CHAPTER

06

Molecular basis of inheritance

Nucleic acids

Nucleic acids, the building blocks of life, are macromolecules that carry genetic information. They are made up of repeating units called *nucleotides*, which are composed of a sugar molecule, a phosphate group, and a nitrogenous base.

There are *two* main types of nucleic acids in living organisms: ***ribonucleic acid (RNA)*** and ***deoxyribonucleic acid (DNA).***

Search for genetic material

Frederick Griffith conducted pioneering experiments with *Streptococcus pneumoniae*, which led to the discovery of the transforming principle – the genetic material responsible for transferring traits from one strain of bacteria to another.

Avery, Macleod, and *McCarty* followed up on Griffith's work and conclusively demonstrated that DNA is the hereditary material. Their experiments revealed that **DNA** carries the genetic code and determines the traits and characteristics of an organism. The *Hershey-Chase* experiment with bacteriophages further confirmed that *DNA is the genetic material* passed from one generation to the next.

In most organisms, DNA is the primary genetic material. **RNA**, on the other hand, plays a crucial role in the transfer and expression of genetic information. It functions as messenger RNA (mRNA) in the translation of proteins.

Nucleosides and ***nucleotides*** are the basic units that make up DNA and RNA. A nucleoside is formed by linking a ***nitrogenous base*** to a ***pentose sugar*** through ***N-glycosidic linkage.*** A nucleotide, on the other hand, consists of a nitrogenous base, a pentose sugar, and a phosphate group.

Nitrogenous bases are of two types: ***purines*** (adenine, guanine) and ***pyrimidines*** (cytosine, uracil, thymine).

RNA, a type of nucleic acid, differs from DNA in several ways. RNA contains the nitrogenous base ***uracil*** instead of ***thymine***. Additionally, RNA contains the sugar ribose, while DNA contains deoxyribose.

RNA plays a variety of roles in the cell. It acts as an ***adapter molecule***, helping to translate the genetic information stored in DNA into functional proteins. RNA also has structural and catalytic functions, making it a versatile molecule.

In some *viruses*, ***RNA*** serves as the genetic material instead of DNA. Although both RNA and DNA can function as genetic material, ***DNA*** is generally preferred due to its *greater stability*. In fact, DNA evolved from RNA, which was the first nucleic acid to arise in early life forms.

The pairing of nitrogenous bases in DNA is crucial to its function. *Adenine* pairs with *thymine* through ***two hydrogen bonds***, while *guanine* pairs with *cytosine* through ***three hydrogen bonds***.

Central dogma

The central dogma in molecular biology describes the flow of genetic information from **DNA to RNA to protein**. It emphasizes the importance of DNA as the carrier of genetic information and the central role of proteins in the expression of genetic information.

Genetic material in Prokaryotic and Eukaryotic cells

The genetic material In prokaryotic and eukaryotic cells differs in their organization and composition.

Prokaryotic cells store their genetic material in a region called the *nucleoid*. The DNA in the nucleoid is negatively charged, and it is held together with some positively charged proteins.

In contrast, ***eukaryotic cells*** have a set of proteins called *histones*, which are positively charged. These histones come together to form a structure called the ***histone octamer***. The DNA in eukaryotic cells is negatively charged and is wrapped around the histone octamer to form a ***nucleosome***, which is the basic unit of compaction in the genome.

Chromatin structure

To achieve a higher level of chromatin packaging, a group of proteins known as ***Non-Histone Chromosomal (NHC) proteins*** work together. These proteins are distinct from histone proteins and are essential for the proper organization of chromatin structure.

Euchromatin and Heterochromatin

Euchromatin and ***Heterochromatin*** are two types of chromatin regions found in cells. *Euchromatin* refers to the loosely packed regions of chromatin that stain light and are considered to be active, while *heterochromatin* refers to the densely packed regions of chromatin that stain dark and are generally considered to be inactive.

DNA Replication

DNA replication is a process that occurs **semi conservatively**. This means that the two strands of the DNA double-helix separate and act as a template for the synthesis of new complementary strands. Complementary H-bonding guides this process, which is *catalyzed* by several sets of *enzymes*, including ***DNA-dependent DNA polymerase,*** which uses a DNA template to catalyze the polymerization of deoxynucleotides; ***DNA helicase***, which unwinds DNA strands to form a replication fork; and ***DNA ligase***, which facilitates the joining of DNA strands by catalyzing the formation of phosphodiester bonds.

During replication, the ***3' → 5' strand*** undergoes **continuous replication**, while the ***5' → 3'*** strand undergoes **discontinuous replication**. DNA replication begins at a specific and fixed position of the DNA molecule, known as the **origin of replication**.

RNA

There are following three types of RNA:

Messenger RNA (mRNA): This type of RNA provides the template for transcription. It carries genetic information from the DNA in the nucleus to the ribosomes in the cytoplasm, where it is translated into a protein.

Transfer RNA (tRNA): This RNA brings amino acids to the ribosome during protein synthesis and reads the genetic code on the mRNA. tRNA is an adapter molecule that can read the code on one end and bind to the specific amino acid on the other end.

Ribosomal RNA (rRNA): This RNA plays a structural and catalytic role during translation. It forms the main component of the ribosome, where it catalyzes the formation of peptide bonds between amino acids.

Note: ***tRNA*** has five loops (anticodon loop, amino acid acceptor end, T-loop, D-loop, and variable loop) and is shaped like a clover leaf shaped molecule.

Eukaryotes

Transcription in prokaryotes and eukaryotes

Transcription is the process of creating an RNA copy of genetic information from DNA. This involves copying a segment of DNA, or just one of its two strands.

In prokaryotes, such as bacteria, the mRNA produced during transcription is directly functional and can be translated without further processing.

Eukaryotes, on the other hand, have genes that are split into ***exons*** (*coding sequences*) and ***introns*** (*non-coding sequences)*. After transcription, the introns are removed and the exons are spliced together to produce functional RNA.

A transcription unit In DNA is composed of ***three*** regions: ***a promoter,*** which initiates transcription; ***a structural gene,*** which contains the information that is transcribed; and ***a terminator***, which signals the end of transcription.

Post transcriptional modifications

After transcription, the ***initial RNA*** product, called **heteronuclear RNA (hnRNA)**, undergoes two crucial modifications.

The first process is ***capping***, where a *methyl guanosine triphosphate i*s added to the ***5' end*** of the ***hnRNA*** molecule. This cap protects the RNA from degradation and helps it to be recognized by the cellular machinery responsible for translation.

The second modification is tailing, where *200-300 adenylate, residues* are added to the ***3' end*** of the ***hnRNA*** molecule in a template-independent manner. This tail, also known as a ***poly-A tail***, plays a role in stabilizing the RNA molecule and promoting its transport out of the nucleus for translation in the cytoplasm.

Genetic code

The genetic code Is a critical biological concept that describes the relationship between the sequence of nucleotides on mRNA and the sequence of amino acids in the resulting polypeptide.

(i) Dr. Har Gobind Khorana developed a chemical method for synthesizing RNA molecules with defined base combinations to study the genetic code.
(ii) The genetic code Is ***unambiguous*** and ***specific***, meaning that each codon codes for only one amino acid.
(iii) Codons, the three-nucleotide sequences on mRNA, are ***triplet*** and ***degenerate***, meaning that some amino acids can be coded by more than one codon.
(iv) The genetic code Is ***universal***, meaning that each codon codes for the same amino acid in all organisms.
(v) The ***AUG*** codon has a **dual function**, as it codes for the amino acid ***methionine*** and serves as an ***initiation codon*** for protein synthesis.
(vi) Three codons, **UAA, UGA, and UAG**, do not code for any amino acid and instead function as ***stop codons***, signalling the end of protein synthesis.

Translation

Translation is the crucial process of polymerizing amino acids into a functional ***polypeptide***. During this process, proteins are synthesized with the aid of ribosomes from mRNA. Here are some important points to consider:

Ribosomes are present as small and large subunits when they are inactive.

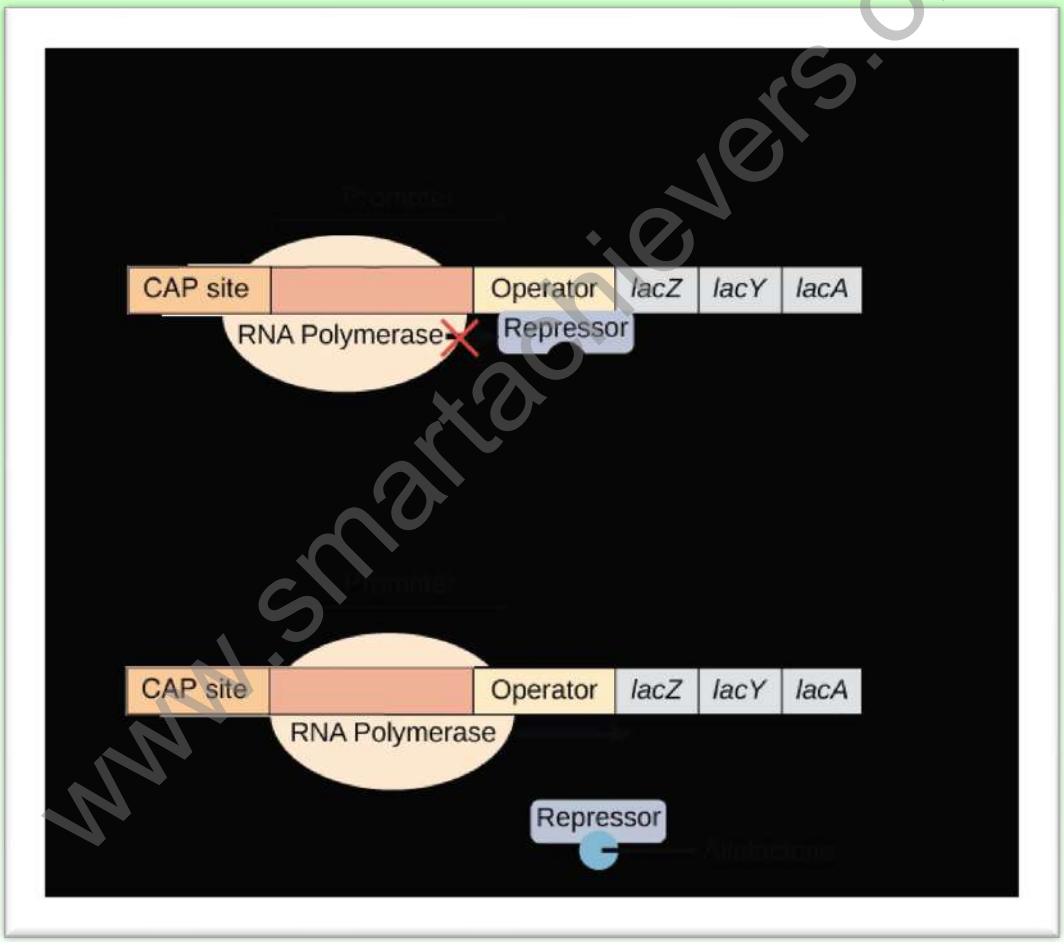
There are three distinct phases of translation: initiation, elongation, and termination.

(i) **Initiation** is the first step of polypeptide synthesis, where the ribosome identifies the start codon (AUG) and the initiator tRNA brings the first amino acid.
(ii) During **elongation**, the ribosome moves along the mRNA and adds amino acids one by one to the growing polypeptide chain until a stop codon is reached.
(iii) **Termination** is the final phase of polypeptide synthesis. The completed polypeptide chain is released from the ribosome, and the ribosome dissociates into its subunits to be reused for further rounds of protein synthesis.

Gene Expression in Prokaryotes and Eukaryotes

Gene expression is a complex process that is regulated at various levels in prokaryotes and eukaryotes. In ***prokaryotes***, the rate of initiation of transcription plays a significant role in regulating gene expression. On the other hand, ***eukaryotes*** regulate gene expression at four levels, including ***transcriptional level, processing level, transport of mRNA from the nucleus to the cytoplasm,*** and ***translational level***.

One transcriptionally regulated system in prokaryotes is the operon, which consists of a ***polycistronic*** structural gene that is regulated by a common promoter and regulatory genes. Examples of operons include the ***lac*** (lactose) operon, **ara** (arabinose) operon, ***his*** (histidine) operon, ***val*** (valine) operon, among others. The ***lac*** operon, which codes for genes responsible for the metabolism of ***lactose***, was proposed by Francois Jacob and Jacque Monod and serves as a prototype (inducible) operon in bacteria.



Human genome project

The Human Genome Project was an ambitious and groundbreaking initiative that spanned over 13 years. The primary objective of this project was to determine the sequence of every single base pair in the human genome.

The project involved a collaborative effort between researchers from across the globe and utilized cutting-edge technology to identify and sequence the three billion nucleotide base pairs that comprise the human genome.

Here are the key points of the Human Genome Project:

1. The Human Genome Project (HGP) was an international research effort launched in **1990** to determine the complete sequence of the human genome.
2. The human genome is the entire set of DNA instructions that make up the genetic blueprint for human life.
3. The project involved scientists from around the world collaborating to ***map*** and ***sequence*** the human genome.
4. The primary goal of the project was to identify and map all of the approximately ***20,000-25,000*** genes in the human genome and to determine the sequence of the **3 billion** DNA base pairs that make up the *genome*.
5. The project provided a wealth of insights into the genetic basis of human disease and has opened up new avenues for research in fields such as *biotechnology* and *personalized medicine*.
6. The Human Genome Project has led to the development of new technologies and techniques for DNA sequencing and analysis, which have since been applied to many other areas of biological research.
7. The project has had a profound impact on our understanding of genetics and has paved the way for advances in fields such as ***gene therapy, genetic testing***, and ***precision medicine.***

Goals of human genome project

1. **To map and sequence the entire human genome**: The HGP aimed to create a complete map and sequence of the **3 billion base pairs** that make up the human genome. This involved identifying and locating all of the genes, as well as other regions of the genome that play a role in gene regulation and function.
2. **To understand the function of genes**: The HGP aimed to identify all of the genes in the human genome and understand their functions. This information would be useful in understanding how genes contribute to health and disease.
3. **To identify genetic variations:** The HGP aimed to identify genetic variations that are responsible for differences in susceptibility to diseases, response to drugs, and other traits. This information could be used to develop personalized medicine.
4. **To develop new technologies**: The HGP aimed to develop new technologies for sequencing and analysing DNA, which could be used for other areas of research and medicine.

Methodologies of human genome project

Several different methodologies were used during the course of the project, some of which are described below:

- **Sequencing**: The most significant methodology used in the HGP was DNA sequencing. Sequencing is the process of determining the precise order of nucleotides in a DNA molecule. The HGP used two main sequencing strategies: *the whole-genome shotgun sequencing approach and the hierarchical shotgun sequencing approach.*
- **Mapping**: Before the DNA could be sequenced, it needed to be mapped. Mapping is the process of identifying the location of specific genes or markers on a chromosome. Mapping was achieved using several different techniques, including *restriction fragment length polymorphism (RFLP) analysis, microsatellite analysis, and single nucleotide polymorphism (SNP) analysis.*
- **Bioinformatics**: The HGP generated a vast amount of genomic data, which required sophisticated computational tools to analyze and interpret. Bioinformatics is the application of computational techniques to biological data. Bioinformatics tools were used to manage, analyze, and visualize the genomic data generated by the HGP.
- **Genetics**: The HGP also utilized classical genetics techniques, such as linkage analysis and pedigree analysis, to identify the genes responsible for inherited diseases.
- **Functional analysis**: Once the genome was sequenced, researchers needed to determine the functions of the genes and other non-coding regions. Functional analysis techniques, such as gene expression analysis, protein-protein interaction analysis, and knock-out studies, were used to determine the function of genes and other genomic elements.

DNA fingerprinting

DNA fingerprinting, also known as ***DNA profiling*** or ***genetic fingerprinting***, is a forensic technique used to identify individuals based on their unique genetic code. It involves comparing the DNA of two or more samples to determine whether they come from the same individual or related individuals.

The process of DNA fingerprinting involves several steps:

1. **Sample Collection:** DNA samples are collected from the person or object being tested. This can be done using a variety of methods, such as blood, saliva, hair, or skin cells.

2. **DNA Extraction**: The DNA is extracted from the sample using a chemical process that breaks open the cells and releases the DNA.

3. **PCR Amplification:** Polymerase Chain Reaction (PCR) is used to amplify specific regions of the DNA sample. This makes it easier to analyze and compare the DNA.

4. **Gel Electrophoresis**: The amplified DNA fragments are separated based on their size using a technique called gel electrophoresis. The DNA fragments are placed in a gel and an electrical charge is applied, causing the DNA to move through the gel. Smaller fragments move faster and farther than larger ones, creating a unique pattern of bands.

5. **DNA Analysis:** The DNA bands are visualized using a staining agent and the pattern is compared between samples. If the banding patterns are identical, the samples are considered a match.

DNA fingerprinting has many practical applications, including criminal investigations, paternity testing, and identifying victims of natural disasters or mass casualty events. It is a powerful tool for identifying individuals and has become an important part of forensic science.

Molecular Basis of Inheritance

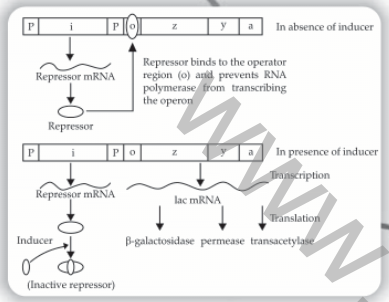
Human Genome Project

- To identify all the estimated genes in human DNA
- To determine the sequences of the 3 billion base pairs
- To provide tools for data analysis

Lac operon

The operon controlling lactose metabolism

- Structural gene
- Operator gene
- Promoter gene
- Repressor
- Inducer



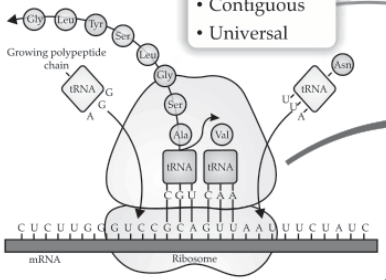
Gene expression and regulation

Definition: Sequence of nucleotides (nitrogen bases) in mRNA that contains information for protein synthesis (translation).

Features:

- Triplet
- Unambiguous
- Degenerate
- Contiguous
- Universal

Genetic Code



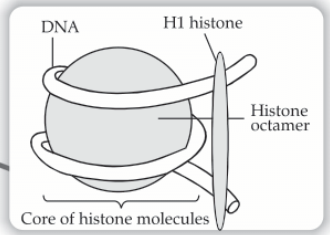
Translation

Transcription

Central Dogma

DNA —transcription→ mRNA —translation→ Protein

DNA packaged nucleosome



Double Helix

Polynucleotide Chain

Made of Nucleotide

Linked to the 5'- and 3'- carbon deoxyribose

Phosphate group

Sugar

- Ribose in RNA
- Deoxyribose in DNA

Nitrogenous Base

- C, T (only in DNA), U (Only in RNA)
- A, G

Salient Features

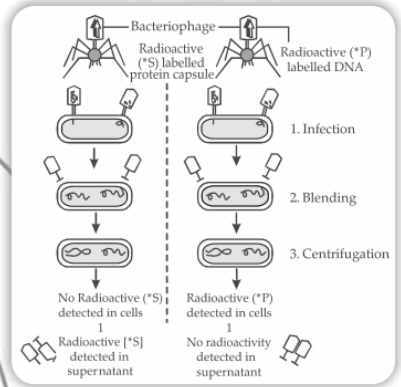
- Two polynucleotide chains.
- They have anti-parallel polarity.
- 2 H-bond : A=T; 3 H-bond : G≡C.
- Two chains coiled in a right -handed fashion
- Plane of one base pair stacks over the other

Search for genetic material

Griffith exp.

- S-strain ® Inject into mice ® Mice die
- R-strain ® Inject into mice ® Mice live
- S-strain (Heat killed) ® Inject into mice ® Mice live
- S-strain (Heat killed) + R-strain (live) ® Inject into mice ® Mice die
- Conclusion: Some 'transforming principle', transferred from heat-killed S-strain to R-strain.

Hershey and Chase exp.

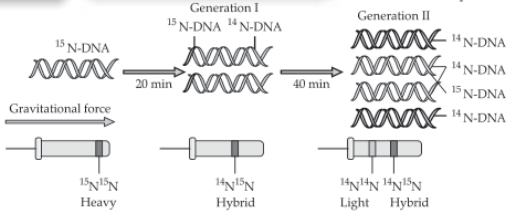


Biochemical Nature

- Discovered by Oswald Avery, Colin MacLeod and Maclyn McCarty.
- Conclusion: DNA is the hereditary material.

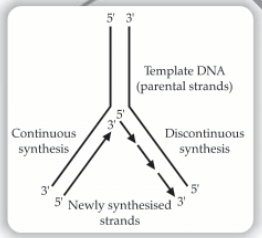
Semi-Conservative DNA Replication

Meselson and Stahl experiment



Replication

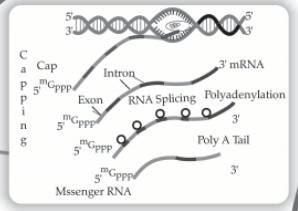
Process



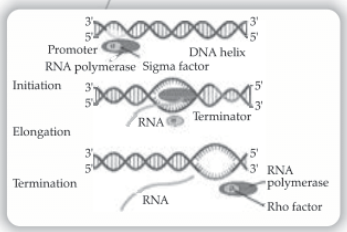
Types of RNA

- mRNA (messenger RNA) : Protein synthesis.
- rRNA (ribosomal RNA) : Structural & catalytic role during translation.
- tRNA (transfer RNA or sRNA or soluble RNA) : Brings amino acids for protein synthesis and reads the genetic code.

In Eukaryotes



In Prokaryotes



Definition: The process of copying genetic information from one strand of the DNA into RNA.

Units:

- A promoter.
- The structural gene.
- A terminator.

Trace the Mind Map

- First Level
- Second Level
- Third Level

Practice Questions

1.Which of the following factors determines the length of DNA?

(a) Position of nucleotides

(b) Number of nnucleotides

(c)Both (a) and (b)

(d) None of the above

2.Which of the following matches is incorrect?

(a) A bacteriophage (^{1} ′ 174) –5386 nucleotides

(b) Bacteriophage lamda – 48502 base pairs

(C) E. coli – 4.6×10^6 bp

(d) Haploid content of human DNA – 3.3×10^6 bp

3.How are nitrogenous bases linked to sugar in a nucleotide?

(a) Hydrogen bond

(b) Phosphodiester bond

c) N-glycosidic bond

(d) O-glycosidic bond

4.Which of the following options correctly completes the sentence: When a phosphate group is linked to …A… group of nucleosides through …B… bond, a corresponding …C… is formed.

(a) A–5’ OH, B–phosphodiester bond, C–nucleotide

(b) A–3’ OH, B–phosphodiester bond, C–nnucleotidec

C) A–2’ OH, B–phosphodiester bond, C–nucleotide

(d) A–5’ OH, B–phosphodiester bond, C–nucleoside

5.Which of the following options correctly identifies pyrimidines and purines?

(a) Pyrimidines include adenine and guanine

(b) Pyrimidines include cytosine, uracil and thymine

C) Purines include adenine and thymine

(d) Purines include guanine and cytosine

6.Which of the following is not a component of a nucleotide?

(a) A nitrogenous base (b) A phosphate group

(c) A ribose sugar (d) A deoxyribose sugar

7.Which of the following scientists did not contribute to the discovery of the structure of DNA?

(a) Rosalind Franklin (b) James Watson

(c) Francis Crick (d) Charles Darwin

8.Which of the following nitrogenous bases is not found in DNA?

(a) Adenine (b) Thymine (c) Guanine (d) Uracil

9.Which of the following is not a type of RNA?

(a) Messenger RNA (b) Transfer RNA

(c) Ribosomal RNA (d) Deoxyribonucleic acid

10.Which of the following is not a type of DNA mutation?

(a) Substitution (b) Deletion (c) Addition (d) Replication

11.Which of the following is not a characteristic of the double helix structure of DNA?

(a) Two strands of nucleotides are held together by hydrogen bonds

(b) The sugar-phosphate backbone of each strand is oriented in the same direction

c) The nitrogenous bases are located on the outside of the helix

(d) The two strands are complementary to each other\

12.Which of the following is not a function of RNA?

(a) To carry genetic information from DNA to ribosomes

(b) To serve as a template for protein synthesis

(c) To catalyze chemical reactions

(d) To store genetic information

13.Which of the following is not a characteristic of the genetic code?

(a) It is universal (b) It is redundant

(c) It is non-overlapping (d) It is self-replicating

14.Which term describes the lightly stained, transcriptionally active part of chromatin?

(a) Euchromatin (b) Heterochromatin

(c) Chromatosome (d) Chromonemata

15.What did Griffith's experiments reveal?

(a) DNA was identified as the genetic material.

(b) RNA was identified as the genetic material.

(c) Something from dead organisms could transform living cells.

(d) Viruses can live in bacteria.

16.Which isotopes did Hershey and Chase use in their experiments?

(a) 32P and 35S (b) 35P and 32S

(c) 34P and 31S (d) 30P and 32S

17.What did Hershey and Chase conclude about the viral infecting agent in their experiment?

(a) Protein (b) DNA (c) RNA (d) Both (b) and (c)

18.Which of the following organisms have RNA as their genetic material?

(a) All bacteria (b) Tobacco Mosaic Viruses (TMV)

(c) QB bacteriophage (d) Both (b) and (c)

19.Who conducted the experiment that experimentally proved the semiconservative mode of DNA replication?

(a) Mathew Meselson (b) Franklin Stahl (c) Both (a) and (b) (d) Watson and Crick

20.Taylor conducted similar experiments like Meselson and Stahl in 1958. What was the experimental organism of Taylor?

(a) Vicia faba (b) Fungi (c) E. Coli (d) Protista

21.Which enzyme is responsible for the synthesis of DNA from RNA template?

(a) DNA polymerase I (b) RNA polymerase I

(c) Reverse transcriptase (d) Ligase

22.Which type of RNA molecule carries amino acids to the ribosome during translation?

(a) Messenger RNA (mRNA) (b) Transfer RNA (tRNA)

(c) Ribosomal RNA (rRNA) (d) Small nuclear RNA (snRNA)

23.Which type of RNA molecule makes up the structure of ribosomes?

(a) Messenger RNA (mRNA) (b) Transfer RNA (tRNA)

(c) Ribosomal RNA (rRNA) (d) Small nuclear RNA (snRNA)

24.What is the function of small nuclear RNA (snRNA)?

(a) To carry amino acids to the ribosome

(b) To synthesize proteins from mRNA templates

(c) To modify and process pre-mRNA molecules

(d) To regulate gene expression by binding to mRNA molecules

25.Which type of RNA molecule is synthesized using a DNA template during transcription?

(a) Messenger RNA (mRNA) (b) Transfer RNA (tRNA)

(c) Ribosomal RNA (rRNA) (d) All of the above

26.Which of the following is not a component of a nucleotide?

(a) Nitrogenous base (b) Phosphate group

(c) Deoxyribose sugar (d) Amino acid group

27..What does “degeneracy” mean in the context of genetic code?

(a) one amino acid has more than one code triplet

(b) one amino acid has only one code triplet

c) codons which specify the same amino acids differ only in the third base of the triplet

(d) Both (a) and (c)

28.Which of the following statements is incorrect about tRNA molecules?

(a) It has an anticodon loop that has bases complementary to the code

(b) It has an amino acid acceptor end to which it binds to amino acids

c) tRNA are not specific for each amino acid

(d) tRNA looks like a clover leaf

29.Which of the following processes refers to the polymerization of amino acids to form a polypeptide?

(a) transcription (b) replication (c) translation (d) polymerization

30.Which of the following processes occur(s) during the charging or aminoacylation of tRNA?

(a) Activation of amino acids in the presence of ATP

(b) Linking of amino acids to their cognate tRNA

c) Both (a) and (b) (d) None of the above

31.What do UTRs present on mRNA refer to?

(a) Untranscribed regions at both 5’ end and 3’ end (b) Untranslated regions at 5’ end

(c) Untranslated regions at both 5’ end and 3’ end (d) Untranslated regions at 3’ end

32.Which enzyme uses lactose as a substrate?

(a) galactosidase (b) a-galactosidase (c) b-galactosidase (d) g-galactosidase

33.How is lactose transported into cells?

(a) b-galactosidase (b) permease (c) transacetylase (d) transferase

34.Why glucose and galactose cannot act as an inducer for lac operon?

(a) Because they cannot bind with the repressor

(b) Because they can bind with the repressor

(c) Because they can bind with the operator

(d) Because they can bind with the regulator

35.Which of the following options is true for the Human Genome Project (HGP)?

(a) It was launched in the year 1990 and was called a mega project

(b) The total estimated cost of the project would be 9 billion US ddollars

c)It aims to identify all 20000-25000 genes in human DNA

(d) All of the above

36.Identify the incorrect pair.

(a) Expressed sequence tags — Genes that are expressed as RNA

(b) Sequence annotation — Sequencing genome with coding sequences

c) Automated DNA sequences — Work on the principle developed by Frederick Sanger

(d) None of the above

37.DNA fingerprinting involves identifying the differences in some specific regions in the DNA sequence called

(a) non-repetitive DNA (b) coding DNA

(c) non-coding DNA (d) repetitive DNA

38.Which of the following enzymes is responsible for unwinding the DNA double helix during DNA replication?

(a) Helicase (b) Polymerase (c) Ligase (d) Topoisomerase

39.In eukaryotic cells, DNA is organized into structures called:

(a) Chromosomes (b) Plasmids (c) Ribosomes (d) Nucleosomes

40.Which of the following is an example of a point mutation?

(a) Deletion of a large segment of DNA (b) Inversion of a DNA segment

(c) Substitution of one nucleotide for another (d) Duplication of a DNA segment

41.In the lac-operon model, lactose molecules function as :

(a) Inducers which bind with the operator gene.

(b) Repressors which bind with the operator gene.

c) Inducers which bind with the repressor protein.

(d) Corepressors which bind with repressor protein.

42.Nonsense codons take part in

(a) helping protein synthesis.

(b) termination gene message for polypeptide synthesis.

c) initiating gene message for polypeptide synthesis.

(d) synthesis of nonprotein amino acids.

43. Eukaryotes differ from prokaryotes in mechanism of DNA replication due to :

(a) different enzymes for opening of strands. (b) DNA primers instead of RNA primers.

(c) unidirectional rather than bidirectional. (d) discontinuous rather than semi discontinuous.

44. Which of the following codons code for phenylalanine?

(a) UUA (b) UUU (c) UCU (d) UAA

45.. Crossing over that results in genetic recombination in higher organisms occurs between :

(a) Sister chromatids of a bivalent. (b) Nonsister chromatids of a bivalent.

(c) Two daughter nuclei. (d) Two different bivalents.

46.What is the main function of tRNA in relation to protein synthesis?

(a) Initiates transcription. (b) Inhibits protein synthesis.

c) Identifies amino acids and transport them to ribosomes. (d) Proof reading.

47. Which of the following would you expect to find in an inducible system?

(a) A repressor protein, which is bound to DNA in absence of any other factor.

(b) A repressor protein, which is bound to DNA in the presence of a co-repressor.

c) An activator protein, which is bound to DNA in the absence of any other factor.

(d) An activator protein, which is bound to DNA only in the absence of air inhibitor.

48. What effect would you expect if gene expression of the lac operon were completely repressed?

(a) The cell would be more efficient without 'wasting' the energy required for the low level of Lac Z,

Lac Y, and Lac A gene expression.

(b) All lactose would accumulate within the cell and become toxic.

c) Lactose would not be converted into the inducer and the operon could not be induced.

(d) All of the above.

49. Choose the incorrect statement regarding the observations drawn from the human genome project.

(a) Repetitive sequences are stretches of RNA.

(b) Less than 2 per cent of the genome codes for protein.

c) SNPs help in tracing human history.

(d) Repetitive sequences make up a very large portion of the human genome.

50. How many of the given statements (i-iv) is/are correct?

(i) In transcription, adenosine pairs with uracil.

(ii) Regulation of lac operon by repressor is referred to as positive regulation.

(i) The human genome has approximately 50,000 genes.

(iv) Haemophilia is a sex-linked recessive disease.

(a) Two (b) Three (c) Four (d) One

Answers

1. Answer: (b) number of nucleotides

Explanation: The length of DNA refers to the number of nucleotides present in it. The nucleotides are the basic building blocks of DNA and each nucleotide is composed of a sugar molecule, a phosphate group, and a nitrogenous base. The position of nucleotides does not affect the length of DNA.

2.answer: © E. coli – 4.6 $\times 10^6$ ′ bp

Explanation: The length of the E. coli genome is approximately 4.6 million base pairs (4.6 $\times 10^6$ bp). Therefore, option © is incorrect.

3.answer: © N-glycosidic bond

Explanation: Nitrogenous bases are linked to sugar by N-glycosidic bond. This bond is formed between the nitrogenous base and the C1' carbon of the sugar molecule.

4. answer: (a) A–5¢ OH, B–phosphodiester bond, C–nucleotide

Explanation: When a phosphate group is linked to the 5' OH group of the sugar molecule of a nucleoside through a phosphodiester bond, a corresponding nucleotide is formed. The 5' end of the nucleotide has a free phosphate group and the 3' end has a free hydroxyl (OH) group.

5.answer: (b) Pyrimidines include cytosine, uracil and thymine

Explanation: Pyrimidines are one of the two types of nitrogenous bases found in DNA and RNA. They include cytosine, uracil (found in RNA), and thymine (found in DNA). Purines include adenine and guanine.

6. Explanation: A nucleotide is composed of a nitrogenous base, a phosphate group, and a sugar. However, the sugar can either be ribose (in RNA) or deoxyribose (in DNA). Therefore, option (d) is incorrect.

7. Explanation: Rosalind Franklin, James Watson, and Francis Crick are all credited with contributing to the discovery of the structure of DNA. Charles Darwin, on the other hand, is known for his work on the theory of evolution. Therefore, option (d) is incorrect.

8. Explanation: Uracil is a nitrogenous base found in RNA, but it is not found in DNA. Instead, DNA uses thymine as one of its four nitrogenous bases. Therefore, option (d) is incorrect.

9. Explanation: RNA stands for ribonucleic acid, while DNA stands for deoxyribonucleic acid. Therefore, option (d) is incorrect.

10. Explanation: Replication is the process by which DNA copies itself, while substitution, deletion, and addition are all types of mutations that can occur during replication. Therefore, option (d) is incorrect.

11.Explanation: The nitrogenous bases are located on the inside of the helix, while the sugar-phosphate backbones are on the outside. Therefore, option © is incorrect.

12.Explanation: RNA can carry genetic information and serve as a template for protein synthesis, as well as catalyze chemical reactions. However, RNA does not store genetic information in the same way that DNA does. Therefore, option (d) is incorrect.

13.Explanation: The genetic code is universal (meaning that the same codons code for the same amino acids in all organisms), redundant (meaning that multiple codons can code for the same amino acid), and non-overlapping (meaning that each nucleotide is only part of one codon). However, the genetic code is not self-replicating. Therefore, option (d) is incorrect.

14.The correct answer is (a) euchromatin. Euchromatin is a lightly stained region of chromatin that remains loosely packed during the interphase stage of the cell cycle. This region is transcriptionally active and allows for gene expression and DNA replication. In contrast, heterochromatin is a more tightly packed region of chromatin that is not transcriptionally active and is often involved in structural functions, such as maintaining chromosome shape.

15.The correct answer is (c) Something from dead organisms could change the living cells. In Frederick Griffith's experiments in 1928, he discovered that something from the heat-killed cells of a pathogenic strain of bacteria could transform a non-pathogenic strain into a pathogenic one. This was the first demonstration of what we now know as bacterial transformation, where genetic material can be transferred from one bacterium to another. Griffith's experiment was significant because it demonstrated that genetic information could be transferred between cells, but he did not identify the specific molecule responsible for this transformation.

16.The correct answer is (a) 32P and 35S. In 1952, Alfred Hershey and Martha Chase used radioactive isotopes to study the genetic material of viruses. They used two isotopes, 32P and 35S, to label the DNA and protein components of the virus, respectively. 32P is a radioactive isotope of phosphorus that is incorporated into the DNA backbone, while 35S is a radioactive isotope of sulfur that is incorporated into the protein coat of the virus. By infecting bacteria with these labeled viruses, Hershey and Chase were able to demonstrate that only the DNA component of the virus was transferred to the bacterial host during infection, not the protein.

17.The correct answer Is (b) DNA. Hershey and Chase's experiment showed that the viral infecting agent was DNA, not protein. By using the radioactive isotope 32P to label the DNA in the virus and 35S to label the protein coat, they were able to demonstrate that only the DNA was transferred to the bacterial host during infection. This provided strong evidence that DNA, not protein, was the genetic material responsible for inheritance and replication.

18.Answer: both (b) and (c)

Explanation: RNA is the genetic material for both Tobacco Mosaic Viruses and QB bacteriophage. In bacteria, DNA is the genetic material.

19. Answer: c), both (a) and (b)

Explanation: Mathew Meselson and Franklin Stahl conducted the experiment that experimentally proved the semiconservative mode of DNA replication.

20.Answer: (a) Vicia faba

Explanation: Taylor's experimental organism was Vicia faba.

21.Answer: © Reverse transcriptase

Explanation: Reverse transcriptase is an enzyme that can synthesize a single-stranded DNA molecule from an RNA template. This process is called reverse transcription and is used by retroviruses such as HIV to convert their RNA genome into DNA, which can then be integrated into the host genome.

22.Answer: (b) Transfer RNA (tRNA)

Explanation: Transfer RNA (tRNA) is a type of RNA molecule that carries amino acids to the ribosome during translation. Each tRNA molecule has a specific anticodon sequence that matches a codon on the mRNA molecule, allowing it to deliver the correct amino acid to the growing polypeptide chain.

23.Answer: © Ribosomal RNA (rRNA)

Explanation: Ribosomal RNA (rRNA) is a type of RNA molecule that makes up the structure of ribosomes. Ribosomes are the cellular organelles responsible for synthesizing proteins from mRNA templates. The rRNA molecules within the ribosome help to align the mRNA and tRNA molecules during translation and also catalyze the formation of peptide bonds between amino acids.

24.Answer: © To modify and process pre-mRNA molecules

Explanation: Small nuclear RNA (snRNA) is a type of RNA molecule that is involved in the processing of pre-mRNA molecules. During splicing, snRNA molecules combine with proteins to form small nuclear ribonucleoprotein particles (snRNPs), which help to identify and remove introns from the pre-mRNA molecule.

25. Answer: (d) All of the above

Explanation: During transcription, all three types of RNA molecules (mRNA, tRNA, and rRNA) are synthesized using a DNA template. RNA polymerase enzymes are responsible for catalyzing the synthesis of these RNA molecules, using one of the DNA strands as a template.

26.Answer: (d) Amino acid group

Explanation: A nucleotide is composed of a nitrogenous base (adenine, guanine, cytosine, or thymine), a phosphate group, and a sugar molecule (either ribose in RNA or deoxyribose in DNA). Amino acids are the building blocks of proteins and are not components of nucleotides.

27.Explanation: Degeneracy in genetic code means that multiple codons can code for the same amino acid. Option © is correct, as codons that specify the same amino acids differ only in the third base of the triplet. Option (a) is also correct, as some amino acids have more than one codon that codes for them.

28. Explanation: Option © is incorrect as tRNA molecules are specific for each amino acid. Each tRNA has a unique anticodon sequence that corresponds to a specific codon on the mRNA and also has a specific binding site for a particular amino acid.

29. Explanation: The process of polymerization of amino acids to form a polypeptide is referred to as translation. Option © is correct.

30. Explanation: Both (a) and (b) occur during the charging or aminoacylation of tRNA. First, the amino acid is activated in the presence of ATP, forming an aminoacyl-AMP intermediate. Then, the activated amino acid is linked to the appropriate tRNA molecule by an enzyme called aminoacyl-tRNA synthetase. Option (c) is correct.

31. Explanation: UTRs refer to the untranslated regions present at both the 5’ and 3’ ends of mRNA. These regions are not translated into protein but play important roles in the regulation of gene expression. Option © is correct.

32. Answer: The correct answer is © b-galactosidase. This enzyme cleaves lactose into glucose and galactose.

33. Answer: Lactose is transported into cells through a specific transporter called permease. The correct answer is (b).

34. Answer: Glucose and galactose cannot act as inducers for the lac operon because they can bind to the lac repressor and prevent it from releasing from the lac operator, which is required for the transcription of the lac operon. The correct answer is (b).

35. Answer: All of the options are true for the Human Genome Project (HGP). It was launched in 1990 as a mega project, the estimated cost was around 9 billion US dollars, and it aimed to identify all the genes in the human genome. The correct answer is (d).

36. Answer: The correct answer is (b). Sequence annotation is the process of identifying the functional elements of a genome sequence, including coding and non-coding regions. It is not limited to only coding sequences. Therefore, option (b) is incorrect.

37.Answer: DNA fingerprinting involves identifying the differences in some specific regions in the DNA sequence called non-coding DNA. These regions include variable number tandem repeats (VNTRs) or short tandem repeats (STRs). The correct answer is ©.

38. Answer: (a) Helicase. Helicase is an enzyme that unwinds the DNA double helix during DNA replication, allowing the DNA to be copied.

39.Answer: (a) Chromosomes. In eukaryotic cells, DNA is organized into structures called chromosomes, which consist of DNA wrapped around proteins called histones.

40.Answer: © Substitution of one nucleotide for another. A point mutation is a change in a single nucleotide in a DNA sequence. Substitution is one type of point mutation, where one nucleotide is replaced by another.

41.In the lac-operon model, lactose molecules function as inducers which bind with the repressor protein. The lac-operon is a model that explains the regulation of gene expression in prokaryotic cells. The lac-operon consists of three genes, lacZ, lacY, and lacA, that encode proteins necessary for lactose metabolism. The lac-operon is under the control of a promoter and an operator region. The operator region is bound by a repressor protein, which inhibits transcription of the lac genes. Lactose, which is a disaccharide of glucose and galactose, can act as an inducer of the lac-operon by binding with the repressor protein, changing its shape and preventing it from binding to the operator region. This allows RNA polymerase to bind to the promoter region and initiate transcription of the lac genes.Therefore, the correct option is © Inducers which bind with the repressor protein.

42.Nonsense codons take part in termination gene message for polypeptide synthesis. Nonsense codons, also known as stop codons or termination codons, are a group of three mRNA nucleotides (UAA, UAG, and UGA) that signal the termination of protein synthesis during translation. When a ribosome encounters a nonsense codon, it does not recognize any tRNA molecule that matches it. As a result, the ribosome releases the polypeptide chain, and the newly synthesized protein is terminated.

Therefore, the correct option is (b) termination gene message for polypeptide synthesis.

43.Eukaryotes differ from prokaryotes in the mechanism of DNA replication due to DNA primers instead of RNA primers. DNA replication is the process by which a cell makes a copy of its DNA. In eukaryotes, the process of DNA replication is more complex than in prokaryotes. One of the major differences is the presence of RNA primers in prokaryotes, while eukaryotes use DNA primers to initiate replication. DNA primers are short sequences of DNA that are complementary to the template strand of DNA and are synthesized by the enzyme primase. These primers provide a starting point for DNA polymerase to add nucleotides and extend the new DNA strand.Therefore, the correct option is (b) DNA primers instead of RNA primers.

44.The codon UUU codes for phenylalanine. Codons are sequences of three nucleotides that code for a specific amino acid during protein synthesis. Phenylalanine is an essential amino acid that is used to build proteins. There are 64 possible codons that can be formed by combining four nucleotides in groups of three. Each codon codes for a specific amino acid or serves as a stop signal. Therefore, the correct option is (b) UUU.

45.Crossing over those results in genetic recombination in higher organisms occurs between nonsister chromatids of a bivalent. Crossing over is the exchange of genetic material between homologous chromosomes during meiosis. This process results in genetic recombination, which increases genetic diversity in offspring. In higher organisms, crossing over occurs between nonsister chromatids of homologous chromosomes, specifically during prophase I of meiosis. This exchange occurs at regions called chiasmata, which form between non-sister chromatids of the homologous chromosomes. Therefore, the correct option is (b) Nonsister chromatids of a bivalent.

46.(c) Identifies amino acids and transport them to ribosomes.

Explanation: The main function of tRNA (transfer RNA) in relation to protein synthesis is to identify and transport specific amino acids to the ribosomes during translation. Each tRNA molecule has an anticodon sequence that matches a specific codon sequence on the mRNA, and it carries the corresponding amino acid. The tRNA recognizes the codon on the mRNA and delivers the correct amino acid to the growing polypeptide chain.

47.(c) An activator protein, which is bound to DNA in the absence of any other factor.

Explanation: An inducible system is a type of gene regulation in which the transcription of genes is turned on by the presence of a specific molecule or signal. In an inducible system, an activator protein, which is bound to DNA in the absence of any other factor, would be expected. This activator protein is activated by the inducer, which binds to it and causes a conformational change that allows it to bind to DNA and activate transcription.

48.(b) All lactose would accumulate within the cell and become toxic.

Explanation:The lac operon is a system of genes in bacteria that are responsible for the metabolism of lactose. If gene expression of the lac operon were completely repressed, the cell would not be able to metabolize lactose, and all lactose molecules would accumulate within the cell and become toxic. Therefore, option (b) is the correct answer.

49.(a) Repetitive sequences are stretches of RNA.

Explanation: Repetitive sequences are DNA sequences that occur in multiple copies throughout the genome. These sequences do not code for proteins, but they have other functions, such as regulating gene expression and maintaining the structure of chromosomes. Repetitive sequences make up a very large portion of the human genome. Option (a) is incorrect because repetitive sequences are stretches of DNA, not RNA.

50.(d) One

Explanation: Only statement (iv) is correct. Adenosine pairs with uracil in RNA, not in transcription (I is incorrect). The regulation of the lac operon by repressor is referred to as negative regulation, not positive regulation (ii is incorrect). The human genome has approximately 20,000-25,000 genes, not 50,000 (iii is incorrect). Hemophilia is a sex-linked recessive disease (iv is correct). Therefore, option (d) is the correct answer.