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16 | GENE REGULATION

REVIEW QUESTIONS

1 Control of gene expression in eukaryotic cells occurs at which level(s)?

A Only the transcriptional level

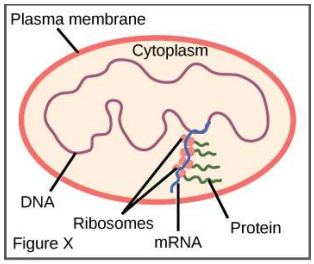
B Epigenetic and transcriptional levels

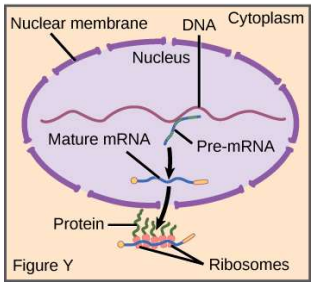
C Epigenetic, transcriptional, and translational levels

D Epigenetic, transcriptional, translational, and post-translational levels

Solution The solution is (D). Eukaryotes exhibit a tightly regulated mechanism of gene expression. Control of gene expression in eukaryotic cells occurs at the epigenetic, transcriptional, translational, and post-translational levels.

2 What do Figures X and Y in the figure illustrate?





A Transcription and translation in a eukaryotic cell (Figure X) and a prokaryotic cell (Figure Y)

B Transcription and translation in a prokaryotic cell (Figure X) and a eukaryotic cell (Figure Y)

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C Transcription in a eukaryotic cell (Figure X) and translation in a prokaryotic cell (Figure Y)

D Transcription in a prokaryotic cell (Figure X) and translation in a eukaryotic cell (Figure Y)

Solution The solution is (B). Figure X depicts coupled transcription and translation in prokaryotes. Eukaryotes show compartmentalization within their cells; therefore, transcription occurs inside the nucleus and translation occurs in the cytosol. Figure Y shows transcription and translation in eukaryotes.

3 If glucose is absent but lactose is present, the *lac* operon will be —

A activated

B repressed

C partially activated

D mutated

Solution The solution is (A). Lactose acts as an inducer of the *lac* operon. When glucose is present, catabolite repression occurs and the lactose operon is repressed.

4 What would happen if the operator sequence of the *lac* operon contained a mutation that prevented the repressor protein from binding the operator?

A In the presence of lactose, the *lac* operon will not be transcribed.

B In the absence of lactose, the *lac* operon will be transcribed.

C The cAMP-CAP complex will not increase RNA synthesis.

D The RNA polymerase will not bind the promoter.

Solution The solution is (B). If the repressor cannot bind to the operator, the *lac* operon will be transcribed when lactose is absent, since the RNA polymerase can bind to the promoter and initiate transcription.

5 What would happen if the operator sequence of the *trp* operon contained a mutation that prevented the repressor protein from binding to the operator?

A In the absence of tryptophan, the genes trpA–E will not be transcribed.

B In the absence of tryptophan, only genes trpE and trpD will be transcribed.

C In the presence of tryptophan, the genes trpA–E will be transcribed.

D In the presence of tryptophan, the trpE gene will not be transcribed.

Solution The solution is (C). If the operator sequence of the *trp* operon contained a mutation that prevented the repressor protein from binding to the operator, constitutive expression of the *trp* operon would occur regardless of the presence or absence of the tryptophan in the medium.

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6 What are epigenetic modifications?

- **A** Addition of reversible changes to histone proteins and DNA
- **B** Removal of nucleosomes from the DNA
- **C** Addition of more nucleosomes to the DNA
- **D** Mutation of the DNA sequence

Solution The solution is (A). Epigenetic modifications do not change the sequence of the DNA and only bring about reversible changes in histone, proteins, and DNA.

7 Which statement about epigenetic regulation is false?

- **A** Histone protein charge becomes more positive when acetyl groups are added.
- **B** DNA molecules are modified within CpG islands.
- **C** Methylation of DNA and histones causes nucleosomes to pack tightly together.
- **D** Histone acetylation results in the loose packing of nucleosomes.

Solution The solution is (A). Acetylation has the effect of changing the overall charge of the histone tail from neutral to negative. Acetylation disrupts the association between nucleosomes and DNA, leading to weaker binding of the nucleosomal components.

8 What is true of epigenetic changes?

- **A** They only allow gene expression.
- **B** They allow movement of histones.
- **C** They change the DNA sequence.
- **D** They are always heritable.

Solution The solution is (B). Epigenetic modifications result in the movement of histones to open or close a chromosomal region. Open chromosomal regions can be transcribed, while closed chromosomal regions cannot be transcribed.

9 The binding of what is required for transcription start?

- **A** A protein
- **B** DNA polymerase
- **C** RNA polymerase
- **D** A transcription factor

Solution The solution is (C). The binding of RNA polymerase is required for transcription initiation.

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10 What would be the outcome of a mutation that prevented DNA-binding proteins from being produced?

A Decreased transcription because transcription factors would not bind to transcription-binding sites

B Decreased transcription because enhancers would not be able to bind to transcription factors

C Increased transcription because repressors would not be able to bind to promoter regions

D Increased transcription because RNA polymerase would be able to increase binding to promoter regions

Solution The solution is (B). Enhancer regions are the binding sites for the transcription factors. When a DNA-binding protein binds to DNA, the shape of the DNA changes. This shape change allows activators bound to the enhancer regions to interact with transcription factors bound to the promoter region and the RNA polymerase.

11 What will result from the binding of a transcription factor to an enhancer region?

A Decreased transcription of an adjacent gene

B Increased transcription of a distant gene

C Alteration of the translation of an adjacent gene

D Initiation of the recruitment of RNA polymerase

Solution The solution is (B). Enhancers are the DNA sequences that influence the rate of transcription by up-regulating the gene expression.

12 What is involved in post-transcriptional control?

A Control of RNA splicing

B Ubiquitination

C Proteolytic cleavage

D Phosphorylation

Solution The solution is (A). Post-transcriptional control includes the control of RNA splicing after transcription.

13 Gene A is thought to be associated with color blindness. The protein corresponding to gene A is isolated. Analysis of the protein recovered shows there are actually two different proteins that differ in molecular weight that correspond to gene A.

What is one reason that two proteins may correspond to the gene?

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A One protein had a 5’ cap and a poly-A tail in its mRNA, and the other protein did not.

B One protein had a 5’ UTR and a 3’ UTR in its RNA, and the other protein did not.

C The gene was alternatively spliced.

D The gene produced mRNA molecules with differing stability.

Solution The solution is (C). The alternative splicing of any gene can lead to the formation of proteins varying in their molecular weights.

14 Binding of an RNA-binding protein will change the stability of the RNA molecule in what way?

A Increase

B Decrease

C Neither increase nor decrease

D Either increase or decrease

Solution The solution is (D). Binding of an RNA-binding protein (RBP) will either increase or decrease the stability of the RNA molecule depending on the specific RBP that binds.

15 A mutation in the 5’UTR that prevents any proteins from binding to the region will —

A increase or decrease the stability of the RNA molecule

B prevent translation of the RNA molecule

C prevent splicing of the RNA molecule

D increase or decrease the length of the poly-A tail

Solution The solution is (A). The binding of RBP’s to the 5’UTR can increase or decrease the stability of an RNA molecule, depending on the specific RBP that binds. Any mutation in the 5’UTR can increase or decrease the stability of the RNA molecule.

16 What can post-translational modifications of proteins affect?

A mRNA splicing

B 5’ capping

C 3’ polyadenylation

D Chemical modifications

Solution The solution is (D). Chemical modifications occur post-translationally and can affect protein function.

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17 A mutation is found in eIF-2, which impairs the initiation of translation. The mutation could affect all but one of the following functions of eIF-2.

Which function would NOT be affected?

A The mutation prevents eIF-2 from binding to RNA.

B The mutation prevents eIF-2 from being phosphorylated.

C The mutation prevents eIF-2 from binding to GTP.

D The mutation prevents eIF-2 from binding to the 40S ribosomal subunit.

Solution The solution is (B). When eIF-2 is wildtype, it does not usually undergo phosphorylation and translation occurs. Mutation can lead to phosphorylation of eIF-2. Phosphorylated eIF-2 undergoes a conformational change and cannot bind to GTP. Therefore, the initiation complex cannot form properly and translation cannot occur.

18 What does the addition of an ubiquitin group to a protein do?

A Increases the stability of the protein

B Decreases translation of the protein

C Increases translation of the protein

D Marks the protein for degradation

Solution The solution is (D). The addition of an ubiquitin group to a protein marks the protein for degradation.

19 What are cancer-causing genes called?

A Transformation genes

B Tumor suppressor genes

C Oncogenes

D Proto-oncogenes

Solution The solution is (C). Cancer-causing genes are called oncogenes.

20 Targeted therapies are used in patients with a certain gene expression pattern. A targeted therapy that prevents the activation of the estrogen receptor in breast cancer would be beneficial to what type of patient?

A Patients who express the EGFR receptor in normal cells

B Patients with a mutation that inactivates the estrogen receptor

C Patients with over-expression of ER alpha in their tumor cells

D Patients with over-expression of VEGF, which helps in tumor angiogenesis

Solution The solution is (C). A targeted therapy can prove to be beneficial for patients showing over-expression of estrogen receptors.

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21 In a new cancer treatment, a cold virus is genetically modified so that it binds to, enters, and is replicated in cells, causing them to burst. The modified cold virus cannot replicate when wildtype p53 protein is present in the cell.

How does this treatment treat cancer without harming healthy cells?

A The modified virus only infects and enters cancer cells.

B The modified virus replicates in normal and cancer cells.

C The modified virus only infects and enters normal cells.

D The modified virus replicates only in cancer cells.

Solution The solution is (D). The treatment can treat cancer when the modified virus replicates only in cancer cells.

22 A drug designed to switch silenced genes back on in cancer cells would result in what?

A Methylation of DNA and deacetylation of histones

B Methylation of DNA and acetylation of histones

C Deacetylation of DNA and methylation of histones

D Acetylation of DNA and demethylation of histones

Solution The solution is (A). Preventing methylation of DNA and acetylation of histones can switch on the silenced genes.

23 What are positive cell-cycle regulators that can cause cancer when mutated called?

A Transformation genes

B Tumor suppressor genes

C Oncogenes

D Mutated genes

Solution The solution is (C). Positive cell-cycle regulators that can cause cancer when mutated are called oncogenes.

CRITICAL THINKING QUESTIONS

24 What best distinguishes prokaryotic and eukaryotic cells?

A Prokaryotes possess a nucleus whereas eukaryotes do not, but eukaryotes show greater compartmentalization that allows for greater regulation of gene expression.

B Eukaryotic cells contain a nucleus whereas prokaryotes do not, and eukaryotes show greater compartmentalization that allows for greater regulation of gene expression.

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C Prokaryotic cells are less complex and perform highly regulated gene expression, whereas eukaryotes perform less-regulated gene expression.

D Eukaryotic cells are more complex and perform less-regulated gene expression, whereas prokaryotic cells perform highly regulated gene expression.

Solution The solution is (B). Eukaryotic cells contain a nucleus whereas prokaryotes do not, allowing greater regulation of gene expression in eukaryotes.

25 Which statement is correct regarding the distinction between prokaryotic and eukaryotic gene expression?

A Prokaryotes regulate gene expression at the level of transcription, whereas eukaryotes regulate at multiple levels including epigenetic, transcriptional, and translational.

B Prokaryotes regulate gene expression at the level of translation, whereas eukaryotes regulate at the level of transcription to manipulate protein levels.

C Prokaryotes regulate gene expression with the help of repressors and activators, whereas eukaryotes regulate expression by degrading mRNA transcripts, thereby controlling protein levels.

D Prokaryotes control protein levels using epigenetic modifications, whereas eukaryotes control protein levels by regulating the rate of transcription and translation.

Solution The solution is (A). Because prokaryotes perform transcription and translation at the same time, they regulate gene expression at the transcription level whereas eukaryotes regulate gene expression at multiple levels.

26 All the cells of one organisms share the genome. However, during development, some cells develop into skin cells while others develop into muscle cells. How can the same genetic instructions result in two different cell types in the same organism? Thoroughly explain your answer.

Solution Different genetic programs are turned on or off when cells differentiate into different cell types (e.g. skin cells, muscle cells, etc.) As a result, cells express genes needed for the tissue in which they are located.

27 Which statement describes prokaryotic transcription of the *lac* operon?

A When lactose and glucose are present in the medium, transcription of the *lac* operon is induced.

B When lactose is present but glucose is absent, the *lac* operon is repressed.

C Lactose acts as an inducer of the *lac* operon when glucose is absent.

D Lactose acts as an inducer of the *lac* operon when glucose is present.

Solution The solution is (C). Environmental stimuli can increase or induce transcription in prokaryotic cells. In this example, lactose in the environment will induce the

transcription of the *lac* operon, but only if glucose is not available in the environment.

28 The *lac* operon consists of regulatory regions such as the promoter as well as the structural genes lacZ, lacY, and lacA, which code for proteins involved in lactose metabolism. What would be the outcome of a mutation in one of the structural genes of the *lac* operon?

A Mutation in structural genes will stop transcription.

B Mutated lacY will produce an abnormal β galactosidase protein.

C Mutated lacA will produce a protein that will transfer an acetyl group to β galactosidase.

D Transcription will continue but lactose will not be metabolized properly.

Solution The solution is (D). A mutation in one of the structural genes of the *lac* operon will not prevent transcription of the operon. However, depending on the type of mutation in the gene, an abnormal protein may be produced, which could prevent metabolism of lactose.

29 In some diseases, alteration to epigenetic modifications turns off genes that are normally expressed. Hypothetically, how could you reverse this process to turn these genes back on?

Solution Sample answer: To turn these genes back on, you would have to reverse the epigenetic modifications. For example, if the genes are turned off due to methylation, removing the methyl groups should turn the genes back on.

30 Flowering Locus C (FLC) is a gene that is responsible for flowering in certain plants. FLC is expressed in new seedlings, which prevents flowering. Upon exposure to cold temperatures, FLC expression decreases and the plant flowers. FLC is regulated through epigenetic modifications.

What type of epigenetic modifications is present in new seedlings and after cold exposure?

A In new seedlings, histone acetylations are present; upon cold exposure, methylation occurs.

B In new seedlings, histone deacetylations are present; upon cold exposure, methylation occurs.

C In new seedlings, histone methylations are present; upon cold exposure, acetylation occurs.

D In new seedlings, histone methylations are present; upon cold exposure, deacetylation occurs.

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Solution The solution is (A). Methylation of DNA causes nucleosomes to pack tightly together. Transcription factors cannot bind the DNA, and genes are not expressed. Histone acetylation results in loose packing of nucleosomes. Transcription factors can bind the DNA, and genes are expressed. Since the FLC gene is expressed in new seedlings, the corresponding DNA likely has histone acetylation. Since gene expression of the FLC gene decreases upon cold exposure, the corresponding DNA is likely methylated in response to cold temperatures.

31 A mutation within the promoter region can alter gene transcription. How can this happen?

A Mutated promoters decrease the rate of transcription by altering the binding site for the transcription factor.

B Mutated promoters increase the rate of transcription by altering the binding site for the transcription factor.

C Mutated promoters alter the binding site for transcription factors to increase or decrease the rate of transcription.

D Mutated promoters alter the binding site for transcription factors and thereby cease transcription of the adjacent gene.

Solution The solution is (C). A mutation in the promoter region can change the binding site for a transcription factor that normally binds to increase transcription. The mutation could either decrease the ability of the transcription factor to bind, thereby decreasing transcription, or it can increase the ability of the transcription factor to bind, thus increasing transcription.

32 What could happen if a cell had too much of an activating transcription factor present?

A The transcription rate would increase, altering cell function.

B The transcription rate would decrease, inhibiting cell functions.

C The transcription rate decreases due to clogging of the transcription factors.

D The transcription rate increases due to clogging of the transcription factors.

Solution The solution is (A). If too much of an activating transcription factor were present, then transcription would be increased in the cell. This could lead to dramatic alterations in cell function.

33 The *wnt* transcription pathway is responsible for key changes during animal development. The transcription pathway shown in the figure uses arrows to represent activation and perpendicular symbols to represent repression of *wnt* gene products.

Based on the pathway, how would blocking *wnt* gene expression affect the production of Bar-1?

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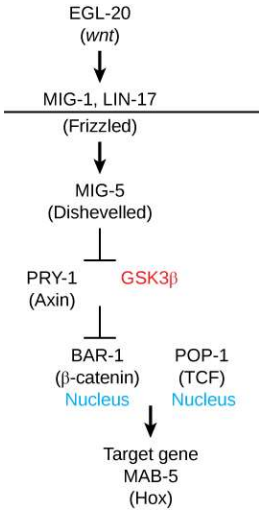

Solution Sample answer: Bar-1 production would decrease. If *wnt* production is blocked, then MIG-1, LIN-17 are not produced, which results in MIG-5 not being produced either. When MIG-5 is not produced, PRY-1 is produced because there is no inhibition from MIG-5. Once PRY-1 is produced, it will repress BAR-1 production.

34 How can RBPs prevent miRNAs from degrading an RNA molecule?

A RBPs can bind first to the RNA, thus preventing the binding of miRNA, which degrades RNA.

B RBPs bind the miRNA, thereby protecting the mRNA from degradation.

C RBPs methylate miRNA to inhibit its function and thus stop mRNA degradation.

D RBPs direct miRNA degradation with the help of a DICER protein complex.

Solution The solution is (A). RNA-binding proteins (RBP) bind to the RNA and can either increase or decrease the stability of the RNA. If they increase the stability of the RNA molecule, the RNA will remain intact in the cell for a longer period of time than normal. Since both RBPs and miRNAs bind to the RNA molecule, RBP can potentially bind first to the RNA and prevent the binding of the miRNA that will degrade it.

35 How can external stimuli alter post-transcriptional control of gene expression?

A UV rays can alter methylation and acetylation of proteins.

B RNA-binding proteins are modified through phosphorylation.

C External stimuli can cause deacetylation and demethylation of the transcript.

D UV rays can cause dimerization of the RNA-binding proteins.

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Solution The solution is (B). External stimuli can modify RNA-binding proteins (i.e., through phosphorylation of proteins) to alter their activity.

36 Protein modifications can alter gene expression in many ways. How can phosphorylation of proteins alter gene expression?

A Phosphorylation of proteins can alter translation, RNA shuttling, RNA stability, or post-transcriptional modification.

B Phosphorylation of proteins can alter DNA replication, cell division, pathogen recognition, and RNA stability.

C Phosphorylated proteins affect only translation and can cause cancer by altering the p53 function.

D Phosphorylated proteins affect only RNA shuttling, RNA stability, and post-translational modifications.

Solution The solution is (A). Because proteins are involved in every stage of gene regulation, phosphorylation of a protein (depending on the protein that is modified) can alter accessibility to the chromosome; can alter translation (by altering the transcription factor binding or function); can change nuclear shuttling (by influencing modifications to the nuclear pore complex); can alter RNA stability (by binding or not binding to the RNA to regulate its stability); can modify translation (increase or decrease); or can change post-translational modifications (add or remove phosphates or other chemical modifications).

37 Changes in epigenetic modifications alter the accessibility and transcription of DNA. How could environmental stimuli, such as ultraviolet light exposure, modify gene expression?

A UV rays could cause methylation and deacetylation of the genes that could alter the accessibility and transcription of DNA.

B UV rays could cause phosphorylation and acetylation of the DNA and histones, which could alter the transcriptional capabilities of the DNA.

C UV rays could cause methylation and phosphorylation of the DNA bases, which could become dimerized, rendering no accessibility of DNA.

D UV rays can cause methylation and acetylation of histones, making the DNA more tightly packed and leading to inaccessibility.

Solution The solution is (A). Environmental stimuli, such as ultraviolet light exposure, can alter the modifications to the histone proteins or DNA. Such stimuli may change an actively transcribed gene into a silenced gene by removing acetyl groups from histone proteins or by adding methyl groups to DNA.

38 New drugs are being developed that decrease DNA methylation and prevent the removal of acetyl groups from histone proteins. How could these drugs affect gene expression to help kill tumor cells?

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A These drugs maintain the demethylated and the acetylated forms of the DNA to keep transcription of necessary genes on.

B The demethylated and the acetylated forms of the DNA are reversed when the silenced gene is expressed.

C The drug methylates and acetylates the silenced genes to turn them back on.

D Drugs maintain DNA methylation and acetylation to silence unimportant genes in cancer cells.

Solution The solution is (A). These drugs will keep the histone proteins and the DNA methylation patterns in the open chromosomal configuration so that transcription is feasible. If a gene is silenced, these drugs could reverse the epigenetic configuration to re-express the gene.

39 How can understanding the gene expression pattern in a cancer cell tell you something about that specific form of cancer?

A Understanding gene expression patterns in cancer cells will identify the faulty genes, which is helpful in providing the relevant drug treatment.

B Understanding gene expression will help diagnose tumor cells for antigen therapy.

C Gene profiling would identify the target genes of the cancer-causing pathogens.

D Breast cancer patients who do not express EGFR can respond to anti-EGFR therapy.

Solution The solution is (A). Understanding which genes are expressed in a cancer cell can help diagnose the specific form of cancer. It also can help identify treatment options for that patient. For example, if a breast cancer tumor expresses EGFR in high numbers, it might respond to specific anti-EGFR therapy. If that receptor is not expressed, it would not respond to that therapy.

40 What is personalized medicine? How can it be used to treat cancer?

A Personalized medicines would vary based on the type of mutations and the gene's expression pattern.

B The medicines are given based on the type of tumor found in an individual's body.

C The personalized medicines are provided based only on the symptoms of the patient.

D The medicines tend to vary depending on the severity and the stage of the cancer.

Solution The solution is (A). The design of drugs on the basis of gene expression patterns within individual tumors is the basis of personalized medicine. With an increased understanding of gene regulation and gene function, medicines can be designed specifically to target diseased cells without harming healthy cells. Cancer is a heterogeneous disease with many different mutations and gene-signaling pathways, leading to the development and progression of the disease. By identifying the gene expression patterns in individuals and within individual tumors, treatments can be

developed and prescribed to target only those genes and pathways that are abnormal.

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41 What is found in both prokaryotes and eukaryotes?

A 3’ poly-A tails

B 5’ caps

C Promoters

D Introns

Solution The solution is (C). In prokaryotic as well as in eukaryotic genes, regulation of transcription takes place with the help of promoters.

42 The enzyme polyadenylate polymerase catalyzes the addition of adenosine monophosphate to the 3’ ends of mRNAs to form a poly-A tail. If the enzyme were blocked so that it could not function, the result would be —

A increased mRNA stability in eukaryotes and decreased mRNA stability in prokaryotes

B decreased mRNA stability in eukaryotes and no effect in prokaryotes

C no effect in eukaryotes and increased mRNA stability in prokaryotes

D no effect in eukaryotes and decreased mRNA stability in prokaryotes

Solution The solution is (B). In eukaryotes, poly-A tails provide mRNA with stability and protection against random endonucleases. In prokaryotes, this modification is absent.

43 What are two ways in which gene regulation differs and two ways in which it is similar in prokaryotes and eukaryotes?

A Prokaryotes show co-transcriptional translation, whereas eukaryotes perform transcription prior to translation; in both cell types, regulation occurs through the binding of transcription factors, activators, and repressors.

B Prokaryotes perform transcription prior to translation, whereas eukaryotes show co-transcriptional translation—that is, the processes occur in the same organelle.

C Prokaryotes show co-transcriptional translation that is regulated prior to translation, whereas eukaryotes perform transcription prior to translation that is regulated only at the level of transcription. In both domains, transcription factors, activators, and repressors provide regulation.

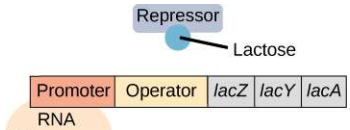
D Prokaryotes show cotranscriptional translation that occurs in the nucleus whereas eukaryotes show transcription prior to translation. In both cell types, regulation occurs using transcription factors, activators, and repressors.

Solution The solution is (A). In prokaryotes, RNA transcription and protein formation occur almost simultaneously. In eukaryotes, RNA transcription occurs prior to protein formation and takes place in the nucleus. Translation of RNA to protein occurs in the cytoplasm. In prokaryotes, gene expression is regulated primarily at the transcriptional level, for example through operons. In eukaryotes, gene expression is regulated at many levels (epigenetic, transcriptional, post-transcriptional, translational, and post-translational). In both prokaryotes and eukaryotes, gene expression can be regulated through transcription-factor binding of promoters. In both prokaryotes and eukaryotes, repressors can suppress transcription and activators can increase transcription in response to external stimuli.

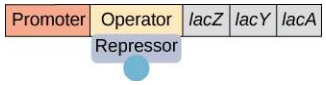
44 Lactose digestion in *E. coli* begins with its hydrolysis by the enzyme galactosidase. The gene encoding β-galactosidase, lacZ, is part of a coordinately regulated operon containing other genes required for lactose utilization.

Which figure correctly depicts the interactions at the lac operon when lactose is NOT being utilized?

A



B



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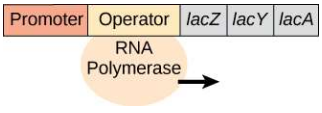

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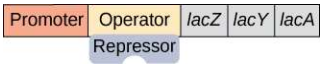

Solution The solution is (D). The correct configuration when lactose is not being utilized is RNA polymerase on promoter and repressor protein bound to lactose, not bound to DNA.

45 What would be the result of a mutation in the repressor protein that prevented it from binding lactose?

A The repressor will bind to lactose when it is removed from the operator.

B The repressor will bind the operator in the presence of lactose.

C The repressor will not bind the operator in the presence of lactose.

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D The repressor will not bind the operator in the absence of lactose.

Solution The solution is (B). The active repressor normally binds to lactose if it is present. If the repressor is mutated, then it will not be able to bind with lactose and will, in turn, bind to the operator site and suppress the operon and RNA synthesis.

46 What type of modification might be observed in the GR gene in all newborn rats?

A The DNA will have many methyl molecules.

B The DNA will have many acetyl molecules.

C The DNA will have few methyl groups.

D The histones will have many acetyl groups.

Solution The solution is (A). DNA, when methylated at many locations, suppresses the expression of the gene. Therefore, the GR genes would not be expressed in the newborn rats.

47 What type of modification will be observed in the GR gene in the highly nurtured rats?

A The DNA will have many methyl molecules.

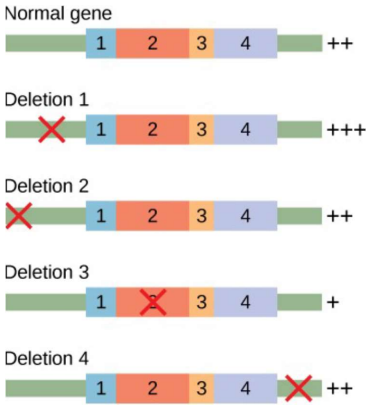
B The DNA will have many acetyl molecules.

C The DNA will have few methyl groups.

D The histones will have few acetyl groups.

Solution The solution is (C). The highly nurtured pups will show a greater amount of GR gene expression, thereby showing very few methylated molecules in the DNA. The low methylation would be responsible for the higher expression of the GR gene.

48 The level of transcription of a gene is tested by creating deletions in the gene as shown in the illustration. These modified genes are tested for their level of transcription: (++) normal transcription levels; (+) low transcription levels; (+++) high transcription levels.



Which deletion is in an enhancer involved in regulating the gene?

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A Deletion 1

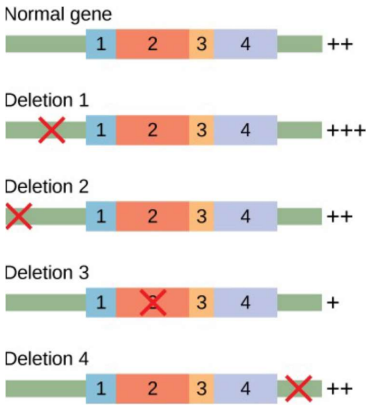
B Deletion 2

C Deletion 3

D Deletion 4

Solution The solution is (C). Deletion 3 is an enhancer involving in regulating the gene. There are deletions in the gene sequence in Deletion 3 which reduces the transcription level.

49 In the figure, which deletion is in a repressor involved in regulating the gene?



A Deletion 1

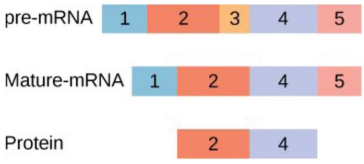
B Deletion 2

C Deletion 3

D Deletion 4

Solution The solution is (A). Deletion 1 is in a repressor, as there is a sudden increase in the level of transcripts when it is induced. If it were not a repressor, then the level of transcript would be lower, proving that is it a repressor.

50 The diagram shows different regions (1–5) of a pre-mRNA molecule, a mature-mRNA molecule, and the protein corresponding to the mRNA.



A mutation in which region is most likely to be damaging to the cell?

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A Region 1

B Region 2

C Region 3

D Region 5

Solution The solution is (B). Region 2 seems to be encoding a gene. Any mutation in this region would likely produce a nonfunctional protein, damaging the cell.

51 What do regions 1 and 5 correspond to?

A Exons

B Introns

C Promoters

D Untranslated regions

Solution The solution is (D). The untranslated regions are useful for post-transcriptional regulation. The 5'UTR (leader sequence) contains the ribosome-complex binding site and 3'UTR (trailer sequence) contains binding sites for regulatory proteins.

52 What are regions 1 through 5 in the diagram?

A Regions 1, 3, and 5 are exons; regions 2 and 4 are introns.

B Regions 2 and 4 are exons; regions 1, 3, and 5 are introns.

C Regions 1 and 5 are exons; regions 2, 3, and 4 are introns.

D Regions 2, 3, and 4 are exons; regions 1 and 5 are introns.

Solution The solution is (A). Regions 1, 3, and 5 are the exons. These are the DNA regions encoding a useful gene. In between every exon, larger introns are present, corresponding to regions 2 and 4 in the diagram.

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53 A mutation results in the formation of the mutated mature-mRNA as indicated in the diagram. What type of mutation occurred, and what is the likely outcome of the mutation?

A Mutation in the GU-AG sites of introns produced a nonfunctional protein.

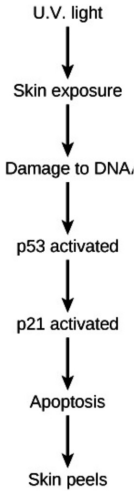
B A transversion mutation in the introns led to alternative splicing, producing a functional protein.

C A transversion mutation in the GU-AG site mutated this mRNA, producing a nonfunctional protein.

D Transition mutations in the introns could produce a functional protein.

Solution The solution is (A). The mutation caused a failure in recognition of the intron 2 end and instead appears to have recognized the end of the next intron (intron 4). This caused excision of introns 2, 3, and 4. The most likely outcome of this mutation is a truncated protein that will be nonfunctional.

54 The diagram illustrates the role of p53 in response to UV exposure. What would be the result of a mutation in the p53 gene that inactivates it?



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A Skin will peel in response to UV exposure.

B Apoptosis will occur in response to UV exposure.

C No DNA damage will occur in response to UV exposure.

D No peeling of skin will occur in response to UV exposure.

Solution The solution is (D). Mutation in p53 would restrict its function, causing no activation of p21 and also no apoptosis, leading to no peeling of the skin.

55 What will NOT occur in response to UV exposure if a p53 mutation inactivates the p53 protein?

A Damage to DNA, p53 activation, and p21 activation

B p21 activation and apoptosis

C p21 activation

D p53 activation, p21 activation, and apoptosis

Solution The solution is (C). If p53 inactivates due to a mutation, then p21 will get inactivated too. As a result, apoptosis will not take place.

56 What happens when tryptophan is present?

A The repressor binds to the operator, and RNA synthesis is blocked.

B RNA polymerase binds to the operator, and RNA synthesis is blocked.

C Tryptophan binds to the repressor, and RNA synthesis proceeds.

D Tryptophan binds to RNA polymerase, and RNA synthesis proceeds.

Solution The solution is (A). In the *trp* operon, the tryptophan binds to the inactive apo-repressor and makes it active. This active repressor would bind to the operator site, blocking RNA synthesis.

57 What happens in the absence of tryptophan?

A RNA polymerase binds to the repressor.

B The repressor binds to the promoter.

C The repressor dissociates from the operator.

D RNA polymerase dissociates from the promoter.

Solution The solution is (C). The absence of tryptophan would inactivate the repressor, dissociating it from the operator. This apo-repressor now remains in the cell in an inactive form, allowing the operon to synthesize RNA.

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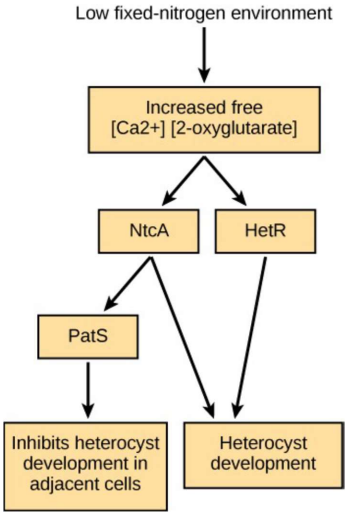
58 *Anabaena* is a simple multicellular photosynthetic cyanobacterium. In the absence of fixed nitrogen, certain newly developing cells along a filament express genes that code for nitrogen-fixing enzymes and become non-photosynthetic heterocysts. The specialization is advantageous because some nitrogen-fixing enzymes function best in the absence of oxygen. Heterocysts do not carry out photosynthesis, but instead provide adjacent cells with fixed nitrogen and receive fixed carbon and reduced energy carriers in return. As shown in the diagram, when there is low fixed nitrogen in the environment, an increase in the concentration of free calcium ions and 2-oxyglutarate stimulates the expression of genes that produce two transcription factors (NtcA and HetR) that promote the expression of genes responsible for heterocyst development. HetR also causes production of a signal, PatS, that prevents adjacent cells from developing as heterocysts.



Based on your understanding of the ways in which signal transmission mediates cell function, which prediction is most consistent with the information given?

A In an environment with low fixed nitrogen, treating the *Anabaena* cells with a calcium-binding compound should prevent heterocyst differentiation.

B A strain that overexpresses the PatS gene should develop many more heterocysts in a low nitrogen environment.

C In an environment with abundant fixed nitrogen, free calcium levels should be high in all cells, preventing heterocysts from developing.

D In environments with abundant fixed nitrogen, loss of the HetR gene should induce heterocyst development.

Solution The solution is (A). As increased calcium stimulates the expression of heterocyst development genes, providing Anabaena cells with calcium-binding compound inhibits heterocyst development.

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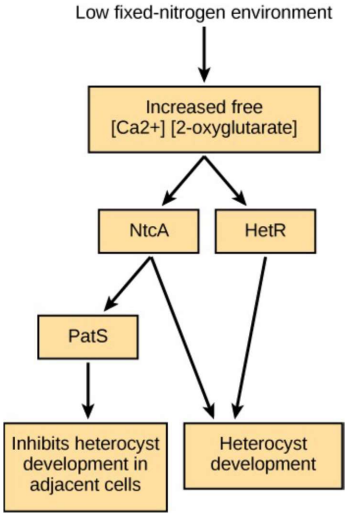
59 Which statement about *Anabaena* is false?



A Decreasing the concentration of free calcium ions will prevent heterocyst development.

B In the presence of fixed nitrogen, NtcA will not be expressed.

C Low fixed nitrogen levels result in increased PatS levels.

D A mutation in NtcA that makes it nonfunctional also will allow adjacent cells to develop as heterocysts.

Solution The solution is (D). The NtcA gene is responsible for heterocyst development whereas the HetR gene promotes PatS gene, which controls the heterocyst development in adjacent cells.

SCIENCE PRACTICE CHALLENGE QUESTIONS

16.4 Eukaryotic Transcriptional Gene Regulation

60 The operon model describes expression in prokaryotes. **Describe** this model and the essential difference in the way in which expression is regulated in eukaryotes.

Solution Sample answer: An operon is a cluster of genes involved in the same biochemical pathway. The genes are transcribed together, and are all under the control of the same promoter. In eukaryotes, genes are not clustered into operons, and a different promoter regulates each gene.

An operon includes structural genes involved in a single biochemical pathway which are under the same control and transcribed into a single mRNA. Either the operon is active and all structural genes are transcribed or the operon is off and none of the

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genes are transcribed. Upstream of the structural genes are located the regulatory sequences that include a promoter where RNA polymerase binds and operators where repressors bind. The genes encoding the repressor proteins are usually not part of the operon. Activator sequences can be located upstream of the promoter. Operons are found in bacteria with few exceptions in some organisms such as yeast and *C. elegans*.

In eukaryotic cells, genes are generally transcribed individually. Each gene is preceded by its own promoter upstream (at the 5′ end) and a transcription terminator at the 3′ end. Genes encoding proteins involved in the same pathway are nevertheless expressed individually.

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