Genetics Analysis and Principles 7th edition Brooker Solutions Manual

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Chapter 1: Overview of Genetics

Key Terms

Alleles
Amino acid
Behavioral traits
Biological evolution
Carbohydrates
Cellular level
Central dogma of genetics
Chromosomes
Codon
Deoxyribonucleic acid (DNA)
Diploid
Discovery-based science
Environment
Enzymes
Evolution
Gametes
Gene
Gene expression
Gene mutations
Genetic approach
Genetic code
Genetic cross
Genetic variation
Genome
Haploid
Homologs
Hypothesis testing
Karyotype
Lipids
Loss-of-function allele
Loss-of-function mutation
Macromolecules
Messenger RNA (mRNA)
Model organisms
Molecular level
Morphological traits
Morphs
Natural selection
Norm of reaction
Nucleic acids
Nucleotides
Organismal level
Phenylketonuria (PKU)
Physiological traits
Polypeptides
Population level
Proteins
Proteome
Ribonucleic acid (RNA)
Scientific method
Species
Somatic cells
Traits
Transcription
Translated (translation)

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Chapter Outline

Introduction

1. The Human Genome Project began in 1990 as a project between the National Institutes of Health (NIH) and the Department of Energy (DOE). The project was completed in 2003.
   a. human genome contains approximately 3 billion nucleotide base pairs (Figure 1.1)
   b. project is 99.99% accurate (1 error in 10,000 nucleotides)
2. Human Genome Project should enable scientists to:
   a. determine the number of genes in humans
   b. examine the relationship between genes and living cells
   c. study the evolution of the species
   d. understand developmental genetics
   e. explore the relationship between genetic mutations and disease
   f. develop new technologies for genetic studies
3. Modern genetic studies result in developments that affect our daily lives.
   a. The development of new medicines such as Humulin. Humulin is human insulin manufactured by *E. coli* bacteria.
   b. Cloning of mammals, such as Dolly the sheep by Ian Wilmut and associates (1997) (Figure 1.2)
   c. production of transgenic organisms (Figure 1.3)

1.1 The Molecular Expression of Genes

Learning Outcomes:

1. Describe the biochemical composition of cells.
2. Explain how proteins are largely responsible for cell structure and function.
3. Outline how DNA stores the information to make proteins.

1. Genes represent the basic unit of heredity, while a trait represents the characteristics of an organism. Genes provide the blueprint that determines an organism's traits.

Living Cells Are Composed of Biochemicals

1. Small organic molecules provide energy for cellular functions as well as the building blocks for larger molecules.
2. There are Four categories of biologically important organic molecules that are made of repetitive subunits. These organic molecules are called macromolecules.
   a. nucleic acids
   b. proteins
   c. carbohydrates
   d. lipids
3. Larger cellular structures, such as chromosomes, are built from combinations of macromolecules and smaller molecules (Figure 1.4).

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Each Cell Contains Many Different Proteins That Determine Cellular Structure and Function

1. Cellular characteristics are determined primarily by proteins.
2. A cell's proteome consists of all of the proteins that a cell makes at a given time.
3. General roles of proteins include: enzymatic functions, cellular support, transport across the cell membrane, biological motors, cell-to-cell recognition, and cell signaling.
4. Most enzymes are proteins that accelerate a chemical reaction (catalyst).
   a. catabolic enzymes break down molecules and release energy
   b. anabolic enzymes synthesize larger molecules

DNA Stores the Information for Protein Synthesis

1. DNA stores the information needed for synthesis of cellular proteins.
2. DNA is made of nucleotides. Each nucleotide includes a nitrogenous base, which is either adenine (A), thymine (T), cytosine (C), or guanine (G).
3. The information in the DNA contains the information the sequence of amino acids in a protein.
   a. the genetic code is used to relate the genetic information to the correct amino acid
4. In cells, DNA is found in chromosomes (Figure 1.5). The information on a chromosome is organized as genes.
   a. on average, a human chromosome contains approximately1000 genes

The Information in DNA is Accessed During the Process of Gene Expression

1. Gene expression refers to the use of the genetic information to affect the characteristics of cells.
2. Process includes two steps (Figure 1.6):
   a. information in the DNA is copied into RNA by transcription (genes that contain the information for the synthesis of proteins are copied into messenger RNA (mRNA)).
   b. the RNA is then translated into a functional protein.
3. The distinctive structure of a protein determines is cellular function.

1.2 The Relationship Between Genes and Traits

Learning Outcomes:

1. Outline how the expression of genes leads to an organism's traits.
2. Define genetic variation.
3. Discuss the relationship between genes and traits.
4. Describe how genes are transmitted in sexually reproducing species.
5. Explain the process of evolution.

The Molecular Expression of Genes Within Cells Leads to an Organism's Traits

1. A trait is the displayed characteristic of an organism.
2. Morphological traits are associated with the appearance of an organism (eye color, height, etc.).
3. Physiological traits are associated with the ability of the organism to function, such as metabolic functions.

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4. Behavioral traits are associated with how an organism responds to its environment.
5. Genetics spans four levels of biological organization (Figure 1.7):
    a. molecular level – the processes of transcription and translation
    b. cellular level – the function of a protein within the cell
    c. organismal level – the observed traits of an organism
    d. population level – the occurrence of the trait in a population under given conditions
6. Alternate forms of a gene are called alleles. Different alleles of a gene have different DNA sequences.

Inherited Differences in Traits Are Due to Genetic Variation

1. Genetic variation is the differences in inherited traits among individuals of a population (Figure 1.8).
2. For species that occupy wide geographic ranges, these differences may be drastic. These are very distinct forms of a single species are called morphs.
3. Genetic variation is due to changes in the nucleotide sequence of the DNA. These variations may be caused by:
    a. gene mutations at the nucleotide level
    b. major structural changes in a chromosome
    c. variation in the total number of chromosomes in an organism

Traits Are Governed by Genes and by the Environment

1. The external environment in which an organism exists may influence that organism's traits.
2. The term norm of reaction refers to the effects of environmental variation on an individual's traits.
3. Example is the human disease phenylketonuria (PKU), which encodes a gene called phenylalanine hydrolase. This gene allows for the metabolism of the phenylalanine amino acid.
    a. Mutations causing a defect in this gene mean that toxic levels of phenylalanine accumulate in the blood, causing mental impairment and developmental problems.
    b. The defective allele is present in 1 in 8,000 individuals in the U.S.

During Reproduction, Genes Are Passed from Parent to Offspring

1. Gregor Mendel first established that genetic information was passed from parent to offspring as discrete units (genes).
2. Sexually reproducing species are usually diploid (two copies of each chromosome, or 2n).
3. The copies of each chromosome are called homologs (Figure 1.10a).
4. Gametes are haploid (one copy of each chromosome, also known as the n number) (Figure 1.10b).
5. Sexual reproduction increases genetic variation in a population.
6. Somatic cells, also known as body cells, are diploid in a diploid organism.

The Genetic Composition of a Species Evolves from Generation to Generation

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1. The change in the genetic composition of a species over time is called biological evolution, or simply evolution.
2. Charles Darwin proposed the theory of natural selection as the mechanism for biological evolution.
3. Over a long period of time, the accumulation of many genetic changes may lead to rather striking modifications in a species' characteristics (Figure 1.11).

1.3Fields of Genetics

Learning Outcomes:

1. Compare and contrast the three major fields of genetics: transmission, molecular, and population genetics.

1. Genetics is a broad field encompassing molecular, cellular, organism, and population biology.
2. Experimentally, geneticists often focus their efforts on model organisms – organisms studied by many different researchers so they can compare their results and determine scientific principles that apply more broadly to other species.
3. Figure 1.12 shows some common model genetic organisms.

Transmission Genetics Explores the Inheritance Patterns of Traits as They Are Passed from Parents to Offspring

1. Framework provided by Gregor Mendel who suggested that genetic determinants (genes) were discrete units that were passed from generation to generation.
2. Studies of transmission genetics rely on controlled genetic crosses and pedigree analyses to examine how traits are passed from parents to offspring.

Molecular Genetics Focuses on a Biochemical Understanding of the Hereditary Material

1. The workings of the genetic material at the molecular level.
2. Molecular geneticists use a genetic approach to study mutant genes with an abnormal function. These loss of function mutations help geneticists understand the normal role of the gene in the organism.

Population Genetics Is Concerned with Genetic Variation and Its Role in Evolution

1. Involves the use of mathematical theories explain the prevalence of certain genes in a population.
2. Provides a link between the study of transmission genetics (Mendel) and natural selection (Darwin).
3. Population geneticists study the relationship between genetic variation and the environment that an organism inhabits.

1.4 The Science of Genetics

Learning Outcomes:

1. Discuss how genetics is an experimental science.
2. Outline different strategies for solving problems in genetics.

Genetics is an Experimental Science

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1. Uses hypothesis testing, also known as the scientific method, and discovery-based science.
2. Hypothesis testing involves gathering of data to support or refute a putative conclusion.
3. Discovery-based science involves gathering of data without a preconceived hypothesis.

Genetics TIPS Will Help You to Improve Your Problem-Solving Skills
1. Genetics TIPS are solved problems that walk students through the problem-solving process.
2. Genetics TIPs are presented throughout chapters 2 through 29, in the chapter and at the end of the chapter.
3. Many different problem-solving strategies are used in the Genetics TIPS: Define key terms, Make a drawing, Predict the outcome, Compare and contrast, Relate structure and function, Describe the steps, Propose a hypothesis, Design and experiment, Analyze data, and Make a calculation.
4. Genetics TIPS provides students with practice at applying these problem-solving skills.

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ANSWERS TO CONCEPT CHECK QUESTIONS AND END OF CHAPTER QUESTIONS

CHAPTER 1

Note: The answers to the Comprehension questions are in Appendix B.

Concept check questions (in figure legends)

FIGURE 1.1 Understanding our genes may help to diagnose inherited diseases. It may also lead to the development of drugs to combat diseases. Other answers are possible.

FIGURE 1.2 Many ethical issues are associated with human cloning. Is it the wrong thing to do? Does it conflict with an individual's religious views? And so on.

FIGURE 1.3 Because females mate only once, sorting out the male mosquitoes and releasing sterile males into the environment can limit mosquito reproduction.

FIGURE 1.4 DNA is a macromolecule.

FIGURE 1.5 DNA and proteins are found in chromosomes. A small amount of RNA may also be associated with chromosomes when transcription is occurring, and, as discussed in Chapter 17, some non-coding RNAs may bind to chromosomes.

FIGURE 1.6 The information to make a polypeptide is stored in DNA.

FIGURE 1.7 The dark-colored butterfly has a more active pigment-synthesizing enzyme.

FIGURE 1.8 Genetic variation is the reason these frogs look different.

FIGURE 1.9 These are examples of variation in chromosome number.

FIGURE 1.10 A corn gamete contains 10 chromosomes. (The leaf cells are diploid.)

FIGURE 1.11 The horse populations have become adapted to their environment, which has gradually changed over the course of many years.

FIGURE 1.12 There are several possible examples of other model organisms, including rats and frogs.

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End-of-chapter Questions:

Conceptual Questions

C1. There are many possible answers. Some common areas to discuss might involve the impact of genetics in the production of new medicines, the diagnosis of diseases, the production of new kinds of food, and the use of DNA fingerprinting to solve crimes.

C2. A chromosome is a very long polymer of DNA. A gene is a specific sequence of bases within that polymer; the sequence of bases distinguishes a gene from other genes. Genes are located in chromosomes, which are found within living cells.

C3. The structure and function of proteins govern the structure and function of living cells. The cells of the body determine an organism's traits.

C4. At the molecular level, a gene (a sequence of bases in DNA) is first transcribed into RNA. Most genes are transcribed into an mRNA, which encodes a polypeptide. The genetic code within the mRNA is used to synthesize a polypeptide with a particular amino acid sequence. This second process is called translation.

C5.

A. Molecular level. This is a description of a how an allele affects protein function.
B. Cellular level. This is a description of how protein function affects cell structure.
C. Population level. This is a description of how the two alleles affect members of a population.
D. Organism level. This is a description of how the alleles affect the traits of an individual.

C6. Genetic variation is the occurrence of genetic differences within members of the same species or among different species. Within any population, variation may occur in the genetic material. Variation may occur in particular genes, so some individuals carry one allele and other individuals carry a different allele. An example would be alleles that cause differences in coat color among mammals. Variation may also occur in chromosome structure and number. In plants, differences in chromosome number can affect disease resistance.

C7. An extra chromosome (specifically an extra copy of chromosome 21) causes Down syndrome.

C8. You can pick almost any trait. For example, flower color in petunias would be an interesting choice. Some petunias are red and others are purple. There must be different alleles of a flower color gene that affect this trait in petunias. In addition, the amounts of sunlight, fertilizer, and water also affect the intensity of flower color.

C9. The term *diploid* means that a cell has two copies of each type of chromosome. In humans, nearly all of the cells are diploid except for gametes (i.e., sperm and egg cells). Gametes usually have only one set of chromosomes.

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C10. A DNA sequence is a sequence of nucleotides. Each nucleotide may have one of four different bases (i.e., A, T, G, or C). When we speak of a DNA sequence, we focus on the sequence of bases.

C11. The genetic code is the way in which the sequence of bases in mRNA is read to produce a sequence of amino acids within a protein.

C12.
A. A gene is a segment of DNA. For most genes, the expression of the gene results in the production of a functional protein. The functioning of proteins within living cells affects the traits of an organism.
B. A gene is a segment of DNA that usually encodes the information for the production of a specific protein. Genes are found within chromosomes. Many genes are found within a single chromosome.
C. An allele is an alternative version of a particular gene. For example, suppose that a plant has a flower color gene. One allele of this gene may produce a white flower, and a different allele may produce an orange flower. The white allele and the orange allele are then two versions of the flower color gene.
D. A DNA sequence is a sequence of nucleotides. The information within a DNA sequence (which is transcribed into an RNA sequence) specifies the amino acid sequence within a polypeptide.

C13. The statement in part A is not correct. Individuals do not evolve. Populations evolve because certain individuals are more likely to survive and reproduce and pass their genes to succeeding generations.

C14.
A. How genes and traits are transmitted from parents to offspring.
B. How the genetic material functions at the molecular and cellular levels.
C. Why genetic variation exists in populations, and how it changes over the course of many generations.

Experimental Questions

E1. A genetic cross involves breeding two different individuals.

E2. DNA sequencing is used primarily by molecular geneticists. The sequence of DNA is a molecular characteristic of DNA. However, as you will learn throughout this textbook, the sequence of DNA is also of interest to transmission and population geneticists.

E3. You would see 47 chromosomes instead of 46. There would be three copies of chromosome 21 instead of two copies.

E4.
A. Transmission geneticists. Dog breeders are interested in how genetic crosses affect the traits of dogs.
B. Molecular geneticists. *E. coli* is a good model organism for studying genetics at the molecular level.

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C. Both transmission geneticists and molecular geneticists. Fruit flies are easy to cross for studying the transmission of genes and traits from parents to offspring. Molecular geneticists have also studied many genes in fruit flies to see how they function at the molecular level.
D. Population geneticists. Most wild animals and plants would be of interest to population geneticists. In the wild, you cannot make controlled crosses. But you can study genetic variation within a population and try to understand its relationship to the environment.
E. Transmission geneticists. Agricultural breeders are interested in how genetic crosses affect the outcome of traits.

E5. You need to follow the scientific method. You can take a look at an experiment in another chapter to see how the scientific method is followed.

CHAPTER 2

Note: The answers to Comprehension questions are in Appendix B.

Concept check questions (in figure legends)

FIGURE 2.2 The male gamete is found within pollen grains.

FIGURE 2.3 The white-flowered plant is providing the sperm, and the purple-flowered plant is providing the eggs.

FIGURE 2.4 A true-breeding line maintains the same trait over the course of several generations of self-fertilization.

FIGURE 2.6 Segregation means that the *T* and *t* alleles separate from each other, and so a gamete receives one of them, but not both.

FIGURE 2.7 According to this hypothesis, two different genes are linked. The alleles of the same gene are not linked.

FIGURE 2.9 Independent assortment allows for new combinations of alleles of different genes to be found in future generations of offspring.

FIGURE 2.10 Such a parent could make two types of gametes, *Ty* and *ty*, in equal proportions.

FIGURE 2.12 Horizontal lines connect two individuals that have offspring together, and they connect all of the offspring produced by the same two parents.

End-of-chapter Questions:

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Conceptual Questions

C1. Mendel's work showed that genetic determinants are inherited in a dominant/recessive manner. This was readily apparent in many of his crosses. For example, when he crossed two true-breeding plants for a trait such as height (i.e., tall versus dwarf), all the F_1 plants were tall. This was not consistent with blending. Perhaps more striking was the result obtained in the F_2 generation: 3/4 of the offspring were tall and 1/4 were dwarf. In other words, the F_2 generation displayed phenotypes that were like the parental generation. There did not appear to be a blending to create an intermediate phenotype. Instead, the genetic determinants did not seem to change from one generation to the next.

C2. In plants, cross-fertilization occurs when the pollen and eggs come from different plants, whereas in self-fertilization, they come from the same plant.

C3. The genotype is the type of genes that an individual inherits whereas the phenotype is the individual's observable traits. Tall pea plants, red hair in humans, and vestigial wings in fruit flies are phenotypes. Homozygous, *TT,* in pea plants; a heterozygous carrier of the cystic fibrosis allele; and homozygotes for the cystic fibrosis allele are descriptions of genotypes. It is possible to have different genotypes and the same phenotype. For example, a pea plant that is *TT* or *Tt* would both have a tall phenotype.

C4. A true-breeding organism is a homozygote that has two copies of the same allele.

C5. Conduct a cross in which the unknown individual is bred to an individual that carries only recessive alleles for the gene in question.

C6. Diploid organisms contain two copies of each type of gene. When they make gametes, only one copy of each gene is found in a gamete. Two alleles cannot stay together within the same gamete.

C7. B. This statement is not correct because these are alleles of different genes.

C8. Genotypes: 1 *Tt* :1 *tt*
Phenotypes: 1 tall : 1 dwarf

C9. The recessive phenotype must be a homozygote. The dominant phenotype could be either homozygous or heterozygous.

C10. Here, *c* is the recessive allele for constricted pods; *Y* is the dominant allele for yellow color. The cross is *ccYy* × *CcYy.* Follow the directions for setting up a Punnett square, as described in Chapter 2. The genotypic ratio is 2 *CcYY* : 4 *CcYy* : 2 *Ccyy* : 2 *ccYY* : 4 *ccYy* : 2 *ccyy.* This 2:4:2:2:4:2 ratio can be reduced to a 1:2:1:1:2:1 ratio.
The phenotypic ratio is 6 smooth pods, yellow seeds : 2 smooth pods, green seeds : 6 constricted pods, yellow seeds : 2 constricted pods, green seeds. This 6:2:6:2 ratio can be reduced to a 3:1:3:1 ratio.

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C11. The genotypes are 1 *YY* : 2 *Yy* : 1 *yy*.
The phenotypes are 3 yellow : 1 green.

C12. Offspring with a nonparental phenotype are consistent with the law of independent assortment. If two different traits were always transmitted together as unit, it would not be possible to get nonparental combinations of traits. For example, if a true-breeding parent had two dominant traits and was crossed to a true-breeding parent having the two recessive traits, the F_2 offspring could not have one recessive and one dominant trait. However, because independent assortment can occur, it is possible for F_2 offspring to have one dominant and one recessive trait.

C13. (a) It behaves like a recessive trait because unaffected parents sometimes produce affected offspring. In such cases, the unaffected parents are heterozygous carriers.
(b) It behaves like a dominant trait. An affected offspring always has an affected parent. However, recessive inheritance cannot be ruled out.

C14.
A. Barring a new mutation during gamete formation, the probability is 100% because the parents must be heterozygotes in order to produce a child with a recessive disorder.
B. Construct a Punnett square. There is a 50% chance of heterozygous offspring.
C. Use the product rule. The chance of being phenotypically unaffected is 0.75 (i.e., 75%), so the answer is $0.75 \times 0.75 \times 0.75 = 0.422$, which is 42.2%.
D. Use the binomial expansion equation where $n = 3$, $x = 2$, $p = 0.75$, $q = 0.25$. The answer is 0.422, or 42.2%.

C15.
A. 100% because they are genetically identical.
B. Construct a Punnett square. You know the parents are heterozygotes because they produced a blue-eyed child. The fraternal twin is not genetically identical, but she or he has the same parents as their twin. The answer is 25%.
C. The probability that an offspring inherits the allele is 50% and the probability that this offspring will pass it on to his/her offspring is also 50%. You use the product rule: (0.5)(0.5) = 0.25, or 25%.
D. Barring a new mutation during gamete formation, the chance is 100% because they must be heterozygotes in order to produce a child with blue eyes.

C16. First construct a Punnett square. The chances are 75% of producing a solid pup and 25% of producing a spotted pup.
A. Use the binomial expansion equation where $n = 5$, $x = 4$, $p = 0.75$, $q = 0.25$. The answer is 0.396, or 39.6% of the time.
B. You can use the binomial expansion equation for each litter. For the first litter, $n = 6$, $x = 4$, $p = 0.75$, $q = 0.25$; for the second litter, $n = 5$, $x = 5$, $p = 0.75$, $q = 0.25$. Because the litters are in a specified order, you use the product rule and multiply the probability of the first litter times the probability of the second litter. The answer is 0.070, or 7.0%.
C. To calculate the probability of the first litter, you use the product rule and multiply the probability of the first pup (0.75) times the probability of the remaining four. You use the binomial expansion equation to calculate the probability of the remaining four, where $n = 4$, $x = 3$, $p = 0.75$, $q = 0.25$.

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The probability of the first litter is 0.316. To calculate the probability of the second litter, you use the product rule and multiply the probability of the first pup (0.25) times the probability of the second pup (0.25) times the probability of the remaining five. To calculate the probability of the remaining five, you use the binomial expansion equation, where $n = 5$, $x = 4$, $p = 0.75$, $q = 0.25$. The probability of the second litter is 0.025. To get the probability of these two litters occurring in this order, you use the product rule and multiply the probability of the first litter (0.316) times the probability of the second litter (0.025). The answer is 0.008, or 0.8%.

D. Because the order of the first two is specified, you use the product rule and multiply the probability of the firstborn (0.75) times the probability of the second born (0.25) times the probability of the remaining four. You use the binomial expansion equation to calculate the probability of the remaining four pups, where $n = 4$, $x = 2$, $p = 0.75$, $q = 0.25$. The answer is 0.040, or 4.0%.

C17. If *B* is the black allele, and *b* is the white allele, the male is *bb,* the first female is probably *BB,* and the second female is *Bb.* You are uncertain of the genotype of the first female. She could be *Bb,* although it is unlikely because she didn't produce any white pups out of a litter of eight.

C18.

A. Use the product rule:
(1/4)(1/4)=1/16

B. Use the binomial expansion equation, where
$n = 4$, $p = ¼$, $q = ¾$, $x = 2$:
$P = 0.21$, or 21%

C. Use the product rule:
(1/4)(3/4)(3/4) = 0.14, or 14%

C19. The parents must be heterozygotes, so the probability is 1/4.

C20.

A. 1/4

B. 1, or 100%

C. (3/4)(3/4)(3/4) = 27/64 = 0.42, or 42%

D. Use the binomial expansion equation, where
$n = 7$, $p = 3/4$, $q = 1/4$, $x = 3$:
$P = 0.058$, or 5.8%

E. The probability that the first plant is tall is 3/4. To calculate the probability that among the next four, any two will be tall, use the binomial expansion equation, where $n = 4$, $p = 3/4$, $q = 1/4$, and $x = 2$:
$P = 0.21$
Then calculate the overall probability of these two events:
(3/4)(0.21) = 0.16, or 16%

C21.

A. *T Y R, T y R, T Y r, T y r*

B. *T Y r, t Y r*

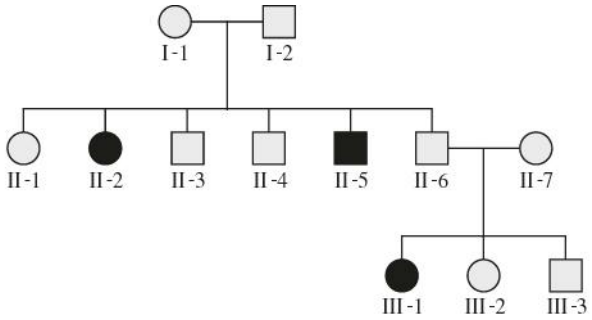
C. *T Y R, T Y r, T y R, T y r, t Y R, t Y r, t y R, t y r*

D. *t Y r, t y r*

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C22. The gamete violates the law of segregation because it has two copies of one gene. The two alleles for the *A* gene did not segregate from each other.

C23. It is recessive inheritance. The pedigree is shown next. Affected individuals are shown with filled symbols.



The mode of inheritance appears to be recessive. Unaffected parents (who must be heterozygous) produce affected children.

C24. Based on the pedigree provided, the disease is likely to be a dominant trait because an affected child always has an affected parent. In fact, it is a dominant disorder.

C25.

A. 3/16
B. (9/16)(9/16)(9/16) = 729/4096 = 0.18
C. (9/16)(9/16)(3/16)(1/16)(1/16) = 243/1,048,576 = 0.00023, or 0.023%
D. Another way of looking at this is that the probability it will have round, yellow seeds is 9/16. Therefore, the probability that it will not is 1 – 9/16 = 7/16.

C26. It is impossible for F_1 individuals to be true-breeding because they are all heterozygotes.

C27. This problem is a bit unwieldy, but you can solve it using the multiplication method.
For height, the ratio is 3 tall : 1 dwarf.
For seed texture, the ratio is 1 round : 1 wrinkled.
For seed color, they are all yellow.
For flower location, the ratio is 3 axial : 1 terminal.
Thus, the product is
(3 tall + 1 dwarf)(1 round + 1 wrinkled)(1 yellow)(3 axial + 1 terminal)
Multiplying this out, the answer is
9 tall, round, yellow, axial
9 tall, wrinkled, yellow, axial
3 tall, round, yellow, terminal
3 tall, wrinkled, yellow, terminal
3 dwarf, round, yellow, axial
3 dwarf, wrinkled, yellow, axial
1 dwarf, round, yellow, terminal

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1 dwarf, wrinkled, yellow, terminal

C28. 2 *TY, tY,* 2 *Ty, ty, TTY, TTy,* 2 *TtY,* 2 *Tty*
This question is a bit tricky, but you get 2 *TY* and 2 *Ty* because either of the two *T* alleles could combine with *Y* or *y.* Also, you get 2 *TtY* and 2 *Tty* because either of the two *T* alleles could combine with *t* and then combine with *Y* or *y.*

C29. The drone is *sB* and the queen is *SsBb.* According to the laws of segregation and independent assortment, the male can make only *sB* gametes, while the queen can make *SB, Sb, sB,* and *sb,* in equal proportions. Therefore, male offspring will be *SB, Sb, sB,* and *sb,* and female offspring will be *SsBB, SsBb, ssBB,* and *ssBb.* The phenotypic ratios, assuming an equal number of males and females, will be:

Males	*Females*
1 normal wings/black eyes	2 normal wings, black eyes
1 normal wings/white eyes	2 short wings, black eyes
1 short wings/black eyes	
1 short wings/white eyes	

C30. The genotype of the F_1 plants is *Tt Yy Rr.* According to the laws of segregation and independent assortment, the alleles of each gene will segregate from each other, and the alleles of different genes will randomly assort into gametes. A *Tt Yy Rr* individual could make eight types of gametes: *TYR, TyR, Tyr, TYr, tYR, tyR, tYr,* and *tyr,* in equal proportions (i.e., 1/8 of each type of gamete). To determine genotypes and phenotypes, you could make a large Punnett square that would contain 64 boxes. You would need to line up the eight possible gametes across the top and along the side, and then fill in the 64 boxes. Alternatively, you could either the multiplication method or forked-line method described in Figure 2.11. The genotypes and phenotypes are as follows:
1 *TT YY RR*
2 *TT Yy RR*
2 *TT YY Rr*
2 *Tt YY RR*
4 *TT Yy Rr*
4 *Tt Yy RR*
4 *Tt YY Rr*
8 *Tt Yy Rr* = 27 tall, yellow, round
1 *TT yy RR*
2 *Tt yy RR*
2 *TT yy Rr*
4 *Tt yy Rr* = 9 tall, green, round
1 *TT YY rr*
2 *TT Yy rr*
2 *Tt YY rr*
4 *Tt Yy rr* = 9 tall, yellow, wrinkled
1 *tt YY RR*
2 *tt Yy RR*
2 *tt YY Rr*

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4 *tt Yy Rr* = 9 dwarf, yellow, round
1 *TT yy rr*
2 *Tt yy rr* = 3 tall, green, wrinkled
1 *tt yy RR*
2 *tt yy Rr* = 3 dwarf, green, round
1 *tt YY rr*
2 *tt Yy rr* = 3 dwarf, yellow, wrinkled
1 *tt yy rr* = 1 dwarf, green, wrinkled

C31. Construct a Punnett square to determine the probability of these three phenotypes. The probabilities are 9/16 for round, yellow; 3/16 for round, green; and 1/16 for wrinkled, green. Use the multinomial expansion equation described question 4 in More Genetic TIPS, where $n = 5$, $a = 2$, $b = 1$, $c = 2$, $p = 9/16$, $q = 3/16$, $r = 1/16$. The answer is 0.007, or 0.7%.

C32. The wooly haired male is a heterozygote, because he has the trait and his mother did not. (He must have inherited the normal allele from his mother.) Therefore, he has a 50% chance of passing the wooly allele to his offspring; his offspring have a 50% of passing the allele to their offspring; and those grandchildren have a 50% chance of passing the allele to their offspring (the wooly haired man's great-grandchildren). Because this is an ordered sequence of independent events, you use the product rule: $0.5 \times 0.5 \times 0.5 = 0.125$, or 12.5%. Because no other Scandinavians are on the island, the chance is 87.5% for the offspring being normal (because they could not inherit the wooly hair allele from anyone else). You use the binomial expansion equation to determine the probability that one out of eight great-grandchildren will have wooly hair, where $n = 8$, $x = 1$, $p = 0.125$, $q = 0.875$. The answer is 0.393, or 39.3%.

C33.

A. Construct a Punnett square. Because it is a rare disorder, you would assume that the mother is a heterozygote and the father is homozygous for the normal allele. The chances are 50% that the man in his thirties will have the allele.

B. Use the product rule: 0.5 (chance that the man has the allele) times 0.5 (chance that he will pass it to his offspring), which equals 0.25, or 25%.

C. You use the binomial expansion equation. From part B, you calculated that the probability of an affected child is 0.25. Therefore the probability of an unaffected child is 0.75. For the binomial expansion equation, $n = 3$, $x = 1$, $p = 0.25$, $q = 0.75$. The answer is 0.422 or 42.2%.

C34. Use the product rule. If the woman is a heterozygote, there is a 50% chance of having an affected offspring at each birth: $(0.5)^7 = 0.0078$, or 0.78%. This is a pretty small probability. If the woman has an eighth child who is unaffected, however, she has to be a heterozygote, because it is a dominant trait. She would have to pass a normal allele to an unaffected offspring. The answer is 100%.

Experimental Questions

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E1. Pea plants are relatively small and hardy. They produce both pollen and eggs within the same flower. Because a keel covers the flower, self-fertilization is quite easy. In addition, cross-fertilization is possible by the simple manipulation of removing the anthers in an immature flower and later placing pollen from another plant. Finally, peas exist in several variants.

E2. The difference lies in where the pollen comes from. In self-fertilization, the pollen and eggs come from the same plant. In cross-fertilization, they come from different plants.

E3. Two generations would take two growing seasons. About 1 and 1/2 years.

E4. According to Mendel's law of segregation, the genotypic ratio should be 1 homozygote dominant : 2 heterozygotes : 1 homozygote recessive. The data table considers only the plants with a dominant phenotype. The genotypic ratio should be 1 homozygote dominant : 2 heterozygotes. The homozygote dominants would be true-breeding while the heterozygotes would not be true-breeding. This 1:2 ratio is very close to what Mendel observed.

E5. In a single-factor cross, the experimenter is only concerned with the outcome of a single trait. In a two-factor cross, the experimenter follows the pattern of inheritance for two different traits.

E6. All three offspring had black fur. The ovaries from the albino female could only produce eggs with the dominant black allele (because they were obtained from a true-breeding black female). The actual phenotype of the albino mother does not matter. Therefore, all offspring are heterozygotes (*Bb*) and have black fur.

E7. The data are consistent with two genes (let's call them gene 22 and gene 24) that exist in two alleles each, a susceptible allele and a resistant allele. The observed data approximate a 9:3:3:1 ratio. This is the expected ratio if two genes are involved, and if resistance is dominant to susceptibility.

E8. If you construct a Punnett square according to Mendel's laws, you expect a 9:3:3:1 ratio. Because a total of 556 offspring were observed, the expected numbers of offspring with different phenotypes are
556 × 9/16 = 313 round, yellow
556 × 3/16 = 104 wrinkled, yellow
556 × 3/16 = 104 round, green
556 × 1/16 = 35 wrinkled, green
If you plug the observed and expected values into the chi square equation, you get a value of 0.51. With four categories, your degrees of freedom equal $n - 1$, or 3. If you look up the value of 0.51 in the chi square table (see Table 2.1), you see that it falls between the P values of 0.80 and 0.95. This means that the probability is between 80% and 95% that any deviation between observed results and expected results was caused by random sampling error. Therefore, you accept the hypothesis. In other words, the results are consistent with the law of independent assortment.

E9. No, the law of independent assortment applies to transmission patterns of two or more genes. In a single-factor cross, you are monitoring only the transmission pattern of a single gene.

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E10.

A. Let c^+ represent normal wings and c represent curved wings and e^+ represent gray body and e represent ebony body.
Parental Cross: $cce^+e^+ \times c^+c^+ee$.
F_1 generation is heterozygous: c^+ce^+e
An F_1 offspring crossed to a fly with curved wings and ebony body is represented as follows:
$c^+ce^+e \times ccee$
The F_2 offspring will have this 1:1:1:1 ratio of genotypes:
$c^+ce^+e : c^+cee : cc\ e^+e : ccee$

B. The phenotypic ratio of the F_2 flies will be 1:1:1:1:
normal wings, gray body : normal wings, ebony bodies : curved wings, gray bodies : curved wings, ebony bodies

C. From part B, the F_2 generation consists of 1/4 of each category. There are a total of 444 offspring. The expected number of each category is 1/4 × 444, which equals 111.

$$\chi^2 = \frac{(114-111)^2}{111} + \frac{(105-111)^2}{111} + \frac{(111-111)^2}{111} + \frac{(114-111)^2}{111}$$

$$\chi^2 = 0.49$$

With 3 degrees of freedom, a value of 0.49 or greater is likely to occur between 80% and 95% of the time. Therefore, the experimental data are consistent with the expected outcome.

E11. You would expect a ratio of 3 normal : 1 long neck. In other words, there should be 1/3 as many long-necked mice as normal mice. If you multiply 522 times 1/3, the expected value is 174. However, only 62 were observed. Therefore, it appears that 174 – 62, or 112, mice died during early embryonic development; 112 divided by 174 gives us the percentage that died, which equals 0.644, or 64.4%.

E12. Follow the same basic chi square analysis used before. You expect a 3:1 ratio, or 3/4 of the dominant phenotype and 1/4 of the recessive phenotype.
The observed and expected values are as follows (rounded to the nearest whole number):

Observed*	Expected	$\frac{(O-E)^2}{E}$
5,474	5,493	0.066
1,850	1,831	0.197
6,022	6,017	0.004
2,001	2,006	0.012
705	697	0.092
224	232	0.276
882	886	0.018
299	295	0.054
428	435	0.113
152	145	0.338
651	644	0.076
207	215	0.298

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787	798	0.152
277	266	0.455
	χ^2 =	2.15

*Due to rounding, the observed and expected values may not add up to precisely the same number. Because n = 14, there are 13 degrees of freedom. If you look up the value 2.15 in the chi square table, you have to look between 10 and 15 degrees of freedom. In either case, a value of 2.15 or greater is expected to occur more than 99% of the time. Therefore, the data are consistent with the law of segregation.

E13. This means that a deviation value of 1.005 or greater (between the observed and expected data) would occur 80% of the time. In other words, it is fairly likely to obtain this value due to random sampling error. Therefore, you accept the hypothesis.

E14. The dwarf parent with terminal flowers must be homozygous for both genes, because it is expressing these two recessive traits: *ttaa,* where *t* is the recessive dwarf allele, and *a* is the recessive allele for terminal flowers. The phenotype of the other parent is dominant for both traits. However, because this parent was able to produce dwarf offspring with axial flowers, it must have been heterozygous for both genes: *TtAa.*

E15. The hypothesis is that disease sensitivity and herbicide resistance are dominant traits and they are governed by two genes that assort independently. According to this hypothesis, the F_2 generation should yield a ratio of 9 disease sensitive, herbicide resistant : 3 disease sensitive, herbicide sensitive : 3 disease resistant, herbicide resistant : 1 disease resistant, herbicide sensitive. Because there are a total of 288 offspring produced, the expected numbers would be

9/16 × 288 = 162 disease sensitive, herbicide resistant
3/16 × 288 = 54 disease sensitive, herbicide sensitive
3/16 × 288 = 54 disease resistant, herbicide resistant
1/16 × 288 = 18 disease resistant, herbicide sensitive

$$\chi^2 = \frac{(157-162)^2}{162} + \frac{(57-54)^2}{54} + \frac{(54-54)^2}{54} + \frac{(20-18)^2}{18}$$

$$\chi^2 = 0.54$$

If you look up this value in the chi square table under 3 degrees of freedom, the value lies between the 0.95 and 0.80 probability values. Therefore, you expect a value equal of 0.54 or greater, at least 80% of the time, due to random sampling error. Therefore, you would accept the hypothesis.

Questions for Student Discussion/Collaboration

1. The methods for making a Punnett square and using the multiplication method are described in the chapter. Presumably, the multiplication method (or the forked-line method) will work a lot faster.

2. If you construct a Punnett square, the following probabilities will be obtained:
tall with axial flowers 3/8
dwarf with terminal flowers 1/8

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The probability of being tall with axial flowers or dwarf with terminal flowers is then:
3/8 + 1/8 = 4/8 = 1/2
You use the product rule to calculate the probability of the ordered events of the first three offspring being tall and axial or dwarf and terminal, and fourth offspring being tall and axial:
(1/2)(1/2)(1/2)(3/8) = 3/64 = 0.047 = 4.7%

3. Ignore the other genes. The cross is *Rr* × *RR*. All of the offspring will have round seeds. The probability is 100%

CHAPTER 3

Note: The answers to Comprehension questions are in Appendix B.

Concept check questions (in figure legends)

FIGURE 3.1 *Compartmentalization* means that the cells have membrane-bound compartments.

FIGURE 3.2 The chromosomes would not be spread out very well, and would probably be overlapping. It would be difficult to see individual chromosomes.

FIGURE 3.3 Homologs are similar in size and banding pattern, and they carry the same types of genes. However, the alleles of a given gene may be different on two homologs.

FIGURE 3.4 FtsZ assembles into a ring at the future site of the septum and recruits other proteins to this site to produce a cell wall between the two daughter cells.

FIGURE 3.5 In the G_1 phase of the cell cycle, a cell may be preparing to divide. By comparison, the G_0 phase is the phase in which a cell is either temporarily not progressing through the cell cycle or never dividing again.

FIGURE 3.6 Homologs are genetically similar; one is inherited from the mother and the other from the father. By comparison, chromatids are the product of DNA replication. The chromatids within a pair of sister chromatids are genetically identical.

FIGURE 3.7 One end of a kinetochore microtubule is attached to a kinetochore on a chromosome. The other end is within the centrosome.

FIGURE 3.8 Anaphase.

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