6

Molecular Basis of Inheritance

Multiple Choice Questions (MCQs)

Q. 1 In a DNA strand the nucleotides are linked together by

(a) glycosidic bonds (b) phosphodiester bonds
(c) peptide bonds (d) hydrogen bonds

Ans. *(b)* (In a DNA strand the nucleotides are linked together by 3′–5′ phosphodiester linkage (bonds) to form a dinucleotide. More nucleotides can be joined in such a manner to form a polynucleotide chain.

Q. 2 A nucleoside differs from a nucleotide. It lacks the

(a) base (b) sugar
(c) phosphate group (d) hydroxyl group

Ans. *(c)* A nitrogenous base is attached to the pentose sugar by an N-glycosidic linkage to form a nucleoside, *i.e.,* Nucleoside=Nitrogen base+Pentose sugar.

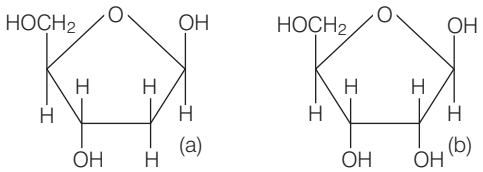
When a phosphate group is attached to the 5′-OH of a nucleoside through phosphodiester linkage, a nucleotide is formed, *i.e.,* Nucleotide = Nitrogen base + Pentose sugar + Phosphate (PO_4).

So, a nucleoside differs from a nucleotide as it lacks the phosphate group.

Q. 3 Both deoxyribose and ribose belong to a class of sugars called

(a) trioses (b) hexoses (c) pentoses (d) polysaccharides

Ans. *(c)* Both deoxyribose and ribose belong to the class pentoses as it contains 'S' carbon atoms.



Structure of (a) deoxyribose (b) ribose sugar

Q. 4 The fact that a purine always paired base through hydrogen bonds with a pyrimidine base leads to, in the DNA double helix

(a) the antiparallel nature
(b) the semiconservative nature
(c) uniform width throughout DNA
(d) uniform length in all DNA

Ans. *(c)* The diameter of the strand is always constant due to a pairing of purine (adenine and guanine) and pyrimidine (cytosine and thymine). This specific bonding gives uniform width to the DNA.

Q. 5 The net electric charge on DNA and histones is

(a) both positive
(b) both negative
(c) Both (a) and (b)
(d) zero

Ans. *(c)* DNA consists of a nitrogenous base, pentose sugar and a phosphate group. DNA has negative charge due to the presence of phosphate group (PO_4^{3-}).

Histones are rich in the basic amino acid residues lysines and arginines, which carry positive charges in their side chains. Therefore, histones are positively charged.

Q. 6 The promoter site and the terminator site for transcription are located at

(a) 3′ (downstream) end and 5′ (upstream) end, respectively of the transcription unit
(b) 5′ (upstream) end and 3′ (downstream) end, respectively of the transcription unit
(c) the 5′ (upstream) end
(d) the 3′ (downstream) end

Ans. *(c)* The promoter is the binding site for RNA polymerase for initiation of transcription.

The promoter is located towards 5′-end (upstream) of the structural gene of coding strands and provides the binding site for RNA polymerase.

Q. 7 Which of the following statements is the most appropriate for sickle-cell anaemia?

(a) It cannot be treated with iron supplements
(b) It is a molecular disease
(c) It confers resistance to acquiring malaria
(d) All of the above

Ans. *(d)* Sickle-cell anaemia is an autosome linked recessive trait. In this genetic disorder point mutation in β-globin chain results in change of glutamate (glutamic acid) to valine at sixth position. Only the homozygous individuals for $Hb^S{}_2$, *i.e.,* Hb^SHb^S show the diseased phenotype. The heterozygous individuals (Hb^S/Hb^A) are carriers.

It is also known that heterozygotes, having both types of haemoglobin, show resistance to malaria infection because the body targets the *P. falciparum* (protozoan) infected cells for destruction of RBC.

Q. 8 One of the following is true with respect to AUG

(a) it codes for methionine only
(b) it is also an initiation codon
(c) it codes for methionine in both prokaryotes and eukaryotes
(d) All of the above

Thinking Process

Three adjacent nitrogenous bases constitute a codon which specifies the placement of one amino acid in a polypeptide.

Ans. *(d)* Polypeptide synthesis is signalled by two initiation codons commonly AUG or methionine codon and rarely GUG or valine codon. Since there are 64 triplet codons and only 20 amino acids, the incorporation of some amino acids must be influenced by more than one codon.

Only tryptophan (UGG) and methionine (AUG) are specified by single codons. AUG codes for methionine in both prokaryotes and eukaryotes.

Q. 9 The first genetic material could be

(a) protein (b) carbohydrates (c) DNA (d) RNA

Ans. *(d)* RNA was the first genetic material. There is now enough evidence to suggest that essential life processes (such as metabolism, translation, splicing, etc.), evolved around RNA.

RNA used to act as a genetic material as well as a catalyst (there are some important biochemical reactions in living systems that are catalysed by RNA catalysts and not by protein enzymes). But, RNA being a catalyst was reactive and hence unstable.

Therefore, DNA has evolved from RNA with chemical modifications that make it more stable. DNA being double-stranded and having complementary strand further resists changes by evolving a process of repair.

Q. 10 With regard to mature *m*RNA in eukaryotes

(a) exons and introns do not appear in the mature RNA
(b) exons appear but introns do not appear in the mature RNA
(c) introns appear but exons do not appear in the mature RNA
(d) both exons and introns appear in the mature RNA

Ans. *(b)* In eukaryotes, the monocistronic structural genes have interrupted coding sequences *i.e.,* the genes in eukaryotes are split. The coding sequences or expressed sequences are defined as exons.

These sequences (exons) appear in mature or processed RNA. The exons are interrupted by introns or intervening sequences which do not appear in mature or processed RNA.

Q. 11 The human chromosome with the highest and least number of genes in them are respectively

(a) chromosome 21 and Y (b) chromosome 1 and X
(c) chromosome 1 and Y (d) chromosome X and Y

Ans. *(c)* In humans, chromosome 1 has highest genes (2968 approx.) and the Y has the fewest (231 approx.) genes.

Q. 12 Who amongst the following scientists had no contribution in the development of the double helix model for the structure of DNA?

(a) Rosalind Franklin (b) Maurice Wilkins
(c) Erwin Chargaff (d) Meselson and Stahl

Ans. *(d)* It was only in 1953 that **James Watson** and **Francis Crick**, based on the *X*-ray diffraction data produced by **Maurice Wilkins** and **Rasalind Franklin**, proposed a very simple but famous double helix model for the structure of DNA.

Erwin Chargaff observed that for a double-stranded DNA, the ratios between adenine and thymine and guanine and cytosine are constant and equals one.

On the other bond **Matthew Meselson** and **Franklin Stahl** in 1958 performed experiments on *E.coli* to prove that DNA replication is semi-conservative. But had no contribution it the development of double helix model.

Q. 13 DNA is a polymer of nucleotides which are linked to each other by 3′–5′ phosphodiester bond. To prevent polymerisation of nucleotides, which of the following modifications would you choose?

(a) Replace purine with pyrimindines
(b) Remove/Replace 3′ OH group in deoxy ribose
(c) Remove/Replace 2′ OH group with some other group in deoxy ribose
(d) Both (b) and (c)

Ans. ***(b)*** The enzyme called DNA polymerase progressively adds deoxyribonucleotides to the free 3′-end of the growing polynucleotide chain so, that replication of the 3′–5′ strand of the DNA molecule is continuous (growth of the new strand in 5′ → 3′ direction).

So, to prevent polymerisation of nucleotides 3′ OH group in deoxyribose should be replaced/removed.

Q. 14 Discontinuous synthesis of DNA occurs in one strand, because

(a) DNA molecule being synthesised is very long
(b) DNA dependent DNA polymerase catalyses polymerisation only in one direction (5′→ 3′)
(c) it is a more efficient process
(d) DNA ligase has to have a role

Thinking Process

The replication of 3′ → 5′ strand is continuous and it is called leading strand, while the replication of second strand (5′→ 3′ strand) of the DNA molecules is discontinuous and it is known as the lagging strand.

Ans. ***(b)*** DNA polymerase adds deoxyribonucleotides to the free 3′-end of the growing polynucleotide chain so, that replication of the 3′→ 5′ strand of the DNA molecule is continuous (growth of the new strand in 5′ → 3′ direction).

Since, DNA dependent DNA polymerase catalyses polymerisation only in one direction (5′ → 3′), discontinuous synthesis of DNA occurs in the other strand.

Q. 15 Which of the following steps in transcription is catalysed by RNA polymerse?

(a) Initiation (b) Elongation (c) Termination (d) All of these

Ans. ***(b)*** The DNA dependent RNA polymerase helps in DNA replication by catalysing the polymerisation in only one direction, *i.e.*, 5′ → 3′.

Q. 16 Control of gene expression takes place at the level of

(a) DNA-replication (b) transcription
(c) translation (d) None of these

Thinking Process

Regulation of gene expression refers to a very broad term that may occur at various levels.

Ans. ***(b)*** Considering that gene expression results in the formation of a polypeptide, it can be regulated at several levels. *In eukaryotes, the regulation could be exerted at*

(i) transcriptional level (formation of primary transcript)
(ii) processing level (regulation of splicing)
(iii) transport of *m*RNA from nucleus to the cytoplasm
(iv) translational level

While, in prokaryotes, control of the rate of transcriptional initiation is the predominant site for control of gene expression.

Q. 17 Regulatory proteins are the accessory proteins that interact with RNA polymerase and affect its role in transcription. Which of the following statements is correct about regulatory protein?

(a) They only increase expression
(b) They only decrease expression
(c) They interact with RNA polymerase but do not affect the expression
(d) They can act both as activators and as repressors

Thinking Process

Regulatory protein is a term used in genetics to describe a protein involved in regulating gene expressions. There are often needed to switch a gene on (activator) or to switch off a gene (represssor).

Ans. ***(d)*** Regulatory sequences (proteins) control the functions of structural genes and are at called regulatory genes. The important regulatory genes are promoters, terminators, operators and repressor.

To regulate the process of transcription, transcription factors (a sequence of specific DNA-binding factor) alone or with other proteins, promoter (as on activator) or stop as a repress or the binding site of RNA polymerase to DNA.

Q. 18 Which was the last human chromosome to be completely sequenced?

(a) Chromosome 1
(b) Chromosome 11
(c) Chromosome 21
(d) Chromosome-X

Ans. ***(a)*** Chromosome 1 was the last completed chromosome, sequenced two decades after the beginning of the human Genome Project (hGP). It is the designation for the largest human chromosome.

Q. 19 Which of the following are the functions of RNA?

(a) It is carrier of genetic information from DNA to ribosomes synthesising polypeptides
(b) It carries amino acids to ribosomes
(c) It is a constituent component of ribosomes
(d) All of the above

Thinking Process

RNA is a single chain polyribonucleotide which functions as carrier of coded genetic or hereditary information from DNA to cytoplasm for taking part in protein and enzyme synthesis.

Ans. ***(d)*** *r*RNA, *m*RNA and *t*RNA are major classes of RNAs that are involved in gene expression.
*r*RNAs bind protein molecules and give rise to ribosomes.
*m*RNA carries coded information for translation into polypeptide formation.
*t*RNA is called soluble or adaptor RNA and carries amino acids to *m*RNA during protein synthesis.

Q. 20 While analysing the DNA of an organism a total number of 5386 nucleotides were found out of which the proportion of different bases were Adenine = 29%, Guanine = 17%, Cytosine = 32%, Thymine = 17%. Considering the Chargaffs rule it can be concluded that

(a) it is a double-stranded circular DNA
(b) it is single-stranded DNA
(c) it is a double-stranded linear DNA
(d) No conclusion can be drawn

Ans. ***(b)*** According to Chargaff's rules of base pairing,

(i) The amount of adenine is always equal to the amount of thymine and the amount of guanine is always equal to the amount of cytosine.

(ii) Adenine is joined to thymine with two hydrogen bonds and guanine is joined to cytosine by three hydrogen bonds.

(iii) The ratio of adenine to thymine and that of guanine to cytosine is always equal to one,

i.e., $$\frac{A}{T} = \frac{G}{C} = 1$$

In the given organism, the DNA is not following the Chargaff's rule, hence it can be concluded that it is a single-stranded DNA, not double-stranded.

Q. 21 In some viruses, DNA is synthesised by using RNA as template. Such a DNA is called

(a) A-DNA (b) B-DNA (c) *c*DNA (d) *r*DNA

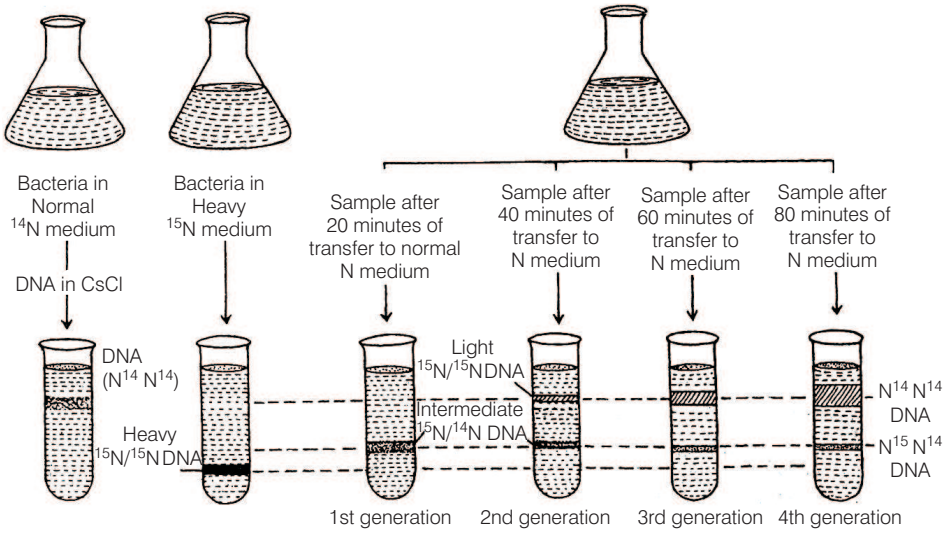
Ans. ***(c)*** In some viruses, like retroviruses (*e.g.,* HIV), an enzyme called reverse transcriptase is used to generate complementary DNA (*c*DNA) from an RNA template. This process is termed reverse transcription.

Q. 22 If Meselson and Stahl's experiment is continued for four generations in bacteria, the ratio of 15_N / 15_N : 15_N / 14_N : 14_N / 14_N containing DNA in the fourth generation would be

(a) 1:1:0 (b) 1:4:0 (c) 0:1:3 (d) 0:1:7

Ans. ***(d)*** Meselson and Stahl found that DNA of the first generation was hybrid or intermediate (^{15}N and ^{14}N). It settled in caesium chloride at a level higher than the fully labelled DNA of parent bacteria (^{15}N ^{15}N). The second generation of bacteria after 40 minutes, contained two types of DNA, 50% light (N^{14} N^{14}) and 50% intermediate (N^{15} N^{14}).

The third generation of bacteria after 60 minutes contained two types of DNA, 25% intermediate (N^{15} N^{14}) and 75% light (N^{14} N^{14}) in 1:3 ratio. The fourth generation after 80 minutes contained 12.5% N^{15} N^{14} and 87.5% N^{14} N^{14} DNA in 1:7 ratio.



Meselson and Stahl's experiment

Q. 23 If the sequence of nitrogen bases of the coding strand of DNA in a transcription unit is

5' - A T G A A T G - 3',

the sequence of bases in its RNA transcript would be

(a) 5′ - A U G A A U G - 3′ (b) 5′ - U A C U U A C - 3′
(c) 5′ - C A U U C A U - 3′ (d) 5′ - G U A A G U A - 3′

Ans. *(a)* 5′ - A T G A A T G - 3′ (coding strand)
↓
5′- T A C T T A C - 3′ (complementary strand)
↓
5′ -A U G A A U G - 3′ (RNA)

Q. 24 The RNA polymerase holoenzyme transcribes

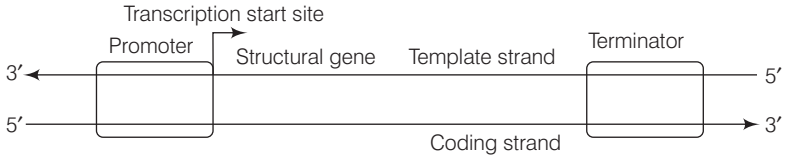
(a) the promoter, structural gene and the terminator region
(b) the promoter and the terminator region
(c) the structural gene and the terminator regions
(d) the structural gene only

Thinking Process

In prokaryotes, the structural gene is polycistronic and continuous. In bacteria (prokaryotes), the transcription of all the three types of RNA (mRNA, tRNA and rRNA) is catalysed by single DNA dependent enzyme, called the RNA polymerase.

Ans. *(c)* In *E. coli* bacterium, the RNA polymerase has co-factors β, β', α, α' and ω along with σ (sigma) factor, to catalyse the process. The transcription is completed in three steps.

Initiation σ (sigma) factor recognises the start signal and promotor region on DNA which then along with RNA polymerase binds to the promoter to initiate transcription.



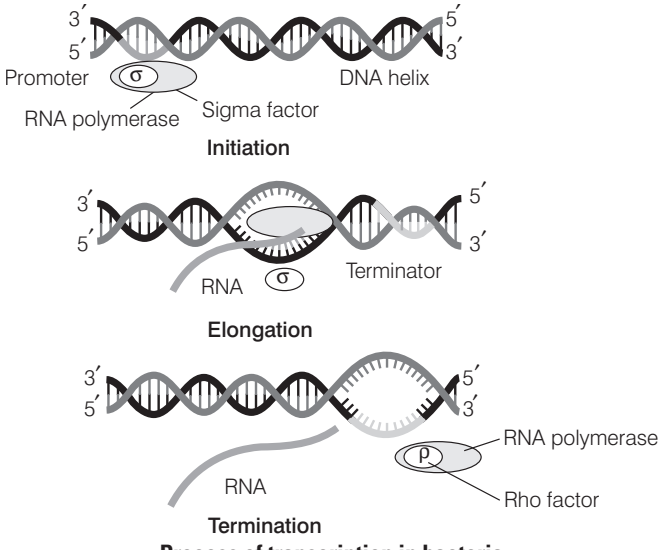
Schematic structure of a transcription unit

Elongation The RNA polymerase after initiation of RNA transcription loses the σ factor but continues the polymerisation of ribonucleotides to form RNA.

Termination Once the RNA polymerase reaches the termination region of DNA, the RNA polymerase is separated from DNA-RNA hybrid, as a result nascent RNA separates. This process is called termination which is facilitated by a termination factor ρ (rho).

In prokaryotes, *m*RNA does not require any processing, so both transcription and translation occur in the cytosol. It can be said that transcription and translation are coupled together.

Representation of initiation, elongation and termination are as given



Process of transcription in bacteria

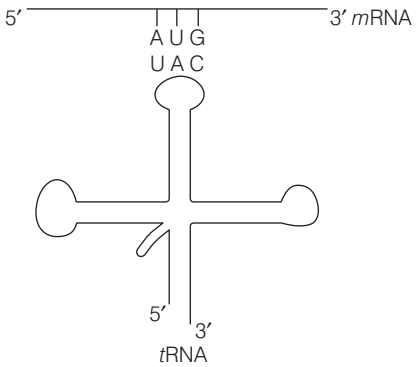
Q. 25 If the base sequence of a codon in *m*RNA is 5'-AUG-3', the sequence of *t*RNA pairing with it must be

(a) 5′ - UAC - 3′ (b) 5′ - CAU - 3′ (c) 5′ - AUG - 3′ (d) 5′ - GUA - 3′

Ans. ***(a)*** 5′ - A U G - 3′ (codon in *m*RNA)

| | |

5′ - U A C - 3′ (*t*RNA)



Q. 26 The amino acid attaches to the *t*RNA at its

(a) 5′-end (b) 3′-end (c) Anti codon site (d) DHU loop

Ans. ***(b)*** AA-binding site (amino acid binding site) lies at the 3′ end opposite the anticodon and has CCA-OH group. It is the site where amino acid attaches to the *t*RNA.

Q. 27 To initiate translation, the *m*RNA first binds to

(a) the smaller ribosomal sub-unit (b) the larger ribosomal sub-unit
(c) the whole ribosome (d) No such specificity exists

Thinking Process

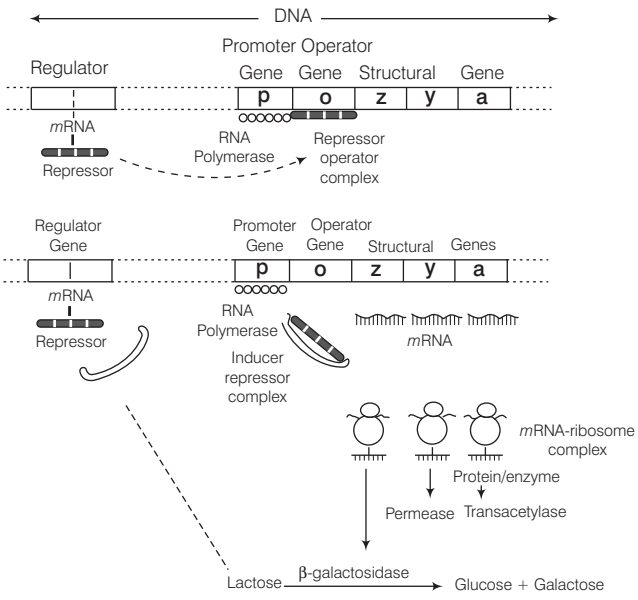
The cellular factory responsible for synthesising proteins is the ribosome.

Ans. *(a)* The ribosome consists of structural RNAs and about 80 different proteins. In its inactive state, it exist as two subunits, a large subunit and a small subunit. When the smaller subunit encounters the *m*RNA, the process of translation of the *m*RNA to protein begins .

Q. 28 In *E. coli*, the *lac* operon gets switched on when

(a) lactose is present and it binds to the repressor
(b) repressor binds to operator
(c) RNA polymerase binds to the operator
(d) lactose is present and it binds to RNA polymerase

Ans. *(a)*



Jacob and Monod model of an inducible operon

In case of lactose presence

(i) Lactose acts as an inducer which binds to the repressor and forms an inactive repressor.
(ii) The repressor fails to bind to the operator region.
(iii) The RNA polymerase binds to the operator and transcript *lac m*RNA.
(iv) *lac m*RNA is polycistronic, *i.e.,* produces all three enzymes, β-galactosidase, permease and transacetylase.
(v) The *lac* operon is switched on.

In case of lactose absence

(i) When lactose is absent, *i* gene regulates and produces repressor *m*RNA which translate repression.
(ii) The repressor protein binds to the operator region of the operon and as a result prevents RNA polymerase to bind to the operon.
(iii) The operon is switched off.

Very Short Answers Type Questions

Q. 1 What is the function of histones in DNA packaging?

Ans. *Functions of histones in DNA packaging are*

(i) Histones as units of octamer participate in primary packaging of DNA.

(ii) Basic histone proteins neutralise the acidic DNA molecule.

Q. 2 Distinguish between heterochromatin and euchromatin. Which of the two is transcriptionally active?

Ans. Densely packed and dark stained chromatin regions are called hetorochromation, while, loosely packed light stained regions are called euchromatin.

Euchromation is transcriptionally active and is transcribed into *m*RNA. Due to very tight coiling heterochromatin can not be transcribed and is inert/inactive form.

Q. 3 The enzyme DNA polymerase in *E.coli* is a DNA dependent polymerase and also has the ability to proofread the DNA strand being synthesised Explain. Discuss the dual polymerase.

Ans. In bacteria, three types of DNA polymerases are there. All of them can add nucleotides in 5′→ 3′ direction. They process exonuclease activity as well. DNA polymerase III can proofread the newly synthesised strand and senses the wrong base insertions.

It deletes wrong bases and helps correct the mistake by putting in the right one, DNA polymerase. The only mistake it cannot corrects substitution of uracil in place of thymin.

It can repair any damages done to DNA by UV exposure, etc., or the left over proofreading mistakes. It detects mutation caused by UV, removes mismatched pairs and puts back the right ones.

Q. 4 What is the cause of discontinuous synthesis of DNA on one of the parental strands of DNA? What happens to these short stretches of synthesised DNA?

Ans. Synthesis of DNA always takes place in 5′→ 3′ direction. In a double stranded DNA both strands are anti parallel and complementary. During DNA synthesis as both strands act as templates, only one strand, *i.e.,* 3′→ 5′ can synthesis complementary strand in 5′→ 3′ direction.

The other strand, *i.e.,* 5′→ 3′ has to be synthesised in small stretches in opposite direction as replication fork moves to right. That is why DNA synthesis is discontinuous on one of the parental strands of DNA. These small stretches called Okazaki fragments are joined together by DNA ligase enzyme that closes the nicks.

Q. 5 Given below is the sequence of coding strand of DNA in a transcription unit 3′ AATGCAGCTAT TAGG-5′ write the sequence of

(a) its complementary strand

(b) the *m*RNA

Ans. According to base complementary rules,

(a) 5'TTACGTCGATAATCC-3' (b) 5'CGAUUAUCGACGUAA-3'

RNA uses the base uracil (U) rather than thymine (T). So, in RNA the base pairs are

Adenine (A) pairs with uracil (U)

Guanine (G) pairs with cytosine (C).

Q. 6 What is DNA polymorphism? What is it important to study it?

Ans. DNA polymorphism refers to the variation in DNA arising through mutation at non-coding sequences.

A special type of polymorphism, called VNTR (Variable Number of Tandem Repeats), is composed of repeated copies of a DNA sequence that lie adjacent to one another on the chromosome. Since, polymorphism is the basis of genetic mapping of human genome, therefore, it forms the basis of DNA fingerprinting too.

The single nucleotide polymorphisms are used in locating diseases and tracing of human history as well as in case of paternity testing.

Q. 7 Based on your understanding of genetic code, explain the formation of any abnormal haemoglobin molecule. What are the known consequences of such a change?

Thinking Process

It is the case of sickle-cell anaemia.

Ans. Due to point mutation in β-globin chain of haemoglobin molecule, glutamic acid (Glu) is replaced by valine (Val) at the sixth position.

Under stress condition erythrocytes lose their circular shape and become sickle-shaped. As a result, the cells cannot pass through narrow capillaries. Blood capillaries are clogged and thus affect blood supply to different organs.

Q. 8 Sometimes cattle or even human beings give birth to their young ones that are having extremely different sets of organs like limbs/position of eye(s) etc. Comment.

Ans. Sometimes cattle or even human beings give birth to their young ones that are having extremely different of organs like limbs/position of eye etc. It happens due to the disturbance in coordinated regulation of expression in sets of genes, which are associated with organ development.

Q. 9 In a nucleus, the number of ribonucleoside triphosphates is 10 times the number of deoxy *x* 10 ribonucleoside triphosphates, but only deoxy ribonucleotides are added during the DNA replication. Suggest a mechanism.

Ans. DNA polymerase enzyme is highly specific to recognise only deoxy ribonucleoside triphosphates. Therefore, it cannot hold RNA β-nucleotides.

Q. 10 Name a few enzymes involved in DNA replication other than DNA polymerase and ligase. Name the key functions for each of them.

Ans. The enzymes involved in DNA replication other than DNA polymerase and ligase are listed below with their functions.

(i) Helicase — Opens the helix
(ii) Topoisomerases — Removes the super coiling of DNA
(iii) Primase — Synthesises RNA primer
(iv) Telomerase — To synthesis the DNA of telomeric end of chromosomes.

Q. 11 Name any three viruses which have RNA as the genetic material.

Ans. In some viruses, RNA is the genetic material.
e.g., Tobacco mosaic viruscs, QB bacteriophage, HIV, influenza virus, etc.

Short Answer Type Questions

Q. 1 Define transformation in Griffith's experiment. Discuss how it helps in the identification of DNA as the genetic material.

Ans. In **Griffith's experiment**, transformation can be defined as a change in the genetic constitution of an organism by picking out up DNA from the environment (from dead organisms).

Transformation helps in identification of DNA as a genetic material. When heat was used to kill the virulent bacteria, they died but not their genetic material (DNA). This DNA when picked up by non-virulent bacteria made them capable of causing infection.

Since, ability to cause infection could be passed on by these organisms to their progeny, it was concluded that DNA was the material that was inherited.

Q. 2 Who revealed biochemical nature of the transforming principle?

Ans. Oswald, Avery, Colin MacLeod and Maclyn McCarty revealed biochemical nature of the transforming principle.

They reported **Griffith's experiment** in an *in vitro* system in order to determine biochemical nature of transforming principle.

They reported that DNA from the heat-killed S-type bacteria caused the transformation of non-virulent R-type bacteria into virulent S-type bacteria. They also discovered that proteases and RNase did not affect transformation while DNase inhibited the process. They concluded that DNA is the hereditary material.

Q. 3 Discuss the significance of heavy isotope of nitrogen in the Meselson and Stahl's experiment.

Thinking Process

Meselson *and* ***Stahl*** *used heavy isotope of* ^{15}N *in the nutrient medium to grow Escherichia coli (E. coli), for several generations.*

Ans. They performed experiments on *E. coli* to prove that DNA replication is semi-conservative. They first grew the bacteria in a medium containing $^{15}NH_4Cl$ (in which ^{15}N is the heavy istope of nitrogen) for many generations.

Then they transferred the cells into a medium with normal $^{14}NH_4Cl$ (in which ^{14}N is the lighter isotope) and took the samples at various definite time intervals as the cells multiplied. The extracted DNAs were centrifuged and measured to get their densities.

The DNA extracted from the culture after one generation of transfer from then ^{15}N mediun to ^{14}N mediun, (*i.e.,* after 20 minutes *E.coli* divides every 20 minutes) showed an intermediate hybrid density, *i.e.,* both heavy and light nitrogen, which proved the semi-conservative nature of DNA.

Q. 4 Define a cistron. Giving examples differentiate between monocistronic and polycistronic unit.

Ans. A cistron is stretch of base sequences that codes for one polypeptide chain including adjacent control regions. It may also code for a *t*RNA, *r*RNA molecule or may perform other specific functions including regulating functions of other cistrons.

This term has replaced the definition of a gene. Monocistronic transcription unit will have all the regulatory and coding sequences for a single polypeptide, whereas polycistronic may have coding sequences for more than one polypeptide.

In eukaryotic cells almost all the messenger RNAs are monocistronic. In prokaryotes, *lac* operon coding sequence would be an example of polycistronic DNA region.

Q. 5 Give any six features of the human genome.

Ans. *Salient features of human genome*

(i) The human genome contains 3164.7 million nucleotide bases.

(ii) The average gene consists of 30000 the largest know human gene being dystrophin at 2.4 Million bases.

(iii) The total number of genes is estimated to be 30000 and 99.9% nucleotide bases are exactly the same in all people.

(iv) The functions are unknown for over 50% of the discovered genes.

(v) Less than 2% of the genome codes for proteins.

(vi) The human genome contains large repeated sequences.

(vii) The repeated sequence is thought to have no direct coding functions but they throw light on chromosome structures, dynamics and evolution.

(viii) Chromosome I has most genes (2968) and the Y has the fewest genes (231).

(ix) Scientists have identified about 1.4 million locations where single base DNA sequence differences called **SNPs** or Single Nucleotide Polymorphisms occur in humans.

Q. 6 During DNA replication, why is it that the entire molecule does not open in one go? Explain replication fork. What are the two functions that the monomers (dNTPs) play?

Ans. While replicating, the entire DNA molecule to keep the whole molecule stabilised does not open in one go because it would be highly expens energetically. Actually unwiding creates tension in the molecule as uncoiled parts.

Actually, unwinding creates tension in the molecule as uncoiled parts start forming super coils due to the interaction of exposed nucleotides.

Instead, helicase enzyme acts on the double strand at *ori* site (origin of replication) and a small stretch is unzipped. Immediately, it is held and stabilised by single strand binding proteins.

Slowly with the help of enzymes, exposed strands are copied as a point of unwinding moves and ahead in both directions.

It gives an appearance of Y-shaped structure which is called replication fork.

The two functions that the monomer units of NTPs play are

(i) They pair up with exposed nucleotides of the template strand and make phosphodiester linkages and release a pyrophosphate.

(ii) Hydrolysis of this pyrophosphate by enzyme pyrophosphatase releases energy that will facilitate making hydrogen bonds between free nucleotides and bases of the template strand.

Q. 7 Retroviruses do no follow central dogma. Comment.

Ans. Retroviruses do not follow central dogma of biology (DNA → RNA → Protein) because their genetic material is not DNA. Instead they have RNA that is converted to DNA by the enzyme reverse transcriptase.

Q. 8 In an experiment, DNA is treated with the compound which tends to place itself amongst the stacks of nitrogenous base pairs. As a result of this, the distance between two consecutive base increases. From 0.34–0.44 nm calculate the length of DNA double helix (which has 2×10^9 bp) in the presence of saturating of this compound.

Ans. The length of DNA double helix = $2 \times 10^9 \times 0.44 \times 10^{-9}$/ bp.

Q. 9 What would happen if histones were to be mutated and made rich in acidic amino acids such as aspartic acid and glutamic acid in place of basic amino acids such as lysine and arginine?

Ans. If histones were mutated and made rich in acidic amino acids. They will not be able to serve the purpose of keeping the DNA coiled around them. This is because DNA is negatively charged molecule and histones are positively charged because of basic amino acids.

So, they are attracted to each other. If histones become negatively charged, instead of binding, they will rather repel DNA. The packaging of DNA in eukaryotes would not happen. Consequently, the chromatin fibre would not be formed.

Q. 10 Recall the experiments done by Frederick Griffith, Avery, MacLeod and McCarty, where DNA was speculated to be the genetic material. If RNA, instead of DNA was the genetic material, would the heat killed strain of *Pneumococcus* have transformed the R-strain into virulent strain? Explain.

Ans. RNA is more liable and prone to degradation (owing to the presence of 2'OH group in its ribose). Hence, heat-killed S-stain may not have retained its ability to transform the R-strain into virulent form if RNA was its genetic material.

Q. 11 You are repeating the Hershey-Chase experiment and are provided with two isotopes ^{32}P and ^{15}N (in place of ^{35}S in the original experiment). How does you expect your results to be different?

Ans. Use of ^{15}N will be inappropriate because method of detection of ^{32}P and ^{15}N different (^{32}P being a radioactive isotope while ^{15}N is non-radioactive but is the heavier isotope of nitrogen).

Even if ^{15}N was radioactive then its presence would have been detected, both inside the cell (^{15}N incorporated as introgenous base in DNA) as well as in the supernatant, because ^{15}N would also get incorporated in amino group of amino acids in proteins. Hence, the use of ^{15}N would not give any conclusive results.

Q. 12 There is only one possible sequence of amino acids when deduced from a given nucleotides. But multiple nucleotides sequence can be deduced from a single amino acid sequence. Explain this phenomena.

Ans. Some amino acids are coded by more then one codon (known as degeneracy of codons), hence, on deducing a nucleotide sequence from an amino acid sequence, multiple nucleotide sequence will be obtained, *e.g.,* Ile (Isoleucine) has three codons AUU, AUC, AUA. Hence, a dipeptide Met-Ile can have the following nucleotide sequence.

(i) AUG-AUU (ii) AUG-AUC (iii) AUG-AUA

And if, we deduce amion acid sequence from the above nucleotide sequences, all the three will code for Met-Ile.

Q. 13 A single base mutation in a gene may not 'always' result in loss or gain of function. Do you think the statement is correct? Defined your answer.

Ans. The statement is correct. Because of degeneracy of codons, mutations at third base of codon, usually does not result into any change is phenotype. This is called silent mutations.

On other hand, if codon is changed in away that now it specifies another amino acid, it may other the protein function as it happens in cse of β-globulin of haemoglobin protein. Where a substitution of valine instead of glutamic acid causes change in its structure and function, and resulting into sickle-cell trait.

Q. 14 A low level of expression of *lac* operon occurs at all the time. Can you explain the logic behind this phenomena.

Ans. In the complete absence of expression of lac operon, permease will not be synthesised which is essential for transport of lactose from medium into the cells. And if lactose cannot be transported into the cell, then it cannot act as inducers. Hence, cannot relieve the *lac* operon from its repressed state.

Q. 15 How has the sequencing of human genome opened new windows for treatment of various genetic disorders. Discuss amongst your classmates.

Thinking Process

In 1990, US department of energy and National Institute of Health Embarked and Coordinated on the project of sequencing human genome called HGP or Human Genome Project.

Ans. The sequencing of human genome helped in enhancing the basic understanding of genetics and immunity to various disorders. Various genes that cause genetic disorders were identified with the help of this project.

It was found that more than 1200 genes are responsible for common human cardiovascular diseases, endocrine diseases (like diabetes), neurological, disorders (like Alzeimer's disease, cancers and many more. These diseases can be treated easily by knowing the particular gene responsible for the particular disease.

Q. 16 The total number of genes in humans is far less (< 25000) than the previous estimate (up to 140000 gene). Comment.

Ans. The total number of genes is estimated at 25000 much lower than previous estimates of 140000 that had been based on extrapolations from gene-rich areas as opposed to a composite of gene-rich and gene-poor areas.

Almost all (99.9%) nucleotide bases are exactly the same in all people. Functions for over 50% discovered genes are not known yet. Scientist have identified about 1.4 million locations where single-base DNA difference (SNPs or Single Nucleotide Polymorphisms) occur in humans.

This information promises to revolutionise the processes of finding chromosomal locations for disease-associated sequence and tracing human history.

Q. 17 Now, sequencing of total genomes is getting less expensive day by day. Soon it may be affordable for a common man to get his genome sequenced. What in your opinion could be the advantage and disadvantage of this development?

Ans. Human genome helps to find out the complete genome sequence of the human. It has many advantages and disadvantages.

Some important advantages

It provides the knowledge of the effects of variations of DNA among individuals can revolutionise the ways to diagnose, treat and prevent many diseases that affect humans. It also provides clues to the understanding of human biology. It helps to find out the human evolution. Identification through DNA forensics is also possible.

Some important disadvantages

People might discover and untreatable genetic disease. People may abuse the knowledge obtained from the HGP. Problem can occur for the ownership of the genetic test result and the patenting of human genes and DNA. People believe that they are special and unique in their own ways and may wish to remain like that.

Q. 18 Would it be appropriate to use DNA probes such as VNTR in DNA fingerprinting of a bacteriophage?

Ans. Bacteriophage does not have repetitive sequences such as VNTRs in its genome, as its genome is very small and have all the coding sequence. DNA finger printing is not done for phages.

Q. 19 During *in vitro* synthesis of DNA, a researcher used 2′, 3′-dideoxy cytidine triphosphate as raw nucleotide in place of 2′-deoxy cytidine. What would be the consequence?

Ans. Further polymerisation would not occur, as the 3′ OH on sugar is not there to add a new nucleotide for forming ester bond.

Q. 20 That background information did Watson and Crick have made available for developing a model of DNA? What was their contribution?

Ans. **Watson** and **Crick** had the following informations which helped them to develop a model of DNA.

(i) **Chargaff's** Law suggesting A = T and C = G

(ii) **Wilkins** and **Rosalind Franklin**'s work on DNA crystal's X-ray diffraction studies about DNAs physical structure.

Watson and **Crick** proposed

(a) Pattern of complementary bases pair

(b) Semi-conservative replication

(c) Mutation through tautomerism

Q. 21 What are the functions of

(i) methylated guanine cap?

(ii) poly-A 'tail' in a mature on RNA?

Ans. **(i)** Methylated guanine cap helps in binding of *m*RNA to smaller ribosomal sub-unit during initiation of translation.

(ii) Poly-A tail provides longevity to *m*RNA's life. Tail length and longevity of *m*RNA are positively correlated.

Q. 22 Do you think that the alternate splicing of exons may enable a structural gene to code for several isoproteins from one and the same gene? If yes, how? If not, why so?

Ans. Functional *m*RNA of structural genes need not always include all of its exons. This alternate splicing of exons is sex-specific, tissue-specific and even developmental stage-specific. By such alternate splicing of exons, a single gene may encode for several isoproteins and/or proteins of similar class.

In absence of such a kind of splicing, there should have been new genes for every protein/isoprotein. Such an extravagancy has been avoided in natural phenomena by way of alternate splicing.

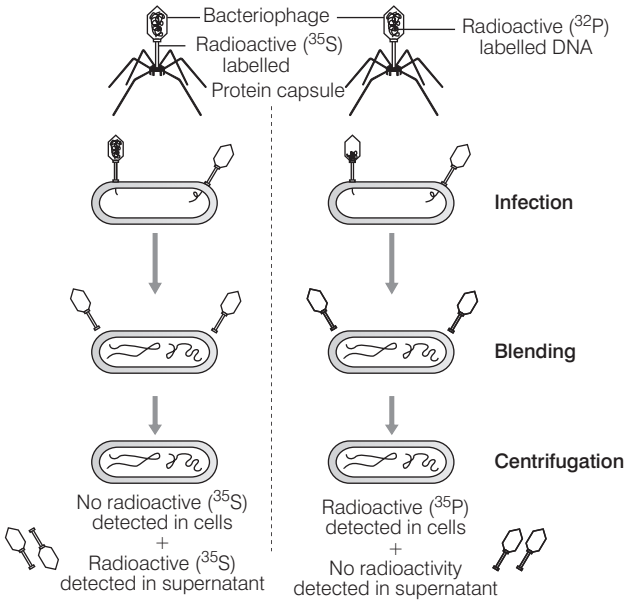
Q. 23 Comment on the utility of variability in number of tandem repeats during DNA fingerprinting.

Ans. Tandemness in repeats provides many copies of the sequence for finger-printing and variability in nitrogen base sequences present in them. Being individual-specific, this proves to be useful in the process of DNA fingerprinting.

Long Answer Type Questions

Q. 1 Give an account of Hershey and Chase experiment. What did it conclusively prove? If both DNA and proteins contained phosphorus and sulphur do you think the result would have been the same?

Ans. **Hershey** and **Chase** conducted experiments on bacteriophage to prove that DNA is the genetic material.



Hershey and Chase experiment

(i) Some bacteriophage virus were grown on a medium that contained radioactive phosphorus (^{32}P) and some in another medium with radioactive sulphur (^{35}S).

(ii) Viruses grown in the presence of radioactive phosphorus (^{32}P) contained radioactive DNA.

(iii) Similar viruses grown in presence of radioactive sulphur (^{35}S) contained radioactive protein.

(iv) Both the radioactive virus types were allowed to infect *E. coli* separately.

(v) Soon after infection, the bacterial cells were gently agitated in blender to remove viral coats from the bacteria.

(vi) The culture was also centrifuged to separate the viral particle from the bacterial cell.

Observations and Conclusions

(i) Only radioactive ^{32}P was found to be associated with the bacterial cell, whereas radioactive ^{35}S was only found in surrounding medium and not in the bacterial cell.

(ii) This indicates that only DNA and not protein coat entered the bacterial cell.

(iii) This proves that DNA is the genetic material which is passed from virus to bacteria and not protein.

If both DNA and proteins contained phosphorus and sulphur, the result might change.

In case (i)

Radioactive ^{35}S and ^{32}P labelled protein capsule + Bacteriophage $\longrightarrow$ No radioactive ^{35}S and ^{32}P Detected in cells + Radioactivity (^{35}S and ^{32}P) detected in supernatant

In case (ii)

Radioactive ^{35}S and ^{32}P lebelled DNA + Bacteriophage $\longrightarrow$ Radioactive ^{32}P and ^{35}S Detected in cells + No radioactivity detected in supernatant

Q. 2 During the course of evolution why DNA was choosen over RNA as genetic material. Give reasons by first discussing the desired criteria in a molecule that can act as genetic material and in the light of biochemical differences between DNA and RNA.

Ans. *A molecule that can act as a genetic material must fulfil the following*

(i) It should be able to generate its replica (replication).

(ii) It should chemically and structurally be stable.

(iii) It should provide the scope for slow changes (mutation) that are required for evolution.

(iv) It should be able to express itself in the form of Mendelian.

Biochemical differences between DNA and RNA

(i) Both nucleic acid (DNA and RNA) are able to direct their duplication proteins fails for the first criteria.

(ii) RNA is reactive, it also acts are catalyst, hence DNA is less reactive and structurally more stable than RNA.

(iii) Presence of thymine at the place of uracil also confers additional stability to DNA.

Q. 3 Give an account of post transcriptional modifications of a eukaryotic *m*RNA.

Thinking Process

Post-transcriptional modifications include the modification of the mRNA transcript synthesised by RNA polymerase II (in eukaryotes).

Ans. **Post-transcriptional Modifications**

The primary transcripts are non-functional, containing both the coding region, exon and non-coding region, intron in RNA and are called heterogenous RNA or *hn*RNA.

In eukaryotes, three types of RNA polymerases are found in the nucleus

(i) **RNA polymerase I** transcribes *r*RNAs (28 S and 5.8 S).

(ii) **RNA polymerase II** transcribes the precursor of *m*RNA (called heterogeneous nuclear RNA or *hn*RNA).

(iii) **RNA polymerase III** transcribes *t*RNA, 5 S *r*RNA and *sn*RNAs (small nuclear RNAs).

The *hn*RNA undergoes two additional processes called **capping** and **tailing**.

In capping, an unusual nucleotide, methyl guanosine triphosphate is added to the 5′-end of *hn*RNA.

In tailing, adenylate residues (about 200-300) are added at 3′-end in a template independent manner.

Now the *hn*RNA undergoes a process where the introns are removed and exons are joined to form *m*RNA by the process called **splicing**.

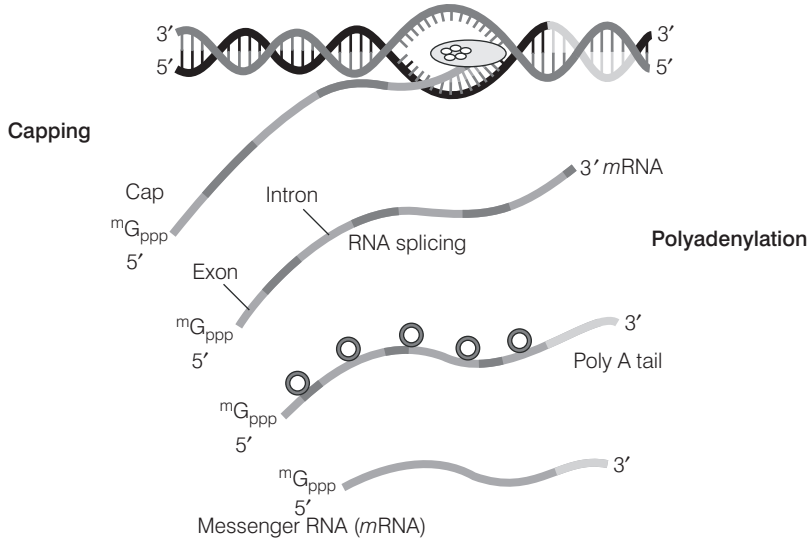


Diagram representation of a post transcriptional modification in eukaryotes

Note *In prokaryotes, mRNA does not require any processing.*

Q. 4 Discuss the process of translation in detail.

Thinking Process

Translation is the process of synthesis of protein from mRNA with the help of ribosome. A translational unit in mRNA from 5′→3′ comprises of a start codon, region coding for a polypeptide, a stop codon and Untranslated Regions (UTRs) at both 5′-end and 3′-end for efficient process.

Ans. *There are three-stages of protein synthesis*

(i) **Initiation**

Assembly of Ribosomes on m*RNA* In prokaryotes, initiation requires the large and small ribosome subunits, the *m*RNA, initiation *t*RNA and three Initiation Factors (IFs).

Activation of Amino Acid Amino acids become activated by binding with aminoacyl *t*RNA synthetase enzyme in the presence of ATP.

$$\text{Amino acid (AA)} + \text{ATP} \xrightarrow[\text{synthetases}]{\text{Aminoacy}\,t\,\text{RNA}} \text{AA-AMP-Enzyme complex} + P_i$$

Transfer of Amino Acid to t*RNA* The AA-AMP-enzyme complex formed reacts with specific *t*RNA to form aminoacyl *t*RNA complex.

$$\text{AA-AMP-Enzyme complex} + t\text{RNA} \longrightarrow \text{AA}\,t\text{RNA} + \text{AMP} + \text{Enzyme}.$$

The cap region of *m*RNA binds to the smaller subunit of ribosome.

The ribosome has two sites, A-site and P-site.

The smaller subunit first binds the initiator *t*RNA then and then binds to the larger subunit so, that initiation codon (AUG) lies on the P-site.

The initiation *t*RNA, *i.e.,* methionyl *t*RNA then binds to the P-site.

(ii) **Elongation**

Another charged aminoacyl *t*RNA complex binds to the A-site of the ribosome.

Peptide bond formation and movement along the *m*RNA called translocation. A peptide bond is formed between carboxyl group (—COOH) of amino acid at P-site and amino group (—NH) of amino acid at A-site by the enzyme peptidyl transferase.

The ribosome slides over *m*RNA from codon to codon in the 5′→3′ direction.

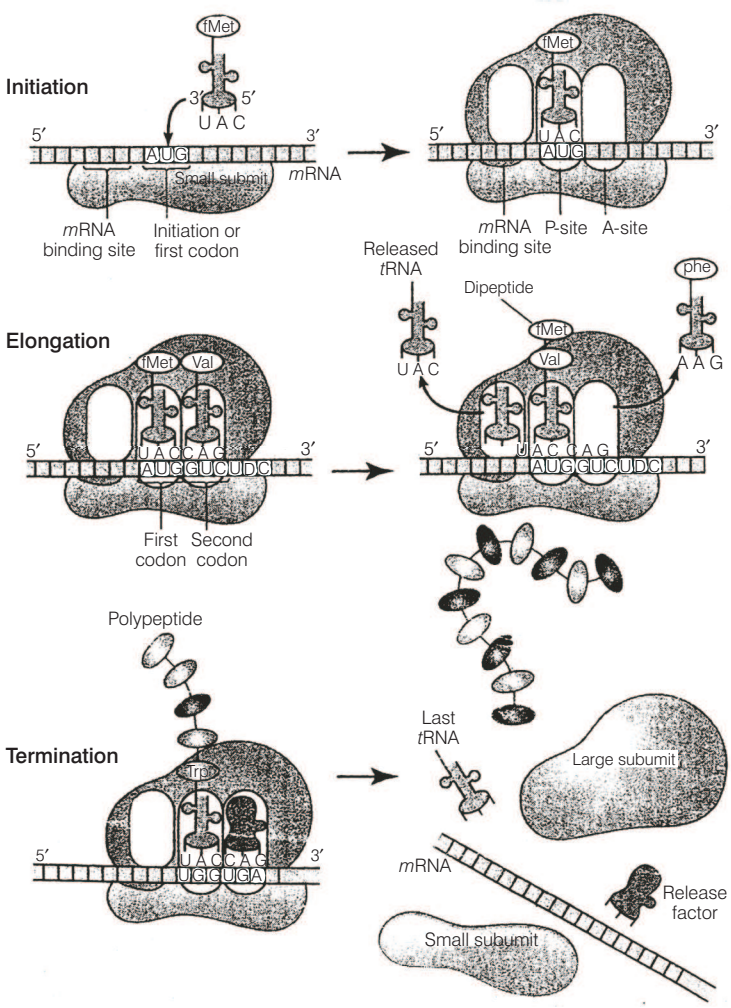
According to the sequence of codon, amino acids are attached to one another by peptide bonds and a polypeptide chain is formed.

(iii) **Termination**

When the A-site of ribosome reaches a termination codon which does not code for any amino acid, no charged *t*RNA binds to the A-site.

Dissociation of polypeptide from ribosome takes place which is catalysed by a '**release factor**'.

There are three **termination codons,** *i.e.*, UGA, UAG and UAA.



Process of translation

Q. 5 Define an operon, giving an example, explain an inducible operon.

Ans. The concept of operon was first proposed in 1961, by **Jacob** and **Monad**. An operon is a unit of prokaryotic gene expression which includes coordinately regulated (structural) genes and control elements which are recognised by regulatory gene product.

Components of an Operon

(i) **Structural gene** The fragment of DNA which transcribe *m*RNA for polypeptide synthesis.

(ii) **Promoter** The sequence of DNA where RNA polymerase binds and initiates transcription of structural genes is called promoter.

(iii) **Operator** The sequence of DNA adjacent to promoter where specific repressor protein binds is called operator.

(iv) **Regulator gene** The gene that codes for the repressor protein that binds to the operator and suppresses its activity as a result of which transcription will be switched off.

(v) **Inducer** The substrate that prevents the repressor from binding to the operator, is called an inducer. As a result transcription is switched on. It is a chemical of diverse nature like metabolite, hormone substrate, etc.

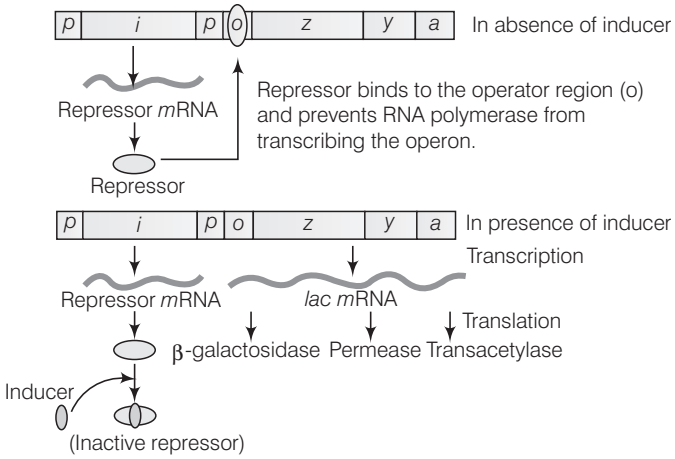
Inducible Operon System

An inducible operon system is a regulated unit of genetic material which is switched on in response to the presence of a chemical. *e.g.,* the lactose or *lac*-operon of *E.coli*.

The lactose operon The *lac z*, *y*, *a* genes are transcribed from a *lac* transcription unit under the control of a single promoter. They encode enzyme required for the use of lactose as a carbon source. The *lac i* gene product, the lac repressor, is expressed from a separate transcription unit upstream from the operator.

lac operon consists of **three structural genes** (z, y and a), operator, promoter and a separate regulatory gene.

The three structural genes (*a*, *y* and *a*) transcribe a polycistronic *m*RNA.



***Lac* operon**

Gene *z* codes for β-galactosidase (β-gal) enzyme which breaks lactose into galactose and glucose.

Gene *y* codes for permease, which increases the permeability of the cell to lactose.

Gene *a* codes for enzyme transacetylase, which catalyses the transacetylation of lactose in its active form.

When Lactose is Absent

(i) When lactose is absent, *i* gene regulates and produces repressor *m*RNA which translate repression.

(ii) The repressor protein binds to the operator region of the operon and as a result prevents RNA polymerase to bind to the operon.

(iii) The operon is **switched off.**

When Lactose is Present

(i) Lactose acts as an inducer which binds to the repressor and forms an inactive repressor.

(ii) The repressor fails to bind to the operator region.

(iii) The RNA polymerase binds to the operator and transcript *lac m*RNA.

(iv) *lac m*RNA is polycistronic, *i.e.,* produces all three enzymes, β-galactosidase, permease and transacetylase.

(v) The *lac* operon is **switched on.**

Q. 6 'There is a paternity dispute for a child'. Which technique can solve the problem? Discuss the principle involved.

Ans. DNA fingerprinting is the technique used in solving the paternity dispute for a child. DNA fingerprinting is a technique of determining nucleotide sequences of certain areas of DNA which are unique to each individual.

The basis of DNA fingerprinting is DNA polymorphism. Although the DNA from different individuals is more alike than different, there are many regions of the human chromosomes that exhibit a great deal of diversity. Such variable sequences are termed 'polymorphic' (meaning many forms).

A special type of polymorphism, called VNTR (Variable Number of Tandem Repeats), is composed of repeated copies of a DNA sequence that lie adjacent to one another on the chromosome. Since, polymorphism is the basis of genetic mapping of human.

Q. 7 Give an account of the methods used in sequencing the human genome.

Ans. Sequencing of human genome has made it possible to understand the link between various genes and their functions. If there are any gene defects that express as disorders or that increase the susceptibility of an individual to a disease then specific gene therapies can be worked out

Methodologies of human genome sequencing

The methods involve two major approaches

(i) **Expressed Sequence Tags** (ESTs) This method focusses on identifying all the genes that are expressed as RNA.

(ii) **Sequence annotation** It is an approach of simply sequencing the whole set of genome that contains all the coding and non-coding sequences, and later assigning different regions in the sequence with functions.

For sequencing, first the total DNA from cell is *i.e.*, solated and broken down in relatively small sizes as fragments.

There DNA fragments are cloned in suitable host using suitable vectors. When bacteria is used as vector, they are called Bacterial Artificial Chromosomes (BAC) and when yeast is used as vector, they are called Yeast Artificial Chromosomes (YACs).

Frederick Sanger developed a principle according to which the fragments of DNA are sequenced by automated DNA sequences.

On the basis of overlapping regions on DNA fragments, these sequences are arranged accordingly. For alignment of these sequences, specialised computer-based programmes were developed.

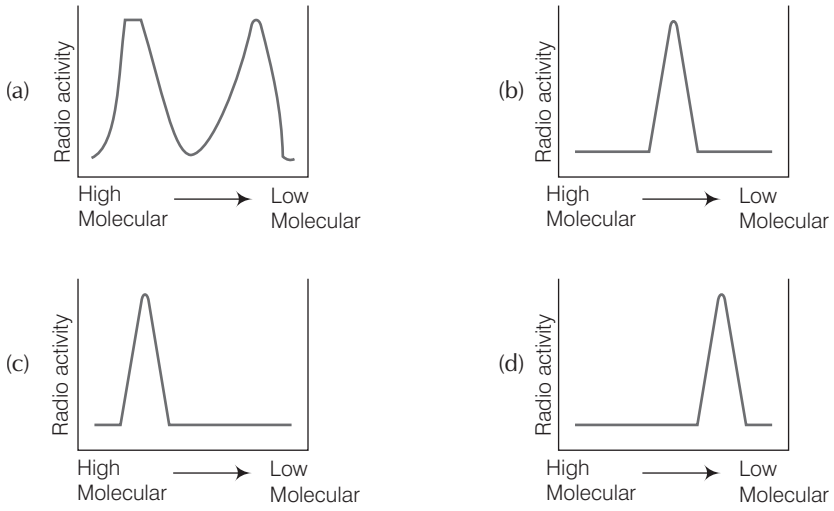
Finally, the genetic and physical maps of the genome were constructed by collecting information about certain repetitive DNA sequences and DNA polymorphism, based on endonuclease recognition sites.

Q. 8 List the various markers that are used in DNA fingerprinting.

Ans. **Dr. Alec Jeffreys** developed the technique of DNA fingerprinting in an attempt to identify DNA marker for inherited diseases.

DNA fingerprinting uses short nucleotide repeats called Variable Number Tandem Repeats (VNTRs) as markers. VNTRs vary from person to person and are inherited from one generation to the next. Only closely individuals have similar VNTRs.

Q. 9 Replication was allowed to take place in the presence of radioactive deoxynucleotides precursors in *E.coli* that was a mutant for DNA ligase. Newly synthesised radioactive DNA was purified and strands were separated by denaturation. These were centrifuged using density gradient centrifugation. Which of the following would be a correct result?



Ans. In above case, as *E.coli* is a mutant for DNA ligase, it will result in no further joining of Okazaki fragments on lagging strand.

This will ultimately result into the formation of both high molecular weight fragments (on leading strands) and low molecular weight fragments (on lagging strand). Hence, only the graph (a) could be the appropriate result after centrifugation.