12 Genomes

Chapter Outline

Chapter 12 draws attention to the genome. An organism's genome is the complete DNA sequence that constitutes its full set of genes plus the rest of its DNA. Mistakes in the copying of DNA (*mutations*) provide evolutionary possibilities in the face of environmental uncertainty. Natural selection's effects are especially apparent at the level of the phenotype, but as phenotypic variation is largely based on variation in the genome, genomic studies provide detailed evolutionary insight into life's variations. Genomic analysis allows detailed studies of gene/protein structure/function, which demonstrate key evidence for the presence of evolutionary connections among all living organisms.

Genomes have been characterized for many viruses, prokaryotes, and eukaryotes. Prokaryotic cells are produced via binary fission, and each resulting cell typically has the full set of genes as well as other DNA. Cell replication, called *mitosis* in eukaryotes, includes copying all of an organism's DNA so that each eukaryotic cell has the full genome. Viruses have the capacity to take advantage of, and even insert DNA into, the genomes of both prokaryotes and eukaryotes. Genomic analysis provides detailed examples of viral enhancement of host genomes.

Chapter 12 includes material characterized in **Big Idea 3.** The heritable information in cells that effects change is their genes (i.e., their DNA or genome). The genome typically includes much more information than a single cell might use, but different information (different genes) in the genome can be activated in response to different signals found in the environment. These responses usually promote homeostasis in the organism. Specific parts of the AP Biology curriculum that are covered in Chapter 12 include:

- **3.A.1:** DNA, and in some cases RNA, is the primary source of heritable information.
- **3.A.3:** The chromosomal basis of inheritance provides an understanding of the pattern of passage (transmission) of genes from parent to offspring.
- **3.C.3:** Viral replication results in genetic variation, and viral infection can introduce genetic variation into the hosts.

Chapter Review

Concept 12.1 *discusses the methods for sequencing genomes and analyzing gene products. The "instructions for life" are found in every cell that has the full complement of DNA. Sequencing the genome started as an expensive and laborious process, but it has been greatly accelerated by automated techniques. Even so, DNA is typically an incredibly long molecule; the single DNA molecule that comprises human chromosome one has 246,000,000 base pairs.*

Genomic studies provide insight into protein structure and function, as proteins are among the direct products of gene expression. More than one protein can be the product of a gene being expressed; one large protein from a single gene can be cut up into several smaller proteins, each of which might serve a different role in the cell. For the approximately 24,000 genes in the human genome, there are about 75,000 proteins known. Because many proteins serve as enzymes in the synthesis of lipids and other biomolecules, the analysis of the full set of active biomolecules has its own label: metabolomics.

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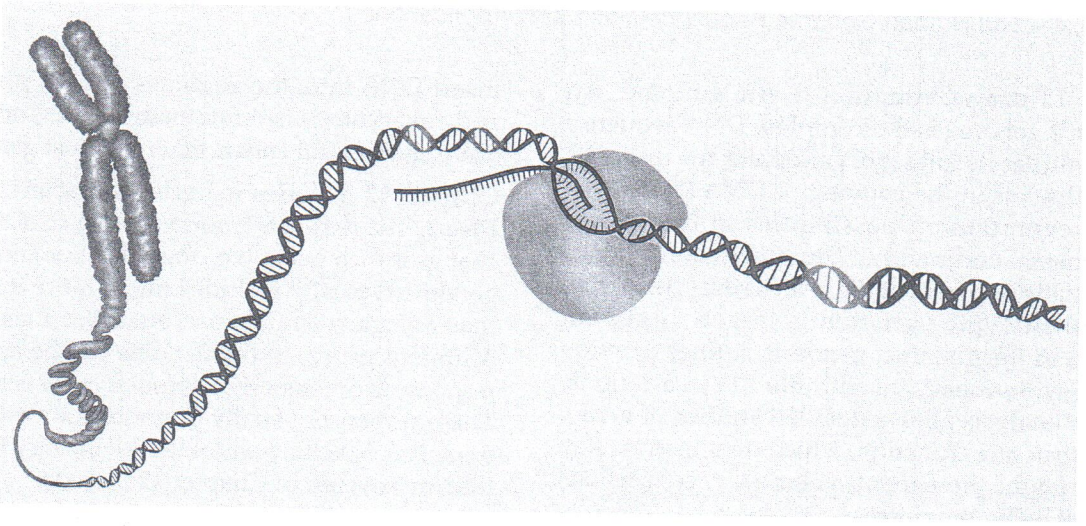
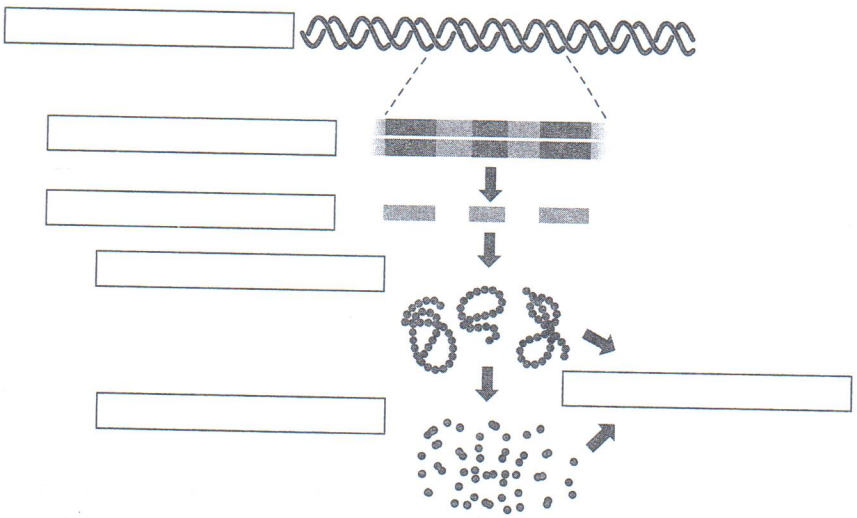
Genomic analysis spans many areas of interest, including evolutionary biology, molecular details of genetic function in health and disease, RNA functions, open reading frames, intron analysis, protein synthesis, and chromosome stability. Comparing DNA sequences provides insight into the molecular basis of evolutionary changes that cause related organisms to separate from their common ancestor. Recall that certain parts of the DNA sequence code specifically for the start and stop of transcription, and you will appreciate how far genomic analysis has advanced in a short amount of time.

1. On the diagram below, label terminator of transcription, promoter of transcription, centromere, telomere, RNA polymerase, and mRNA. Then add a labeled bracket for the open reading frame.



2. On the diagram below, label mRNA, phenotype, genome, metabolome, proteome, and genes.



Concept 12.2 *notes that prokaryotic genomes are relatively small, compact, and diverse. Organisms are broadly described as either eukaryotes or prokaryotes, with the latter including bacteria and all of the other microbes that lack membrane-bound organelles. Genomic packaging in the prokaryotes is typically minimal and compact, taking place on a single chromosome. In fact, the first genome to be fully sequenced was that of a prokaryote. The first synthetic genome/organism assembled by biologists was also prokaryotic in most of its characteristics.*

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Very few prokaryotic genes have introns, suggesting efficiency in gene expression by these haploid organisms. Genomic analysis of different prokaryotes has revealed the evolutionary expansion of key functions, such as molecular uptake of nutrients from the environment and the metabolism of fuel molecules. It is also apparent that some sets of base sequences move around in the DNA and can be loaded onto plasmids, greatly enhancing biotechnology-based efforts to understand life.

3. Imagine that you are studying two strains of related bacteria: one is non-pathogenic but has antibiotic resistance, and the other is pathogenic but lacks antibiotic resistance. Speculate on the possible consequences of contamination in these two strains if you were to rely only on antibiotic soaps to "sterilize" your hands and equipment while going back and forth between the bacterial strains.

4. *Escherichia coli* has 4,288 protein-coding genes, 243 energy-metabolism genes, and 427 genes with products that take up molecules from the environment, whereas *Mycoplasma genitalium* has only 482, 31, and 34 genes in those categories, respectively. Discuss the differences between these two prokaryotes from a genomic viewpoint.

Concept 12.3 *reviews the large and complex genomes of eukaryotes. The packaging of the eukaryotic genome is necessarily complex, due to its large size and greater number of genes compared to prokaryotes. Eukaryotic DNA is packaged in structures clearly recognized as chromosomes. Many parts of eukaryotic DNA are not transcribed and/or translated and thus serve purposes other than coding for proteins (e.g., telomeres and spacers). Eukaryotes are diploid, with two copies of each gene present in each cell (except for the haploid gametes, sperm, and egg). Among animals, developmental genes are broadly shared, reflecting a conserved evolutionary history in the genes controlling development.*

5. Construct an argument to explain why the claim that DNA codes for proteins is too limited to provide a good description of "life's instruction book."

6. Complete the table below by filling in the appropriate genomic characteristics of prokaryotes and eukaryotes.

	Prokaryotes	Eukaryotes
Complexity		
DNA location		
Chromosomes		
RNA splicing		
Size (number of base pairs)		
Number of gene copies		
Proportion of DNA that is translated		
Number of genes		

7. Discuss the claim that viruses directly increase genomic variation in prokaryotes and eukaryotes. Include a discussion of transposons in your answer.

8. In analyzing the genomes of diverse eukaryotes, scientists have found many stretches of gene duplication. Assume that an original DNA sequence is associated with an essential protein, and that the duplicate sequence is no longer identical to the original sequence. Discuss gene duplication as an evolutionary opportunity for changing the phenotype.

Concept 12.4 *describes the many applications of human-genome study. Human DNA includes some six billion base pairs, packaged in 23 pairs of chromosomes. Genomic diversity is small; humans are much more alike than they are different, with 97 percent of DNA sequences being identical from one person to the next.*

9. A newspaper story reported that the genomes of persons with African–American ancestry have fewer genetic components for resistance to malarial infection, compared to the genomes of persons with African-only ancestry. Describe methodology that could have been used to generate these results.

10. Following up on the finding described in Question 9, discuss the idea that African–Americans have faced different selective pressures than those faced by Africans.

11. If you knew the heights of 100 people whose individual genomes had been fully sequenced, how could you use the sequencing information to determine how height is passed on from one individual to another?

12. Consider the population of people described in Question 11. Describe challenges you might have in drawing satisfactory conclusions about differences in their intelligence.

Science Practices & Inquiry

In the AP Biology Curriculum Framework, there are seven **Science Practices**. In this chapter, we focus on **Science Practice 6:** The student can work with scientific explanations and theories. More specifically, we focus on **Science Practice 6.4:** The student can make claims and predictions about natural phenomena based on scientific theories and models.

Question 13 provides you with enough information to justify the claim that humans can manipulate heritable information by identifying at least two commonly used technologies (**Learning Objective 3.5**).

13. Discuss two technologies that researchers can use to manipulate heritable information. Identify each technology, explain how it is used, and then give an example of its use.