given chromosome, several recombination events may occur, causing extensive shuffling of alleles.

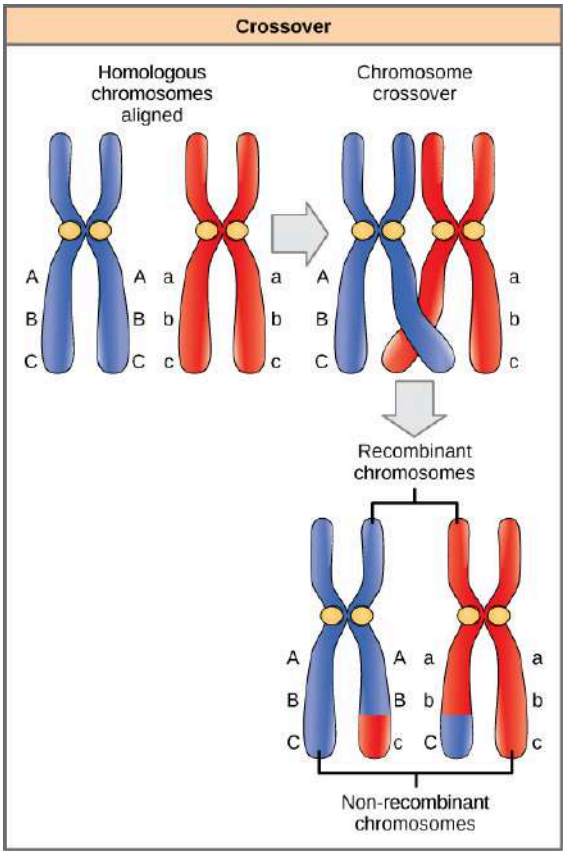


Figure 12.18 The process of crossover, or recombination, occurs when two homologous chromosomes align during meiosis and exchange a segment of genetic material. Here, the alleles for gene C were exchanged. The result is two recombinant and two non-recombinant chromosomes.

When two genes are located in close proximity on the same chromosome, they are considered linked, and their alleles tend to be transmitted through meiosis together. To exemplify this, imagine a dihybrid cross involving flower color and plant height in which the genes are next to each other on the chromosome. If one homologous chromosome has alleles for tall plants and red flowers, and the other chromosome has genes for short plants and yellow flowers, then when the gametes are formed, the tall and red alleles will go together into a gamete and the short and yellow alleles will go into other gametes. These are called the parental genotypes because they have been inherited intact from the parents of the individual producing gametes. But unlike if the genes were on different chromosomes, there will be no gametes with tall and yellow alleles and no gametes with short and red alleles. If you create the Punnett square with these gametes, you will see that the classical Mendelian prediction of a 9:3:3:1 outcome of a dihybrid cross would not apply. As the distance between two genes increases, the probability of one or more crossovers between them increases, and the genes behave more like they are on separate chromosomes. Geneticists have used the proportion of recombinant gametes (the ones not like the parents) as a measure of how far apart genes are on a chromosome. Using this information, they have constructed elaborate maps of genes on chromosomes for well-studied organisms, including humans.

Mendel's seminal publication makes no mention of linkage, and many researchers have questioned whether he encountered linkage but chose not to publish those crosses out of concern that they would invalidate his independent assortment postulate. The garden pea has seven chromosomes, and some have suggested that his choice of seven characteristics was not a coincidence. However, even if the genes he examined were not located on separate chromosomes, it is possible that he simply did not observe linkage because of the extensive shuffling effects of recombination.

Testing the Hypothesis of Independent Assortment

To better appreciate the amount of labor and ingenuity that went into Mendel's experiments, proceed through one of Mendel's dihybrid crosses.

Question: What will be the offspring of a dihybrid cross?

Background: Consider that pea plants mature in one growing season, and you have access to a large garden in which you can cultivate thousands of pea plants. There are several true-breeding plants with the following pairs of

traits: tall plants with inflated pods, and dwarf plants with constricted pods. Before the plants have matured, you remove the pollen-producing organs from the tall/inflated plants in your crosses to prevent self-fertilization. Upon plant maturation, the plants are manually crossed by transferring pollen from the dwarf/constricted plants to the stigmata of the tall/inflated plants.

Hypothesis: Both trait pairs will sort independently according to Mendelian laws. When the true-breeding parents are crossed, all of the F_1 offspring are tall and have inflated pods, which indicates that the tall and inflated traits are dominant over the dwarf and constricted traits, respectively. A self-cross of the F_1 heterozygotes results in 2,000 F_2 progeny.

Test the hypothesis: Because each trait pair sorts independently, the ratios of tall:dwarf and inflated:constricted are each expected to be 3:1. The tall/dwarf trait pair is called *T/t*, and the inflated/constricted trait pair is designated *I/i*. Each member of the F_1 generation therefore has a genotype of *TtIi*. Construct a grid analogous to **Figure 12.16**, in which you cross two *TtIi* individuals. Each individual can donate four combinations of two traits: *TI*, *Ti*, *tI*, or *ti*, meaning that there are 16 possibilities of offspring genotypes. Because the *T* and *I* alleles are dominant, any individual having one or two of those alleles will express the tall or inflated phenotypes, respectively, regardless if they also have a *t* or *i* allele. Only individuals that are *tt* or *ii* will express the dwarf and constricted alleles, respectively. As shown in **Figure 12.19**, you predict that you will observe the following offspring proportions: tall/inflated:tall/constricted:dwarf/inflated:dwarf/constricted in a 9:3:3:1 ratio. Notice from the grid that when considering the tall/dwarf and inflated/constricted trait pairs in isolation, they are each inherited in 3:1 ratios.

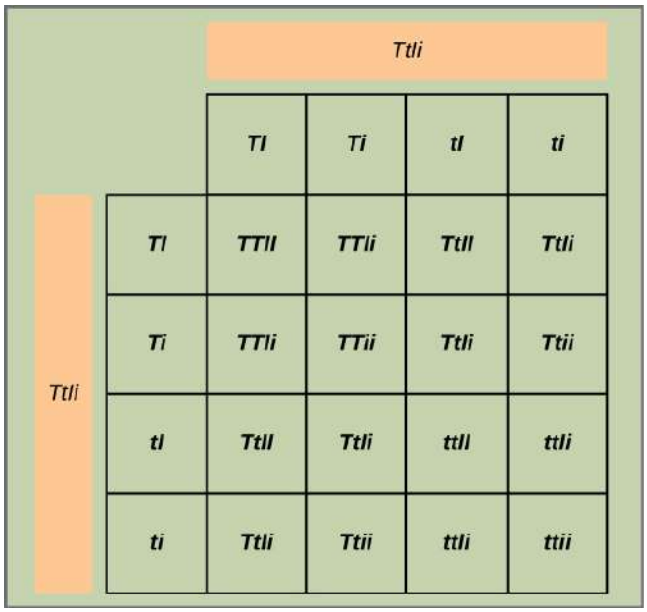


Figure 12.19 This figure shows all possible combinations of offspring resulting from a dihybrid cross of pea plants that are heterozygous for the tall/dwarf and inflated/constricted alleles.

Test the hypothesis: You cross the dwarf and tall plants and then self-cross the offspring. For best results, this is repeated with hundreds or even thousands of pea plants. What special precautions should be taken in the crosses and in growing the plants?

Analyze your data: You observe the following plant phenotypes in the F_2 generation: 2706 tall/inflated, 930 tall/constricted, 888 dwarf/inflated, and 300 dwarf/constricted. Reduce these findings to a ratio and determine if they are consistent with Mendelian laws.

Form a conclusion: Were the results close to the expected 9:3:3:1 phenotypic ratio? Do the results support the prediction? What might be observed if far fewer plants were used, given that alleles segregate randomly into gametes? Try to imagine growing that many pea plants, and consider the potential for experimental error. For instance, what would happen if it was extremely windy one day?

science practices CONNECTION for AP® Courses

Think About It

In the shepherd's-purse plant (*Capsella bursa-pastoris*), seed shape is controlled by two genes, *A* and *B*. When both the *A* and *B* loci are homozygous recessive (*aabb*), the seeds are ovoid. However, if the dominant allele for either or both of these genes is present, the seeds are triangular. Based on this information, what are the expected phenotypic ratios for a cross between plants that are heterozygous for both traits?

What is the expected ratio of phenotypes from a dihybrid cross? How do you explain the difference between the expected dihybrid cross ratio and ratio observed in the shepherd's-purse plant?

Epistasis

Mendel's studies in pea plants implied that the sum of an individual's phenotype was controlled by genes (or as he called them, unit factors), such that every characteristic was distinctly and completely controlled by a single gene. In fact, single observable characteristics are almost always under the influence of multiple genes (each with two or more alleles) acting in unison. For example, at least eight genes contribute to eye color in humans.

LINK TO LEARNING

Eye color in humans is determined by multiple genes. Use the **Eye Color Calculator (http://openstaxcollege.org/l/eye_color_calc)** to predict the eye color of children from parental eye color.

A couple produces a green-eyed child. Both of the parents have brown eyes. Explain how this is genetically possible.

a. Both parents are homozygous for the dominant trait of brown eyes.

b. Both parents are heterozygous, having the green trait on the green-blue eye gene.

c. Both parents are heterozygous with the recessive trait of brown eyes.

d. Both parents are homozygous having the green trait on the green-blue eye gene.

In some cases, several genes can contribute to aspects of a common phenotype without their gene products ever directly interacting. In the case of organ development, for instance, genes may be expressed sequentially, with each gene adding to the complexity and specificity of the organ. Genes may function in complementary or synergistic fashions, such that two or more genes need to be expressed simultaneously to affect a phenotype. Genes may also oppose each other, with one gene modifying the expression of another.

In **epistasis**, the interaction between genes is antagonistic, such that one gene masks or interferes with the expression of another. "Epistasis" is a word composed of Greek roots that mean "standing upon." The alleles that are being masked or silenced are said to be hypostatic to the epistatic alleles that are doing the masking. Often the biochemical basis of epistasis is a gene pathway in which the expression of one gene is dependent on the function of a gene that precedes or follows it in the pathway.

An example of epistasis is pigmentation in mice. The wild-type coat color, agouti (*AA*), is dominant to solid-colored fur (*aa*). However, a separate gene (*C*) is necessary for pigment production. A mouse with a recessive *c* allele at this locus is unable to produce pigment and is albino regardless of the allele present at locus *A* (**Figure 12.20**). Therefore, the genotypes *AAcc*, *Aacc*, and *aacc* all produce the same albino phenotype. A cross between heterozygotes for both genes (*AaCc* x *AaCc*)

would generate offspring with a phenotypic ratio of 9 agouti:3 solid color:4 albino (**Figure 12.20**). In this case, the *C* gene is epistatic to the *A* gene.

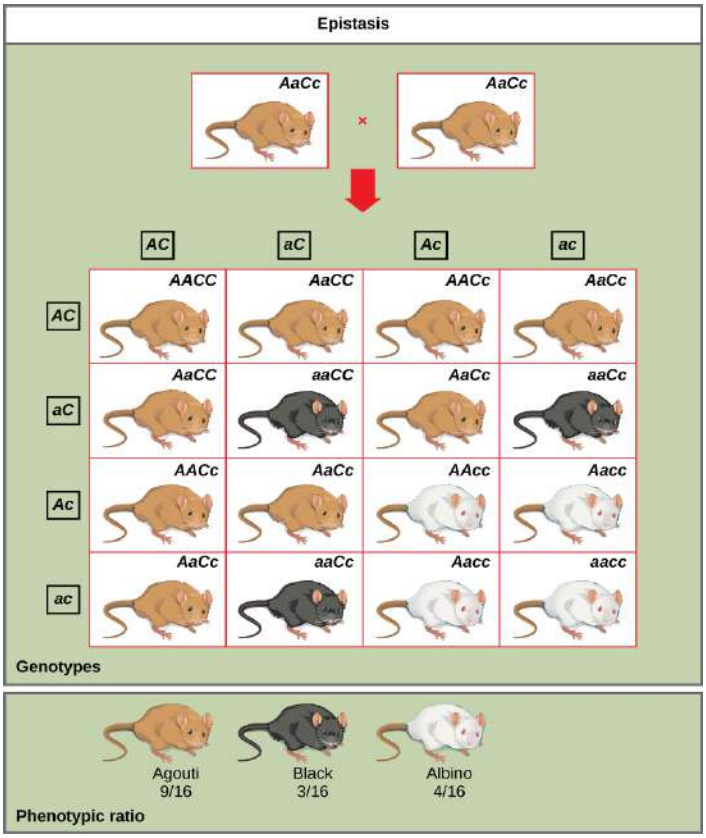


Figure 12.20 In mice, the mottled agouti coat color (*A*) is dominant to a solid coloration, such as black or gray. A gene at a separate locus (*C*) is responsible for pigment production. The recessive *c* allele does not produce pigment, and a mouse with the homozygous recessive *cc* genotype is albino regardless of the allele present at the *A* locus. Thus, the *C* gene is epistatic to the *A* gene.

Epistasis can also occur when a dominant allele masks expression at a separate gene. Fruit color in summer squash is expressed in this way. Homozygous recessive expression of the *W* gene (*ww*) coupled with homozygous dominant or heterozygous expression of the *Y* gene (*YY* or *Yy*) generates yellow fruit, and the *wwyy* genotype produces green fruit. However, if a dominant copy of the *W* gene is present in the homozygous or heterozygous form, the summer squash will produce white fruit regardless of the *Y* alleles. A cross between white heterozygotes for both genes (*WwYy* × *WwYy*) would produce offspring with a phenotypic ratio of 12 white:3 yellow:1 green.

Finally, epistasis can be reciprocal such that either gene, when present in the dominant (or recessive) form, expresses the same phenotype. In the shepherd's purse plant (*Capsella bursa-pastoris*), the characteristic of seed shape is controlled by two genes in a dominant epistatic relationship. When the genes *A* and *B* are both homozygous recessive (*aabb*), the seeds are ovoid. If the dominant allele for either of these genes is present, the result is triangular seeds. That is, every possible genotype other than *aabb* results in triangular seeds, and a cross between heterozygotes for both genes (*AaBb* x *AaBb*) would yield offspring with a phenotypic ratio of 15 triangular:1 ovoid.

As you work through genetics problems, keep in mind that any single characteristic that results in a phenotypic ratio that totals 16 is typical of a two-gene interaction. Recall the phenotypic inheritance pattern for Mendel's dihybrid cross, which considered two non-interacting genes—9:3:3:1. Similarly, we would expect interacting gene pairs to also exhibit ratios expressed as 16 parts. Note that we are assuming the interacting genes are not linked; they are still assorting independently into gametes.

For an excellent review of Mendel's experiments and to perform your own crosses and identify patterns of inheritance, visit the **Mendel's Peas (http://openstaxcollege.org/l/mendels_peas)** web lab.

Explain how Mendel's experiments help modern-day farmers breed crops that exhibit preferred traits, like tall height or large fruit size.

a. by providing information about the variety of pea plants

b. by providing information about soil condition

c. by providing information about organic feritilizers

d. by providing information about the inheritance of traits and the concept of dominance

KEY TERMS

allele gene variations that arise by mutation and exist at the same relative locations on homologous chromosomes

autosomes any of the non-sex chromosomes

blending theory of inheritance hypothetical inheritance pattern in which parental traits are blended together in the offspring to produce an intermediate physical appearance

codominance in a heterozygote, complete and simultaneous expression of both alleles for the same characteristic

continuous variation inheritance pattern in which a character shows a range of trait values with small gradations rather than large gaps between them

dihybrid result of a cross between two true-breeding parents that express different traits for two characteristics

discontinuous variation inheritance pattern in which traits are distinct and are transmitted independently of one another

dominant trait which confers the same physical appearance whether an individual has two copies of the trait or one copy of the dominant trait and one copy of the recessive trait

dominant lethal inheritance pattern in which an allele is lethal both in the homozygote and the heterozygote; this allele can only be transmitted if the lethality phenotype occurs after reproductive age

epistasis antagonistic interaction between genes such that one gene masks or interferes with the expression of another

F_1 first filial generation in a cross; the offspring of the parental generation

F_2 second filial generation produced when F_1 individuals are self-crossed or fertilized with each other

genotype underlying genetic makeup, consisting of both physically visible and non-expressed alleles, of an organism

hemizygous presence of only one allele for a characteristic, as in X-linkage; hemizygosity makes descriptions of dominance and recessiveness irrelevant

heterozygous having two different alleles for a given gene on the homologous chromosome

homozygous having two identical alleles for a given gene on the homologous chromosome

hybridization process of mating two individuals that differ with the goal of achieving a certain characteristic in their offspring

incomplete dominance in a heterozygote, expression of two contrasting alleles such that the individual displays an intermediate phenotype

law of dominance in a heterozygote, one trait will conceal the presence of another trait for the same characteristic

law of independent assortment genes do not influence each other with regard to sorting of alleles into gametes; every possible combination of alleles is equally likely to occur

law of segregation paired unit factors (i.e., genes) segregate equally into gametes such that offspring have an equal likelihood of inheriting any combination of factors

linkage phenomenon in which alleles that are located in close proximity to each other on the same chromosome are more likely to be inherited together

model system species or biological system used to study a specific biological phenomenon to be applied to other different species

monohybrid result of a cross between two true-breeding parents that express different traits for only one characteristic

P_0 parental generation in a cross

phenotype observable traits expressed by an organism

product rule probability of two independent events occurring simultaneously can be calculated by multiplying the individual probabilities of each event occurring alone

Punnett square visual representation of a cross between two individuals in which the gametes of each individual are denoted along the top and side of a grid, respectively, and the possible zygotic genotypes are recombined at each box in the grid

recessive trait that appears "latent" or non-expressed when the individual also carries a dominant trait for that same characteristic; when present as two identical copies, the recessive trait is expressed

recessive lethal inheritance pattern in which an allele is only lethal in the homozygous form; the heterozygote may be normal or have some altered, non-lethal phenotype

reciprocal cross paired cross in which the respective traits of the male and female in one cross become the respective traits of the female and male in the other cross

sex-linked any gene on a sex chromosome

sum rule probability of the occurrence of at least one of two mutually exclusive events is the sum of their individual probabilities

test cross cross between a dominant expressing individual with an unknown genotype and a homozygous recessive individual; the offspring phenotypes indicate whether the unknown parent is heterozygous or homozygous for the dominant trait

trait variation in the physical appearance of a heritable characteristic

X-linked gene present on the X, but not the Y chromosome

CHAPTER SUMMARY

12.1 Mendel's Experiments and the Laws of Probability

Working with garden pea plants, Mendel found that crosses between parents that differed by one trait produced F_1 offspring that all expressed the traits of one parent. Observable traits are referred to as dominant, and non-expressed traits are described as recessive. When the offspring in Mendel's experiment were self-crossed, the F_2 offspring exhibited the dominant trait or the recessive trait in a 3:1 ratio, confirming that the recessive trait had been transmitted faithfully from the original P_0 parent. Reciprocal crosses generated identical F_1 and F_2 offspring ratios. By examining sample sizes, Mendel showed that his crosses behaved reproducibly according to the laws of probability, and that the traits were inherited as independent events.

Two rules in probability can be used to find the expected proportions of offspring of different traits from different crosses. To find the probability of two or more independent events occurring together, apply the product rule and multiply the probabilities of the individual events. The use of the word "and" suggests the appropriate application of the product rule. To find the probability of two or more events occurring in combination, apply the sum rule and add their individual probabilities together. The use of the word "or" suggests the appropriate application of the sum rule.

12.2 Characteristics and Traits

When true-breeding or homozygous individuals that differ for a certain trait are crossed, all of the offspring will be heterozygotes for that trait. If the traits are inherited as dominant and recessive, the F_1 offspring will all exhibit the same phenotype as the parent homozygous for the dominant trait. If these heterozygous offspring are self-crossed, the resulting F_2 offspring will be equally likely to inherit gametes carrying the dominant or recessive trait, giving rise to offspring of which one quarter are homozygous dominant, half are heterozygous, and one quarter are homozygous recessive. Because homozygous dominant and heterozygous individuals are phenotypically identical, the observed traits in the F_2 offspring will exhibit a ratio of three dominant to one recessive.

Alleles do not always behave in dominant and recessive patterns. Incomplete dominance describes situations in which the heterozygote exhibits a phenotype that is intermediate between the homozygous phenotypes. Codominance describes the simultaneous expression of both of the alleles in the heterozygote. Although diploid organisms can only have two alleles

for any given gene, it is common for more than two alleles of a gene to exist in a population. In humans, as in many animals and some plants, females have two X chromosomes and males have one X and one Y chromosome. Genes that are present on the X but not the Y chromosome are said to be X-linked, such that males only inherit one allele for the gene, and females inherit two. Finally, some alleles can be lethal. Recessive lethal alleles are only lethal in homozygotes, but dominant lethal alleles are fatal in heterozygotes as well.

12.3 Laws of Inheritance

Mendel postulated that genes (characteristics) are inherited as pairs of alleles (traits) that behave in a dominant and recessive pattern. Alleles segregate into gametes such that each gamete is equally likely to receive either one of the two alleles present in a diploid individual. In addition, genes are assorted into gametes independently of one another. That is, alleles are generally not more likely to segregate into a gamete with a particular allele of another gene. A dihybrid cross demonstrates independent assortment when the genes in question are on different chromosomes or distant from each other on the same chromosome. For crosses involving more than two genes, use the forked line or probability methods to predict offspring genotypes and phenotypes rather than a Punnett square.

Although chromosomes sort independently into gametes during meiosis, Mendel’s law of independent assortment refers to genes, not chromosomes, and a single chromosome may carry more than 1,000 genes. When genes are located in close proximity on the same chromosome, their alleles tend to be inherited together. This results in offspring ratios that violate Mendel's law of independent assortment. However, recombination serves to exchange genetic material on homologous chromosomes such that maternal and paternal alleles may be recombined on the same chromosome. This is why alleles on a given chromosome are not always inherited together. Recombination is a random event occurring anywhere on a chromosome. Therefore, genes that are far apart on the same chromosome are likely to still assort independently because of recombination events that occurred in the intervening chromosomal space.

Whether or not they are sorting independently, genes may interact at the level of gene products such that the expression of an allele for one gene masks or modifies the expression of an allele for a different gene. This is called epistasis.

REVIEW QUESTIONS

1. Mendel performed hybridizations by transferring pollen to the female ova from what part of the male plant?

a. anther
b. pistil
c. stigma
d. seed

2. Which is one of the seven characteristics that Mendel observed in pea plants?

a. flower size
b. leaf shape
c. seed texture
d. stem color

3. Imagine you are performing a cross involving garden pea plants. What F_1 offspring would you expect if you cross true-breeding parents with green seeds and yellow seeds? Yellow seed color is dominant over green.

a. 100 percent yellow-green seeds
b. 100 percent yellow seeds
c. 50 percent yellow, 50 percent green seeds
d. 25 percent green, 75 percent yellow seeds

4. Consider a cross to investigate the pea pod texture trait, involving constricted or inflated pods. Mendel found that the traits behave according to a dominant/recessive pattern in which inflated pods were dominant. If you performed this cross and obtained 650 inflated-pod plants in the F_2 generation bred from true-breading stock, approximately how many constricted-pod plants would you expect to have?

a. 600
b. 165
c. 217
d. 468

5. The observable traits expressed by an organism are described as its

a. alleles
b. genotype
c. phenotype
d. zygote

6. A recessive trait will be observed in individuals that are what for that trait?

a. diploid
b. heterozygous
c. homozygous or heterozygous
d. homozygous

7. If black and white true-breeding mice are mated and the result is all gray offspring, what inheritance pattern would

this be indicative of?

a. codominance
b. dominance
c. incomplete dominance
d. multiple alleles

8. The ABO blood groups in humans are controlled by the IA, IB, and I alleles. The IA allele encodes the A blood group antigen, IB encodes B, and I encodes O. Both A and B are dominant to O. If a heterozygous blood type A parent (iAi) and a heterozygous blood type B parent (iBi) mate, one quarter of their offspring will have AB blood type (IAIB) in which both antigens are expressed equally. Therefore, the ABO blood groups are an example of _____.

a. codominance and incomplete dominance
b. incomplete dominance only
c. multiple alleles and incomplete dominance
d. multiple alleles and codominance

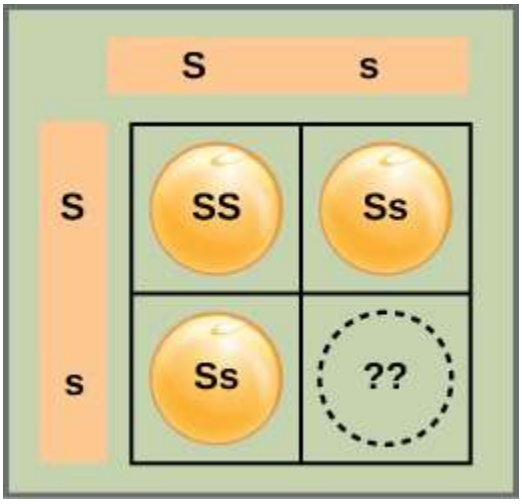
9. In a mating between two individuals that are heterozygous for a recessive lethal allele that is expressed in utero, what genotypic ratio (homozygous dominant : heterozygous : homozygous recessive) would you expect to observe in the off-spring?

a. 1 : 2 : 1
b. 3 : 1 : 1
c. 1 : 2 : 0
d. 0 : 2 : 1

10. The forked line and probability methods make use of what probability rule?

a. monohybrid rule
b. product rule
c. sum rule
d. test cross

11.



In pea plants, smooth seeds (S) are dominant to wrinkled seeds (s). In a genetic cross of two plants that are heterozygous for the seed shape trait, the Punnett square is shown. What is the missing genotype?

a. SS
b. Ss
c. sS
d. ss

12. If the inheritance of two traits fully obeys Mendelian laws of inheritance, where may you assume that the genes are located?

a. on any autosomal chromosome or chromosomes
b. on Y chromosomes
c. on the same chromosome
d. on separate chromosomes

13. How many different offspring genotypes are expected in a trihybrid cross between parents heterozygous for all three traits? How many phenotypes are expected if the traits behave in a dominant and recessive pattern?

a. 64 genotypes; 16 phenotypes
b. 16 genotypes; 64 phenotypes
c. 8 genotypes; 27 phenotypes
d. 27 genotypes; 8 phenotypes

14. Four-o' clock flowers may be red, pink or white. In the crossing of a true-breeding red and true-breeding white plants, all the offspring are pink. Use a Punnett square to determine the correct genotype of the offspring if the red parent has genotype RR and the white parent has genotype rr.

a. RR and Rr
b. Rr and rr
c. Rr only
d. RR only

15. Which cellular process underlies Mendel's law of independent assortment?

a. Chromosomes align randomly during meiosis.

b. Chromosomes can exchange genetic material during crossover.

c. Gametes contain half the number of chromosomes of somatic cells.

d. Daughter cells are genetically identical to parent cells after mitosis.

16. While studying meiosis, you observe that gametes receive one copy of each pair of homologous chromosomes and one copy of the sex chromosomes. This observation is the physical explanation of Mendel's law of _____.

a. dominance

b. independent assortment

c. random distribution of traits

d. segregation

17. In some primroses, the petal color blue is dominant. A cross between a true-breed blue primrose and a white primrose yields progeny with white petals. A second gene at another locus prevented the expression of the dominant coat color. This is an example of _____.

a. codominance

b. hemizygosity

c. incomplete dominance

d. epistasis

18.

Cross 1: Swollen pods X shriveled pods	
F1	314 swollen; 298 shriveled
Cross 2: swollen F1 X swollen F1	
F2	594 swollen 97 shriveled

Purple flowers (P) are dominant over red flowers (p) and long pollen grains are dominant over round pollen grains. When purple flowers and long pollen grain plants were crossed with plants with white flowers and round pollen grains, all the F_1 plants showed purple flowers and long pollen grains. The F_1 plants were crossed and the results are in the table. What conclusions about the physical relationship between the traits can be drawn from the experiment?

a. The traits are probably linked.

b. The traits follow the law of independent assortment

c. The traits are located on different chromosomes

d. There was epistasis.

19. When the expression of one gene pair masks or modifies the expression of another, the genes show _____.

a. codominance

b. epistasis

c. incomplete dominance

d. partial linkage

CRITICAL THINKING QUESTIONS

20. Describe one reason why the garden pea was an excellent model system for studying inheritance.

a. The garden pea has flowers that close tightly to promote cross-fertilization.

b. The garden pea has flowers that close tightly to prevent cross-fertilization.

c. The garden pea does not mature in one season and is a perennial plant.

d. Male and female reproductive parts attain maturity at different times, promoting self-fertilization.

21. How would you perform a reciprocal cross to test stem height in the garden pea?

a. First cross is performed by transferring the pollen of a heterozygous tall plant to the stigma of a true breeding dwarf plant. Second cross is performed by transferring the pollen of a heterozygous dwarf plant to the stigma of a true breeding tall plant.

b. First cross is performed by transferring the pollen of a true breeding tall plant to the stigma of a true breeding dwarf plant. Second cross is performed by transferring the pollen of a true breeding dwarf plant to the stigma of a true breeding tall plant.

c. First cross is performed by transferring the pollen of a true breeding tall plant to the stigma of a heterozygous dwarf plant. Second cross is performed by transferring the pollen of a heterozygous dwarf plant to the stigma of a true breeding tall plant.

d. First cross is performed by transferring the pollen of a heterozygous tall plant to the stigma of a heterozygous dwarf plant. Second cross is performed by transferring the pollen of a heterozygous tall plant to the stigma of a heterozygous dwarf plant.

22. Flower position in pea plants is determined by a gene with axial and terminal alleles. Given that axial is dominant to terminal, list all of the possible F_1 and F_2 genotypes and phenotypes from a cross involving parents that are homozygous for each trait. Express genotypes with conventional genetic abbreviations.

a. F_1: All AA-axial; F_2: AA-Axial and aa-terminal.

b. F_1: All aa-terminal; F_2: AA-Axial and Aa-terminal.

c. F_1: AA-axial and Aa-terminal; F_2: All AA-axial.

d. F_1: All Aa-axial; F_2: AA-Axial, Aa-Axial, and aa-terminal.

23. Use a Punnett square to predict the offspring in a cross between a dwarf pea plant (homozygous recessive) and a tall pea plant (heterozygous). What is the phenotypic ratio of the offspring?

a. 1 Tall : 1 dwarf

b. 1 tall : 2 dwarf

c. 3 tall : 1 dwarf

d. 1 dwarf : 4 tall

24. Can a human male be a carrier of red-green color blindness?

a. Yes, males can be the carriers of red-green color blindness, as color blindness is autosomal dominant.

b. No, males cannot be the carriers of red-green color blindness, as color blindness is X-linked.

c. No, males cannot be the carriers of red-green color blindness, as color blindness is Y-linked.

d. Yes, males can be the carriers of red-green color blindness, as color blindness is autosomal recessive.

25. Use the probability method to calculate the genotypes and genotypic proportions of a cross between AABBCc and Aabbcc parents.

a. Possible genotypes are AABBcc, AaBbCc, AaBbcc and the ratio $1 : 2 : 1$.

b. Possible genotypes are AABbcc, AaBbCc, AaBbcc and the ratio $1 : 3 : 1$.

c. Possible genotypes are AABbCc, AABbcc, AaBbCc, AaBbcc and the ratio $1 : 1 : 1 : 1$.

d. Possible genotypes are AABbcc, AaBbCC, AaBbcc and the ratio $1 : 1 : 1$.

26. How does the segregation of traits result in different combinations of gametes at the end of meiosis?

a. The chromosomes randomly align during metaphase I at the equator, and separation of homologous chromosomes occurs during anaphase I. Similarly separation of sister chromatids occurs at anaphase II of meiosis II. At the end of meiosis II, four different gametic combinations are produced, each containing a haploid set of chromosomes.

b. The chromosomes randomly align during anaphase I at the equator. Separation of bivalent chromosomes occur during metaphase I of meiosis I. Similarly, separation of sister chromatids occurs at metaphase II of meiosis II. At the end of meiosis II, four different gametic combinations are produced, each containing a haploid set of chromosomes.

c. The chromosomes randomly align during prophase I at the equator, and separation of sister chromatids occurs during metaphase I of meiosis I. Similarly separation of bivalent chromosomes occur at metaphase II of meiosis II. At the end of meiosis II, four different gametic combinations are produced, each containing a diploid set of chromosomes.

d. The chromosomes randomly align during prophase I at the equator, and separation of bivalent chromosomes occur during anaphase I of meiosis I. Similarly, separation of homologous chromosomes occurs at metaphase II of meiosis II. At the end of meiosis II, four different gametic combinations are produced, each containing a diploid set of chromosomes.

27. In Section 12.3, "Laws of Inheritance," an example of epistasis was given for summer squash. Cross white WwYy heterozygotes to demonstrate the phenotypic ratio of 12 white : 3 yellow : 1 green that was given in the text.

a. 12 offspring are white, as the W gene is epistatic to the Y gene. Three offspring are yellow, because w is not epistatic. Green offspring is obtained when the recessive form of both genes (wwyy) are present.

b. 12 offspring are white as W gene is hypostatic to Y gene. Three offspring are yellow because Y is epistatic to w. Green offspring is obtained when the dominant form of both the genes (WWYY) is present.

c. 12 offspring are white as W gene is dominant. Three offspring are yellow because Y is dominant and w is recessive. Green offspring is obtained when the recessive form of both the genes (wwyy) is present, showing codominance.

d. 12 offspring are white as W is epistatic to Y gene. Three offspring are yellow because Y is hypostatic to w. Green offspring is obtained when the recessive form of both the genes (wwyy) are present, showing codominance.

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28. The trait for widow's peak can be considered a monoallelic dominant trait in humans. If a man with a widow's peak and a woman with a straight hairline have a child together, what is the probability that the child will inherit the widow's peak if you know that the father's mother had a straight hairline?

a. 0.25

b. 0.5

c. 0.75

d. 1

29. Don't like Brussels sprouts? Blame your genes. The chemical PTC (phenylthiocarbamide), which is nearly identical to a compound found in the cabbage family, tastes very bitter for some people. Others cannot detect a taste. The ability to taste PTC is incompletely dominant and is controlled by a gene on chromosome 7. A woman who finds Brussel sprouts mildly distasteful (in other words, who can taste PTC weakly) has a child with a man who hates Brussel sprouts (in other words, who can taste PTC strongly). What is the probability that their son likes Brussel sprouts (in other words, cannot taste PTC)?

a. 0

b. 0.25

c. 0.5

d. 1

30. Tay-Sachs disease is an autosomal recessive disorder that causes severe problems in neurons. Children who receive two copies of the gene rarely live beyond the age of five. There is no cure for the disease. During a genetic screening, a couple is told that both partners carry the recessive gene. What kind of issue must the couple confront?

a. scientific

b. financial

c. ethical

d. educational

31. A couple has three daughters. What is the probability that the next child they have will be a daughter?

a. 0%

b. 25%

c. 50%

d. 100%

32. What is the probability that a couple will have three daughters?

a. $\frac{1}{2}$

b. $\frac{1}{3}$

c. $\frac{1}{6}$

d. $\frac{1}{8}$

33. Petunias can be blue, red, or violet. When a blue flower is crossed with a red flower, all the resulting flowers are violet. When a violet flower is crossed with a red flower, about half of the flowers are violet and half are red. How do you characterize the color trait?

a. complete dominance

b. codominance

c. incomplete dominance

d. sex-linked

34. Petunias can be blue, red, or violet. When a blue flower is crossed with a red flower, all the resulting flowers are violet. Two violet petunias are crossed. Which is the most probable result of the cross?

a. 75% of the flowers are blue and 25% of the flowers are red.

b. 50% of the flowers are blue and 50% of the flowers are red.

c. 75% of the flowers are red and 25% are blue.

d. 25% of the flowers are blue, 50% of the flowers are violet, and 25% of the flowers are red.

35. Fruit flies (*Drosophila melanogaster*) with a wild-type phenotype have gray bodies and red eyes. Certain mutations can cause changes to these traits. Mutant flies may have a black body and/or cinnabar eyes. To study the genetics of these traits, a researcher crossed a true-breeding wild-typed male fly with a true-breeding female fly with a black body and cinnabar eyes. All of the F1 progeny displayed a wild type phenotype. Which of the following is correct about the traits observed?

a. Gray body and cinnabar eyes are dominant.

b. Eye color is sex-linked.

c. Body color is sex-linked.

d. Gray body and red eyes are dominant.

36.

Body Color	Eye Color	Number Predicted
Gray	Red	244
Black	Cinnabar	244
Gray	Cinnabar	244
Black	Red	244

Female flies from the F_1 generation were crossed with true-breeding male flies with black bodies and cinnabar eyes. The table represents the predicted outcome and the data obtained from the cross. What was the assumption that lead to the predicted numbers?

a. The traits assort independently.

b. The traits are located on the X chromosome.

c. The traits are on the same chromosome.

d. The female flies were homozygous for wild type alleles.

37. Cats can be black, yellow, or calico (black and yellow patches). Coat color is carried on the X chromosome. What type of inheritance is color coat in cats?

1. Complete dominance
2. Codominance
3. Incomplete dominance
4. Sex-linked

a. 2

b. 3

c. 2,4

d. 3,4

38. Cats can be black, yellow or calico (black and yellow patches). Coat color is carried on the X chromosome. A yellow cat is crossed with a black cat. Assume that the offspring are both male and female. What are the phenotypes of the offspring and in what proportions?

a. All the cats are yellow.

b. All the cats are black.

c. All the cats are calico.

d. There is not enough information to answer the question.

SCIENCE PRACTICE CHALLENGE QUESTIONS

39. The gene *SLC24A5* encodes an antiporter membrane protein that exchanges sodium for calcium (R. Ginger et

al., JBC, 2007). This process has a role in the synthesis of the melanosomes that cause skin pigmentation. A mutation in this gene affecting a single amino acid occurs in humans. The homozygous mutant gene is found in 99% of humans with European origins. Both the wild type and mutant display codominance.

A. Representing the wild-type form of the gene as +/+ and the mutant form of the gene as m/m for two homozygous parents, **construct** a Punnett square for this cross using the first grid below. **Annotate your representation** to **identify** the phenotypes with high (H), intermediate (I), and low (L) melanosome production. Use the second grid to represent an F_2 generation from the offspring of the first cross. Use annotation to show the phenotype.

F_1	m	m
+		
+		

Table 12.6

F_2		

Table 12.7

B. **Draw** sister chromatids at anaphase II for both parents in the F_1 generation and annotate your drawing to **identify** each genotype of the gametes using the cells of the Punnett square.

C. **Explain** which of Mendel's laws is violated by codominance.

D. Suppose that these data were available to evaluate the claim that the wild-type and mutant forms of *SLC24A5* are codominant:

F_2		
Phenotype	**Observed**	**Expected**
H	1206	
I	2238	
L	1124	

Table 12.8

Complete the table. **Explain** the values expected in terms of the genotype of the offspring.

E. Using a c^2 statistic at the 95% confidence level, **evaluate** the claim that the wild-type and mutant forms of *SCLO24A5* are codominant. The definition of the statistic $X_c^2 = \sum \frac{(O_i - E_i)^2}{E_i}$ where X is the chi-square test statistic, c is the significant level of the test (we will use 0.05), O is the observed value for variable *i*, and E is the expected value for variable *i*. The Chi-square statistic table is provided in the AP Biology Exam.

Degrees of Freedom								
p	1	2	3	4	5	6	7	8
0.05	3.84	5.99	7.82	9.49	11.07	12.59	14.07	15.51

Table 12.9

40. Adrenoleukodystrophy (ALD) is a genetic disorder in which lipids with very high molecular weights are not metabolized and accumulate within cells. Accumulation of these fats in the brain damages the myelin that surrounds nerves. This progressive disease has two causes: an autosomal recessive allele, which causes neonatal ALD, and a mutation in the ABCD1 gene located on the X chromosome. A controversial treatment is the use of Lorenzo's oil, which is expensive; despite this treatment, neurological degradation persists in many patients. Gene therapy as a potential treatment is currently in trials but is also very costly.

An infant patient exhibits symptoms of neonatal ALD, which are difficult to distinguish from the X-linked form of the disease. The infant's physician consults electronic health records to construct a pedigree showing family members who also presented symptoms similar to ALD. The pedigree is shown in this diagram. The infant patient is circled. Symbols for males (o) and females (m) are filled when symptoms are present.

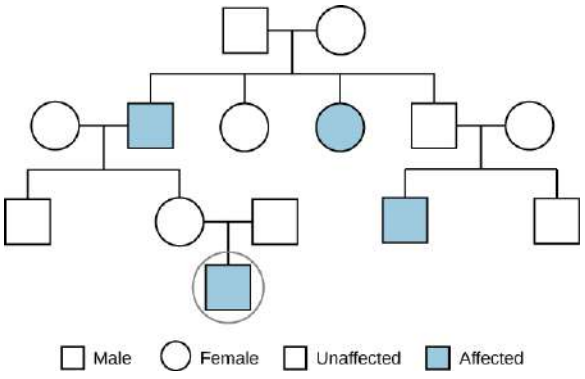

Figure 12.21

A. Using the pedigree, **explain** which form of ALD (neonatal or X-linked) is present in the infant.

B. Sharing of digital records among health providers is one method proposed to improve the quality and reduce the cost of health care in the U.S. The privacy of electronic

health records is a concern. **Pose three questions** that must be addressed in developing policies that balance the costs of treatments and diagnoses, patient quality of life, and risks to individual privacy.

41. Two genes, A and B, are located adjacent to each other (linked) on the same chromosome. In the original cross (P_0), one parent is homozygous dominant for both traits (AB), whereas the other parent is recessive (ab).

Characteristic	Alleles	Chromosome
Seed color	yellow (I) / green (i)	1
Seed coat & flowers	colored (A) / white (a)	1
Mature pods	smooth (V) / wrinkled (v)	4
Flower stalk	from leaf axils (Fa) / umbellate at top of plant (fa)	4
Height	> 1 m (Le) / ~0.5 m (le)	4
Unripe pods	green (Gp) / yellow (gp)	5
Mature seeds	smooth (R) / wrinkled (r)	7

Table 12.10

A. **Describe** the distribution of genotypes and phenotypes in F_1.

B. **Describe** the distribution of genotypes and phenotypes when F_1 is crossed with the ab parent.

C. **Describe** the distribution of genotypes and phenotypes when F_1 is crossed with the AB parent.

D. **Explain** the observed non-Mendelian results in terms of the violation of the laws governing Mendelian genetics.

42. Gregor Mendel's 1865 paper described experiments on the inheritance of seven characteristics of *Pisum sativum* shown in the first column in the table below. Many years later, based on his reported outcomes and analysis of the inheritance of a single characteristic, Mendel developed the concepts of genes, their alleles, and dominance. These concepts are defined in the second column of the table using conventional symbols for the dominant allele for each characteristic. Even later, the location of each of these genes on one of the seven chromosomes in *P. sativum* were determined, as shown in the third column.

A. Before the acceptance of what Mendel called "factors" as the discrete units of inheritance, the accepted model was that the traits of progeny were "blended" traits of the parents. **Evaluate the evidence** provided by Mendel's experiments in disproving the blending theory of inheritance.

B. Mendel published experimental data and analysis for two experiments involving the inheritance of more than a single characteristic. He examined two-character inheritance of seed shape and seed color. He also reported three-character inheritance of seed shape, seed color, and flower color. **Evaluate the evidence** provided by the multiple-character experiments. **Identify** which of the following laws of inheritance depend upon these multiple-character experiments for support:

a. During gamete formation, the alleles for each gene segregate from each other so that each gamete carries only one allele for each gene.

b. Genes for different traits can segregate independently during the formation of gametes.

c. Some alleles are dominant, whereas others are recessive. An organism with at least one dominant allele will display the effect of the dominant allele.

d. All three laws can be inferred from the single-character experiments.

C. As shown in the table above, some chromosomes contain the gene for more than one of the seven characteristics Mendel studied, for example, seed color and flowers. The table below shows, with filled cells above the dashed diagonal line, the combinations of characteristics for which Mendel reported results. In the cells below the dotted diagonal line, **identify with an X** each cell where deviations from the law or laws identified in part B might be expected.

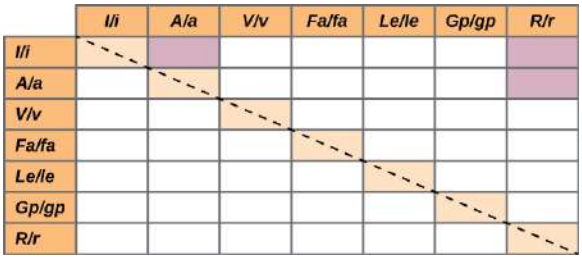

Figure 12.22

D. **Explain** the reasons for the expected deviations for those combinations of characteristics identified in part C.

E. In one of the experiments reported by Mendel, deviations from the law identified in part B might be expected. **Explain** how the outcomes of this experiment were consistent with Mendel's laws.

43. A dihybrid cross involves two traits. A cross of parental types AaBb and AaBb can be represented with a Punnett square:

	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AaBb
Ab	AAbB	AAbb	AabB	Aabb
aB	aABB	aABb	aaBB	aaBb
ab	aAbB	aAbb	aabB	aabb

Figure 12.23

This representation clearly organizes all of the possible genotypes and reveals the 9:3:3:1 distribution of phenotypes and a 4×4 grid of 16 cells. Expressed as a fraction of the 16 possible genotypes of the offspring, the phenotypic ratio describes the probability of each phenotype among the offspring: 3 (AA, Aa, aA) × 3 (BB, bB, Bb)/16 = 9/16; 3 (AA, Aa, aA) × 1 (bb) /16 = 3/16; 1 (aa) × 3 (BB, bB, Bb) = 3/16; and 1 (aa) × 1 (bb) = 1/16.

A. Using the probability method, calculate the likelihood of these phenotypes from each dihybrid cross:

- recessive in the gene with alleles A and a from the cross AaBb × aabb
- dominant in both genes from the cross AaBb × aabb
- recessive in both genes from the cross AaBb × aabb
- recessive in either gene from the cross AaBb × aabb

A Punnett square representation of a trihybrid cross, such as the self-cross of AaBbCc, is more cumbersome because there are eight columns and rows (2×2×2 ways to choose parental genotypes) and 64 cells. A less tedious representation is to calculate the number of each type of genotype in the offspring directly by counting the unique permutations of the letters representing the alleles. For example, the probability of the cross AaBbCc × AaBbCc is 3 (AA, Aa, aA) × 3 (BB, Bb, bB) × 3 (CC, Cc, cC)/64 = 27/64.

B. Using the probability method, **calculate** the likelihood of these phenotypes from each trihybrid cross:

- recessive in all traits from the cross AaBbCc × aabbcc
- recessive in the gene with alleles C and c and dominant in the other two traits from the cross AaBbCc × AaBbCc
- dominant in the gene with alleles A and a and recessive in the other two traits from the cross AaBbcc × AaBbCc

C. The probability method is an easy way to calculate the likelihood of each particular phenotype, but it doesn't simultaneously display the probability of all possible phenotypes. The forked line representation described in the text allows the entire phenotypic distribution to be displayed. Using the forked line method, calculate the probabilities in a cross between *AABBCc* and *Aabbcc* parents:

- all traits are recessive: aabbcc
- traits are dominant at each loci, A?B?C?
- traits are dominant at two genes and recessive at the third
- traits are dominant at one gene and recessive at the other two

44. Construct a representation showing the connection between the process of meiosis and the transmission of six possible phenotypes from parents to F2 offspring. The phenotypes are labeled A, a, B, b and C, c. Expression of each phenotype is controlled by a separate Mendelian gene. Your representation should show the proportion of every possible combination of phenotypes (e.g., ABC, AbC, etc.) that will be present in the F2 offspring.