DOPAMINE
SCIENTIFIC TEAM

Test bank - Molecular biology - Lectures 5 to 10

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Lecture 5 - DNA replication

Q1 . Which of the following best explains why mammalian cells do not require an enzyme analogous to DNA Polymerase I found in *E. coli*? *Book question*

A. DNA synthesis in mammalian cells occurs without the need for RNA primers.

B. DNA Polymerase I is replaced by DNA polymerase α, which performs all its functions in mammalian cells.

C. Mammalian cells use specialized enzymes like RNase H, and DNA polymerase δ to perform the functions of DNA Polymerase I.

D. DNA replication in mammalian cells is error-free, so no repair enzymes are needed.

Q2. You treat cells with an RNA polymerase inhibitor and observe its effects on DNA synthesis at the replication fork. How would this treatment most likely affect the synthesis of the leading and lagging strands of DNA? *Book question*

A. Neither strand would be affected, as RNA polymerase is not involved in DNA replication.

B. The leading strand would be affected only, but the lagging strand would continue to be synthesized normally.

C. Both strands would be affected, as RNA polymerase is essential for synthesizing RNA primers needed for DNA replication.

D. The lagging strand would be affected only, as RNA polymerase is required only for discontinuous DNA synthesis.

Q3.Which of the following best describes the difference between the actions of topoisomerases I and II during DNA replication? *Book question*

A. Topoisomerase I relaxes DNA supercoils by creating single-strand breaks, while topoisomerase II introduces double-strand breaks to relieve supercoiling.

B. Topoisomerase I creates double-strand breaks to prevent DNA tangling, while topoisomerase II cuts only one strand to relax DNA.

C. Both topoisomerase I and II create single-strand breaks but differ in the enzymes they use to reseal the breaks.

D. Topoisomerase I is involved only in transcription, while topoisomerase II functions exclusively during DNA replication.

Q4. What would happen if the proofreading function of DNA polymerase were impaired?

A. DNA replication would occur faster but with fewer mutations.

B. DNA replication would be unaffected because other enzymes can proofread.

C. The mutation rate during replication would increase significantly.

D. The replication fork would not be able to open properly.

Q5 . What is the likely consequence if DNA polymerase synthesized DNA without its 3′ to 5′ exonuclease activity?

A. DNA replication would occur normally but at a slower rate.

B. Mismatched nucleotides would accumulate, increasing mutation rates.

C. The leading strand would not be synthesized at all.

D. Okazaki fragments would not be joined properly.

Q6 . Why is the lagging strand synthesized in shorter fragments rather than continuously?

A. The DNA polymerase synthesizes DNA only in the 5′ to 3′ direction, requiring frequent restarting on the lagging strand.

B. The helicase only unwinds the lagging strand in short sections.

C. Single-strand binding proteins interfere with continuous synthesis on the lagging strand.

D. The lagging strand is more prone to mutations, requiring pauses for repair.

Q7 .If DNA ligase were defective, what immediate effect would this have on the DNA replication process?

A. DNA polymerase would fail to synthesize new DNA strands.

B. RNA primers would not be added.

C. Okazaki fragments on the lagging strand would remain unjoined.

D. DNA helicase would be unable to unwind the DNA helix.

Q8 . Which of the following best describes the difference between DNA polymerase I and DNA polymerase III in *E. coli*?

A . DNA polymerase I synthesizes the leading strand, while DNA polymerase III synthesizes the lagging strand.

B. DNA polymerase I synthesizes RNA primers, while DNA polymerase III removes them.

C. DNA polymerase I removes RNA primers and fills in gaps, while DNA polymerase III synthesizes most of the new DNA.

D. DNA polymerase I only works in eukaryotic cells, while DNA polymerase III is exclusive to prokaryotes.

Q9 .Which enzyme prevents DNA from becoming too tightly coiled ahead of the replication fork during replication?

A. DNA polymerase

B. DNA helicase

C. DNA ligase

D. Topoisomerase

Q10 . Arrange the following steps in the correct order during DNA replication:

1. RNA primers are synthesized.
2. DNA strands are unwound by helicase.
3. DNA polymerase synthesizes new DNA strands.
4. RNA primers are removed and replaced with DNA.
5. Okazaki fragments are joined by ligase.

A) 2 → 1 → 3 → 4 → 5

B) 1 → 2 → 3 → 4 → 5

C) 2 → 3 → 1 → 5 → 4

D) 3 → 1 → 4 → 2 → 5

Answers : C C A C B A C C D A

Lecture 6 - PCR

Q1. You are studying the levels of a specific mRNA in blood cells compared to brain cells. Using real-time PCR, you find that the minimum detectable fluorescence (threshold cycle, Ct) is reached after 10 cycles for RNA from blood cells and 13 cycles for RNA from brain cells. What is the relative concentration of the mRNA in blood cells compared to brain cells? *Book question* - explanation below

A. The mRNA concentration in blood cells is 2 times that in brain cells.
B. The mRNA concentration in blood cells is 4 times that in brain cells.
C. The mRNA concentration in blood cells is 8 times that in brain cells.
D. The mRNA concentration in blood cells is 16 times that in brain cells.

Q2. How do primers determine the region of DNA that is amplified in PCR? *Book question*

A. Primers bind randomly to the DNA, allowing the polymerase to amplify any region.
B. Primers bind specifically to complementary sequences flanking the target DNA, defining the start and end of the amplified region.
C. Primers attach to the RNA transcript, guiding the polymerase to the target DNA.
D. Primers degrade non-target DNA, leaving only the desired region for amplification.

Q3.In qPCR using SYBR Green, how is DNA detected?

A. SYBR Green binds to single-stranded DNA and fluoresces during denaturation.
B. SYBR Green binds to double-stranded DNA and fluoresces only when bound.
C. SYBR Green binds to RNA and fluoresces during annealing.
D. SYBR Green binds to primers and fluoresces during extension.

Q4 . A qPCR experiment is performed to quantify the expression of a specific mRNA in two tissues. The Ct value for Liver is 18, and for Heart, it is 21. What does this suggest about the mRNA levels?

A. The mRNA levels are higher in the Heart than in the Liver.
B. The mRNA levels are higher in the Liver than in the Heart.
C. The mRNA levels are equal in both tissues.
D. qPCR cannot determine mRNA levels.

Q5. What is the effect of setting the annealing temperature too low during PCR?

A. Primers bind nonspecifically, resulting in amplification of unwanted DNA sequences.
B. Primers fail to bind, leading to no amplification.
C. Only GC-rich regions are amplified.
D. Amplification occurs with high specificity.

Q6. How does TaqMan qPCR achieve multiplexing?

A. By using primers that bind to multiple targets
B. By increasing the number of cycles in the PCR reaction
C. By using SYBR Green to detect all targets simultaneously
D. By using different fluorescent dyes on each probe for different targets

Q7 .Why is TaqMan qPCR considered more reproducible than SYBR Green qPCR?

A. It uses lower annealing temperatures for improved efficiency.
B. It requires fewer reagents.
C. It specifically detects the target DNA via probes, reducing nonspecific signals.
D. It amplifies all double-stranded DNA in the sample.

Q8. What is the primary reason Taq polymerase is widely used in PCR?

A. It can withstand high denaturation temperatures without losing activity.
B. It synthesizes RNA more efficiently than other polymerases.
C. It has a built-in proofreading ability to ensure accuracy.
D. It binds directly to primers without requiring a template.

Q9.You perform PCR and observe multiple bands of different sizes on an agarose gel. What does this indicate?

A. Primer-dimer formation.
B. Successful amplification of the target sequence.
C. Nonspecific amplification due to poor primer design.
D. Complete degradation of the DNA template.

Q10 .During PCR, what is the purpose of the annealing step?

A. To separate the double-stranded DNA
B. To allow primers to bind to the complementary sequences on the template DNA
C. To synthesize new DNA strands
D. To degrade non-target DNA

Answers : C B B B A D C A C B

Explanation of Q1 : Each PCR cycle doubles the amount of amplified DNA.

- The difference in Ct values is **3 cycles** (13 - 10).
- $2^3 = 8$, so the mRNA concentration in blood cells is **8 times higher** than in brain cells.

Lecture 7 - DNA sequencing

Q1. Why do DNA sequencing reactions contain all four normal nucleotides as well as one dideoxynucleotide? *Book question*

A. To allow the synthesis of a complementary DNA strand without termination
B. To enable random incorporation of the dideoxynucleotide, causing chain termination at specific points
C. To distinguish between coding and non-coding regions of the DNA sequence
D. To amplify the DNA fragments during sequencing

Q2.What is the basic approach used in next-generation sequencing? ***Book question***

A. DNA is separated into single strands and sequenced directly without amplification.
B. DNA is fragmented, adapters are ligated, fragments are immobilized on a solid surface, amplified into clusters, and sequenced by synthesis using fluorescently labeled nucleotides.
C. Entire DNA is sequenced in one long read without fragmentation or labeling.
D. DNA fragments are sequenced by incorporating radioactive nucleotides and analyzed using autoradiography.

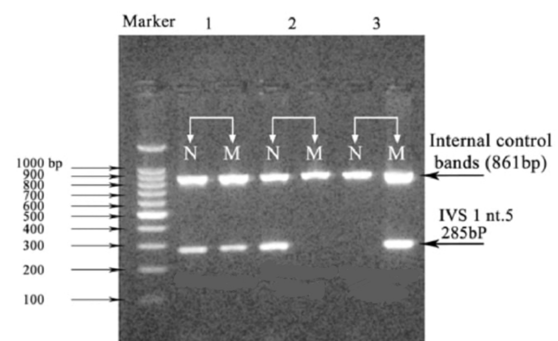
Q3. How is the DNA sequence read from the gel or electropherogram?

A. By matching the sequence with a standard DNA library
B. From bottom to top, starting with the smallest fragment
C. By reading the intensity of the fluorescent signals in no specific order
D. From top to bottom, starting with the largest fragment

Q4. Why does the incorporation of a dideoxynucleotide into a growing DNA strand terminate DNA synthesis?

A. It introduces a mutation in the DNA strand
B. It prevents the addition of more nucleotides by blocking the DNA polymerase active site
C. It lacks a 3′ hydroxyl group, preventing further nucleotide addition
D. It disrupts the base-pairing rules

Q5 . A patient sample was collected, and their genome underwent DNA sequencing followed by gel electrophoresis. What can be determined about Gene 2? (at 300 bp)



A. The patient is homozygous for this gene.
B. The patient is heterozygous for this gene.
C. The gene exhibits no structural variation in this patient.
D. The banding pattern indicates a potential technical artifact.

Answers : B B B C A

Lectures 8 , 9 & 10 - Transcription

Q1. What is the primary role of sigma (σ) factors in bacterial RNA synthesis? ***Book question***

A. Terminate transcription by recognizing stop codons
B. Assist in mRNA splicing during post-transcriptional modification
C. Facilitate the binding of RNA polymerase to specific promoter regions
D. Catalyze the synthesis of ribosomal RNA (rRNA)

Q2. You are studying a gene that is transcribed at a low level and find that it has the –10 promoter sequence TGTAGT instead of the consensus sequence at that position. How could you determine if this –10 sequence is responsible for the low-level transcription of your gene? ***Book question***

A. Delete the entire gene and observe if transcription stops.
B. Replace the –10 sequence with the consensus sequence and measure transcription levels.
C. Introduce a mutation in the coding region and measure changes in transcription.
D. Increase the number of sigma (σ) factors in the cell and observe if transcription increases.

Q3.How can different promoters drive transcription of different classes of genes in bacteria? Book question

A. Different promoters are recognized by specific sigma (σ) factors that bind RNA polymerase.
B. Promoters produce different types of RNA polymerase enzymes for each gene class.
C. Promoters signal the ribosome to begin transcription of specific genes.
D. Promoters encode transcription factors that modify gene sequences.

Q4. What is the molecular basis for the difference in hydrogen bonding between GC and AT base pairs that contributes to transcription termination in *E. coli*? ***Book question***

A. The higher number of hydrogen bonds in GC pairs destabilizes the hairpin structure, preventing termination.
B. AT base pairs, having fewer hydrogen bonds, cause the RNA-DNA hybrid to be less stable, promoting dissociation after hairpin formation.
C. GC base pairs destabilize the transcription complex by forming unstable RNA-DNA hybrids.
D. The hydrogen bonding pattern of AT pairs strengthens the interaction between RNA polymerase and the DNA template, promoting elongation.

Q5. Which of the following is true about DNA replication compared to transcription?

A. Both strands of DNA are used as templates in replication, while only one strand is used in transcription.
B. Only one strand of DNA is used as a template in replication, while both strands are used in transcription.
C. Replication involves the synthesis of RNA, while transcription involves the synthesis of DNA.
D. Both processes use both strands of DNA as templates.

Q6. Which of the following is a difference between RNA polymerase and DNA polymerase?

A. RNA polymerase requires a primer, while DNA polymerase does not.

B. RNA polymerase does not require a primer, while DNA polymerase does.

C. Both RNA and DNA polymerases require primers to initiate synthesis.

D. Neither RNA nor DNA polymerase requires a primer.

Q7. During RNA synthesis, how does the RNA molecule interact with the DNA template?

A. The entire RNA molecule remains permanently bonded to the DNA template.

B. The RNA molecule is temporarily bonded to the DNA template and separates as it elongates.

C. The RNA molecule never binds to the DNA template during transcription.

D. Only the 5′ end of RNA remains bonded to DNA throughout transcription.

Q8.Which of the following is the most likely advantage of organizing bacterial genes into polycistronic operons?

A. It allows independent regulation of each gene in the operon.

B. It prevents translation of unnecessary proteins in a metabolic pathway.

C. It ensures simultaneous and coordinated expression of genes involved in related functions.

D. It increases the transcription rate of individual genes in the operon.

Q9.What distinguishes the upstream region of a gene from the downstream region?

A. The upstream region refers to sequences following the transcription start site, while the downstream region refers to sequences before it.

B. The upstream region includes regulatory elements like the promoter, while the downstream region contains the gene's coding sequence.

C. The upstream region contains only introns, while the downstream region contains only exons.

D. The upstream region starts at the +1 site, while the downstream region starts at the -35 site.

Q10. How does the stem-loop structure destabilize the RNA polymerase during transcription termination?

A. It prevents RNA polymerase from forming phosphodiester bonds.

B. It disrupts the RNA-DNA hybrid and weakens RNA polymerase binding to the DNA template.

C. It modifies the sigma factor, preventing further elongation.

D. It attracts termination factors that degrade RNA polymerase.

Q11.Which multi-subunit factor is involved in DNA unwinding and transcription initiation in eukaryotes?

A. RNA polymerase II

B. TFIID

C. TFIIH

D. SWI/SNF complex

Q12. What would happen if cohesin is non-functional during transcription?

A. Enhancer-promoter interactions would be unstable, leading to reduced transcription efficiency.

B. RNA polymerase would fail to bind to the core promoter.

C. The Mediator complex would dissociate from the transcription machinery.

D. DNA would fail to loop, but transcription would remain unaffected.

Q13. What is the final output of Chromatin Immunoprecipitation (ChIP)?

A. A purified protein sample.

B. A list of all RNA transcripts.

C. The identification of specific DNA sequences bound by the protein of interest.

D. A fully assembled chromatin structure.

Q14. Why are introns transcribed if they do not encode proteins?

A. To stabilize the RNA during translation.

B. To act as templates for protein folding.

C. To regulate transcription rates.

D. To allow alternative splicing for generating multiple protein

Q15. What distinguishes the 5′ cap structure from the rest of the mRNA molecule?

A. It consists of ribose sugars instead of deoxyribose.

B. It contains a methylated guanosine connected by a 5′-to-5′ triphosphate bond.

C. It is a region of double-stranded RNA.

D. It is made of poly-A sequences that protect the mRNA.

Answers : C B A C A B B C B B C A C D B