

I'm not robot!

characterize subsets of particular cancers, enabling more refined treatments. Breast **▲** Figure 18.4 cancer is one example (see Figure 16.21). Human gene Ultimately, medical records may include microarray chip, an individual's DNA sequence, a sort of genetic bar code, with regions highlighted that predispose the person to specific diseases. The use of such sequences for personalized medicine—disease prevention and treatment—has great potential. Systems biology is a very efficient way to study emergent properties at the molecular level. Novel properties emerge at each level of biological complexity as a result of the arrangement of building blocks at the underlying level (see Concept 1.1). The more we can learn about the arrangement and interactions of the components of genetic systems, the deeper will be our understanding of whole organisms. The rest of this chapter surveys what we've learned from genomic studies. CONCEPT CHECK 18.2 1. What role does the Internet play in current genomics and proteomics research? 2. Explain the advantage of the systems biology approach to studying cancer versus studying a single gene at a time. 3. MAKE CONNECTIONS The ENCODE pilot project found that at least 75% of the genome is transcribed into RNAs, far more than could be accounted for by protein-coding genes. Suggest some roles that these RNAs might play. (Review Concepts 14.3 and 15.3.) For suggested answers, see Appendix A. CONCEPT 18.3 Genomes vary in size, number of genes, and gene density The sequences of thousands of genomes have been completed, with tens of thousands of genomes either in progress or considered permanent drafts (because they require more work than it would be worth to complete them). Among sequences in progress are 550 metagenomes. In the completely sequenced group, about 3,000 are genomes of bacteria, and 180 are genomes of archaea. There are 60 completed eukaryotic species and 875 permanent drafts. Among these are vertebrates, invertebrates, protists, fungi, and plants. Next, we'll discuss what we've learned about genome size, number of genes, and gene density, focusing on general trends. CHAPTER 18 GENOMES AND THEIR EVOLUTION 361 Genome Size Comparing the three domains (Bacteria, Archaea, and Eukarya), we find a general difference in genome size between prokaryotes and eukaryotes (Table 18.1). While there are some exceptions, most bacterial genomes have between 1 and 6 million base pairs (Mb); the genome of *E. coli*, for instance, has 4.6 Mb. Genomes of archaea are, for the most part, within the size range of bacterial genomes. (Keep in mind, however, that many fewer genomes of archaea have been completely sequenced, so this picture may change.) Eukaryotic genomes tend to be larger: The genome of the single-celled yeast *Saccharomyces cerevisiae* (a fungus) has about 12 Mb, while most animals and plants, which are multicellular, have genomes of at least 100 Mb. There are 165 Mb in the fruit fly genome, while humans have 3,000 Mb, about 500 to 3,000 times as many as a typical bacterium. Aside from this general difference between prokaryotes and eukaryotes, a comparison of genome sizes among eukaryotes fails to reveal any systematic relationship between genome size and the organism's phenotype. For instance, the genome of *Paris japonica*, the Japanese canopy plant, contains 149 billion base pairs (149,000 Mb), about 50 times the size of the human genome. On a finer scale, comparing two insect species, the cricket (*Anabrus simplex*) genome turns out to have 11 times as many base pairs as the *Drosophila melanogaster* genome. There is a wide range of genome sizes within the groups of unicellular eukaryotes, insects, amphibians, and plants and less of a range within mammals and reptiles. Number of Genes The number of genes also varies between prokaryotes and eukaryotes: Bacteria and archaea, in general, have fewer genes than eukaryotes. Free-living bacteria and archaea have from 1,500 to 7,500 genes, while the number of genes in eukaryotes ranges from about 5,000 for unicellular fungi (yeasts) to at least 40,000 for some multicellular eukaryotes. Within the eukaryotes, the number of genes in a species is often lower than expected from considering simply the size of its genome. Looking at Table 18.1, you can see that the genome of the nematode *C. elegans* is 100 Mb in size and contains 20,100 genes. The *Drosophila* genome, in comparison, is much bigger (165 Mb) but has about two-thirds the number of genes—14,000 genes. Considering an example closer to home, we noted that the human genome contains 3,000 Mb, well over ten times the size of either the *D. melanogaster* or *C. elegans* genome. At the outset of the Human Genome Project, biologists expected somewhere between 50,000 and 100,000 genes to be identified in the completed sequence, based on the number of known human proteins. As the project progressed, the estimate was revised downward several times, and the ENCODE project has established the number to be fewer than 21,000. This relatively low number, similar to the number of genes in the nematode 362 UNIT TWO GENETICS Table 18.1 Genome Sizes and Estimated Numbers of Genes* Organism Haploid Genome Size (Mb)† Number of Genes Genes per Mb‡ Bacteria *Haemophilus influenzae* 1.8 1,700 940 *Escherichia coli* 4.6 4,400 950 Archaea *Archaeoglobus fulgidus* 2.2 2,500 1,130 *Methanosarcina barkeri* 4.8 3,600 750 12 6,300 525 *Caenorhabditis elegans* (nematode) 100 20,100 200 *Arabidopsis thaliana* (mustard family plant) 120 27,000 225 *Drosophila melanogaster* (fruit fly) 165 14,000 85 Eukaryotes *Saccharomyces cerevisiae* (yeast, a fungus) 430 42,000 95 *Zea mays* (corn) *Oryza sativa* (rice) 2,300 32,000 14 *Ailuropoda melanoleuca* (giant panda) 2,400 21,000 9 *Homo sapiens* (human) 3,000

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