

Genetics

A Conceptual Approach

Seventh Edition



Benjamin A. Pierce

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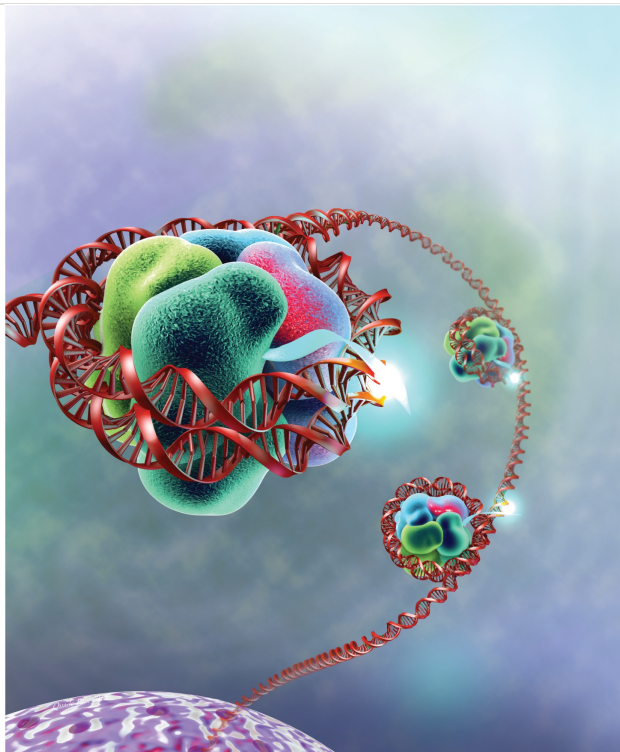
A Conceptual Approach

Seventh Edition

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To my parents, Rush and Amanda Pierce; my children, Sarah Pierce Dumas and Michael Pierce; and my genetic partner, friend, and soul mate for 39 years, Marlene Tyrrell

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Letter from the Author



Marlene Tyrrell

I still remember the excitement I felt when I was in your place, taking my first genetics course. I was intrigued by the principles of heredity, which allow one to predict what offspring will look like even before they are born; I was fascinated to learn that these principles have their foundation in the chemistry of an elegant molecule called DNA; and I was captivated to find that genetics underlies evolution, the process responsible for life's endless diversity and beauty. These elements of genetics still impress and excite me today. One of the great things about teaching genetics is the chance to convey that excitement to students.

This book has been written in different places: in my office at Southwestern University, on the back porch of my home overlooking the hills of central Texas, in the mountains of northern New Mexico, and in airports and hotel rooms around the country. Regardless of location, whenever I write, I try to imagine that I'm sitting with a small group of students, having a conversation about genetics. My goal as the author of *Genetics: A Conceptual Approach* is to have that conversation with you. I want to become a trusted guide on your journey through introductory genetics. In this book, I've tried to share some of what I've learned in my years of teaching genetics. I provide advice and encouragement at places where students often have difficulty, and I tell stories of the people, places, and experiments of genetics—past and present—to keep the subject relevant, interesting, and alive. My goal is to help you learn the necessary details, concepts, and problem-solving skills while encouraging you to see the elegance and beauty of the larger landscape.

Educational research demonstrates that students learn best when they are actively engaged with their subject, and this has been my own experience in teaching and learning. In this seventh edition of *Genetics: A Conceptual Approach*, I wanted to share some active learning tools that I use in my own classroom: think-pair-share and concept mapping questions—exercises designed for small group work—as well as extensive problem sets at the end of each chapter. Additional group learning exercises and digital learning tools are provided on the SaplingPlus web site. I encourage you to take advantage of these resources and work with

other students in learning genetics.

At Southwestern University, my office door is always open, and my students often drop by to share their experiences, concerns, and triumphs. I learn as much from my students as they learn from me, and I would love to learn from you—by email (pierceb@southwestern.edu), by telephone (512-863-1974), or in person (Southwestern University, Georgetown, Texas).

Ben Pierce

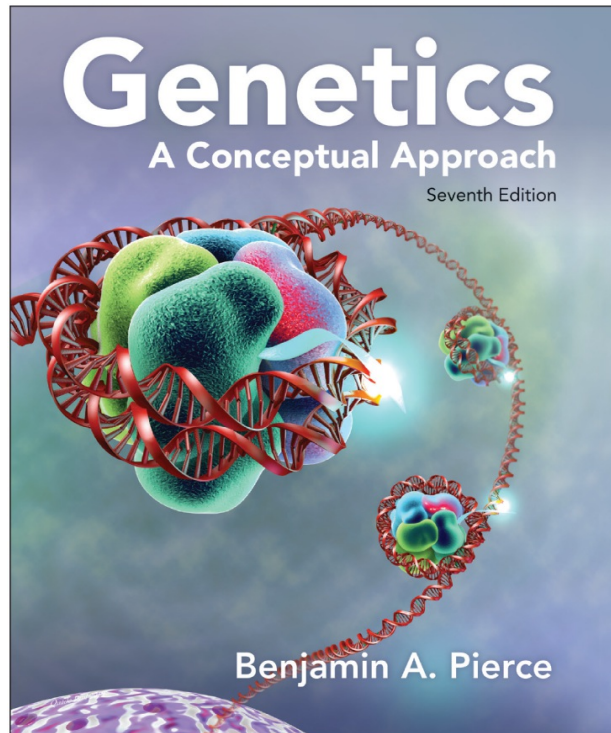
PROFESSOR OF BIOLOGY

AND HOLDER OF THE LILLIAN NELSON PRATT CHAIR

SOUTHWESTERN UNIVERSITY

A conceptual approach to success in genetics

With ***Genetics: A Conceptual Approach***, Ben Pierce brings a master teacher's experience to his introductory genetics textbook, clarifying this complex subject by focusing on the big picture of genetics concepts and how they connect to one another.



Cover and Title Page Illustration: Echo Medical Media

The new seventh edition continues this mission by expanding upon the powerful pedagogy and tools that have made this title so successful. New question types, more learning guidelines for students, and an updated art program round out a powerful text. Improvements to the online resources in SaplingPlus give students the conceptual and problem solving understanding they need for success.

New to the seventh edition:

CONNECTING PROBLEMS allow students to connect concepts across chapters. These questions ask students to integrate what they have learned over several chapters, and to apply what they learned to problem solving or data analysis.

CONCEPT MAPPING EXERCISES help students conceptually map out topics within a chapter by including key terms and describing how they are connected. Creating connections between concepts and ideas is critically important for effective learning. These new concept mapping exercises are designed to help students build an understanding of the relationships among important concepts and terms by creating a visual map that depicts these relationships. These problems can be assigned as homework, or students can work on them in groups, allowing them to discuss how to organize the concepts in a map.

END-OF-CHAPTER LEARNING OBJECTIVES help frame the concepts covered in each section. A set of Learning Objectives, one for each major section of the chapter (followed by key concepts for that section), helps students identify the main learning goals for each chapter.

Powerful tools for problem solving

Genetics: A Conceptual Approach features powerful tools, both in the text and online in SaplingPlus, to teach and reinforce the problem-solving skills students need for success in genetics.

DATA ANALYSIS PROBLEMS draw on examples from published research articles and ask students to apply the concepts they learned to analyze real data.

26. Honeybees have haplodiploid sex determination:



queens (females) are diploid, developing from fertilized eggs, whereas drones (males) are haploid, developing from unfertilized eggs. Otto Mackensen studied linkage relations among eight mutations in honeybees (O. Mackensen. 1958. *Journal of Heredity* 49:99–102). The following table gives the results of two of Mackensen's crosses, including three recessive mutations: *cd* (cordovan body color), *h* (hairless), and *ch* (chartreuse eye color).

Queen genotype **Phenotypes of drone (male) progeny**

$cd \quad h^+$	294 cordovan, 236 hairless, 262
$cd^+ \quad h$	cordovan and hairless, 289 wild type
$h \quad ch^+$	3131 hairless, 3064 chartreuse, 96
$h^+ \quad ch$	chartreuse and hairless, 132 wild type

- Only the genotype of the queen is given. Why is the genotype of the male parent not needed for mapping these genes? Would the genotype of the male parent be required if we examined female progeny instead of male progeny?
- Determine the nonrecombinant and recombinant progeny for each cross, and calculate the map distances between *cd*, *h*, and *ch*. Draw a linkage map illustrating the linkage arrangements among these three genes.

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NEW! CONNECTING QUESTIONS

help students synthesize concepts from different chapters to understand the big picture. The new questions ensure that students get the bigger picture of the science of genetics and, much like real geneticists, learn to use information from different fields within genetics in problem solving.

Section 8.3



***29.** Red–green color blindness is a human X-linked recessive disorder (see Chapter 4). A young man with a 47,XXY karyotype (Klinefelter syndrome) is color blind. His 46,XY brother is also color blind. Both parents have color vision. In which parent and where in meiosis did the nondisjunction that gave rise to the young man with Klinefelter syndrome take place? Assume that no crossing over took place in prophase I of meiosis (see Chapter 2).

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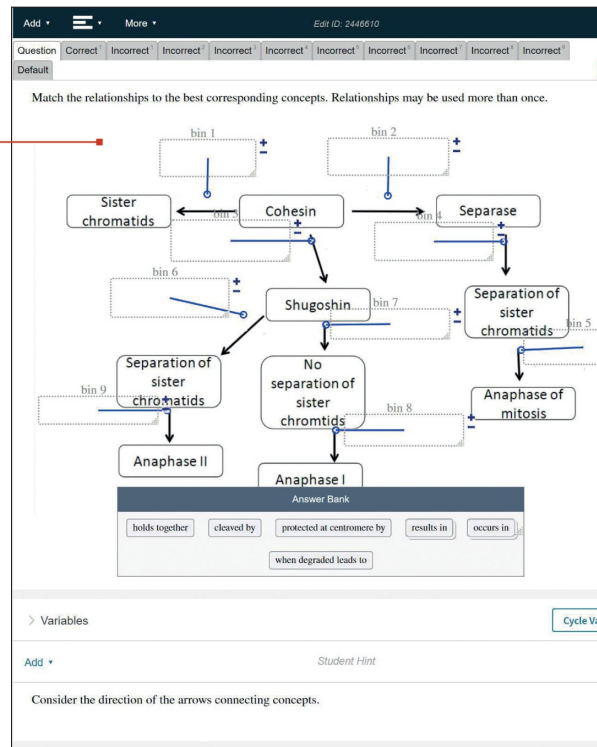
NEW! CONCEPT MAPPING QUESTIONS, available in the book and in SaplingPlus, ask students to build a visual representation of a topic.

Section 2.3

3. Create a concept map that outlines the role of cohesin in the separation of sister chromatids and homologous chromosomes in mitosis and meiosis.

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Concept mapping problems available in SaplingPlus allow students to test their skill through automatically graded exercises.



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SaplingPlus: Tools for Success

SaplingPlus is the online companion to *Genetics: A Conceptual Approach* and combines Sapling’s acclaimed automatically graded online homework with a powerful e-book and an extensive suite of engaging multimedia learning resources. Problems feature hints for when students get stuck, answer-specific feedback to help them learn from their mistakes, and solutions to reinforce what they’ve learned.

SAPLING ONLINE HOMEWORK

Sapling's scaffolded support of hints, answer-specific feedback, and stepped out solutions provide a powerful formative assessment experience.

In a dihybrid cross, the possible offspring genotype combinations for two genes are predicted. In this example, short stems are recessive and tall stems are dominant, whereas white flowers are recessive and purple flowers are dominant. Stephen crossed two heterozygotes, or $TtPp$ individuals, which produced 656 offspring. Each of the two $TtPp$ individuals can produce one of four possible allele combinations, which include TP , Tp , tP , and tp .

The Punnett square shows a $TtPp \times TtPp$ dihybrid cross.

	TP	Tp	tP	tp
TP	TTPP	TTpP	TtPP	TtPp
Tp	TTpP	TTpp	TtPp	Ttpp
tP	TtPP	TtPp	ttPP	ttPp
tp	TtPp	Ttpp	ttPp	ttpp

Based on this dihybrid cross, 1/16 offspring are predicted to have short size number of pp offspring, multiply 656 by 1/16. Therefore, the predicted

Optional hints keep students from getting stuck.

Students receive feedback specific to their incorrect answers, helping them learn from their mistakes.

E-BOOK
SaplingPlus incorporates a powerful e-book along with plentiful online resources, giving students a single place to read, study, and assess their knowledge.

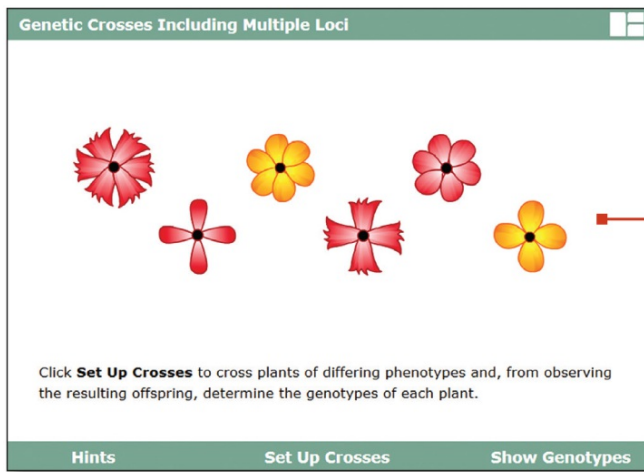
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SaplingPlus also includes tools to help students prepare for class and study for their exams. LearningCurve adaptive quizzing ties back to the e-book and is a great tool to help students learn basic concepts and do assigned readings before coming to lecture. SaplingPlus also includes a wealth of multimedia and problem solving resources to help students make the most of their study time.

LEARNINGCURVE

Put "testing to learn" into action. Based on research, LearningCurve really works: Game-like quizzing motivates students and adapts to their needs based on their performance. It is the perfect tool to get them to engage before class and review after! Additional reporting tools and metrics help teachers get a handle on what their class knows and doesn't know.

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MULTIMEDIA

SaplingPlus also includes powerful multimedia assets, such as **videos and animations**, to help students visualize complex processes.

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Tools for active learning

Genetics: A Conceptual Approach includes support for professors to implement more active learning in the classroom.






NEW! ACTIVE LEARNING HUB with in-class activities is now in SaplingPlus. It contains PowerPoints and worksheets to help you easily implement more active learning in your classroom.

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paternal in origin and the light ones are maternal). Fill out the charts below to determine the chromosome number in the cells of this organism throughout mitosis and meiosis. Also, determine the number of DNA molecules and the amount of DNA (in picograms), as well as the ploidy of the cell, at each stage of the cell cycle. (For meiosis, assume no recombination takes place.) Then answer the questions that follow.

Part 1: Mitosis

Mitosis

	G1	S	G2	Prophase and prometaphase	Metaphase	Anaphase	Telophase and cytokinesis
							
Chromosomes per cell	6						
Chromosome status							
DNA (molecules) per cell	6						
DNA (picograms) per cell	20						

IN-CLASS ACTIVITIES

encourage students to apply the concepts that they learn and work, and learn, in groups.

New and Reorganized Content

The seventh edition addresses recent discoveries in genetics corresponding to our ever-changing understanding of inheritance, the molecular nature of genetic information, epigenetics, and genetic evolution. This edition also focuses on updating the new research techniques that have become available to geneticists in the past few years. For example, this edition provides expanded coverage of CRISPR-Cas systems and reorganized and updated content in the chapters on molecular genetic analysis and epigenetics.

New and updated content includes:

- Eight new chapter-opening stories, including [“Mapping Fear and Aggression in Dogs” \(Chapter 4\)](#), [“Hominin History in Ancient DNA” \(Chapter 12\)](#), [“Wrecks on the DNA Highway” \(Chapter 13\)](#), and [“Sequencing Earth’s Biodiversity” \(Chapter 20\)](#)
- New Concept Mapping exercises
- New Connecting Concepts problems
- New Learning Objectives in chapter summaries
- Revised section on the cutting edge of genetics (Chapter 1)
- Revised section on binary fission in prokaryotes (Chapter 2)
- Revised and updated coverage of mandatory genetic screening of newborns; updated information on noninvasive prenatal screening; and a new section on genealogies and genetic testing for ancestry (Chapter 6)
- Updated discussion of aneuploidy in humans (Chapter 8)
- Updated discussion of bacterial and archaeal diversity; revised discussion of gene mapping in bacteria; a new section called “Bacterial Defense Mechanisms” and expanded coverage of CRISPR-Cas in bacteria; a new section called “Zika virus”; and an updated discussion of the microbiome (Chapter 9)
- New discussion of topologically associated domains in chromatin structure (Chapter 11)
- Revised and updated discussion of eukaryotic origins of replication (Chapter 12)
- New section on internal mRNA modifications (Chapter 14)
- Updated discussion of variation in translation initiation sites (Chapter 15)
- Revised discussion of transcription factors; new discussion of super enhancers, as well as updated discussion of insulators and regulatory neighborhoods (Chapter 17)
- New discussion of single-cell genomic sequencing to estimate rates of somatic mutations, as well as updated discussion of tautomeric shifts (Chapter 18)
- Extensively updated CRISPR-Cas coverage; new discussion of environmental DNA (eDNA); revised discussion of gene libraries; updated discussion of next-generation and third-generation DNA sequencing methods; updated information on the CODIS system for DNA fingerprinting; and updated information on gene therapy currently in use (Chapter 19)
- New information on DNA and protein databases; expanded discussion of heat maps; new information on applications of RNA sequencing; and added discussion of the interactome (Chapter 20)
- Extensively reorganized and updated epigenetics content; new discussion of epigenome-wide association studies (Chapter 21)
- New section on mapping gene expression in *Drosophila* embryos; updated information on epigenetic modifications affecting eye development in blind cave fish (Chapter 22)
- Updated cancer statistics; a new discussion of autophagy; and an expanded discussion of the factors that contribute to metastasis (Chapter 23)
- Updated information on the wolves of Isle Royale (Chapter 25)
- A new section called “Interpreting Phylogenetic Trees” (Chapter 26)

Acknowledgments

I am indebted to many people for help with this and previous editions of *Genetics: A Conceptual Approach*. I learned much from my genetics teachers: Ray Canham, who first exposed me to genetics and instilled in me a lifelong love for the subject, and Jeff Mitton, who taught me the art of genetic research. I've learned from the thousands of genetics students who have filled my classes over the past 39 years, first at Connecticut College, then at Baylor University, and now at Southwestern University. Their intelligence, enthusiasm, curiosity, and humor have been a source of motivation and pleasure throughout my professional life. I have also learned from students worldwide who have used earlier editions of this book and kindly shared with me, through emails and phone calls, their thoughts about the book and how it could be improved.

I am grateful for the wonderful colleagues who surround me daily at Southwestern University and whose friendship, advice, and good humor sustain my work. The small classes, close interaction of students and faculty, and integration of teaching and research have made working at Southwestern University personally and professionally rewarding. I thank Edward Burger, President of Southwestern University, and Alisa Gaunder, Dean of the Faculty, for sustaining this supportive academic environment, for their creativity and inspiration, and for their continued friendship and collegiality.

Writing a modern science textbook requires a team effort, and I have been blessed with an outstanding team at W. H. Freeman and Macmillan Learning. General Manager Susan Winslow has been a champion of this book for a number of years; I value her support, strategic vision, and commitment to education. Sandy Lindelof, Executive Program Director, has been an outstanding leader of the project. Her encouragement, attention to detail, creativity, and great sense of perspective have been tremendous assets. Throughout the revision process, I interacted daily with Senior Development Editor Maria Lokshin, who has been instrumental in shaping this edition. Maria's hard work, passion for excellence, superior knowledge of genetics, great organizational skills, and good humor made working on this edition both rewarding and fun, in spite of a demanding schedule.

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I am grateful to the Faculty Advisory Board for their invaluable input on the new features of the textbook and new Sapling content. The board includes Eugenia Ribeiro-Hurley (Fordham University), David Kass (Eastern Michigan University), Brian Kreiser (University of Southern Mississippi), Karly Ackermann (South Dakota State University), Kari Loomis (University of Massachusetts), Agata Becalska (MacEwan University),

and Amanda Moehring (Western University).

As always, I am grateful to the Macmillan Learning sales representatives, regional managers, and STEM specialists who introduce my book to genetic instructors throughout the world. I have greatly enjoyed working with this sales staff; their expertise, hard work, and great service are responsible for the success of Macmillan books.

A number of colleagues served as reviewers of this book, kindly lending me their technical expertise and teaching experience. Their assistance is gratefully acknowledged. Any remaining errors are entirely my own.

Marlene Tyrrell (my spouse and best friend for 39 years), our children and their spouses (Sarah, Matt, Michael, and Amber), and now my F₂ progeny (Ellie, Beckett, and Caroline) provide love, support, and inspiration for everything I do.

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Genetics

A Conceptual Approach

CHAPTER 1

Introduction to Genetics



Ansel Adams/National Park Archives at College Park, MD.

A Hopi pueblo on Black Mesa. Albinism, a genetic condition, arises with high frequency among the Hopi people and occupies a special place in the Hopi culture.

Albinism in the Hopis

Rising a thousand feet above the desert floor, Black Mesa dominates the horizon of the Enchanted Desert and provides a familiar landmark for travelers passing through northeastern Arizona. Black Mesa is not only a prominent geological feature but also, more significantly, the ancestral home of the Hopi Native Americans. Fingers of the mesa reach out into the desert, and alongside or on top of each finger is a Hopi village. Most of the villages are quite small, having only a few dozen inhabitants, but they are incredibly old. One village, Oraibi, has existed on Black Mesa since 1150 C.E. and is the oldest continuously occupied settlement in North America.

In 1900, Aleš Hrdlička, an anthropologist and physician working for the American Museum of Natural History, visited the Hopi villages of Black Mesa and reported a startling discovery. Among the Hopis were 11 white people—not Caucasians but white Hopi Native Americans. These Hopis had a genetic condition known as albinism ([Figure 1.1](#)).



© The Field Museum, #CSA118. Charles Carpenter.

1.1 Albinism among the Hopi Native Americans. The Hopi girl in the center of this photograph, taken around 1900, displays albinism.

Albinism is caused by a defect in one of the enzymes required to produce melanin, the pigment that darkens our skin, hair, and eyes. People with albinism either don't produce melanin or produce only small amounts of it and, consequently, have white hair, light skin, and no pigment in the irises of their eyes. Melanin normally protects the DNA of skin cells from the damaging effects of ultraviolet radiation in sunlight, and melanin's presence in the developing eye is essential for proper eyesight.

The genetic basis of albinism was first described by the English physician Archibald Garrod, who recognized in 1908 that the condition was inherited as an autosomal recessive trait, meaning that a person must receive two copies of an albino mutation—one from each parent—to have albinism. In recent years, the molecular nature of the mutations that lead to albinism has been elucidated. Albinism in humans is caused by a mutation in any one of several different genes that control the synthesis and storage of melanin; many different types of mutations can occur at each gene, any one of which may lead to albinism. The form of albinism found among the Hopis is most likely oculocutaneous albinism (albinism affecting the eyes and skin) type 2, caused by a defect in the *OCA2* gene on chromosome 15.

The Hopis are not unique in having people with albinism among the members of their tribe. Albinism is found in almost all human ethnic groups. It is described in ancient writings and has probably been present since humankind's beginnings. What is unique about the Hopis is the high frequency of albinism in their population. In most human groups, albinism is rare, present in only about 1 in 20,000 individuals. In the villages on Black Mesa, it reaches a frequency of 1 in 200, a hundred times higher than in many other populations.

Why is albinism so frequent among the Hopis? The answer to this question is not completely known, but geneticists who have studied albinism in the Hopis speculate that the high frequency of the albino mutation is related to the special place that albinism occupied in the Hopi culture. For much of their history, the Hopis considered members of their tribe with albinism to be important and special. Having a number of people with albinism in one's village was considered a good sign, a symbol that the people of the village contained particularly pure Hopi blood. Members of the tribe with albinism performed in Hopi ceremonies and held positions of leadership, often as chiefs, healers, and religious leaders.

Hopis with albinism were also given special treatment in everyday activities. The Hopis have farmed small garden plots at the foot of Black Mesa for centuries. Every day throughout the growing season, the men of the tribe trekked to the base of Black Mesa and spent much of the day in the bright southwestern sunlight tending gardens of corn and vegetables. With little or no melanin pigment in their skin, people with albinism are extremely susceptible to sunburn and have an increased incidence of skin cancer when exposed to the sun. Furthermore, many don't see well in bright sunlight. Therefore, the male Hopis with albinism were excused from farming and allowed to remain behind in the village with the women of the tribe, performing other duties.

Throughout the growing season, the men with albinism were the only male members of the tribe in the village with the women during the day, and thus they may have enjoyed a mating advantage, which helped pass on their albino genes. In addition, the special considerations given to Hopis with albinism allowed them to avoid the detrimental effects of albinism—increased skin cancer and poor eyesight. The small size of the Hopi tribe probably also played a role by allowing chance to increase the frequency of the albino mutation. Regardless of the factors that led to the high frequency of albinism, the Hopis clearly respected and valued the members of their tribe who possessed this particular trait. Unfortunately, people with genetic conditions in many societies are often subject to discrimination and prejudice. > TRY [PROBLEMS 1 AND 26](#)



THINK-PAIR-SHARE

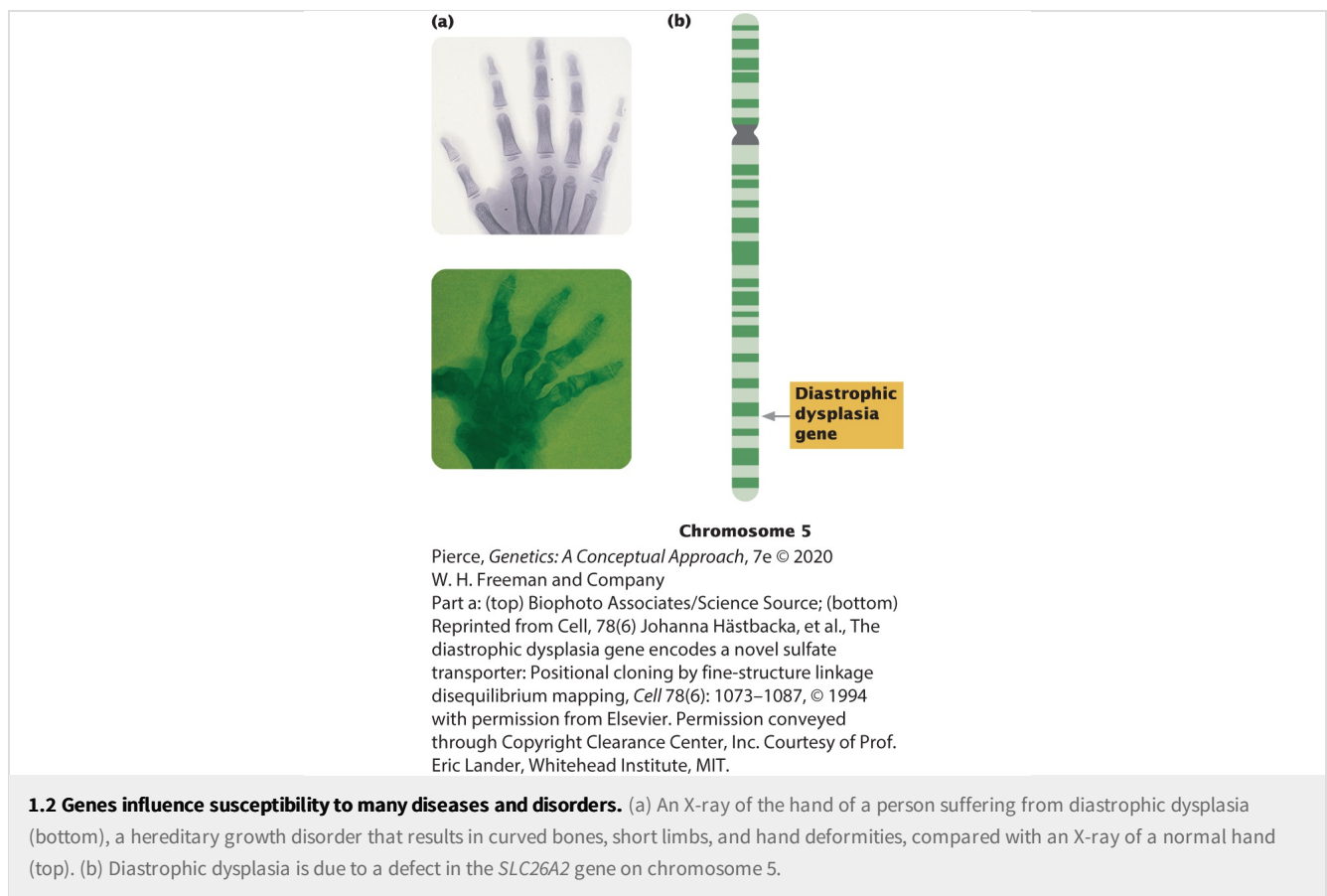
- Albinism occupied a special place in the Hopi culture; individuals who possessed this trait were valued by members of the tribe. What are some examples of genetic traits that, in contrast, sometimes result in discrimination and prejudice?
- Albinism in humans can be caused by mutations in any one of several different genes. This situation, in which the same phenotype may result from variation in several different genes, is referred to as genetic heterogeneity. Is genetic heterogeneity common? Are most genetic traits in humans the result of variation in a single gene, or are there many genetic traits that result from variation in several genes, as albinism does?

Genetics is the study of heredity, how inherited variation is encoded, replicated, and expressed, and how it evolves over time. This definition encompasses the three major subdivisions of genetics: transmission genetics, molecular genetics, and population genetics. The study of heredity and inherited variation is one of the most rapidly advancing areas of science, with important new discoveries reported every month. Look at almost any major news source, and chances are that you will see articles related to genetics: on the sequencing of new genomes, such as those of the sunflower, barley, the axolotl, and Darwin's finches; on the discovery of genes that affect major diseases, including amyotrophic lateral sclerosis (ALS), depression, and cancer; on analyses of DNA from long-extinct organisms, such as a 700,000-year-old Pleistocene horse; or on the identification of genes that affect birth weight, skin pigmentation, height, and learning ability in humans. Even among advertisements, you are likely to see ads for genetic testing to determine a person's ancestry or the pedigree of your dog. These new findings and applications of genetics often have significant economic and ethical implications, making the study of genetics relevant, timely, and interesting.

This chapter introduces you to genetics and reviews some concepts that you may have encountered in your general biology course. We begin by considering the importance of genetics to each of us, to society, and to students of biology. We then turn to the history of genetics and how the field as a whole developed. The final part of the chapter presents some fundamental terms and principles of genetics that are used throughout the book.

1.1 Genetics Is Important to Us Individually, to Society, and to the Study of Biology

Albinism among the Hopis illustrates the important role that genes play in our lives. This one genetic alteration, among the 20,000 genes that humans possess, completely changes the life of a Hopi who possesses it. It alters his or her occupation, role in Hopi society, and relations with other members of the tribe. We all possess genes that influence our lives in significant ways. Genes affect our height, weight, hair color, and skin pigmentation. They affect our susceptibility to many diseases and disorders (Figure 1.2) and even contribute to our intelligence and personality. Genes are fundamental to who and what we are, but they alone do not define us. Many factors—genetic and environmental—help determine our traits. A fundamental problem in genetics is separating the genetic and environmental influences on individual variation.



Although the science of genetics is relatively new compared with sciences such as astronomy and chemistry, people have understood the hereditary nature of traits and practiced genetics for thousands of years. The rise of agriculture began when people started to apply genetic principles to the domestication of plants and animals. Today, the major crops and animals used in agriculture are quite different from their wild progenitors, having undergone extensive genetic alteration that increased their yields and provided many desirable traits, such as disease and pest resistance, special nutritional qualities, and characteristics that facilitate harvest. The Green Revolution, which expanded food production throughout the world in the 1950s and 1960s, relied heavily on the application of genetic methods and principles (Figure 1.3). Today, genetically engineered corn, soybeans, canola (rapeseed), squash, sugar beets, and other crops constitute a significant proportion of all the food produced worldwide.



Left: Bettmann/Getty Images. right: IRRI.

1.3 In the Green Revolution, genetic techniques were used to develop new high-yielding strains of crops. (Left) Norman Borlaug, a leader in the development of new varieties of wheat, which led to the Green Revolution. Borlaug was awarded the Nobel Peace Prize in 1970. (Right) Modern, high-yielding rice plant (left) and traditional rice plant (right).

The pharmaceutical industry is another area in which genetics plays an important role. Numerous drugs and food additives are synthesized by fungi and bacteria that have been genetically manipulated to make them efficient producers of these substances. The biotechnology industry employs molecular genetic techniques to develop and mass-produce substances of commercial value. Antimalarial drugs, growth hormone, insulin, clotting factor, antiviral drugs, enzymes, antibiotics, vaccines, and many other compounds are now produced commercially by genetically engineered bacteria and other organisms ([Figure 1.4](#)). Genetics has also been used to generate bacterial strains that remove minerals from ore, break down toxic chemicals, and help produce biofuels.



Traimak_Ivan/Getty Images.

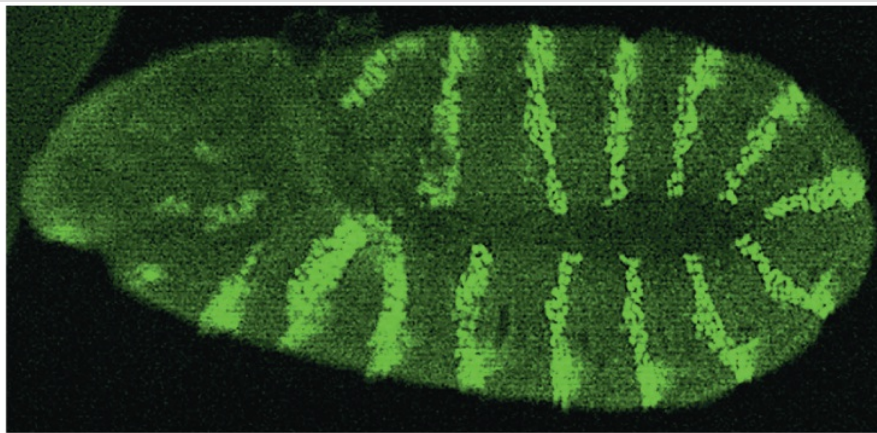
1.4 The biotechnology industry uses molecular genetic methods to produce substances of economic value.

Genetics also plays a critical role in medicine. Physicians recognize that many diseases and disorders have a hereditary component, including rare genetic disorders such as sickle-cell anemia and Huntington disease, as well as many common diseases such as asthma, diabetes, and hypertension. Advances in genetics have resulted in important insights into the nature of diseases such as cancer and in the development of diagnostic tests, including tests that identify disease-causing mutations as well as pathogens. Genomic data are helping to usher in the era of personalized medicine. Rapid, low-cost sequencing methods now allow us to obtain a person's complete genome sequence, which provides important information about that person's susceptibilities to diseases and likely responses to particular treatments. And gene therapy—the direct alteration of genes to treat human diseases—has now been administered to thousands of patients, although its use is still experimental and limited.

THINK-PAIR-SHARE [Question 1](#) 

The Role of Genetics in Biology

Although an understanding of genetics is important to all people, it is critical to the student of biology. Genetics provides one of biology's unifying principles: all organisms use genetic systems that have a number of features in common. Genetics also undergirds the study of many other biological disciplines. Evolution, for example, is genetic change taking place over time, so the study of evolution requires an understanding of genetics. Developmental biology relies heavily on genetics: tissues and organs develop through the regulated expression of genes ([Figure 1.5](#)). Even such fields as taxonomy, ecology, and animal behavior are making increasing use of genetic methods. The study of almost any field of biology or medicine is incomplete without a thorough understanding of genes and genetic methods.



Steven Paddock.

1.5 The key to development lies in the regulation of gene expression. This early fruit-fly embryo illustrates the localized expression of the *engrailed* gene, which helps determine the development of body segments in the adult fly.

Genetic Diversity and Evolution

Life on Earth exists in a tremendous array of forms and features, occupying almost every conceivable environment. Life is also characterized by adaptation: many organisms are exquisitely suited to the environment in which they are found. The history of life is a chronicle of new forms of life emerging, old forms disappearing, and existing forms changing.

Despite their tremendous diversity, living organisms have an important feature in common: all use similar genetic systems. The complete set of genetic instructions for any organism is its **genome**, and all genomes are encoded in nucleic acids—either DNA or RNA. The coding system for genomic information is also common to all life: genetic instructions are in the same format and, with rare exceptions, the code words are identical. Likewise, the process by which genetic information is copied and decoded is remarkably similar for all forms of life. These common features suggest that all life on Earth evolved from the same primordial ancestor, which arose between 3.5 billion and 4 billion years ago. Biologist Richard Dawkins describes life as a river of DNA that runs through time, connecting all organisms past and present.

That all organisms have similar genetic systems means that the study of one organism's genes reveals principles that apply to other organisms. Investigations of how bacterial DNA is replicated (copied), for example, provide information that applies to the replication of human DNA. It also means that genes can often function in foreign cells, which makes genetic engineering possible. Unfortunately, the similarity of genetic systems is also the basis for diseases such as AIDS (acquired immune deficiency syndrome), in which viral genes are able to function—sometimes with alarming efficiency—in human cells.

Life's diversity and adaptations are products of evolution, which is simply genetic change over time. Evolution is a two-step process: first, inherited differences arise randomly, and then the proportion of individuals with particular differences increases or decreases. Genetic variation is therefore the foundation of all evolutionary change and is ultimately the basis of all life as we know it. Techniques of molecular genetics are now routinely used to decipher evolutionary relationships among organisms; for example, analysis of DNA isolated from Neanderthal fossils has yielded new information concerning the relationship between Neanderthals and modern humans, demonstrating that Neanderthals and the ancestors of modern humans interbred some 30,000 to 40,000 years ago. Genetics and the study of genetic variation are critical to understanding the past, present, and future of life. > **TRY PROBLEM 17**

THINK-PAIR-SHARE [Question 2](#) 

CONCEPTS

Our genes affect many of our physical features as well as our susceptibility to many diseases and disorders. Genetics contributes to advances in agriculture, pharmaceuticals, and medicine and is fundamental to modern biology. All organisms use similar genetic systems, and genetic variation is the foundation of the diversity of all life.

✓ CONCEPT CHECK 1

What are some of the implications of all organisms having similar genetic systems?

- That all life forms are genetically related
- That research findings on one organism's gene function can often be applied to other organisms
- That genes from one organism can often function in another organism
- All of the above

DNA in the Biosphere

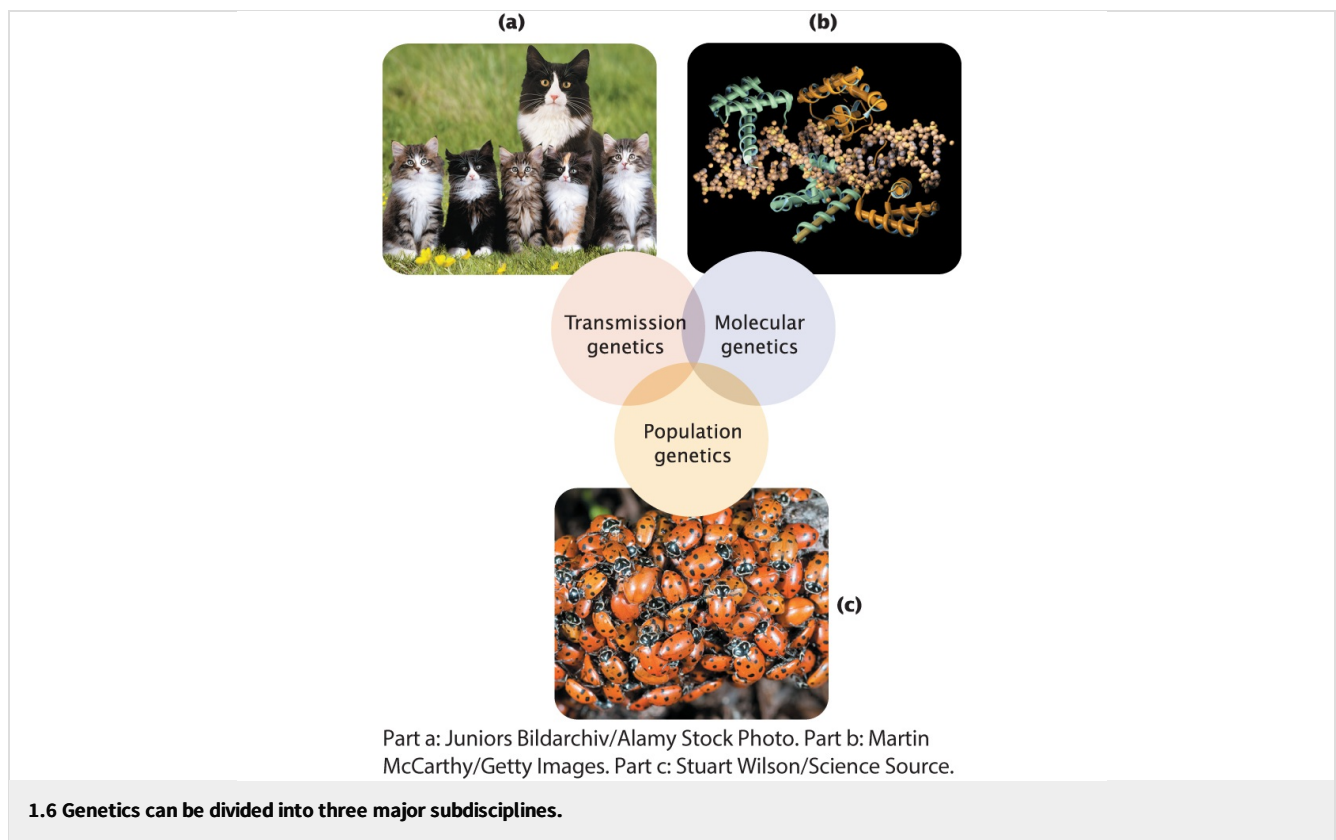
Each DNA molecule is very small, but because all cells contain genetic information, there is a tremendous amount of DNA in the world. Scientists estimate that the total amount of DNA in the biosphere is 5.3×10^{31}

megabase pairs (millions of base pairs), altogether weighing some 50 billion tons. Storing the information content of the world's DNA would require 10^{21} computers, each with the average storage capacity of the world's four most powerful supercomputers.

Scientists are now cataloging and measuring the world's biodiversity through analysis of DNA. For example, researchers aboard the ship *Tara* surveyed the world's oceans for organisms by isolating DNA from seawater during a three-and-a-half-year voyage. They collected 35,000 seawater samples and extracted DNA from each. The DNA was then sequenced and analyzed, revealing the presence of 150,000 genetically distinct types of eukaryotes. Most of these eukaryotes were newly discovered single-celled organisms. The researchers also detected 5000 viruses, only 39 of which were previously known to science. In an effort named the Earth BioGenome Project (EBP), scientists have recently proposed sequencing the genomes of 1.5 million known eukaryotic species on Earth. (See the Suggested Readings for this chapter in your SaplingPlus for the reference to these studies and many others mentioned in the book.)

Divisions of Genetics

The study of genetics consists of three major subdisciplines: transmission genetics, molecular genetics, and population genetics ([Figure 1.6](#)). Also known as classical genetics, [transmission genetics](#) encompasses the basic principles of heredity and how traits are passed from one generation to the next. This subdiscipline addresses the relation between chromosomes and heredity, the arrangement of genes on chromosomes, and gene mapping. Here, the focus is on the individual organism—how an individual inherits its genetic makeup and how it passes its genes to the next generation.



[Molecular genetics](#) concerns the chemical nature of the gene itself: how genetic information is encoded, replicated, and expressed. It includes the cellular processes of replication, transcription, and translation (by which genetic information is transferred from one molecule to another) and gene regulation (the processes that control the expression of genetic information). The focus in molecular genetics is the gene and its

structure, organization, and function.

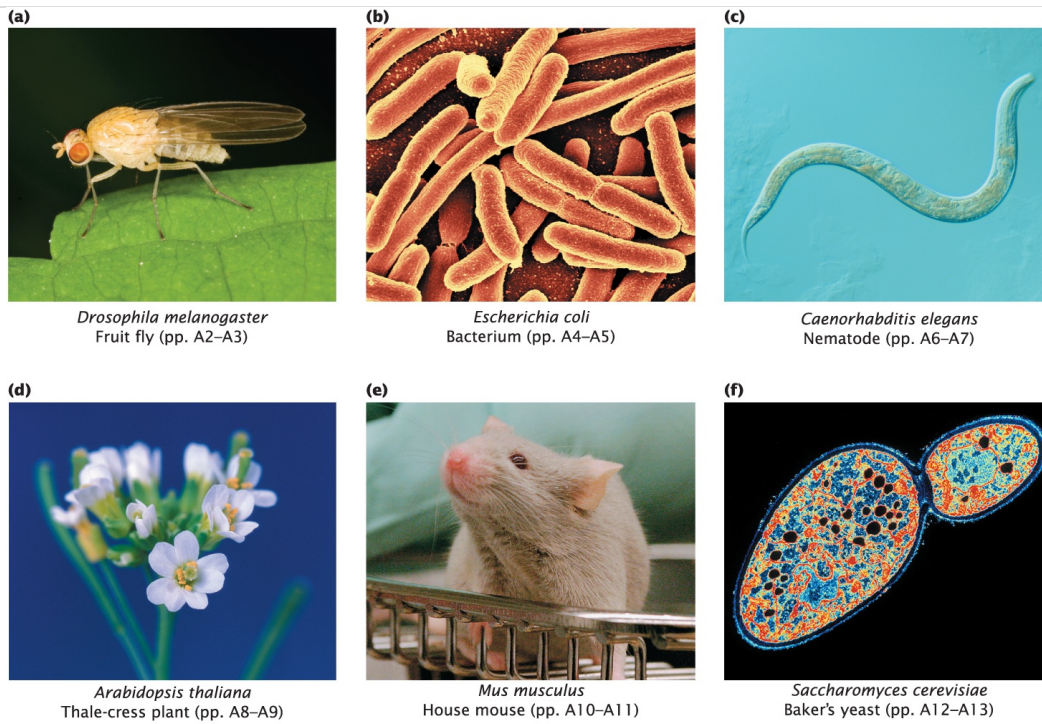
Population genetics explores the genetic composition of populations (groups of individuals of the same species) and how that composition changes geographically and with the passage of time. Because evolution is genetic change, population genetics is fundamentally the study of evolution. The focus of population genetics is the group of genes found in a population.

Division of the study of genetics into these three subdisciplines is convenient and traditional, but we should recognize not only that they overlap but also that each one can be further divided into a number of more specialized fields, such as chromosomal genetics, biochemical genetics, and quantitative genetics. Alternatively, genetic studies can be subdivided by organism (fruit fly, corn, or bacterial genetics), and each of these organisms may be studied at the levels of transmission, molecular, and population genetics. Modern genetics is an extremely broad field, encompassing many interrelated subdisciplines and specializations.

› TRY **PROBLEM 18**

Model Genetic Organisms

Through the years, genetic studies have been conducted on thousands of different species, including almost all major groups of bacteria, fungi, protists, plants, and animals. Nevertheless, a few species have emerged as **model genetic organisms**—organisms that are widely used in genetic research and that can serve as models for the genetic systems of other organisms, like humans, which, for various reasons, may be more difficult to study. Genetic models typically have characteristics that make them particularly useful for genetic analysis and about which a tremendous amount of genetic information has accumulated. Six model organisms that have been the subject of intensive genetic study are *Drosophila melanogaster*, a species of fruit fly; *Escherichia coli*, a bacterium present in the gut of humans and other mammals; *Caenorhabditis elegans*, a soil-dwelling nematode (roundworm); *Arabidopsis thaliana*, the thale-cress plant; *Mus musculus*, the house mouse; and *Saccharomyces cerevisiae*, baker's yeast (**Figure 1.7**). The life cycles and genetic characteristics of these model genetic organisms are described in more detail in the Reference Guide to Model Genetic Organisms located at the end of this book (pp. A1–A13). This Reference Guide will be a useful resource as you encounter these organisms throughout the book.

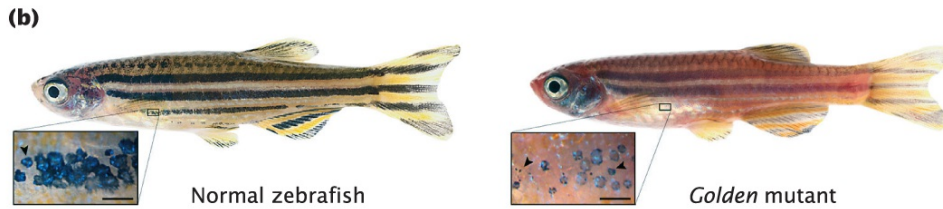
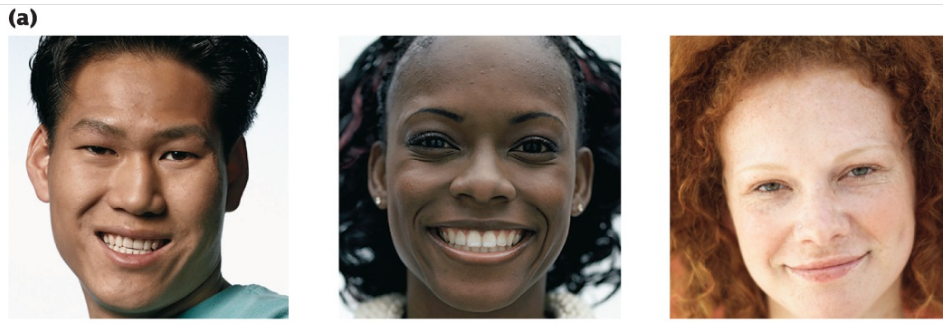


Part a: © Alfred Schaubhuber/ImageBROKER/Alamy Stock Photo. Part b: Pasieka/Science Source. Part c: Sinclair Stammers/Science Source. Part d: Peggy Greb/ARS/USDA. Part e: AP Photo/Joel Page. Part f: Biophoto Associates/Science Source.

1.7 Model genetic organisms are species with features that make them useful for genetic analysis.

At first glance, these lowly and sometimes unappreciated creatures might seem unlikely candidates for model genetic organisms. However, all possess life cycles and traits that make them particularly suitable for genetic study, including a short generation time, large but manageable numbers of progeny, adaptability to a laboratory environment, and the ability to be housed and propagated inexpensively. Other species that are frequently the subjects of genetic research and considered genetic models include *Neurospora crassa* (bread mold), *Zea mays* (corn), *Danio rerio* (zebrafish), and *Xenopus laevis* (clawed frog). Although not generally considered a model genetic organism, *Homo sapiens* has also been subjected to intensive genetic scrutiny; special techniques for the genetic analysis of humans are discussed in [Chapter 6](#).

The value of model genetic organisms is illustrated by the use of zebrafish to identify genes that affect skin pigmentation in humans. For many years, geneticists recognized that differences in pigmentation among human ethnic groups were genetic ([Figure 1.8a](#)), but the genes causing these differences were largely unknown. The zebrafish has become an important model in genetic studies because it is a small vertebrate that produces many offspring and is easy to rear in the laboratory. The mutant zebrafish called *golden* has light pigmentation due to the presence of fewer, smaller, and less dense pigment-containing structures called melanosomes in its cells ([Figure 1.8b](#)).



Part a: (left) Barbara Penoyar/Getty Images; (center) Amos Morgan/Getty Images; (right) Stockbyte/Getty Images. Part b: Keith Cheng/Jake Gittlen Cancer Research Foundation Penn State College of Medicine.

1.8 The zebrafish, a model genetic organism, has been instrumental in helping identify genes encoding pigmentation differences among humans. (a) Humans differ in degree of skin pigmentation. (b) The zebrafish *golden* mutation is caused by a gene that controls the amount of melanin in melanosomes.

Keith Cheng and his colleagues hypothesized that light skin in humans might result from a mutation that is similar to the *golden* mutation in zebrafish. Taking advantage of the ease with which zebrafish can be manipulated in the laboratory, they isolated and sequenced the gene responsible for the *golden* mutation and found that it encodes a protein that takes part in calcium uptake by melanosomes. They then searched a database of all known human genes and found a similar gene called *SLC24A5*, which encodes a protein that has the same function in human cells. When they examined human populations, they found that light-skinned Europeans often possess one form of this gene, whereas darker-skinned Africans, East Asians, and Native Americans usually possess a different form. Many other genes also affect pigmentation in humans, as illustrated by the mutations in the *OCA2* gene that produce albinism among the Hopis (discussed in the introduction to this chapter). Nevertheless, *SLC24A5* appears to be responsible for 24% to 38% of the differences in pigmentation between Africans and Europeans.

This example illustrates the power of model organisms in genetic research. However, we should not forget that all organisms possess unique characteristics and that the genetics of model organisms do not always accurately reflect the genetic systems of other organisms.

CONCEPTS

The three major divisions of genetics are transmission genetics, molecular genetics, and population genetics. Transmission genetics examines the principles of heredity; molecular genetics deals with the gene and the cellular processes by which genetic information is transferred and expressed; population genetics concerns the genetic composition of groups of organisms and how that composition changes geographically and over time. Model genetic organisms are species that have received special emphasis in genetic research; they have characteristics that make them useful for genetic analysis.

✓ CONCEPT CHECK 2

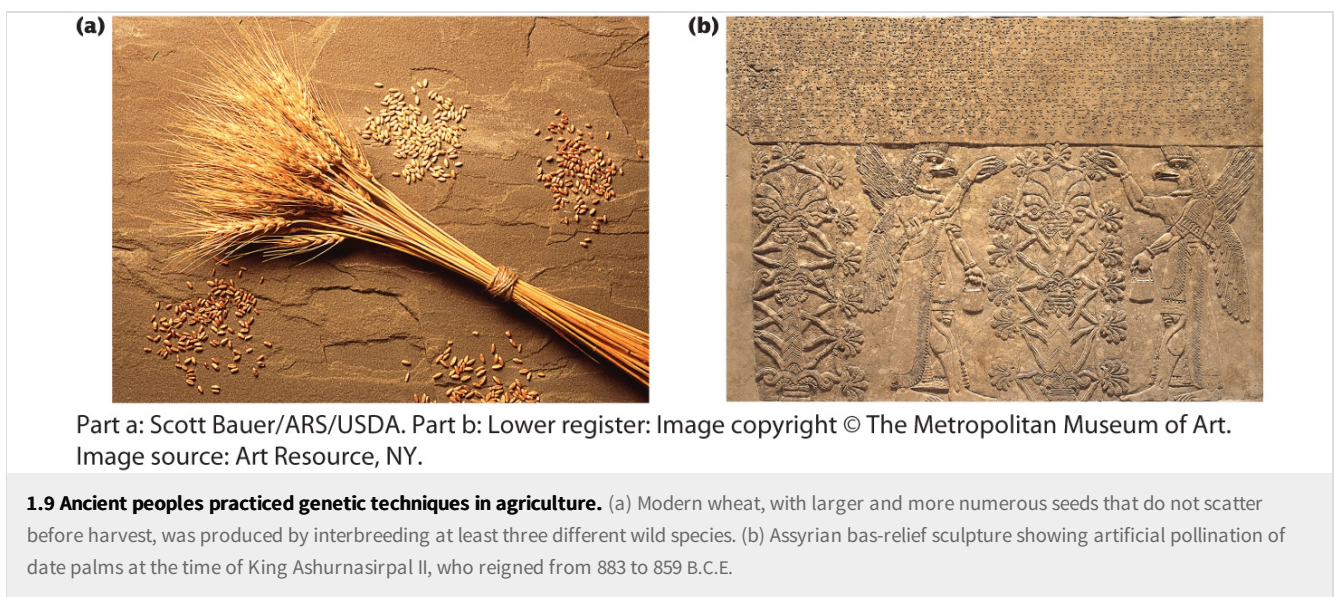
Would the horse make a good model genetic organism? Why or why not?

1.2 Humans Have Been Using Genetic Techniques for Thousands of Years

Although the science of genetics is young—almost entirely a product of the past 120 years or so—people have been using genetic principles for thousands of years.

The Early Use and Understanding of Heredity

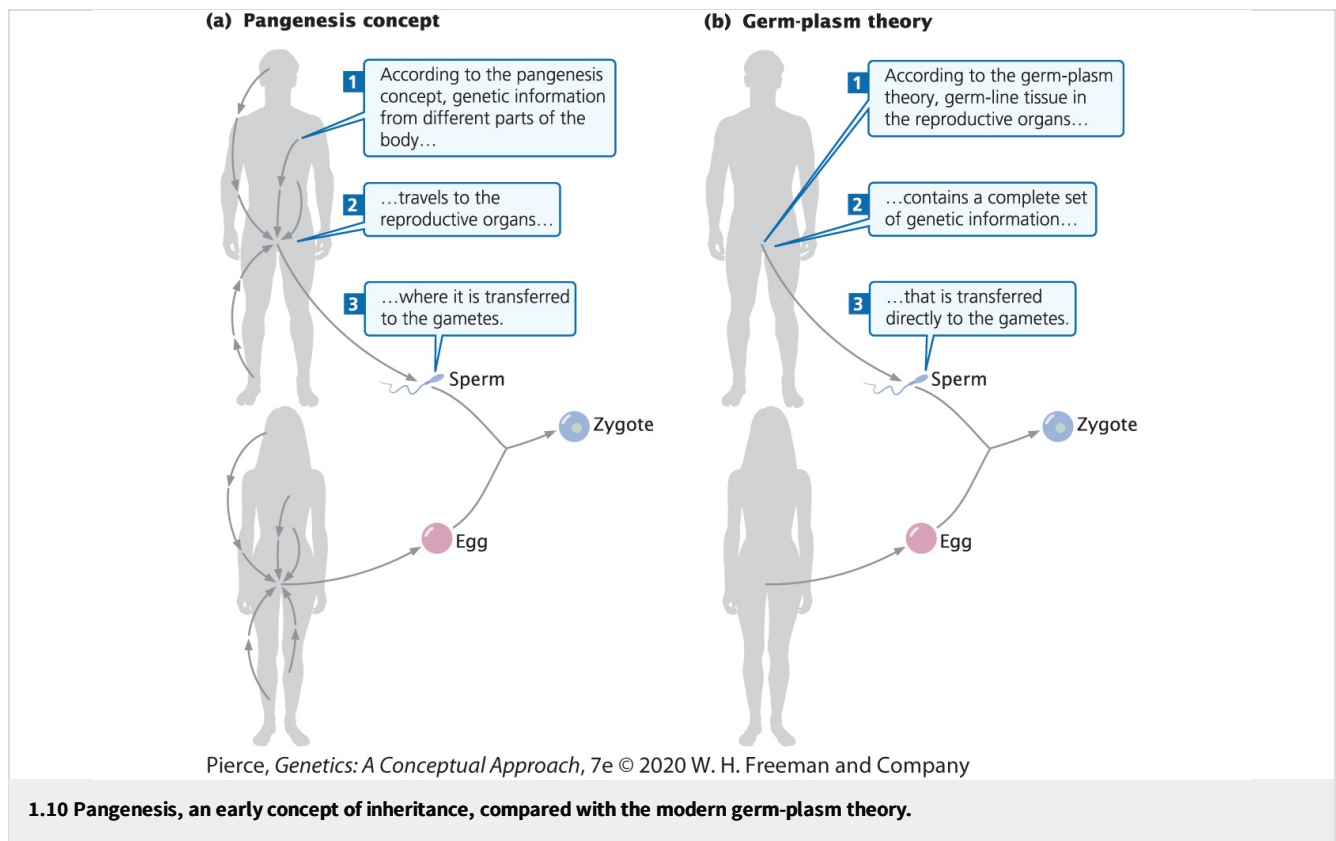
The first evidence that people understood and applied the principles of heredity in earlier times is found in the domestication of plants and animals, which began between approximately 10,000 and 12,000 years ago; early farming villages appeared in the Middle East between 11,000 and 11,500 years ago. The first domesticated organisms included wheat, peas, lentils, barley, dogs, goats, and sheep ([Figure 1.9a](#)). By 4000 years ago, genetic techniques of selective breeding were already in use in the Middle East. The Assyrians and Babylonians developed several hundred varieties of date palms that differed in fruit size, color, taste, and time of ripening ([Figure 1.9b](#)). Other crops and domesticated animals were developed by cultures in Asia, Africa, and the Americas in the same period.



Ancient writings demonstrate that early humans were also aware of their own heredity. Hindu sacred writings dating to 2000 years ago suggest that many traits are inherited from the father and that differences between siblings are produced by the mother. The Talmud—the Jewish book of religious laws based on oral traditions dating back thousands of—years, presents an uncannily accurate understanding of the inheritance of hemophilia. It directs that if a woman bears two sons who die of bleeding after circumcision any additional sons that she bears should not be circumcised, nor should the sons of her sisters be circumcised. This advice accurately corresponds to the X-linked pattern of inheritance of hemophilia (discussed further in [Chapter 6](#)).

Some early concepts of heredity were incorrect but reflect human interest in heredity and our attempts to explain the inheritance of traits. The ancient Greeks gave careful consideration to human reproduction and heredity. Greek philosophers developed the concept of [pangenesis](#), in which each part of the body contains genetic information for that particular part. Specific particles, later called gemmules, carry information

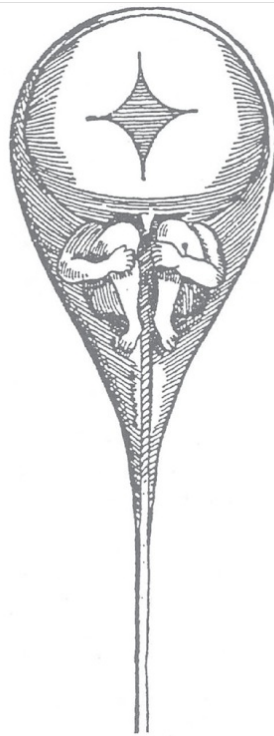
from various parts of the body to the reproductive organs, from which they are passed to the embryo at the moment of conception (**Figure 1.10a**). Although incorrect, the concept of pangenesis was highly influential and persisted until the late 1800s.



The concept of pangenesis led the ancient Greeks to propose the notion of the **inheritance of acquired characteristics**, according to which traits acquired in a person's lifetime become incorporated into that person's hereditary information and are passed on to offspring; for example, they proposed that people who developed musical ability through diligent study would produce children who were innately endowed with musical ability. Jean-Baptiste Lamarck (1744–1829) was a proponent of this idea and incorporated it into his theory of biological change. The notion of the inheritance of acquired characteristics is also no longer accepted, but it remained popular through the twentieth century.

Although the ancient Romans contributed little to an understanding of human heredity, they successfully developed a number of techniques for animal and plant breeding; their techniques were based on trial and error rather than any general concept of heredity. Little new information was added to the understanding of genetics in the next thousand years.

Additional developments in our understanding of heredity occurred during the seventeenth century. Dutch eyeglass makers began to put together simple microscopes in the late 1500s, enabling Robert Hooke (1635–1703) to discover cells in 1665. Microscopes provided naturalists with new and exciting vistas on life. Perhaps it was excessive enthusiasm for this new world of the very small that gave rise to the idea of **preformationism**: that inside the egg or sperm there exists a fully formed miniature adult, a *homunculus*, which simply enlarges in the course of development (**Figure 1.11**). Preformationism meant that all traits were inherited from only one parent—from the father if the homunculus was in the sperm or from the mother if it was in the egg. Although many observations suggested that offspring possess a mixture of traits from both parents, preformationism remained a popular concept throughout much of the seventeenth and eighteenth centuries.



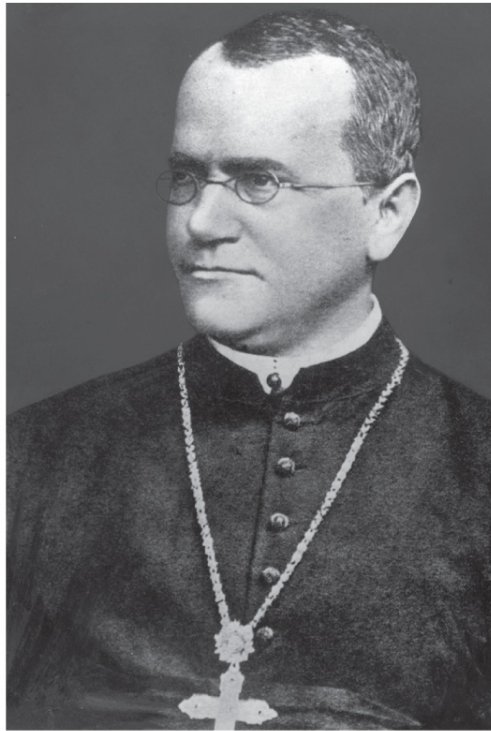
Science Source.

1.11 Preformationists in the seventeenth and eighteenth centuries believed that sperm or eggs contained a fully formed human (the homunculus). Shown here is a drawing of a homunculus inside a sperm.

Another early notion of heredity was **blending inheritance**, which proposed that the traits of offspring are a blend, or mixture, of parental traits. This idea suggested that the genetic material itself blends, much as blue and yellow pigments blend to make green paint; it also suggested that after having been blended, genetic differences could not be separated in future generations, just as green paint cannot be separated into blue and yellow pigments. Some traits do *appear* to exhibit blending inheritance; however, we realize today that individual genes do not blend.

The Rise of the Science of Genetics

In 1676, Nehemiah Grew (1641–1712) reported that plants reproduce sexually. With this information, a number of botanists began to experiment with crossing plants and creating hybrids, including Gregor Mendel (1822–1884; **Figure 1.12**), who went on to discover the basic principles of heredity. Mendel's conclusions, which were not widely known in the scientific community until 35 years after their publication, laid the foundation for our modern understanding of heredity, and he is generally recognized today as the father of genetics.



Hulton Archive/Getty Images.

1.12 Gregor Mendel is the father of modern genetics. Mendel first discovered the principles of heredity by crossing different varieties of pea plants and analyzing the transmission of traits in subsequent generations.

Developments in cytology (the study of cells) in the 1800s had a strong influence on genetics. Robert Brown (1773–1858) described the cell nucleus in 1833. Building on the work of others, Matthias Jacob Schleiden (1804–1881) and Theodor Schwann (1810–1882) proposed the concept that came to be known as the [cell theory](#) in 1839. According to this theory, all life is composed of cells, cells arise only from preexisting cells, and the cell is the fundamental unit of structure and function in living organisms. Biologists interested in heredity began to examine cells to see what took place in the course of cell reproduction. Walther Flemming (1843–1905) observed the division of chromosomes in 1879 and published a superb description of mitosis. By 1885, biologists generally recognized that the cell nucleus contains the hereditary information.

Charles Darwin (1809–1882), one of the most influential biologists of the nineteenth century, put forth the theory of evolution through natural selection and published his ideas in *On the Origin of Species* in 1859. Darwin recognized that heredity was fundamental to evolution, and he conducted extensive genetic crosses with pigeons and other organisms. He never understood the nature of inheritance, however, and this lack of understanding was a major omission in his theory of evolution.

In the last half of the nineteenth century, cytologists demonstrated that the nucleus had a role in fertilization. Near the close of that century, August Weismann (1834–1914) finally laid to rest the notion of the inheritance of acquired characteristics. He cut off the tails of mice for 22 consecutive generations and showed that the tail length in descendants remained stubbornly long. Weismann proposed the [germ-plasm theory](#), which holds that the cells in the reproductive organs carry a complete set of genetic information that is passed to the egg and sperm ([Figure 1.10b](#)).

The year 1900 was a watershed in the history of genetics. Gregor Mendel's pivotal 1866 publication on experiments with pea plants, which revealed the principles of heredity (considered in more detail in [Chapter 3](#)), was rediscovered. Once the significance of his conclusions was recognized, other biologists immediately began to conduct similar genetic studies on mice, chickens, and other organisms. The results of these investigations showed that many traits indeed follow Mendel's rules. Some of the early concepts of

heredity are summarized in [Table 1.1](#).

TABLE 1.1 Early concepts of heredity

Concept	Proposed	Correct or Incorrect
Pangenes	Genetic information travels from different parts of the body to reproductive organs.	Incorrect
Inheritance of acquired characteristics	Acquired traits become incorporated into hereditary information.	Incorrect
Preformationism	Miniature organism resides in sex cells, and all traits are inherited from one parent.	Incorrect
Blending inheritance	Genes blend and mix.	Incorrect
Germ-plasm theory	All cells contain a complete set of genetic information.	Correct
Cell theory	All life is composed of cells, and cells arise only from cells.	Correct
Mendelian inheritance	Traits are inherited in accord with defined principles.	Correct

In 1902, after the acceptance of Mendel's theory of heredity, Walter Sutton (1877–1916) proposed that genes, the units of inheritance, are located on chromosomes. Thomas Hunt Morgan (1866–1945) discovered the first mutant fruit fly in 1910 and used fruit flies to unravel many details of transmission genetics. Ronald A. Fisher (1890–1962), John B. S. Haldane (1892–1964), and Sewall Wright (1889–1988) laid the foundation for population genetics in the 1930s by integrating Mendelian genetics and evolutionary theory.

Geneticists began to use bacteria and viruses in the 1940s; the rapid reproduction and simple genetic systems of these organisms allowed detailed study of the organization and structure of their genes. At about this same time, evidence accumulated that DNA was the repository of genetic information. James Watson (b. 1928) and Francis Crick (1916–2004), along with Rosalind Franklin (1920–1958) and Maurice Wilkins (1916–2004), described the three-dimensional structure of DNA in 1953, ushering in the era of molecular genetics (see [Chapter 10](#)).

By 1966, the chemical structure of DNA and the system by which it determines the amino acid sequence of proteins had been worked out. Advances in molecular genetics led to the first recombinant DNA experiments in 1973, which provided techniques for combining genetic material from different sources and touched off another revolution in genetic research. Walter Gilbert (b. 1932) and Frederick Sanger (1918–2013) developed methods for sequencing DNA in 1977. The polymerase chain reaction (PCR), a technique for quickly amplifying tiny amounts of DNA, was developed by Kary Mullis (1944–2019) and others in 1983. PCR has subsequently become one of the most widely used tools in molecular biology.

In 1990, gene therapy was used for the first time to treat human genetic disease in the United States, and the Human Genome Project was launched. By 1995, the first complete DNA sequence of a free-living organism—the bacterium *Haemophilus influenzae*—had been determined, and the first complete sequence of a eukaryotic organism (yeast) was reported a year later. A rough draft of the human genome sequence was reported in 2000 (see [Chapter 20](#)), and the sequence was essentially completed in 2003, bringing in another new era in genetics. Building on prior research by several groups, Jennifer Doudna and Emmanuelle Charpentier in 2012 modified the CRISPR-Cas system found in bacteria to develop a powerful new technology for editing the genome. ▶ **TRY PROBLEM 23**

The Cutting Edge of Genetics

With exciting advances being made every year, genetics remains at the forefront of biological research. Rapid methods for sequencing DNA are being used to sequence the genomes of numerous species, from

cockroaches to orangutans to hot peppers to roses. New DNA sequencing techniques are capable of sequencing single DNA molecules, allowing longer and longer sequence reads that facilitate assembling of whole genomes.

Genetics continues to play a major role in agriculture. For example, many people complain about the bland taste of store-bought tomatoes. Geneticists are now using modern genetic techniques to locate genes that are responsible for loss of flavor in commercial tomatoes. In one study, researchers quantified natural compounds that enhance flavor in 400 varieties of tomatoes and identified compounds that were missing or low in poor-tasting commercial varieties. They then used genome sequencing to identify genes that affect the missing flavors, and this information is being used to breed back into commercial varieties compounds that enhance flavor, producing better-tasting tomatoes. Other plant scientists are studying the genetics of volatile organic compounds in flowers, with the goal of engineering fragrance. There is currently a project underway to completely sequence the genomes of 10,000 plant species.

Today, genomic studies provide key insights into evolution. For example, how many types of giraffes are there? Previously, biologists thought there was a single species, but analysis of DNA sequences has now revealed the presence of four distinct species. In 2016, researchers identified the gene responsible for the evolution of industrial melanism in peppered moths of Britain, where dark moths became more frequent during times of pollution. They discovered that the mutation that produced the dark (*carbonaria*) form of the moths was a large transposable element (a mobile genetic sequence) which inserted into a gene that normally controls cell division and wing development in moths. Whereas archaeologists previously studied fossils, ancient pottery, and tools to understand human ancestry, researchers are now isolating DNA from ancient remains to reconstruct human history. Genome sequences have been analyzed from more than 1000 ancient humans and are being used to answer important questions about the spread of agriculture, the development of languages, and human migration. Genome sequencing of ancient DNA has demonstrated that early *Homo sapiens* interbred with other hominins, including Neanderthals and Denisovans.

Other researchers are unraveling genetic underpinnings of development. Snakes evolved from four-legged ancestors but began to lose their limbs about 150 million years ago. Today, most snakes have lost all vestiges of their limbs (although a few species such as pythons have vestigial pelvises and leg bones). Geneticists have now isolated genes that control the absence of limbs in snakes. When genetic engineers inserted a snake version of an enhancer (a genetic element that controls gene expression) into mice, these mice developed truncated limbs instead of legs.

New research has made CRISPR-Cas9—the powerful genome editing technology that is now widely used in genetic research—more accurate and flexible than ever. New developments have harnessed the ability of CRISPR-Cas9 to provide additional functions, including detection of DNA molecules, editing of RNA, activation of gene expression, and changing of specific base pairs of DNA. CRISPR-Cas was recently used to successfully repair defective genes that cause heart disease in human embryos.

Genetic research continues to provide important information and tools for medicine. Researchers are developing blood tests that detect DNA and proteins shed by tumors, providing the potential for early detection of cancer. Genetics information is being used to develop vaccines to combat infectious diseases such as HIV, Zika, and Ebola. And human gene therapy is being harnessed to treat a number of diseases and disorders, including leukemia, blindness, deafness, blood disorders, cancer, and metabolic disorders. Recently researchers have identified genes that allow Tibetans to live in high altitudes and other genes that allow traditional divers in Southeast Asia to stay underwater for longer periods of time.

As sequencing becomes more affordable, the focus of DNA-sequencing efforts is shifting from the genomes of different species to individual differences within species. In the not-too-distant future, many people will possess a copy of their entire genome sequence, which can be used to help assess the risk of acquiring various diseases and to tailor their treatment should they arise. This ever-widening scope of genetics raises significant ethical, social, and economic issues.

This brief overview of the history of genetics, from the first domestication of crops to present-day whole-genome sequencing, is not intended to be comprehensive; rather, it is designed to provide a sense of the accelerating pace of advances in genetics. In the chapters to come, we will learn more about the experiments and the scientists who helped shape the discipline of genetics.

THINK-PAIR-SHARE [Question 3](#) 

CONCEPTS

Humans first applied genetic methods to the domestication of plants and animals between approximately 10,000 and 12,000 years ago. Developments in plant hybridization and cytology in the eighteenth and nineteenth centuries laid the foundation for the field of genetics today. After Mendel's work was rediscovered in 1900, the science of genetics developed rapidly, and today it is one of the most active areas of science.

CONCEPT CHECK 3

How did developments in cytology in the nineteenth century contribute to our modern understanding of genetics?

1.3 A Few Fundamental Concepts Are Important for the Start of Our Journey into Genetics

Undoubtedly, you learned some genetic principles in other biology classes. Let's take a few moments to review some fundamental genetic concepts.

CELLS ARE OF TWO BASIC TYPES: EUKARYOTIC AND PROKARYOTIC

Structurally, cells consist of two basic types, although evolutionarily, the story is more complex (see [Chapter 2](#)). Prokaryotic cells lack a nuclear membrane and do not generally possess membrane-bounded organelles, whereas eukaryotic cells are more complex, possessing a nucleus and membrane-bounded organelles such as chloroplasts and mitochondria.

THE GENE IS THE FUNDAMENTAL UNIT OF HEREDITY

The precise way in which a gene is defined often varies depending on the biological context. At the simplest level, we can think of a gene as a unit of information that encodes a genetic characteristic. We will expand this definition as we learn more about what genes are and how they function.

GENES COME IN MULTIPLE FORMS CALLED ALLELES

A gene that specifies a characteristic may exist in several forms, called alleles. For example, a gene for coat color in cats may exist as an allele that encodes black fur or as an allele that encodes orange fur.

GENES CONFER PHENOTYPES

One of the most important concepts in genetics is the distinction between traits and genes. Traits are not inherited directly. Rather, genes are inherited, and genes, along with environmental factors, determine the expression of traits. The genetic information that an individual organism possesses is its genotype; the trait is its phenotype. For example, the albinism seen in some Hopis is a phenotype, and the information in *OCA2* genes that causes albinism is a genotype.

GENETIC INFORMATION IS CARRIED IN DNA AND RNA

Genetic information is encoded in the molecular structure of nucleic acids, which come in two types: deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). Nucleic acids are polymers consisting of repeating units called nucleotides; each nucleotide consists of a sugar, a phosphate, and a nitrogenous base. The nitrogenous bases in DNA are of four types: adenine (A), cytosine (C), guanine (G), and thymine (T). The sequence of these bases encodes genetic information. DNA consists of two complementary nucleotide strands. Most organisms carry their genetic information in DNA, but a few viruses carry it in RNA. The four nitrogenous bases of RNA are adenine, cytosine, guanine, and uracil (U).