Chapter 21: Genomes and Their Evolution

21.1 Describe how the Human Genome Project contributed to DNA sequencing technology.
21.2 Explain how scientists use bioinformatics to analyze genomes and their functions.
21.3 For a range of genomes, compare and contrast genome size, number of genes, and gene density.
21.4 Describe the composition of the genome of a multicellular eukaryote, such as that of humans.
21.5 Identify the changes to DNA that contribute to evolution of the genome.
21.6 Explain how comparing genome sequences and developmental processes helps us learn about evolution.

What can we learn from the evolution of genomes from vastly different species? What can we learn from comparing genomes from our most closely related species? These and other big-picture questions will be addressed in this chapter. New techniques and new ideas characterize this chapter. As you work through the chapter, focus on the concepts of evolution and how those concepts apply to genomes

Study Tip: Figure 21.1 shows questions that can be explored by sequencing and comparing genomes. These questions introduce the topics to be discussed in this chapter. What are they?

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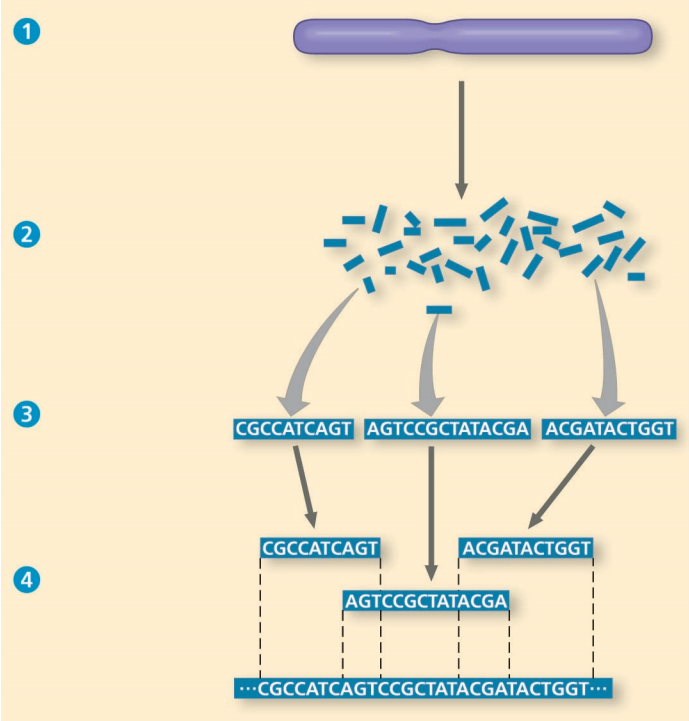
Concept 21.1 The Human Genome Project fostered development of faster, less expensive sequencing techniques

LO 21.1: Describe how the Human Genome Project contributed to DNA sequencing technology.

1. What is *genomics*? How does *bioinformatics* support genomic research?

2. The *whole-genome shotgun approach* is widely used today to sequence genomes. Using the figure below, describe the four major steps to this technique.



3. What is the approach known as *metagenomics*?

4. What is the value of using *metagenomics* to study an environment like the human gut, which contains many species?

Concept 21.2 Scientists use bioinformatics to analyze genomes and their functions

LO 21.2: Explain how scientists use bioinformatics to analyze genomes and their functions.

5. *Bioinformatics* is the application of statistics and computer science to the field of molecular biology. The NCBI maintains a site that you may use if you do an investigation involving BLAST or other genetic analysis. Figure 21.3 in your text shows a screenshot of a typical entry and information gleaned from the NCBI website. Describe four important examples of information that is available through bioinformatics data on the NCBI website.

6. What is the goal of *gene annotation*?

7. What is the *proteome?* What is the goal of scientists who study *proteomics*?

8. What role does *systems biology* play in trying to understand the underlying biology of cancer?

9. How might a human gene microarray chip be of medical importance in cancer treatment?

Concept 21.3 Genomes vary in size, number of genes, and gene density

LO 21.3: For a range of genomes, compare and contrast genome size, number of genes, and gene density.

10. How do prokaryotic genomes of the two domains Bacteria and Archaea compare to eukaryotic genomes?

11. What is the relationship between size and complexity of a eukaryotic species and the size of its genome?

12. Compare the DNA in bacterial genomes to the DNA in eukaryotic genomes with reference to function of the DNA, introns, length of genes, and nonprotein-coding DNA.

13. How is it possible for humans to have so few genes, in fact approximately the same number of genes as a nematode worm, and yet make so many proteins?

Concept 21.4 Multicellular eukaryotes have a lot of noncoding DNA and many multigene families

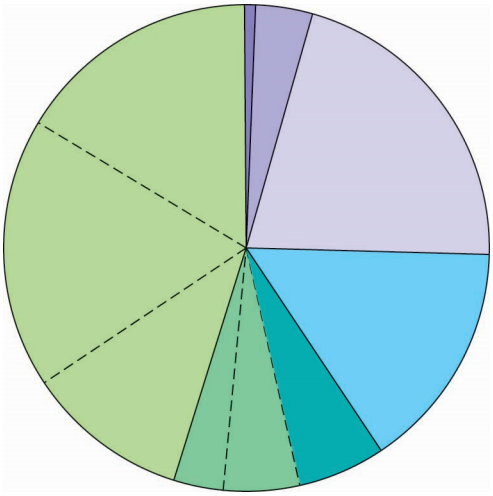
LO 21.4: Describe the composition of the genome of a multicellular eukaryote, such as that of humans.

14. Define the following two terms.

    pseudogenes

    repetitive DNA

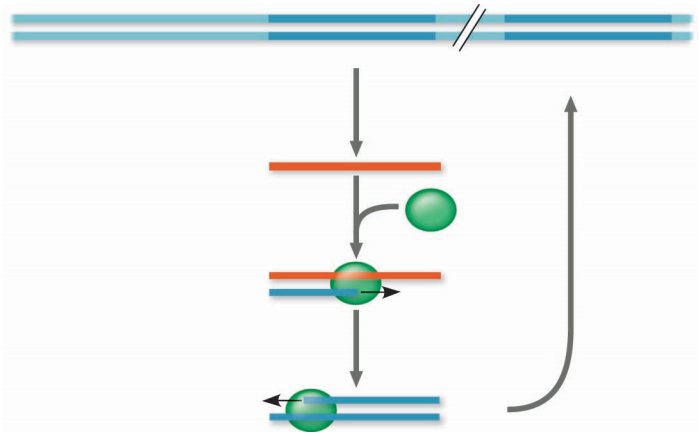
15. Using Figure 21.6 in your text as a guide, label the types of DNA sequences in the human genome and give their percentages.



16. What are *transposable elements*, and what percentage of our genome is made of them?

17. What is the difference between a "copy and paste" transposon and a "cut and paste" transposon?

18. *Retrotransposons* move by means of an RNA intermediate. Use Figure 21.9 in your text to label *DNA, RNA, reverse transcriptase, retrotransposon, new copy of retrotransposon,* and *insertion site.* Explain how these common transposons accomplish this movement.



19. What is the role of *reverse transcriptase*? How might retroviruses be related to retrotransposons?

20. Transposons and retrotransposons comprise 20–50% of most mammalian genomes. What possible function might they have?

21. What are *short tandem repeats (STRs)*, and why are Earl Washington (see p. 437 in your text) and The Innocence Project interested in them?

22. Describe and give an example of each of the following:

    multigene families of identical DNA sequences

    multigene families of nonidentical genes

23. How is fetal hemoglobin different from adult hemoglobin? What is the selective advantage of these different ß-globin genes?

Concept 21.5 Duplication, rearrangement, and mutation of DNA contribute to genome evolution

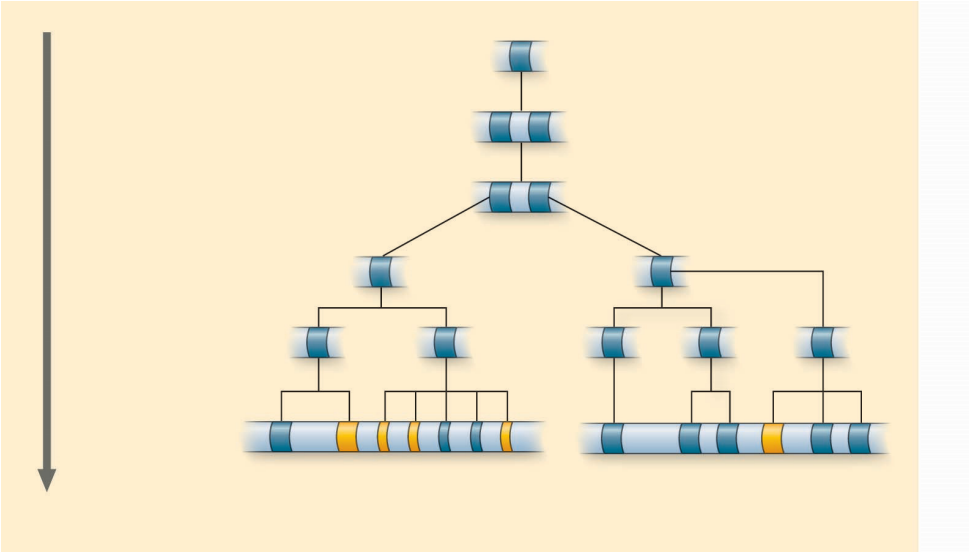
LO 21.5: Identify the changes to DNA that contribute to evolution of the genome.

24. Explain how polyploidy could facilitate the evolution of genes.

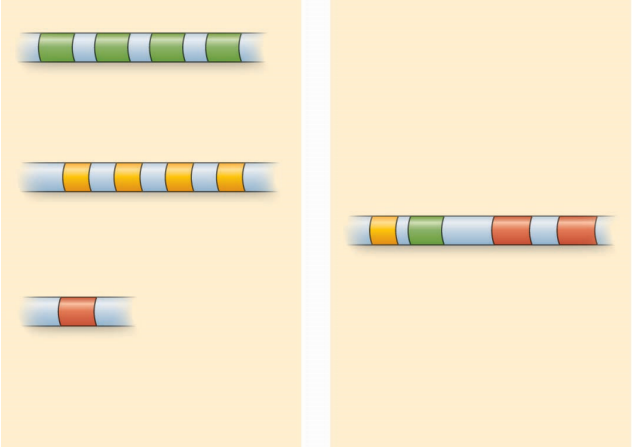
25. Describe how the chromosome banding pattern showing telomeres and centromeres may explain why there are different haploid chromosome numbers for humans (n = 23) and chimpanzees (n = 24).

26. What is the evolutionary significance of the relationship between the genes on human chromosome 16 and those same blocks of genes on mouse chromosomes 7, 8, 16, and 17?

27. A good summary of several processes involved in genomic evolution can be found in the globin gene families. Label and explain these processes (including duplication, mutation, and transposition) as described in Figure 21.14 in your text.



28. Using Figure 21.16 in your text as a guide, label and then explain how *exon shuffling* can lead to new proteins with novel functions. Use the concept of protein domains in your answer.



29. Transposable elements contribute to genome evolution in several ways. Describe three.

Concept 21.6 Comparing genome sequences provides clues to evolution and development

LO 21.6: Explain how comparing genome sequences and developmental processes helps us learn about evolution.

30. When comparing genomes, we find that the more_____ in sequence the genes and genomes of two species are, the more closely related those species are in their _____ history.

31. What does it mean to say that a gene is *highly conserved*?

32. In human evolution, the genes that appear to be evolving the fastest are those that code for transcription factors. Why does this make sense?

33. Why is the amount of DNA variation among humans small compared to many other species?

34. Explain why there is such genetic diversity among African genomes when compared to European or Asian genomes.

35. What is *evo-devo*, and how does it relate to understanding the evolution of genomes?

36. Explain what a *homeobox* is and describe how it functions.

Test Your Understanding Answers, p. 466

Now you should be ready to test your knowledge. Place your answers here:

1. _____ 2. _____ 3. _____