Past papers

بسم الله الرحمن الرحيم

FINAL – Lecture #7-15

Molecular Biology

﴿ وَإِن تَتَوَلَّوْا يَسْتَبْدِلْ قَوْمًا غَيْرَكُمْ ثُمَّ لَا يَكُونُوا أَمْثَالَكُم ﴾

اللهم استعملنا ولا تستبدلنا

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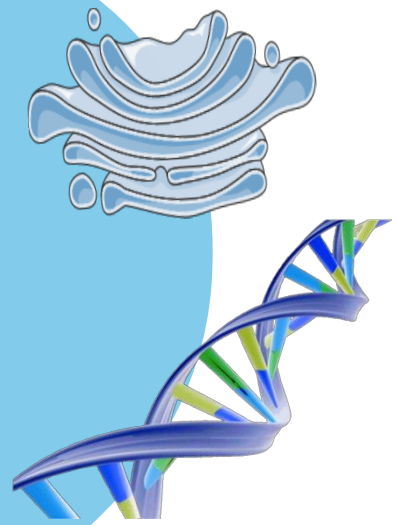


Past Papers for Lecture (7)

1) What statement is true about the C & H band in the following fluorescent DNA-sequencing SDS-PAGE print:

- a. There is a difference of 5 nucleotides between them
- b. One of them contains more disulfide bridges than the other
- c. They possess the same amount of negative charges
- d. Their 3’-terminal nucleotide is 2’,5’-dideoxyribonucleotide
- e. The gel must contain a reducing agent for them to be separated

- Answer:A

2) In fluorescent DNA sequencing, fluorescent labels are added to:

- a. Deoxyribonucleotides (dNTPs)
- b. Dideoxyribonucleotides (ddNTPs)
- c. Primers
- d. DNA polymerase
- e. Ribonucleotides (NTPs)

Answer:B

3) Choose the wrong statement about next-generation sequencing:

- a. We use unique adapters for different DNA fragments
- b. We use the same primer for all fragments
- c. We take advantage of the overlapping DNA fragments to combine them
- d. We use DNA polymerase in the process
- e. The terminal added nucleotide must be modified to add another one

Answer:A

4)Using fluorescent-based DNA sequencing, an insertion mutation in both alleles results in the following

- a. Insertion of a new peak and change of color of all subsequent peaks
- b. Insertion of a new peak and shift of all other peaks to the right
- c. Nothing happens
- d. The disappearance of a peak representing the site of insertion
- e. The presence of an overlapping peak representing the site of insertion

Answer: B

5)In next-generation sequencing, when the incorporated nucleotide is activated and lights up, the other unincorporated nucleotides do not light up because

- a. They are linked to the solid platform and cannot be activated
- b. They cannot be activated
- c. They light up but faintly
- d. They are removed after the addition of the right one
- e. They light up but at a different wavelength

Answer: D

6)the following is needed for next generation sequencing:

- A. DNA adapters
- B. Probes
- C. Taq polymerase
- D. Dideoxynucleotide
- E. Multiple pairs of gene-specific primers

Answer: A

7)The sequence of the original DNA strand is

ANSWER: 5’TACAGTTCCAAG 3’

8)your performed fluorescence based DNA sequencing of the coding region of the hormone gene in two plants; one has a functioning hormone and other does not. you found identical homology except for one position where the peak totally changed colors. This indicates:

- A. one heterozygous single point to mutation
- B. Polymorphism
- C. Bese insertion
- D. two homozygous single point mutation
- E. frameshift mutation due to the deletion

Answer: D

9)All of the following are advantages of using fluorescence-based sequencing over radioactivity-based sequencing except:

- A. It detects heterozygosity
- B. It is automated
- C. It is safe and cheap
- D. It is fast

Answer: A

10)Why we use DNA adapters in next generation sequencing?

- A. To anneal with primers
- B. To stabilize the DNA strands

Answer: A

11)What is the primary purpose of DNA sequencing?

- A) To determine the exact order of nucleotides in a DNA molecule
- B) To create DNA mutations
- C) To synthesize DNA enzymes
- D) To replicate viral genomes
- E) To modify gene expression

Answer: A

12)What method is typically used to determine the sequence of nucleotides in DNA sequencing?

- A) Restriction enzyme digestion
- B) Fluorescence-based detection
- C) Protein synthesis
- D) Lipid profiling
- E) Carbohydrate analysis

Answer: B

13)Which of the following is NOT true about next-generation sequencing?

- A) It involves fragmenting DNA into smaller pieces
- B) It uses fluorescently labeled nucleotides
- C) It is primarily used for protein synthesis
- D) It allows for the rapid sequencing of large amounts of DNA
- E) It can be used to sequence entire genomes quickly

Answer: C

14)In DNA sequencing, what is the role of a primer?

- A) It degrades the DNA strands
- B) It initiates DNA synthesis
- C) It enhances the fluorescence of nucleotides
- D) It prevents DNA replication
- E) It detects mutations

Answer: B

15)What does a 'dideoxynucleotide' accomplish in the context of DNA sequencing?

- A) It accelerates DNA polymerase action
- B) It acts as a regular substrate for DNA synthesis
- C) It terminates DNA synthesis
- D) It repairs DNA mutations
- E) It binds to the primer

Answer: C

16)Which technology uses a camera to detect the colors emitted by fluorescently labeled nucleotides during sequencing?

- A) Sanger sequencing
- B) Restriction fragment length polymorphism (RFLP)
- C) Next-generation sequencing
- D) Polymerase chain reaction (PCR)
- E) Southern blotting

Answer: C

17)What is true about next-generation sequencing compared to traditional methods?

- A) It is slower and more expensive
- B) It can only sequence small fragments of DNA
- C) It uses radioactivity to detect DNA sequences
- D) It allows simultaneous sequencing of multiple DNA fragments
- E) It requires larger DNA samples for sequencing

Answer: D

18)What is the function of fluorescent tags in DNA sequencing?

- A) To break the DNA strands into smaller pieces
- B) To enhance the action of DNA polymerase
- C) To visualize the incorporation of nucleotides
- D) To initiate the replication of DNA
- E) To act as a primer for DNA synthesis

Answer: C

19)In fluorescence-based DNA sequencing, what does the presence of different colors indicate?

- A) The type of nucleotide added
- B) The concentration of DNA polymerase
- C) The effectiveness of the primer
- D) The temperature of the reaction
- E) The speed of the gel electrophoresis

Answer: A

20)Which is NOT a component used in the preparation of a DNA sequencing reaction?

- A) Template DNA
- B) DNA polymerase
- C) RNA primers
- D) Dideoxynucleotides
- E) Deoxynucleotides

Answer: C

21)What does the termination of DNA chain elongation during sequencing depend on?

A) Addition of a deoxynucleotide
B) Addition of a dideoxynucleotide
C) Presence of a DNA primer
D) Activity of RNA polymerase
E) None of the above

Answer: B

22)In automated DNA sequencing, what role does the sensor play?

- A) It synthesizes new DNA strands
- B) It detects the fluorescent signals from labeled nucleotides
- C) It separates DNA fragments by size
- D) It replicates the DNA template
- E) It adds primers to the reaction

Answer: B

23)What advancement does next-generation sequencing offer over traditional methods?

- A) It requires radioactive labeling
- B) It uses only one type of fluorescent dye
- C) It can sequence multiple DNA fragments simultaneously
- D) It is less accurate than older methods
- E) It only sequences small DNA fragments

Answer: C

24)What does the size of a DNA fragment in gel electrophoresis indicate about its sequence?

- A) Longer fragments have more adenine bases
- B) Shorter fragments move faster through the gel
- C) Color of the fragment indicates its base sequence
- D) Each fragment size corresponds to a specific gene
- E) Fragment size shows the number of repeated sequences

Answer: B

25)How does the resolution of gel electrophoresis aid in DNA sequencing?

- A) It increases the speed of the reaction
- B) It allows separation of fragments differing by a single nucleotide
- C) It decreases the need for fluorescent tags
- D) It enhances the activity of DNA polymerase
- E) It reduces the cost of sequencing

Answer: B

26)What is the primary reason for using next-generation sequencing in research?

- A) To increase the use of radioactive materials
- B) To decrease the accuracy of gene identification
- C) To reduce the time and cost of sequencing
- D) To avoid using DNA polymerase
- E) To sequence only small DNA fragments

Answer: C

27)DNA sequencing refers to the:

- A) technique used to determine the sugar sequence and DNA
- B) technique used to determine the phosphate sequence in DNA molecule
- C) technique used to determine the base sequence in DNA molecule
- D) All of the above

Answer: C

28)In classic, old-fashioned, radioactive-based Sanger DNA sequencing, a substrate does not allow the addition of another deoxyribonucleotide because

a. It is a monophosphate
b. It is a ribonucleoside
c. It is missing a (-OH) group at carbon 2 of the sugar
d. It needs to be activated
e. It is missing a (-OH) group at carbon 3 of the sugar

Answer : E

Past Papers for Lectures (8-13)

Q1) Changing the position of this sequence from upstream of a gene to its downstream would not affect the expression of this gene:

- A. Enhancer
- B. Promoter
- C. A CpG island
- D. A transcription initiation site
- E. Promoter proximal element

Answer : A

Q2) Which of the following steps is NOT correct about producing mature RNA (mRNA)?

- A. Adding a cap to the 5’- untranslated region (5’-UTR) of the RNA
- B. Introns are removed from RNA
- C. A poly-A-tail is added to the 3’- end of the RNA
- D. Exons are joined together
- E. Binding of miRNA to the 3’-untranslated region of mRNA.

Answer : E

Q3) Although enhancers in human genes can change location and still be functional, this change of position is limited to a certain distances because of:

- A. the formation of topologically associating domains
- B. the presence of many other regulatory elements including enhancers
- C. the monocistronic nature of human genes
- D. the restrictive length of enhancers
- E. the number of proteins that can bind to enhancers and promoters

Answer :A

Q4) Which of the following sentences does best describe the core promoter?

- A. Region of DNA in front (downstream) of a structural gene mainly composed of proximal-elements
- B. Consensus sequences that bind activator proteins and enhance the transcription
- C. Region of DNA usually in front (upstream) of a gene that binds RNA polymerase and initiates gene expression
- D. A cluster of prokaryotic genes that are transcribed together
- E. Region of an mRNA between the 5’- end and the translation start site

Answer: C

Q5) during transcription and elongation of RNA in prokaryotic cells, the two strands are separated from each other by:

- A. DNA gyrase
- B. the RNA polymerase itself
- C. helicase
- D. the AT-rich regions of genes
- E. the sigma subunit

Answer : B

Q6) In eukaryotes, which of the following general transcription factors bind to the TATA box?

- A. TFIID
- B. TFIIE
- C. TFIIB
- D. TFIIF
- E. TFIIA

Answer :A

Q7) in eukaryotes, the pre-mRNA is

- A. the mRNA that is non-coding
- B. the mRNA that is ready for transcription
- C. the mRNA that is not poly-adenylated
- D. the mRNA that is not capped
- E. the mRNA that is not spliced

Answer :E

Q8) in eukaryotic genomes, promoter-proximal elements are NOT this

- A. they are binding sites of gene-specific transcriptional regulatory factors
- B. they can be located upstream of the core promoter
- C. they can either induce or suppress transcription
- D. they can change positions or be flipped and still be functional
- E. they are found in the promoters of genes that participate in similar end-points

Answer :D

Q9) the consensus sequence for the termination of transcription in prokaryotic cells functions in this manner

- A. it destabilizes the interaction of the RNA polymerase to the DNA
- B. it causes the RNA polymerase to stop until it dissociate spontaneously
- C. it attracts transcription termination proteins to the site
- D. it forces the RNA polymerase to move in the opposite direction
- E. it encodes an endonuclease-specific sequence

Answer :A

Q10) instead of a sigma subunit of the RNA polymerase in prokaryotic cells , eukaryotic cells have this

- A. an intrinsic activity of RNA polymerase
- B. a proof-reading mechanism
- C. enhancers
- D. regulatory transcriptional protein
- E. general transcription factors

Answer : E

Q11) In eukaryotes, which of the following molecules can tell you the sequence of introns and exons?

- A. Polypeptide
- B. Complementary DNA (cDNA)
- C. miRNA
- D. mRNA
- E. Pre-mRNA

Answer : E

Q12) In bacteria, which of the following RNA polymerase enzyme subunits is responsible for promoter recognition?

- A. The beta (β) subunit
- B. The epsilon (ε) subunit
- C. The delta (δ) subunit
- D. The sigma (σ) subunit
- E. The gamma (γ) subunit

Answer : D

Q13)All of the following are true regarding polyadenylation EXCEPT:

- A.Takes place in the nucleus.
- B.200-300 adenine residues are added to the 3’ end of the mRNA
- C.Carried out by RNA polymerase II.
- D. Is needed to stabilize the mRNA.
- E.Adenine nucleotides are added after the polyadenylation sequence AAUAAA.

Answer : C

Q14) Which of the following is not a function of the 5’ cap?

- A. Adenylates the 3’ end.
- B.Regulates nuclear export.
- C. Increases half-life of mRNA.
- D. Plays a role in translation.

Answer : A

Q15) Which of the following has a function similar to operons in eukaryotes?

- A. Enhancers
- B. Silencers
- C.PPE
- D. Promotors

Answer :C

Q16)Which f the following is correct?

- A. Enhancers can be located upstream or downstream of the gene.
- B. Enhancers can be located up to 50 kilo BP away from the gene.
- C. Mediators mediate the attachment of activators to the pre-initiation complex.
- D. All of the above are correct

Answer :D

Q17) Which of the following is correct?

- A. TFIIH has a kinase and a helicase-like function.
- B.TFIIB binds to the BRE element in promoters.
- C. There have to be 4 core components in EACH eukaryotic promoter region.
- D. TFIIE can attract TFIIH.
- E. More than one of the above are correct.

Answer : E

Q18) Which of the following correctly describes a core component of promoters in eukaryotes?

- A.TATA box at -10
- B. Initiator at -2 ~> -6
- C. Downstream promoter element at +16 ~> +20
- D.TFIIB recognition element at -37 ~> -32

Answer :D

Q19) On which side of the gene is the promoter located?

- A. 3’ side
- B. 5’ side
- C. It can be located on any side.

Answer : B

Q20). Which of the following is correct about alternative splicing?

- A. Alternative removal of introns
- B. Alternative connecting of exons
- C. Exons are moved and can be put before or after any exon D) All of the above are incorrect

Answer :B

Q21) hormone response elements are examples of

- A. insulators
- B. CpG island
- C. promoter-proximal elements
- D.core promoters
- E. enhancers

Answer :C

Q22) True about promoters in eukaryotes:

- A. Have promoter proximal elements downstream of the core promoter region
- B. Have a downstream and upstream promoter
- C. Have TATA box downstream of the initiator
- D. The promoter is always downstream
- E. RNA polymerase starts transcription from the -1 site

Answer :B

Q23) It has been found by researchers that enhancers are still functional even after flipping or changing location, this is due to:

- A. DNA looping
- B. Promoter proximal elements
- C. Mediator protein
- D. More than one of the above
- E. None of the above

Answer: A

Q24) True about polyadenylation:

- A. It is the addition of a methyl guanosine at the 5’ end of DNA
- B. Recruits proteins necessary for splicing
- C. Helps in the degradation of mRNA
- D. Helps in exporting RNA to the cytoplasm
- E. All of the above are true

Answer: D

Q25) What is a distinct advantage of mature human-mRNA compared to other types of RNA?

- a. It contains shine-dalgarno sequence
- b. It has a 3’-cap
- c. It has a poly-A tail
- d. It contains introns
- e. It contains the promoter region

Answer :C

Q26) What is the purpose of the poly-A tail in mRNA processing?

- A) To degrade the mRNA
- B) To assist in the attachment of the ribosome
- C) To protect mRNA from enzymatic degradation
- D) To signal the end of transcription

Answer: C

Q27) What does the TATA box represent in gene regulation?

- A) An enhancer element
- B) A silencer sequence
- C) A basal promoter region
- D) An exon
- E) None of the above

Answer: C

Q28) Which statement is TRUE about the regulatory regions of genes?

- A) They only include exons.
- B) They are only found in prokaryotes.
- C) They include elements like enhancers and silencers.
- D) They are not involved in transcriptional control.
- E) All statements are false.

Answer: C

Q29) What is the significance of the core promoter in gene expression?

- A) It is the site where RNA polymerase binds.
- B) It contains the repressor region of the promoter.
- C) It does not play a role in transcription initiation.
- D) It only contains enhancers and silencers.
- E) None of the above

Answer: A

Q30) Which statement correctly describes the role of enhancers in gene regulation?

- A) They decrease the transcription of adjacent genes.
- B) They bind directly to RNA polymerase.
- C) They enhance the transcription of genes by binding at distant sites.
- D) They are only active in prokaryotes.
- E) None of the above

Answer: C

Q31) gene amplification results in :

A) increasing number of chromosomes
B) initiation of gene expression
C) changing the ploidy nature of chromosomes (that is, haploid or diploid)
D) increasing protein level produced from the amplified gene
E) changing zygosity of genes (that is, homozygous and heterozygous)

Answer: D

Q32) Gene amplification is :

A) Increased quantity of DNA in a restricted region of a chromosome
B) Producing multiple copies of chromosomes
C) Not useful to cancer cells
D) None of the above
E) All of the above

Answer: A

Q33) What is the action of cyclic AMP (cAMP) on the lac operon?

A) It binds the RNA polymerase stabilizing its binding to the promoter.

B) It binds the repressor preventing its binding to the promoter.

C) It binds catabolite activating protein (CAP) stimulating its binding upstream of the promoter.

D) It binds to and activates beta galactosidase.

E) It binds to and stabilizes the polycistronic mRNA.

Answer: C

Q34) The following mutation would cause constitutive expression of the Lac operon :

A) Deletion of the promoter
B) Deletion of the lac *i* gene.
C) Inability of allolactose to bind to the lac repressor
D) Constant binding of catabolite-activating protein (CAP) upstream of the promoter
E) Constant binding of the RNA polymerase to the promoter

Answer: B

Option E (Constant binding of RNA polymerase) → NOT sufficient to cause constitutive expression because regulation by the repressor still exists.

Q35) It is necessary for the gene that codes for the repressor of lac operon to be near the structural genes :

A) False
B) True

Answer: A

Q36) As more and more lactose is metabolized what is expected to happen?

A) Decrease in transcription of the lac operon because of the increase of glucose.

B) Increase in transcription because of the increase of lactose.

C) Decrease in transcription because of the decrease of Allolactose.

D) NONE of the above

Answer: A

Q37) It is said that some promoters are "leaky" because :

A) the phenomenon is also called basal expression
B) interaction are based on reversible, non- covalent forces
C) they are mutated
D) repressors are not produced all the time
E) repressors are repressed themselves

Answer: B

Q38) One of the following is NOT a regulation by epigenetics :

A) Methylation of histones
B) A point mutation of the promoter regions
C) Methylation of cytosines within promoter regions
D) Binding of noncoding RNAs to promoters regions
E) Conversion of heterochromatin to euchromatin

Answer: B

Q39) In the presence of glucose, one the following is NOT NECESSARILY true in regards to the lac operon :

A) The enzyme adenylyl cyclase is not active
B) CAP is not bound to upstream of the promoter region
C) The lac repressor is always bound to the operator
D) cAMP levels are low
E) CAP cannot stimulate the RNA polymerase

Answer: C

Q40) how do transcriptional repressors with DNA-binding domains only function?

A) they chemically modify the bases within promoters
B) they modify the chromatin structure of promoters
C) they compete with activators in binding to promoters
D) they change the DNA sequence of promoters
E) they prevent enhancers-promoter interaction

Answer: C

Q41) what is the effect of a repressed mutation within the permease gene of the lac operon?

A) the lac operon is regulated normally
B) there will be high levels of cAMP in cells
C) the lac repressor will be mostly bound to the operator
D) the lac I gene will not be expressed
E) the lac operon will be turned on most of the time

Answer: C

Q42) A bacterial gene (gene A) ordinarily makes a protein that binds to DNA, a mutation of (gene A) decreases the expression of another gene, (gene B). We can conclude that :

A) gene A is a positive regulator of gene B.
B) gene A is a negative regulator of gene B.
C) gene B is a positive regulator of gene A.
D) gene B is a negative regulator of gene A.
E) genes A and B regulate one another.

Answer: A

Q43) Deacetylation of histones has which of the following effects?

A) Uncoiling of histone structure, preventing it from being accessed by transcriptional machinery.

B) Uncoiling of histone structure, allowing it to be accessed by transcriptional machinery.

C) Coiling of histone structure, preventing it from being accessed by transcriptional machinery.

D) Coiling of histone structure, allowing it to be accessed by transcriptionalMachinery.

Answer: C

Q44) the Xist gene on the X chromosome produces

A) a cytosine methyltransferase
B) a long non-coding RNA
C) a micro RNA
D) a gene repressor protein
E) a histone modifying

Answer: B

Q45) one of the following is NOT true regards to histone acetylation?

A) the interaction between DNA and histones become weaker
B) the extended "tail" of histones is the part that is acetylated
C) histone acetylation activates transcription
D) the amino acid lysine is the main target of the enzyme, histone acetyltransfrase
E) transcription factor II H (TFIIH) is responsible for histone acetylation

Answer: E

Q46) One of the following in NOT a cis-acting element :

A) Iron response element binding protein
B) GC-rich box (-35 sequence)
C) Enhancer
D) Shine-Dalgarno sequence
E) Iron-response element

Answer: A

Q47) A repressor has DNA binding domain and a repressing domain, a function special to it is :

A) Competing with the activator for binding to DNA
B) Stimulate transcription by interaction with general transcription factors
C) Prevent transcription by interacting with general transcription factors
D) Competing with the repressor for binding to DNA
E) Doesn't affect transcription

Answer: C

Q48) Not true about lncRNA produced by xist gene of chromosome X :

A) Leads to a phenomenon known as dosage compensation
B) Inactivates the same chromosome from which it was transcribed
C) Leads to formation of Barr body
D) Causes the activation of genes in the complementary chromosome
E) Only acts on the cis level

Answer: E

Q49) Not true about a possible function of an activation domain of transcription activation protein :

A) Modification of chromatin structure into euchromatin
B) Binding of H1
C) Modifying histone methylation
D) More than one of the above
E) None of the above

Answer: B

Past Papers for Lectures (14 & 15)

Q1) you performed in situ hybridization (ISH) and immunohistochemistry (IHC) for a steroid nuclear receptor such as the androgen receptor in the presence or absence of a steroid hormone. Where would expect STRONG cellular staining of RNA and proteins to be at?

A) + hormone; ISH: cytoplasmic; IHC: nuclear
B) no hormone; ISH: cytoplasmic; IHC: nuclear
C) no hormone; ISH: nuclear ;IHC: nuclear
D) + hormone; ISH: nuclear; IHC: cytoplasmic
E) with or without hormones; ISH: cytoplasmic; IHC: nuclear

Answer: A

Q2) the MAIN purpose of measuring the expression of a housekeeping gene in northern blotting is to :

A) confirm the cellular localization of RNA molecules
B) confirm the sizes of tested RNA molecules
C) ensure that probes are specific
D) ensure applying equal amounts of total RNA samples in a gel
E) confirm that cells have active transcriptional activities

Answer: D

Q3) In situ hybridization done on a tissue section reveals staining in one region, and immunohistochemistry reveals staining in another, This indicates:

A) A pre-mRNA exists in one region of the tissue, but it is modified somewhere else
B) A protein exists in one region of the tissue, but it is modified somewhere else
C) A gene is expressed in one region, but its protein product is localized somewhere else
D) A gene is expressed, but the protein is degraded
E) Both mRNA and protein are modified

Answer: C

Q4) The reason behind analyzing the expression of a housekeeping gene in Northern blotting is :

A) To ensure the expression of all genes is a sample
B) To measure the stability of mRNA in a sample
C) To ensure equal loading of total RNA of a sample
D) To estimate the length (size) of mRNA molecules
E) To determine the splicing of mRNA molecules

Answer: C

Q5) One of the following doesn't need nucleic acid probes :

A) Gel electrophoresis
B) Dot blotting
C) Southern blotting
D) Northern blotting
E) In situ hybridization

Answer: A

Q6) HindIII is a restriction endonuclease. Which of the following is most likely to be the recognition sequence for this enzyme?

A) AAGAAG

B) AAGAGA

C) AAGCTT

D) AAGGAA

E) AAGTTC

Answer: C

(Palindromic sequence)

Q7) The following is a sequence you expect NOT to be recognized by a restriction endonuclease :

A) CTTAAG
B) AGCT
C) GCAGCA
D) ATATAT
E) GGATCC

Answer: C

Q8) This particular advantage of plasmids makes them favorable vectors for the production of large amounts of a recombinant human protein in bacteria :

A) They carry antibiotic-resistance genes
B) The promoter they contain is human
C) They are small
D) They can be replicated in bacterial cells
E) They are bacterial in nature

Answer: D

Q9) It is difficult to use a restriction enzyme that cuts (shown as *) within one of these restriction sites for cloning purposes :

A) GCA*TGC
B) GCGCGCG*C
C) *AAAATTTT
D) AGC*T
E) C*GCG

Answer: A

Q10) You studied the promoter region of the gene Ahramerica using the luciferase reporter assay. Its length is 1000 bp (from-1000 to - 1 bp, upstream to downstream). You deleted portions of it gradually and measured gene expression compared to a positive control that has 100% expression and negative control of 5% expression. (Full promoter = 85%; from - 800 to -1 bp = 150% ; from -600 to -1bp = 67%; from -400 to -1 bp = 63%; from -200 to -1 = 80%; from -50 to - 1 = 20%;from -50 to -1. = 7%). **Based on the following results, This is NOT a correct interpretation:**

A) Region - 800 to -600 bp contains an activating region

B) Region -1000 to -800 bp contains a repressor region

C) Region -600 to -400 contains a repressor region

D) Region - 400 to -200 bp contains a repressor region

E) Region -200 to -50 bp contains an activating region

Answer: C

Q11) You have created both a genomic DNA library and a cDNA library from skin stem cells and from differentiated skin cells by fragmenting the DNA using the same restriction enzyme. What would you expect?

A) The cDNA libraries will be identical
B) A cDNA library cannot be created from differentiated cells
C) A genomic library cannot be created from stem cells
D) The genomic libraries will be identical
E) All libraries will be identical to each other

Answer: D

Q12) You want to study the regulatory sequence of the hormone gene including the promoter, promoter proximal element and silencer. you perform a reporter gene assay. one of the following is true:

A) you need to make cDNA from the hormone mRNA
B) you need the coding region of the hormone without introns
C) you need to use the Lac as a reporter gene
D) you need to create an expression vector that contains different regions of regulatory sequence
E) you need to create a recombinant hormone with luciferase

Answer: D

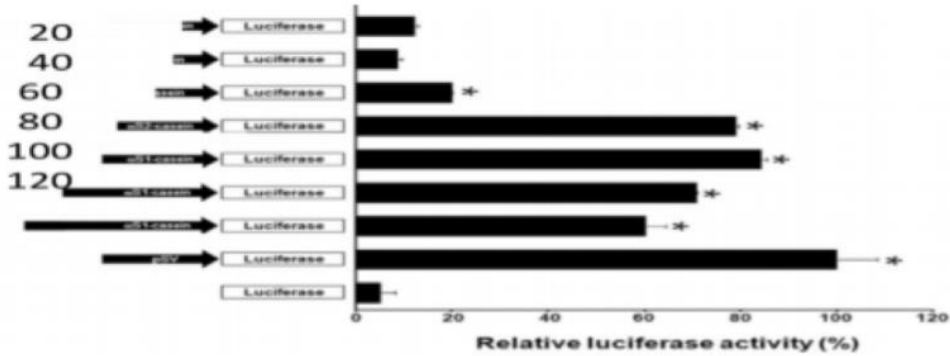
Q13) The luciferase reporter assay is used to :

A) Identify transcription start sites
B) Identify introns and exons within eukaryotic genes
C) Identify termination sequences of genes
D) Identify genes
E) Identify regulatory sequences within promoters

Answer: E

Q14) The promoter of a specific gene only is placed upstream of a "reporter gene"luciferase gene in a plasmid, the plasmid is transfected (inserted) into the cells ,and the expression level of luciferase is measured, what can you tell?

A) There is inhibitor region within 80 and 100.
B) There is repressor region within 100 and 120.
C) Gene is transcribed at best when there is no promoter.
D) Promoter does NOT affect the transcription.



Answer: B

Q15) The best technique to discover the expression of a novel gene is :

A) Protein tagging
B) DNA sequencing
C) DNA microarray
D) PCR
E) RNA sequencing

Answer: E

Q16) Using radioactive-based DNA microarray, comparative expression cannot be done on the same slide (the solid platform) because :

A) Radioactivity has a low level of detection
B) Radioactivity has no distinct color
C) There is a lower hybridization capability of glass slides
D) The amount of probes on the slide is very little to handle two samples
E) Using two labeled samples means high radioactivity and this is unhealthy

Answer: B

Q17) This technique allows you to identify the change of expression of hundreds to thousands of genes, known and unkown ones, with their alternatively spliced variants :

A) Real -time PCR of cDNA
B) Reporter gene assay
C) Next generation DNA sequencing
D) DNA microarray
E) RNA sequencing

Answer: E

Q18) This technique allows you to investigate the change of expression in several thousands of known genes, all at the same time, among plants that express the hormone versus those that do not?

A) Quantitative real-time PCR of cDNA
B) Reporter gene assay
C) DNA microarray
D) Yeast-two hybrid system
E) Quantitative PCR

Answer: C

Q19) Each spot in DNA microarray represents ;

A) A known DNA sequence
B) a protein with high affinity to a DNA sequence
C) A known RNA sequence
D) A heterogeneous population of DNA fragments
E) An unkown DNA fragment

Answer: A

Q20) you expressed the hormone in every plant cell, but the hormone does not function, You want to identify the gene that has a mutation, but their plant genome is composed of 5000 genes. you don't know what the gene is. you can perform this technique and compare the results to the database of the normal genome :

A) Quantitative PCR
B) real time PCR
C) RNA sequencing
D) next generation sequencing
E) fluorescent based sequencing

Answer: C

Q21) A patient has been diagnosed with a particular form of cancer. Appropriate treatment of this cancer, however, requires knowledge of which molecular markers are being expressed by the tumor as compared to normal cells of the same tissue. This is most easily accomplished by which of the following techniques?

A) Southern blotting
B) Southwestern blot
C) MicroRNA analysis
D) Microarray analysis
E) ELISAS

Answer: D

Q22) What is the primary purpose of DNA cloning?

A) To decrease DNA segments
B) To create genetically diverse populations
C) To amplify a DNA segment into many copies
D) To study DNA degradation

Answer: C

Q23) What is a clone in genetic terms?

A) A group of genetically different organisms
B) A group of organisms derived from multiple cells
C) A genetically identical population derived from a single cell
D) A synthetic DNA molecule

Answer: C

Q24) What are restriction endonucleases primarily used for in DNA cloning?

A) To degrade RNA molecules
B) To identify palindromic sequences in DNA
C) To cut DNA at specific recognition sites
D) To replicate DNA segments

Answer: C

Q25) What is recombinant DNA?

A) DNA replicated in a biological system
B) DNA consisting of sequences from different species
C) A single-stranded DNA
D) A visible phenotype in cloning

Answer: B

Q26) How do bacteria protect themselves against foreign DNA using restriction endonucleases?

A) By mutating their own DNA
B) By cleaving foreign DNA
C) By replicating foreign DNA
D) By attaching to plasma membranes

Answer: B

Q27) What role does a vector play in DNA cloning?

A) It degrades DNA fragments
B) It carries the DNA segment of interest into a host cell
C) It restricts the growth of bacteria
D) It identifies recombinant DNA

Answer: B

Q28) Which of the following is NOT a component necessary for a plasmid cloning vector?

A) Origin of replication
B) Selectable gene
C) Ribosomal binding site
D) Restriction site

Answer: C

Q29) What is the function of DNA ligase in the creation of recombinant DNA?

A) To cut DNA strands
B) To degrade unwanted DNA fragments
C) To join DNA fragments together
D) To replicate DNA

Answer: C

Q30) What is meant by 'sticky ends' in DNA cloning?

A) Fragments with no overhangs
B) DNA fragments with covalent bonds
C) Single-stranded overhangs at the end of DNA fragments
D) DNA fragments fully matched with their complementary base

Answer: C

Q31) What is a palindromic sequence in the context of DNA cloning?

A) A sequence that reads the same forward and backward

B) A sequence found only in bacterial DNA

C) A sequence that does not include base pairs

D) A sequence that cuts DNA into blunt ends

Answer: A

Q32) How is recombinant DNA introduced back into bacterial cells?

A) Through restriction endonucleases
B) Through a cloning vector
C) Through a transcription process
D) Through direct injection

Answer: B

Q33) What is the significance of the selectable gene in a plasmid cloning vector?

A) It cuts DNA at specific sites
B) It helps in identifying cells that have taken up the plasmid
C) It attaches the vector to the host DNA
D) It creates sticky ends on DNA fragments

Answer: B

Q34) What does the term 'expression vector' refer to?

A) A vector used only for DNA replication

B) A vector that allows for the production of proteins

C) A vector that does not integrate into the host genome

D) A vector that prevents the expression of certain genes

Answer: B

Q35) How do sticky ends facilitate the formation of recombinant DNA?

A) By allowing DNA fragments to be directly replicated
B) By preventing the action of DNA ligase
C) By enabling complementary DNA fragments to hybridize
D) By signaling the completion of DNA replication

Answer: C

Q36) What is the primary role of the origin of replication in a plasmid vector?

A) To initiate transcription
B) To signal the end of DNA replication
C) To initiate DNA replication
D) To mark the site for protein synthesis

Answer: C

Q37) What is the primary role of luciferase in the Luciferase reporter assay?

A) To generate light in response to gene expression
B) To silence the genes being studied
C) To act as a restriction enzyme
D) To directly interact with DNA
E) To replicate DNA

Answer: A

Q38) Which of these components is essential for a Luciferase reporter assay?

A) D-luciferin
B) Promoter sequence
C) Regulatory element
D) Luciferase enzyme
E) All of the above

Answer: E

Q39) In a Luciferase reporter assay, what indicates a successful transcription of the gene of interest?

A) Decrease in light production
B) No change in light production
C) Increase in light production
D) Change in the color of the cell
E) None of the above

Answer: C

Q40) What does the removal of a repressor region in a promoter likely cause in a Luciferase reporter assay?

A) Decreased expression of luciferase
B) Increased expression of luciferase
C) No change in expression
D) All of the above
E) None of the above

Answer: B

Q41) Why might a promoter with deleted regions lead to no expression of luciferase in a reporter assay?

A) The deletion included the core promoter necessary for RNA polymerase binding.

B) The enhancer elements were overexpressed.

C) The silencer regions were removed, causing uncontrolled expression.

D) All of the above

E) None of the above

Answer: A

Q42) What does the term "negative control" refer to in the context of a Luciferase reporter assay?

A) A scenario where a strong promoter is used to ensure maximum expression.

B) The use of a promoter that does not initiate transcription, resulting in minimal or no luciferase expression.

C) The highest level of luciferase expression observed in the assay.

D) A condition where the repressor region is removed.

E) None of the above

Answer: B

Q43) What is the first step in processing RNA for gene expression analysis?

A) Amplification of DNA
B) Conversion of mRNA to cDNA
C) Protein synthesis from mRNA
D) Extraction of proteins
E) Staining of cells

Answer: B

Q44) Which enzyme is used to convert mRNA into cDNA?

A) DNA polymerase
B) Lipase
C) Reverse transcriptase
D) Catalase
E) Helicase

Answer: C

Q45) In gene expression analysis, what role does a housekeeping gene play?

A) It varies greatly between samples
B) It is only expressed in diseased tissues
C) It is used as a control for normalization
D) It enhances the expression of target genes
E) It suppresses the expression of target genes

Answer: C

Q46) What does the presence of a housekeeping gene indicate in a qPCR experiment?

A) The sample was contaminated
B) The RNA was not properly extracted
C) The sample collection was done properly
D) The primers used were non-specific
E) The enzymes were inactive

Answer: C

Q47) Which method uses microarrays to analyze gene expression?

A) Northern blotting
B) In situ hybridization
C) Transcriptome profiling
D) Protein sequencing
E) Metabolite analysis

Answer: C

Q48) What is NOT true about DNA microarrays?

A) They can analyze thousands of genes simultaneously
B) They use radioactively labeled cDNA for detection
C) They only detect proteins
D) They provide data on gene expression patterns
E) They can compare gene expression in different samples

Answer: C

Q49) What does RNA-seq measure in gene expression analysis?

A) The size of DNA fragments
B) The abundance and variety of transcribed RNA
C) The activity of reverse transcriptase
D) The lipid composition of cells
E) The mineral content in DNA

Answer: B

Q50) What advantage does RNA-seq have over DNA microarrays?

A) It cannot detect novel RNA transcripts
B) It provides less precise data on gene expression
C) It only works with known DNA sequences
D) It identifies both known and unknown transcripts
E) It is less sensitive than microarrays

Answer: D

Q51) What is a primary benefit of RNA sequencing (RNA-seq) over traditional microarray techniques?

A) It requires a larger sample size.
B) It can only analyze known transcripts.
C) It is less sensitive to variations in transcript levels.
D) It can identify both known and novel RNA transcripts.
E) It uses radioactive labels for detection.

Answer: D

Q52) Which application does NOT use cDNA synthesized from mRNA?

A) Northern blotting.
B) Real-time PCR.
C) DNA microarray.
D) RNA sequencing.
E) Proteomic analysis.

Answer: E

Q53) What is the purpose of using housekeeping genes as controls in gene expression studies?

A) To measure the changes in DNA sequence.
B) To confirm the absence of RNA.
C) To standardize measurements against gene expression variations.
D) To enhance the fluorescence in microarray experiments.
E) To identify novel gene functions.

Answer: C

Q54) Which technique is capable of detecting single molecules of RNA in a sample?

A) Northern blotting.
B) In situ hybridization.
C) qPCR.
D) Standard PCR.
E) Gel electrophoresis.

Answer: C

Q55) What is the significance of using different fluorescent tags in comparative DNA microarray analysis?

A) To decrease the sensitivity of the assay.
B) To identify structural variations in DNA.
C) To differentiate between gene expressions in samples.
D) To increase the speed of hybridization.
E) To reduce the cost of the analysis.

Answer: C

Q56) What can you infer about the expression of a housekeeping gene from two samples (a normal cell and a diseased cell) if they both show the same Ct (cycle threshold) value in a qPCR experiment?

A) The gene is not expressed in either sample.
B) The gene is expressed at different levels in the two samples.
C) The gene is expressed at the same level in both samples.
D) The gene is only expressed in the normal cell.

Answer: C

Q57) During cloning, the antibiotic resistance gene in plasmids helps in :

A) Integrating a DNA fragment of interest into a genome
B) Multiply plasmid inside bacterial cells
C) Maintain plasmids in an acceptable size
D) Select the cells that contain a fragment of interest
E) Integrate plasmids inside a genome

Answer: D

Q58) Novel genes can be identified using :

A) Luciferase reporter assay
B) RNA sequencing
C) Cloning of genomic DNA
D) Quantitative PCR
E) PCR

Answer: B

Q59) Which statement about luciferase reporter assay is true?

A) Luciferase degrades the reporter protein over time
B) The light intensity represents natural (typical) luciferase gene activity
C) Luciferase activity directly represents gene expression levels
D) The light intensity represents promoter activity
E) Luciferase catalyzes the conversion of oxyluciferin to luciferin

Answer: D

Q60) What is the first step in the diagnostic procedure of detecting SARS CoV-2 virus from a patient sample?

A) Degrade viral RNA into fragments
B) Isolate viral genetic material from the patient's DNA
C) Use reverse transcriptase
D) Sequence amplified cDNA fragments

Answer: C

Q61) What does each spot on a DNA microarray contain?

A) Gene-specific primer
B) Gene-specific probe
C) Fluorescently-tagged cDNA
D) Amplified DNA sample
E) RNA-bound probes

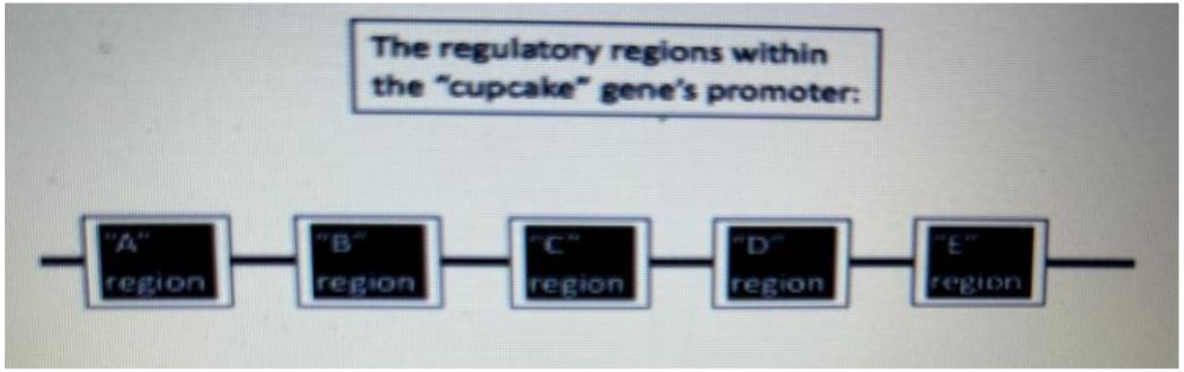
Answer: B

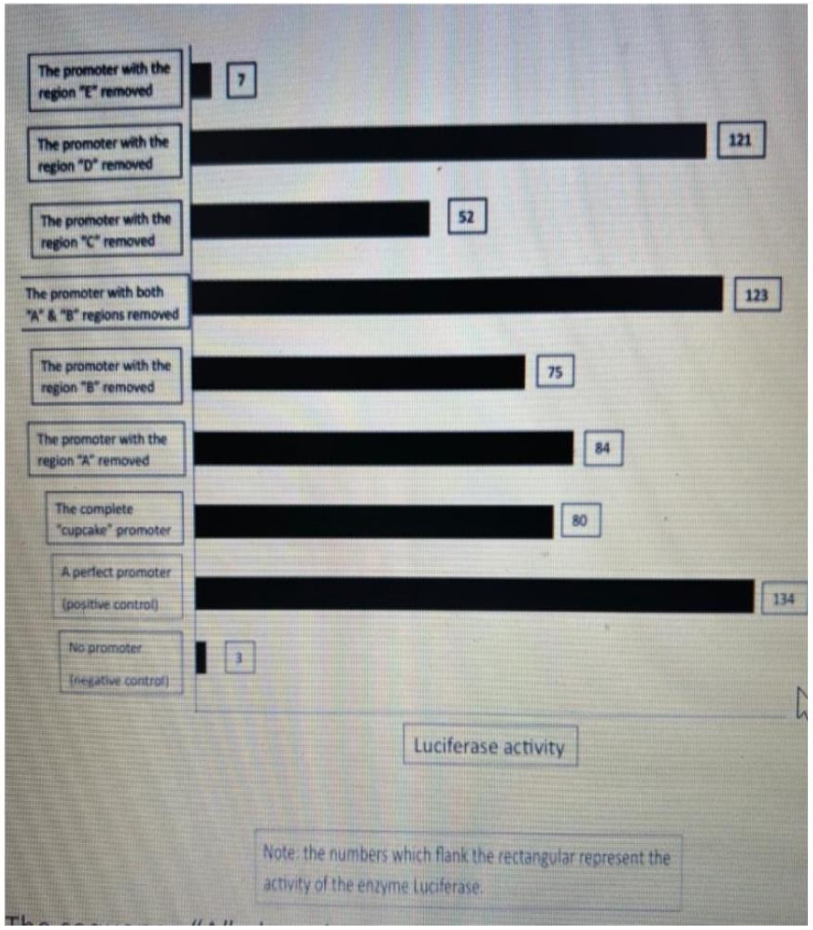
Q62) How do we know the quantity of sequenced RNA's?

A) By knowing the quantity of sequenced cDNA's
B) By knowing the quantity of the probes
C) By knowing the quantity of the primers
D) By knowing the quantity of the mRNA's

Answer: A

Q63) You have the following luciferase reporter assay of the gene "cupcake" which you want to study. Depending on the results in the assay, choose the statement which is most likely to be incorrect:





A) The sequence "E" is the core promoter

B) The sequence "C" is an enhancer

C) The sequences of "A" & "B" are both significant together

D) The sequence "A" alone is a repressor

E) The results of the assay are insufficient to decide

Answer: D

For any feedback, scan the code or click on

Corrections from previous versions:

Versions	Slide # and Place of Error	Before Correction	After Correction
V0 → V1			
V1 → V2			

Additional Resources:

رسالة من الفريق العلمي:

ولا تنسَ إخوتك المستضعفين في غزة من دعائك