

The Genetic Code of Genes and Genomes

Key Concepts

- Inherited traits are affected by genes.
- Genes are composed of the chemical deoxyribonucleic acid (DNA).
- DNA replicates to form (usually identical) copies of itself.
- DNA contains a code specifying what types of enzymes and other proteins are made in cells.
- DNA occasionally mutates, and the mutant forms specify altered proteins.
- A mutant enzyme is an “inborn error of metabolism” that blocks one step in a biochemical pathway for the metabolism of small molecules.
- Traits are affected by environment as well as by genes.
- Organisms change genetically through generations in the process of biological evolution.
- Because of their common descent, organisms share many features of their genetics and biochemistry.

Key Terms

1. complementary base pairing
2. antiparallel
3. central dogma
4. transcription
5. ribosome
6. transfer RNA (tRNA)
7. proteome
8. substrate
9. alkaptonuria
10. phenylketonuria
11. pleiotropic effect or pleiotropy
12. prokaryote

Concepts in Action

- 1.1. (a) false; (b) true; (c) true; (d) false.
- 1.2. The importance of the nucleus in inheritance was implied by its prominence in fertilization. The discovery of chromosomes inside the nucleus, their behavior during cell division, and the observation that each species has a characteristic chromosome number made it likely that chromosomes were the carriers of the genes. Microscopic studies showed that DNA and proteins are both present in chromosomes, but whereas nearly all cells of a given species contain a constant amount of DNA, the amount and kinds of proteins differ greatly in different cell types.

- 1.3.** It was generally believed that the genetic material must be a very complex molecule. Proteins were chemically the most complex macromolecules known at the time. DNA was thought to be a monotonous polymer composed of a simple repeating unit.
- 1.4.** Because the mature T2 phage contains only DNA and protein, the labeled RNA was left behind in material released by the burst cells.
- 1.5.** *Watson and Crick* noted that the nucleotide sequence of the DNA molecule could be replicated if each of the strands were used as a template for the formation of a new daughter strand having a complementary sequence of bases. They also noted that genetic information could be coded by the sequence of bases along the DNA molecule, analogous to letters of the alphabet printed on a strip of paper. Finally, they noted that changes in genetic information could result from errors in replication, and the altered nucleotide sequence could then be perpetuated.
- 1.6.** RNA differs from DNA in that the sugar-phosphate backbone contains ribose rather than deoxyribose. RNA contains the base uracil (U) instead of thymine (T), and RNA usually exists as a single strand (although any particular molecule of RNA may contain short regions of complementary base pairs that can come together to form duplexes).
- 1.7.** Percent C = 37.5%, so percent G = 37.5% also. Percent A + T = 1 - 0.375 - 0.375 = 25%, but because percent A = percent T, it must be that percent A = 12.5%.
- 1.8.** Because A ≠ T and G ≠ C in this DNA, it seems likely that the DNA molecule present in this particular virus is single-stranded.
- 1.9.** 3'-CA-5', because the dinucleotide 3'-CA-5' pairs with 5'-GT-3', so where either strand contains 5'-GT-3', the other contains 3'-CA-5'.
- 1.10.** The repeating Asn results from translation in the reading frame 5'-AAUAAUAAUAAU...-3', and the repeating Ile results from translation in the reading frame 5'-AUAAUAAUAAU...-3'. There is no product corresponding to the third reading frame (5'-UAAUAAUAAU...-3'), because 5'-UAA-3' is a stop codon.
- 1.11.** Most likely the mutant protein does not fold properly and is degraded by proteases.
- 1.12.** It is the case because each codon is exactly three nucleotides in length. In a protein-coding region, an insertion or deletion of anything other than an exact multiple of three nucleotides would shift the reading frame (phase) in which the mRNA is translated. All amino acids downstream of the site of the mutation would be translated incorrectly.
- 1.13.** 5'-TGTCGTATTTGCAAG-3'
- 1.14.** Transcription takes place from left to right, and the mRNA sequence is 5'-UGUCGUAUUUGCAAG-3'.
- 1.15.** Cys-Arg-Ile-Cys-Lys or, using the single-letter abbreviations, CRICK.
- 1.16.** Cys-His-Ile-Cys-Lys, CHICK
- 1.17.** The codon 5'-UGG-3' codes for Trp, and in this random polymer the Trp codon is expected with a frequency of $1/4 \times 3/4 \times 3/4 = 9/64$. The amino acid Val could be specified by either 5'-GUU-3' or 5'-GUG-3'; the former has an expected frequency of $3/4 \times 1/4 \times 1/4 = 3/64$, and the latter of $3/4 \times 1/4 \times 3/4 = 9/64$, totaling 12/64. The amino acid Phe could be specified only by 5'-UUU-3' in this random polymer, so Phe would have an expected frequency of $1/4 \times 1/4 \times 1/4 = 1/64$.
- 1.18.** **(a)** Met-Ser-Thr-Ala-Val-Leu-Glu-Asn-Pro-Gly. **(b)** The mutation changes the initiation codon into a noninitiation codon, so translation will not start with the first AUG; translation will start with the next AUG farther along the mRNA or, if this is too distant, not at all. **(c)** Met-Ser-Thr-Ala-Val-Leu-Glu-Asn-Pro-Gly; there is no change, because both 5'-UCC-3' and 5'-UCG-3' code for serine. **(d)** Met-Ser-Thr-Ala-Ala-Leu-Glu-Asn-Pro-Gly; there is a Val→Ala amino acid replacement because 5'-GUC-3' codes for Val, whereas 5'-GCC-3' codes for Ala. **(e)** Met-Ser-Thr-Ala-Val-Leu; translation is terminated at UAA because 5'-UAA-3' is a "stop" (termination) code.
- 1.19.** **(a)** X, Y, and Z missing, W in excess; **(b)** Y and Z missing, X in excess; **(c)** Z missing, Y in excess.

- 1.20.** The finding that the cells can grow in the presence of Y implies that step C is functional. The finding that the cells cannot grow in the presence of X implies that step B is blocked. The results with W imply that a downstream step is blocked, but do not reveal which one.

Study Questions

- 1.51.** When the base composition of double-stranded DNA from a new species of bacteria was determined, 15% of the bases were found to be cytosine. What is the percentage of adenine in the DNA of this organism?
- A) 15%
 - B) 25%
 - C) 35%
 - D) 45%
- 1.52.** A duplex DNA molecule contains a random sequence of the four nucleotides in equal proportions. What is the average spacing between consecutive occurrences of the sequence 5'-GGGG-3'?
- A) $(1/4)^4$
 - B) 4^4
 - C) 2^4
 - D) 4^2
- 1.53.** The sequence of one strand of DNA is 5'-CCATATGC-3'. The sequence of the complementary strand would be what?
- A) 5'-CCATATGC-3'
 - B) 5'-GGTATACG-3'
 - C) 5'-GCATATGG-3'
 - D) 5'-AAGCGCTA-3'
 - E) 5'-GCAUAUGC-3'
- 1.54.** An RNA molecule folds back upon itself to form a "hairpin" structure held together by a region of base pairing. One segment of the molecule in the paired region has the base sequence 5'-UCAAUGC-3'. What is the base sequence with which this segment is paired?
- A) 5'-GCAUUGA-3'
 - B) 5'-GCAUUGA-3'
 - C) 5'-TCAATGC-3'
 - D) 5'-GCATTGA-3'
- 1.55.** What codon would pair with the anticodon of tRNA^{met} 5'-UAG-3'?
- A) 5'-CAU-3'
 - B) 5'-GAU-3'
 - C) 5'-UAG-3'
 - D) 5'-ATG-3'
 - E) 5'-CUA-3'
- 1.56.** Traits are affected by environment as well as by _____ .
- 1.57.** An enzyme called *reverse transcriptase* can produce a complementary DNA strand from an _____ template.
- 1.58.** If DNA from Baker's yeast has a guanine content of 25%, then what is the content of the adenine?
- 1.59.** If a particular piece of RNA has a uracil content of 25%, then what is its guanine content?
- 1.510.** How many different DNA sequences can encode the amino acid sequence Pro-Met-Arg?