2. Gene - It's Nature, Expression and Regulation

2.0 : Introduction

Q.1. What are the characteristics of living cells and organisms?

Ans: The characteristics of living cells and organisms are:

i) Ability to reproduce.
ii) Transmission of characters from one generation to the next.
iii) Maintaining the continuity of inherited traits.

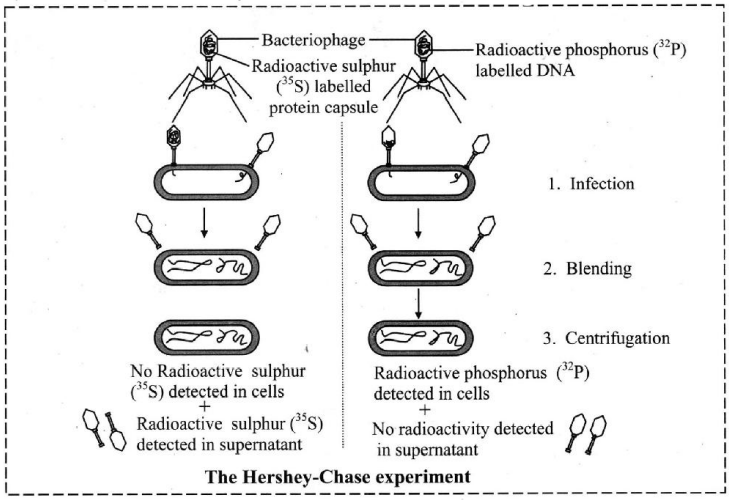
Q.2. Which properties should the genetic material possess ?

Ans: i) Genetic material should be able to express accurately by transcription to mRNA and finally to produce proteins.
ii) Genetic material should have capacity to replicate with minimum errors.
iii) Genetic material should be chemically stable.
iv) Genetic material should be able to undergo inheritable mutation so that evolution can take place.

2.1 : DNA as a genetic material

Q.3. Describe the experiment of Hershey and Chase to prove that DNA is the genetic material. [Mar 2014]

Ans i) Hershey and Chase (1952) worked on viruses which infect bacteria and are called as bacteriophages.
ii) Bacteriophage attaches itself to the bacteria and then its genetic material enters the bacterial cell.
iii) The bacterial cell treats the viral genetic material as its own and subsequently produces more copies.
iv) Hershey and Chase grew some viruses on a medium that contained radioactive phosphorus (^{32}P) and some others on medium that contained radioactive sulphur (^{35}S).
v) Viruses grown in presence of radioactive phosphorus contained radioactive DNA but not radioactive protein, because DNA contains phosphorus.
vi) Viruses grown in presence of radioactive sulphur contained radioactive protein but not radioactive DNA, because DNA does not contain sulphur, but proteins contain sulphur.
vii) Radioactive bacteriophages were allowed to attach to E.coli.
viii) As infection proceeded, the viral coats were removed from the bacteria by agitating them in blender and then separated from bacteria by centrifugation.
ix) Bacteria infected with viruses containing radioactive DNA were radioactive, where as bacteria infected with viruses containing radioactive proteins were not radioactive.
x) This indicates that DNA enters the bacterial cells and not protein.
xi) Thus, by this experiment, Hershey and Chase proved that DNA is the genetic material.



The Hershey-Chase experiment

Q.4. Describe in detail the experiment performed by Griffith.

Ans:i) In 1928, Frederick Griffith performed an experiment with Streptococcus pneumoniae (bacterium responsible for pneumonia).

ii) There are two types of strains of the bacteria:

a. **S-strain** whose cells produce a capsule of polysaccharides (mucous) causing smooth and shiny colonies on agar. This strain is virulent (pathogenic) and causes pneumonia.

b. **R-strain** whose cells lack a capsule and produce dull rough colonies on agar and is oonvirulent.

iii) Griffith performed his experiment by injecting the above strains of bacteria into mice and found the following results:

a. S-strain (virulent) bacteria were injected into mice, the mice developed pneumonia and finally died.

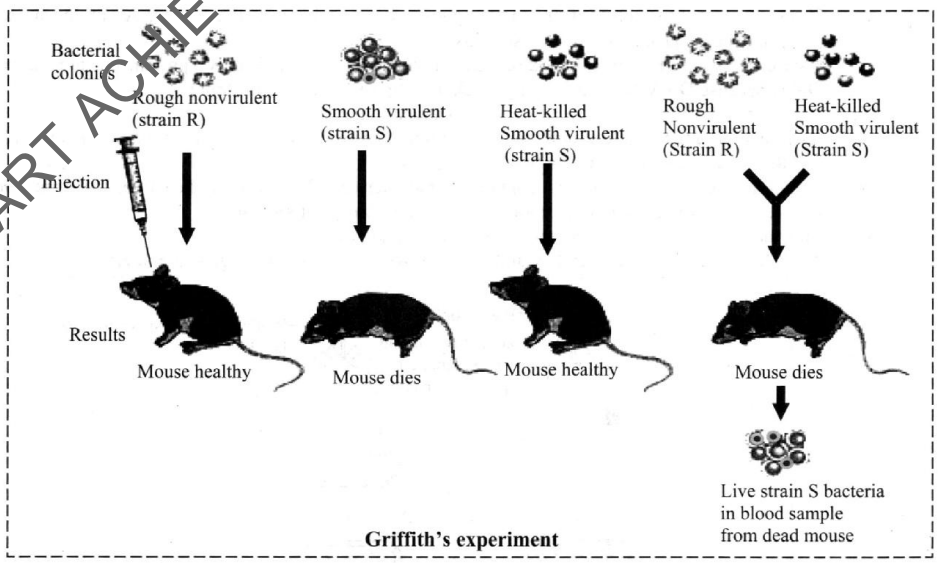
b. R-strain (non-virulent) bacteria were injected into mice, the mice suffered no illness because R-strain was non-pathogenic.

c. Then, Griffith injected heat killed S-strain bacteria into mice, they survived.

d. A mixture of R-strain and heat-killed S-strain were injected into mice, the mice developed pneumonia and died.

iv) He concluded that some genetic factor from heat killed S-strain cells transformed live R-strain cells into live S-strain and produced the disease.

v) Thus, Griffith's experiment helped to identify the transformation of genetic material.



Griffith's experiment

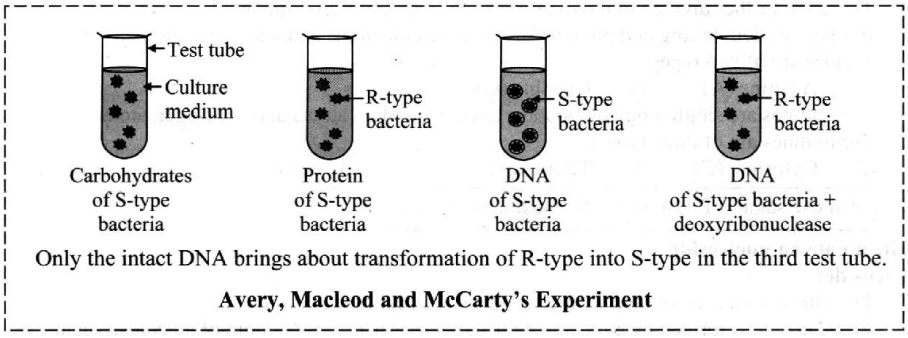
Q.5. Explain the experiment performed by Avery, Macleod and McCarty to prove that 'transforming principle is DNA'.

Ans:i) Avery, Macleod andMcf.arty (1944) purified DNA, RNA, proteins and other materials from heat killed S-type and mixed with R-type to see which ones could transform living R-types to S-types.

ii) Only those mixed with DNA were transformed into S-type bacteria.

iii) When DNA was mixed with Deoxyribonuclease (the enzyme that will digest and destroy DNa) there was no transformation.

iv) For their experiments they used a test tube assay instead of mice. These experiments prove that the transforming principle is DNA.



Avery, Macleod and McCarty's Experiment

2.2 : Modern Concept of Gene

Q.1. Q.6. What are genes ?

Ans:i) Genes are units of inheritance, which are transmitted from one generation to the other. A gene is a segment of DNA that provides instructions for synthesis of a specific protein or a particular type of RNA.

ii) It may be defined as a segment of DNA which is responsible for inheritance and expression of a particular character.

Q.7. Explain the terms introduced by Seymour Denzer.

Ans: i) Cistron

It is a unit of function in DNA system.

It is responsible for expression of a trait. It is a segment of DNA having information for synthesis of a particular protein or RNA. It can be several hundred bp (base pairs) long.

ii) Muton

It is a unit of mutation.

It consists of a few nucleotides, (one to few bp long). It is segment of DNA that can undergo mutation.

iii) Recon

It is a unit of recombination.

It is a segment of DNA that participates in recombination through crossing over during meiosis. It consists of few to many base pairs.

2.3 : DNA : Structure of Eukaryotic DNA

Q.8. Enlist the components of nucleotide.

Ans: A nucleotide is composed of:

i) Pentose sugar (either deoxyribose or ribose)

ii) Phosphate group

iii) Anyone nitrogen base out of four (Adenine, Guanine, Cytosine, Thymine or Uracil)

Q.9. Describe the structure of nucleotide.

Ans: Each nucleotide has the following three components:

Sugar :

i) It is a pentose sugar called deoxyribose ($C_5H_{10}0_4$) or ribose ($C_5H_{10}O_5$).

ii) It is a five carbon compound and has pentagonal ring structure.

Phosphate group :

i) It is derived from phosphoric acid (H_3PO_4).

ii) It helps to link the nucleotides during strand formation.

Nitrogen bases :

i) These are cyclic compounds made up of carbon, hydrogen, oxygen and nitrogen atoms.

ii) The bases are named adenine a), thymine (T), cytosine c), guanine (G) and uracil (U).

iii) These are further divided into two groups - Purines and Pyrimidines.

iv) Purines are double ring compounds, having 5 carbon atoms and 4 nitrogen atoms.

v) Purines are of two types:

a. Adenine a) b. Guanine (G)

Vi) Pyrimidines are single ring compounds, having 4 carbon atoms and 2 nitrogen atoms.

vii) Pyrimidines are of three types:

a. Cytosine c) b. Thymine (T) c. Uracil (U)

Pentose sugar + Phosphate + Nitrogen base = Nucleotide

Q.I0.Write a note on nucleoside.

Ans: Nucleoside :

i) The nitrogen base combined with pentose sugar is called nucleoside.

ii) A nucleoside is formed by attaching a nitrogen base at 1st carbon atom of a pentose sugar.

iii) Nitrogen base is attached to the pentose sugar by glycosidic bond.
iv) The nitrogen base may be a purine or pyrimidine.
v) Nucleoside is basic in nature.
vi) Nucleoside = Pentose sugar + Nitrogen base

Q.11. Write a short note on deoxyribo-nucleotide.

Ans: i) Deoxyribo-nucleotide is the structural unit of DNA.
ii) Each deoxyribo-nucleotide has three components - Deoxyribose sugar, Phosphate group and Nitrogen base.
iii) Deoxyribose sugar is a pentose (five carbon) sugar having pentagonal ring structure.
iv) The phosphate group is phosphoric acid (H_3PO_4). It is involved in strand formation.
v) Nitrogen bases are of two types - Purines (Double ring compounds) and Pyrimidines (Single ring compounds).
vi) Purines include Adenine a) and Guanine (G), while pyrimidines include Cytosine c) and Thymine (T)

Deoxyribonucleotide = Deoxyribose sugar + N-base + Phosphate

Q.12.What is DNA? Describe the double helical structure of eukaryotic DNA.

Ans:DNA (Deoxyribo nucleic acid) is the principal genetic material of all organisms, except some viruses. In 1953, James Watson and Francis Crick proposed the structural model of DNA for which they received the Nobel Prize in 1962.

According to this model, the structure of DNA molecule is as follows:

i) Double Helix :
a. The DNA molecule consists of two strands (chains).
b. The two strands are spirally coiled around each other and around a central imaginary axis in a regular manner to form a double helix.
c. The double helical structure of DNA molecule appears like a twisted ladder and in two dimensional projection shows alternating major and minor grooves.

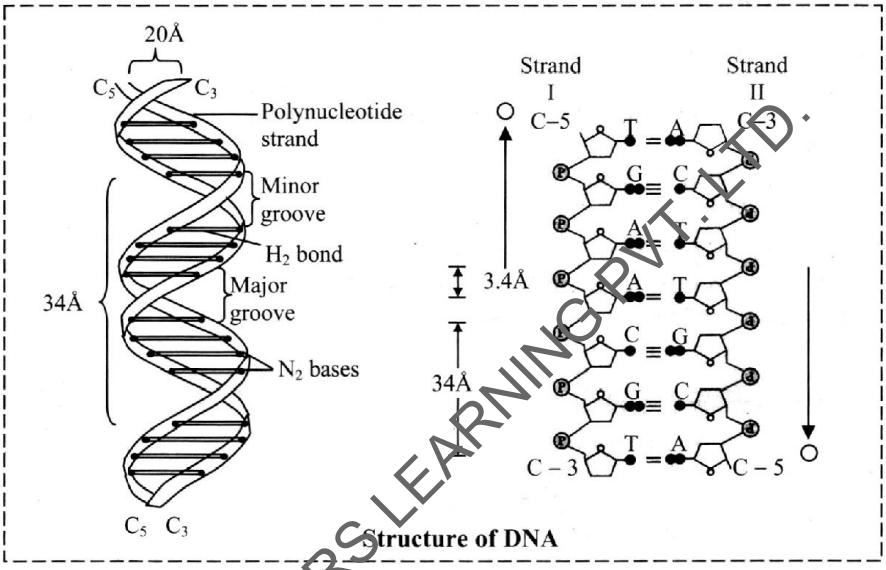
ii) Structure of each strand :
a. Each strand of DNA is a polynucleotide chain, i.e. formed -of many nucleotides.
b. The backbone of each strand consists of alternating deoxyribose sugar and phosphate groups.
c. Each phosphate group is joined to 3^{rd} carbon atom of one deoxyribose sugar molecule and 5^{th} carbon atom of successive deoxyribose molecule of the same strand by phospho-diester bond.
d. Each sugar in the strand has one nitrogen base attached to it at 1st carbon by glycosidic bond.

iii) Base Pairing :
a. The two strands are joined together by pairs of nitrogen bases.
b. In each pair, one base is always purine and the other base is pyrimidine.
c. The base pairing is very specific. The purine base Adenine a) of one strand will always pair with the pyrimidine base Thymine (T) of another strand. .
d. The purine base Guanine (G) of one strand always pairs with the pyrimidine base Cytosine c) of another strand.

iv) Rungs or Transverse bars :
a. The complementary bases of the two strands are held together by weak hydrogen bonds.
b. Adenine and Thymine are held together by two hydrogen bonds (A = T).
c. Guanine and Cytosine are held together by three hydrogen bonds (G == C).
d. The nitrogen containing bases along with hydrogen bonds make up the rungs of the ladder. These are also referred to as transverse bars.

v) Purine - Pyrimidine ratio :
a. In a DNA molecule, total number of A = total number of T and total number of G = total number of C. In other words, A + G = T + C. This is called Chargaff's rule.
b. Thus, purine: pyrimidine ratio is 1 : 1.
c. It may be represented as follows :

$$A + G = T + C \text{ or } \frac{A + G}{T + C} = 1$$



Structure of DNA

vi) Polarity of strands :

Both the polynucleotide strands of DNA show polarity, i.e. direction.

a. One end of each strand has a free' – OR' group at 3rd carbon of deoxyribose sugar.
b. This end of the strand is called 3' end or C–3. It is not linked to any nucleotide.
c. Other end of the strand has a free phosphate group at 5th carbon atom of the deoxyribose sugar.
d. This end of the strand is called 5' end or C– 5. It is also not linked to any nucleotide.
e. One strand of DNA is oriented in 3'–5' and complementary strand is oriented in 5'–3' manner.

vii) Antiparallel strands :

a. The two strands of DNA are parallel to each other, but are placed in opposite direction.
b. One strand runs in (5' to 3') direction, while the other in (3' to 5') direction.
c. Such strands are called antiparallel strands.

viii) Complementary nature of strands :

a. As the base sequence present in one strand of DNA decides the base sequence of the other strand, the strands are regarded as complementary strands.
b. This is because of definite base pairing.

ix) Major grooves and Minor grooves :

a. The strands of DNA undergo right handed coiling around a central imaginary axis.
b. This coiling results in the formation of major (deep) grooves and minor (shallow) grooves.
c. The major and minor grooves occur alternately.

x) Dimensions :

a. The diameter of a DNA molecule is 20m (20 a) . It remains constant throughout the length 0 DNA.
b. The length of one complete turn (spiral or gyre or pitch) is 3.4om (34 a). One turn is the distance between two successive major grooves or minor grooves.
c. In one complete turn ofD A, 10 base pairs are present.
d. Therefore, the distance between the successive base pairs is 0.34 om (3.4 a).

Q.13. What will be the length of eukaryotic D A segment having 10 pairs of nucleotides? [Mar 2013]

Ans: The length of a eukaryotic DNA segment having 10 pairs of nucleotides will be 3.4 om /34 Å

Q.14. Write a note on Chargaff's rule.

Ans: i) In a DNA molecule, total number of purine bases is always equal to total number of pyrimidine bases.

ii) In other words, A + G = T + C. This is called Chargaffs rule.

iii) Thus, purine: pyrimidine ratio is 1 : 1.

iv) It can be represented as $\frac{A+G}{T+C} = 1$ or A + G =T + C.

Q.15.Group the following as nitrogenous bases and nucleosides : Adenine, Cytidine, Thymine, Guanosine, Uracil and Cytosine.

Ans:Nitrogenous bases: Adenine, Thymine, Uracil, Cytosine

Nucleosides : Cytidine, Guanosine.

Q.16. If the sequence of one strand of DNA is written as :
5' ATGC ATGC ATGC ATGC ATGC ATGC ATGC 3'
Write down the sequence of complementary strand.

Ans: 3' TACG TACG TACG TACG TACG TACG TACG 5'

2.4 : Semiconservative replication of DNA

Q.17.Explain the process of DNA replication.

Ans:Replication of DNA :

It is a process in which a DNA molecule produces one or more exact copies or replicas of itself.

Semiconservative method of replication :

After replication, each daughter DNA molecule has one old and other new strand. As parental DNA is partly conserved in each daughter DNA, the process of replication is called semi conservative. In eukaryotes, replication of DNA takes place inside nucleus during S-phase of interphase of the cell cycle. In prokaryotes, however it takes place in the cytoplasm. The model of semi conservative replication was proposed by **Watson and Crick.**

Mechanism of D A replication :

i) **Activation of nucleotides :**
All the four types of DNA nucleotides are found in the nucleoplasm in the form of their monophosphates namely dAMP, dGMP, dTMP and dCMP. They are activated using ATP to form triphosphates, namely dATP, dGTP, dTTP and dCTP respectively. It occurs in presence of enzyme phosphorylase and the process is called activation of nucleotides [dAMP + ATP $\longrightarrow$ dATP + AMP]

ii) **Origin (Initiation) :**
The replication starts at a specific point on DNA molecule called origin or initiation point. In prokaryotes, DNA has single origin point, while in eukaryotes, there are several origin points.

iii) **Incision:**
At the origin, DNA molecule breaks because off ormation of an incision (nick). This incision is made by the activity of endonuclease enzyme, hence hydrogen bonds get broken.

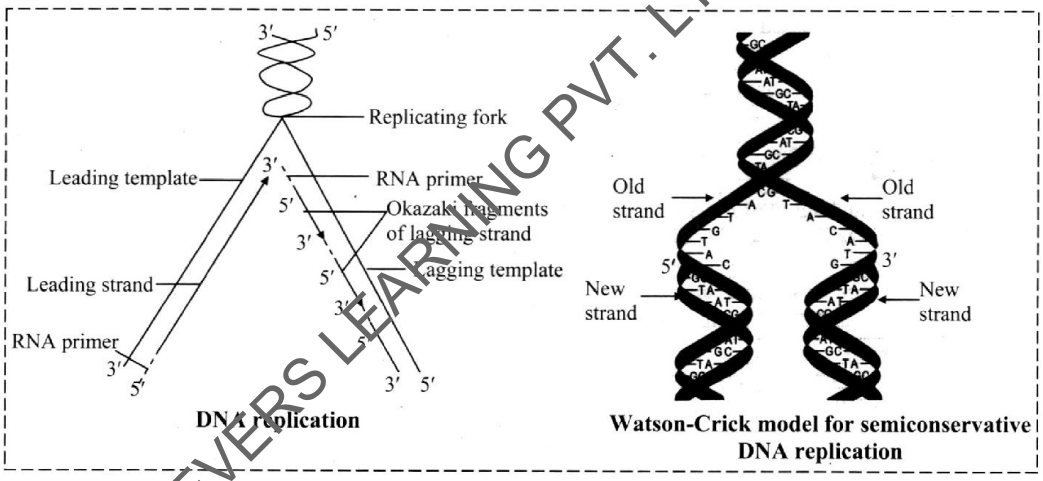
iv) **Unwinding of DNA molecule :**
The two strands start unwinding. This takes place with the help of DNA unwinding protein, i.e. **helicase enzyme.**
By the action of topoisomerase, two strands get separated from each other. Now, the DNA molecule appears as inverted 'Y' shaped structure called replication fork. The portion or unit of DNA undergoing replication is called replicon. The two separated strands of the DNA are stabilized by Single Strand Binding Protein (SSBP) or helix destabilizing protein.

v) **Synthesis of new strand :**
For synthesis of a complementary new strand, each separated strand acts as a template (site) or mould. It is initiated by a small RNA molecule called **RNA primer.** Synthesis of this RNA primer is controlled by **enzyme RNA primase.**
The RNA primer attaches itself at the 3' end of the template strand and attracts the new nucleotides from nucleoplasm. Appropriate nucleotides are selected and are attached by H-bond to their respective complementary bases on the old strand. Synthesis of new strand occurs in the presence of enzyme DNA Polymerase. The successive nucleotides are joined to each other with the help of phosphodiester linkages forming a new strand.

vi) **Leading and Lagging strand :**
During DNA replication, the strand which opens from 3'-5' is called leading template and its complementary strand is called leading strand or continuous strand. It is constructed continuously at a faster rate. The other strand which opens from 5'_3' is called lagging template and its complementary strand is called lagging strand. It is constructed discontinuously at a slower rate. The lagging strand is constructed in the form of short segments called Okazaki fragments which are later joined by the enzyme DNA ligase. The replication of DNA strands always takes place in 3' to 5' direction of template strand, while construction of new strand occurs in 5' to 3' direction, as DNA polymerase shows 5' to 3' direction activity.

vii) Formation of new DNA chains :

In this way for each old strand, a new complementary strand is constructed. Now, one old strand and the other new strand undergo coiling to form two identical daughter DNA molecules at the end of the process.



DNA replication

Watson-Crick model for semiconservative DNA replication

Q.18. Why is DNA replication called semi-conservative ?

Ans: i) During replication of DNA, two DNA molecules are produced from single molecule.

ii) Each daughter molecule has one old and one new strand.

iii) One old strand of DNA is conserved in each DNA.

Due to this property, the method is described as semi-conservative.

Q.19. Write a note on Okazaki fragment.

Ans: i) In semi conservative mode of DNA replication, lagging strands are synthesized discontinuously in small fragments and are called Okazaki fragments.

ii) Each Okazaki fragment is made up of 100-200 nucleotides in eukaryotes and 1000-2000 nucleotides in prokaryotes.

iii) The Okazaki fragments are then joined by the enzyme DNA ligase to give rise to a continuous strand.

Q.20. Distinguish between Leading and Lagging strand.

Ans:

No.	Leading strand	Lagging strand
i)	Leading strand synthesis is continuous.	Lagging strand synthesis is discontinuous.
ii)	Leading strand is synthesized towards the replication fork.	Lagging strand is synthesized away from the replication fork. replication fork.
iii)	Ligase enzyme is not necessary in the sythesis of leading strand.	Ligase enzyme is necessary to join the small fragments of lagging strand.
iv)	Okazaki fragments are not formed in leading strand.	Okazaki fragments are formed in lagging strand.
v)	It requires only one RNA primer to initiate replication	Every fragment require separate RNA primer for initiation of replication.

Q.21. If a double stranded DNA has 20% of cytosine, calculate percentage of adenine in DNA.

Ans: Given ds DNA has 20% of cytosine.

i) According to Chargaffs findings, the amount of cytosine residue is proportional to the amount of guanine residue and amount of adenine residue is proportional to the amount of thymine residue in DNA.

ii) Therefore, based on the above proportionality, the sum of the purines (A + G) equals the sum of the pyrimidines (C + T).

iii) Cytosine pairs with Guanine. As Cytosine is 20%, Guanine is also 20%.

iv) But, A + G = 50%, Guanine is 200/0,so Adenine is 30%.

2.5 : Packaging of DNA

Q.22. How does packaging of DNA take place in a eukaryotic cell ?

Ans:i) In eukaryotes, the packaging and organization of DNA is rather complex. Histones are required for the packaging of DNA. Histones are proteins that are rich in the basic amino acid residues, lysines and arginines which carry positive charge in their side chains

ii) Eight molecules of histones (two each of H2A, H2B, H3 and H4) get organized to form histone octamer.

iii) DNA is negatively charged and it is wrapped around the positively charged histone octamer to form nucleosome.

iv) Under the electron microscope, nucleus shows chromatin network.

v) The nucleosomes in chromatin are seen as 'beads-on-string'.

vi) Around the octomer, DNA molecule is wrapped as 1 and $3/4^{th}$ turn. This DNA is called core DNA and it consists of about 146 bp (base pairs).

vii) Adjacent nucleosomes are linked with small segments of DNA called linker DNA of about 54 bp. (thus the string is, DNA - 2 run or 20 $\overset{o}{A}$ in diameter).

viii) This 'beads-on-string' structure gets condensed into nucleosome fiber, which is 10 run (100 $\overset{o}{A}$) in diameter.

ix) H_1 histone is present in the linker region, and as DNA makes two complete turns, it is present where the DNA starts wrapping the octamer and leaves it. Each nucleosome contains 200 bp of DNA helix.

x) The thin and long nucleosome fibre is coiled like a telephone wire to make solenoid fibre with diameter 30 nm or 300 $\overset{o}{A}$.

xi) The packaging of chromatin at higher levels need additional set of proteins that are collectively called. Non-Histone Chromosomal (NHC) proteins.

xii) A loosely packed region of chromatin that stains light, is called euchromatin and densely packed region that stains dark, is called heterochromatin.

xiii) Euchromatin is considered as transcriptionally active chromatin, while heterochromatin is inactive.

Q.23. Differentiate between Euchromatin and Heterochromatin.

Ans :

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i)	Leading strand synthesis is continous.	Lagging strand synthesis is discontinuous.
ii)	Leading strand is synthesized towards the replication fork.	Lagging strand is synthesized away from the replication fork. replication fork.
iii)	Ligase enzyme is not necessary in the synthesis of leading strand.	Ligase enzyme is necessary to join the small fragments of lagging strand.
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Q.23. Differentiate between Euchromatin and Heterochromatin.

Ans :

No.	Euchromatin	Lagging strand
i)	Euchromatin is considered as transcriptionally active chromatin.	Heterochromatin is considered as transcriptionally inactive chromatin.
ii)	Euchromatin stains lightly.	Heterochromatin stains darkly.
iii)	It is loosely packed region of the chromatin.	It is densely packed region of the chromatin.

Q.24. Why is eukaryotic D A condensed and super coiled?

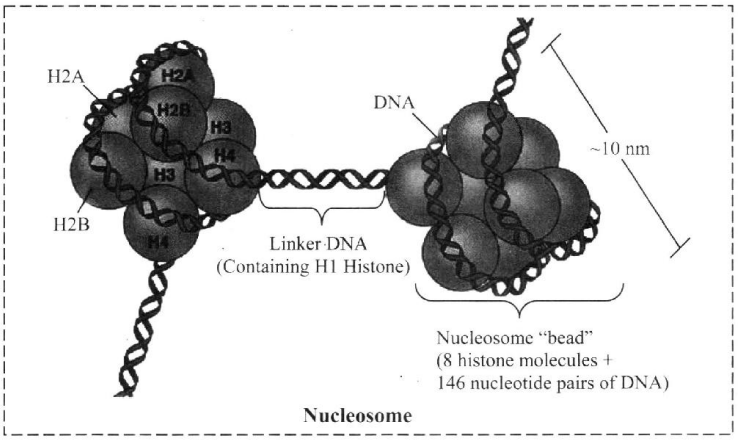
Ans: i) Length of DNA double helix molecule, in a typical mammalian cell is approximately 2.2 meters.

ii) Size of a typical nucleus is approximately 10^{-6}

iii) Such a long DNA molecule has to be accommodated in such a small nucleus.

iv) Hence, eukaryotic DNA is condensed and super coiled.

Q.25. Draw a neat, labelled diagram of Nucleosome.



Nucleosome

2.6 : RNA : General Structure, Types and Function

Q.26.Describe the structure of RNA molecule.

Ans:RNA(Ribose Nucleic Acid) is a type of nucleic acid found in the nucleus as well as in the cytoplasm.

Structure of RNA molecule :

i) RNA molecule is generally single stranded structure which may be simple and straight or may be folded or coiled upon itself.

ii) The RNA single strand is a long chain of ribonucleotides joined by phosphodiester linkages.

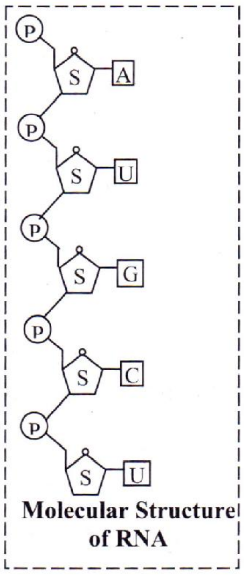
iii) Each nucleotide ofRNA is made up of following components :
Sugar : It is a pentose sugar called ribose ($C_5H_{10}O_S$).It is a five carbon compound and has pentagonal ring structure.
Phosphate group: It is derived from phosphoric acid (H_3P0_4). It helps in linking of nucleotides during strand formation.
Nitrogen bases: The nitrogen bases present in RNA are Purines - adenine and guanine; Pyrimidines - uracil and cytosine (In RNA, thymine is replaced by uracil).

iv) There are four different types of nucleotides present, containing nitrogen bases as A, G, U and C.

v) RNA strand has two ends as 3' or C-3 end and 5' or C-5 end.

vi) In the RNA molecule, if coiling or folding occurs then base pairing takes place between complementary bases (A = U; G ≡ C) present opposite to each other.

vii) As in the RNA molecule, the base pairing is not fixed and definite, the purine: pyrimidine ratio mayor may not be 1:1



Molecular Structure of RNA

Q.27.What is RNA? Mention its types and give the functions of each.

Ans: RNA(Ribose Nucleic Acid) is a type of nucleic acid found in the nucleus as well as in the cytoplasm.

Types of RNA: There are two main types of RNA :

i) Genetic RNA : It acts as genetic material in some viruses.

ii) Non-genetic RNA : It is mainly involved in protein synthesis. There are three different types of nongenetic RNA :

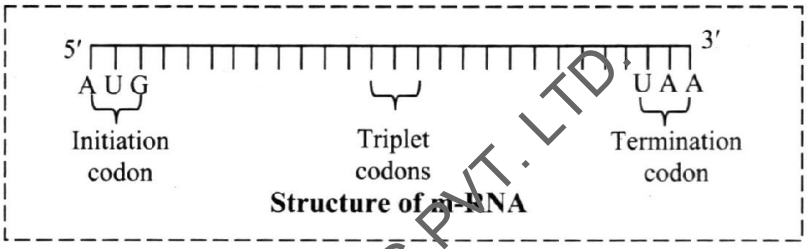
a. Messenger RNA (m-RNa)
b. Ribosomal RNA (r-RNa)
c. Transfer RNA (t-RNa) or Soluble RNA (s-RNa)

a. Messenger RNA (m-RNa) or Informational RNA :

1. It is called messenger RNA because it carries the message for protein synthesis from DNA to the ribosomes (site for protein synthesis) in the form of codons,
2. It is produced on the DNA strand inside nucleus by a process called transcription and then transferred to the cytoplasm.
3. It constitutes about 3-5% of the total RNA content of the cell.
4. It is long RNA and the molecular weight of an average sized m-RNA is about 5,00,000.
5. It is always single stranded, linear and straight (unfolded).
6. It has two ends - 5' end and 3' end.
7. A triplet ofnucleotides on m-RNA is called codon.
8. Each codon 011 m-RNA specifies one amino acid. This is called m-RNA language or genetic code or cryptogram.
9. The codon present at 5' end ofmRNA is **called initiation codon or start codon.** The common initiation codon is AUG or in some cases GUG. AUa and GUG specify amino acids methionine and valine respectively.
10. The codon present at 3' end is called **termination codon or stop codon or non-sense codon (as they do not specify any amino acid).** The termination codon may be UAA

(Ochre) or UAG (Amber) or UGA (Opal).

11. m-RNA is short lived and is degraded soon after protein synthesis.



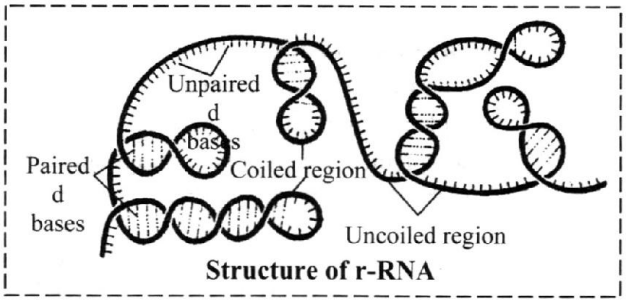
Structure of m-RNA

Functions of m-RNA :

1. It carries genetic information from DNA to ribosomes during protein synthesis.
2. The genetic code of m-RNA gets translated into the sequences of ammo acids to form proteins.

b. Ribosomal RNA (r - RNa) :

1. It is present in ribosomes, hence the name ribosomal RNA.
2. It consists of a single strand. The single strand is folded upon itself in certain regions.



Structure of r-RNA

3. In folded regions, complementary base pairing occurs, while in unfolded regions, it is absent. Hence, r-RNA does not show purine-pyrimidine equality.
4. It constitutes about 80% of the total RNA content of the cell.
5. The molecular weight ranges from 40,000 to 100,000.

Functions of r-RNA :

1. It provides proper binding site for m-RNA on the ribosome.
2. It orients m-RNA molecule in such a way that all the codons are properly read.
3. It releases t-RNA molecule after transfer of activated amino acid to polypeptide chain.
4. It also protects the protein molecule under construction.
5. It also protects m-RNA from RNase enzyme.

c. Transfer RNA (t-RNa) or Soluble RNA (s-RNa) or Supernatant RNA or adapter RNA.

1. It is the smallest of the three types of non-genetic RNA.
2. It transfers activated amino acids to the site of protein synthesis. Hence, it is called transfer RNA.
3. It is also called soluble RNA as these molecules cannot be separated from cytoplasm even by ultra centrifugation technique.
4. The t-RNA molecule consists of a single strand folded upon itself.
5. It constitutes about 10-20% of the total RNA content of the cell.
6. It is made up of73-93 nucleotides with molecular weight of about 23,000-30,000.
7. There are more than 20 different types oft-RNA.
8. Structure oft-RNA can be explained by two models as :

1. Hairpin model :

The t-RNA molecule is folded in such a manner that there is formation of one loop having a triplet of unpaired bases called anticodon. The 5' end has G-nucleotide, while at 3' end, there is a sequence of CCA nucleotides.

2. Clover leaf model (trifoliate leaf model) :

i) The clover leaf model of t-RNA shows presence of three arms, namely - DHU arm, middle arm and T ψ C arm.

ii) These arms have loops at their ends such as amino acyl binding loop, anticodon loop and ribosomal binding loop respectively.

iii) The anticodon loop has anticodon which is a triplet of unpaired nucleotides.

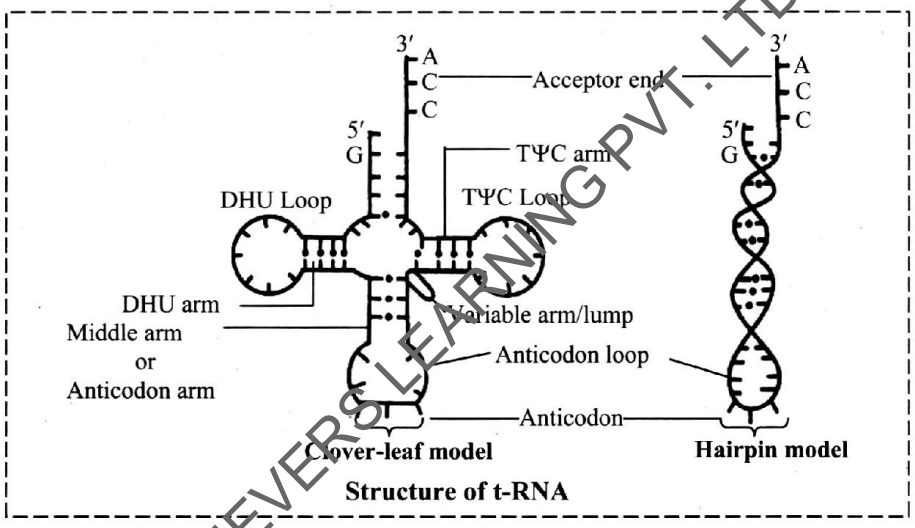
iv) The anticodons present on t-RNA are complementary to codons present on the m-RNA (anticodons are also referred to as nodoc).

v) In addition, it also shows a small lump called variable arm or variable lump.

vi) Like the hair-pin model oft-RNA, it has G nucleotide at 5' end and CCA nucleotides at 3' end.

Functions of t-RNA :

It carries specific type of amino acid at CCA end to the ribosomes during protein synthesis. It places the required amino acid properly in the sequence. (This becomes possible because of complementary nature of codons and anticodons)



Structure of t-RNA

Q.28.Why is D A molecule a more stable genetic material than RNA ?

Ans: In DNA, presence of thymine at the place of uracil confers more stability. In RNA, the - OR group of ribose sugar is a reactive group that makes RNA labile and degradable, while its absence in DNA makes DNA chemically less reactive and more stable.

Additional Information

Q.29. Define the terms :

i) Codogen ii) Codon iii) Anti-codon

Ans:i) **Codogen:** It is the smallest possible sequence (triplet) of nucleotides present on DNA strand which can specify one particular amino acid.

ii) **Codon :** It is the smallest possible sequence (triplet) of nucleotides present on m-RNA strand which can specify one particular amino acid.

iii) **Anti-codon :** It is a triplet of nucleotides present on the loop of middle arm of t-RNA. It is complementary with the codon.

Q.30. Distinguish between DNA and RNA. **[Mar 2008]**

Ans :

No.	DNA	RNA
i)	DNA is the genetic material in almost all living organisms, with the exception of few viruses.	RNA is genetic material only in some viruses.
ii)	It is double stranded.	It is single stranded.
iii)	The pentose sugar is deoxyribose	The pentose sugar is ribose.
iv)	Nitrogen bases of DNA are Adenine, Guanine, Cytosine and Thymine.	Nitrogen bases of RNA are Adenine, Guanine, Cytosine and Uracil
v)	It is the largest macromolecule.	It is medium to small sized macromolecule.
vi)	Nitrogen bases are paired throughout the length.	Nitrogen bases are paired only in loops/ coiled parts.
vii)	DNA is spirally twisted to produce a double helix.	The strands may get folded at places to produce loops.
viii)	Purine and pyrimidine bases are equal in number.	There is no fixed ratio between the amount of purines and pyrimidines.
ix)	It is deoxyribonucleic acid.	It is ribose nucleic acid.
x)	It replicates to form daughter DNA molecules.	It cannot replicate
xi)	It carries information for protein synthesis.	It brings about protein synthesis
xii)	It survives throughout the life span of cell.	It has short life span and it is replaced constantly
xiii)	DNA is of two types : linear and circular.	RNA is of three types : mRNA, rRNA and tRNA

Q.31. Differentiate between the following :

i) t-RNA and m-RNA

Ans:

No.	t-RNA	m- RNA
a)	It is a folded molecule (clover leaf).	It is a linear molecule.
b)	It forms 10 - 20% of total cellular RNA	It forms 3-5% of total cellular RNA
c)	It is the smallest RNA	It is a long and linear RNA
d)	It is twisted and looks like a hair pin or	it does not twist around itself.
	trifoliate clover leaf like structure.	
e)	There are more than 20 different kinds of	There is only one type of m-RNA
	t-RNA	
f)	It has a triplet of nitrogen bases called	It has a triplet of nitrogen bases called
	anticodon	codons.
g)	It carries or tranfers amino acid from cytoplasm to ribosome.	It carries information or message (for the type of protein to be synthesized) from DNA to ribosome.

ii) m-RNA and r-RNA

Ans:

No.	m- RNA	r- RNA
a)	It forms 3-5% of total cellular RNA	It forms 80% of total RNA
b)	It is a long and linear RNA	It is the longest and twisted RNA
c)	It has short life span	It is a permanent RNA
d)	Nitrogen bases do not pair	Nitrogen bases pair
e)	It possesses codons	It does not possess codons
f)	It carries message from DNA to ribosome	It supervises protein synthesis.

2.7 : Protein synthesis

Q.32. What is one gene-one enzyme hypothesis ?

Ans:i) George Beadle and Edward Tatum in 1941 exposed spores of the fungus *Neurospora crassa* tomutagenic agents like X-ray causing mutations in DNA.

ii) They obtained some mutant strains of Neurospora crass a which lacked specific enzyme.

iii) They concluded that a gene is segment of DNA which codes for an enzyme.

iv) It was named as one gene-one enzyme hypothesis.

Q.33.Why has one gene - one enzyme hypothesis been modified to one gene - one polypeptide hypothesi ?

Ans:i) According to one gene - one enzyme hypothesis, one gene synthesizes one enzyme which is responsible for controlling one biochemical reaction.

ii) However, not all genes code for enzymes, they may instead direct the building of structural proteins, such as the collagen in our skin, or the keratin in our hair.

iii) Also, many proteins are made up of more than one polypeptide chains. e.g. haemoglobin consists of four polypeptide chains of two different types - a. chain and B chain which are controlled by different genes. Thus, one gene - one enzyme hypothesis has modified to one gene - one polypeptide hypothesis by Vernon Ingram.

Genetic Code

Q.34. Define Genetic code.

Ans: The sequence of three nucleotides on m-RNA that determines the specific amino acid sequence in the synthesis of proteins is called genetic code.

Q.35. Give the characteristics of genetic code. **[Mar 2013]**

Ans:i) Genetic code is triplet : A single amino acid is specified by a sequence of three nucleotides on mRNA and called as codon. Due to triplet nature, it forms 64 codons.

ii) Genetic code is non-ambiguous : One codon codes for only one particular amino acid. (Exception:

AUG codes for methionine and GUG codes for valine, but if AUG is not available, then GUG codes for methionine, as a start codon in protein synthesis)

iii) **Genetic code is universal :** A codon specifies the same amino acid in all organisms from virus to human beings.

iv) **Genetic code is commaless :** On m-RNA strand, the triplet codons are without punctuations and thus reads continuously and called as commaless.

v) **Genetic code is non-overlapping :** No overlapping between adjacent nucleotide.

vi) **Stop or termination codons :**
The codons are triplet. Out of 64 codons, 61 code for 20 amino acids and 3 codons (UAA, UGA, UAG) do not code for any amino acid. They stop the synthesis of polypeptide chain, hence called as stop or terminating codons. These are also called non-sense codons.

vii) **Initiation codon :**
AUG or GUC which code methionine and valine amino acid respectively.
It initiates the synthesis of polypeptide chain.
It is located at the beginning of the cistron.

viii) Degeneracy: A single amino acid may be specified by many codons e.g. amino acid leucine is coded by CUU, CUC, CUA, CUG, UUA, UUG.

ix) **Polarity :** The genetic code can be read only in 5' to 3' direction.

Q.36.What is degeneracy of genetic code?

Ans:i) There are 61 codons available for coding 20 amino acids.

ii) Two or more codons can code for the same amino acid e.g. Codons GGG, GGA, GGC and GGU code for amino acid glycine.

iii) Thus, genetic code is degenerate.

Q.37.Why is the genetic code considered as commaless ?

Ans: On the mRNA strand, the triplet codons are arranged one after other without any gap or space. Thus, genetic code is considered as commaless.

Q.38. Explain the dual function of AUG codon.

Ans: AUG codon has dual function which are as follows :

i) It codes for Methionine (met) amino acid.

ii) It serves as initiation codon, thus initiates the synthesis of polypeptide chain.

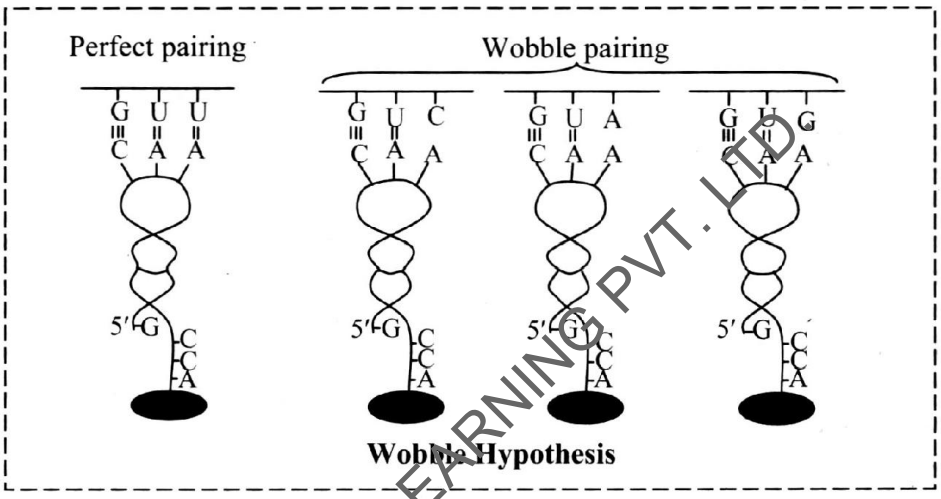
Q.39.What is the role of non-sense codons in protein synthesis ?

Ans: Role of non-sense codons: The codons UAA, UAG and UGA are not recognized by tRNA. For these codons, no tRNA is available for interaction. These codons provide the signal to stop protein synthesis and hence they are called stop signals or terminating codons.

Q.40.Describe the Wobble hypothesis.

Ans:Wobble Hypothesis :

According to Wobble hypothesis, in codon-anticodon pairing the third base may not be complementary. The third base of the codon is called wobble base and this position is called Wobble position. The actual base pairing occurs at first two positions only.



In the above example, though the codon and anticodon do not match perfectly, then also the required amino acid is brought perfectly. This enables the economy oftRNA. GUU, GUC, GUA and GUG code for amino acid - Valine. So, a single tRNA can interact with all the four codons which code for amino acid Valine.

Additional Information

Q41. Write a short note on Selenocysteine.

Ans: Earlier, it was believed that only 20 different types of amino acids are required for formation of proteins. Later, A. Bock et al established that 21st amino acid selenocysteine is also required for synthesis of many proteins. Surprisingly, it is coded by UGA which normally functions as a termination codon. In both, the prokaryotes and eukaryotes, a polypeptide chain typically contains 100-300 amino acids and is formed by specific arrangement of 21 types of amino acids. However, the formation of selenocysteine is dependent on the availability of the element selenium, only 20 amino acids are considered as standard.

Q.42. Why should each codon present in genetic code have 3 bases only and not one or two ?

Ans: i) There are in all 20 different types of essential amino acids required for synthesis of proteins in the cells.

ii) Each amino acid will require at least one specific codon. Thus, there should be at least 20 codons in the genetic code which is composed of only four bases A, U, G and C.

iii) If each codon has only one base/nucleotide- then there will be $4^1 = 4$ codons are possible (not enough to code 20 different amino acids).

iv) If each codon has two bases/nucleotides, then there will be $4^2 = 4 \times 4 = 16$ codons are possible (not enough to code 20 different amino acids)

v) If each codon has three bases/nucleotides, then there will be $4^3 = 4 \times 4 \times 4 = 64$ codons are possible (more than enough to code 20 different amino acids).

Q.43.What is the central dogma of molecular biology ?

Ans: Central dogma of molecular biology can be defined as unidirectional or one way flow of information from DNA to mRNA (Transcription) and from mRNA to protein (Translation).

This can be represented as:

$$\text{DNA} \xrightarrow{\text{Transcription}} \text{mRNA} \xrightarrow{\text{Translation}} \text{Protein}$$

However, in some retroviruses, reverse transcription takes place due to which DNA is synthesized from RNA. This can be represented as :

$$\text{DNA} \underset{\text{Reverse Transcription}}{\overset{\text{Transcription}}{\rightleftharpoons}} \text{mRNA} \xrightarrow{\text{Translation}} \text{Protein}$$

Q.44. Describe the process of transcription in protein synthesis.

Ans: i) Transcription is the formation of mRNA on DNA template. The process takes place in presence of DNA dependent RNA polymerase.

ii) In this process, genetic information from DNA is copied into RNA.

iii) For transcription, promoter, structural gene and terminator are required.

iv) The DNA strand which is used for synthesis of RNA is called antisense or template strand which is oriented in 3' → 5' direction, while the other strand not involved in RNA synthesis is called sense or coding strand, It is oriented in 5' → 3' direction.

v) A small DNA sequence which provides binding site for RNA polymerase is called promoter which is present towards 5' end/upstream, while a small DNA sequence which terminates the transcription process called terminator is present towards 3' end/downstream.

vi) In eukaryotes, the genes are split, having exons and introns. The DNA sequences which are expressed or appear in the mature or processed RNA are the exons, while those not appearing in mature or processed RNA are the introns.

vii) During transcription, the enzyme RNA polymerase binds to the promoter site and brings about the initiation of the process.

viii) The two strands .of DNA separate from each other. According to the base sequence present on the template strand, the complementary RNA nucleotides are selected and joined one after the other to form the mRNA strand (elongation).

ix) A small part ofRNA remains attached to the enzyme. As the enzyme reaches to the terminator region, both the enzyme and newly constructed RNA fall off. This is the termination of transcription.

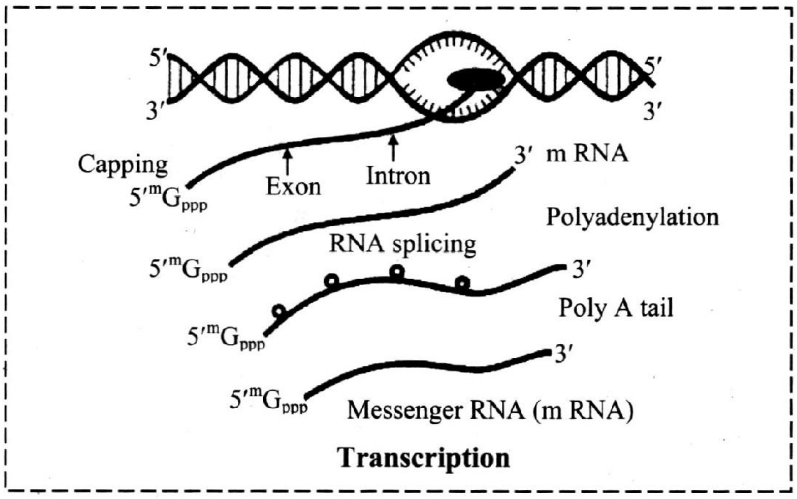
x) Initiation factor (σ) and termination factor (ρ) play an important role in the process.

xi) In prokaryotic organisms such as bacteria, the newly formed RNA do not require further processing, but in eukaryotes the matter is different.

xii) In prokaryotes, single RNA polymerase enzyme undertakes the formation of all RNA.In eukaryotes, there are three types of RNA polymerases; RNA polymerases-I for formation of rRNA, RNA polymerases-II for synthesis of precursor of mRNA, i.e. heterogenous nuclear RNA (hnRNa) and RNA polymerases-III for formation oftRNA and snRNA (small nuclear RNa).

xiii) In eukaryotes, the RNA is non-functional when it is formed and undergoes splicing, capping and tailing which occur inside nucleus. The removal of introns from the RNA is called splicing.

xiv) Addition of an unusual nucleotide methyl guanosine triphosphate at 5' end of hnRNA (having both the introns and exons) is called capping. Addition of adenylate residues at 3' end is called tailing. The hnRNA which has undergone capping, splicing and tailing now functions as mRNA.



Transcription

Q.45.Describe the process of translation in protein synthesis.

Ans: Translation is the process in which the sequence of codons on the mRNA strand is used (read/decoded) and accordingly the amino acids are joined to each other to form a polypeptide chain that makes protein. The process involves the following steps:

i) Activation of amino acids and formation of AA-tRNA complex:
In presence of an enzyme aminoacyl tRNA synthetase, the amino acid (Aa) molecule is activated and each amino acid is attached to the specific tRNA molecule at 3'/CCA end to form aminoacyl-tRNA complex. The reaction requires ATP. This process is called charging oftRNA or aminoacylation of tRNA.

ii) Formation of the polypeptide chain: It is the actual translation which involves the following steps :

Initiation :

It begins with the formation of initiation complex which requires the mRNA having codons for a

polypeptide, the smaller (30S) and larger (50S) sub-units of ribosome, the initial AA1-tRNA complex and ATP and GTP as source of energy.The process of initiation needs initiation factors.

In prokaryotes, the first AA1-tRNA complex has amino acid, N-formyl-metheonine (f-met); In eukaryotes, it is inetheonine (met). The process starts with binding of mRNA on the smaller 30S sub-unit of ribosome.

The start codon AUG is positioned properly.

The AA_1-tRNA complex, i.e. f-met-tRNA complex now gets attached to the start codon AUG. This is done with the help of anticodon UAC of tRNA.

Small and large subunits of ribosome join to form 70S ribosome.

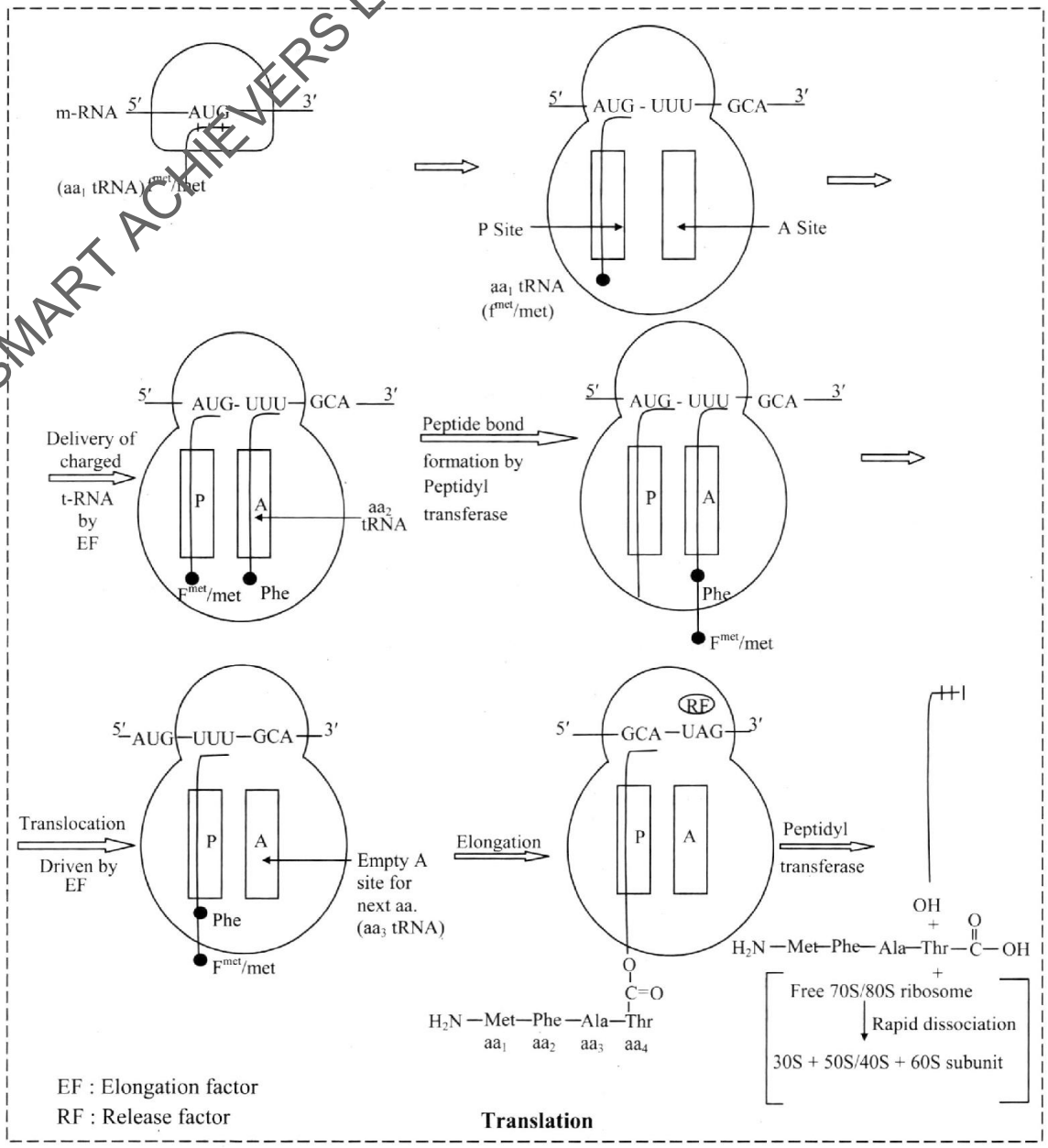
The ribosome has three sit~s namely, Aminoacyl site a), Peptidyl site (P) and Exit site (E).

The empty tRNA leaves from E site.

Only the AA_1-tRNA complex binds at P site directly, while all the other incoming tRNA complexes get attached first at A site and then are shifted to P site.

Polypeptide chain is released from P-site.

In eukaryotes, 40S (smaller sub unit) and 60S (larger sub unit) combine to form 80S type of ribosome.



Elongation :

This is done by formation of peptide linkageslbonds in between the successive amino acid molecules

(AA_1,AA_2,AA_3 and so on). The elongation activity is catalyzed by the enzyme peptidyl transferase.Each tRNA complex brings a specific amino acid. Due to complementary nature of anticodons and codons, the amino acids are placed to their proper positions.During elongation, the ribosome moves along the mRNA in a step wise manner from start to stop codon (5' $\rightarrow$ 3'), one codon ahead each time. This movement is called translocation. In every step of translocation, one amino acid is added in the polypeptide chain causing elongation.

Termination :

When the mRNA reaches the last termination codon, i.e. either UAA, UAG or UGA, termination occurs. In identifying the stop/termination codon and in releasing the polypeptide chain from the site, the release or termination factors Rl, R2 and S play an important role. After termination, the smaller (30S) and larger (50S) sub units of ribosome get separated from each other. In order to increase the cellular efficiency of protein synthesis, many ribosomes may bind to the mRNA strand and form the polypeptide chain for synthesis of protein molecule. Such a structure with many ribosomes bound to mRNA is called polysomes or polyribosome.

Q.46. What is splicing? Why is splicing necessary in eukaryotic genes ?

Ans: The process by which non-coding region (intron) on hnRNA are removed and coding region (exon) are joined to produce mRNA is called splicing.Splicing is necessary in eukaryotes to remove the non-coding introns from hnRNA to produce a meaningful functional mRNA.

Prokaryotes do not have introns in the mRNA.

Q.47.What is hnRNA? Explain the changes that take place in hnRNA during the processing to form m-RNA?

Ans: hnRNA: It is precursor of m-RNA called heterogenous nuclear ribonucleic acid. It undergoes 2 additional processes. i) Capping ii) Tailing.

i) Capping : an unusual nucleotide methyl guanosine triphosphate is added to the 5' end ofhn RNA.

ii) Tailing : the adenylate residues (app. 200-300) are inserted at 3' end. So, fully processed hnRNA is then called m-RNA. It is then transported out of the nucleus for translation process.

Q.48.What is a promoter in a transcription unit? Where is it located in DNA ?

Ans: Promoter is a DNA sequence that provides binding site for RNA polymerase. Promoters are located near the genes they regulate, on the same strand and typically upstream (towards the 5' region of the sense strand).

Q.49.What is a terminator? What is its significance in transcription ?

Ans: The terminator is a component of transcription unit, which defines the end of the process of transcription.It is a code on mRNA for which tRNA has no anticodon and so the polypeptide chain breaks.

Q.50.What is the function of RNA primer during protein synthesis ?

Ans: RNA primer is essential for initiation of new DNA chain. It is formed on the free end of one strand and fork end of another strand. RNA primer attracts complementary nucleotides from the surrounding nucleoplasm. Without RNA primer, DNA polymerase cannot add nucleotides. RNA primer is required to release mRNA.

Q.51. What are polysomes or polyribosomes ?

Ans: In order to increase the cellular efficiency of protein synthesis, many ribosomes may bind to the mRNA strand. Such a structure with many ribosomes bound to mRNA is called polysomes or polyribosome.

Q.52. Distinguish between Transcription in prokaryotes and Transcription in eukaryotes.

Ans:

No.	Transcription in prokaryotes	Transcription in eukaryotes
i)	mRNA is polyscistronic.	mRNA is monocistronic.
ii)	Only one RNA polymerase takes in the process of transcription	Three RNA polymerases take part in the process of transcription.
iii)	Transcription occurs in cytosol (cytoplasmic matrix).	Transcription occurs in nucleus.
iv)	Splicing is not required	Splicing is required for moving introns.

Q.53. Differentiate between template strand and coding strand.

Ans:

No.	Template strand	Coding strand
i)	This is the strand of DNA having $3' \rightarrow 5'$ polarity	This is the strand of DNA having $3' \rightarrow 5'$ polarity.
ii)	It serves as template for transcription as well as codes for RNA	It does not code for any part of RNA during transcription.

Q.54. If the sequence of coding strand in transcription unit is written as follows :

5' ATGC ATGC ATGC ATGC ATGC ATGC ATGC 3'.

Write down the sequence of mRNA.

Ans: For this, template strand will be:

3' TACG TACG TACG TACG TACG TACG TACG 5'

and the sequence of bases in mRNA will be :

5' AUGC AUGC AUGC AUGC AUGC AUGC AUGC 3'

Q.55. Explain the process of charging oftRNA. Why is it essential in translation ?

Ans: In presence of an enzyme aminoacyl tRNA synthetase, the amino acid (Aa) molecule is activated and then each amino acid is attached to the specific tRNA molecule at 3'/CCA end to form aminoacyl-tRNA complex. The reaction needs ATP. This process is called charging oftRNA or aminoacylation oftRNA.

Q.56. Explain (in one or two lines) the function of the following :

i) Promoter ii) tRNA iii) Exons

Ans: i) Promoter : It is the sequence of bases where the RNA polymerase binds for transcription, thus it initiates transcription and also controls the rate of synthesis of m-RNA.

ii) tRNA: It carries specific type of amino acid at CCA end to the ribosomes during protein synthesis. It places the required amino acid properly in the sequence.

iii) Exons: These are parts of DNA coding for RNA. Exon is therefore a region of DNA or gene that becomes a part ofm-RNA and codes for different amino acids.

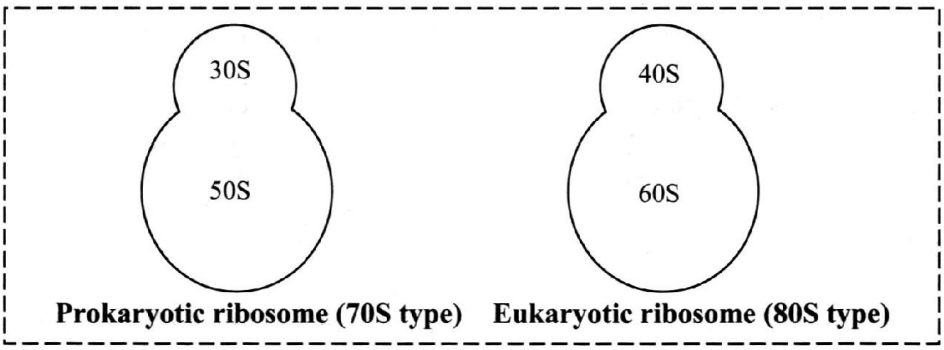
Q.57. Explain the structure of ribosome.

Ans: i) Ribosomes are granular organelles which do not have any enclosed membrane. Ribosomes are present in both prokaryotes and eukaryotes and are associated with protein synthesis.

ii) Ribosomes are composed of approximately 65% r-RNA and 35% proteins.

iii) Each prokaryotic ribosome has two subunits with 30S and 50S sedimentation coefficient, which combine to form 70S type of ribosome.

iv) Similarly, eukaryotic ribosome has two subunits with 40S and 60S sedimentation coefficient, which combine to form.80S type of ribosome. The two unequal and irregularly shaped sub-units fit together to farm a cleft during protein synthesis through which the m-RNA passes as ribosome moves along it at the time of translation.



Q.58. Depending upon chemical nature of template (DNA or RNA) and the nature of nucleic acids synthesized from it (DNA or RNA), list the types of nucleic acid polymerase.

Ans: i) The process of replication requires DNA dependent DNA polymerase. It uses a DNA template to catalyze the polymerization of deoxyribonucleotides.

ii) There is a single DNA dependent RNA polymerase that catalyzes the transcription of all types of

RNA in bacteria. RNA polymerase binds to promoter and initiates transcription (initiation). Here, RNA polymerase is only capable of catalyzing the step of elongation. It associates transiently with 'initiation factor' and 'termination factor' to initiate and terminate the transcription.

iii) In eukaryotes, there are three RNA polymerases in the nucleus. The RNA polymerase I transcribes rRNA (28S, 18S and 5.8S), RNA polymerase III is responsible for transcription oftRNA and snRNA (small nuclear RNa). The RNA polymerase II transcribes precursor of mRNA, i.e. heterogenous nuclear RNA (hnRNa).

Q.59. Where do transcription and translation occur in bacteria and eukaryotes ?

Ans: Transcription and translation in bacteria occur in the cytoplasm of the cell, whereas III eukaryotes, transcription occurs in the nucleus and translation occurs in the cytoplasm.

2.8 : Gene Expression and Gene Regulation

Q. 60. Define the terms – i) Operon ii) Repressors

Ans:i) Operon :

The clusters of genes with related functions are called operons.

ii) Repressors :

Proteins which bind to the operator region of the operon and prevent RNA polymerase from transcribing the operon are called repressors.

Q.61.At which level can gene expression be controlled ?

Ans: Gene expression can be controlled at various levels such as transcriptional or post transcriptional or translational level.

Q.62.Describe the structure of 'Operon'.

Ans: Concept of operon was first proposed by Jacob, Monod and Wollman. A unit of genetic material that functions in a coordinated manner by means of an operator, a promoter, and one or more structural genes that are transcribed together is called operon. The clusters of genes with related functions are called operons.

Components of an operon :

i) One or more structural gene(s):

a. Structural genes have the information to produce enzymes; hence they transcribe the mRNAs for the enzymes.

b. The three structural genes of lac operon (z, y and a) produce a single polycistronic mRNA.

ii) Operator :

a. The sequence of DNA adjacent to promoter where specific repressor protein binds is called operator.

b. The action of operator is controlled by a protein called repressor. It acts as on/off switch for the

iii) Promoter :

a. The sequence of DNA where RNA polymerase binds and initiates transcription of structural genes is called promoter.

b. It initiates transcription and controls the rate of synthesis of mRNA.

iv) Regulator Gene :

a. This gene codes for a protein called repressor.

b. When the repressor binds to the operator, the operator is switched off and transcription does not occur.

c. If the repressor is prevented from binding to the operator, the switch is on and transcription continues.

Hence, the repressor is also called as the regulatory protein.

v) Inducer/Corepressor :

Inducer is a metabolite which binds to the repressor and by changing its configuration, prevents the repressor from binding to the operator. So, the switch remains on and transcription continues; this is the case with inducible operons, e.g. lac operon of *E.coli.*

Q.63.Describe the 'Lac operon'.

Ans:i) Lac operon means lactose operon.

ii) Jacob and Monad proposed the classical model of Lac operon.

iii) The Lac operon has promoter site (P), regulatory site (i) and operator site (O).

iv). Besides this, it has three structural genes, namely z, y and a each producing an enzyme.

v) The following three enzymes are required for the metabolism oflactose in the cell.

Name of gene	Enzyme produced	Function
lac z	β -galactosidase	Lactose $\xrightarrow{\beta-\text{galactosidase}}$ Glucose + Galactose
lac y	Permease	Entry of lactose in the cell
lac a	Transacetylase	Transfers acetyl group from Acetyl CoA to β -galactosidase

vi) If glucose is not available for cells, they will need to use another source of energy such as lactose.

vii) If lactose is **not available,** the repressor will attach to the operator and block RNA polymerase.

viii) Lactose acts as an inducer. If lactose **is available,** it will remove the repressor from the operator, bind with repressor to form inducer-repressor complex and allow RNA polymerase to transcribe mRNA.

ix) RNA polymerase will attach to promoter and if it is not blocked, will begin transcribing mRNA.

x) RNA polymerase first encounters the **lac z** gene which is responsible for making **β -galactosidase**. **β -galactosidase** is the enzyme that hydrolyzes (breaks) the bond between glucose and galactose to make the disaccharide lactose.

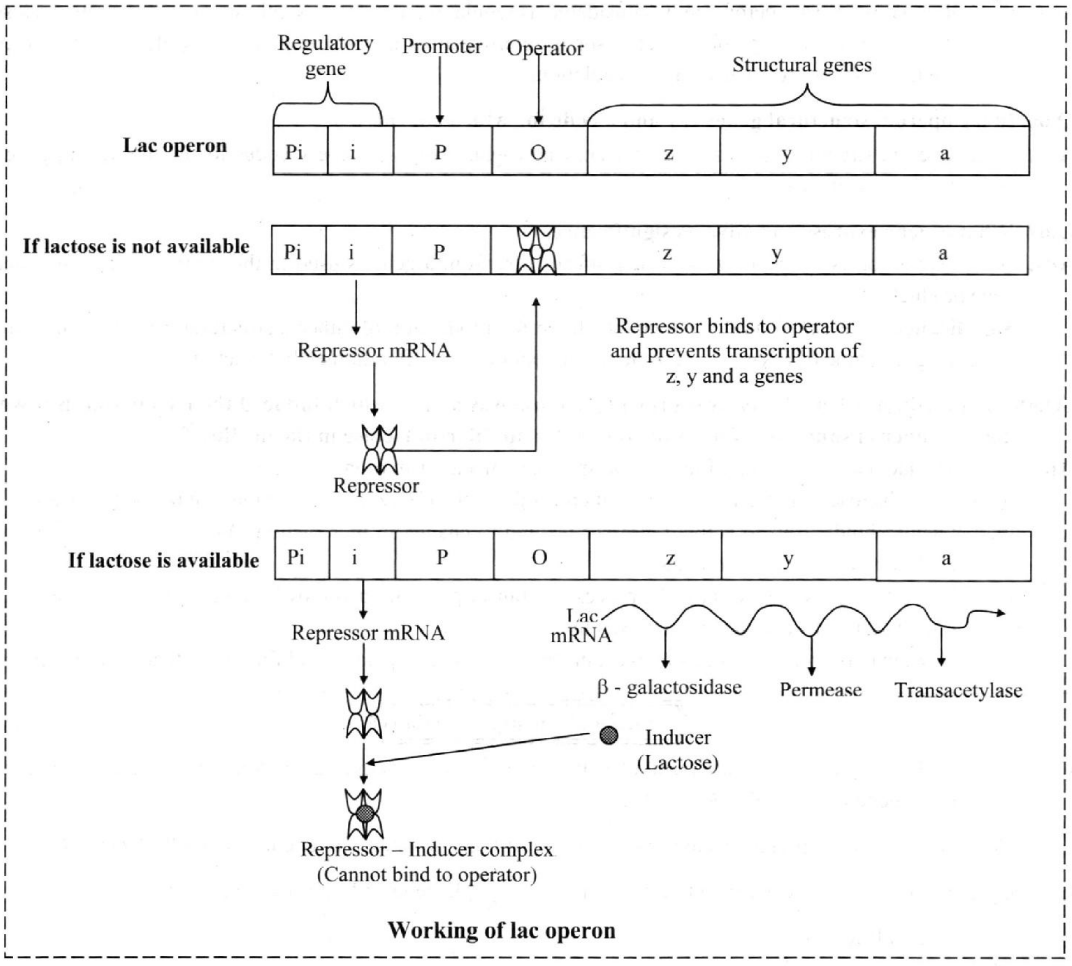
xi) RNA polymerase moves on to the next gene, **lac y** that makes the enzyme permease. It is a transport protein that carries lactose into the cell.

xii) RNA polymerase finally moves to the lac a gene which is responsible for making **transacetylase,** which transfers an acetyl group from acetyl CoA to β -galactosidase.

xiii) β -galactosidase, permease and transacetylase are enzymes in the metabolic pathway used to get energy from lactose.

xiv) After lactose is used up and levels decrease, the repressor will attach to the operator blocking the production of β -galactosidase, permease and transacetylase, so that lactose levels increase.

xv) Once lactose levels increase, the repressor is removed from the operator and RNA polymerase continues to make β -galactosidase, permease and transacetylase, thus enabling the breakdown oflactose.



Working of lac operon

Q.64.Give the names and functions of enzymes involved in lactose metabolism in E. coli. [Oct 2014]

Ans: The names and functions of the enzymes involved in lactose metabolism in E. coli are given in the table below :

Enzyme	Function
β -galactosidase	Lactose $\xrightarrow{\beta-\text{galactosidase}}$ Glucose + Galactose
Permease	Entry of lactose in the cell
Transacetylase	Transfers acetyl group from Acetyl CoA to β -galactosidase

Q.65. Explain the role of lactose in lac operon.

Ans: i) Lactose is the inducer of lac operon (lac stands for lactose).

ii) The inducer binds to the repressor and changes its configuration, so that it cannot bind to the operator. The repressor-inducer complex moves away from the operator and hence the operator switch remains on. RNA polymerase has access to the promotor and hence transcription of the structural genes takes place and lactose is catabolised into glucose and galactose.

iii) Regulation of lac operon can be considered as regulation of enzyme synthesis by its substrate, lactose. Regulation of this operon by repressor is referred to as negative regulation, while that by inducer (lactose) is considered as positive regulation.

Q.66 In lac operon, structural genes z, y and a code for which enzymes ?

Ans: In lac operon, structural gene z codes for enzyme p-galactosidase, gene y codes for Permease and gene a codes for Transacetylase.

Q.67.What is gene expression ? Give its significance.

Ans: Gene expression is the process by which information from a gene is used in the synthesis of a functional gene product.

Significance : The expression of a gene results in the production of either a structural protein or an active protein. eg. Enzyme or RNA. These proteins are required for different metabolic activities.

Q.68. In a medium where *E. coli* was growing, lactose was added, which induced the lac-operon. But why does lac-operon shut down after sometime after addition of lactose in the medium ?

Ans: i) The lac operon is required for the transport and metabolism of lactose in E. coli.

ii) When lactose is added to a medium ,it enters the cells of E.coli by the action of enzyme permease.

iii) Lactose binds itself to active repressor leading to change in its structure. As a result, repressor now fails to bind itself to the operator.

iv) Now, RNA polymerase starts the process of transcription of operon by binding to promoter site P.

v) Finally, all lactose molecules are used up.

vi) Now, inactive repressor turns active, attaches itself to the operator and finally switches off the operon.

Additionai Theory Questions

Q.l. How did Hershey and Chase differentiate between DNA and protein in their experiment while proving that DNA is the genetic material? Refer Q.3.

Q.2.How did Griffith's experiment support the concept of transformation of genetic material? Refer Q.4.

Q.3. Give an account of the experiment performed by Avery, Macleod and McCarty. Refer Q.5.

QA. Define the following terms:

i) Cistron *Refer Q.7 (i).*

ii) Muton *Refer Q.7 (ii).*

iii) Recon *Refer Q.7 (iii).*

Q.5 Give the chemical composition of nucleotide. *Refer Q.8.*

Q.6. Give an account of double helical model of DNA. [Sep 2008] *Refer Q.12.*

Q.7. Describe Watson and Crick model of DNA. [Mar 2009] *Refer Q.12.*

Q.8. Why are DNA strands considered as antiparallel? *Refer Q.12* (vii).

Q.9. Describe the process of replication of eukaryotic DNA. [Mar 2009] *Refer Q.17.*

Q.10.Draw a labelled diagram showing the mechanism of DNA replication. [Mar 2008] ***Refer Q.17.***

Q.l1.Describe the process of replication in deoxyribonucleic acid (DNa). [Mar 2013 Old Course] ***Refer Q.17.***

Q.12.Which property of DNA helix led Watson and Crick to hypothesize semiconservative mode of DNA replication, Explain. ***Refer Q.18.***

Q.13.Write a note on m-RNA. ***Refer Q.27 a).***

Q.l4. Sketch and label the diagram ofm-RNA. [Mar 2008] ***Refer Q.27 a).***

Q.l5. Describe the clover leaf model oft-RNA. ***Refer Q.27 (c).***

Q.16. Sketch and label 'clover leaf model' oft-RNA. [Mar 2014] ***Refer Q.27 (c).***

Q.l7. Draw a neat labelled diagram of the hair pin model oft-RNA. [Mar 2013] ***Refer Q.27 (c).***

Q.l8. What are the properties of genetic code? Refer Q.35.

Q.19. What is operon concept? What are the components of operon? ***Refer Q.62.***

Quick Review

- DNA (Deoxyribonucleic acid) : **Deoxyribo nucleotides**
  - Made up of
    - Join together by Phospho-diester bond
      - i. Phosphoric acid
      - ii. Deoxyribose sugar
    - Join together by glycosidic bond
      - iii. Nitrogen bases
        - Purines
          - Adenine (A)
          - Guanine (G)
        - Pyrimidines
          - Thymine (T)
          - Cytosine (C)
- Gene : Made up of
  - Cistron (unit of function)
  - Muton (unit of mutation)
  - Recon (unit of recombination)
- RNA (Ribonucleic acid) : 3 types
  - m-RNA (Messenger RNA)
  - t-RNA (Transfer RNA)
  - r-RNA (Ribosomal RNA)
- Lac operon : Consists of
  - Promoter site (P)
  - Regulatory site (i)
  - Operator site (O)
  - Three structural genes
    - Gene z : makes enzyme β-galactosidase
    - Gene y : makes enzyme permease
    - Gene a : makes enzyme transacetylase

• Scientists and their contribution :

No.	Scientist	Contribution	Year
i)	F. Griffith	Discovered the phenomenon of transformation	1928
ii)	M. Schlesinger	Demonstrated that the bacteriophages are composed of DNA and protein.	1934
iii)	O.T. Avery, C.M. Macleod and M. McCarty	Proved that the transforming principle is DNA	1944
iv)	A.D. Hershey and M Chase	Demonstrated that only DNA of bacteriophage enters that host i.e. bacterium *Escherichia coli,* where as protein remains behind	1952
v)	Seymour Benzer	Introduced the term cistron, muton and recon.	1955
vi)	Friedrich Miescher	Isolated nuclei and nucleoprotein from pus cells and called it	1869
vii)	J.D. Watson and F.H.C.Crick	Proposed a model for DNA, consisting of two long strands coiled around a common imaginary, central axis to form a double helix.	1953
viii)	E. Chargaff	Demonstrated that in DNA, the number of Adenine and Thymine bases are always equal and so are the number of guanine and cytosine bases.	1950
ix)	Meselson and Stahl	Experimentally proved the semi-conservative nature of DNA replication using heavy isotope of nitrogen N^{15} and *E. coli*	1958
x)	G.W.Beadle and E.L.Tatum	Published their classical study on biochemical genetics of *Neuropora.* Their finding was named one gene – one enzyme hypothesis and got Nobel prize for the in 1958	1941
xi)	Vernon Ingram	Modified one gene – one enzyme hypothesis is one gene– one polypeptide hypothesis.	1957
xii)	M.W. Nirenberg, H.Matthaei and Har Gobind Khorana	Cracked the mRNA genetic code got Nobel prize for that in 1968	1961
xiii)	F.H.C.Crick	Proposed the hypothesis for anticodons of tRNA and explained how several codons meant for same amino acid are recognized by same tRNA.	1965
xiv)	Francois Jacob and J Monod	Proposed the classical model of Lac Operon.	1961

Multiple Choice Questions

1. Which of the following is TRUE?
a) Adenine ≡ Guanine, Thymine = Cytosine
b) Adenine = Guanine, Thymine ≡ Cytosine
c) Adenine = Thymine, Guanine ≡ Cytosine
d) Adenine ≡ Thymine, Guanine = Cytosine

2. m-RNA, t-RNA and r-RNA are the types of
a) genetic RNA
b) non-genetic RNA
c) both a) and b)
d) neither a) nor b)

3. Which of the following is responsible for expression of a trait?
a) Recon b) Muton
c) Cistron d) Codon

4. The two strands of DNA are
a) similar in nature and complementary.
b) anti-parallel and complementary.
c) parallel and complementary.
d) basically different in nature.

5. In DNA, Purine and Pyrimidine ratio is
a) 2:1 b) 1:1
c) 1:2 d) 2:2

6. Purines are
a) single ring compounds
b) double ring compounds
c) open chained
d) sugar compounds

7. Which of the following is a pyrimidine base ?
a) Uracil b) Adenine
c) Guanine d) Riboflavin.

8. How many H–bonds are present between cytosine and guanine ?
a) One c) Two
d) Three d) Four

9. In nucleotide, the nitrogen base is attached to carbon no. 1 of sugar by____bond.
[Mar 2013]
a) glycosidic b) hydrogen
c) phosphodiester d) phosphate

10. The enzyme DNA polymerase has polarity. It can work only in
a) 5' → 3' direction b) 3' → 5' direction
c) RNA synthesis d) translocation

11. Okazaki fragments are joined in a correct sequence by
a) DNA polymerase I
b) DNA ligase
c) RNA polymerase
d) primase

12. In Eukaryotes, DNA replication is
a) semi conservative
b) conservative
c) dispersive
d) anabolic

13. Triplet code in mRNA which is usually the starting point or start signal of protein synthesis is
a) UUA b) AUG
c) UGA d) UGC

14. DNA strand, which is formed continuously in 5' → 3' direction is called
a) lagging strand b) leading strand
c) template strand d) okazaki fragment

15. A nucleosome is a portion of the chromosome containing
a) Only histone
b) Both DNA and histone
c) Only DNA
d) Both DNA and RNA

16. Centraldogma means
a) one way flow of information.
b) two way flow of information.
c) many way flow of information.
d) reverse flow of information.

17. Unwinding of DNA strands is done by which enzyme?
a) Amylase b) Endonuclease
c) Transcriptase d) Helicase

18. A template strand of DNA has base sequence CATGATTAC. New strand synthesized on it will be
a) GATCAUATG b) GTACTAACG
c) GAACTAATG. d) GTACTAATG

19. Formation ofm-RNA from DNA is called as
a) transcription b) translation
c) translocation d) transformation

20. On which strand of DNA, m-RNA is constructed?
a) Sense strand b) Anti-sense strand
c) Both the strands d) Anyone strand

21. The bonds joining two successive nucleotides of DNA strand are called
a) Phospho-diester bonds
b) Covalent bonds
c) Hydrogen bonds
d) Glycosidic bonds

22. Enzyme necessary for transcription is
a) DNA polymerase b) RNA polymerase
c) endonuclease d) RN ase

23. In which of the following stage, does synthesis of polypeptide takes place ?
a) Transcription b) Translation
c) Teminism d) Replication

24. One gene-one enzyme hypothesis was given by
a) Beadle and Tatum
b) Griffith
c) Avery, McCleod and McCarty
d) Hershey and Chase

25. Genetic code translates the language of
a) RNA into that of proteins.
b) proteins into that of DNA.
c) amino acids into that ofRNA.
d) RNA into that of DNA.

26. Which of the following is the smallest RNA ?
a) t-RNA b) m-RNA
c) r-RNA d) ds-RNA

27. Exons and introns are parts of
a) DNA b) RNA
c) m-RNA d) t-RNA

28. Portion of gene which is transcribed but not translated is
a) exon b) intron
c) cistron d) codon

29. Genes express their character by forming
a) enzymes b) carbohydrates
c) fats d) vitamins

30. Genes that are involved in turning on or off the transcription of a set of structural genes are called
a) polymorphic genes b) operator genes
c) redundant genes d) regulatory genes

31. DNA helix model was given by
a) Watson and Crick b) Knoll and Ruska
c) Khorana d) Priestley

32. In the genetic code dictionary, how many codons are used to code for all the 20 essential amino acids ?
a) 64 b) 61
c) 60 d) 20

33. Triplet codon in genetics is
a) fixed b) degenerate
c) ambiguous d) non - wobble

34. The process of removal of introns and joining of exons is called
a) capping b) tailing
c) termination d) splicing

35. Which of the following is a stop codon ?
a) AUG b) GUG
c) UAA d) GGU

36. Which one of the following codes for methionine and also acts as initiator codon?
a) AUG b) AUC
c) ACU d) ACA

37. Operon is
a) sequence of three nitrogen bases determining a single amino acid.
b) a set of closely placed genes regulating a metabolic pathway in prokaryotes.
c) segment of DNA specifying a polypeptide.
d) gene responsible for switching on and switching off of other genes.

38. According to Operon concept, regulator gene forms
a) an inducer b) a repressor
c) a small peptide d) an inhibitor

39. The lac operon consists of
a) four regulatory genes only.
b) one regulatory gene and three structural genes.
c) two regulatory genes and two structural genes.
d) three regulatory genes and three structural genes.

40. The number of adenine molecules in a given DNA segment is 25 and the number of cytosine molecules is 45. The total number of nucleotides in the segment is
a) 70 b) 140
c) 90 d) 50

41. A nucleoside is formed of
a) pentose sugar, phosphate and nitrogen base
b) phosphate and nitrogen base
c) pentose sugar and phosphate
d) pentose sugar and nitrogen base

42. Lac-operon is related with
a) Lactose metabolism
b) Starch metabolism
c) Lipid metabolism
d) Protein metabolism

43. Entry of lactose in cell is influenced by
a) Permease b) Aldolase
c) Ligase d) Transcriptase

Answer Keys

1. c)	2. b)	**3.** c)	**4.** b)	**5.** b)	**6.** b)	**7.** a)	**8.** c)	**9.** a)	**10.** a)
11. b)	**12.** a)	**13.** b)	**14.** b)	**15.** b)	**16.** a)	**17.** d)	**18.** d)	**19.** a)	**20.** b)
21. a)	**22.** b)	**23.** b)	**24.** a)	**25.** a)	**26.** a)	**27.** c)	**28.** b)	**29.** a)	**30.** b)
31. a)	**32.** b)	**33.** b)	**34.** d)	**35.** c)	**36.** a)	**37.** b)	**38.** b)	**39.** d)	**40.** b)
41. d)	**42.** a)	**43.** a)							