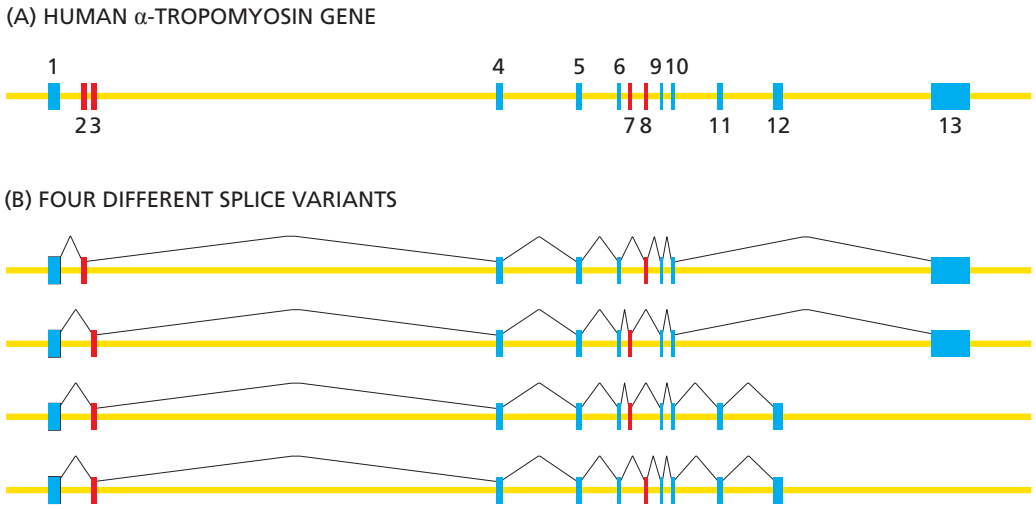
BIO-205-5

Discuss the following exercises in pairs

The human α-tropomyosin gene is alternatively spliced to produce different forms of α-tropomyosin mRNA in different cell types. For all forms of the mRNA, the protein sequences encoded by exon 1 are the same, as are the protein sequences encoded by exon 10. Exons 2 and 3 are alternative exons used in diferent mRNAs, as are exons 7 and 8.



Which of the following statements about exons 2 and 3 is the most accurate? Is that statement also the most accurate one for exons 7 and 8? Explain your answers.

a. Exons 2 and 3 must have the same number of nucleotides.
b. Exons 2 and 3 must each contain an integral number of codons (that is, the number of nucleotides divided by 3 must be an integer).
c. Exons 2 and 3 must each contain a number of nucleotides that when divided by 3 leaves the same remainder (that is, 0, 1, or 2).

You have printed out a set of DNA sequences around the intron/exon boundaries for genes in the β-globin family, and have taken the thick ile to the country to study for the weekend. When you look at the printout, you discover to your annoyance that there's no indication of where in the gene you are. You know that the sequences in **the figure below** come from one of the exon/intron or intron/exon boundaries and that the boundaries lie on the dotted line, but you don't know the order of the intron and exon. You know that introns begin with the dinucleotide sequence GT and end with AG, but you realize that these particular sequences would it *either* as the start *or* the inish of an intron.
If you cannot decide which side is the intron, you will have to cut your weekend short and return to the city (or ind a neighbor with Internet access). In desperation, you consider the problem from an evolutionary perspective. You know that introns evolve faster (sufering more nucleo- tide changes) than exons because they are not constrained by function. Does this perspective allow you to identify the intron, or will you have to pack your bags?

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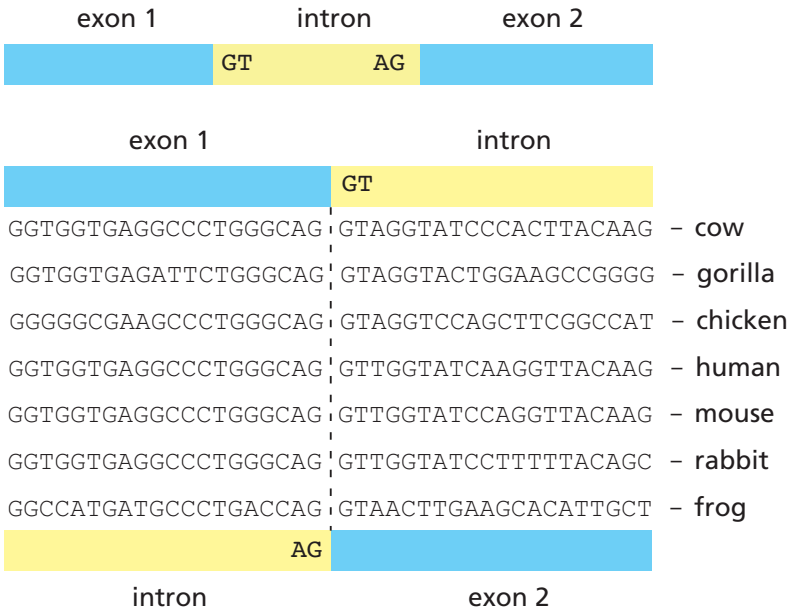

Multiple Choice Questions

1. What can be the impact of a mutation in the -10 or -35 consensus sequence of the bacterial promoter?
    a. Increase in transcription speed.
    b. Decrease in RNA polymerase binding to the promoter.
    c. Transcription starts but with systematic errors.
    d. It does not affect the transcription process.
    e. RNA polymerase will not be able to finish transcription.

2. RNA polymerases do not require an RNA primer
    a. Because ribonucleotides are more stable than deoxyribonucleotides.
    b. Because RNA polymerases can directly bind to the template strand promoter and initiate transcription.
    c. Because RNA is single-stranded.
    d. Because RNA polymerases use different nucleotides.
    e. Because RNA polymerase is more accurate than DNA polymerase.

3. What is the main difference between transcription initiation in prokaryotes and eukaryotes?
    a. Prokaryotes do not require transcription factors.
    b. Prokaryotic RNA polymerase requires a double-stranded promoter to function.
    c. Eukaryotes have multiple RNA polymerases, whereas prokaryotes have only one.
    d. Prokaryotes have many transcription factors, but Eukaryotes do not.
    e. No significant difference.

4. What is the direct consequence of a mutation in the TATA box in Eukaryotes?
    a. Failure of RNA polymerase to bind to the promoter.
    b. Halting of transcription elongation.

c. An error in RNA cleavage.
d. Alteration of the mRNA translation mechanism.
e. No observable change.

5. What is the main effect of elongation factors during transcription in eukaryotes?
    a. Helping to open the DNA double helix.
    b. Stabilizing RNA polymerase to prevent premature dissociation from the DNA.
    c. Speeding up transcription by binding to mRNA.
    d. Modifying the promoter sequence for better transcription.
    e. Inhibiting transcription once the mRNA is completed.

6. What is the function of topoisomerases during transcription?
    a. Prevent RNA polymerase from dissociating from DNA.
    b. Relieve supercoiling tension created during DNA unwinding.
    c. Add ribonucleotides to the RNA strand.
    d. Facilitate transcription initiation by stabilizing DNA.
    e. Help transcription factors associate.

7. What is the main effect of supercoiling tension during transcription?
    a. Prevent RNA polymerase from binding to DNA.
    b. Facilitate wrapping of RNA around histones.
    c. Help open and unwind DNA for transcription.
    d. Promote RNA elongation by aiding ribonucleotide binding.
    e. Slow down topoisomerase activity.

8. Which of the following RNAs is mainly involved in protein <u>translation</u>?
    a. tRNA
    b. miRNA
    c. piRNA
    d. siRNA
    e. snoRNA

<u>TRUE or FALSE</u>

1. Prokaryotes and eukaryotes only use one RNA polymerase for transcription.

2. Multiple RNA polymerases can simultaneously transcribe the same gene.

3. The sigma factor is essential for transcription initiation in eukaryotes.

4. Elongation factors reduce the likelihood that RNA polymerase dissociates prematurely from the DNA strand in both prokaryotes and eukaryotes.

5. The consequences of errors in transcription are less severe than those of errors in DNA replication.

6. The splicing process allows prokaryotes to produce multiple RNAs from a single gene.

7. The transcription of non-coding RNAs (such as siRNA and miRNA) does not require an RNA polymerase.

8. Capping and polyadenylation enzymes function exclusively after RNA polymerase has completed mRNA transcription in eukaryotes.