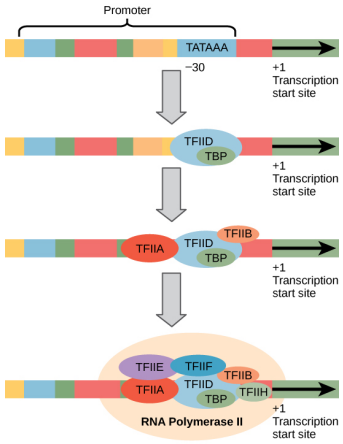
Biology 2e
Unit 3: Genetics
Chapter 15: Genes and Proteins

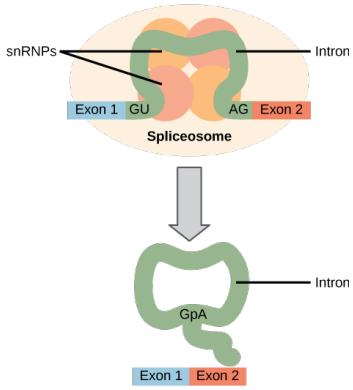
Visual Connection Questions

1. A scientist splices a eukaryotic promoter in front of a bacterial gene and inserts the gene in a bacterial chromosome. Would you expect the bacteria to transcribe the gene?



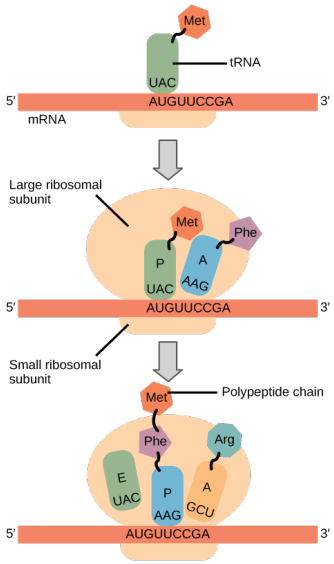
No. Prokaryotes use different promoters than eukaryotes.

2. Errors in splicing are implicated in cancers and other human diseases. What kinds of mutations might lead to splicing errors? Think of different possible outcomes if splicing errors occur.



Mutations in the spliceosome recognition sequence at each end of the intron, or in the proteins and RNAs that make up the spliceosome, may impair splicing. Mutations may also add new spliceosome recognition sites. Splicing errors could lead to introns being retained in spliced RNA, exons being excised, or changes in the location of the splice site.

3. Many antibiotics inhibit bacterial protein synthesis. For example, tetracycline blocks the A site on the bacterial ribosome, and chloramphenicol blocks peptidyl transfer. What specific effect would you expect each of these antibiotics to have on protein synthesis?



Tetracycline: a. tRNA binding to the ribosome; Chloramphenicol: c. growth of the protein chain

Review Questions

4. The AUC and AUA codons in mRNA both specify isoleucine. What feature of the genetic code explains this?

d. degeneracy

5. How many nucleotides are in 12 mRNA codons?

c. 36

6. Which event contradicts the central dogma of molecular biology?

c. Scientists use reverse transcriptase enzymes to make DNA from RNA.

7. Which subunit of the *E. coli* polymerase confers specificity to transcription?

d. σ

8. The -10 and -35 regions of prokaryotic promoters are called consensus sequences because _____.

b. they are similar in all bacterial species

9. Three different bacteria species have the following consensus sequences upstream of a conserved gene.

	Species A	Species B	Species C
-10	TAATAAT	TTTAAT	TATATT
-35	TTGACA	TTGGCC	TTGAAA

Order the bacteria from most to least efficient initiation of gene transcription.

d. A > C > B

10. Which feature of promoters can be found in both prokaryotes and eukaryotes?

b. TATA box

11. What transcripts will be most affected by low levels of α-amanitin?

b. pre-mRNAs

12. How do enhancers and promoters differ?

b. Enhancers increase the efficiency of gene expression, but are not essential for transcription. Promoter recognition is essential to transcription initiation.

13. Which pre-mRNA processing step is important for initiating translation?

d. 7-methylguanosine cap

14. What processing step enhances the stability of pre-tRNAs and pre-rRNAs?

a. methylation

15. A scientist identifies a pre-mRNA with the following structure.

What is the predicted size of the corresponding mature mRNA in base pairs (bp), excluding the 5’ cap and 3’ poly-A tail?

b. 295bp

16. The RNA components of ribosomes are synthesized in the _____.

c. nucleolus

17. In any given species, there are at least how many types of aminoacyl tRNA synthetases?

a. 20

18. A scientist introduces a mutation that makes the 60S ribosomal subunit nonfunctional in a human cell line. What would be the predicted effect on translation?

a. Translation stalls after the initiation AUG codon is identified.

Critical Thinking Questions

19. Imagine if there were 200 commonly occurring amino acids instead of 20. Given what you know about the genetic code, what would be the shortest possible codon length? Explain.

For 200 commonly occurring amino acids, codons consisting of four types of nucleotides would have to be at least four nucleotides long, because $4^4 = 256$. There would be much less degeneracy in this case.

20. Discuss how degeneracy of the genetic code makes cells more robust to mutations.

Codons that specify the same amino acid typically only differ by one nucleotide. In addition, amino acids with chemically similar side chains are encoded by similar codons. This nuance of the genetic code ensures that a single-nucleotide substitution mutation might either specify the same amino acid and have no effect, or may specify a similar amino acid, preventing the protein from being rendered completely nonfunctional.

21. A scientist sequencing mRNA identifies the following strand:
CUAUGUGUCGUAACAGCCGAUGACCCG
What is the sequence of the amino acid chain this mRNA makes when it is translated?

Met Cys Arg Asn Ser Arg

The first step to writing the amino acid sequence is to find the start codon AUG. Then, the nucleotide sequence is separated into triplets: CU **AUG** UGU CGU AAC AGC CGA UGA. We stop the translation at UGA because that triplet encodes a stop codon. When we convert these codons to amino acids, the sequence becomes Met Cys Arg Asn Ser Arg.

22. If mRNA is complementary to the DNA template strand and the DNA template strand is complementary to the DNA nontemplate strand, then why are base sequences of mRNA and the DNA nontemplate strand not identical? Could they ever be?

DNA is different from RNA in that T nucleotides in DNA are replaced with U nucleotides in RNA. Therefore, they could never be identical in base sequence.

23. In your own words, describe the difference between rho-dependent and rho-independent termination of transcription in prokaryotes.

Rho-dependent termination is controlled by the rho protein, which tracks along behind the polymerase on the growing mRNA chain. Near the end of the gene, the polymerase stalls at a run of G nucleotides on the DNA template. The rho protein collides with the polymerase and releases mRNA from the transcription bubble. Rho-independent termination is controlled by specific sequences in the DNA template strand. As the polymerase nears the end of the gene being transcribed, it encounters a region rich in C–G nucleotides. This creates an mRNA hairpin that causes the polymerase to stall right as it begins to transcribe a region rich in A–T nucleotides. Because A–U bonds are less thermostable, the core enzyme falls away.

24. A fragment of bacterial DNA reads:
3’ –TACCTATAATCTCAATTGATAGAAGCACTCTAC– 5’
Assuming that this fragment is the template strand, what is the sequence of mRNA that would be transcribed? (Hint: Be sure to identify the initiation site.)

ACUAUCUUCGUGAGAUG
By examining the DNA sequence, we can see that there is a -10 consensus sequence near the 3’ end of the fragment. If we then count downstream, the +1 initiation site is the T immediately following the sequence AAT. This means the DNA fragment that will serve as the template for transcription has the sequence TGATAGAAGCACTCTAC. The mRNA made from this template will have complementary base pairing with uracil (U) instead of thymine (T). This gives us ACUAUCUUCGUGAGAUG as the transcribed mRNA sequence.

25. A scientist observes that a cell has an RNA polymerase deficiency that prevents it from making proteins. Describe three additional observations that would together support the conclusion that a defect in RNA polymerase I activity, and not problems with the other polymerases, causes the defect.

To determine that a RNA polymerase I mutation or deficiency is causing the defect in protein production, the scientist would need to make observations that provide evidence that RNA polymerases II and III are working in the cell. The observations eliminating RNA polymerase II as the defect could include:

- Transcription of mRNAs in the nucleus
- Presence of processed mRNAs in the cytoplasm

The observations eliminating RNA polymerase III could include:

- Isolation of small nuclear RNAs from the cell
- Isolation of microRNAs from the cell
- Transcription of 5S rRNA in the nucleus
- Presence of tRNAs in the cytoplasm

The observations implicating RNA polymerase I could include:

- A lack of functional ribosomes in the cytoplasm (RNA polymerase I or III)
- A lack of RNA polymerase I protein
- RNA polymerase I protein is non-functional

26. Chronic lymphocytic leukemia patients often harbor nonsense mutations in their spliceosome machinery. Describe how this mutation of the spliceosome would change the final location and sequence of a pre-mRNA.

Nonsense spliceosome mutations would eliminate the splicing step of mRNA processing, so the mature mRNAs would retain their introns and be perfectly complementary to the entire DNA template sequence. However, the mRNAs would still undergo addition of the 5’ cap and poly-A tail, and therefore each has the potential to be exported to the cytoplasm for translation.

27. Transcribe and translate the following DNA sequence (nontemplate strand):
5'- ATGGCCGGTTATTAAGCA-3'

The mRNA would be: 5'-AUGGCCGGUUAUUAAGCA-3'. The protein would be: MAGY. Even though there are six codons, the fifth codon corresponds to a stop, so the sixth codon would not be translated.

28. Explain how single nucleotide changes can have vastly different effects on protein function.

Nucleotide changes in the third position of codons may not change the amino acid and would have no effect on the protein. Other nucleotide changes that change important amino acids or create or delete start or stop codons would have severe effects on the amino acid sequence of the protein.

29. A normal mRNA that reads 5’ –UGCCAUGGUAAUAACACAUGAGGCCUGAAC– 3’ has an insertion mutation that changes the sequence to 5’ –UGCCAUGGUUAAUAACACAUGAGGCCUGAAC– 3’. Translate the original mRNA and the mutated mRNA, and explain how insertion mutations can have dramatic effects on proteins. (Hint: Be sure to find the initiation site.)

Original mRNA: 5’ –UGCC AUG GUA AUA ACA CAU GAG GCC UGA AC– 3’
Translation: Met – Val – Ile – Thr – His – Glu – Ala
Mutated mRNA: 5’ –UGCC AUG G**U**U AAU AAC ACA UGA GGCCUGAAC– 3’
Translation: Met – Val – Asn – Asn – Thr
Insertion mutations can have dramatic effects on proteins because they shift the reading frame for the codons. This changes the amino acids encoded by the mRNA, and can introduce premature start or stop sites.