



MOLECULAR BASIS OF INHERITANCE



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Nucleic acids (DNA & RNA) are the building blocks of genetic material. DNA is the genetic material in most of the organisms. RNA is the genetic material in some viruses. RNA mostly functions as **messengers**.

THE DNA

STRUCTURE OF POLYNUCLEOTIDE CHAIN



Polynucleotides are the polymer of nucleotides. DNA & RNA are **polynucleotides**.

A nucleotide has 3 components:

1

A nitrogenous base.

2

A pentose sugar (ribose in RNA & deoxyribose in DNA).

3

A phosphate group.



Nitrogen bases are 2 types:

Purines: It includes Adenine (A) and Guanine (G). (NEET 2019)

Pyrimidines: It includes Cytosine (C), Thymine (T) & Uracil (U). Thymine (5-methyl Uracil) present only in DNA and Uracil only in RNA.

A nitrogenous base is linked to the pentose sugar through an **N-glycosidic linkage** to form **nucleoside**.

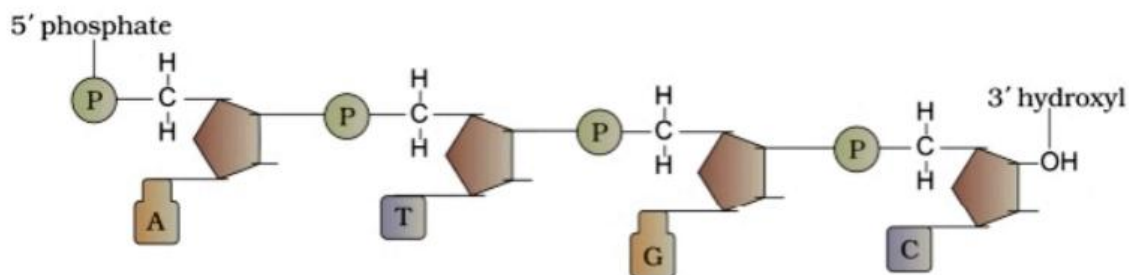
Nitrogen base + sugar + phosphate group = **Nucleotide (deoxyribonucleotide)**.

Nucleosides in RNA	Nucleosides in DNA
Adenosine	Deoxyadenosine
Guanosine	Deoxyguanosine
Cytidine	Deoxycytidine
Uridine	Deoxythymidine

In RNA, every nucleotide residue has an additional -OH group present at 2'-position in the ribose (2'-OH).

2 nucleotides are linked through 3'-5' phosphodiester bond to form **dinucleotide**. (AIPMT 2010)

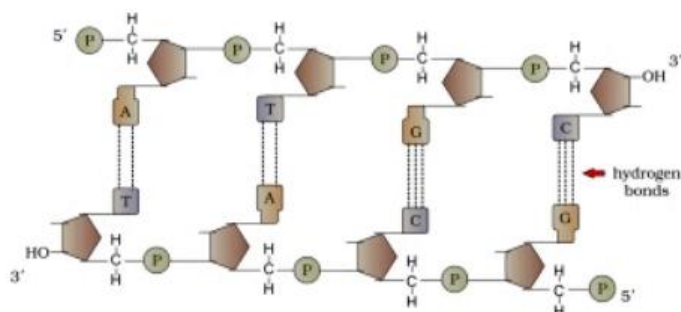
When more nucleotides are linked, it forms **polynucleotide**.



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STRUCTURE OF THE DNA

- ➔ **Friedrich Meischer (1869):** Identified DNA and named it as 'Nuclein'.
- ➔ **James Watson & Francis Crick (1953)** proposed double helix model of DNA. It was based on X-ray diffraction data produced by **Maurice Wilkins & Rosalind Franklin**.
- ➔ DNA is made of 2 polynucleotide chains coiled in a right handed fashion. Its backbone is formed of sugar & phosphates. The bases project inside.
- ➔ The 2 chains have **anti-parallel** polarity, i.e. one chain has the polarity 5'-3' and the other has 3'-5'. (AIPMT 2008)
- ➔ The bases in 2 strands are paired through H-bonds forming base pairs (bp). A=T (2 hydrogen bonds) C≡G (3 hydrogen bonds) (NEET 2020)
- ➔ Purine comes opposite to a pyrimidine. This generates uniform distance between the 2 strands of DNA helix.
- ➔ **Erwin Chargaff's rule:** In DNA, the proportion of A is equal to T and the proportion of G is equal to C.



$$[A] + [G] = [T] + [C]$$

or

$$[A] + [G] / [T] + [C] = 1$$

• ϕ 174 (a bacteriophage) has 5386 nucleotides.

• Bacteriophage lambda has 48502 base pairs (bp).

• *E. coli* has 4.6×10^6 bp.

• Haploid content of human DNA is 3.3×10^9 bp.

Length of DNA = number of base pairs X distance between two adjacent base pairs.

Number of base pairs in human = 6.6×10^9

Hence, the length of DNA = $6.6 \times 10^9 \times 0.34 \times 10^{-9}$

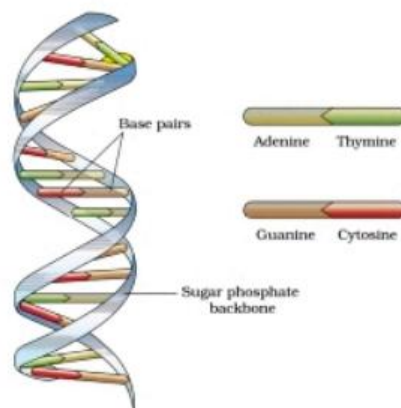
$= 2.2\text{m}$

In *E. coli*, length of DNA = 1.36 mm

$= (1.36 \times 10^{-3} \text{ m})$

The number of base pairs = $1.36 \times 10^{-3} / 0.34 \times 10^{-9}$

$= 4 \times 10^6 \text{ bp}$



PACKAGING OF DNA HELIX

In prokaryotes (E.g. *E. coli*), the DNA is not scattered throughout the cell. DNA, being negatively charged, is held with some positively charged proteins and form 'nucleoid'.

In eukaryotes, there is a set of positively charged, basic proteins called **histones**.

Histones are in positively rich charged basic amino acid residues lysines and arginines.

8 histones form histone **octamer**.

Negatively charged DNA is wrapped around histone octamer to give **nucleosome**.

(NEET 2017)

A typical nucleosome contains 200 bp.

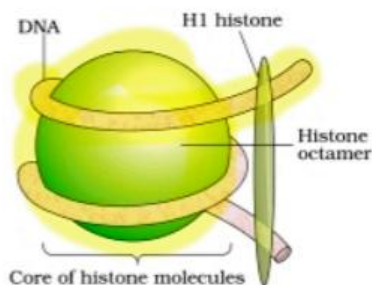
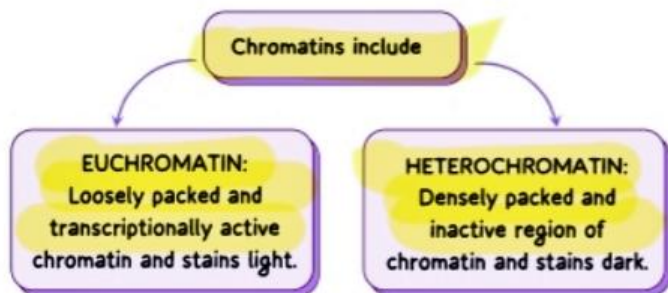
Therefore, the total number of nucleosomes in human = $6.6 \times 10^9 \text{ bp} \div 200 = 3.3 \times 10^7$

Nucleosomes constitute of the repeating unit to chromatin. Chromatin is the thread-like stained bodies.

Nucleosomes in chromatin = 'beads-on-string'.
(AIPMT 2011)

Chromatin is packaged - chromatin fibres - coiled and condensed at metaphase stage to form chromosomes.

Higher level packaging of chromatin requires non histone chromosomal (NHC) proteins.



THE SEARCH FOR GENETIC MATERIAL

1. GRIFFITH'S TRANSFORMING PRINCIPLE EXPERIMENT

Griffith used mice & *Streptococcus pneumoniae*. *Streptococcus pneumoniae* has 2 strains-

Smooth (S) strain (Virulent): Has polysaccharide **mucus** coat. Cause pneumonia.

Rough (R) strain (Non-virulent): No mucus coat. Does not cause Pneumonia.

EXPERIMENT:

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 (Hk) + R-strain (live) ---- Inject into mice ---- Mice die



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He concluded that some 'transforming principle', transferred from heat-killed S-strain to R-strain. It enabled R-strain to synthesize smooth polysaccharide coat and become virulent. This must be due to the transfer of genetic material.

2. BIOCHEMICAL CHARACTERIZATION OF TRANSFORMING PRINCIPLE

Oswald Avery, Colin MacLeod & Maclyn McCarty worked to determine the biochemical nature of transforming principle in Griffith's experiment.

They discovered that Digestion of protein and RNA (using Proteases and RNases) did not affect transformation. So, the transforming substance was not a protein or RNA.

They purified biochemicals (proteins, DNA, RNA etc.) from heat killed S cells using suitable enzymes.

Digestion of DNA with DNase inhibited transformation. It means that DNA caused transformation of R cells to S cells, i.e. DNA was the transforming principle.

3. HERSHEY CHASE EXPERIMENT (BLENDER EXPERIMENT)

- Hershey & Chase grew some bacteriophage viruses on a medium containing radioactive phosphorus (^{32}P) and some others on medium containing radioactive sulphur (^{35}S). (NEET 2017)
- Viruses grown in ^{32}P got radioactive DNA because only DNA contains phosphorus. Viruses grown in ^{35}S got radioactive protein because protein contains sulphur.
- These preparations were used separately to infect *E. coli*.
- After infection, the *E. coli* cells were gently agitated in a blender to remove the virus particles from the bacteria.
- Then the culture was centrifuged to separate lighter virus particles from heavier bacterial cells.
- Bacteria infected with viruses having radioactive DNA were radioactive. i.e., DNA had passed from the virus to bacteria. Bacteria infected with viruses having radioactive proteins were not radioactive. i.e., proteins did not enter the bacteria from the viruses. This proves that DNA is the genetic material.

PROPERTIES OF GENETIC MATERIAL (DNA VS RNA)

A genetic material may have the following properties:

Ability to generate its replica (Replication).

Provide the mutations that are required for evolution. (NEET-II 2016)

Chemical and structural stability.

Ability to express as 'Mendelian Characters'.



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Reasons for stability (less reactivity) of DNA

- Double stranded
- Presence of thymine
- Absence of 2'-OH in nucleotide

Reasons for mutability (high reactivity) of RNA

- Single stranded
- Presence of Uracil
- Presence of 2'-OH in nucleotide

💡 RNA is unstable. So, RNA viruses (E.g. Q. B bacteriophage, Tobacco Mosaic Virus etc.) mutate and evolve faster.

💡 DNA strands are complementary. On heating, they separate. In appropriate conditions, they come together. In Griffith's experiment, some properties of DNA of the heat killed bacteria did not destroy. It indicates the stability of DNA.

💡 For the storage of genetic information, DNA is better due to its stability. But for the transmission of genetic information, RNA is better.

RNA can directly code for the protein synthesis, hence can easily express the characters. DNA is dependent on RNA for protein synthesis.

RNA WORLD



It acts as genetic material and catalyst.



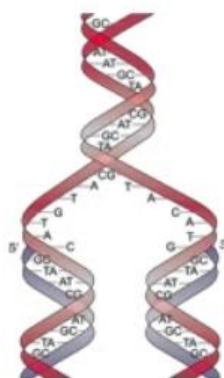
Essential life processes (metabolism, translation, splicing etc.) evolved around RNA.



RNA was the first genetic material.



DNA evolved from RNA for stability.



CENTRAL DOGMA OF MOLECULAR BIOLOGY



It is proposed by Francis Crick. It states that the genetic information flows from DNA - RNA - Protein. (NEET 2013)



In some viruses, flow of information is in reverse direction (from RNA to DNA). It is called reverse transcription.

DNA REPLICATION

Replication is the copying of DNA from parental DNA. Watson & Crick proposed Semi-conservative model of replication. It suggests that the parental DNA strands act as template for the synthesis of new complementary strands. After replication, each DNA molecule would have one parental and one new strand. Matthew Messelson & Franklin Stahl (1958) experimentally proved Semi-conservative model. (AIPT 2000)



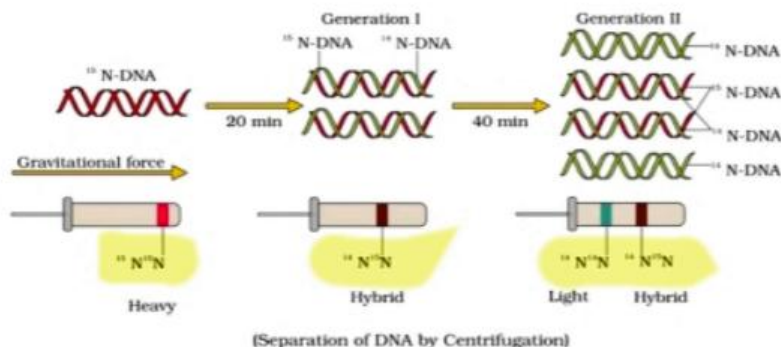
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MESSELSON & STAHL'S EXPERIMENT

They cultured *E. coli* in a medium containing $^{15}\text{NH}_4\text{Cl}$ (^{15}N : heavy isotope of N). ^{15}N was incorporated into both strands of bacterial DNA and the DNA became heavier.

Another preparation containing N salts labeled with ^{14}N is also made. ^{14}N was incorporated in both strands of DNA and became lighter.

These 2 types of DNA can be separated by centrifugation in a CsCl density gradient.



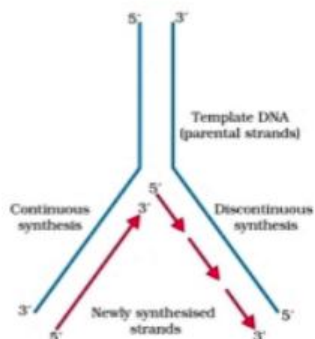
They took *E. coli* cells from ^{15}N medium and transferred to ^{14}N medium. After one generation (i.e. after 20 minutes), they isolated and centrifuged the DNA. Its density was intermediate (hybrid) between ^{15}N DNA and ^{14}N DNA. This shows that the newly formed DNA one strand is old (^{15}N type) and one strand is new (^{14}N type). This confirms semi-conservative replication. After II generation (i.e. after 40 minutes), there was equal amounts of hybrid DNA and light DNA.

Taylor & colleagues (1958) performed similar experiments on *Vicia faba* (faba beans) (NEET-II 2016) using radioactive thymidine to detect distribution of newly synthesized DNA in the chromosomes. It proved that the DNA in chromosomes also replicate semi-conservatively.

THE MACHINERY AND ENZYMES FOR REPLICATION



DNA replication starts at a point called **origin** (ori). A unit of replication with one origin is called a **replicon**. During replication, the 2 strands unwind and separate by breaking H-bonds in presence of an enzyme, **Helicase**.



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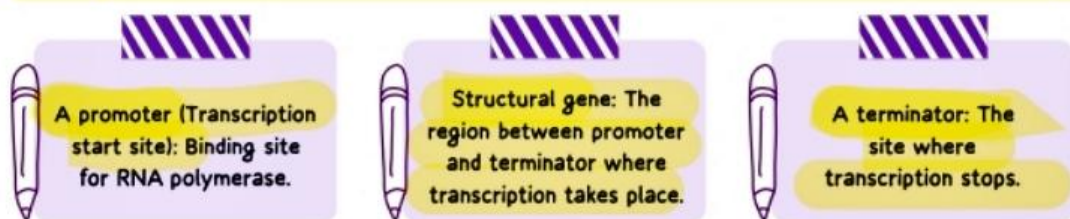
- Unwinding of the DNA molecule at a point forms a structure 'Y'-shaped called replication fork. The separated strands act as templates for the synthesis of new strands. DNA replicates in the 5'-3' direction.
- Deoxyribonucleoside triphosphates (dATP, dGTP, dCTP & dTTP) act as substrate and provide energy for polymerization.
- Firstly, a small RNA primer is synthesized in presence of an enzyme, **primase**.
- In the presence of an enzyme, DNA dependent DNA polymerase, many nucleotides join with one another to primer strand and form a polynucleotide chain (new strand).
- The DNA polymerase forms one new strand (leading strand) in a continuous stretch in the 5'-3' direction (Continuous synthesis).
- The other new strand is formed in small stretches (Okazaki fragments) in 5'-3' direction (Discontinuous synthesis).
- The Okazaki fragments are then joined together to form a new strand by an enzyme, DNA ligase. This new strand is called lagging strand. (NEET 2017)
- If a wrong base is introduced in the new strand, DNA polymerase can do proof reading.
- E. coli* completes replication within 38 minutes. i.e. 2000 bp per second.
- In eukaryotes, the replication of DNA takes place at S phase of the cell cycle. Failure in cell division after DNA replication results in polyploidy.

TRANSCRIPTION

- It is the process of copying genetic information from one strand of the DNA into RNA.
- Here, adenine pairs with uracil instead of thymine.
- During transcription, both strands are not copied because the code for proteins is different in both strands. This complicates the translation.
- If 2 RNA molecules are produced simultaneously, this would be complimentary to each other. It forms a double stranded RNA and prevents translation.

TRANSCRIPTION UNIT

It is the segment of DNA between the sites of initiation and termination of transcription. It consists of 3 regions:



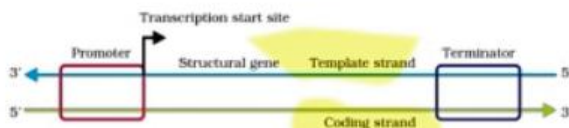
The DNA- dependent RNA polymerase catalyzes the polymerization only in 5'-3' direction.

3'-5' acts as template strand.

5'-3' acts as coding strand.

3'-ATGCATGCAT GCATGCATGCATGC-5' template strand.

5'-TACGTACGTACGTACGTA CGTACG-3' coding strand.



TRANSCRIPTION UNIT AND GENE

Gene: Functional unit of inheritance. It is the DNA sequence coding for RNA molecule.

Cistron: A segment of DNA coding for a polypeptide.

Structural gene in a transcription unit is 2 types:

MONOCISTRONIC STRUCTURAL GENES (SPLIT GENES):

It is seen in eukaryotes. Here, coding sequences (exons or expressed sequences) are interrupted by introns (intervening sequences).

POLYCISTRONIC STRUCTURAL GENES:

It is seen in prokaryotes. Here, there are no split genes

TYPES OF RNA



- mRNA (messenger RNA): Provide template for translation (protein synthesis).
- rRNA (ribosomal RNA): Structural & catalytic role during translation. E.g. 23S rRNA in bacteria acts as *ribozyme*. (NEET-II 2016)
- tRNA (transfer RNA or sRNA or soluble RNA): Brings amino acids for protein synthesis and reads the genetic code.

STEPS OF TRANSCRIPTION IN PROKARYOTES

Initiation



Here, the enzyme RNA polymerase binds at the promoter site of DNA. (AIPMT 2003) This causes the local unwinding of the DNA double helix. An initiation factor (σ factor) present in RNA polymerase initiates the RNA synthesis.

Elongation



The RNA chain is made in a 5'→3' direction. Activated ribonucleoside triphosphates (ATP, GTP, UTP, and CTP) are added during this process as substrates. The nucleotide sequence in the DNA template is complementary to the newly synthesised RNA strand.

Elongation



Only a short stretch of the RNA remains bound to the enzyme. The nascent RNA and RNA polymerase both fall off once the polymerases reach the terminator region. The transcription is stopped when a termination factor (ρ , rho factor) binds to the RNA polymerase.



SALIENT FEATURES OF GENETIC CODE

- Triplet code (three-letter code). (AIPMT 2003)
- 61 codons code for amino acids. 3 codons (UAA, UAG & UGA) do not code for any amino acids. They act as stop codons (Termination codons or non-sense codons). (AIPMT 2009)
- Genetic code is universal. E.g. From bacteria to human
- UUU codes for Phenylalanine. Some exceptions are found in mitochondrial codons, and in some protozoans.
- No punctuations b/w adjacent codons (comma less code).

- The codon is read in mRNA in a contiguous fashion. (AIPMT 2009)
- Genetic code is non-overlapping. (AIPMT 2009)
- A single amino acid is represented by many codons (except AUG for methionine & UGG for tryptophan). Such codons are called degenerate codons. (NEET 2013)
- Genetic code is unambiguous and specific. i.e. one codon specifies only one amino acid. (AIPMT 2010)
- AUG has dual functions. It codes for Methionine and acts as initiator codon. (NEET 2016) In eukaryotes, methionine is the first amino acid and formyl methionine in prokaryotes.



George Gamow suggested that for coding 20 amino acids, the code should be made up of 3 nucleotides.



Har Gobind Khorana developed the chemical method synthesizing RNA molecules with defined combinations of bases (homopolymers & copolymers).



Marshall Nirenberg developed cell-free system for protein synthesis.



Severo Ochoa investigated that polynucleotide phosphorylase enzyme is used to polymerize RNA with defined sequences in a template independent manner.

MUTATIONS AND GENETIC CODE



Relationship between genes & DNA are best understood by mutation studies. Deletions & rearrangements in a DNA may cause loss or gain of a gene and so a function.



Insertion or deletion of one or two bases changes the reading frame from the point of insertion or deletion.



Insertion/ deletion of three or its multiple bases insert or delete one or multiple codon. Hence one or multiple amino acids are inserted /deleted. The reading frame remains unaltered from that point onwards. Such mutations are known as frame-shift insertion or deletion mutations.

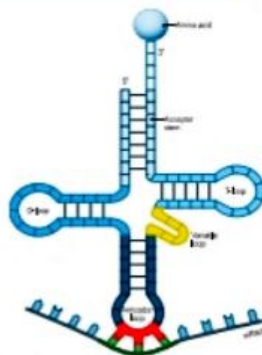


It proves that codon is a triplet and is read contiguously.

t-RNA – THE ADAPTER MOLECULE

tRNA is called adaptor molecule because it has

- An Anticodon loop that has bases complementary to the codon.
- An amino acid acceptor end to which amino acid binds. Ribosome binding loop.
- Enzyme binding loop.
- For initiation, there is another tRNA called initiator tRNA. -
- There are no tRNAs for stop codons.
- Secondary (2-D) structure of tRNA looks like a cloverleaf. (AIPMT 2004)
- 3-D structure looks like inverted 'L'. (AIPMT 2000)



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TRANSLATION (PROTEIN SYNTHESIS)

It takes place in ribosomes. It includes 4 steps:

1. Charging of tRNA

2. Initiation

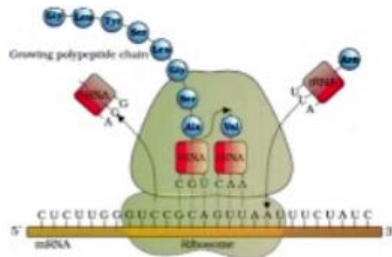
3. Elongation

4. Termination

1. CHARGING (AMINOACYLATION) OF tRNA



Formation of peptide bond needs energy obtained from ATP. For this, amino acids are activated (amino acid + ATP) and linked to their cognate tRNA in presence of aminoacyl tRNA synthetase. Thus, the tRNA becomes charged.



2. INITIATION

- It begins at the 5'-end of mRNA in the presence of an initiation factor.
- The mRNA binds to the small subunit of ribosome.
- Now the large subunit binds to the small subunit to complete the initiation complex.

- Large sub unit has 2 binding sites for tRNA- aminoacyl tRNA binding site (A site) and peptidyl site (P site).
- Initiation codon for methionine is AUG. So methionyl tRNA complex would have UAC at the anticodon site.

3. ELONGATION



At the P site, the first codon of mRNA binds with anticodon of methionyl tRNA complex.



Another aminoacyl tRNA complex with an appropriate amino acid enters the ribosome and attaches to A site. Its anticodon binds to the second codon on the mRNA and a peptide bond is formed between first and second amino acids in presence of an enzyme, peptidyl transferase.



First amino acid and its tRNA are broken. This tRNA is removed from P site and second tRNA at the A site is pulled to P site along with mRNA. This is called **translocation**.



Then 3rd codon comes into A site and a suitable tRNA with 3rd amino acid binds at the A site. This process is repeated.

4. TERMINATION

- When aminoacyl tRNA reaches the termination codon like UAA, UAG & UGA, the termination of translation occurs.
- The polypeptide and tRNA are released from the ribosomes.
- The ribosome dissociates into large and small subunits at the end of protein synthesis.
- A group of ribosomes associated with a single mRNA for translation is called a polyribosome (polysomes). (NEET 2018)
- An mRNA has additional sequences that are not translated (untranslated regions or UTR). UTRs are present at both 5' end (before start codon) and 3'-end (after stop codon). They are required for efficient translation process.



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REGULATION OF GENE EXPRESSION

In eukaryotes, gene expression occurs by following levels:

1. Transcriptional level (formation of primary transcript).

3. Transport of mRNA from nucleus to the cytoplasm.

2. Processing level (splicing).

4. Translational level (formation of a polypeptide).



The metabolic, physiological and environmental conditions regulate expression of genes. E.g. In *E. coli*, the beta-galactosidase enzyme hydrolyses lactose into galactose & glucose. In the absence of lactose, the synthesis of beta-galactosidase stops.



The development and differentiation of embryo into adult are a result of the coordinated expression of several set of genes.



If a substrate is added to growth medium of bacteria, a set of genes is switched on to metabolize it. It is called induction. When a metabolite (product) is added, the genes to produce it are turned off. This is called repression.

OPERON CONCEPT

Each metabolic reaction is controlled by a set of genes"

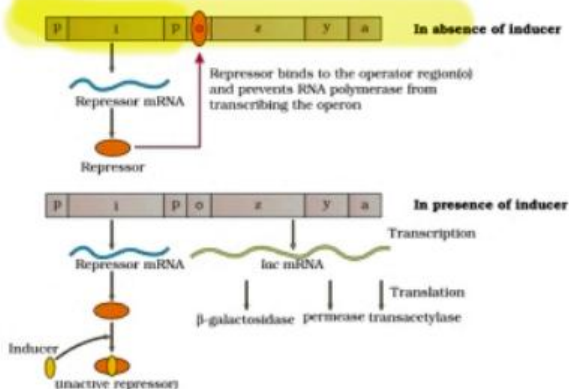
All the genes regulating a metabolic reaction constitute an Operon. E.g. lac operon, trp operon, ara operon, his operon, val operon etc.

Lac Operon in *E. coli*: The operon controlling lactose.

- a) A regulatory or inhibitor
- (i) gene: Codes for the repressor

b) 3 structural genes:

- i. z gene: Codes for β -galactosidase (hydrolyze lactose to galactose and glucose).
- ii. y gene: Codes for permease (increase permeability of the cell to lactose).
- iii. a gene: Codes for a transacetylase.



Lac operon



The genes present in the operon function together in the same or related metabolic pathway. There is an operator region for each operon. (AIPMT 1998)



If there is no lactose (inducer), lac operon remains switched off. (Karnataka NEET 2013) The regulator gene synthesizes mRNA to produce the repressor protein. This protein binds to the operator genes and blocks RNA polymerase movement. So the structural genes are not expressed.



If lactose is provided in the growth medium, the lactose is transported into the *E. coli* cells by the action of permease. Lactose (inducer) binds with repressor protein. So repressor protein cannot bind to operator gene. (NEET 2013) The operator gene becomes free and induces the RNA polymerase to bind with promoter gene. Then, transcription starts.



Regulation of lac operon by repressor is called negative regulation. (NEET 2001)



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HUMAN GENOME PROJECT (HGP)

The entire DNA in the haploid set of chromosomes of an organism is called a **Genome**. In Human genome, DNA is packed in 23 chromosomes. Human Genome Project (1990-2003) is the first mega project in identifying the sequence of nucleotides and mapping of all the genes in human genome. Human genome contains about 3×10^9 bp. HGP was coordinated by the US Department of Energy and National Institute of Health.

GOALS OF HGP

a. Identify all the estimated genes in human DNA.

d. Improve tools for data analysis.

b. Determine the sequences of the 3 billion chemical base pairs that make up human DNA.

e. Transfer related technologies to other sectors.

c. Store this information in databases.

f. Address the ethical, legal and social issues (ELSI) that may arise from the project.

Methodologies of HGP: 2 major approaches.

Expressed Sequence Tags (ESTs): Focused on identifying all the genes that are expressed as RNA. (NEET 2019)

Sequence annotation: Sequencing whole set of genome containing all the coding & non-coding sequence and later assigning different regions in the sequence with functions.



Procedure:

Isolate total DNA from a cell - Convert into random fragments - Clone in suitable host (e.g. BAC & YAC) for amplification - Fragments are sequenced using Automated DNA sequencers (using Frederick Sanger method) -- Sequences are arranged based on overlapping regions. Alignment of sequences using computer programs.

BAC= Bacterial Artificial Chromosomes

YAC= Yeast Artificial Chromosomes

HGP was closely associated with Bioinformatics. Bioinformatics: Application of computer science and information technology to the field of biology & medicine.



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SALIENT FEATURES OF HUMANGENOME

- Human genome contains 3164.7 million nucleotide bases.
- Total number of genes= about 30,000.
- Average gene consists of 3000 bases, but sizes vary. Largest known human gene (dystrophin on X chromosome) contains 2.4 million bases.
- 99.9% nucleotide bases are same in all people. Only 0.1% difference makes every individual unique.
- Functions of over 50% of discovered genes are unknown.
- Chromosome I has most genes (2968) and Y has the fewest (231).

- Less than 2% of the genome codes for proteins.
- Very large portion of human genome is made of Repeated (repetitive) sequences. These are stretches of DNA sequences that are repeated many times. They have no direct coding functions. They shed light on chromosome structure, dynamics and evolution.
- About 1.4 million locations have single-base DNA differences. They are called SNPs (Single nucleotide polymorphism or 'snips').

DNA FINGERPRINTING (DNA PROFILING)



It is the technique to identify the similarities and differences of the DNA fragments of two different individuals. Developed by Alec Jeffreys (1985).

BASIS OF DNA FINGERPRINTING

- DNA carries some non-coding repetitive sequences called variable number tandem repeats (VNTR).
- Number of repeats is specific from person to person.
- The size of VNTR varies from 0.1 to 20 kb.
- Repetitive DNA are separated from bulk genomic DNA as different peaks during density gradient centrifugation.
- The bulk DNA forms a major peak and the small peaks are called satellite DNA. Satellite DNA is classified as micro-satellites, mini satellites etc. based on base composition (A:T rich or G:C rich), length of segment and number of repetitive units (AIPMT MAIN 2012)
- VNTR belongs to mini-satellite DNA (KARNATAKA NEET 2013)
- Any difference in the nucleotide sequence (inheritable mutation) observed in a population is called DNA polymorphism (variation at genetic level).
- Polymorphism is higher in non-coding DNA sequence because mutations in these sequences may not have any immediate effect in an individual's reproductive ability .
- These mutations accumulate generation after generation and cause polymorphism. Important for evolution & speciation, polymorphisms play important role.



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STEPS OF DNA FINGERPRINTING (SOUTHERN BLOTTING TECHNIQUE)

a. Isolation of DNA.

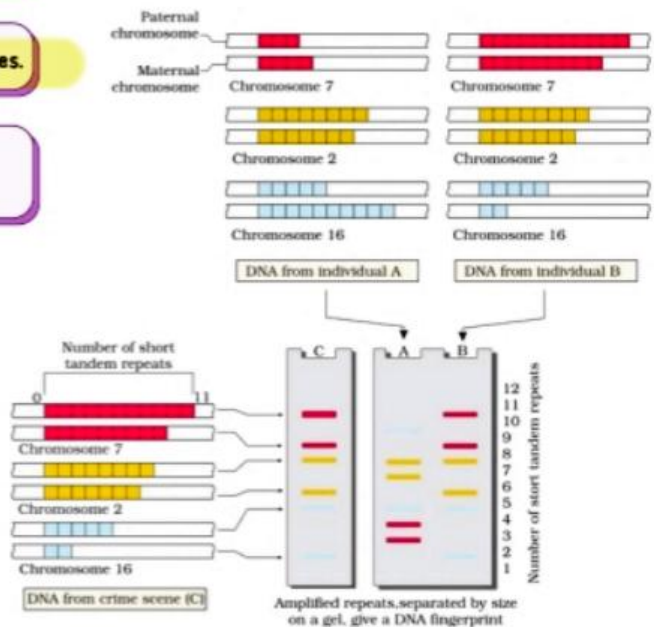
b. Digestion of DNA by restriction endonucleases.

c. Separation of DNA fragments by gel electrophoresis.

d. Transferring (blotting) DNA fragments to synthetic membranes such as nitrocellulose or nylon.

e. Hybridization using radioactive labelled VNTR probe.

f. Detection of hybridized DNA by autoradiography.



The image (in the form of dark & light bands) obtained is called DNA fingerprint. It differs from individual to individual except in monozygotic (identical) twins.



The sensitivity of the technique has been increased by use of polymerase chain reaction (PCR). (NEET I 2016) Therefore, DNA from a single cell is enough for DNA fingerprinting.

APPLICATION OF DNA FINGERPRINTING



Forensic tool to solve paternity, rape, murder etc.



For the diagnosis of genetic diseases.



To determine phylogenetic status of animals.



To determine population and genetic diversities.





BIOLOGY

PHYSICS

CHEMISTRY

MATHS

ENGLISH

REMEDIAL NATURAL SPECIAL CLASS