University of Central Florida (UCF) PCB3063 Genetics Practice Final (Sample)

Study Guide

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Questions

1. What is a significant difference in gamete size between sexes for most species?

   A. Males have larger gametes

   B. Females have larger gametes

   C. Both sexes have equal-sized gametes

   D. Males have smaller gametes

2. How many primers are required for the leading and lagging strands during DNA replication?

   A. One for both leading and lagging strands

   B. One for the leading strand and one for each Okazaki fragment on the lagging strand

   C. Two for the leading strand and one for the lagging strand

   D. One for the lagging strand and zero for the leading strand

3. When does UASg function as an enhancer?

   A. Only in the absence of galactose

   B. When galactose is present

   C. Under all conditions

   D. In the presence of glucose

4. What is the primary function of eukaryotic RNA polymerase IV?

   A. Transcription of mRNA

   B. Transcription of rRNA

   C. Production of siRNA

   D. Encoding tRNA

5. How many chromosomes and DNA molecules are present at Metaphase II of meiosis if the starting cell was diploid with 4 chromosomes?

   A. 2 chromosomes, 2 DNA molecules

   B. 2 chromosomes, 4 DNA molecules

   C. 4 chromosomes, 4 DNA molecules

   D. 4 chromosomes, 8 DNA molecules

6. Where is the regulatory promoter located in eukaryotic RNA transcription?

A. At the end of the coding sequence

B. Immediately downstream of the core promoter

C. Immediately upstream of the core promoter

D. At the transcription termination site

7. Which consensus sequence is located at -10 in bacterial promoters?

A. Rho Box

B. Pribnow Box

C. TATA Box

D. Shine-Dalgarno sequence

8. Increased activity of HAT leads to what change in transcription?

A. Decreased transcription

B. Increased positive charge

C. Increased negative charge

D. Inhibition of transcription

9. What is the chromosome composition of Triplo-X females?

A. 2n=46; XX

B. 2n=45; XO

C. 2n=47; XXX

D. 2n=48; XXXX

10. Where is the core promoter typically located in eukaryotic RNA transcription?

A. Downstream of the transcription start site

B. Within the gene coding region

C. Upstream of the transcription start site

D. At the end of the mRNA transcript

Answers

1. D
2. B
3. B
4. C
5. B
6. C
7. B
8. B
9. C
10. C

Explanations

1. What is a significant difference in gamete size between sexes for most species?

A. Males have larger gametes

B. Females have larger gametes

C. Both sexes have equal-sized gametes

D. Males have smaller gametes

The significant difference in gamete size between sexes in most species is that males produce smaller gametes compared to females. In the context of sexual reproduction, males typically produce sperm, which are generally smaller and more mobile, allowing them to travel and fertilize the larger, immobile eggs produced by females. Females, on the other hand, tend to invest more resources into their larger gametes, which are the eggs. The larger size of the egg provides more nutrients and support for the developing embryo, which is critical for successful reproduction. This biological investment reflects an evolutionary strategy where females provide a greater contribution to the early developmental stages of offspring, while males enhance their reproductive success through the production of numerous small, motile sperm. This difference in gamete size underscores the concept of anisogamy, where there are two distinct types of gametes (small and mobile in males; large and nutrient-rich in females) that drive reproductive strategies in many organisms.

2. How many primers are required for the leading and lagging strands during DNA replication?

A. One for both leading and lagging strands

B. One for the leading strand and one for each Okazaki fragment on the lagging strand

C. Two for the leading strand and one for the lagging strand

D. One for the lagging strand and zero for the leading strand

During DNA replication, the leading strand is synthesized continuously in the direction of the replication fork and requires a single short strand of RNA known as a primer to initiate DNA synthesis. This primer is crucial as DNA polymerase cannot begin synthesizing DNA from scratch; it requires a free 3' hydroxyl (OH) group to which it can add nucleotides. On the lagging strand, however, DNA synthesis occurs in short bursts, producing discrete segments called Okazaki fragments, which are synthesized in the opposite direction of the replication fork. Each Okazaki fragment also requires a primer to provide the necessary 3' OH group for DNA polymerase to extend the new DNA strand. Since there are multiple Okazaki fragments produced along the lagging strand, each of these fragments necessitates its own separate primer. Therefore, the correct response clearly indicates that one primer is required for the leading strand, while a distinct primer is needed for each individual Okazaki fragment on the lagging strand. This results in one primer for the leading strand and a number of primers equal to the number of Okazaki fragments on the lagging strand. This understanding highlights the difference in how the leading and lagging strands are synthesized during DNA replication.

3. When does UASg function as an enhancer?

A. Only in the absence of galactose

B. When galactose is present

C. Under all conditions

D. In the presence of glucose

UASg, or the Upstream Activating Sequence of the GAL genes in yeast, functions as an enhancer specifically in the presence of galactose. This sequence is essential for the transcriptional activation of the GAL genes when galactose is available as a carbon source. In the presence of galactose, UASg binds to transcription factors, primarily Gal4, which then interacts with the transcriptional machinery to enhance the expression of genes required for metabolizing galactose. This regulatory mechanism allows yeast to switch its metabolic pathway in response to the availability of different sugars, showcasing a finely tuned response to environmental changes. When galactose is absent, UASg does not function as an enhancer because the necessary activators are not present, leading to repression of the GAL genes. Similarly, in the presence of glucose, which is a preferred carbon source over galactose, the expression of GAL genes is generally repressed, demonstrating that the presence of glucose prevents UASg from being active in enhancing gene expression. Therefore, the enhancer activity of UASg is conditional, aligning specifically with the presence of galactose.

4. What is the primary function of eukaryotic RNA polymerase IV?

A. Transcription of mRNA

B. Transcription of rRNA

C. Production of siRNA

D. Encoding tRNA

Eukaryotic RNA polymerase IV plays a specialized role in the transcription of certain small RNA molecules, particularly small interfering RNAs (siRNAs) that are involved in RNA interference and the regulation of gene expression. This polymerase is primarily associated with the synthesis of non-coding RNAs that contribute to processes such as silencing transposons and controlling gene expression through mechanisms like heterochromatin formation. The choice related to mRNA transcription is attributed to RNA polymerase II, which is responsible for synthesizing messenger RNA and various other non-coding RNAs. Similarly, rRNA transcription is the function of RNA polymerase I, which synthesizes ribosomal RNA, and tRNA transcription is carried out by RNA polymerase III. Therefore, the main function of RNA polymerase IV in producing siRNAs distinguishes it from the other polymerases that have different roles in the cell. This unique function underscores the complexity of eukaryotic RNA polymerases and their diverse contributions to gene regulation and expression.

5. How many chromosomes and DNA molecules are present at Metaphase II of meiosis if the starting cell was diploid with 4 chromosomes?

A. 2 chromosomes, 2 DNA molecules

B. 2 chromosomes, 4 DNA molecules

C. 4 chromosomes, 4 DNA molecules

D. 4 chromosomes, 8 DNA molecules

To evaluate the state of chromosomes and DNA molecules during Metaphase II of meiosis, it is essential to understand the processes that occur throughout meiosis, particularly the changes that happen in chromosome number and DNA content. Initially, in a diploid organism with 4 chromosomes, during the first meiotic division (meiosis I), homologous chromosomes are separated. This results in two haploid cells, each containing the original 4 chromosomes but with each chromosome consisting of two sister chromatids, making for a total of 8 DNA molecules. In the second meiotic division (meiosis II), which resembles mitosis, the sister chromatids of each chromosome are separated and distributed into newly formed gametes. By the time Metaphase II is reached, the chromosomes have aligned at the metaphase plate, and each chromosome is still made up of two sister chromatids. Therefore, while there are still 4 chromosomes as they did not reduce further in number after meiosis I, the count of DNA molecules remains 8 (4 chromosomes × 2 chromatids each). However, upon the completion of meiosis II and during the transition into the next phase (which might be following the alignment state), the final count in a haploid context typically reflects

6. Where is the regulatory promoter located in eukaryotic RNA transcription?

A. At the end of the coding sequence

B. Immediately downstream of the core promoter

C. Immediately upstream of the core promoter

D. At the transcription termination site

The regulatory promoter is crucial in eukaryotic transcription as it is located immediately upstream of the core promoter. This position allows it to effectively influence the transcription initiation process by interacting with various transcription factors and regulatory proteins that bind to this region. These interactions can enhance or repress the assembly of the transcription machinery at the core promoter, thereby playing a pivotal role in the regulation of gene expression. The regulatory promoter includes specific sequences that are recognized by transcription factors, which will either stimulate or inhibit the transcription process depending on the cell's conditions or developmental stage. This regulatory function is essential in ensuring that genes are expressed at the appropriate levels and times in response to cellular signals. In contrast, other locations mentioned in the incorrect options do not serve the same regulatory purpose. For instance, positions at the end of the coding sequence, immediately downstream, or at the transcription termination site do not influence the initiation of transcription in the way that the regulatory promoter does. This precise positioning allows for the fine-tuning of gene expression, highlighting the regulatory promoter's importance in eukaryotic transcriptional control.

7. Which consensus sequence is located at -10 in bacterial promoters?

A. Rho Box

B. Pribnow Box

C. TATA Box

D. Shine-Dalgarno sequence

The consensus sequence located at -10 in bacterial promoters is known as the Pribnow Box. This sequence is typically characterized by the presence of a conserved sequence that is crucial for the initiation of transcription in prokaryotic organisms. The Pribnow Box generally contains the consensus sequence TATAAT and is recognized by the RNA polymerase during the transcription process. This recognition facilitates the binding of the RNA polymerase to the promoter region and subsequent transcription of downstream genes. In bacterial promoters, the -10 region is essential for the correct positioning of RNA polymerase, allowing it to unwind the DNA and start synthesizing RNA. The Pribnow Box is part of the larger promoter structure that includes the -35 region as well, where another set of sequences play a role in the recruitment of RNA polymerase, but the specific function of the Pribnow Box at -10 is critical for adequate transcription initiation. Understanding the role of these sequences helps clarify the mechanisms of gene expression and regulation within bacterial systems.

8. Increased activity of HAT leads to what change in transcription?

A. Decreased transcription

B. Increased positive charge

C. Increased negative charge

D. Inhibition of transcription

The correct answer highlights the role of histone acetyltransferases (HAT) in modifying chromatin structure and its implications for transcription. HATs add acetyl groups to lysine residues on histone proteins, resulting in a change in the charge of the histones. Specifically, lysine is positively charged at physiological pH, and the addition of an acetyl group neutralizes this positive charge, thereby reducing the overall positive charge of the histones. This reduction in positive charge leads to a more relaxed chromatin structure, which facilitates access for transcription factors and RNA polymerase to the DNA template. Consequently, the transcription of certain genes is enhanced as the chromatin becomes more accessible for the transcription machinery. This underlines the importance of HAT activity in promoting gene expression by altering the ionic nature of histones and enabling a more open and transcriptionally active chromatin state. The other options do not accurately capture the role of HATs; they either imply negative effects on transcription or incorrect changes in charge state. Thus, the reference to increased positive charge directly aligns with the biochemical action of HATs and their functional implications for transcription regulation.

9. What is the chromosome composition of Triplo-X females?

A. 2n=46; XX

B. 2n=45; XO

C. 2n=47; XXX

D. 2n=48; XXXX

Triplo-X females, also referred to as 47,XXX females, have an additional X chromosome beyond the typical female karyotype. In humans, females usually have two X chromosomes, designated as XX, which gives them a diploid chromosome number of 2n=46. However, in the case of Triplo-X females, they have three X chromosomes (XXX), leading to a total chromosome composition of 2n=47. This extra X chromosome can be associated with certain developmental and health characteristics, but many Triplo-X individuals lead relatively normal lives without significant symptoms. This understanding corroborates the correct answer regarding the chromosome composition of Triplo-X females.

10. Where is the core promoter typically located in eukaryotic RNA transcription?

A. Downstream of the transcription start site

B. Within the gene coding region

C. Upstream of the transcription start site

D. At the end of the mRNA transcript

The core promoter in eukaryotic RNA transcription is typically located upstream of the transcription start site. This region is crucial because it contains specific sequences and elements that are recognized by the transcription machinery, including RNA polymerase and various transcription factors. These components are essential for the initiation of transcription, as they help assemble at the promoter to form the transcription initiation complex. In more detail, the core promoter usually includes elements such as the TATA box, which is a conserved sequence found approximately 25-30 base pairs upstream of the transcription start site. The positioning of the core promoter upstream allows it to effectively regulate the expression of the downstream gene by facilitating the necessary interactions for RNA polymerase to begin synthesizing RNA from the DNA template. Understanding the correct location of the core promoter is fundamental in genetics as it highlights how gene expression is orchestrated in eukaryotic cells, showcasing the importance of promoter architecture in the regulation of transcription.