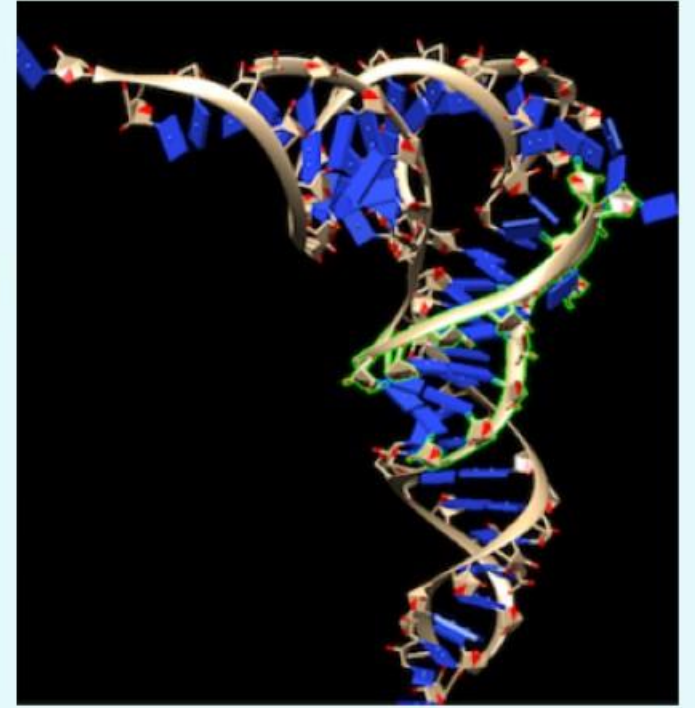
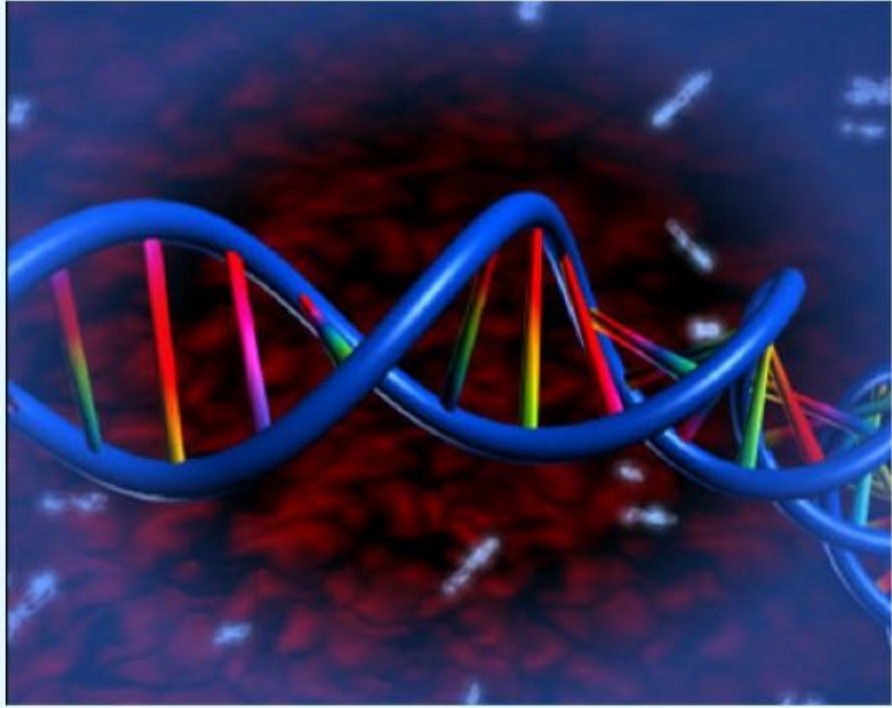


**MOLECULAR BASIS OF
INHERITANCE**

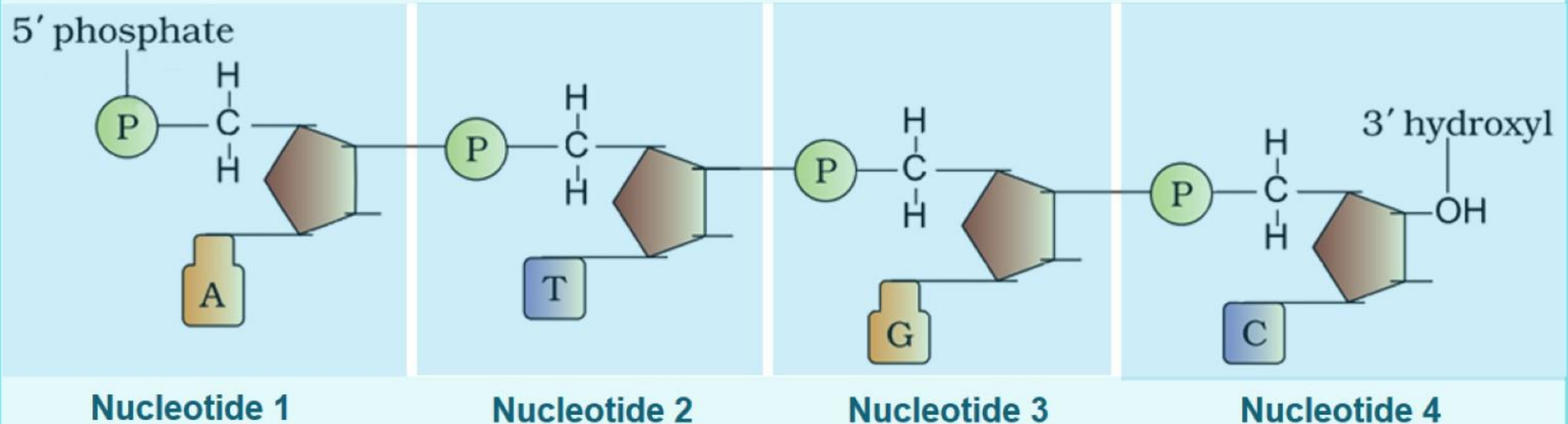


- **Nucleic acids (DNA and RNA)** are the building blocks of genetic material.
- **DNA** is the **genetic material** in most of the organisms.
- **RNA** is the genetic material in some **viruses**.
- **RNA** mostly functions as **messengers**.

THE DNA

STRUCTURE OF POLYNUCLEOTIDE CHAIN

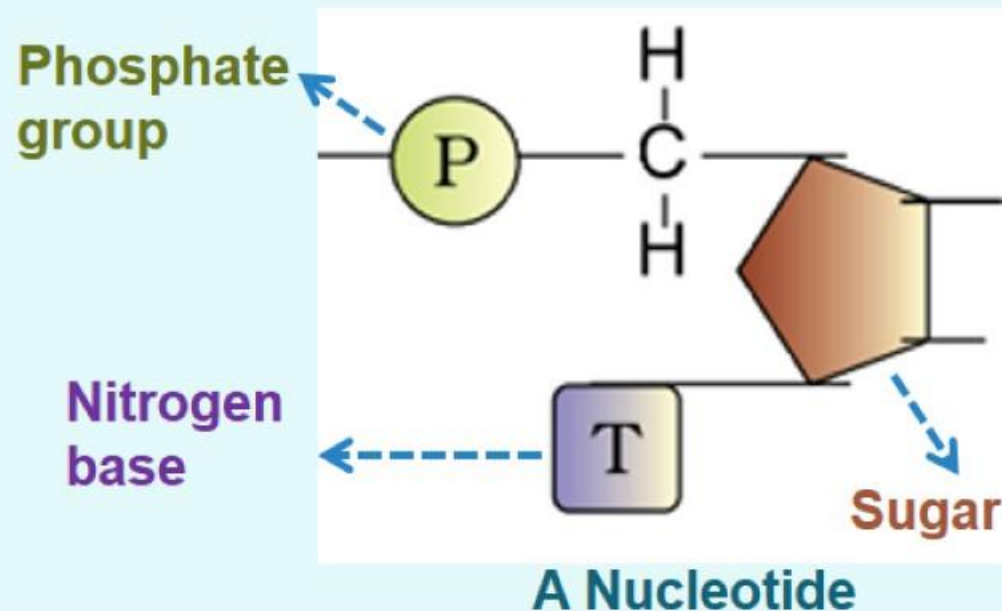
- **Polynucleotides** are the polymer of **nucleotides**.
- DNA and RNA are Polynucleotides.



THE DNA

STRUCTURE OF POLYNUCLEOTIDE CHAIN

- **Polynucleotides** are the polymer of **nucleotides**.
- DNA and RNA are Polynucleotides.



A nucleotide has 3 components

A nitrogenous
base

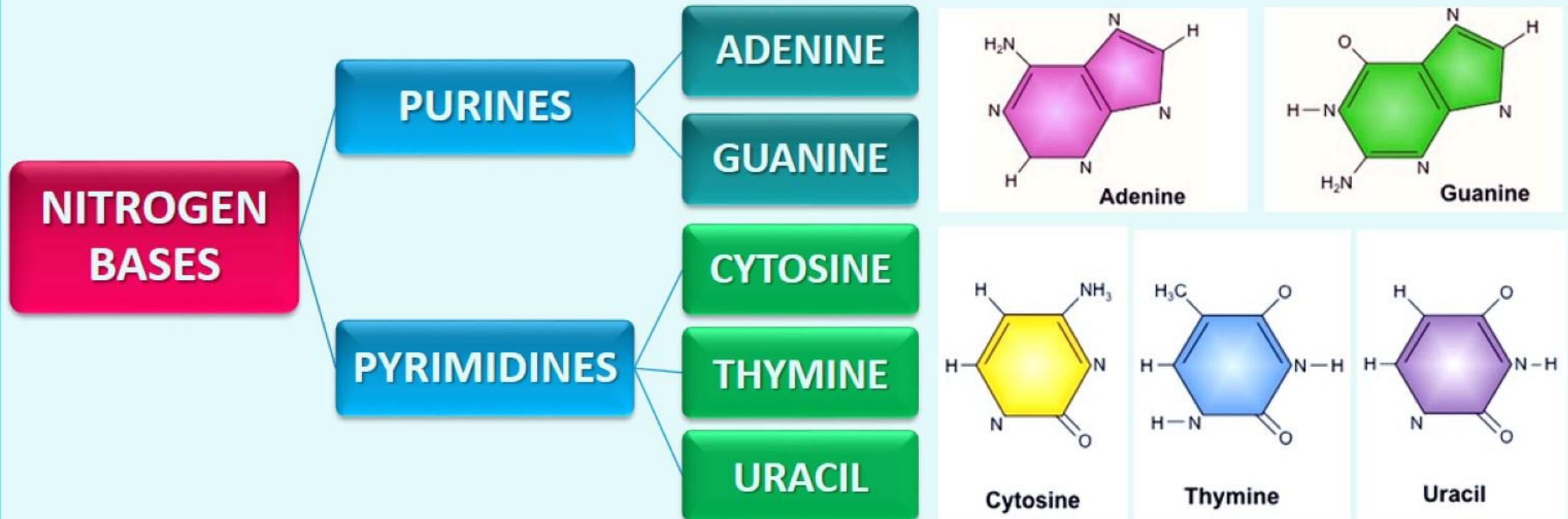
A pentose
sugar
(Ribose in RNA
& deoxyribose
in DNA)

A phosphate
group

THE DNA

bankofbiology.com

STRUCTURE OF POLYNUCLEOTIDE CHAIN



Thymine (5-methyl Uracil) present only in **DNA** and **Uracil** only in **RNA**.

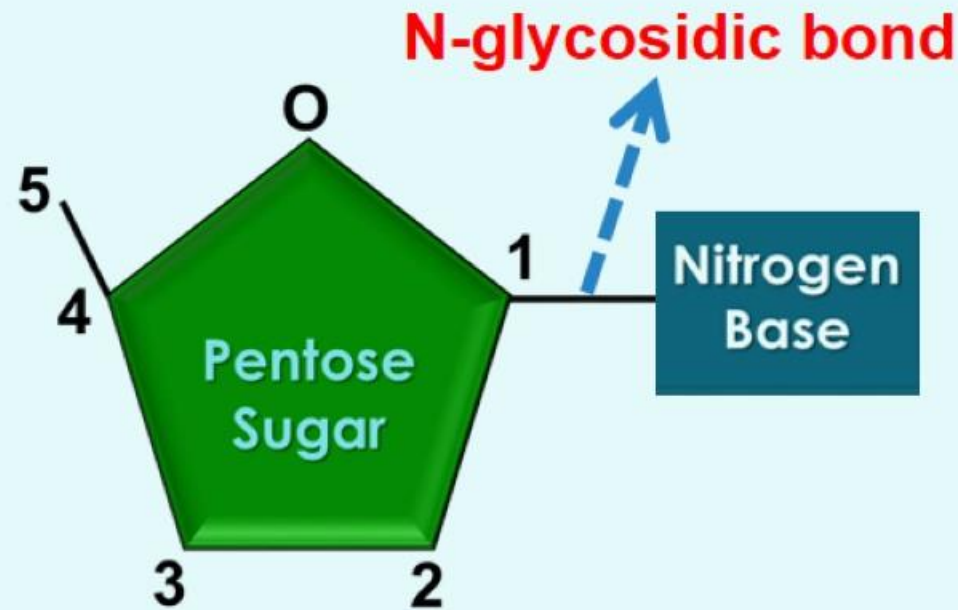
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THE DNA

STRUCTURE OF POLYNUCLEOTIDE CHAIN



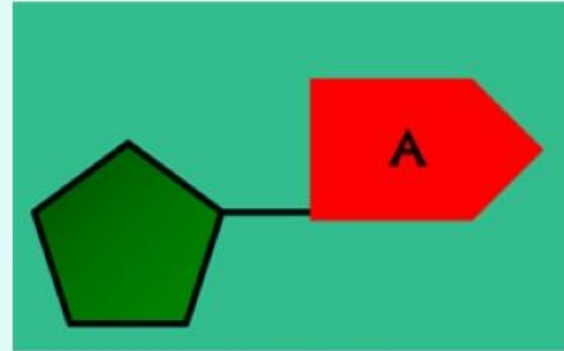
A **nitrogenous base** is linked to the **pentose sugar** through a **N-glycosidic linkage** to form **nucleoside**.



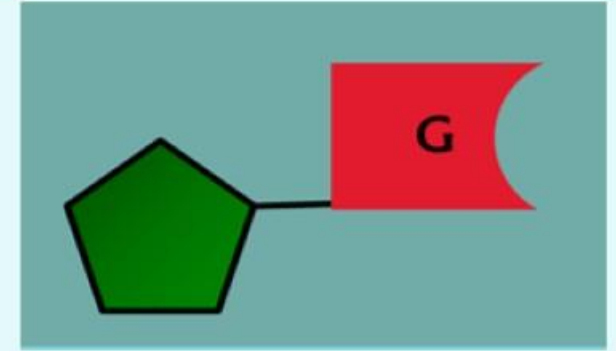
THE DNA

STRUCTURE OF POLYNUCLEOTIDE CHAIN

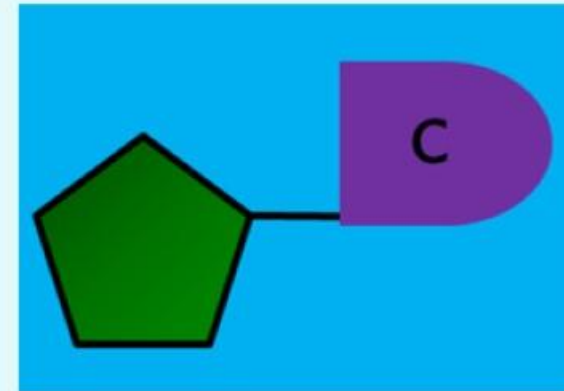
Nucleosides in RNA	Nucleosides in DNA
Adenosine	Deoxyadenosine
Guanosine	Deoxyguanosine
Cytidine	Deoxycytidine
Uridine	Deoxythymidine



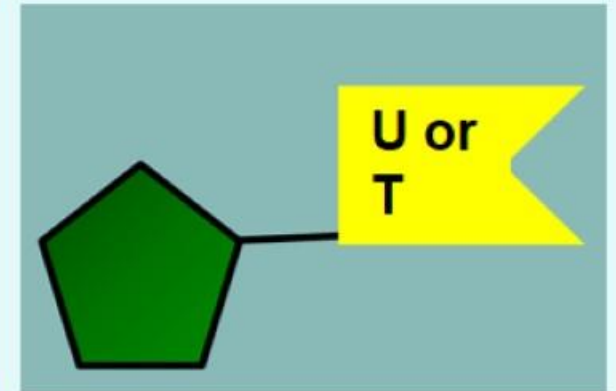
Adenosine / Deoxyadenosine



Guanosine / Deoxyguanosine



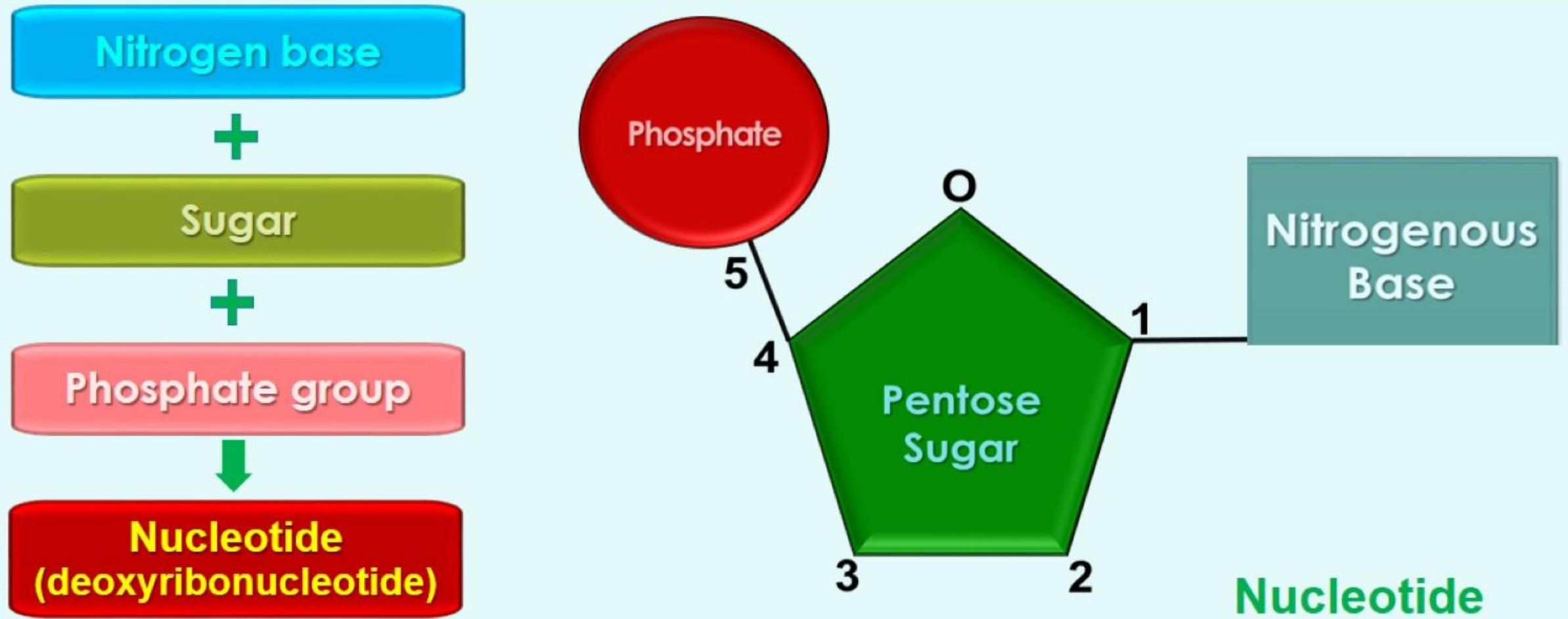
Cytidine / Deoxycytidine



Uridine / Deoxythymidine

THE DNA

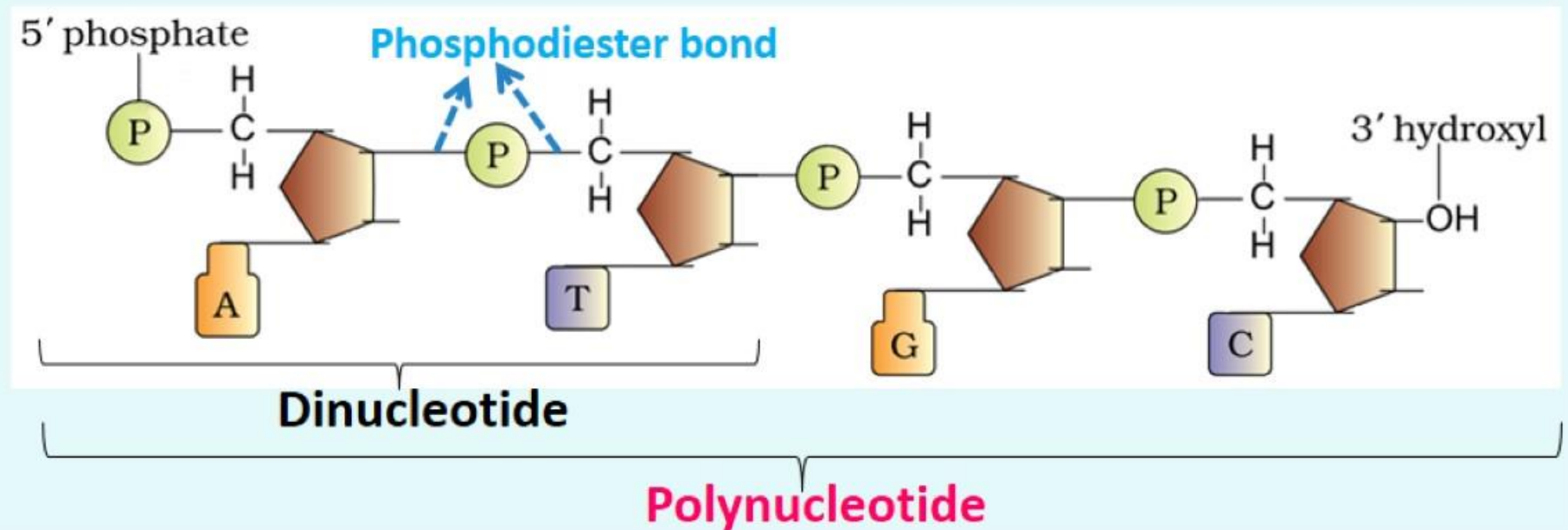
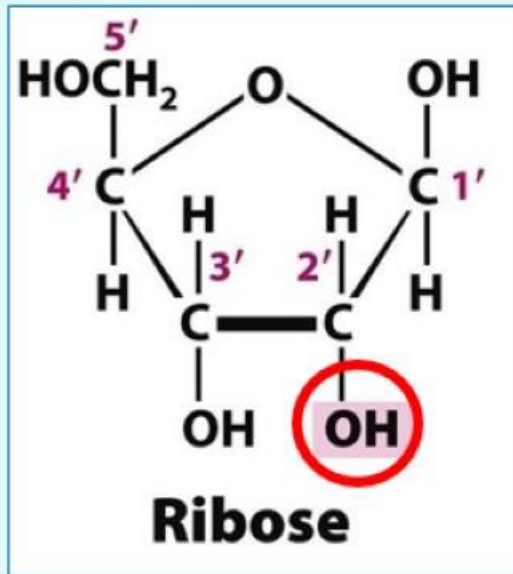
STRUCTURE OF POLYNUCLEOTIDE CHAIN



THE DNA

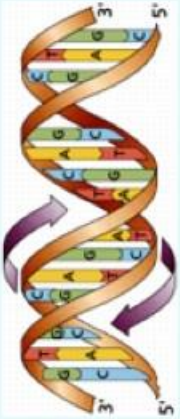
STRUCTURE OF POLYNUCLEOTIDE CHAIN

- In **RNA**, each nucleotide has an additional –OH group at 2'-position of **ribose (2'-OH)**.
- 2 nucleotides are linked through **3'-5' phosphodiester bond** to form **dinucleotide**.
- When more nucleotides are linked, it forms **polynucleotide**.



THE DNA

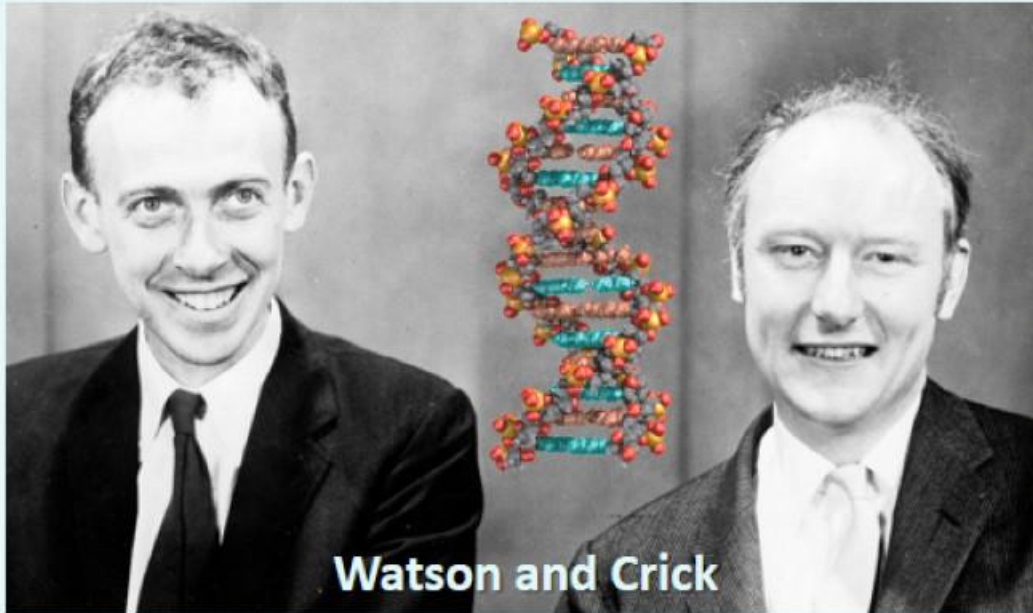
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- **Friedrich Meischer (1869):** Identified DNA and named it as 'Nuclein'.
- **James Watson & Francis Crick** proposed **double helix model** of DNA.
- It was based on X-ray diffraction data produced by **Maurice Wilkins & Rosalind Franklin**.



F. Meischer



Watson and Crick

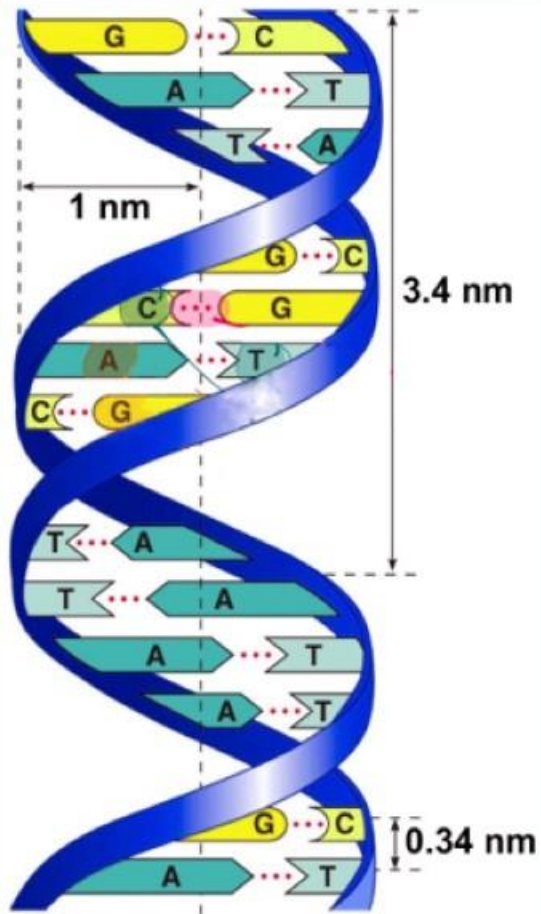


Maurice Wilkins & Rosalind Franklin

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THE DNA

STRUCTURE OF DNA

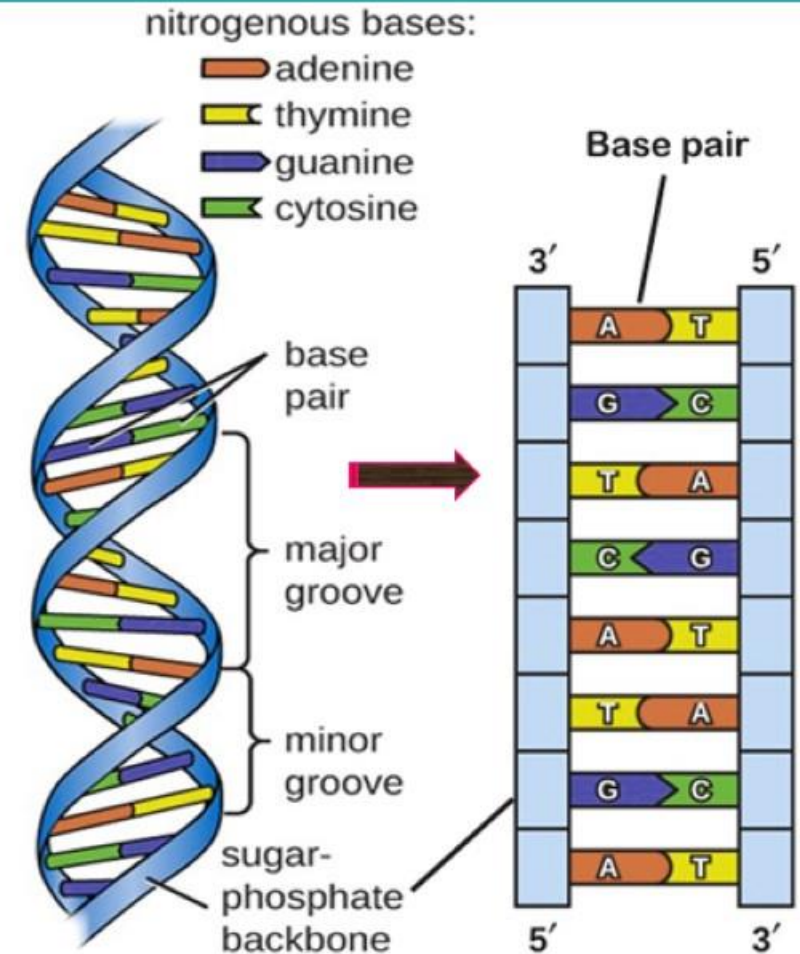


- DNA is made of **2 polynucleotide chains** coiled in a right-handed fashion.
- Pitch of the helix= **3.4 nm (34 Å)**
- Number of base pairs in each turn= **10**
- Distance b/w adjacent base pairs= **0.34 nm (3.4 Å)**

THE DNA

STRUCTURE OF DNA

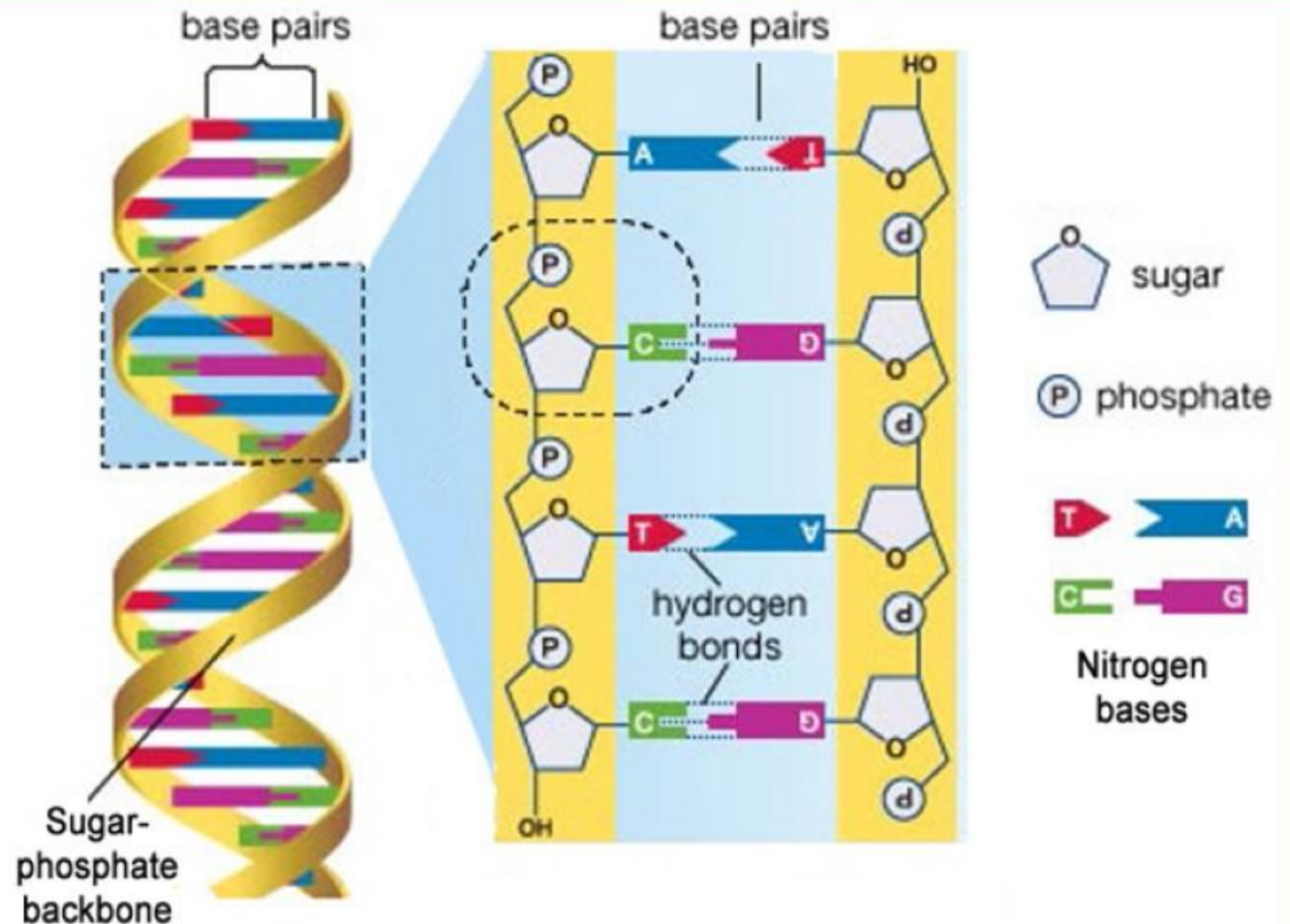
- Backbone of DNA is formed of **sugar & phosphates**.
- The bases project inside.
- The 2 chains have **anti-parallel polarity**, i.e. one chain has the polarity **5'→3'** and the other has **3'→5'**.



THE DNA

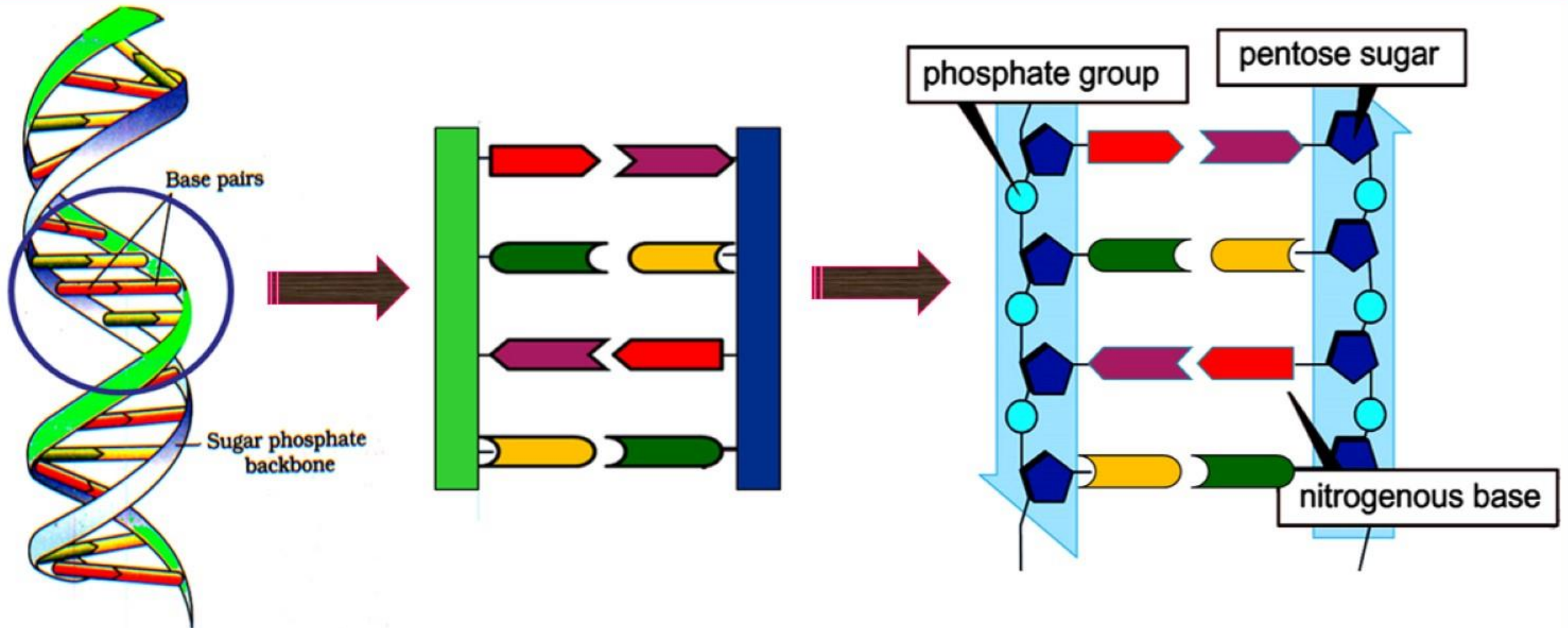
STRUCTURE OF DNA

- The bases in 2 strands are paired through **H-bonds** forming **base pairs (bp)**.
- **A=T** (2 hydrogen bonds)
C≡G (3 hydrogen bonds)
- **Purine** comes opposite to a **pyrimidine**. This generates uniform distance between the 2 strands.



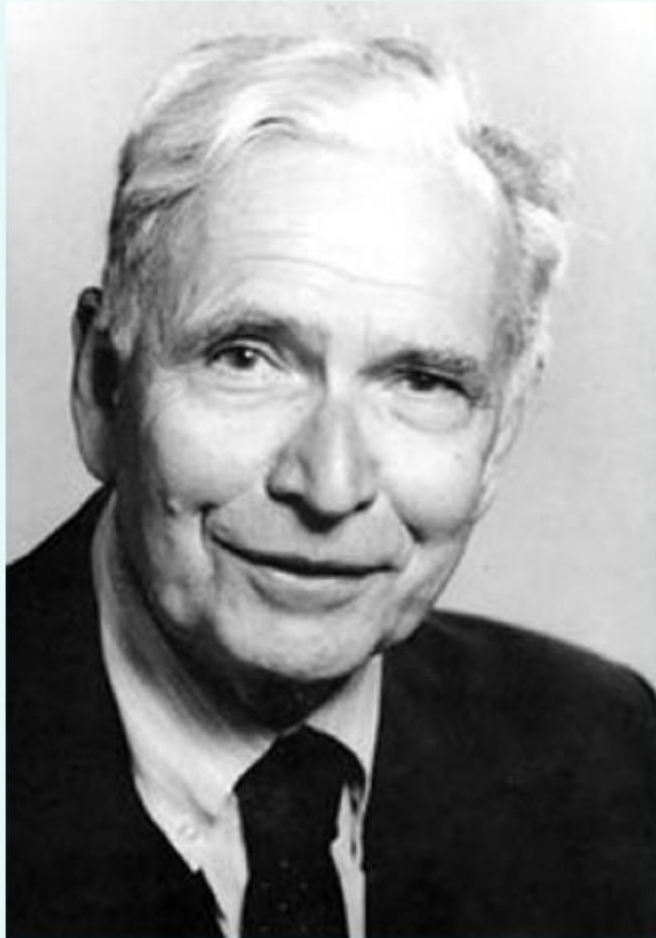
THE DNA

STRUCTURE OF DNA



THE DNA

ERWIN CHARGAFF'S RULE



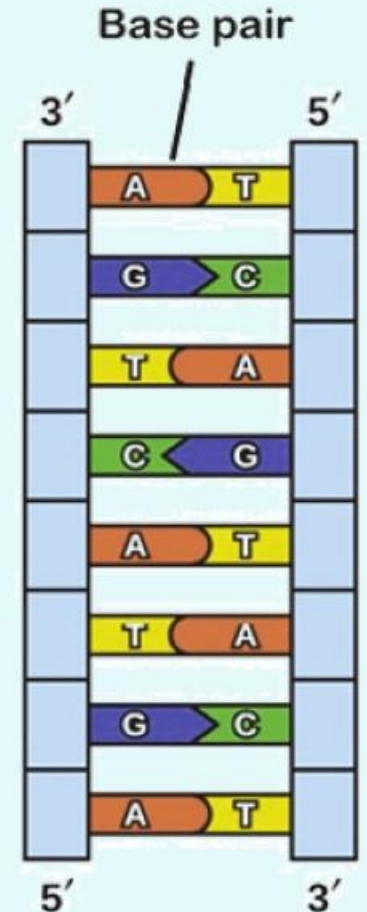
In DNA, the proportion of **A is equal to T**
and the proportion of **G is equal to C.**

Therefore,

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

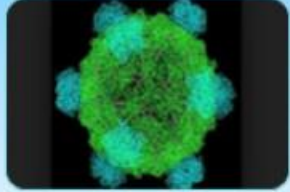
OR

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

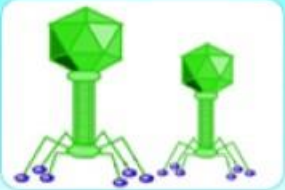


THE DNA

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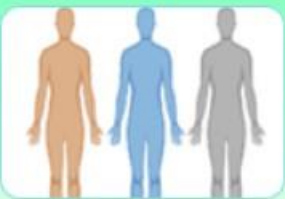
Φ 174 (a bacteriophage) has 5386 nucleotides.



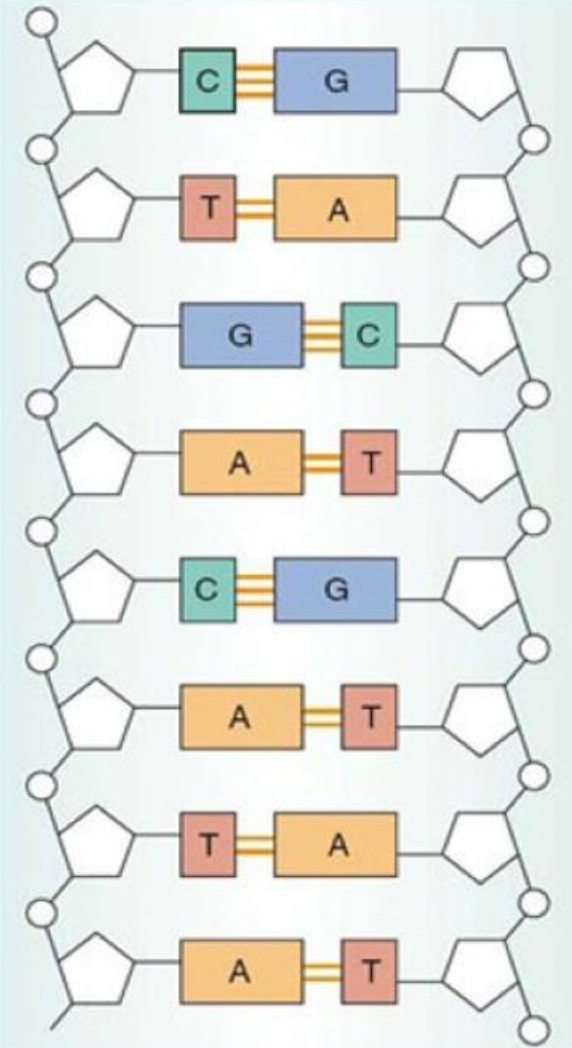
Bacteriophage lambda has 48502 base pairs (bp).



E. coli has 4.6×10^6 bp.



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



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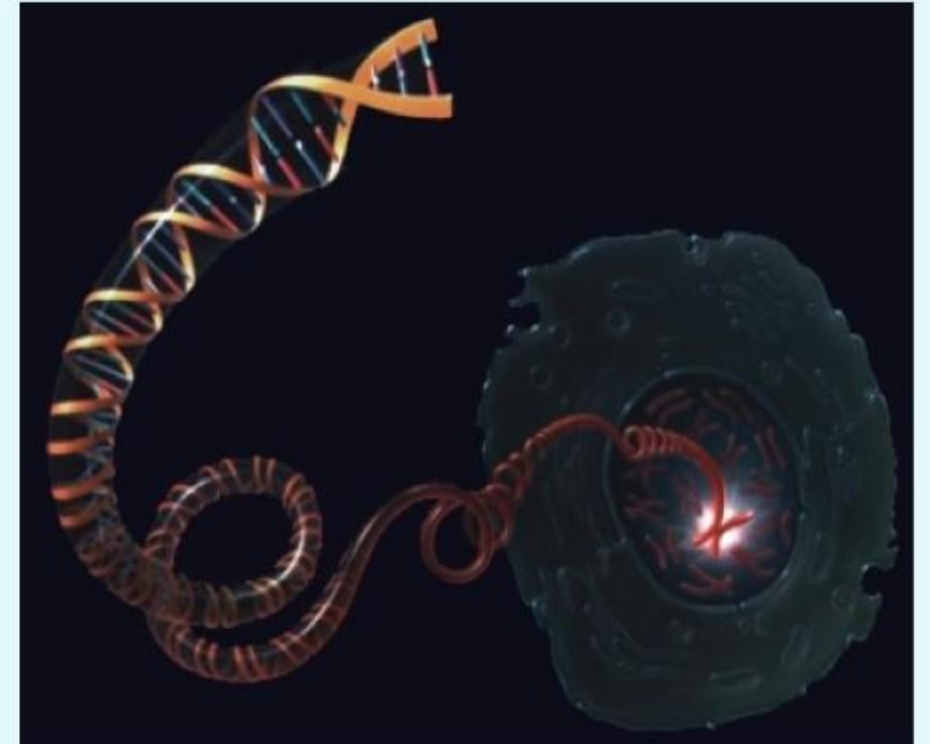
THE DNA

CALCULATION OF LENGTH OF DNA

Length of DNA = number of base pairs X distance b/w 2 adjacent base pairs.

Examples:

- 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 m
- In *E. coli*, length of DNA = 1.36 mm (1.36×10^{-3} m)
 $\therefore$ The number of base pairs = $\frac{1.36 \times 10^{-3}}{0.34 \times 10^{-9}}$
= 4×10^6 bp

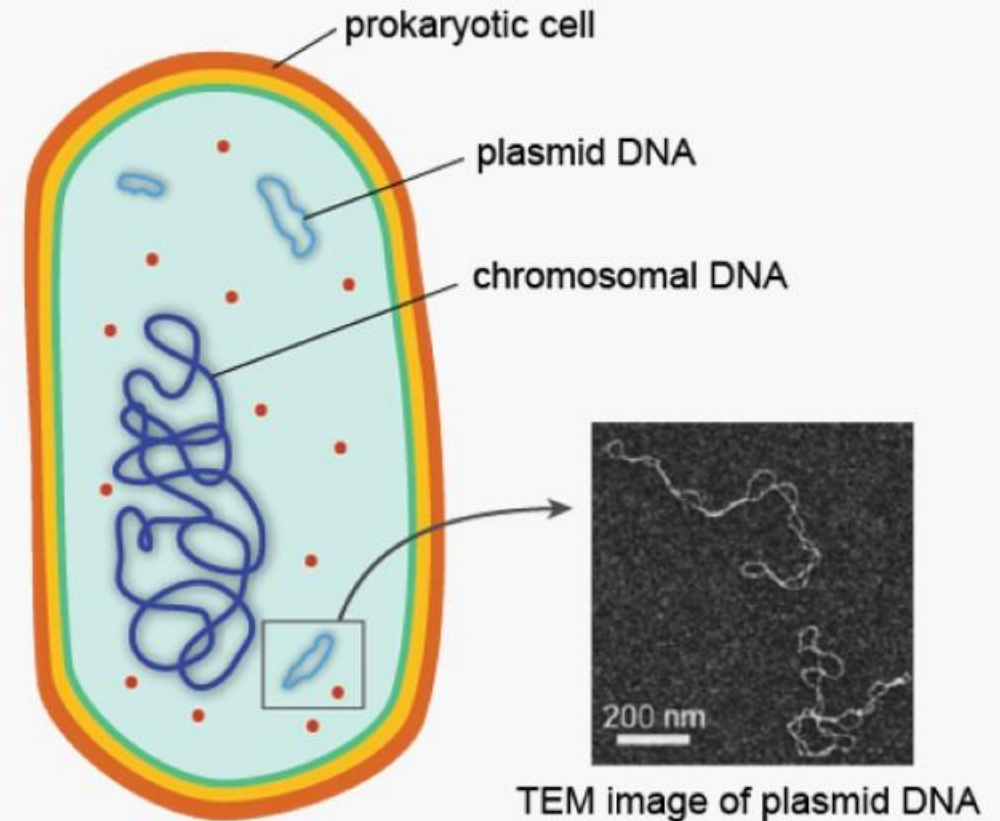
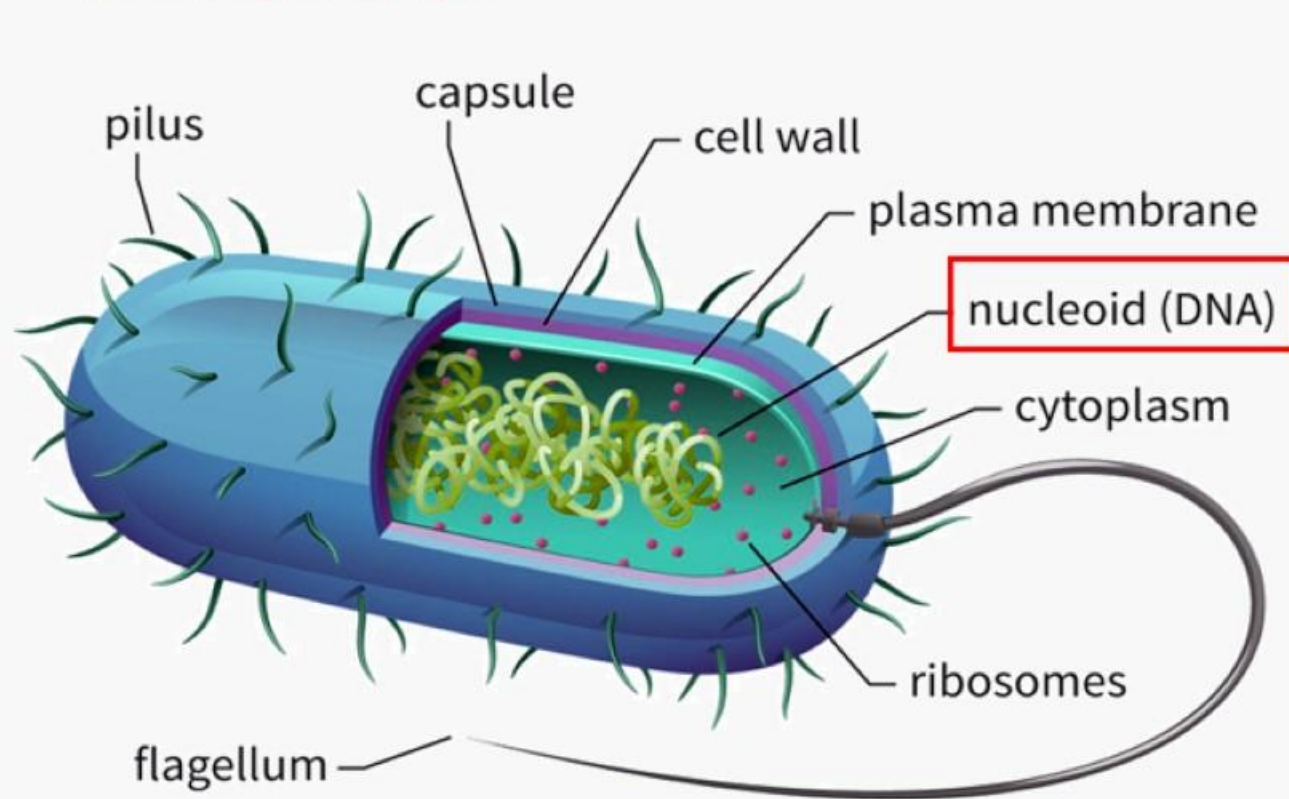


**PACKAGING OF
DNA HELIX**

PACKAGING OF DNA HELIX

IN PROKARYOTES

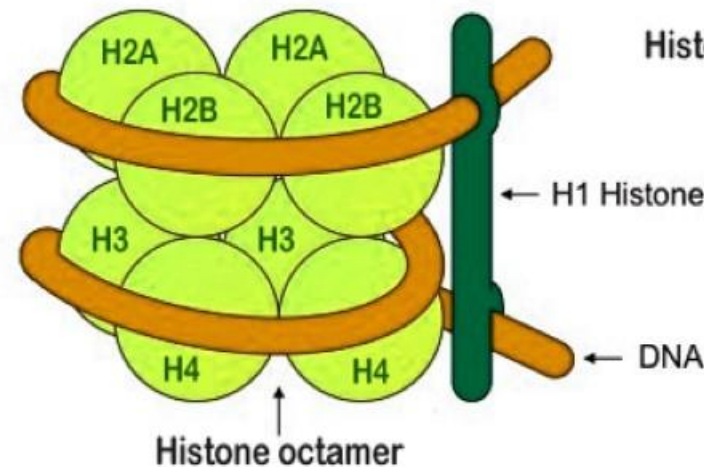
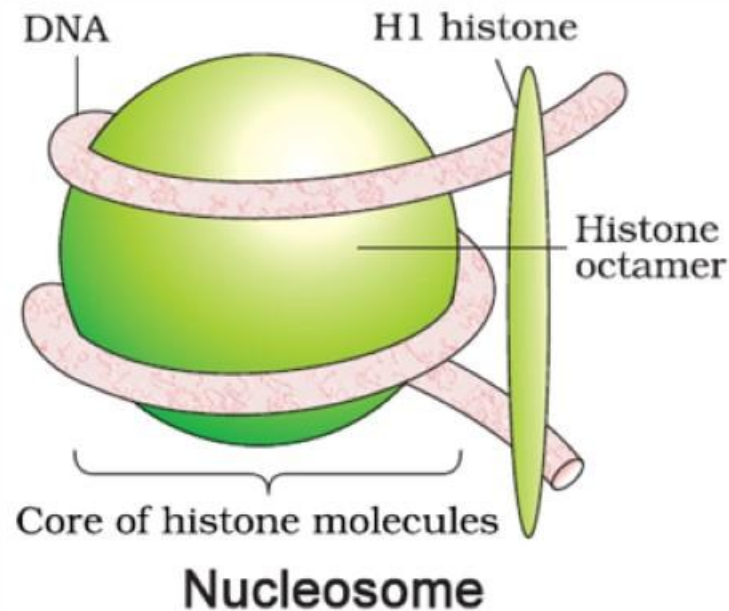
- In prokaryotes (E.g. *E. coli*), the DNA is not scattered throughout the cell.
- DNA is **negatively charged**. So it is held with some positively charged proteins to form **nucleoid**.



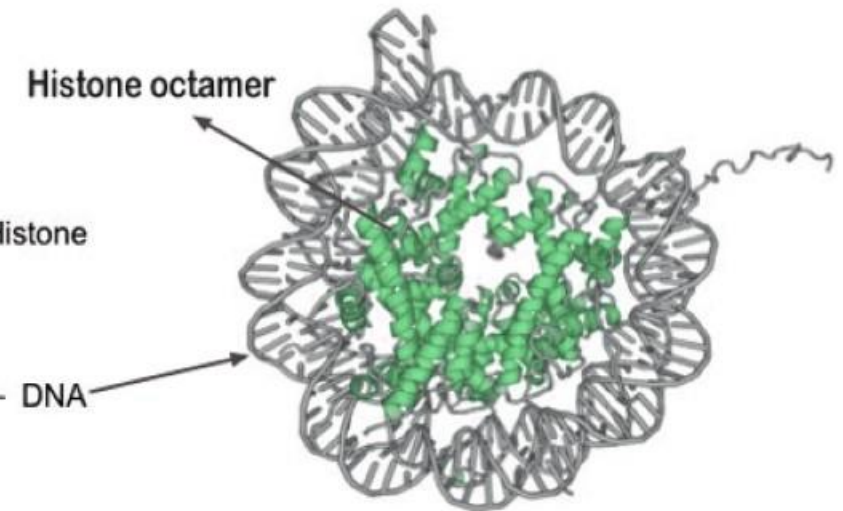
PACKAGING OF DNA HELIX

IN EUKARYOTES

- In eukaryotes, there is a set of positively charged, basic proteins called **histones**.
- Histones are rich in positively charged basic amino acid residues **lysines & arginines**.
- 8 histones form **histone octamer**.
- Negatively charged DNA is wrapped around histone octamer to give **nucleosome**.



A nucleosome molecule (side view)



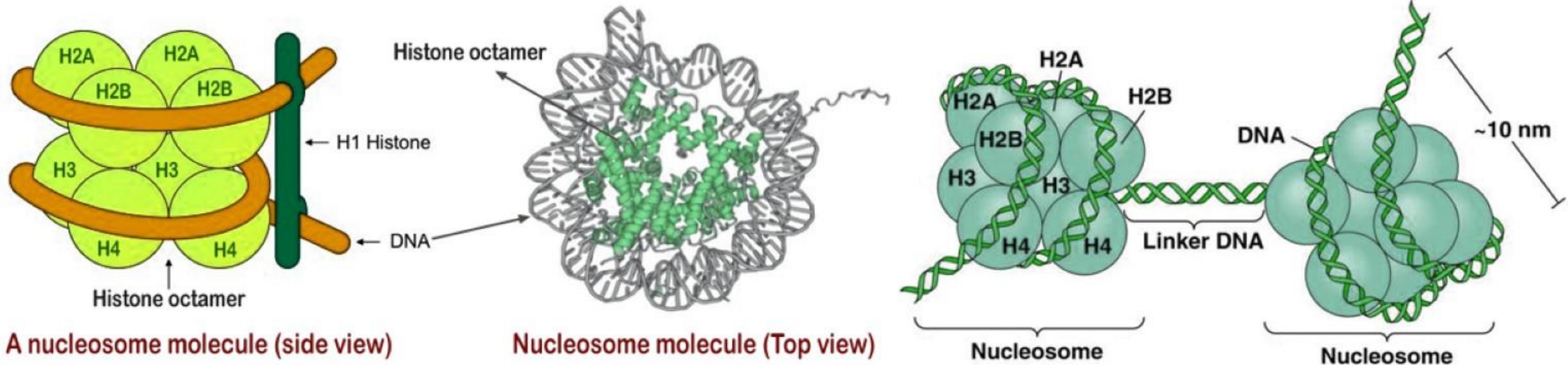
Nucleosome molecule (Top view)

PACKAGING OF DNA HELIX

IN EUKARYOTES

- A typical nucleosome contains **200 bp**.
- Therefore, total number of nucleosomes in human =

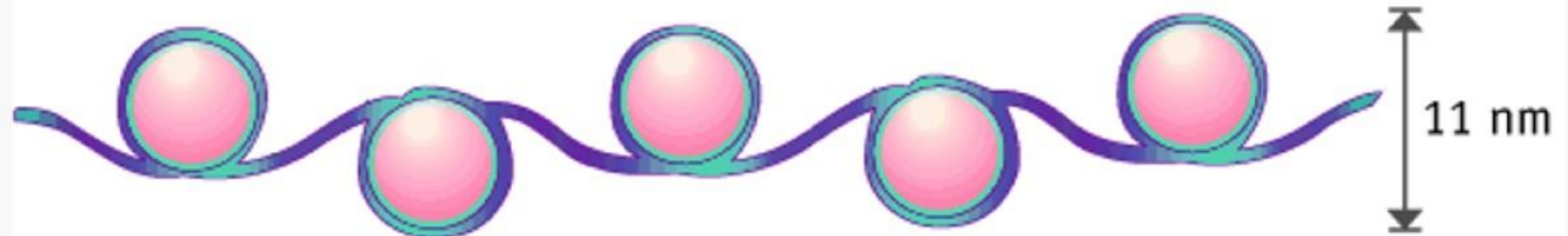
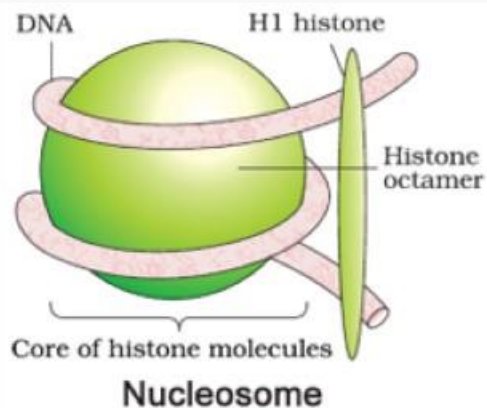
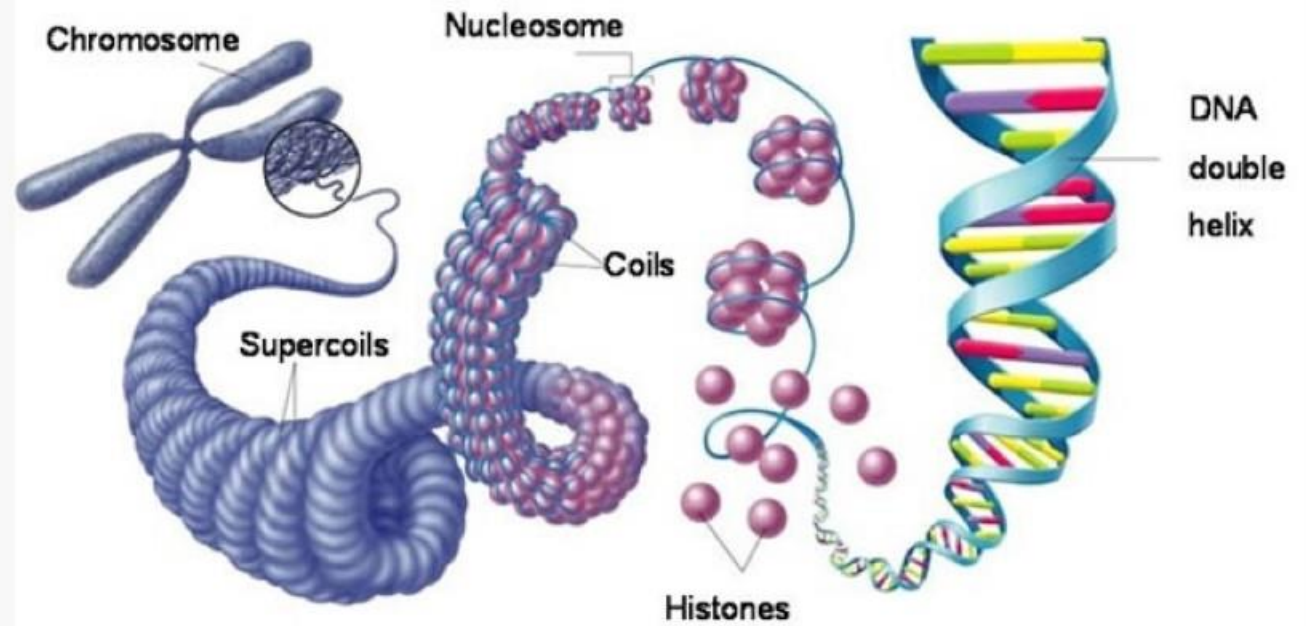
$$\frac{6.6 \times 10^9 \text{ bp}}{200} = 3.3 \times 10^7$$



PACKAGING OF DNA HELIX

IN EUKARYOTES

- Nucleosomes constitute the repeating unit to form **chromatin**.
- Chromatin is the thread-like stained bodies.
- **Nucleosomes in chromatin = 'beads-on-string'.**



Beads-on-string form of chromatin

PACKAGING OF DNA HELIX

IN EUKARYOTES

Chromatin is packaged

Chromatin fibres

Coiled and condensed at metaphase stage

Chromosomes

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

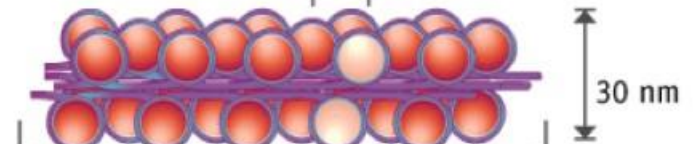
Short region of DNA double helix



"Beads on a string" form of chromatin



30 nm chromatin fibre of packed nucleosomes



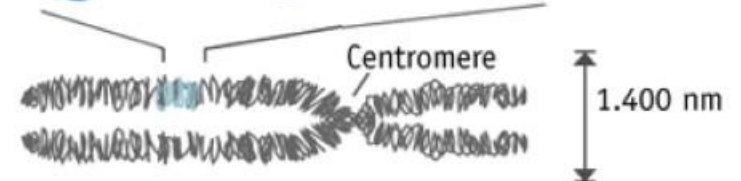
Section of chromosome in an extended form



Condensed section of chromosome



Entire mitotic chromosome



PACKAGING OF DNA HELIX

IN EUKARYOTES

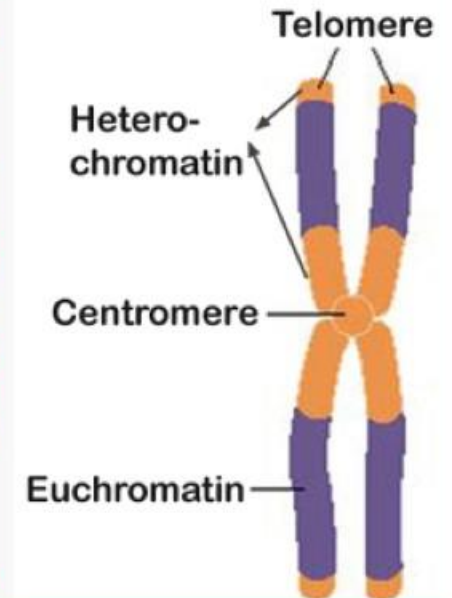
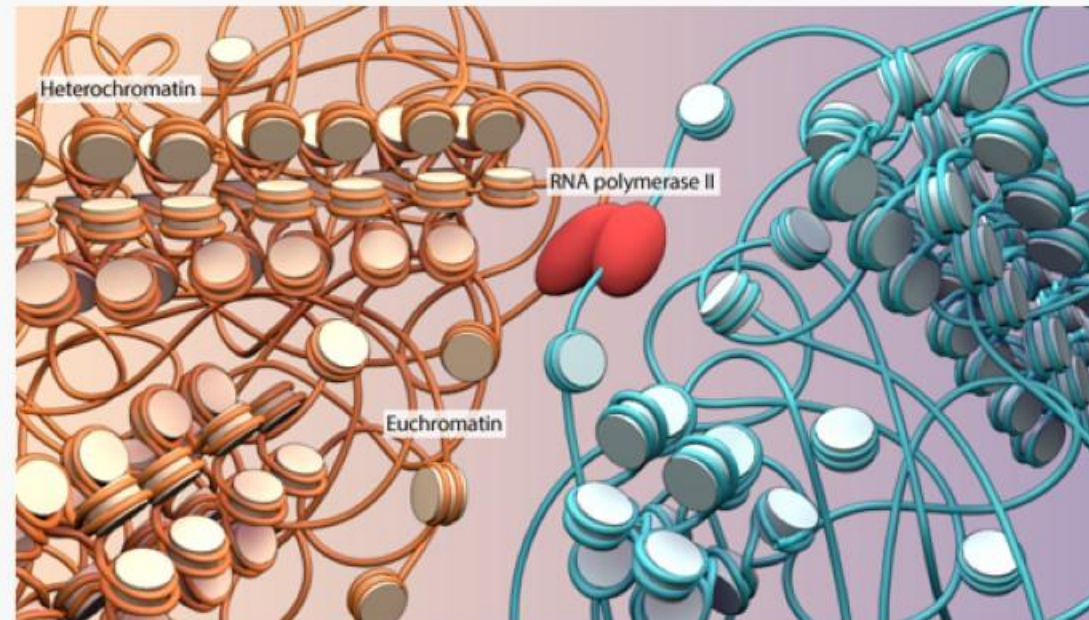
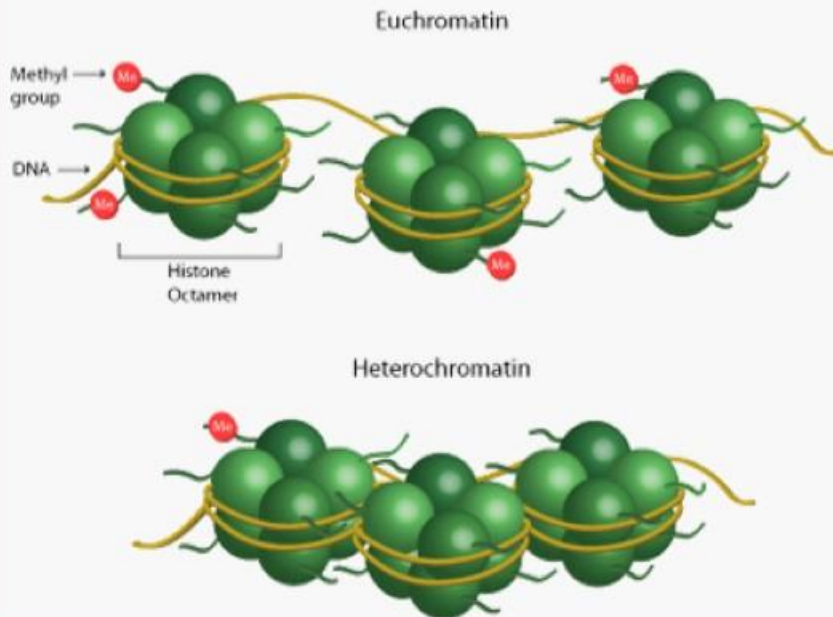
Chromatin has 2 forms

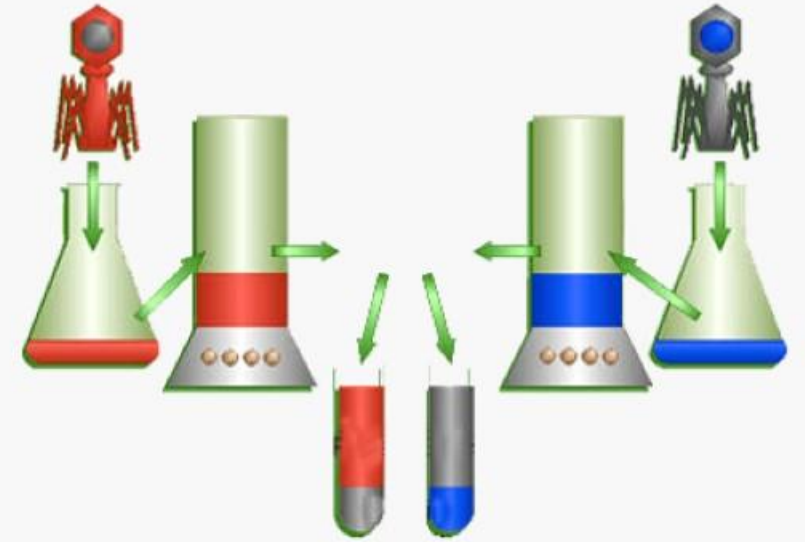
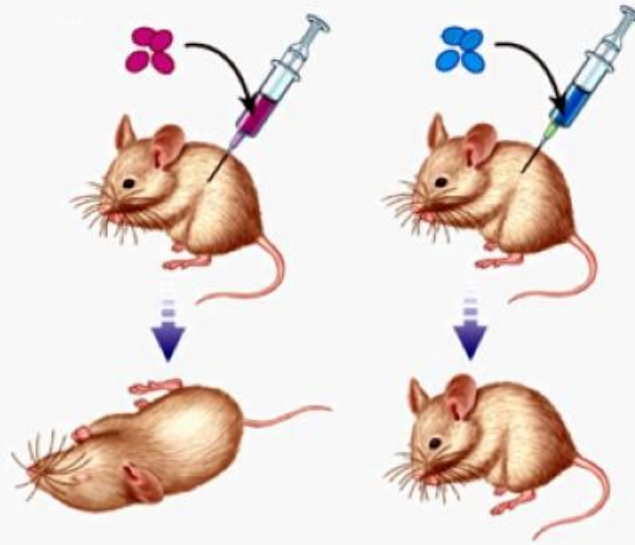
Euchromatin

Loosely packed, transcriptionally active region of chromatin. It stains light.

Heterochromatin

Densely packed, inactive region of chromatin. It stains dark.





THE SEARCH FOR GENETIC MATERIAL

Experiments to prove which is the genetic material...

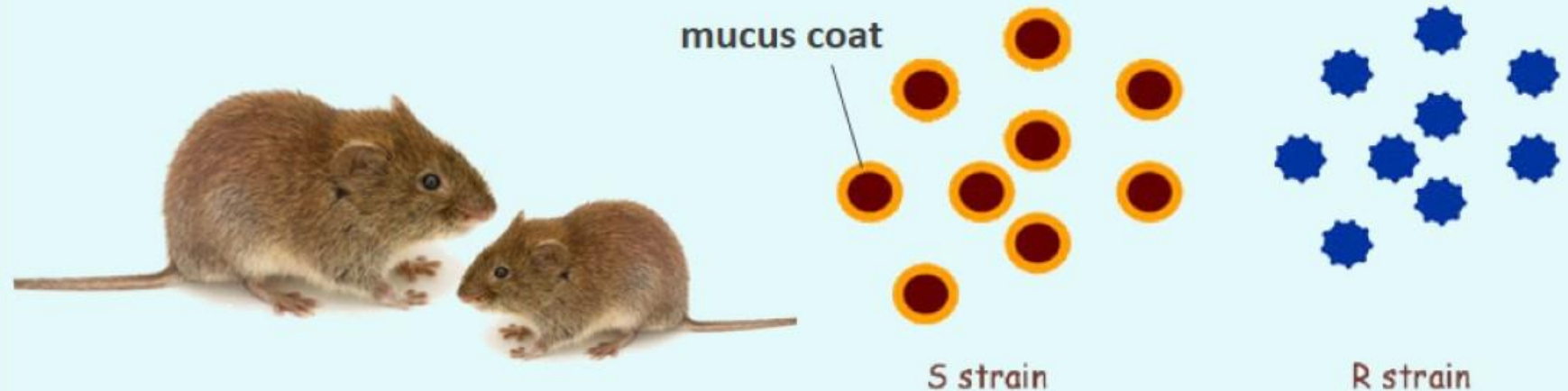
THE SEARCH FOR GENETIC MATERIAL

1

GRIFFITH'S TRANSFORMING PRINCIPLE EXPERIMENT



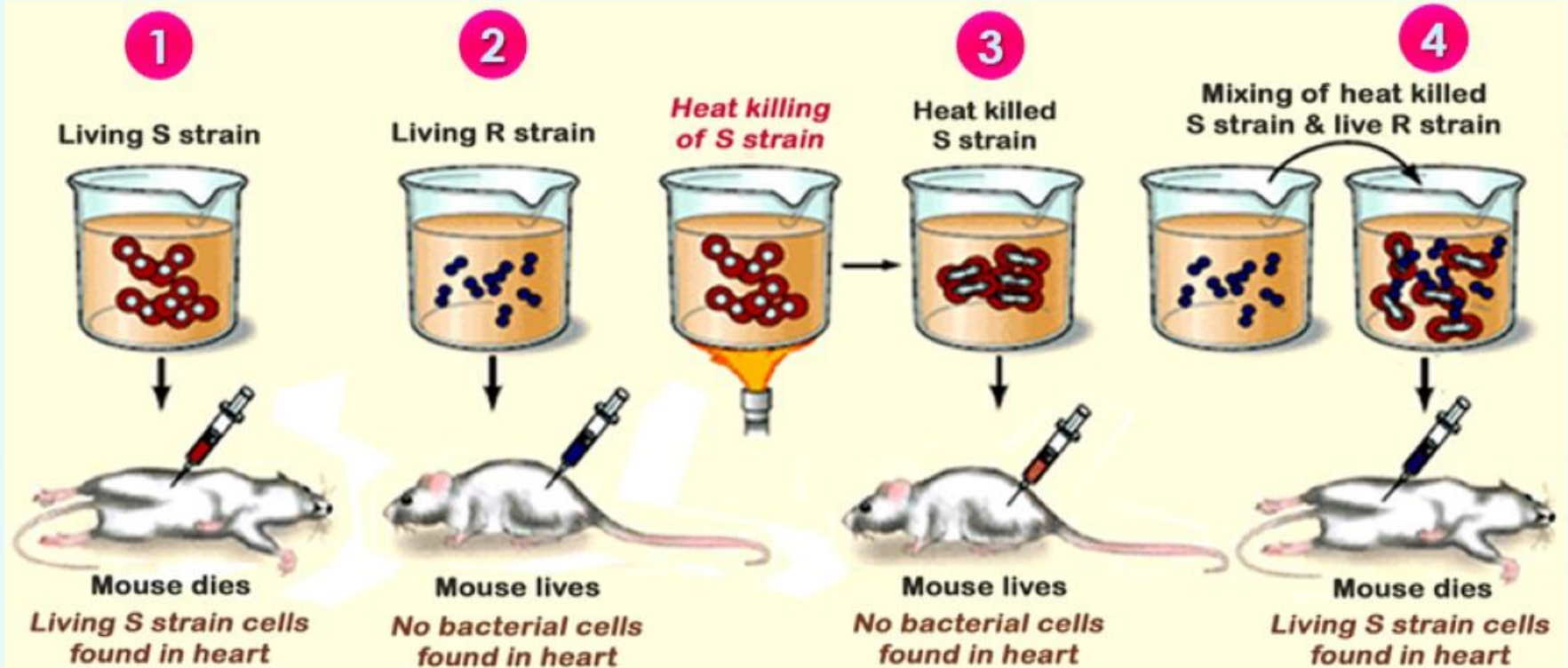
- ▶ Frederick Griffith (1928) used mice & *Streptococcus pneumoniae*.
- ▶ *Streptococcus pneumoniae* has 2 strains:
 - **Smooth (S) strain (Virulent):** Has polysaccharide mucus coat. Cause pneumonia.
 - **Rough (R) strain (Non-virulent):** No mucus coat. Do not cause Pneumonia.



THE SEARCH FOR GENETIC MATERIAL

1

GRIFFITH'S TRANSFORMING PRINCIPLE EXPERIMENT

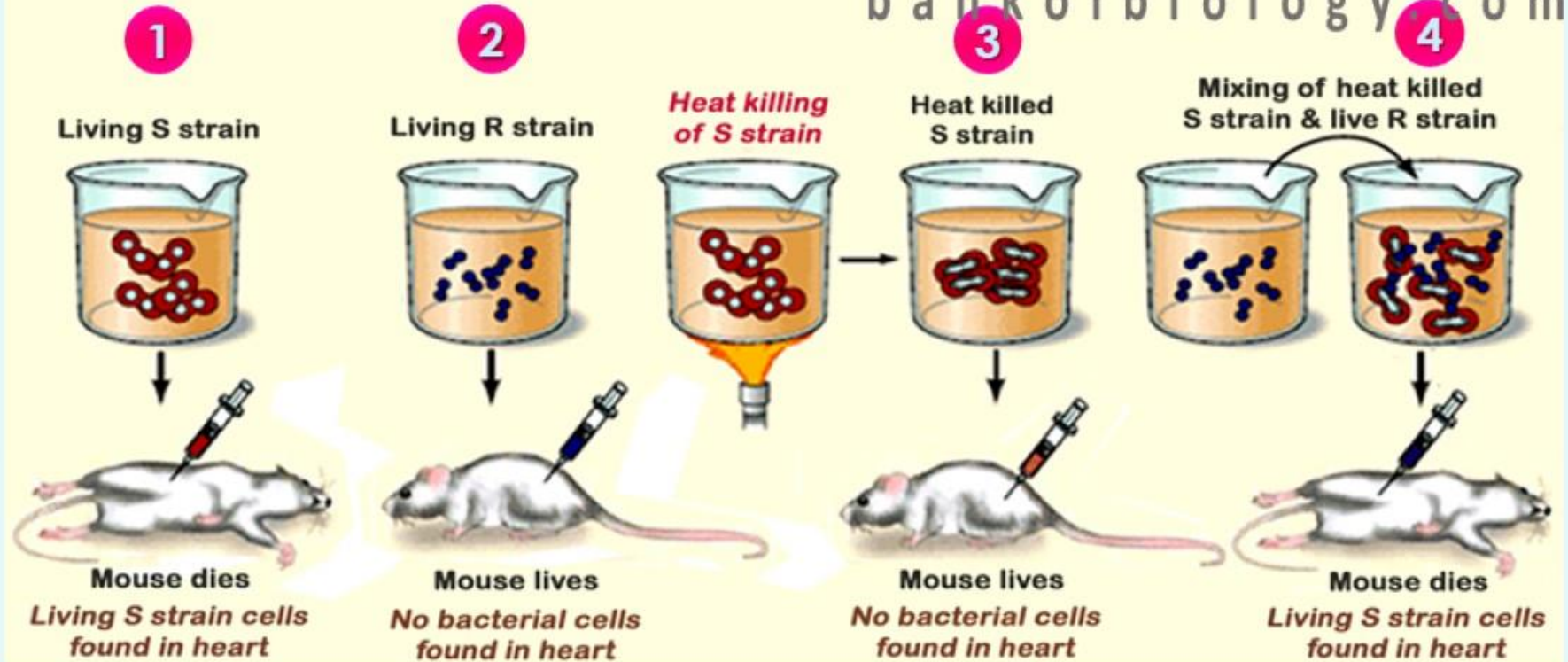


1. S-strain → Inject into mice → Mice die
2. R-strain → Inject into mice → Mice live
3. S-strain (Heat killed) → Inject into mice → Mice live
4. S-strain (Heat killed) + R-strain (live) → Inject into mice → Mice die

THE SEARCH FOR GENETIC MATERIAL

1

GRIFFITH'S TRANSFORMING PRINCIPLE EXPERIMENT



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 is due to the transfer of genetic material.

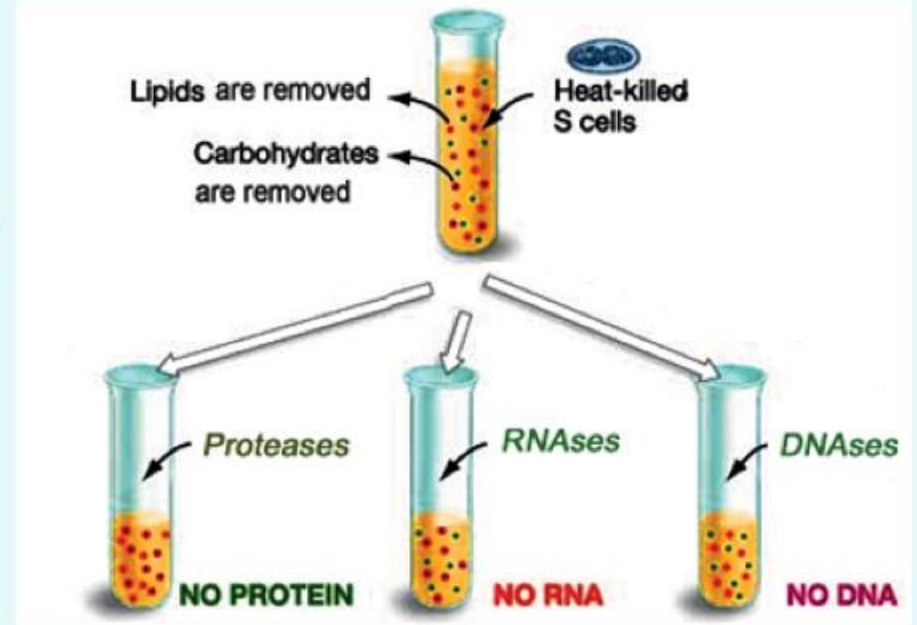
THE SEARCH FOR GENETIC MATERIAL

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



THE SEARCH FOR GENETIC MATERIAL

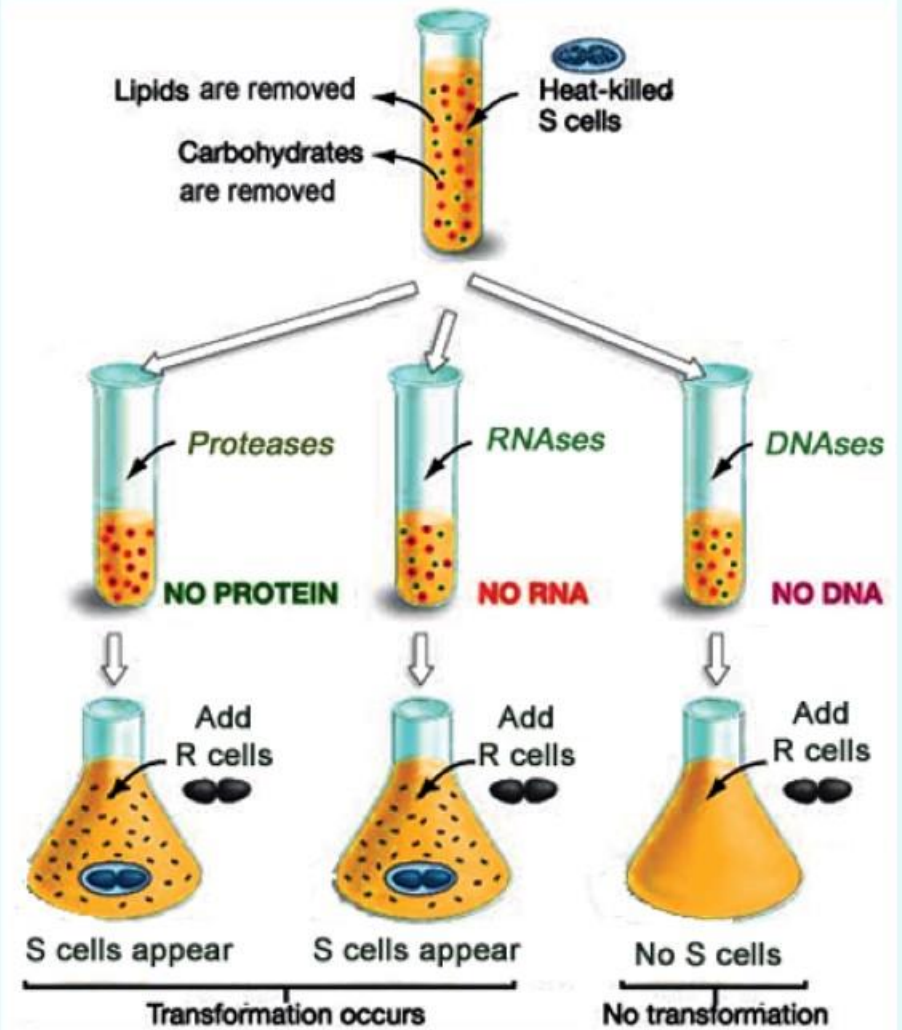
2

BIOCHEMICAL CHARACTERIZATION OF TRANSFORMING PRINCIPLE



They discovered that

- ✓ **Digestion of protein & RNA** (using *Proteases* & *RNases*) **did not affect transformation.** So, transforming substance was not a protein or RNA.
- ✓ **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.**



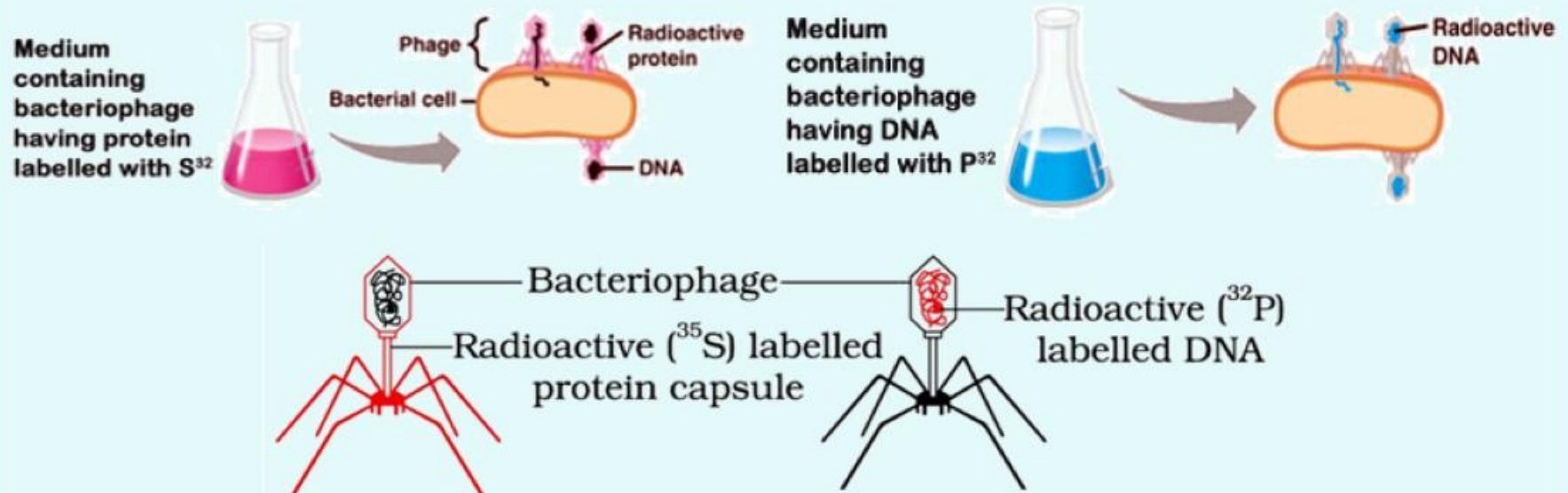
THE SEARCH FOR GENETIC MATERIAL

3

HERSHEY-CHASE EXPERIMENT (BLENDER EXPERIMENT)



- ▶ **Hershey & Chase** grew some **bacteriophage** viruses on a medium containing **radioactive phosphorus (P^{32})** and some others on medium containing **radioactive sulphur (S^{35})**.
- ▶ Viruses grown in **P^{32}** got **radioactive DNA** because only DNA contains phosphorus. Viruses grown in **S^{35}** got **radioactive protein** because protein contains sulphur.



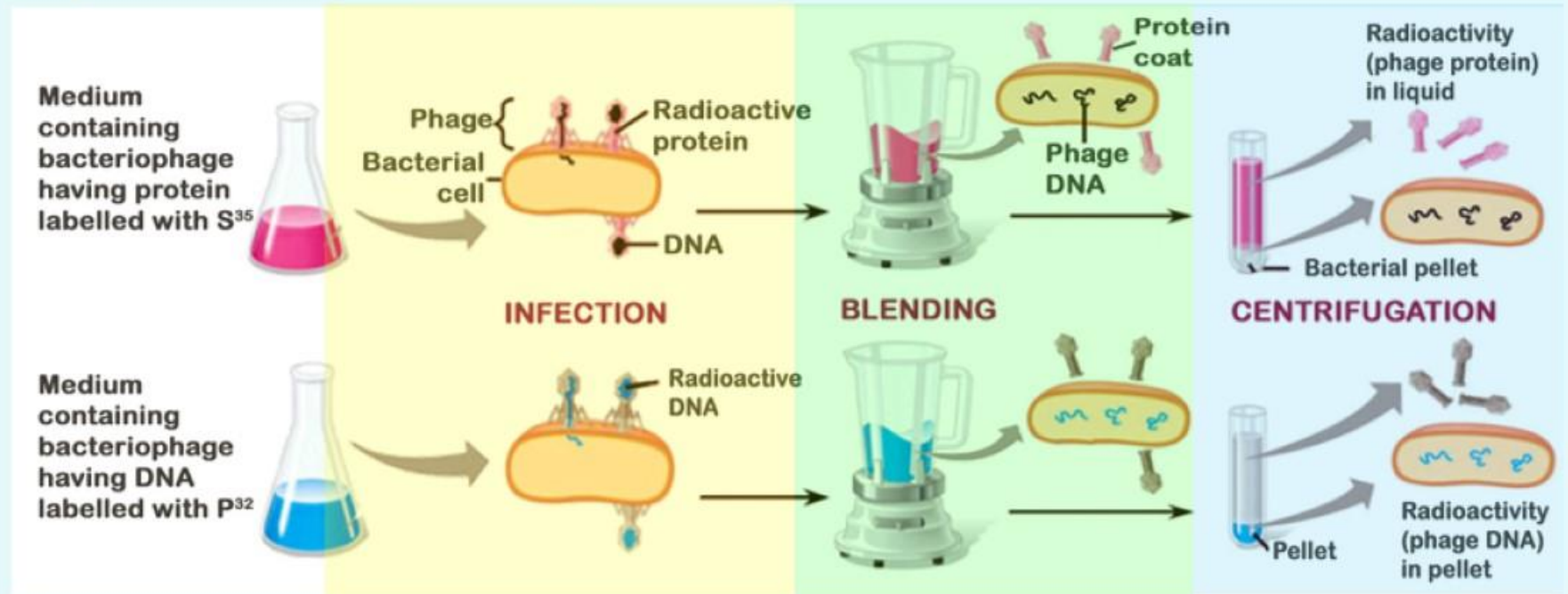
THE SEARCH FOR GENETIC MATERIAL

3

HERSHEY-CHASE EXPERIMENT (BLENDER EXPERIMENT)



- ▶ 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.



THE SEARCH FOR GENETIC MATERIAL

3

HERSHEY-CHASE EXPERIMENT (BLENDER EXPERIMENT)



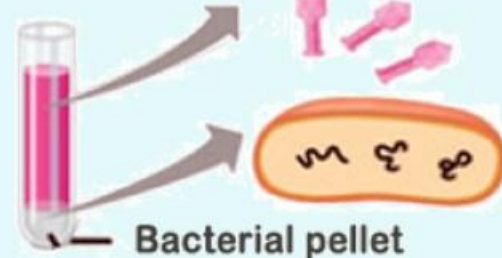
- ▶ Bacteria infected with viruses having radioactive DNA were radioactive. i.e., **DNA had passed from virus to bacteria.**
- ▶ Bacteria infected with viruses having radioactive proteins were not radioactive. i.e., **proteins did not enter the bacteria** from the viruses.


No Radioactive (^{35}S)
detected in cells

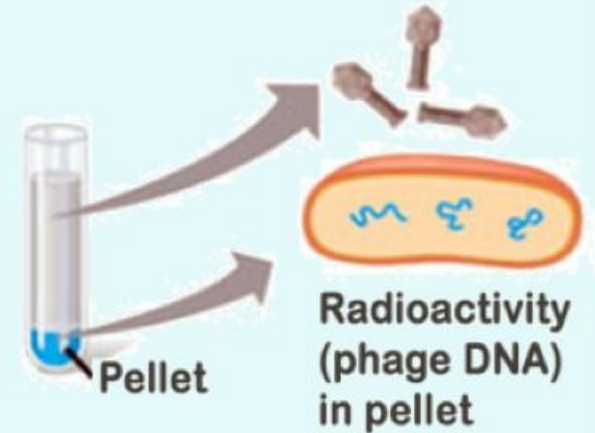
+
Radioactive (^{35}S)
in supernatant



Radioactivity
(phage protein)
in liquid



Bacterial pellet



Pellet

Radioactivity
(phage DNA)
in pellet


Radioactive (^{32}P)
detected in cells

+
No Radioactivity
in supernatant



This proves that **DNA is the genetic material.**

THE SEARCH FOR GENETIC MATERIAL

3

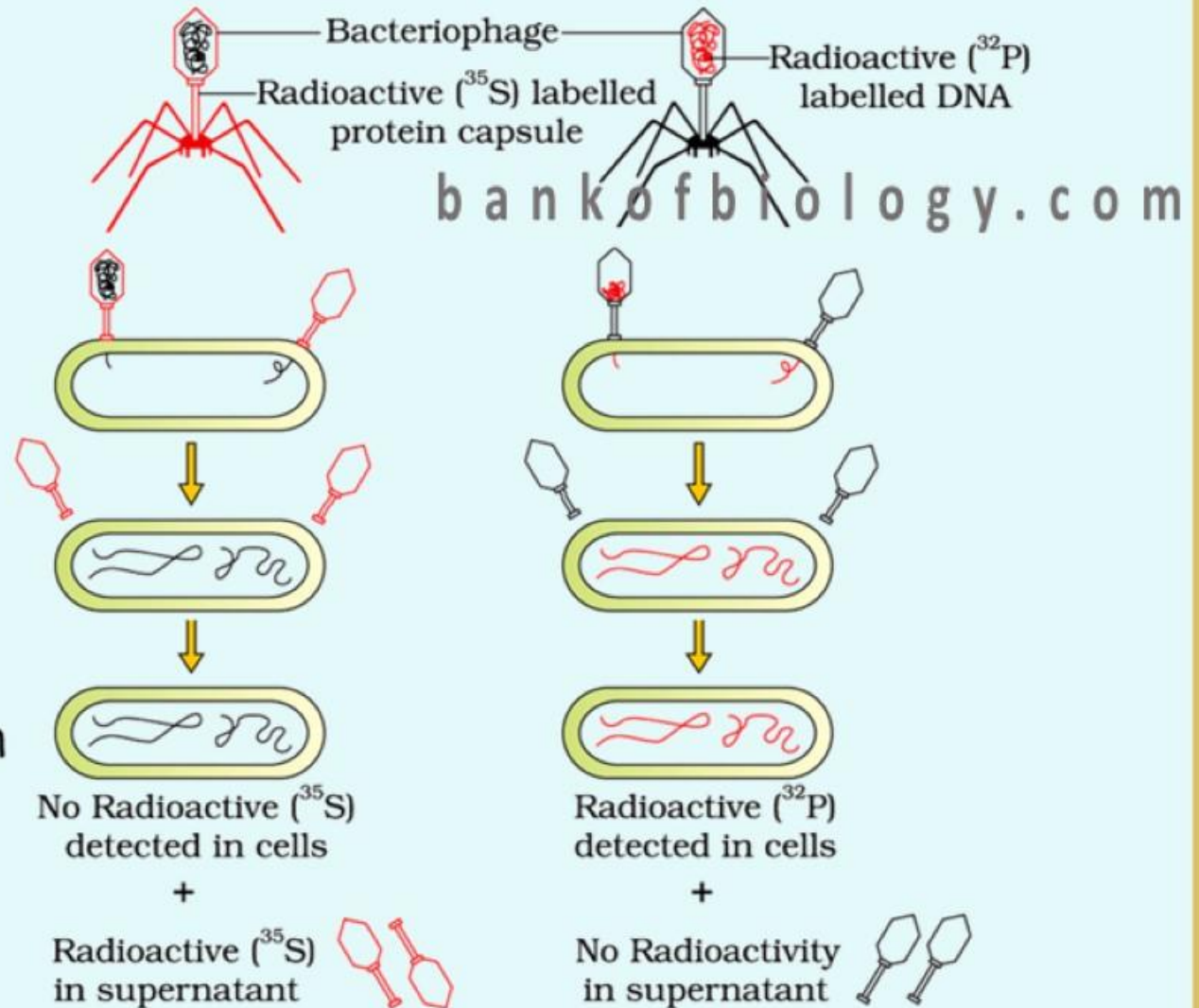
HERSHEY-CHASE EXPERIMENT (BLENDER EXPERIMENT)



1. Infection

2. Blending

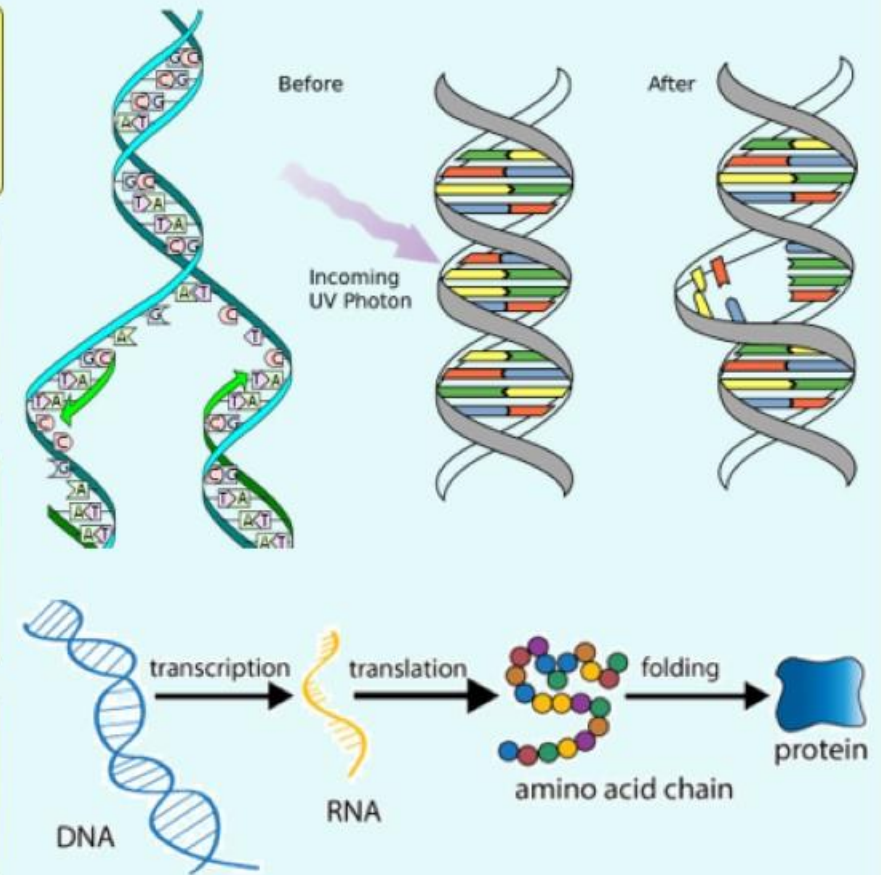
3. Centrifugation



PROPERTIES OF GENETIC MATERIAL

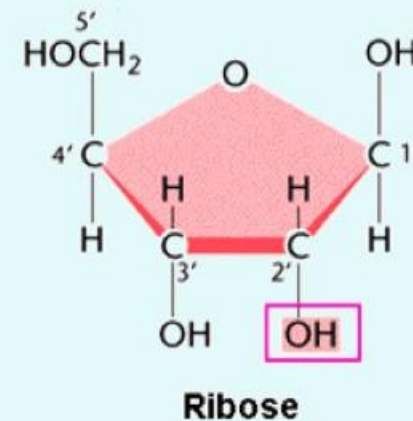
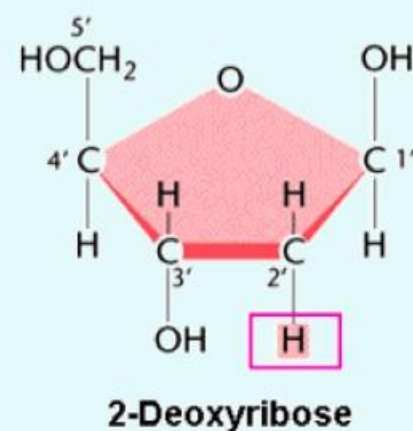
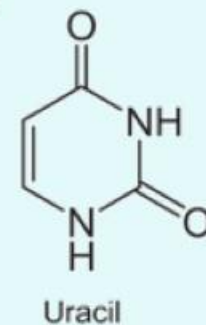
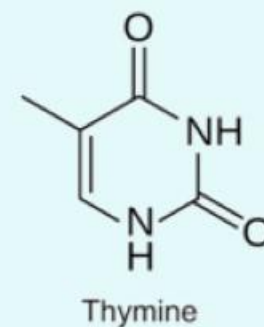
A genetic material must have the following properties:

- ✓ Ability to generate its replica (Replication).
- ✓ Chemical and structural stability.
- ✓ Provide the mutations needed for evolution.
- ✓ Ability to express as 'Mendelian Characters'.



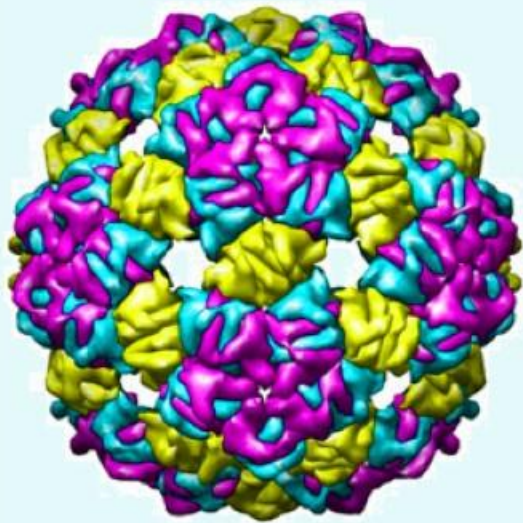
PROPERTIES OF GENETIC MATERIAL

Reasons for stability (less reactivity) of DNA	Reasons for mutability (high reactivity) of RNA
• Double stranded	• Single stranded
• Presence of thymine	• Presence of Uracil
• Absence of 2'-OH in sugar	• Presence of 2'-OH in sugar

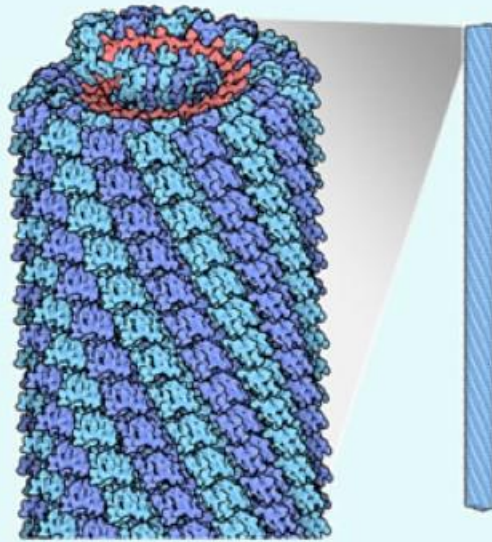


PROPERTIES OF GENETIC MATERIAL

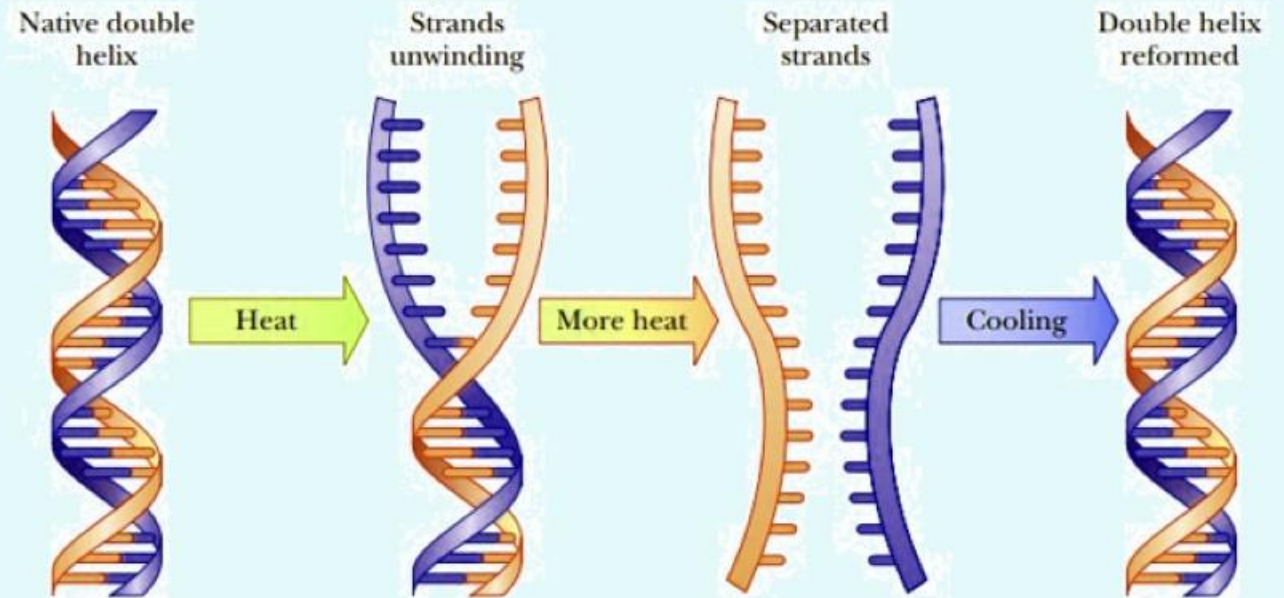
- ▶ Thus **RNA is unstable**. So, **RNA viruses** (E.g. Q.B bacteriophage, Tobacco Mosaic Virus etc.) **mutate and evolve faster**.
- ▶ DNA strands are **complementary**. On heating, they separate. In appropriate conditions, they come together. In Griffith's experiment, some properties of DNA of the heat killed bacteria did not destroy. It indicates the stability of DNA.



Q.B bacteriophage

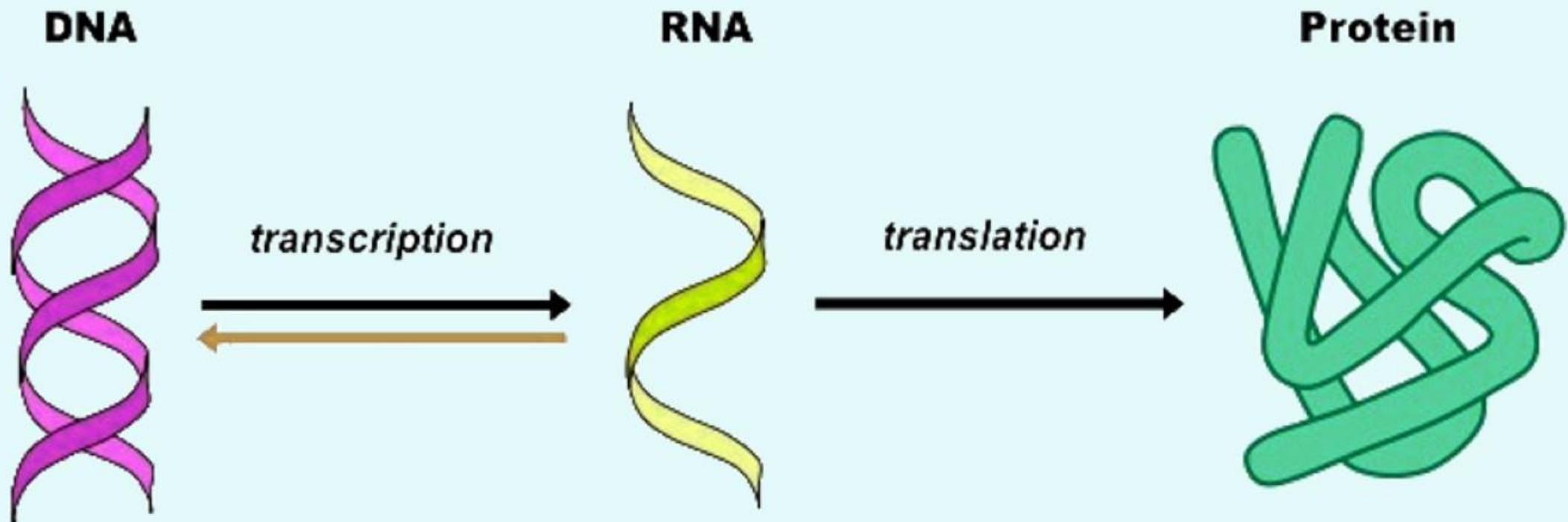


Tobacco Mosaic Virus

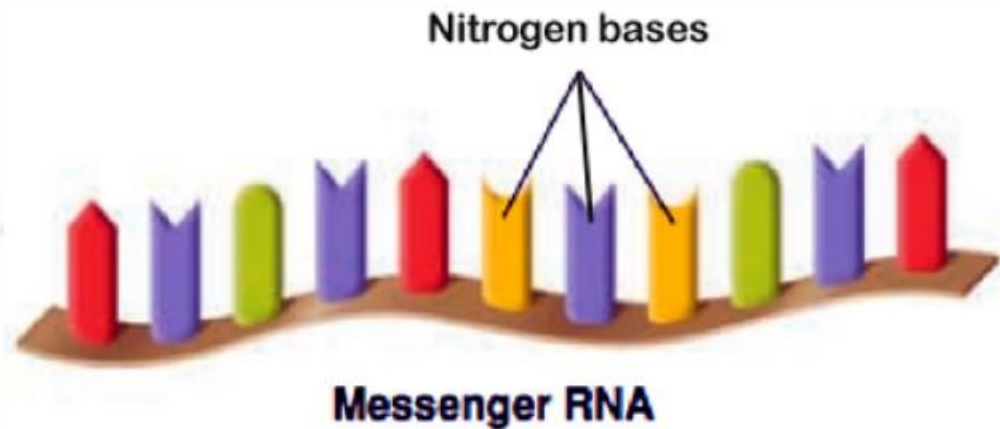


PROPERTIES OF GENETIC MATERIAL

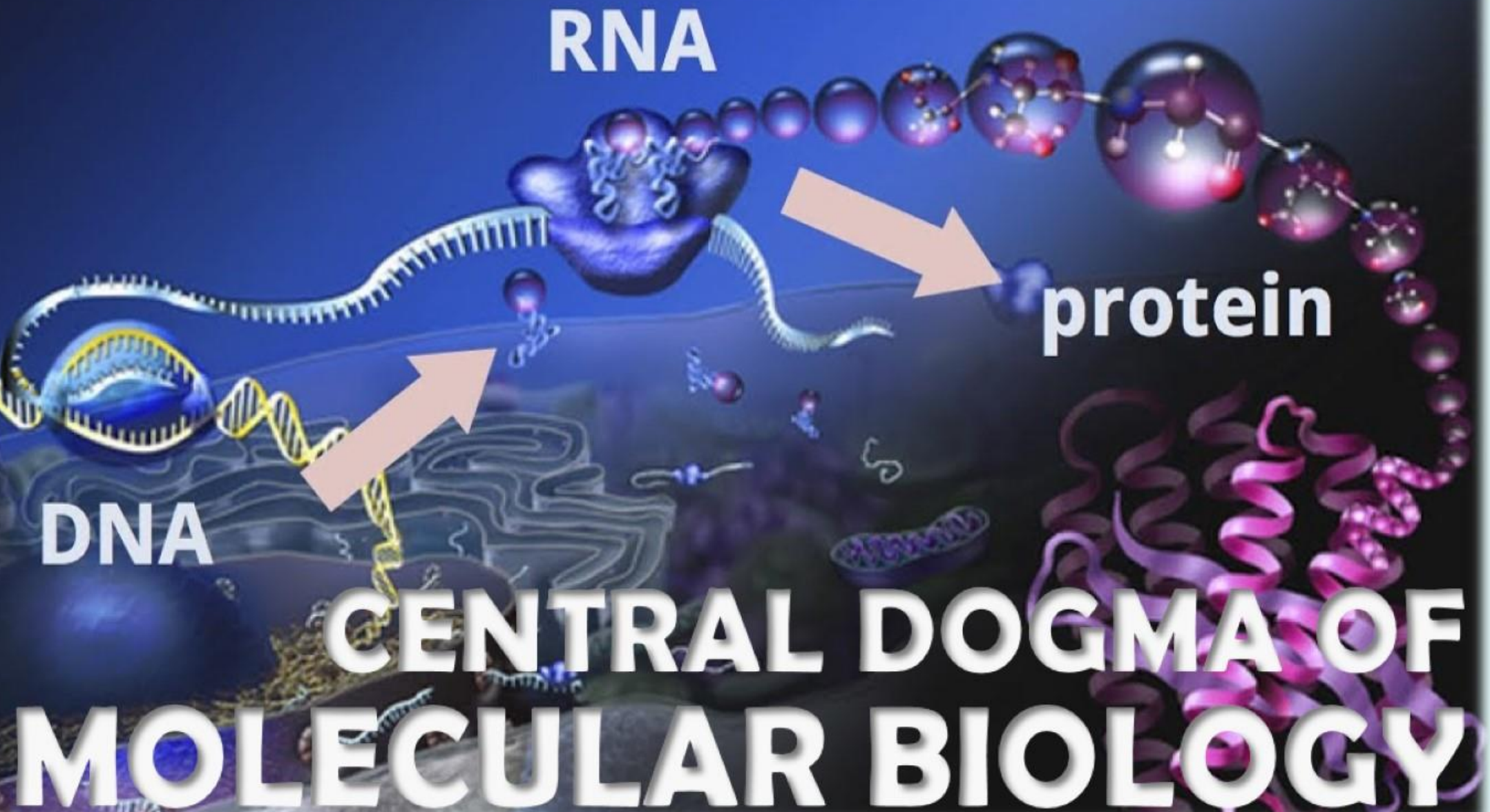
- ▶ For the **storage of genetic information**, DNA is better due to its stability. But for the **transmission of genetic information**, RNA is better.
- ▶ RNA can directly code for the protein synthesis, hence can easily express the characters. **DNA is dependent on RNA for protein synthesis.**



RNA WORLD

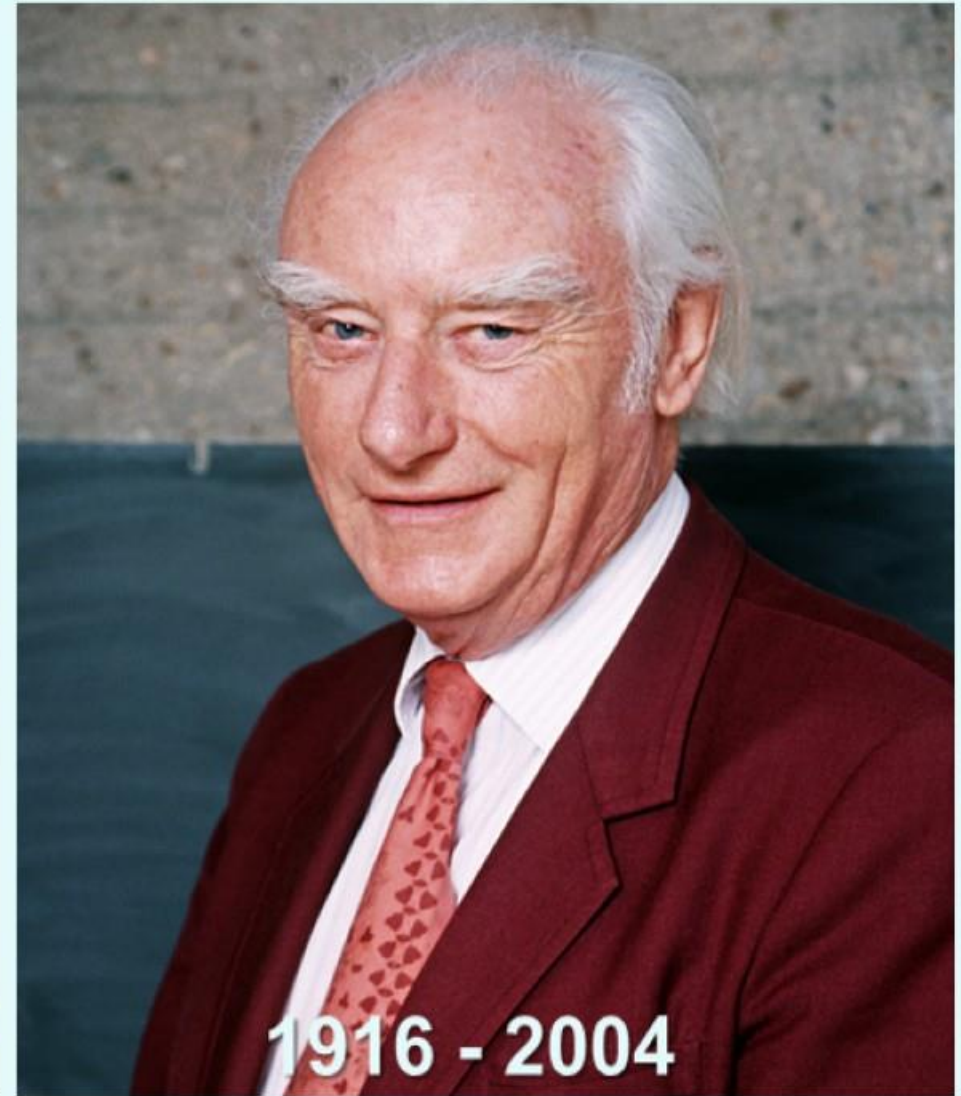
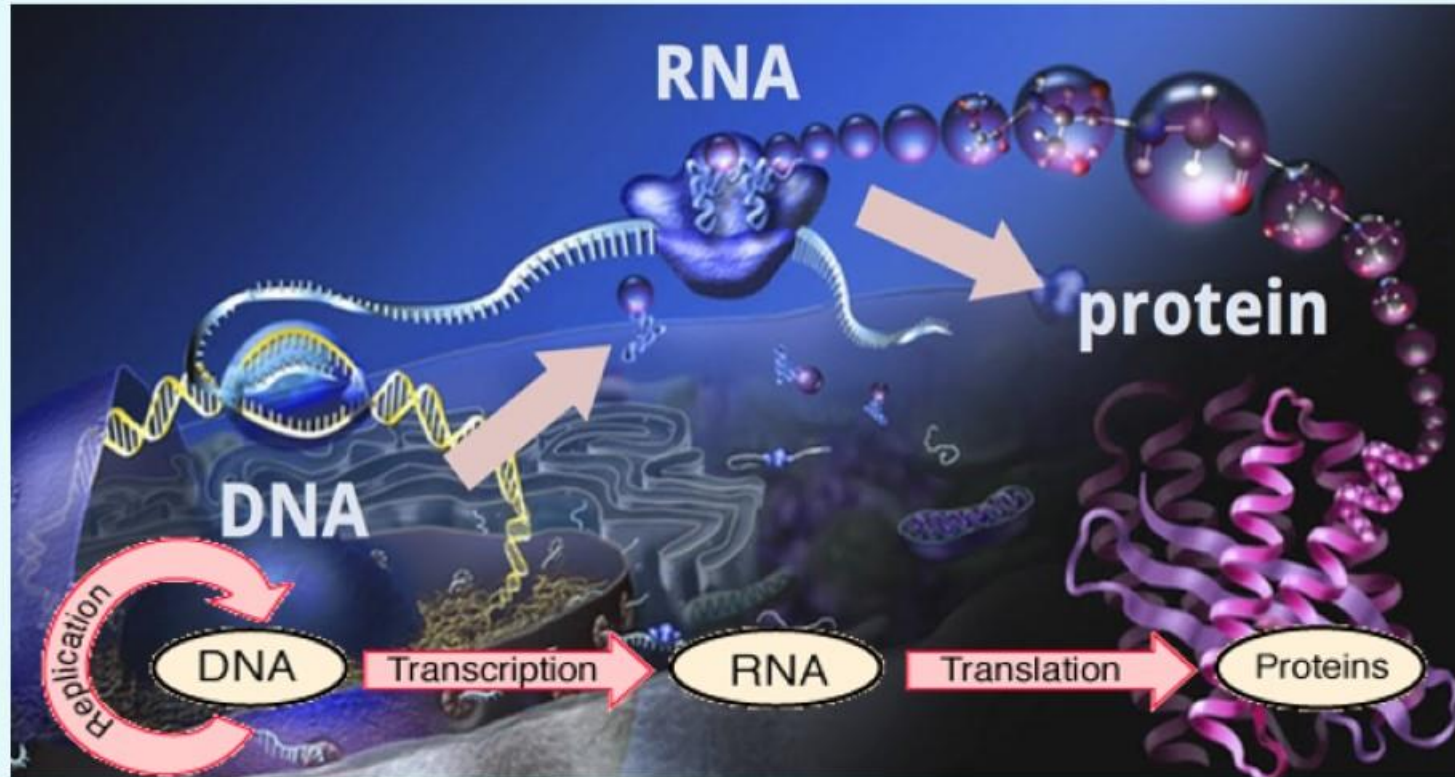


- ▶ RNA was the **first genetic material**.
- ▶ It acts as **genetic material & catalyst**.
- ▶ Essential life processes (**metabolism, translation, splicing etc.**) evolved around RNA.
- ▶ **DNA evolved from RNA** for stability.



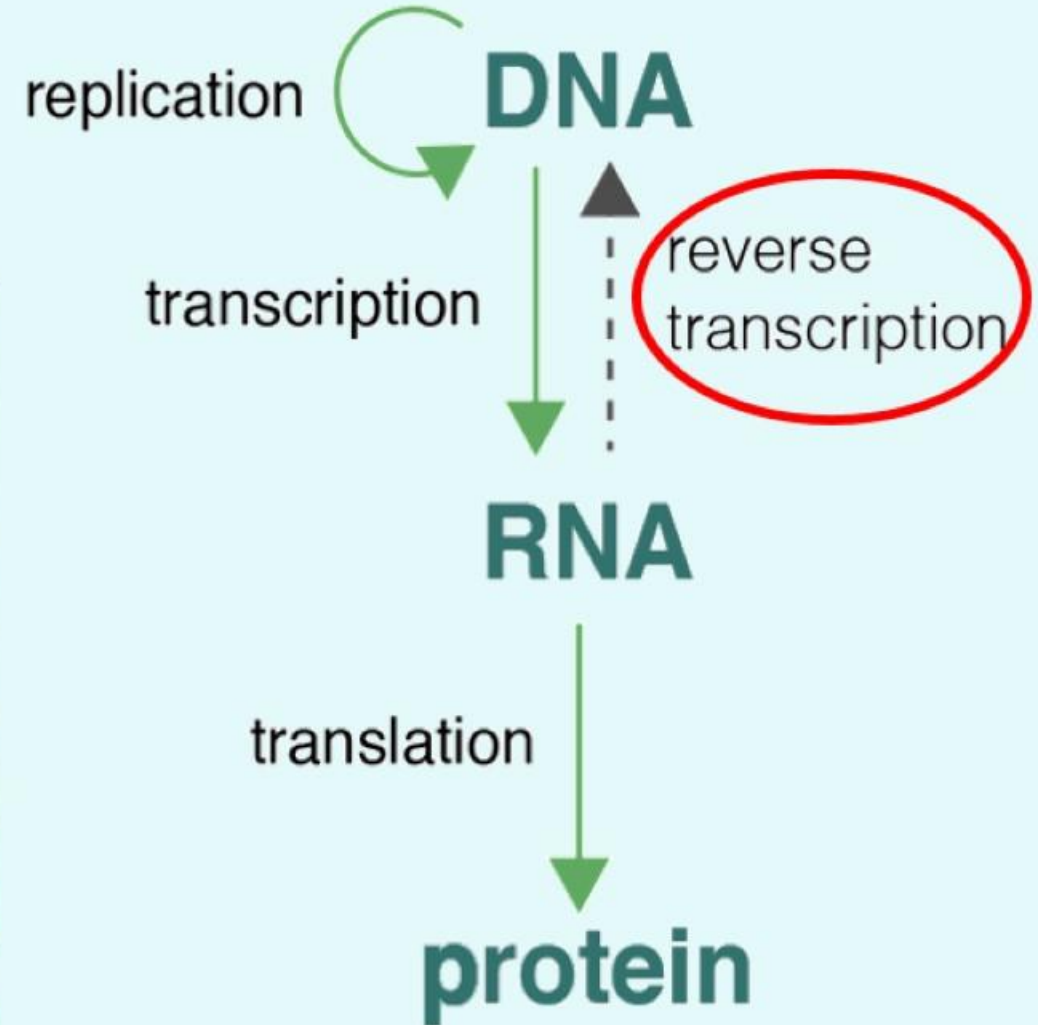
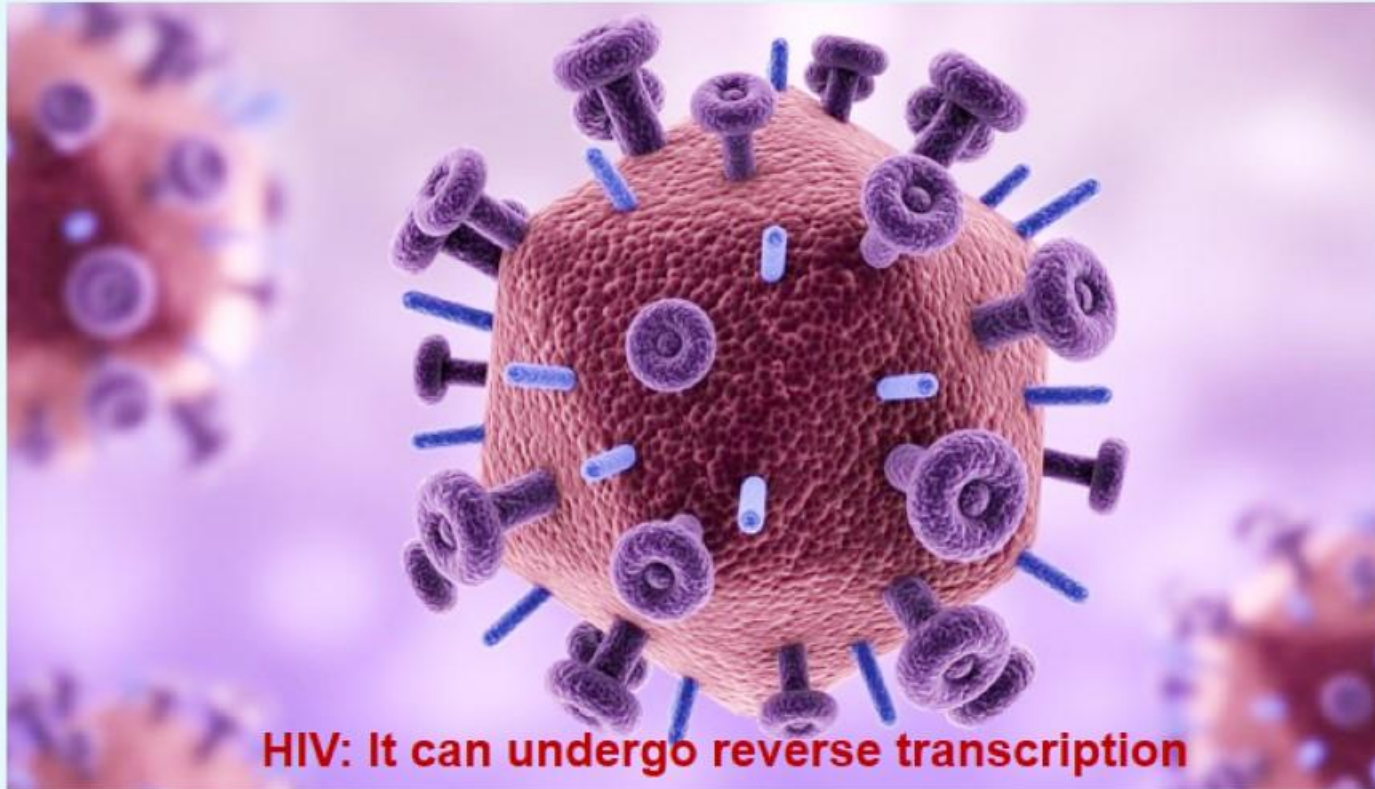
CENTRAL DOGMA OF MOLECULAR BIOLOGY

- It is proposed by **Francis Crick**.
- It states that the genetic information flows from **DNA → RNA → Protein**.



CENTRAL DOGMA OF MOLECULAR BIOLOGY

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





DNA REPLICATION

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) proved Semi-conservative model.



James Watson

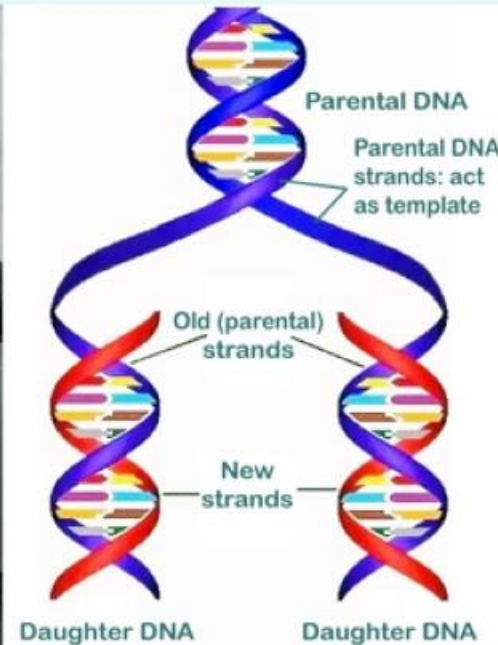
Francis Crick



Watson



Crick



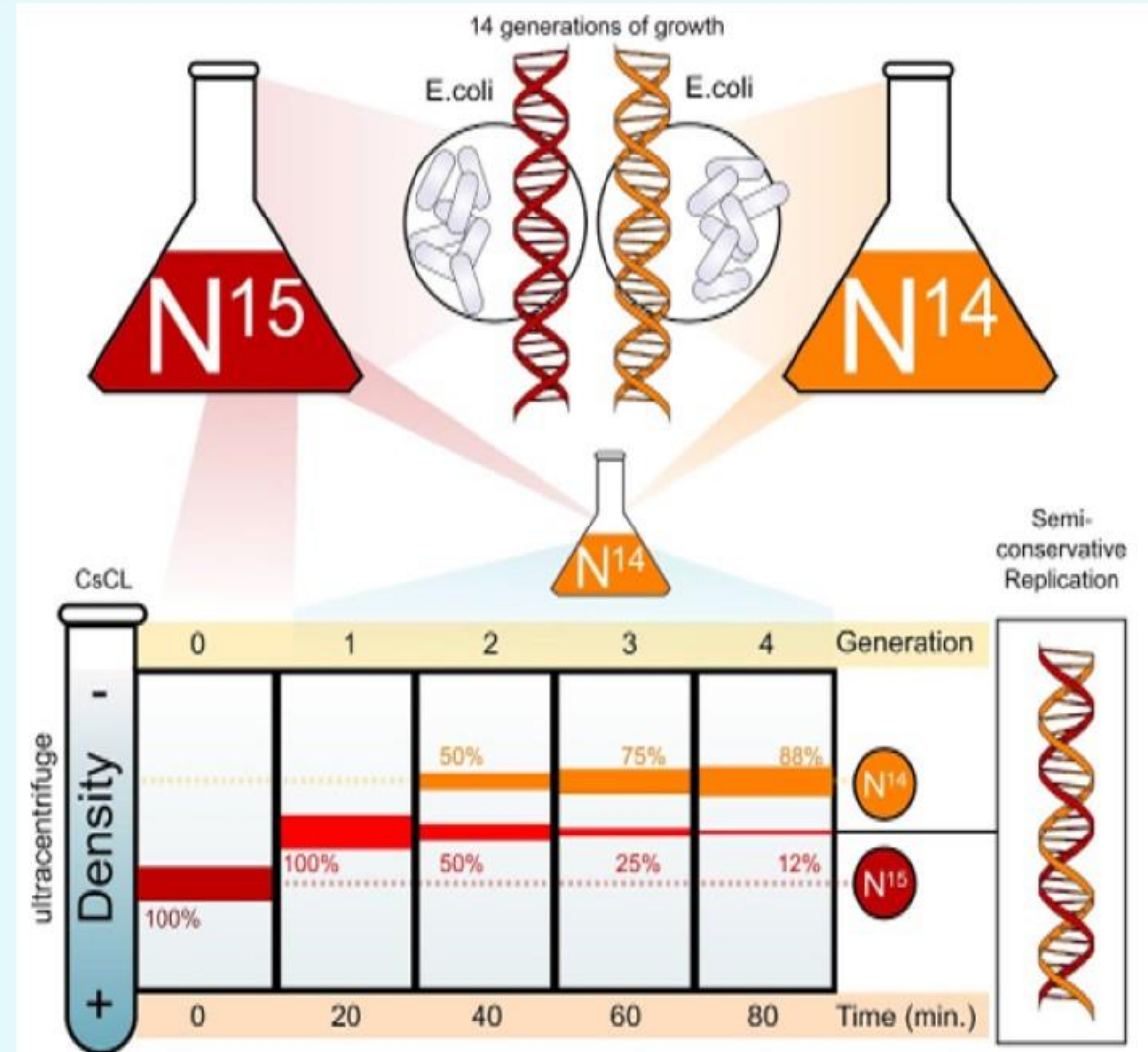
Messelson & Stahl

DNA REPLICATION

MESSELSON & STAHL'S EXPERIMENT

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- They prepared 2 culture media of *E. coli*.
- One preparation contains $^{15}\text{NH}_4\text{Cl}$ salt (^{15}N : heavy isotope of N). So ^{15}N was incorporated into both strands of bacterial DNA and the DNA became **heavier**.
- Other preparation contains ^{14}N salts. So ^{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**.

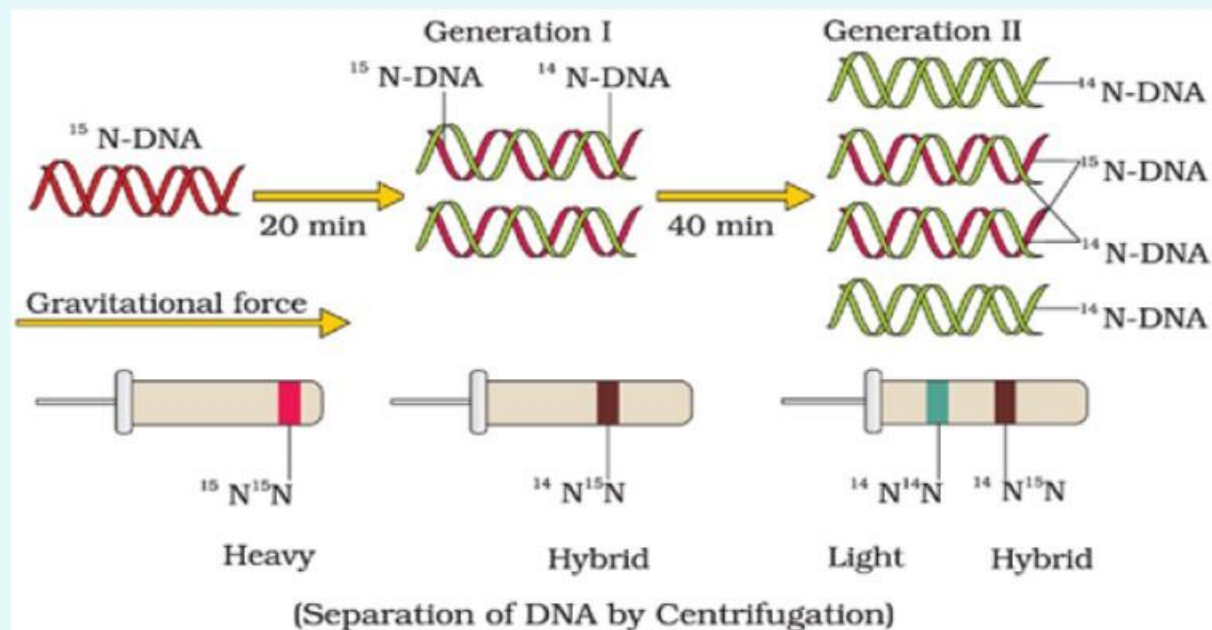
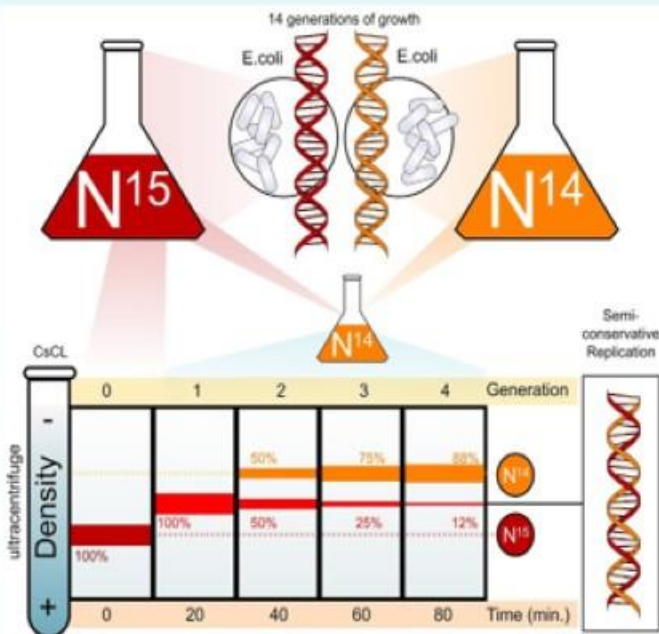


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DNA REPLICATION

MESSELSON & STAHL'S EXPERIMENT

- 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 in 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 min), there was equal amounts of hybrid DNA and light DNA.

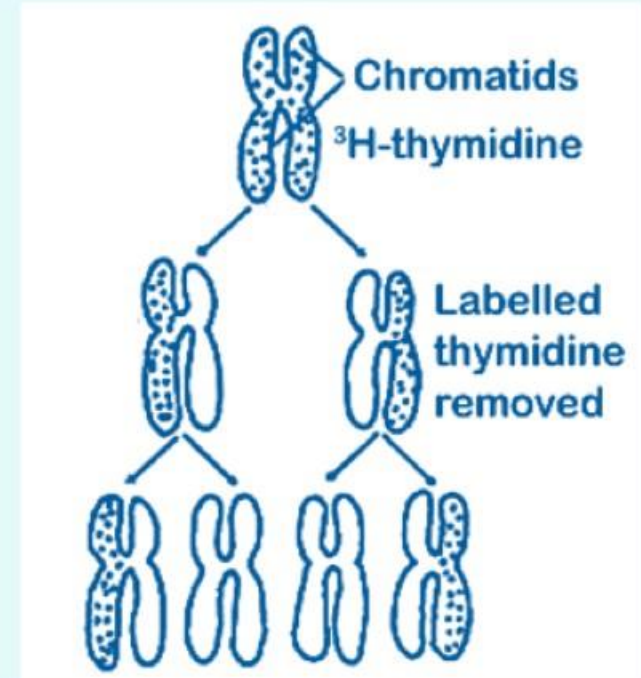
DNA REPLICATION

MESSELSON & STAHL'S EXPERIMENT

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



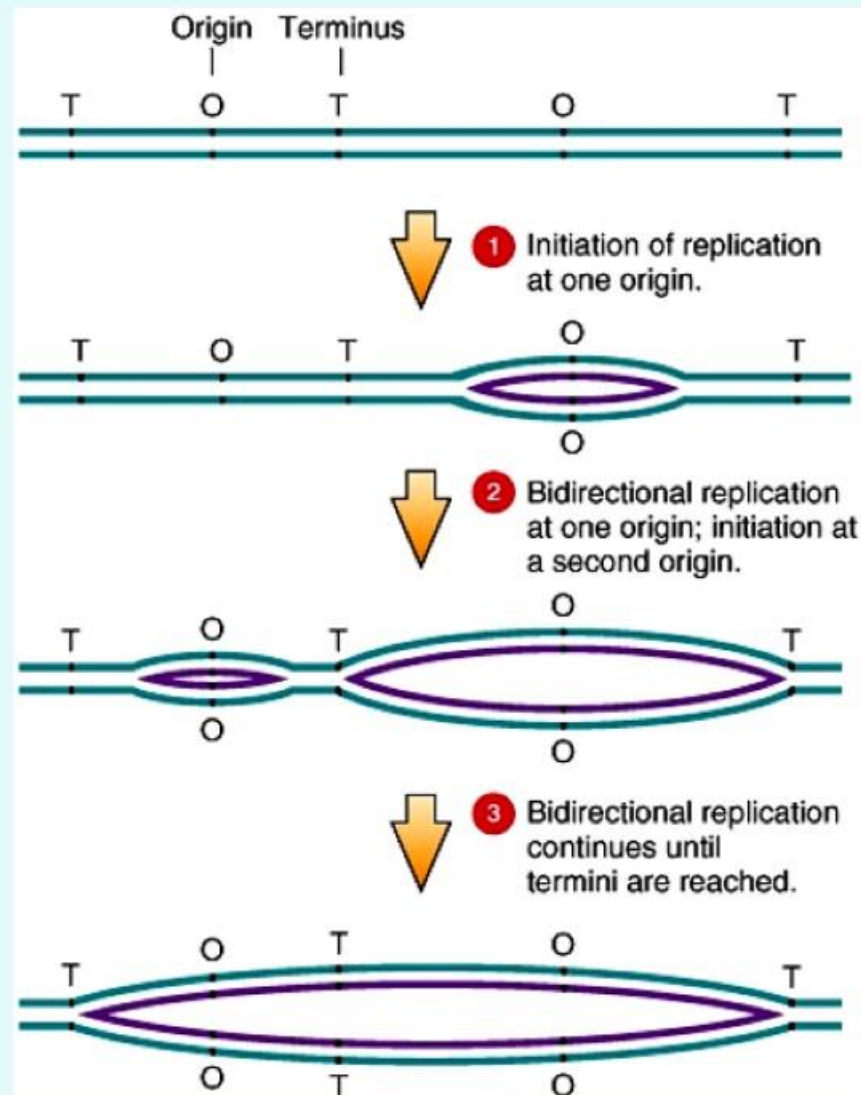
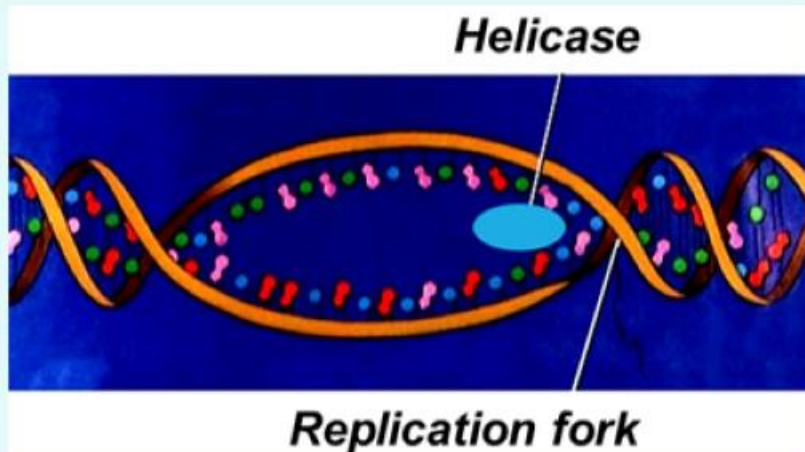
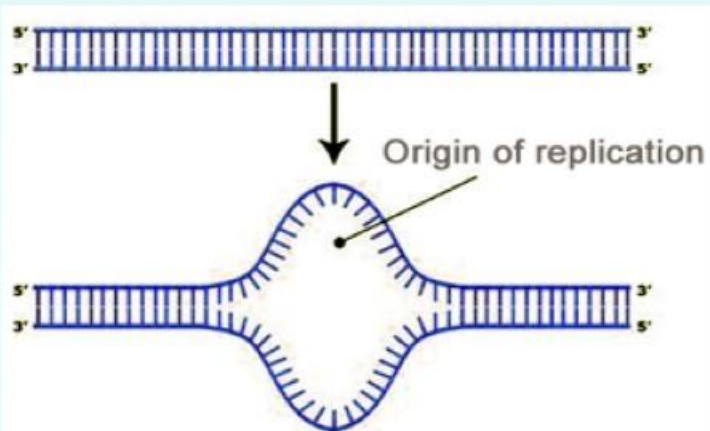
Dr. J. Herbert Taylor



DNA REPLICATION

THE MACHINERY & ENZYMES

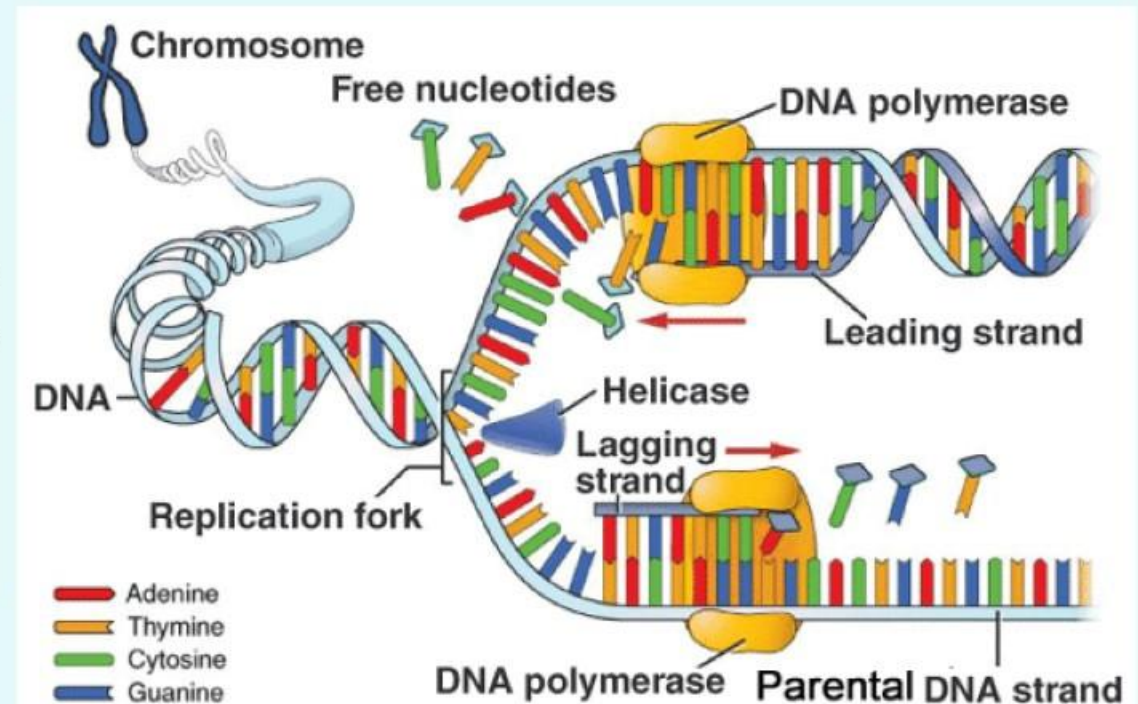
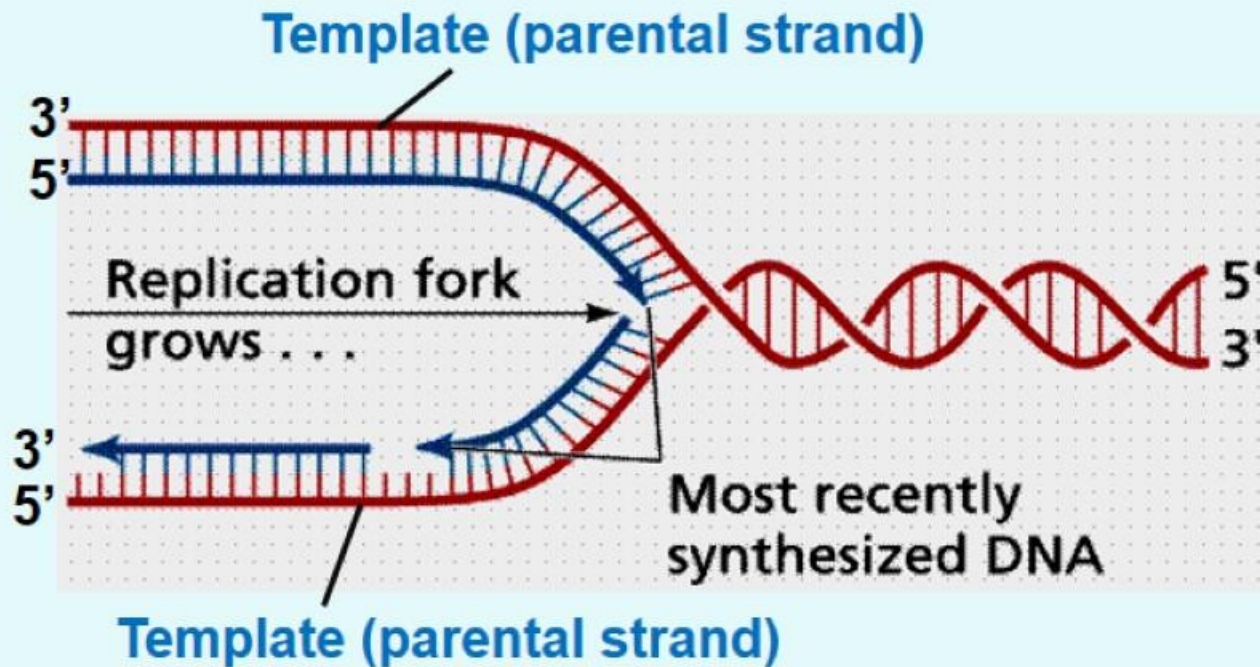
- DNA replication starts at a point called **origin (ori)**.
- A unit of replication with one origin is called a **replicon**.
- During replication, the 2 strands unwind and separate by breaking H-bonds in presence of an enzyme, **Helicase**.
- Unwinding of the DNA molecule at a point forms a 'Y'-shaped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



DNA REPLICATION

THE MACHINERY & ENZYMES

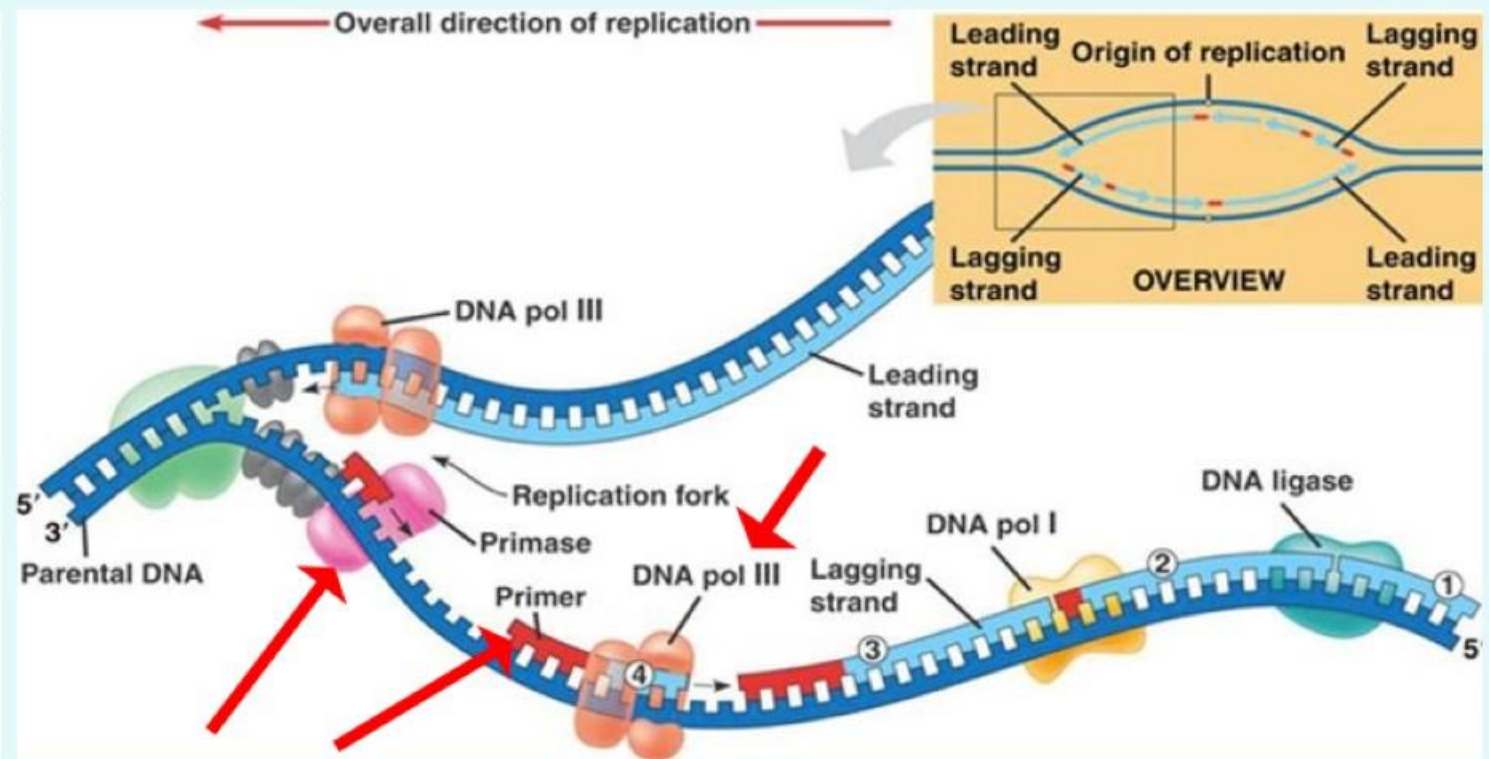
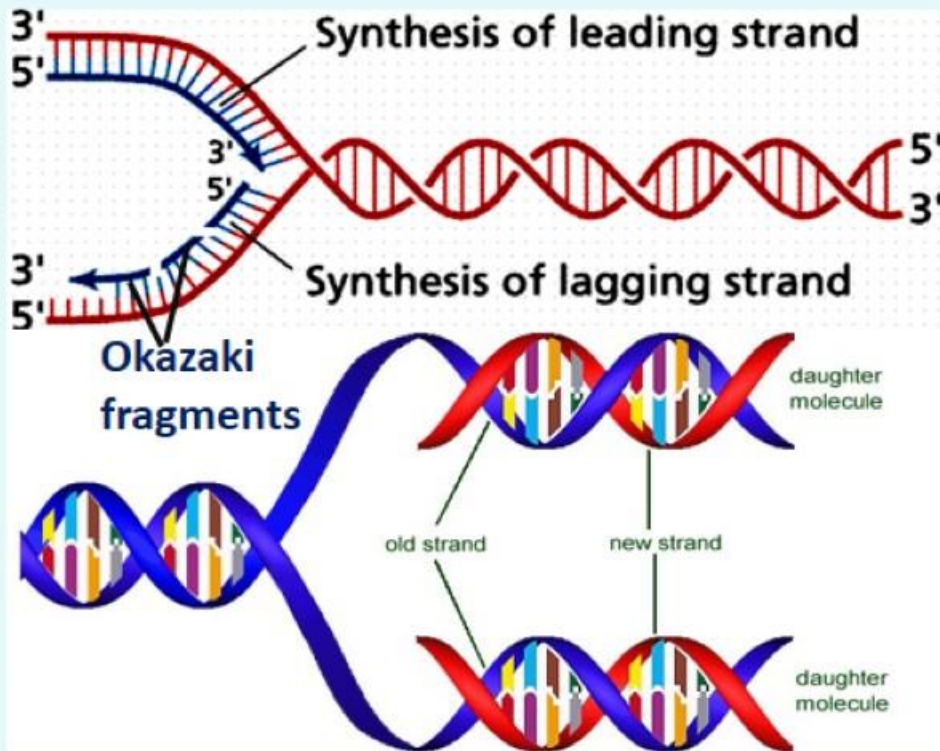
- The separated strands act as **templates** for the synthesis of new strands.
- DNA replicates in the **5'→3'** direction.
- **Deoxyribonucleoside triphosphates (dATP, dGTP, dCTP & dTTP)** act as **substrate** and provide **energy** for polymerization.



DNA REPLICATION

THE MACHINERY & ENZYMES

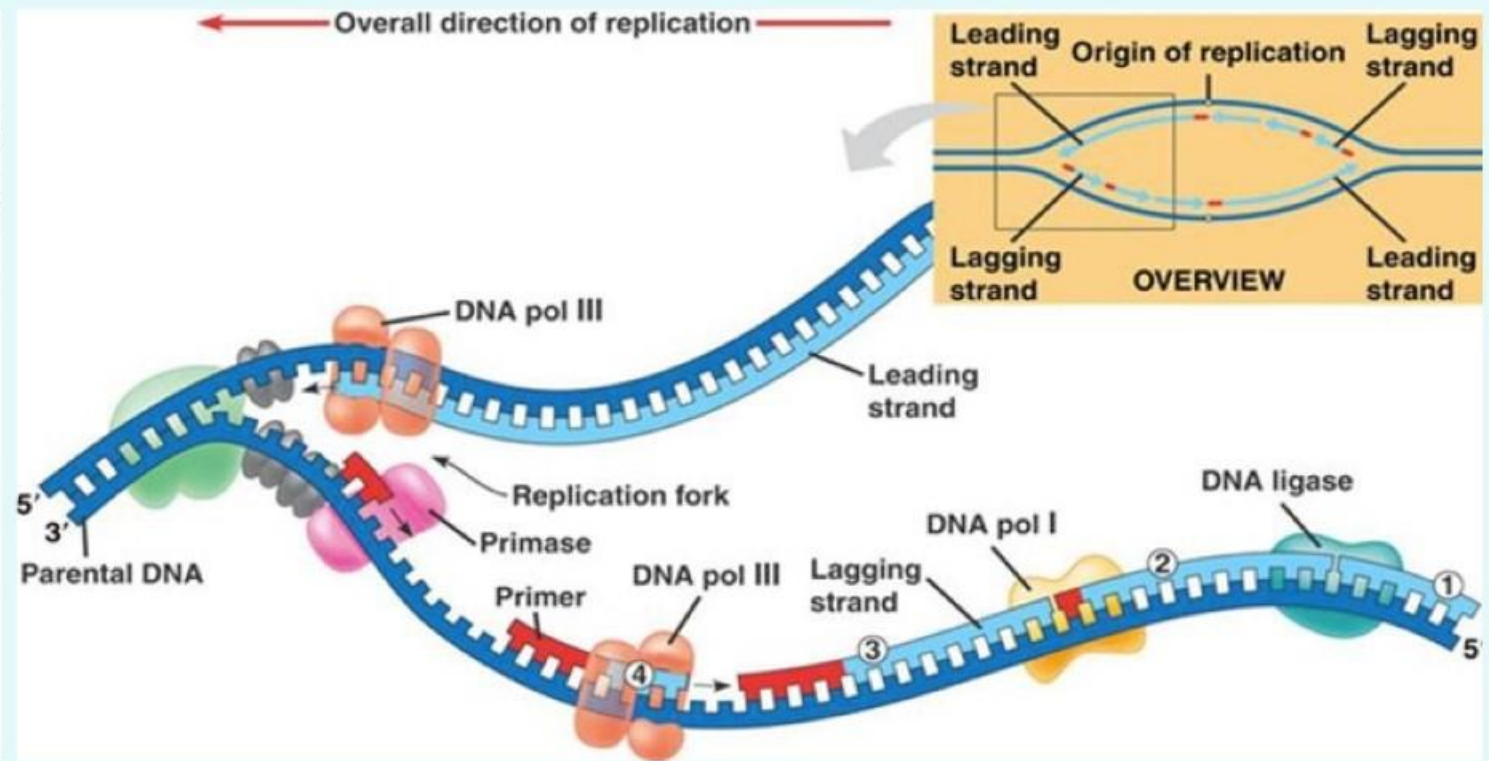
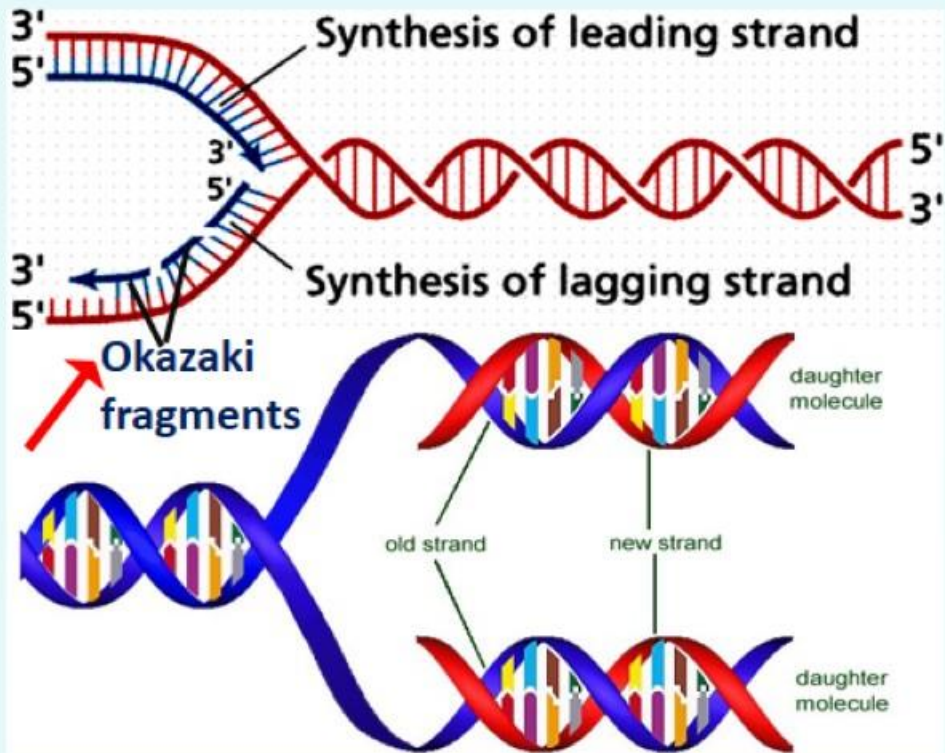
- Firstly, a small **RNA primer** is synthesized in presence of an enzyme, **primase**.
- In presence of an enzyme, DNA dependent **DNA polymerase**, many nucleotides join with one another to primer strand and form a polynucleotide chain (new strand).



DNA REPLICATION

THE MACHINERY & ENZYMES

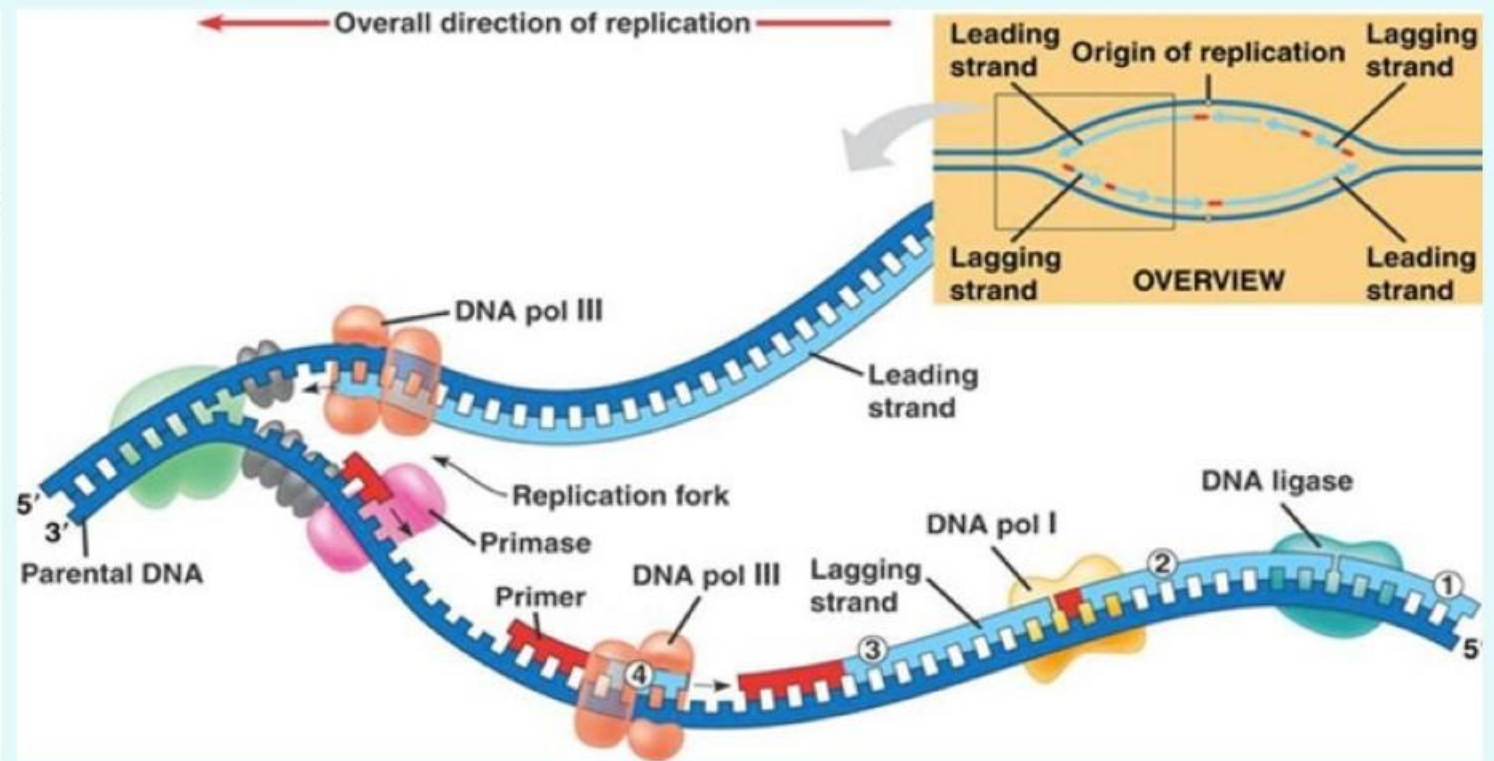
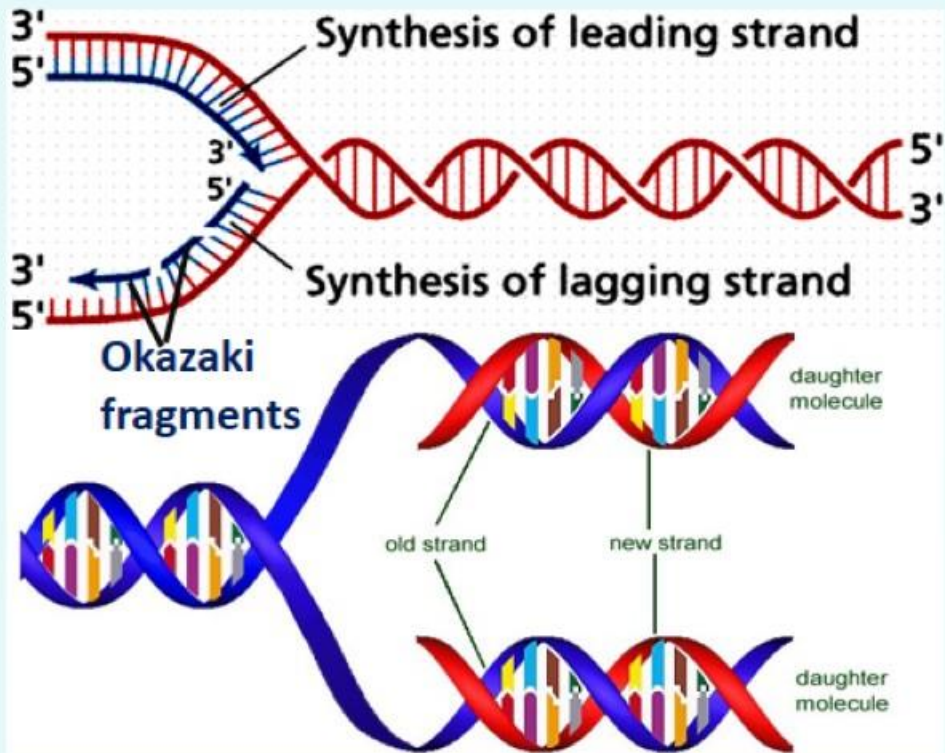
- During replication, one strand is formed as a continuous stretch in 5' → 3' direction (**Continuous synthesis**). This strand is called **leading strand**.
- The other strand is formed in small stretches (**Okazaki fragments**) in 5' → 3' direction (**Discontinuous synthesis**).



DNA REPLICATION

THE MACHINERY & ENZYMES

- The Okazaki fragments are then joined together to form a new strand by an enzyme, **DNA ligase**. This new strand is called **lagging strand**. bankofbiology.com
- If a wrong base is introduced in the new strand, **DNA polymerase** can do **proof reading**.

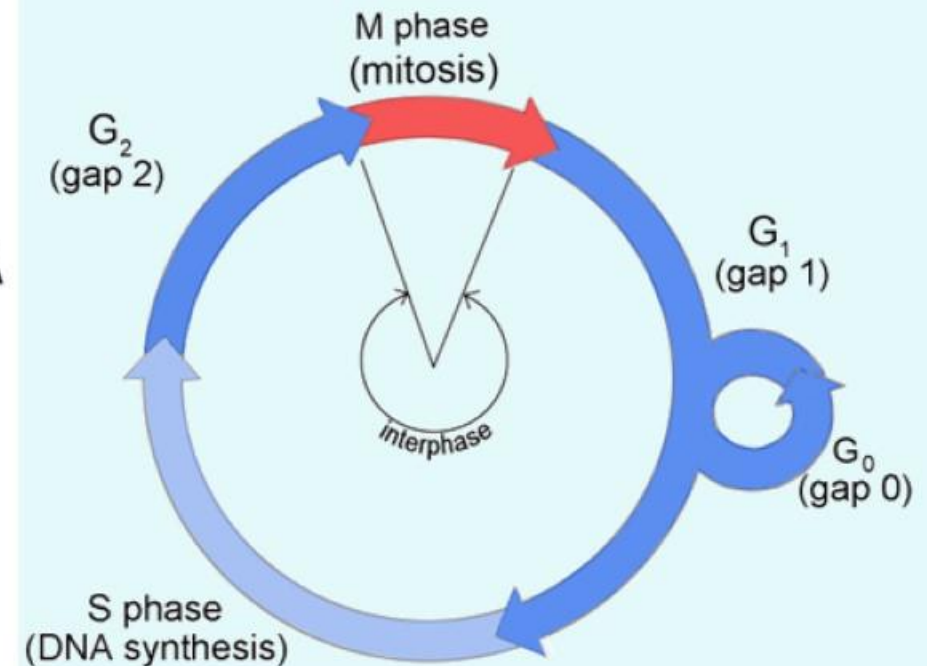
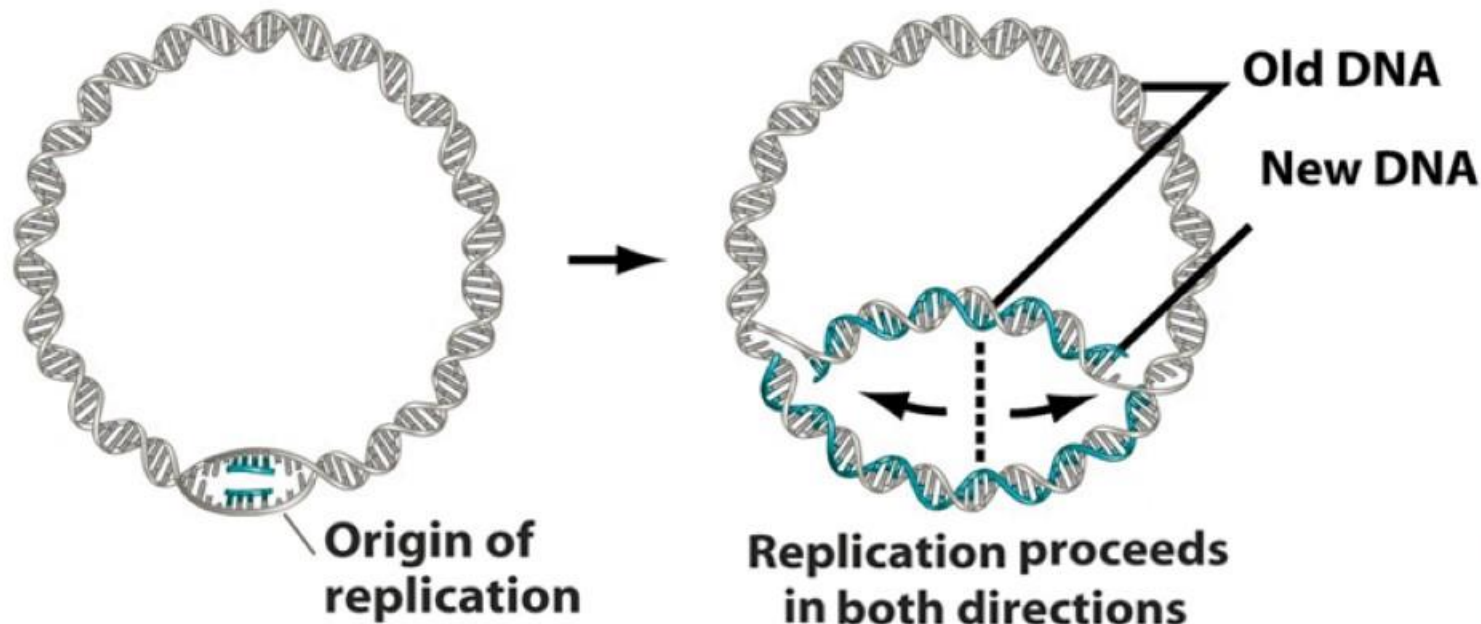


DNA REPLICATION

THE MACHINERY & ENZYMES

- *E. coli* completes replication within **18 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**.

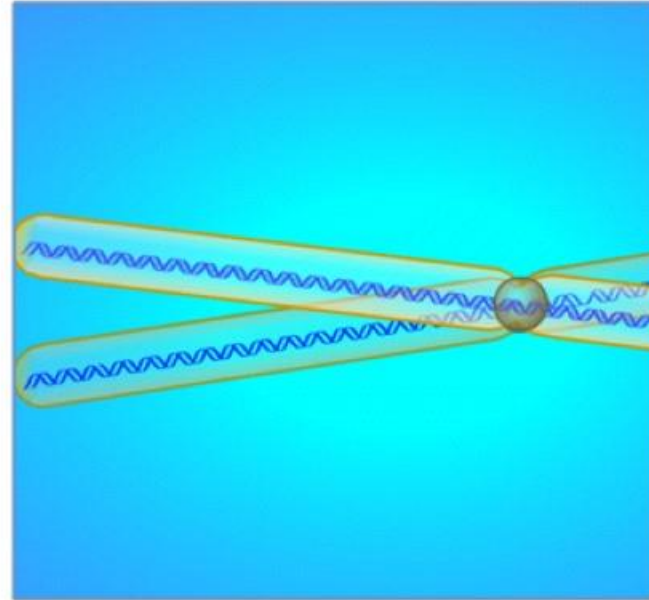
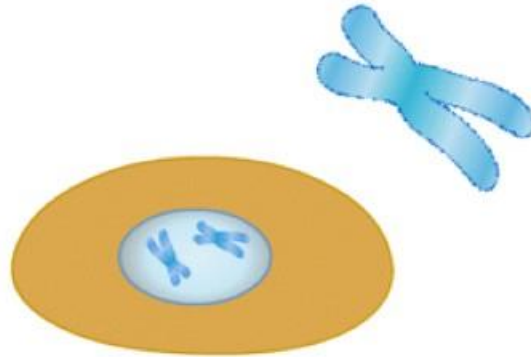
Replication in bacteria



DNA REPLICATION

THE MACHINERY & ENZYMES

- Nuclear Chromosomes
- "Unzipping" DNA
- Complementary Base Pairs
- Simultaneous Replication
- Two New DNA Strands

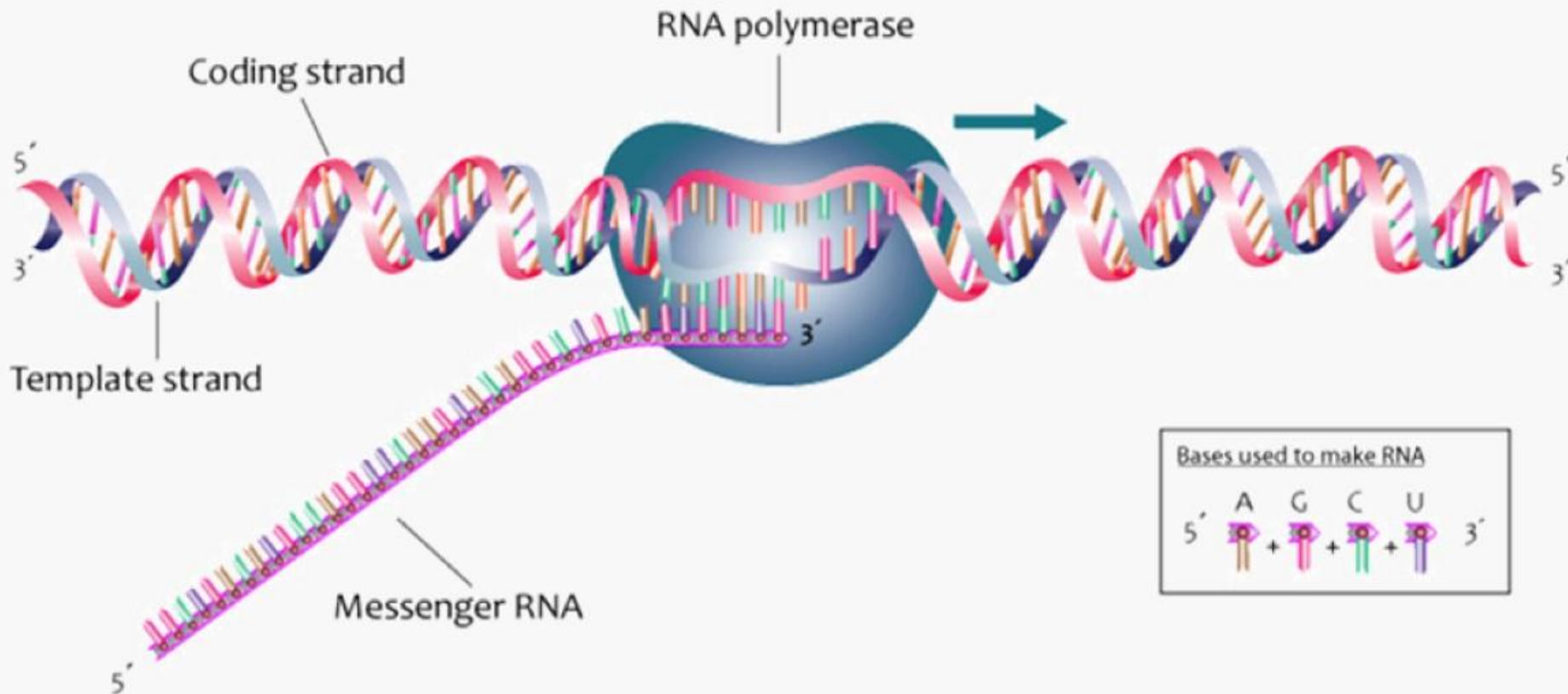


Messenger RNA

TRANSCRIPTION

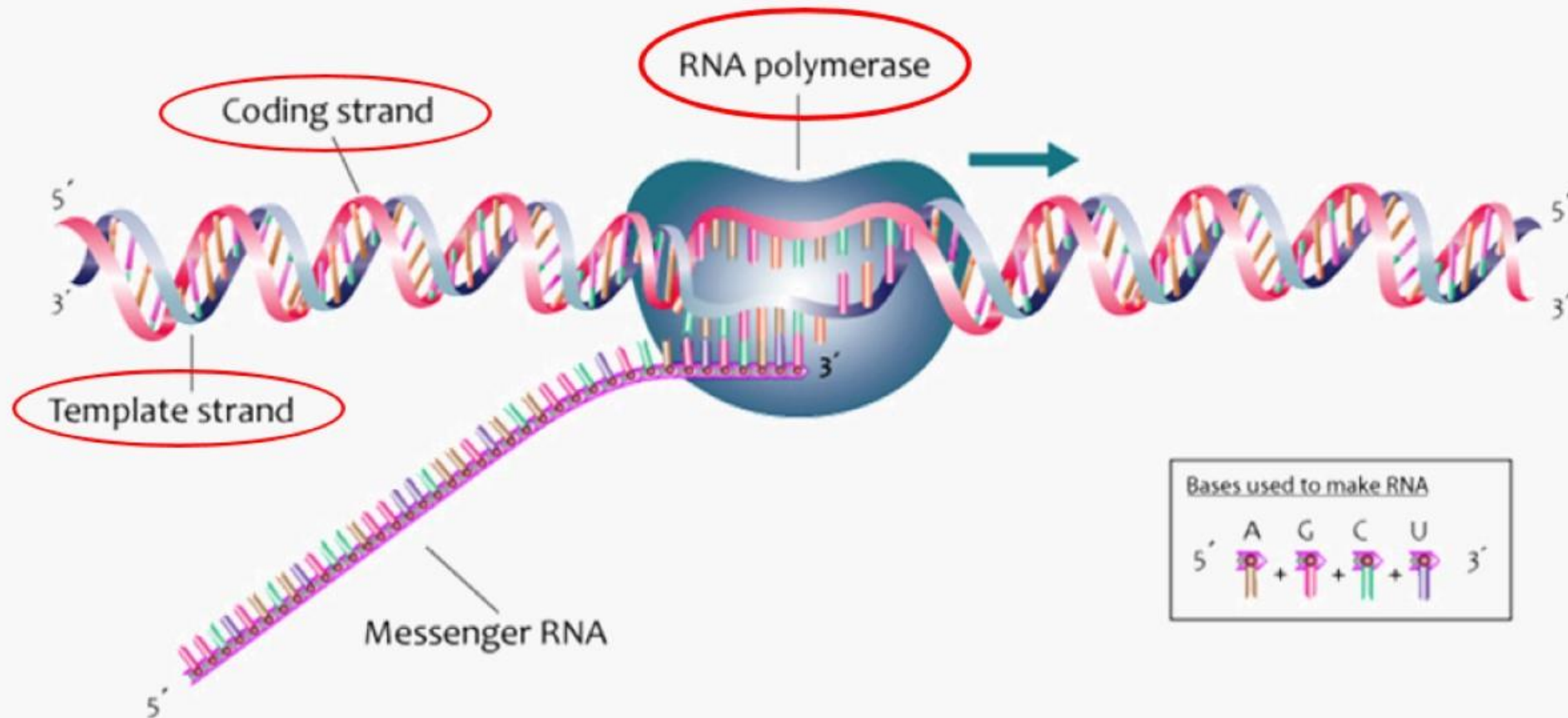
TRANSCRIPTION

- It is the process of **copying genetic information** from one strand of the **DNA into RNA**.
- Here, **adenine** forms base pair with **uracil** instead of **thymine**.



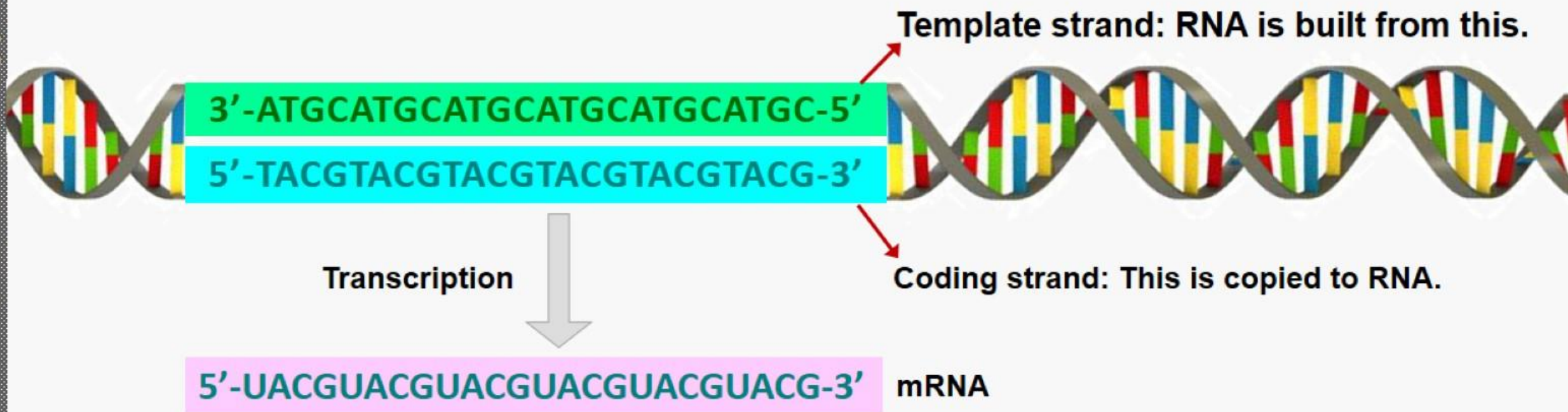
TRANSCRIPTION

- The *DNA- dependent RNA polymerase* catalyzes polymerization only in $5' \rightarrow 3'$ direction.
- $3' \rightarrow 5'$ acts as **template strand** and $5' \rightarrow 3'$ acts as **coding strand**.



TRANSCRIPTION

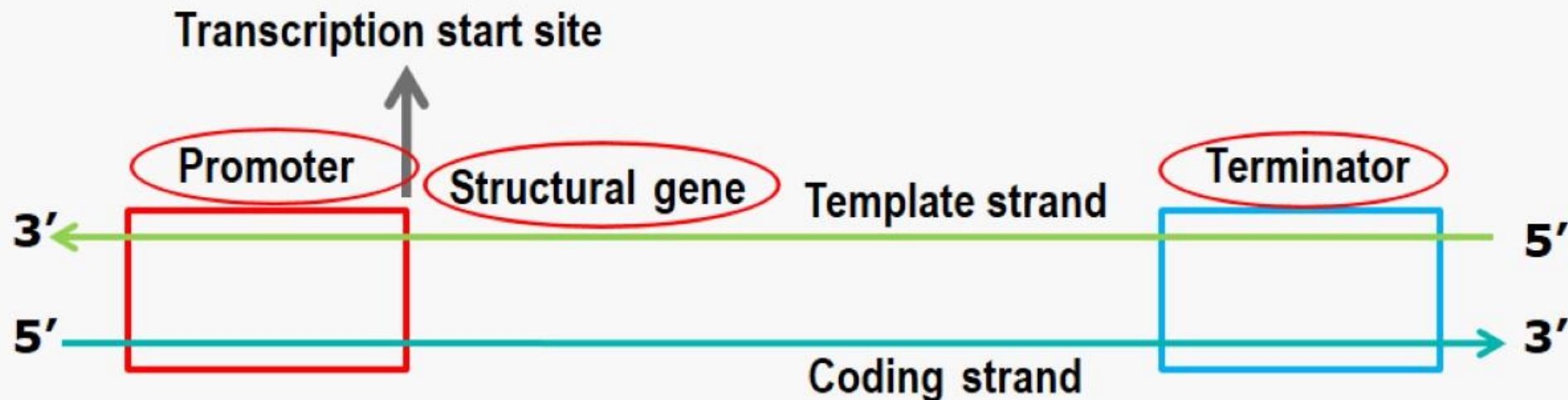
- Both strands are not copied during transcription, because
 - ❖ The **code for proteins is different in both strands**. This complicates the translation.
 - ❖ If **2 RNA molecules** are produced simultaneously, this would be **complimentary** to each other. It forms a **double stranded RNA** and prevents translation.



TRANSCRIPTION

TRANSCRIPTION UNIT

- It is the segment of DNA between the sites of initiation and termination of transcription.
- It consists of 3 regions:
 - **A promoter:** Binding site for *RNA polymerase*. Located towards 5'-end (upstream).
 - **Structural gene:** Region b/w promoter & terminator where transcription takes place.
 - **A terminator:** The site where transcription stops. Located towards 3'-end (downstream).

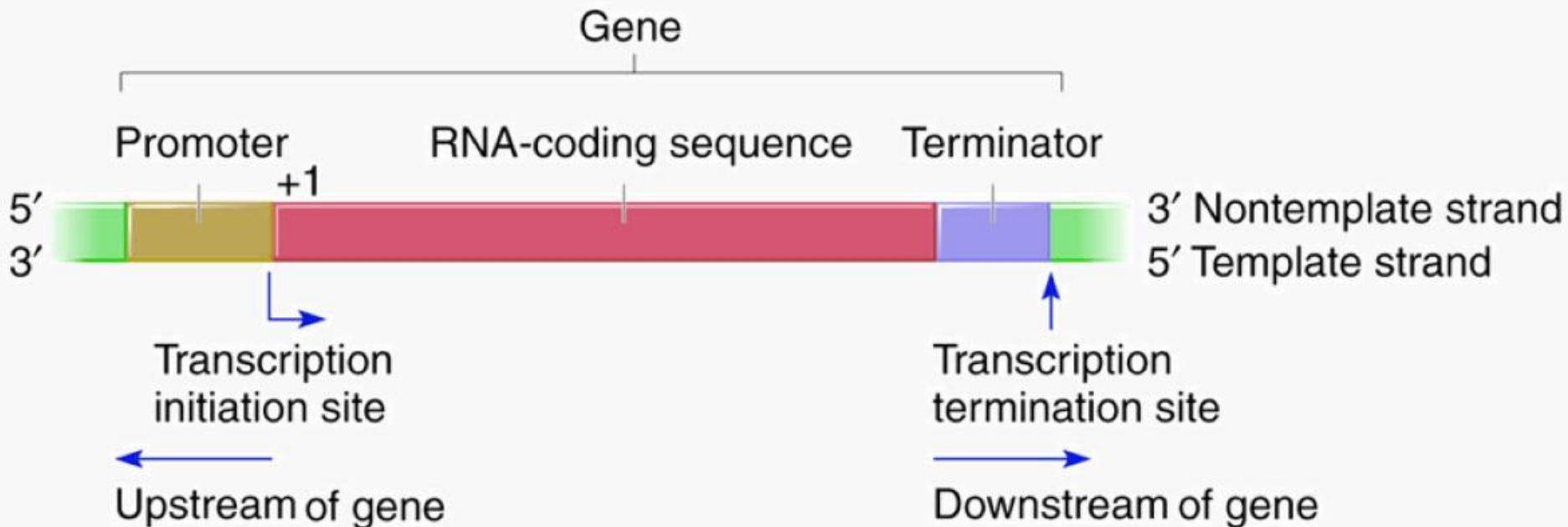


SCHEMATIC STRUCTURE OF A TRANSCRIPTION UNIT

TRANSCRIPTION

TRANSCRIPTION UNIT

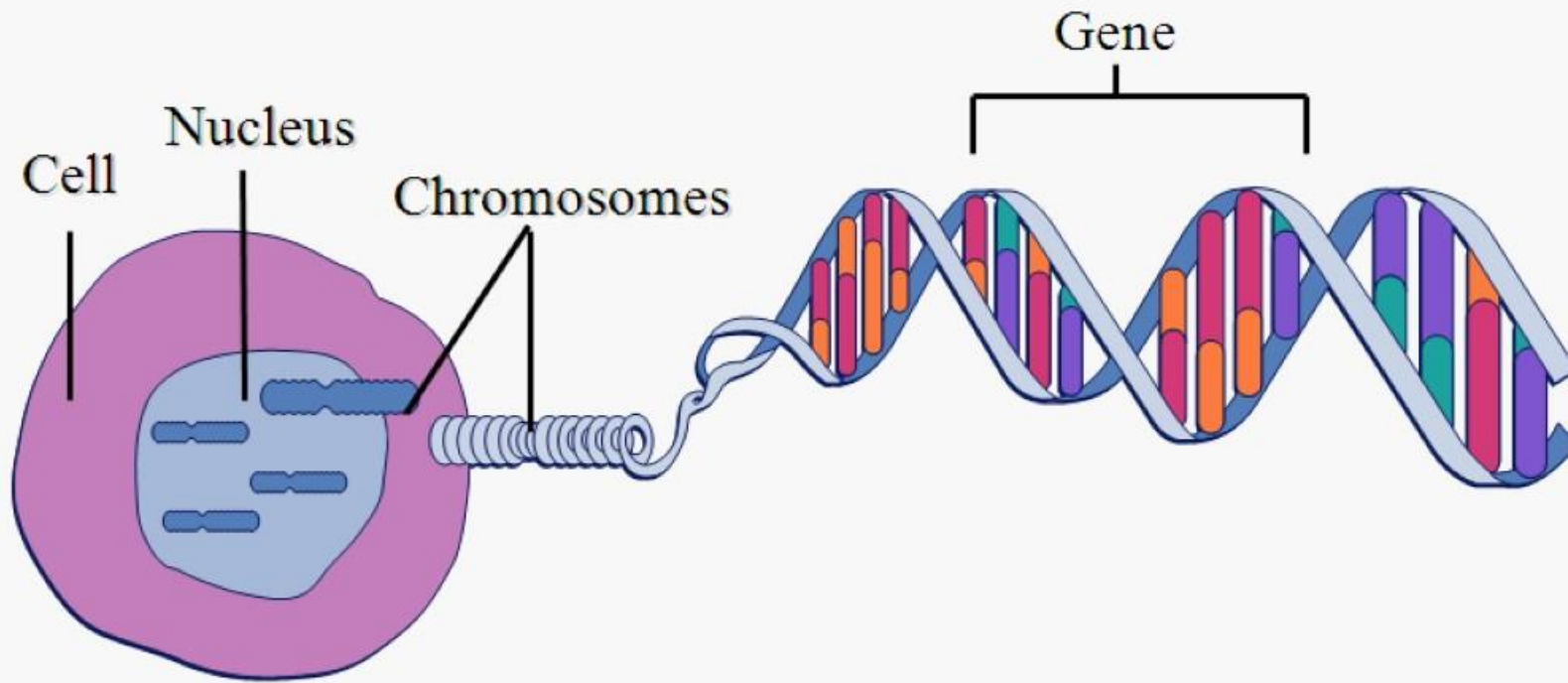
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TRANSCRIPTION

TRANSCRIPTION UNIT & GENE

- **Gene** is a functional unit of inheritance. It is the DNA sequence coding for an RNA (mRNA, rRNA or tRNA).
- **Cistron** is a segment of DNA coding for a polypeptide during protein synthesis. It is the largest element of a gene.



TRANSCRIPTION

TRANSCRIPTION UNIT & GENE

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).
- Exons appear in processed mRNA. Introns do not appear in processed mRNA.

➤ **Polycistronic structural genes:**

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



Monocistronic structural gene



Polycistronic structural gene

TRANSCRIPTION

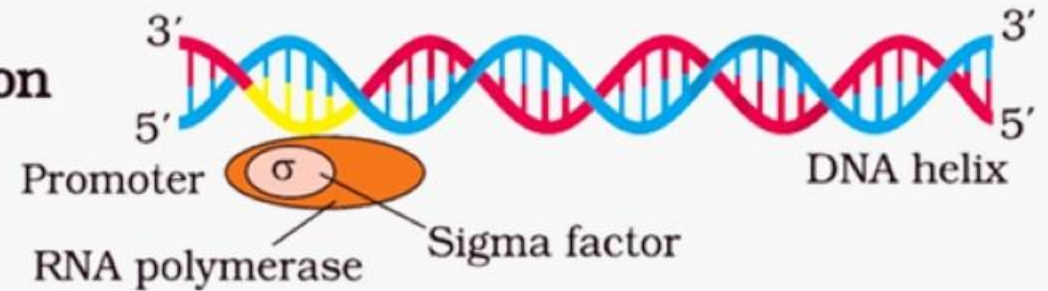
TRANSCRIPTION IN PROKARYOTES

- In bacteria (Prokaryotes), synthesis of all types of RNA are catalysed by a single **RNA polymerase**.

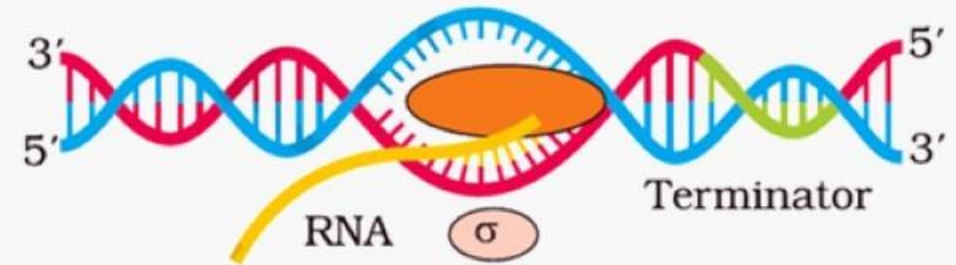
Transcription has 3 steps:

- ✓ **Initiation**
- ✓ **Elongation**
- ✓ **Termination**

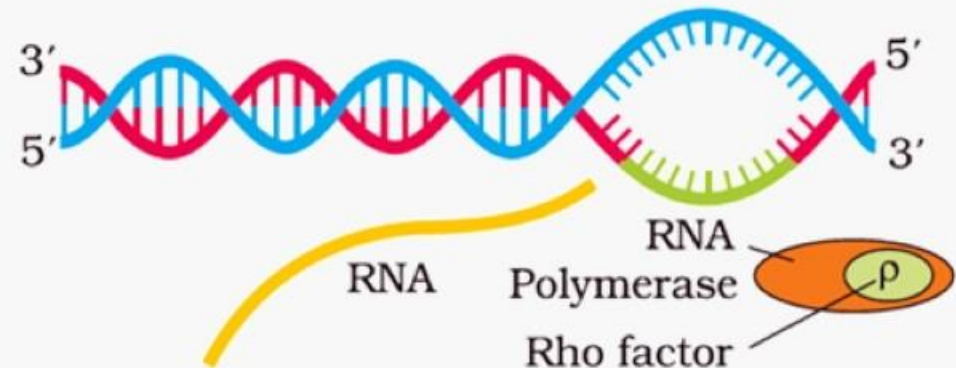
Initiation



Elongation



Termination

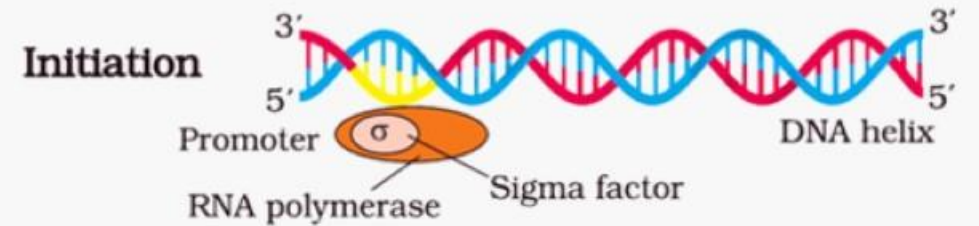
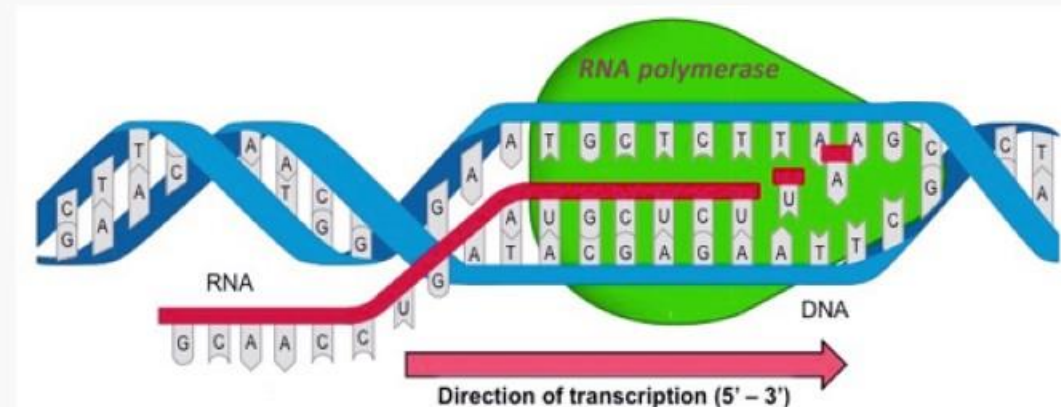
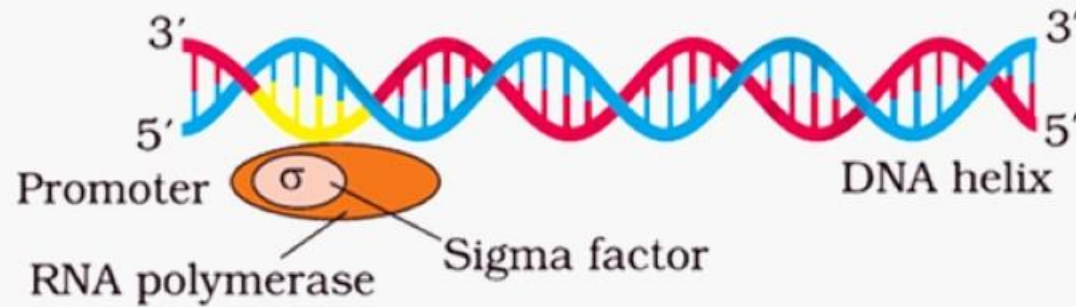


TRANSCRIPTION

TRANSCRIPTION IN PROKARYOTES

Initiation

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

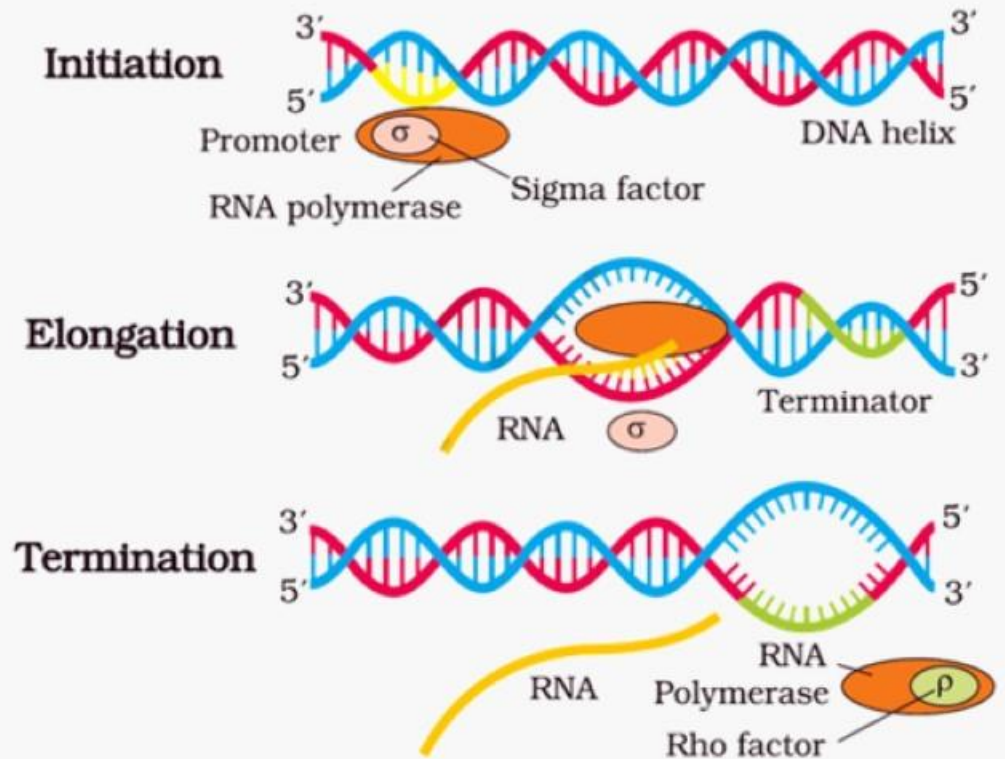
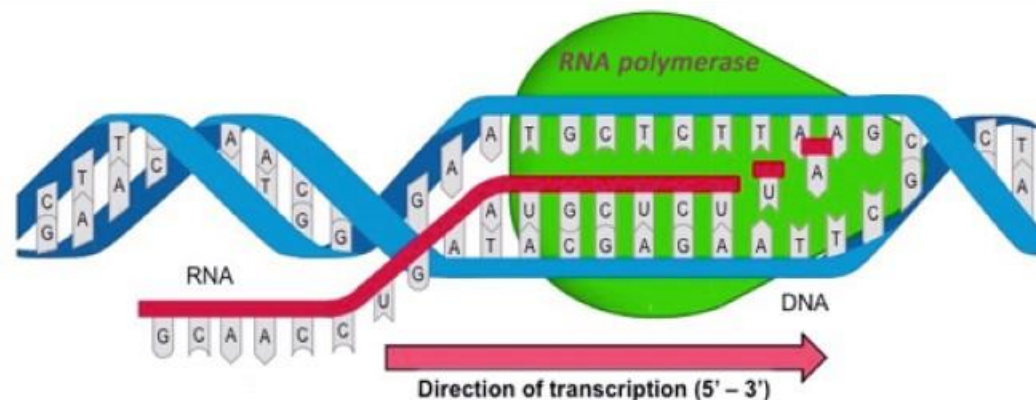
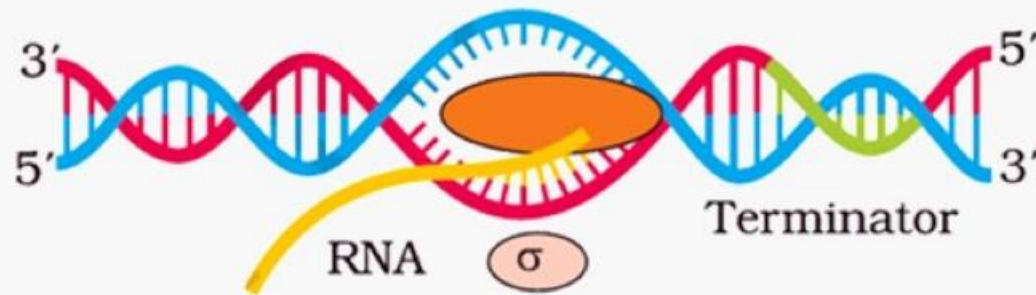


TRANSCRIPTION

TRANSCRIPTION IN PROKARYOTES

Elongation

- RNA chain is synthesized in **5'-3'** direction.
- In this process, activated **ribonucleoside triphosphates (ATP, GTP, UTP & CTP)** are added. This is complementary to the base sequence in the DNA template.

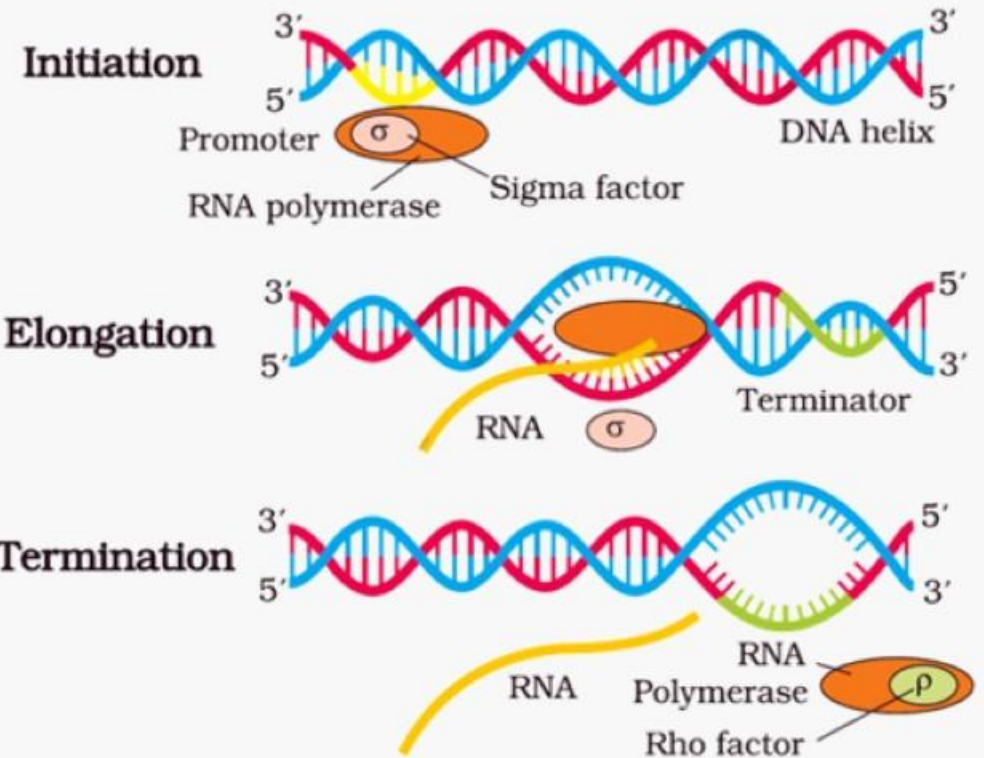
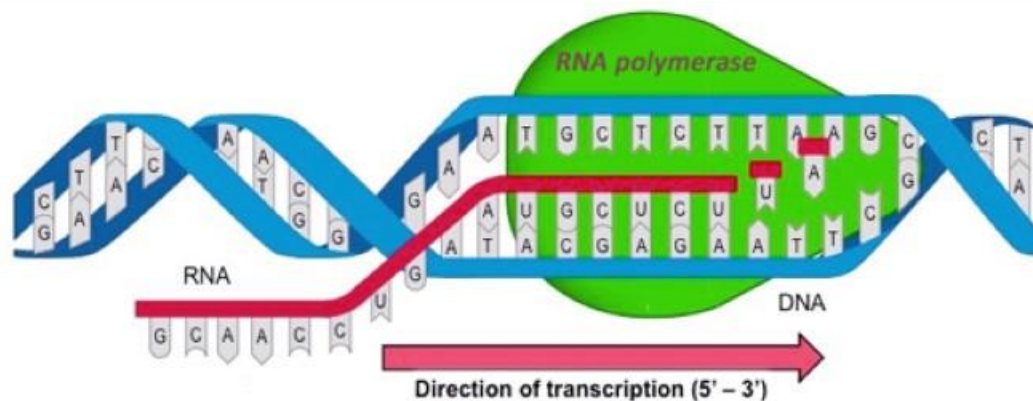
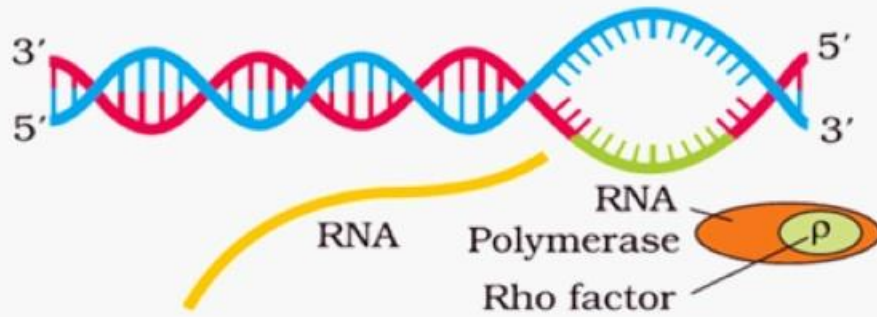


TRANSCRIPTION

TRANSCRIPTION IN PROKARYOTES

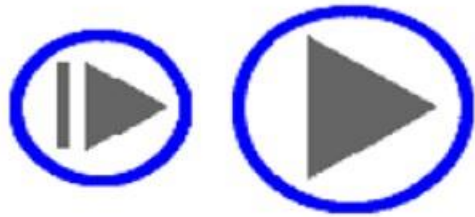
Termination

- A **termination factor (ρ factor)** binds to the *RNA polymerase* and terminates the transcription.

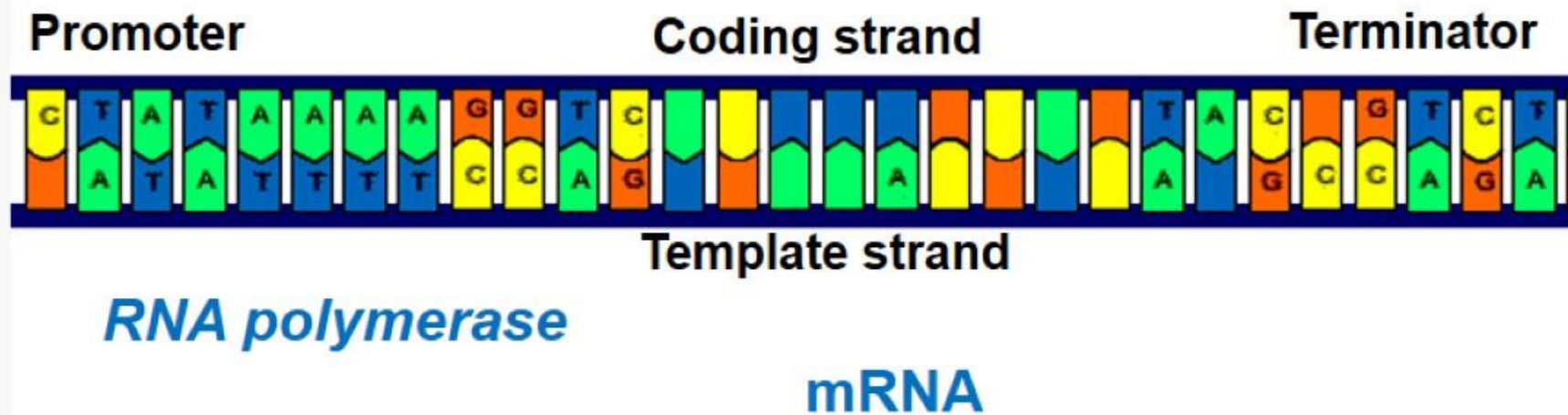


TRANSCRIPTION

TRANSCRIPTION IN PROKARYOTES



Transcription

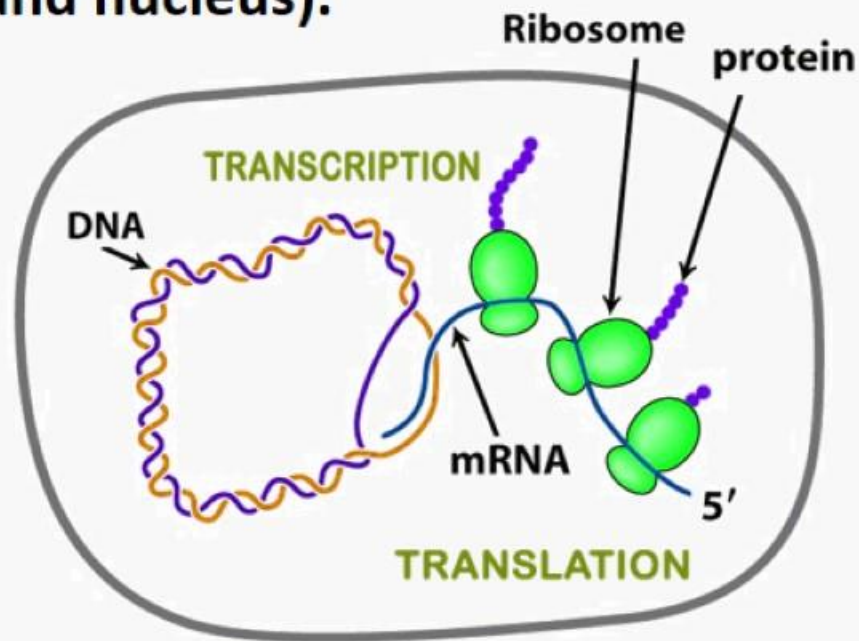


TRANSCRIPTION

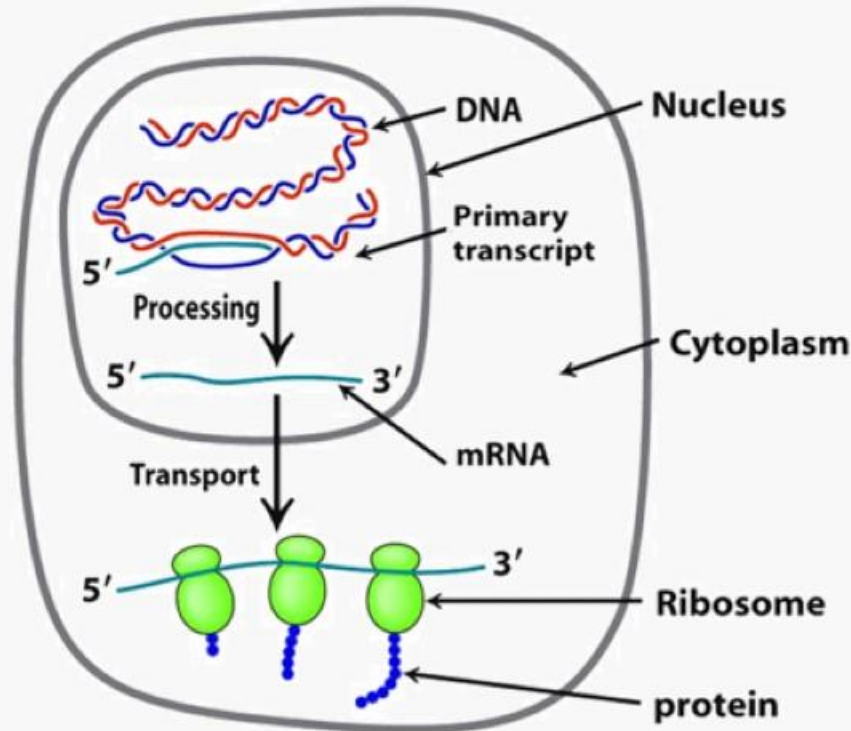
TRANSCRIPTION IN PROKARYOTES

In bacteria, **transcription and translation can be coupled** (translation begins before mRNA is fully transcribed) because

- ✓ mRNA requires **no processing** to become active.
- ✓ **Transcription & translation** take place in **same compartment** (no separation of cytosol and nucleus).



Bacterial cell (Prokaryote)



**Eukaryotic cell.
No coupling of
transcription
and translation**

TRANSCRIPTION

TRANSCRIPTION IN EUKARYOTES

In eukaryotes, there are 2 additional complexities:

1. There are **3 RNA polymerases**.
2. The **primary transcripts (hnRNA)** contain **exons and introns** and are non-functional. Hence introns must be removed.



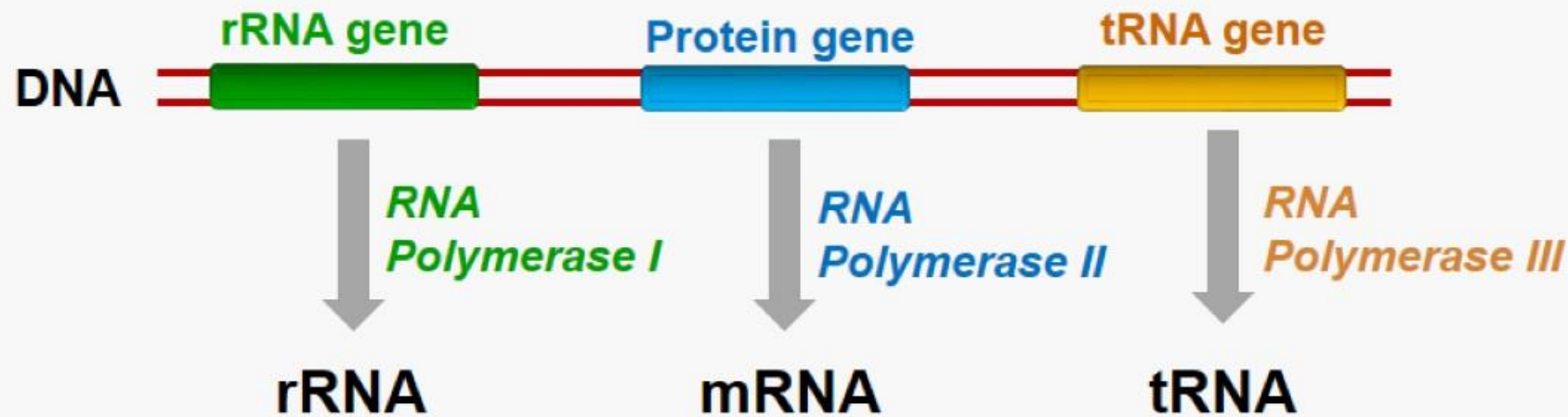
Primary transcripts (hnRNA)

TRANSCRIPTION

TRANSCRIPTION IN EUKARYOTES

3 RNA polymerases in eukaryotes:

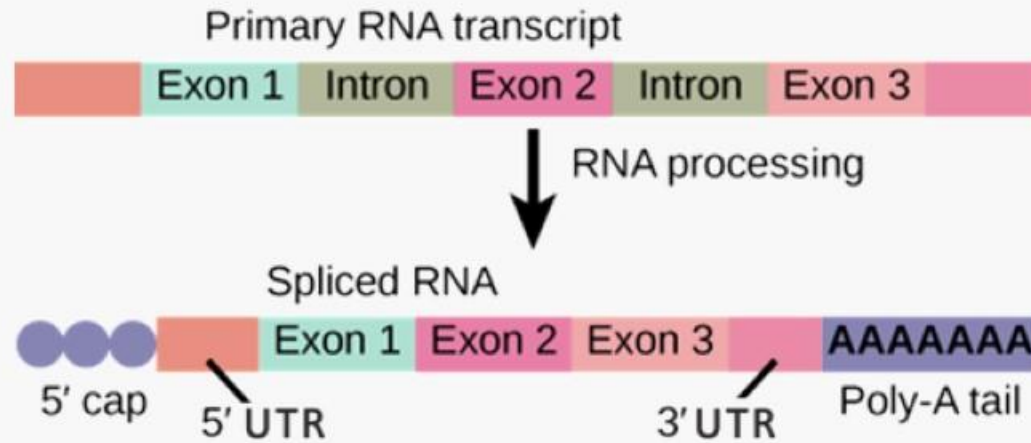
- **RNA polymerase I:** Transcribes **rRNAs** (28S, 18S & 5.8S).
- **RNA polymerase II:** Transcribes the **heterogeneous nuclear RNA (hnRNA)**. It is the precursor of mRNA.
- **RNA polymerase III:** Transcribes **tRNA, 5S rRNA and snRNAs** (small nuclear RNAs).



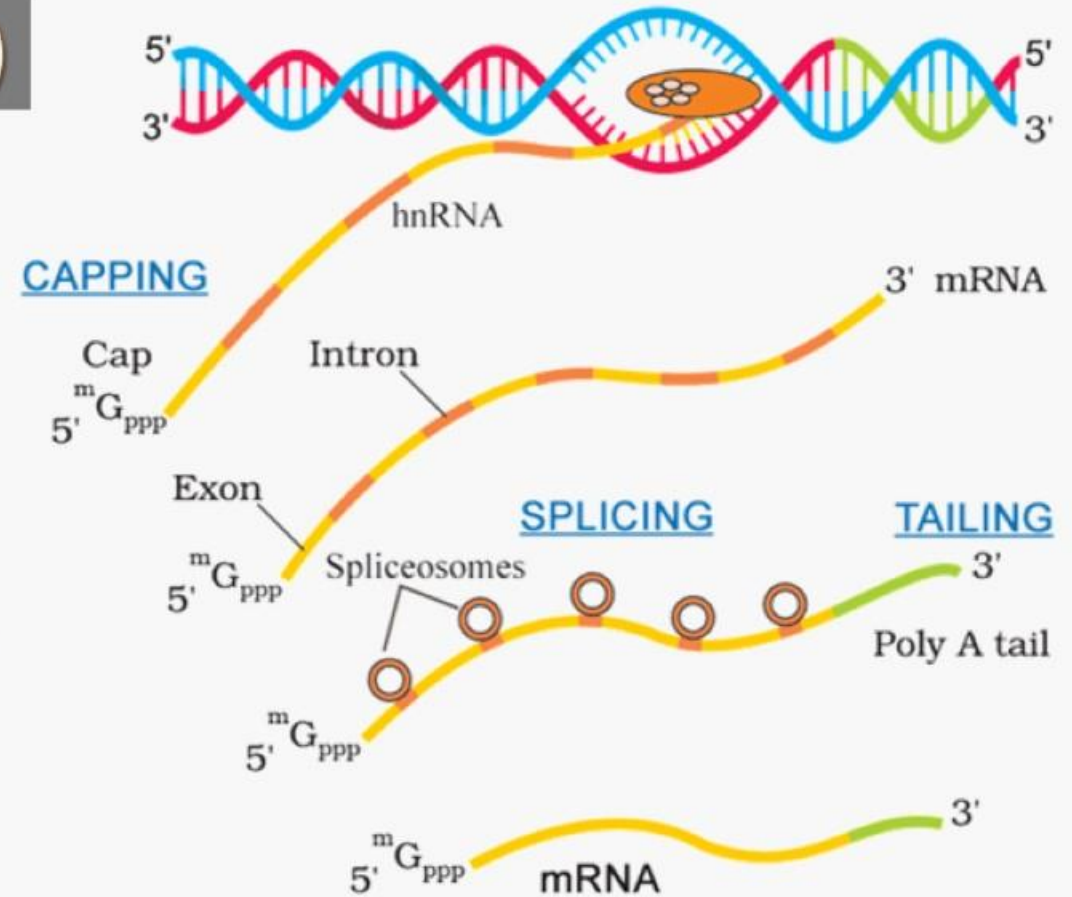
TRANSCRIPTION

TRANSCRIPTION IN EUKARYOTES

Processing of primary transcripts (hnRNA)



1. **Splicing:** From hnRNA, **introns are removed** (by spliceosome) and exons are **spliced** together.
2. **Capping:** Here, a nucleotide **methyl guanosine triphosphate (cap)** is added to 5' end of hnRNA.
3. **Tailing (Polyadenylation):** Here, **adenylate residues (200-300)** are added at 3'-end.



Now, it is the fully processed hnRNA, called mRNA.

GENETIC CODE

- It is the **sequence of nucleotides (nitrogen bases) in mRNA** that contains information for protein synthesis (translation).
- The sequence of 3 bases determining a single amino acid is called **codon**.

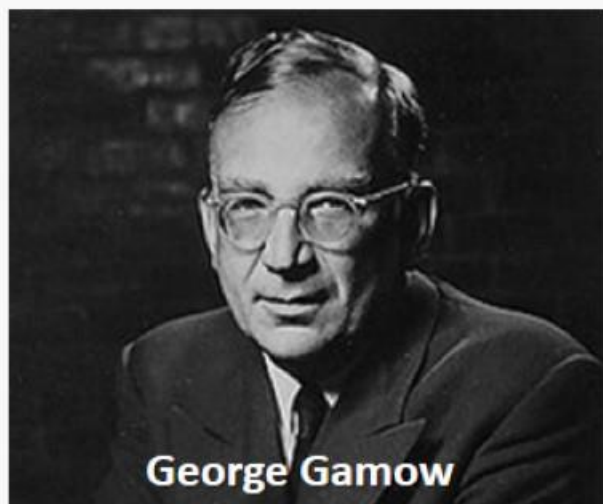
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GENETIC CODE

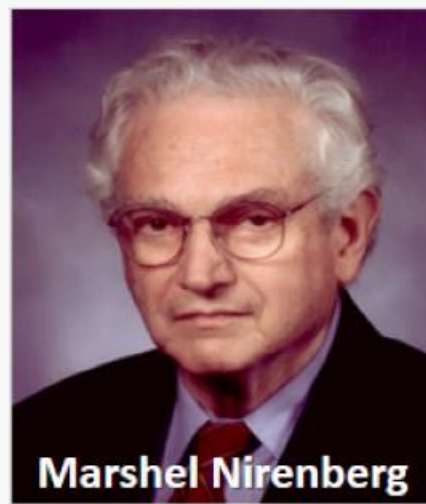
- **George Gamow** suggested that for coding 20 amino acids, the code should be made up of 3 nucleotides. Thus, there are **64 codons** ($4^3 = 4 \times 4 \times 4$).
- **Har Gobind Khorana** developed the chemical method in synthesizing RNA molecules with defined combinations of bases (homopolymers & copolymers).
- **Marshall Nirenberg** developed cell-free system for protein synthesis.
- **Severo Ochoa enzyme** (*polynucleotide phosphorylase*) is used to polymerize RNA with defined sequences in a template independent manner.



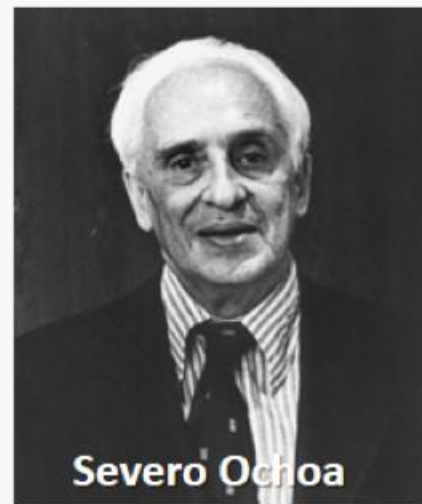
George Gamow



Har Gobind Khorana



Marshall Nirenberg

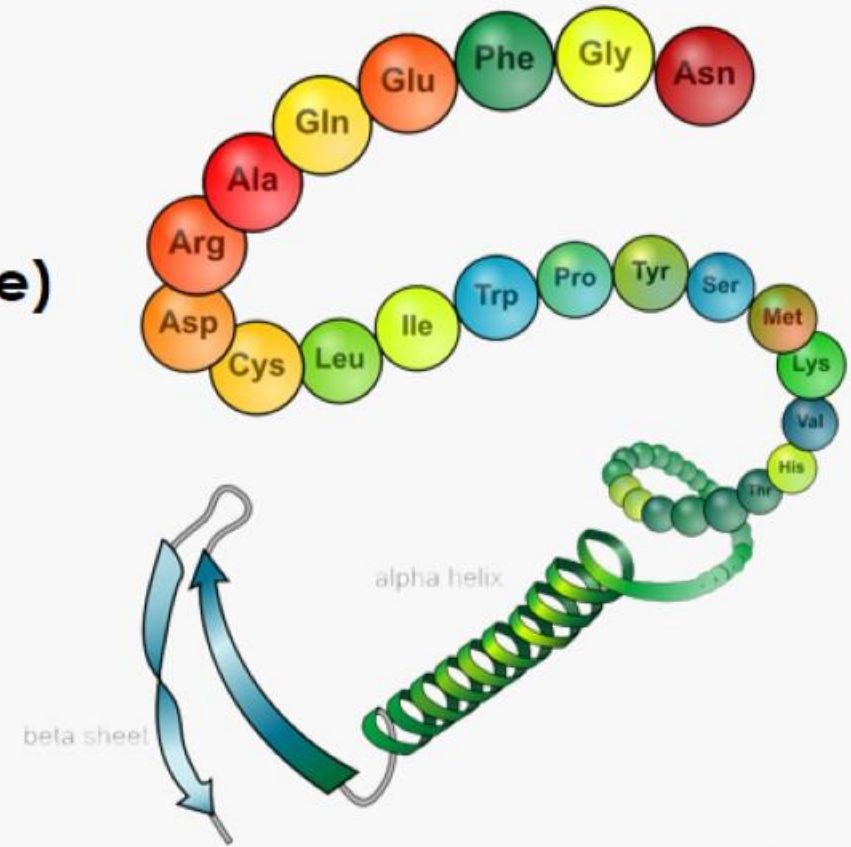


Severo Ochoa

GENETIC CODE

20 types of amino acids involved in translation

- | | |
|------------------------|--------------------------|
| 1. Alanine (ala) | 11. Leucine (leu) |
| 2. Arginine (arg) | 12. Lysine (lys) |
| 3. Asparagine (asn) | 13. Methionine (met) |
| 4. Aspartic acid (asp) | 14. Phenyl alanine (phe) |
| 5. Cystein (cys) | 15. Proline (pro) |
| 6. Glutamine (gln) | 16. Serine (ser) |
| 7. Glutamic acid (glu) | 17. Threonine (thr) |
| 8. Glycine (gly) | 18. Tryptophan (trp) |
| 9. Histidine (his) | 19. Tyrosine (tyr) |
| 10. Isoleucine (iso) | 20. Valine (val) |



GENETIC CODE

CODONS FOR VARIOUS AMINO ACIDS

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THE GENETIC CODE DICTIONARY

	U	C	A	G	
U	UUU Phe UUC phe UUA Leu UUG Leu	UCU Ser UCC Ser UCA Ser UCG Ser	UAU Tyr UAC Tyr UAA Stop UAG Stop	UGU Cys UGC Cys UGA Stop UGG Trp	U C A G
C	CUU Leu CUC Leu CUA Leu CUG Leu	CCU Pro CCC Pro CCA Pro CCG Pro	CAU His CAC His CAA Gln CAG Gln	CGU Arg CGC Arg CGA Arg CGG Arg	U C A G
A	AUU Ile AUC Ile AUA Ile AUG Met	ACU Thr ACC Thr ACA Thr ACG Thr	AAU Asn AAC Asn AAA Lys AAG Lys	AGU Ser AGC Ser AGA Arg AGG Arg	U C A G
G	GUU Val GUC Val GUA Val GUG Val	GCU Ala GCC Ala GCA Ala GCG Ala	GAU Asp GAC Asp GAA Glu GAG Glu	GGU Gly GGC Gly GGA Gly GGG Gly	U C A G

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GENETIC CODE

SALIENT FEATURES OF GENETIC CODE

- **Codon is triplet** (three-letter code).
- 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).
- AUG has dual functions. It codes for Methionine and acts as **initiator codon**. In eukaryotes, **methionine** is the first amino acid and **formyl methionine** in prokaryotes.
- An amino acid is coded by many codons (except AUG for methionine & UGG for tryptophan). Such codons are called **degenerate codons**.



GENETIC CODE

SALIENT FEATURES OF GENETIC CODE

- **No punctuations** b/w adjacent codons (comma less code). The codon is read in mRNA in a contiguous fashion.
- 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.
- Genetic code is **non-overlapping**.
- Genetic code is **unambiguous & specific**. i.e. one codon specifies only one amino acid.

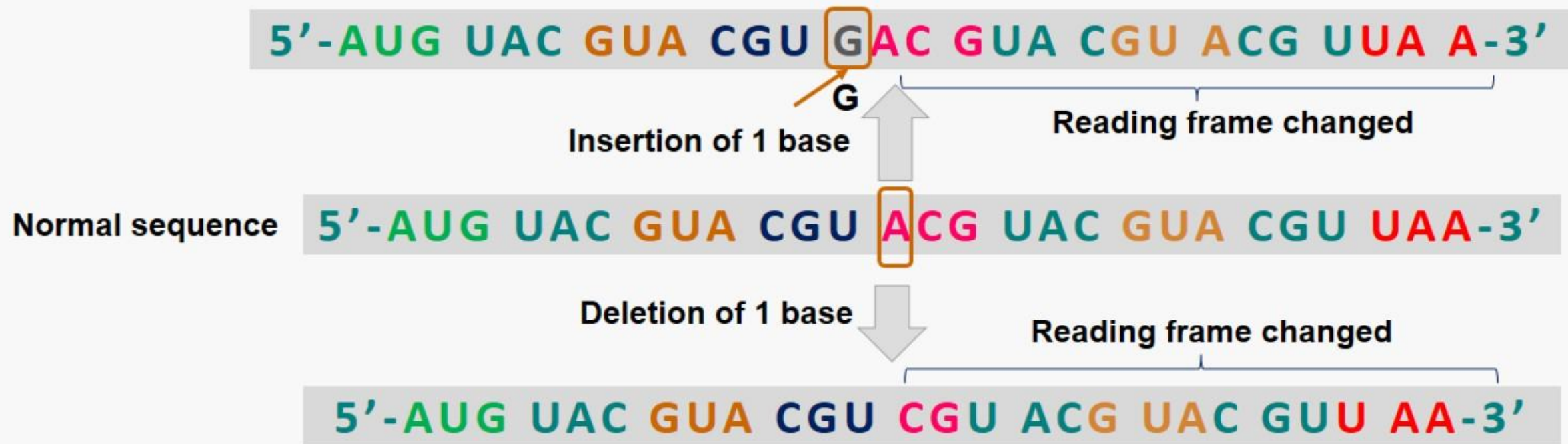
No base ("comma") b/w adjacent codons



GENETIC CODE

MUTATION 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. It is called **frame-shift insertion or deletion mutations**.

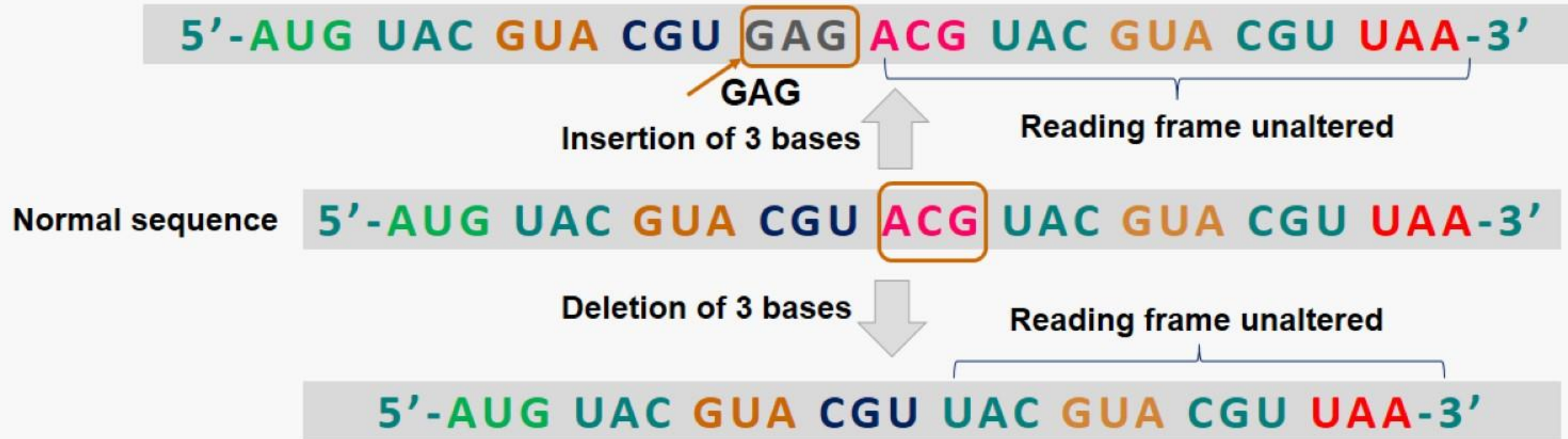


GENETIC CODE

MUTATION AND GENETIC CODE

- Insertion/ deletion of **three or its multiple bases** insert or delete one or multiple codon. The reading frame remains unaltered from that point onwards. Hence one or multiple amino acids are inserted /deleted.
- It proves that codon is a triplet and is read contiguously.

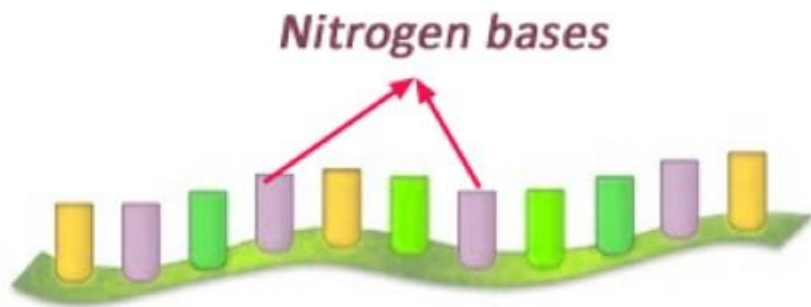
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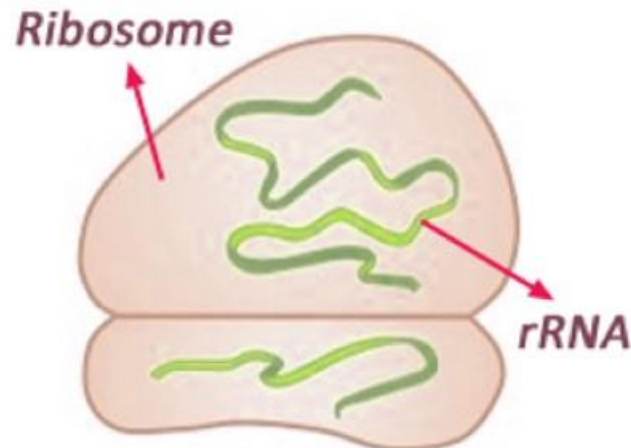
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TYPES OF RNA

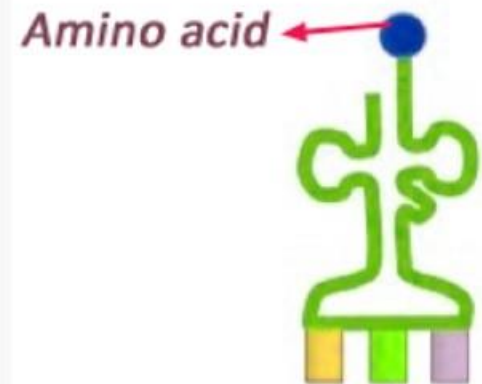
- **mRNA (messenger RNA):** Provide template for translation (protein synthesis).
- **rRNA (ribosomal RNA):** Structural & catalytic role during translation. E.g. 23S rRNA in bacteria acts as ribozyme.
- **tRNA (transfer RNA or sRNA or soluble RNA):** Brings amino acids for protein synthesis and reads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



Messenger RNA (mRNA)



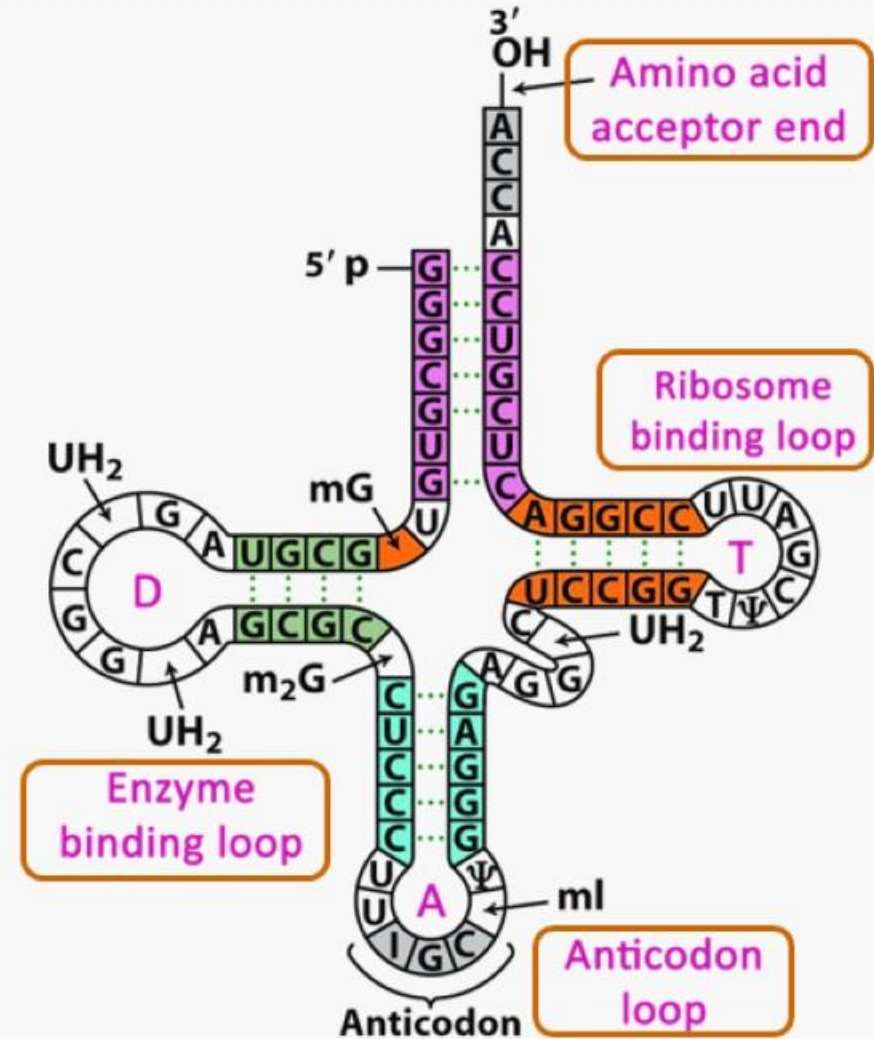
Ribosomal RNA (rRNA)



Transfer RNA (tRNA)

TYPES OF RNA

- **Francis Crick** postulated presence of an adapter molecule that can read the code and to link with amino acids.
- tRNA is called **adapter molecule** because it has
 - **An Anticodon (NODOC) loop** that has bases complementary to the codon.
 - **An amino acid acceptor end** to which amino acid binds.
 - **Ribosome binding loop.**
 - **Enzyme binding loop.**

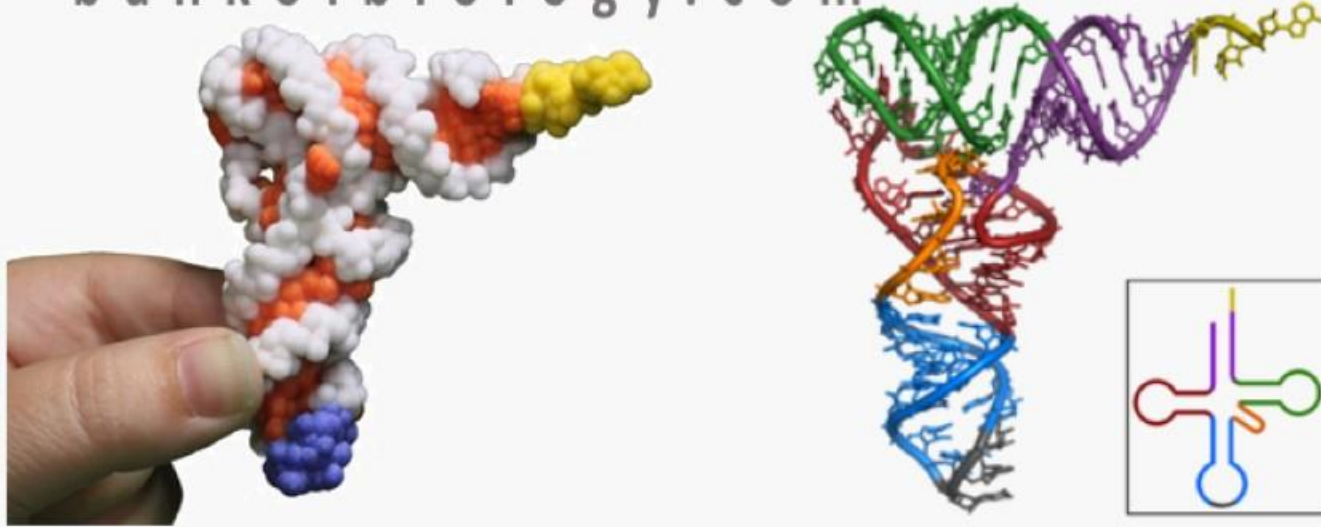


Clover leaf model of tRNA

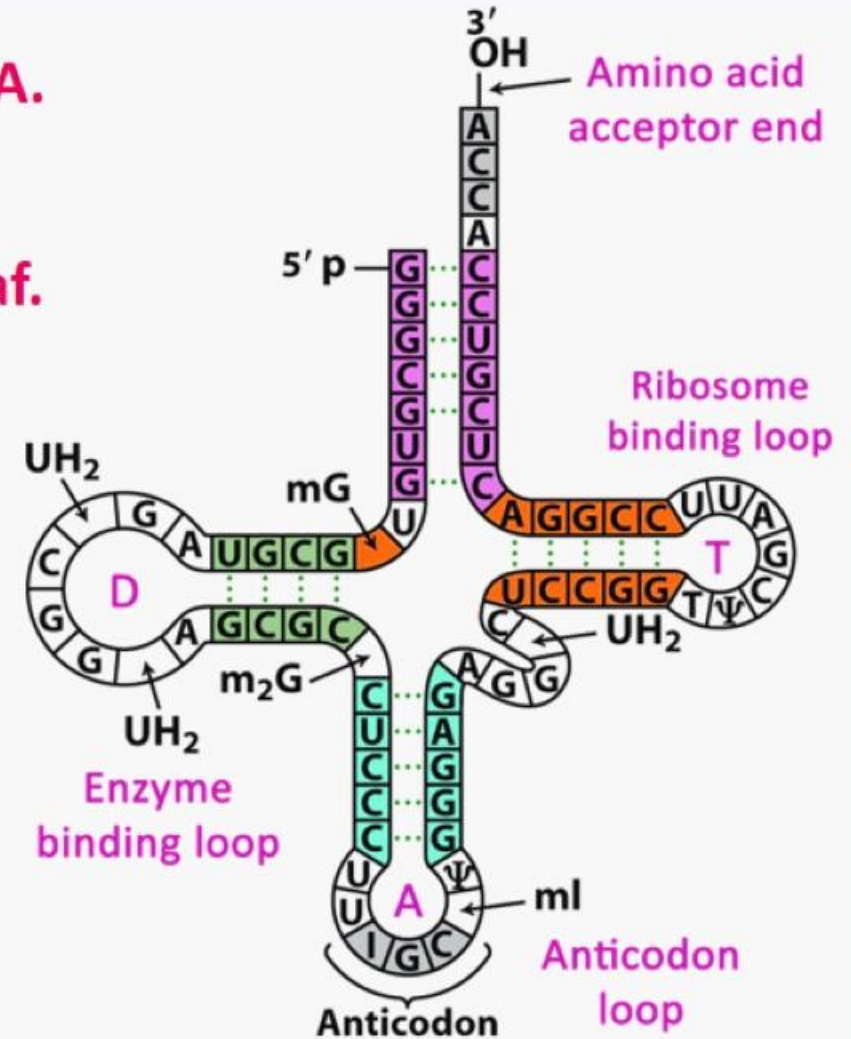
TYPES OF RNA

- 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 **clover-leaf**.
- **3-D structure** looks like **inverted 'L'**.

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3D model of tRNA

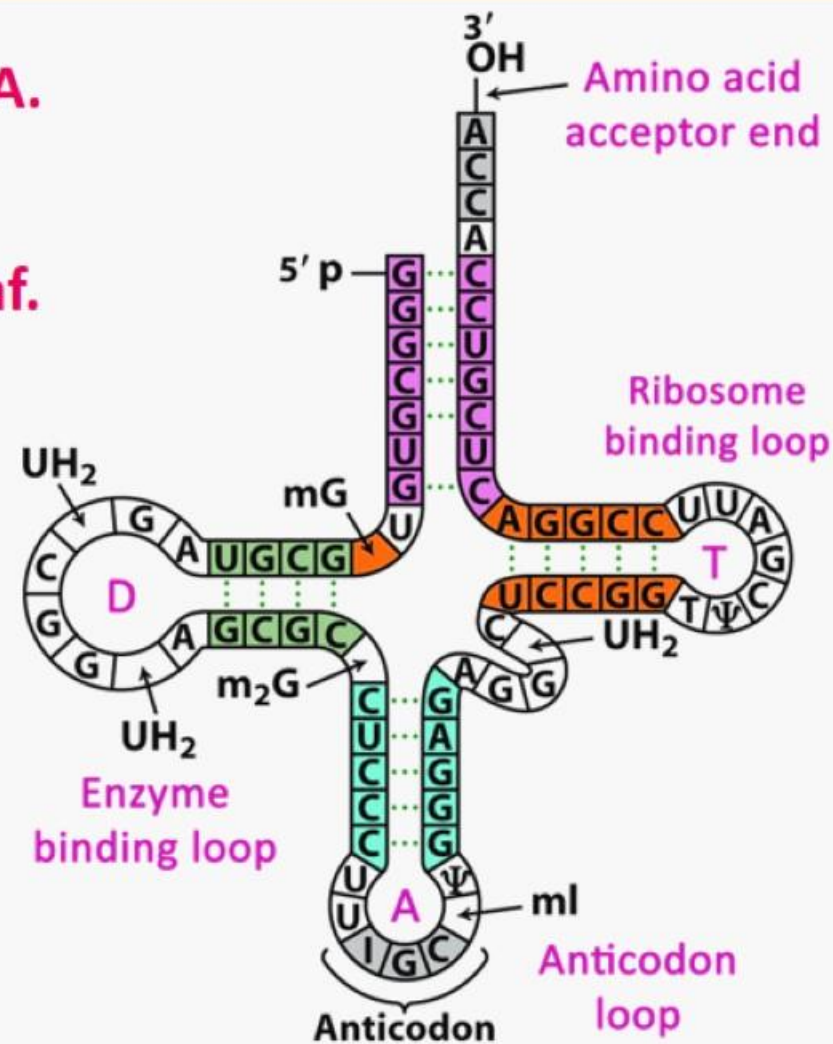
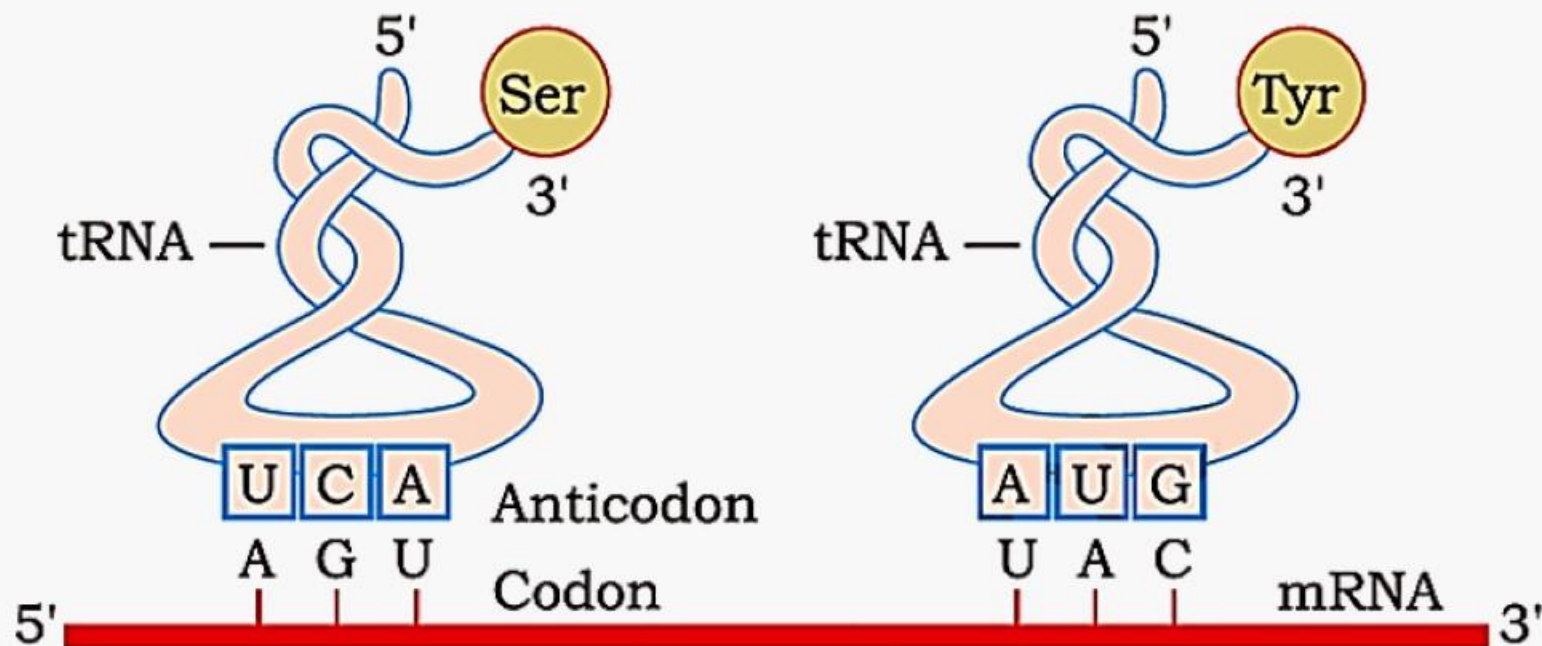


Clover leaf model of tRNA

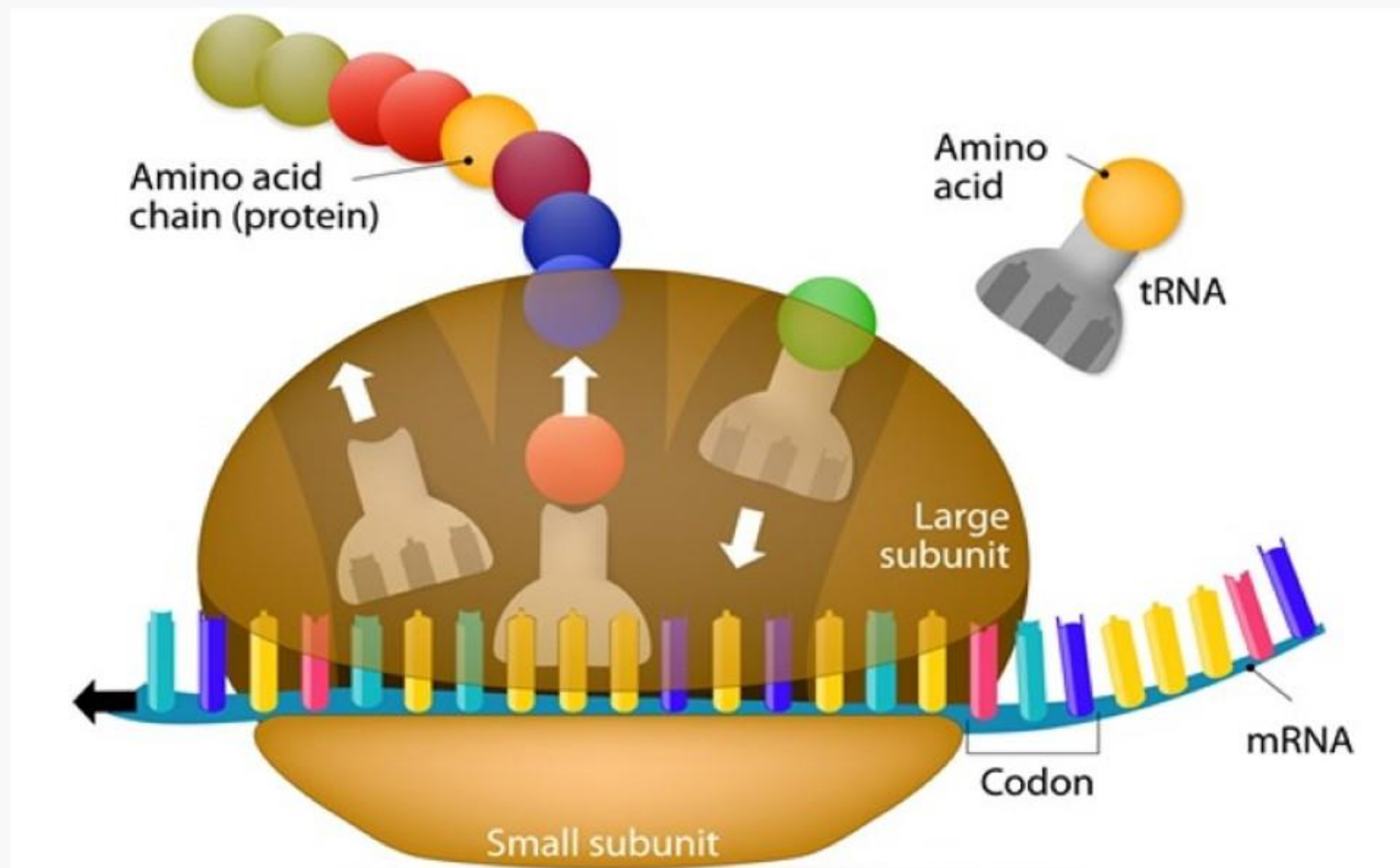
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TYPES OF RNA

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Clover leaf model of tRNA

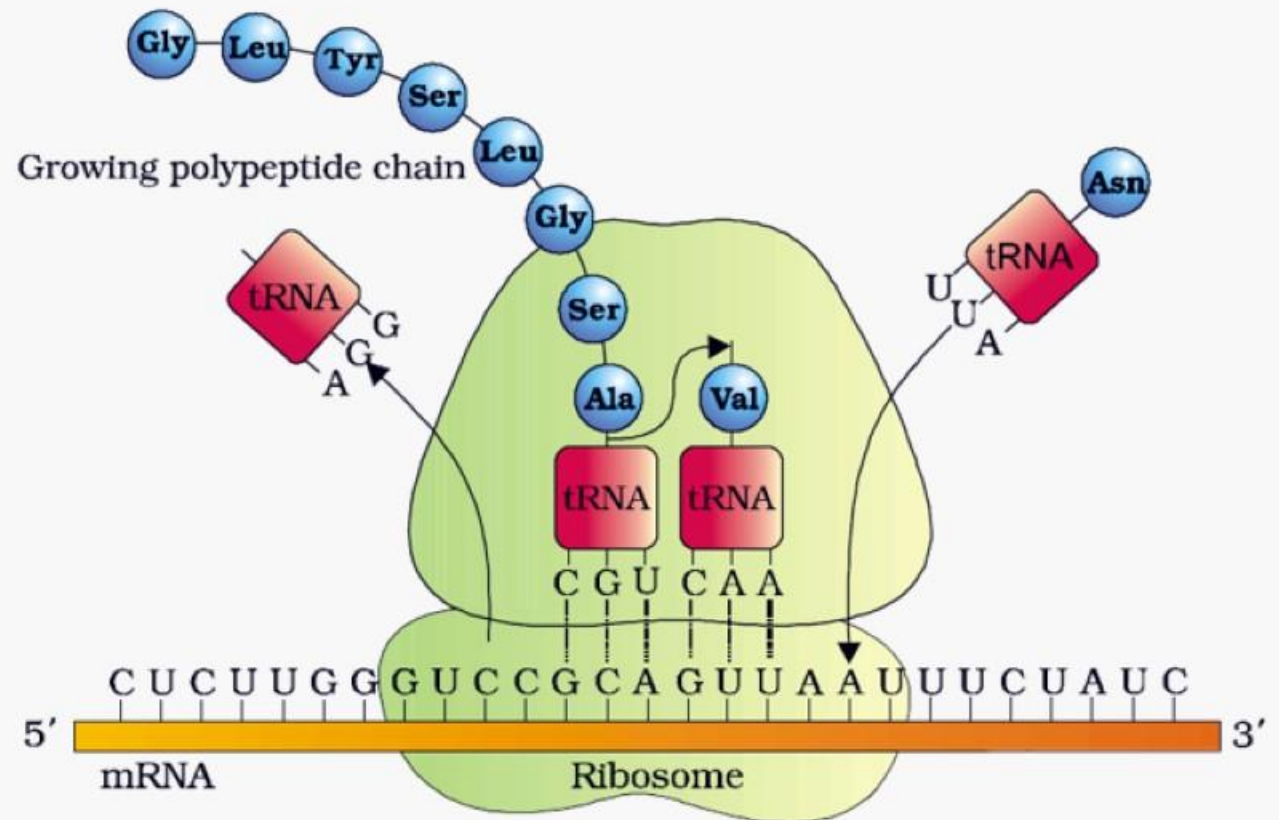


TRANSLATION

TRANSLATION (PROTEIN SYNTHESIS)

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- It is the process of **polymerisation of amino acids** to form a polypeptide based on the sequence of codons in mRNA.
- It takes place in **ribosomes**.
- Ribosome consists of structural RNAs and about 80 types of proteins.
- Ribosome also acts as a catalyst (**23S rRNA** in bacteria is the enzyme-**ribozyme**) for the formation of peptide bond (**peptidyl transferase** enzyme in large subunit of ribosome).



TRANSLATION (PROTEIN SYNTHESIS)

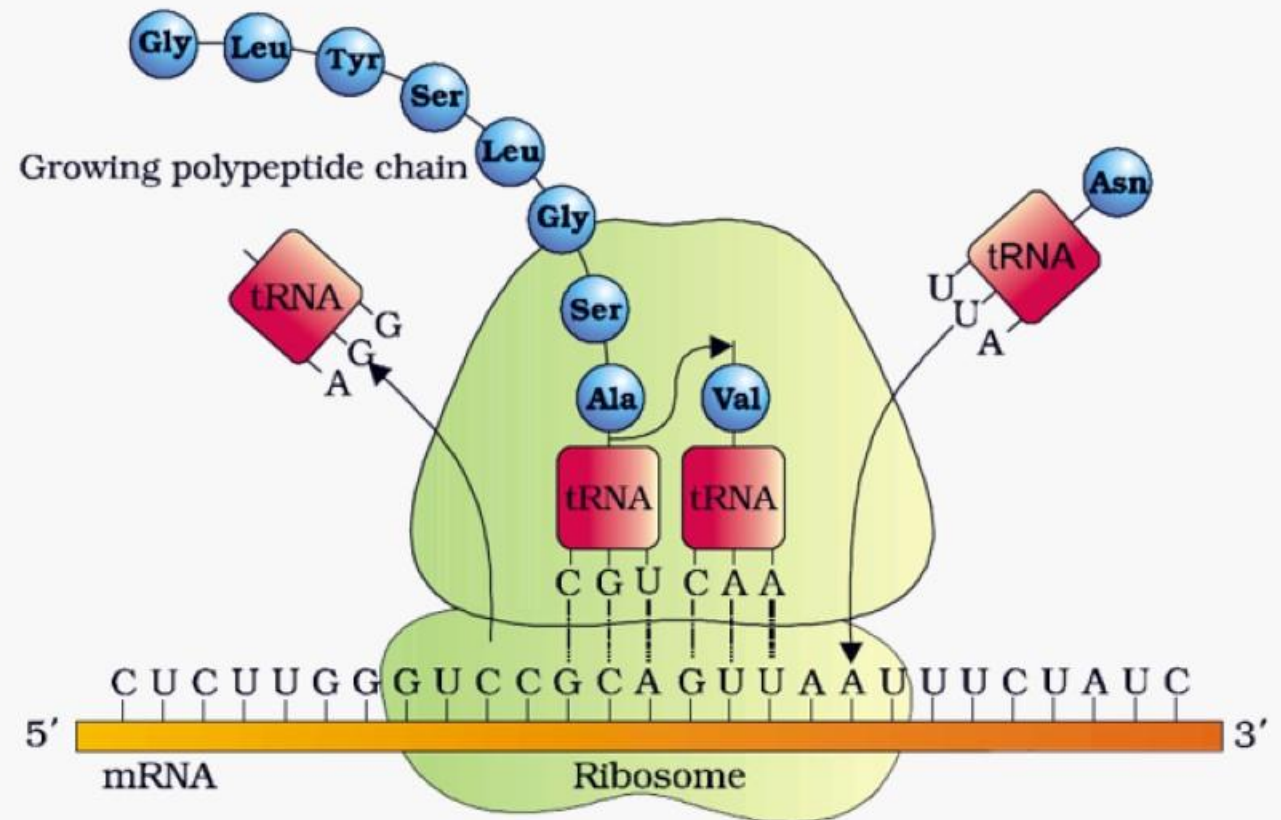
Steps of Translation

CHARGING OF tRNA

INITIATION

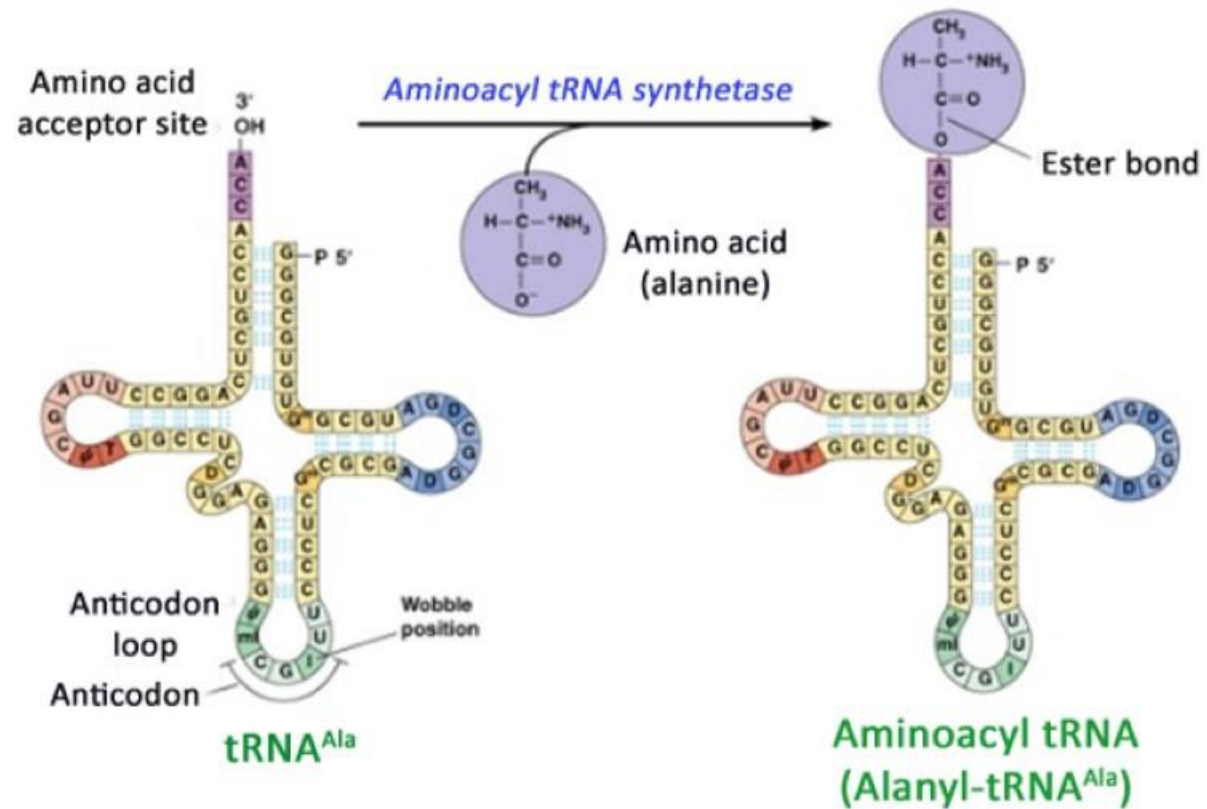
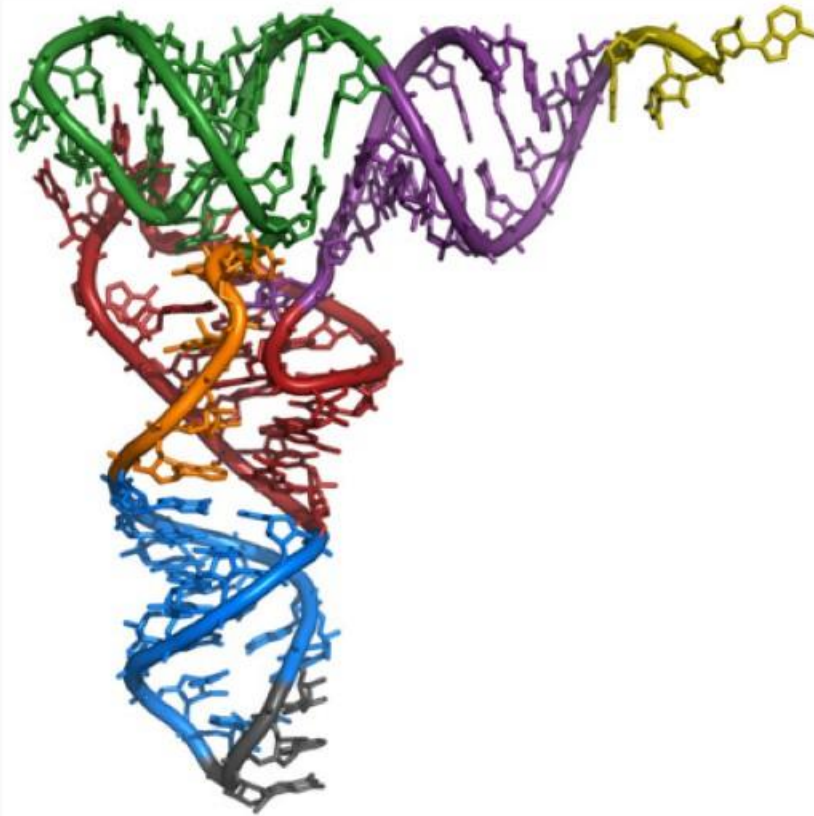
ELONGATION

TERMINATION



TRANSLATION

1. CHARGING (AMINOACYLATION) OF tRNA

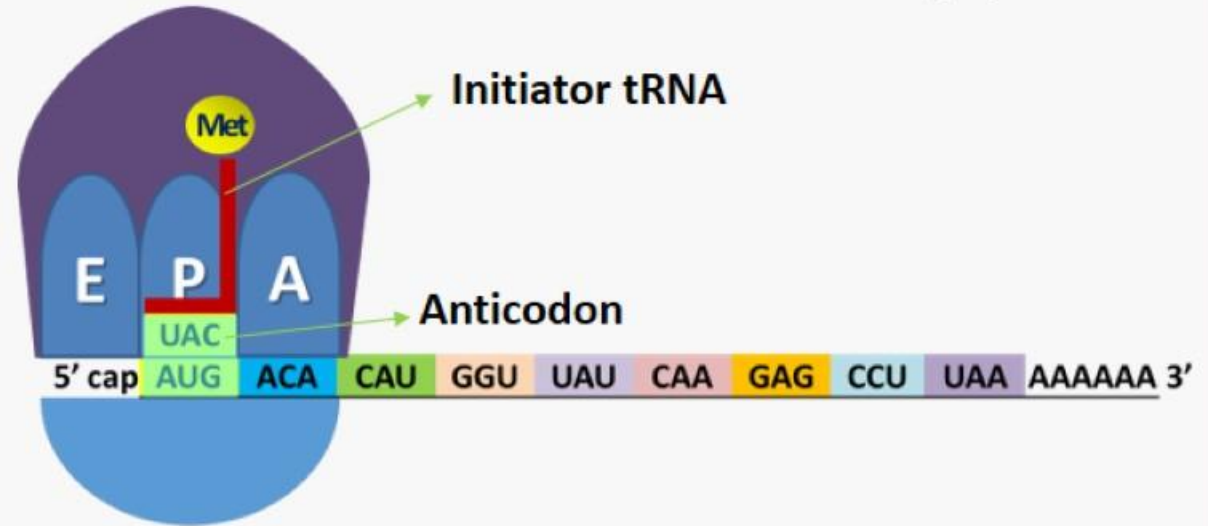
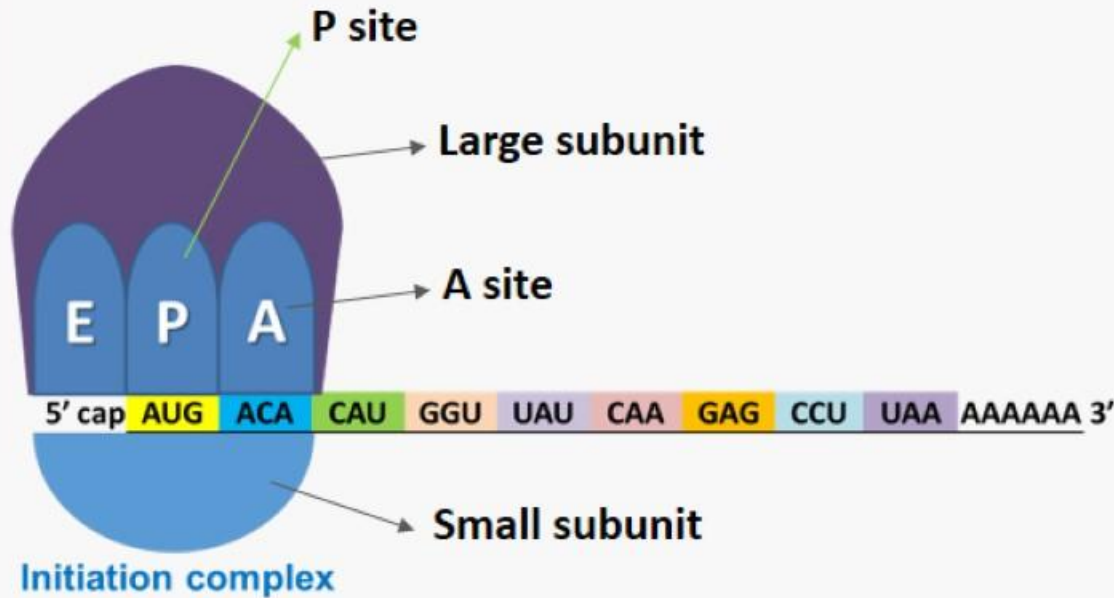


- Formation of **peptide bond** needs energy obtained from **ATP**.
- For this, amino acids are activated (**amino acid + ATP**) and linked to their cognate tRNA in presence of **aminoacyl tRNA synthetase**. Thus, the tRNA becomes charged.

TRANSLATION

2. INITIATION

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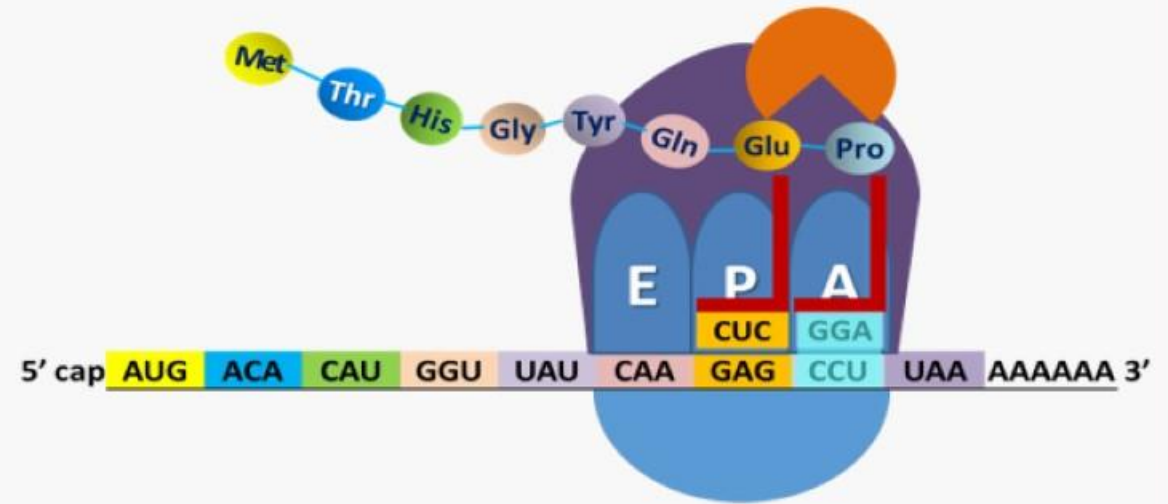
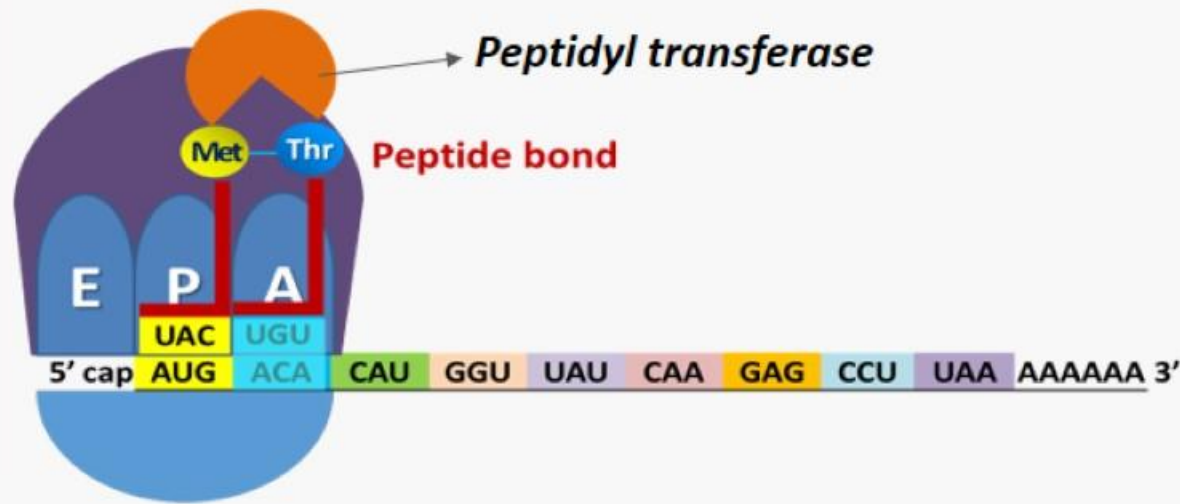


- In this, small subunit of ribosome binds to mRNA at the **start codon (AUG)**.
- Now large subunit binds to small subunit to form **initiation complex**.
- Large subunit consists of **aminoacyl tRNA binding site (A site)** and **peptidyl site (P site)**.
- The **initiator tRNA** (which carries methionine) binds on P site. Its **anticodon (UAC)** recognizes start codon **AUG**.

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TRANSLATION

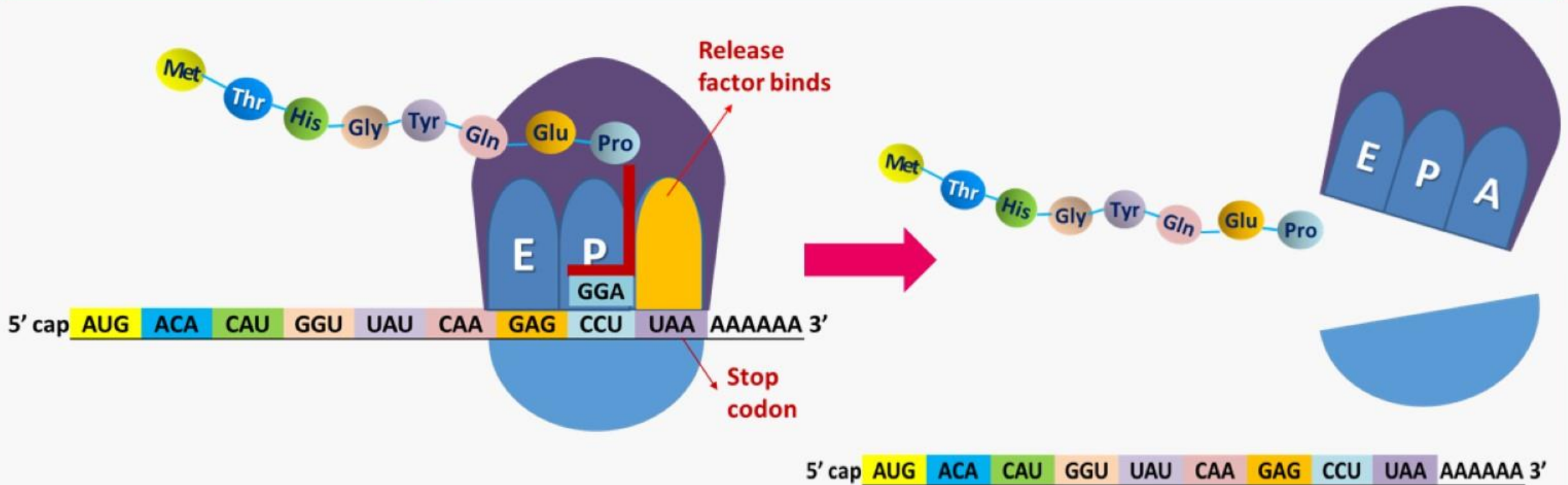
3. ELONGATION



- Second aminoacyl tRNA binds to the A site of ribosome. 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 **peptidyl transferase**.
- First amino acid and its tRNA are broken. This tRNA is removed from P site and second tRNA from A site is pulled to P site along with mRNA. This is called **translocation**.
- These processes are repeated for other codons in mRNA.
- During translation, **ribosome moves from codon to codon**.

TRANSLATION

4. TERMINATION

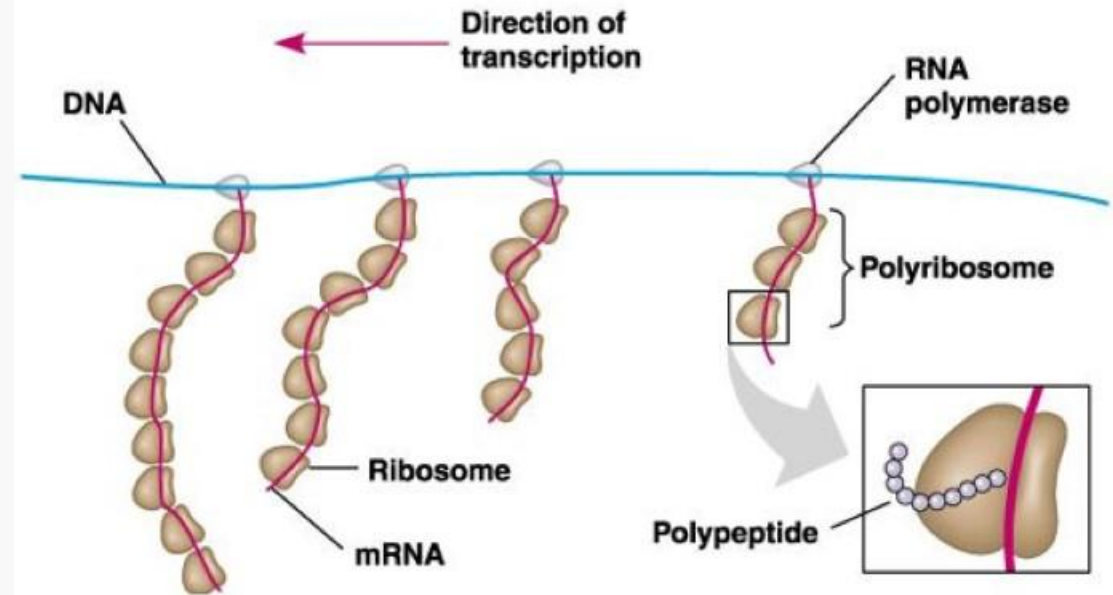


- When a **release factor** binds to the **stop codon**, the translation terminates.
- The **polypeptide** and tRNA are released from the ribosomes.
- The ribosome dissociates into large and small subunits.

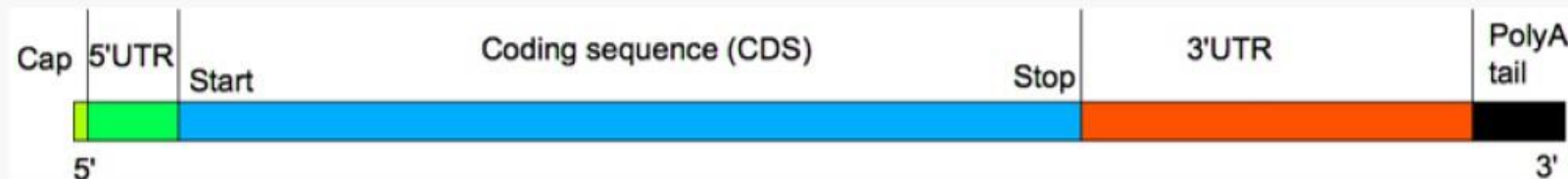
TRANSLATION

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- A group of ribosomes associated with a single mRNA for translation is called a **polyribosome (polysomes)**.

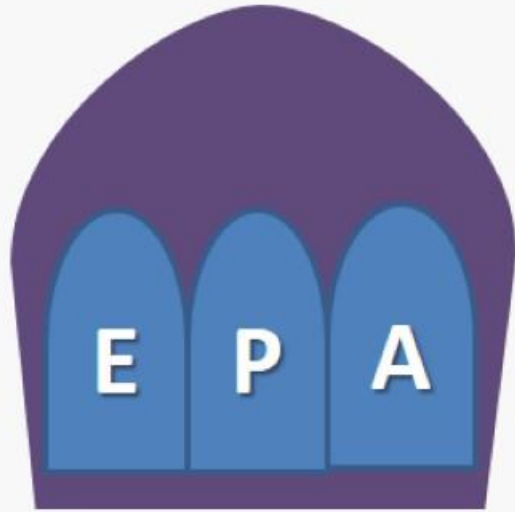


- An mRNA has additional sequences that are not translated (**untranslated regions or UTR**). UTRs are present at both 5'-end (before start codon) and 3'-end (after stop codon). They are required for efficient translation process.

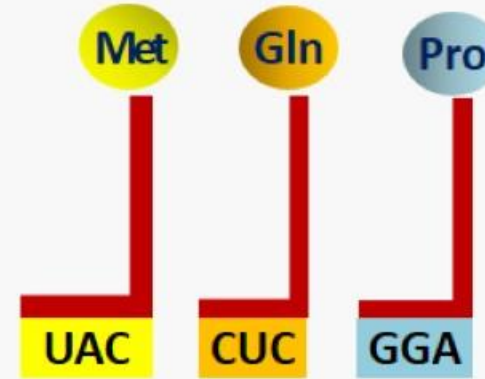


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TRANSLATION IN ACTION



Ribosome
Large
subunit



tRNAs

5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'

mRNA



Ribosome
Small
subunit

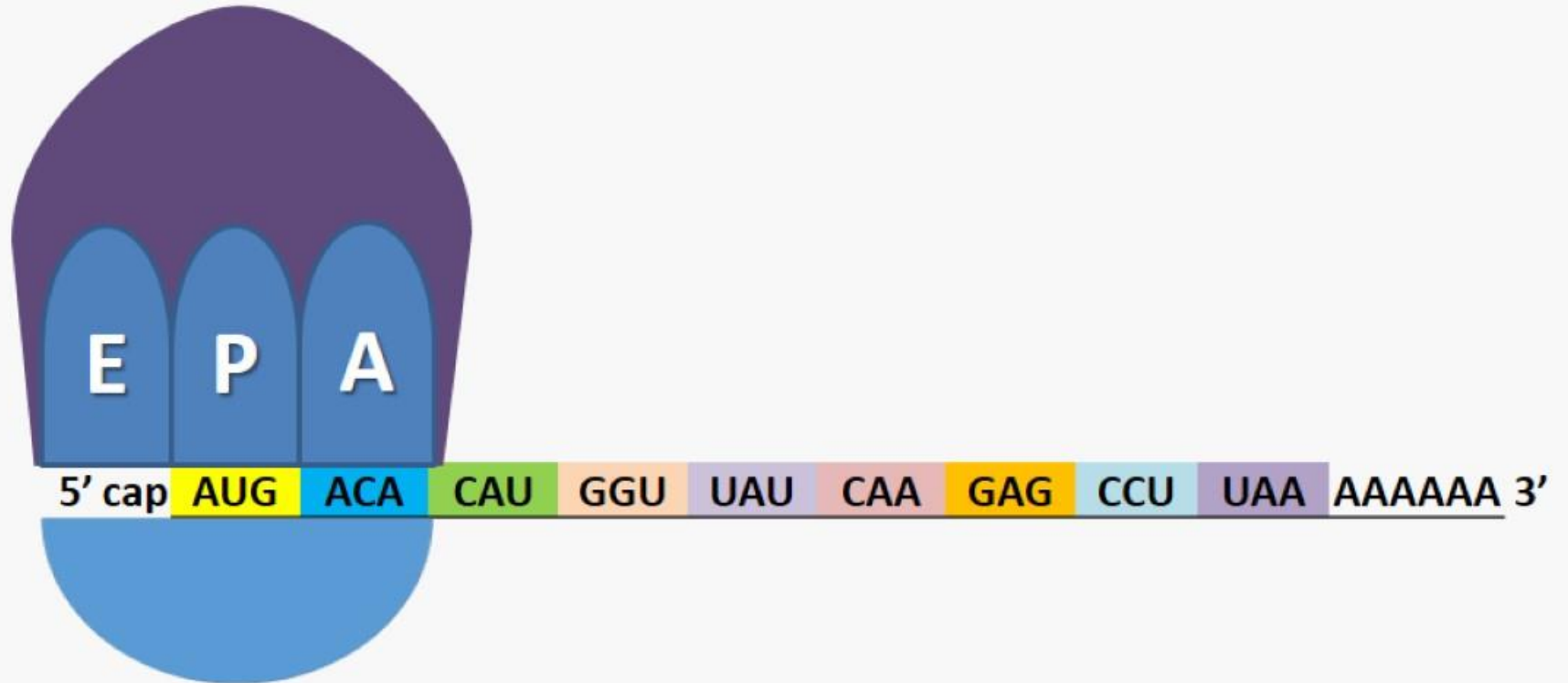
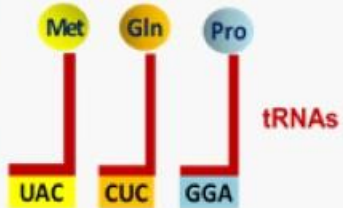
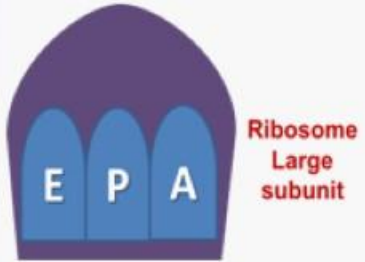


*Peptidyl
transferase*

TRANSLATION IN ACTION

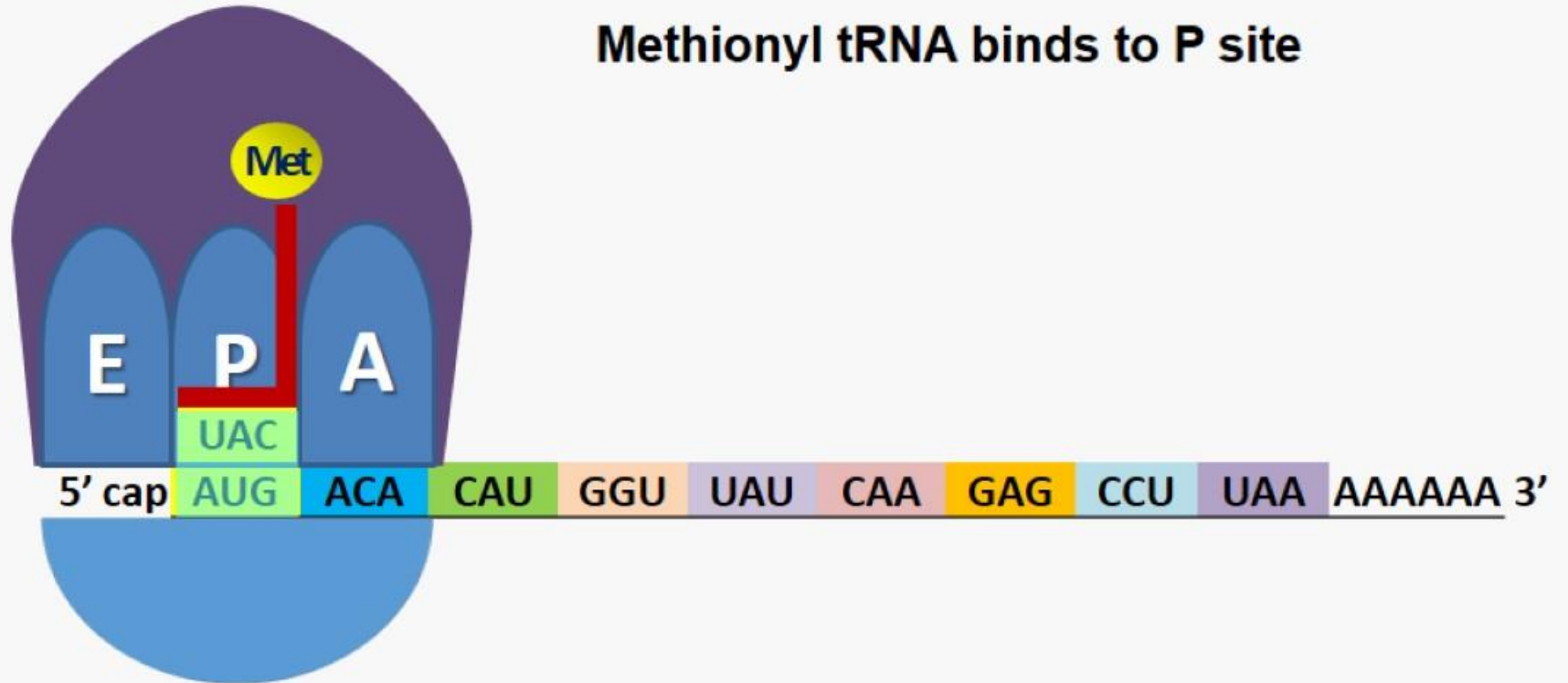
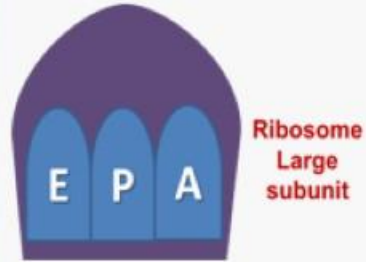
5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'
mRNA

1. Initiation



TRANSLATION IN ACTION

5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'
mRNA

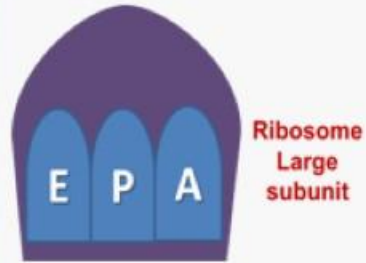


1. Initiation

Methionyl tRNA binds to P site

TRANSLATION IN ACTION

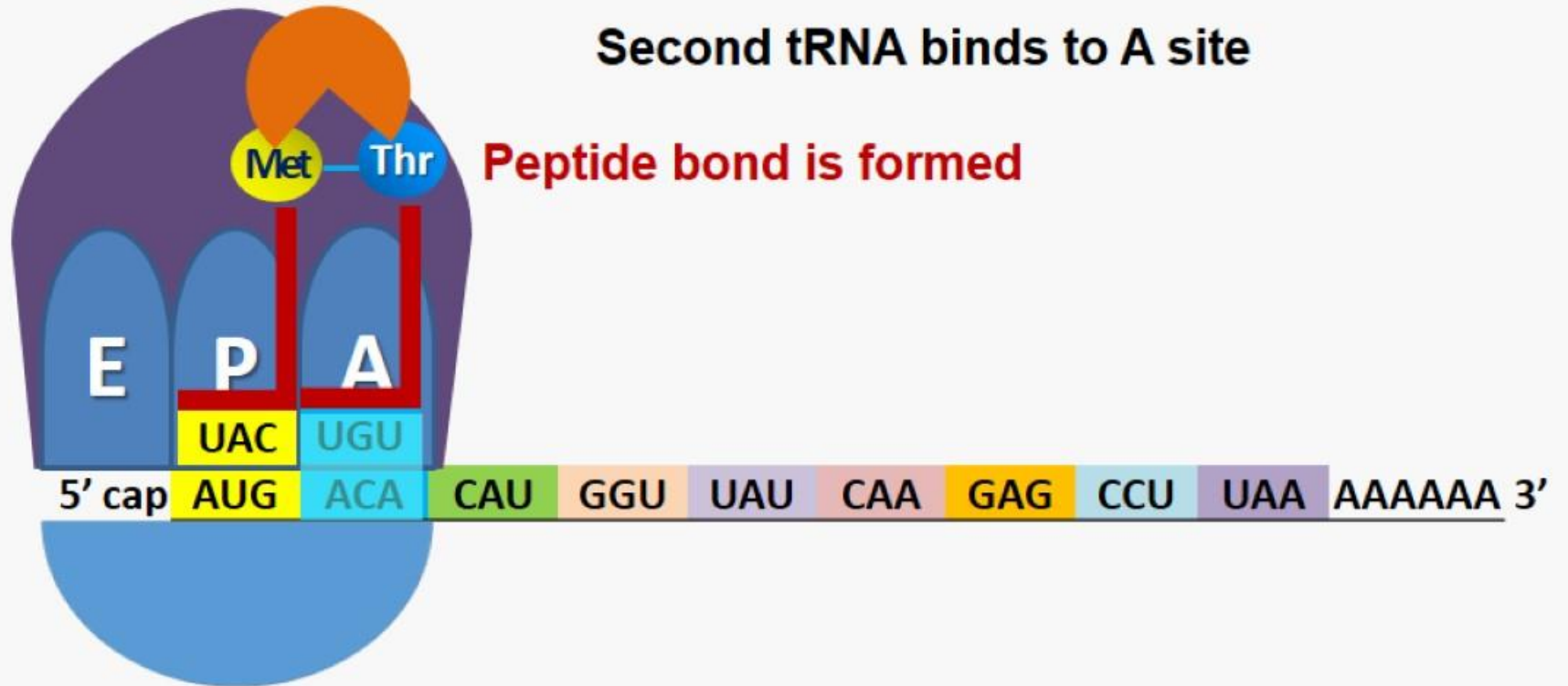
5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'
mRNA



2. Elongation

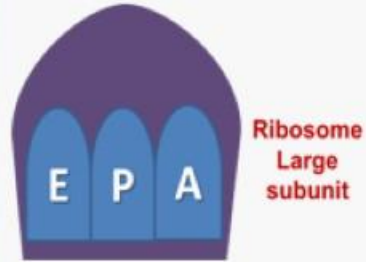
Second tRNA binds to A site

Peptide bond is formed



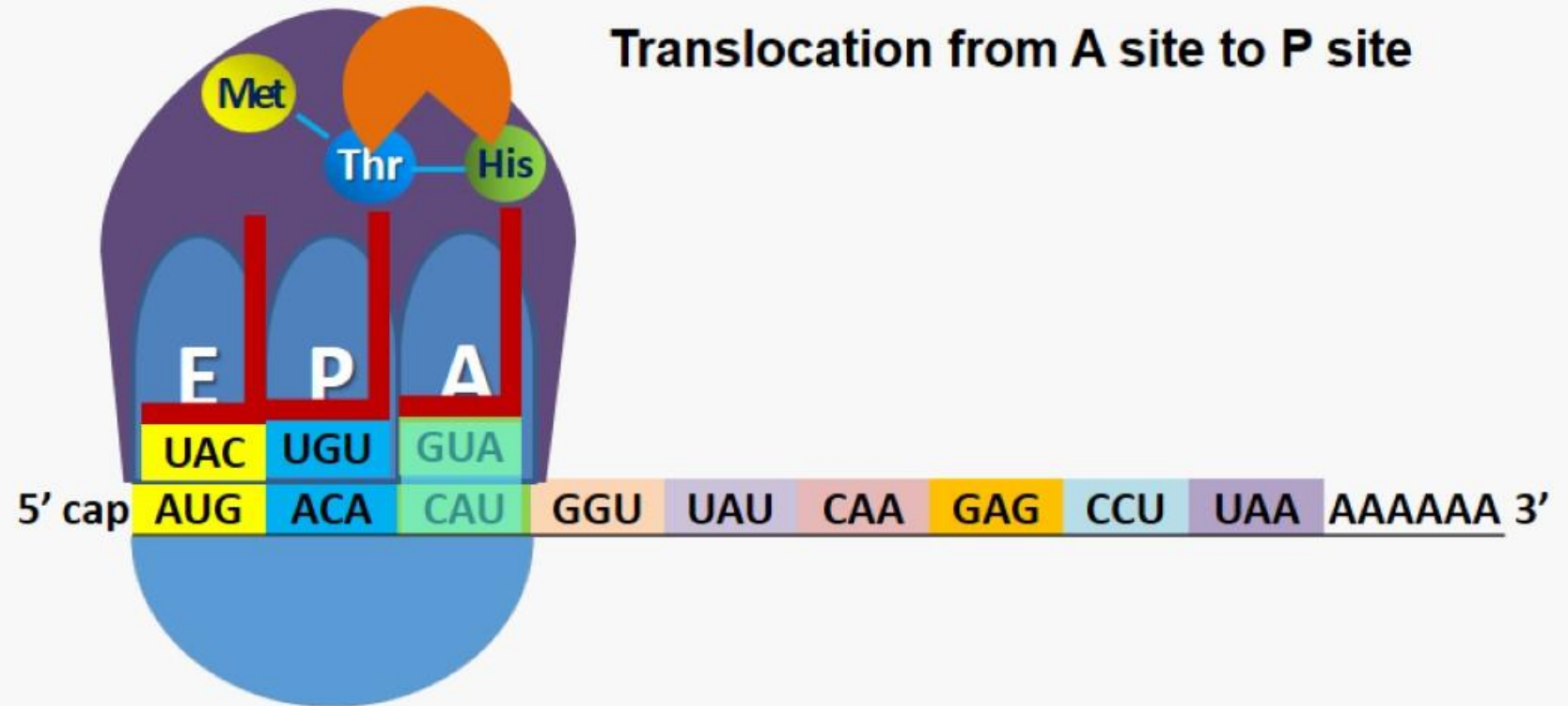
TRANSLATION IN ACTION

5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'
mRNA



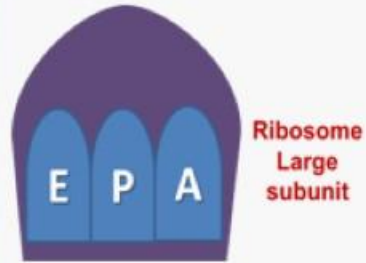
2. Elongation

Translocation from A site to P site

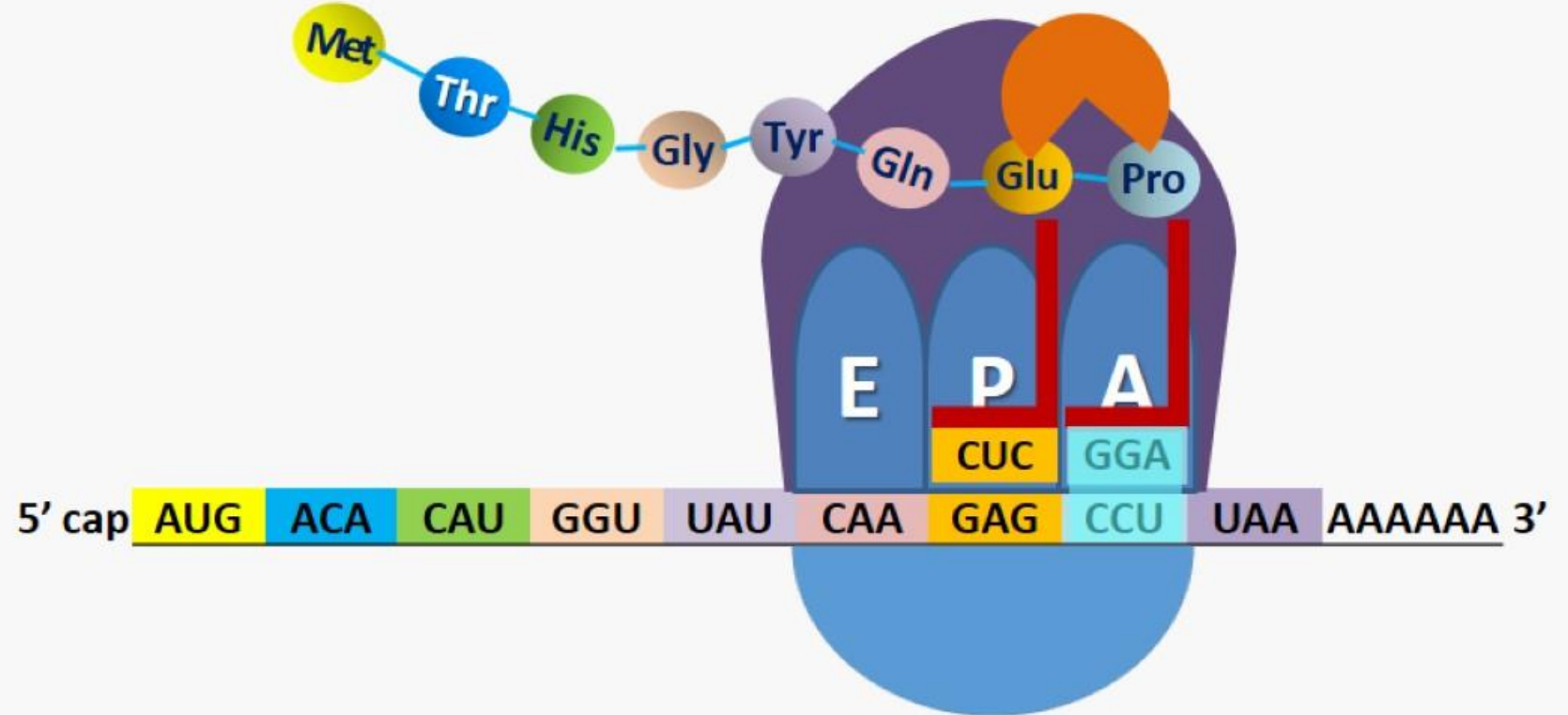


TRANSLATION IN ACTION

5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'
mRNA

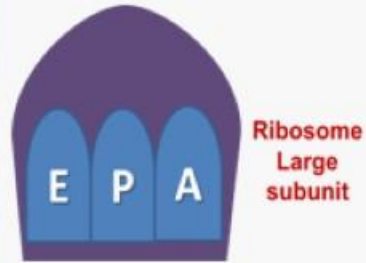


2. Elongation

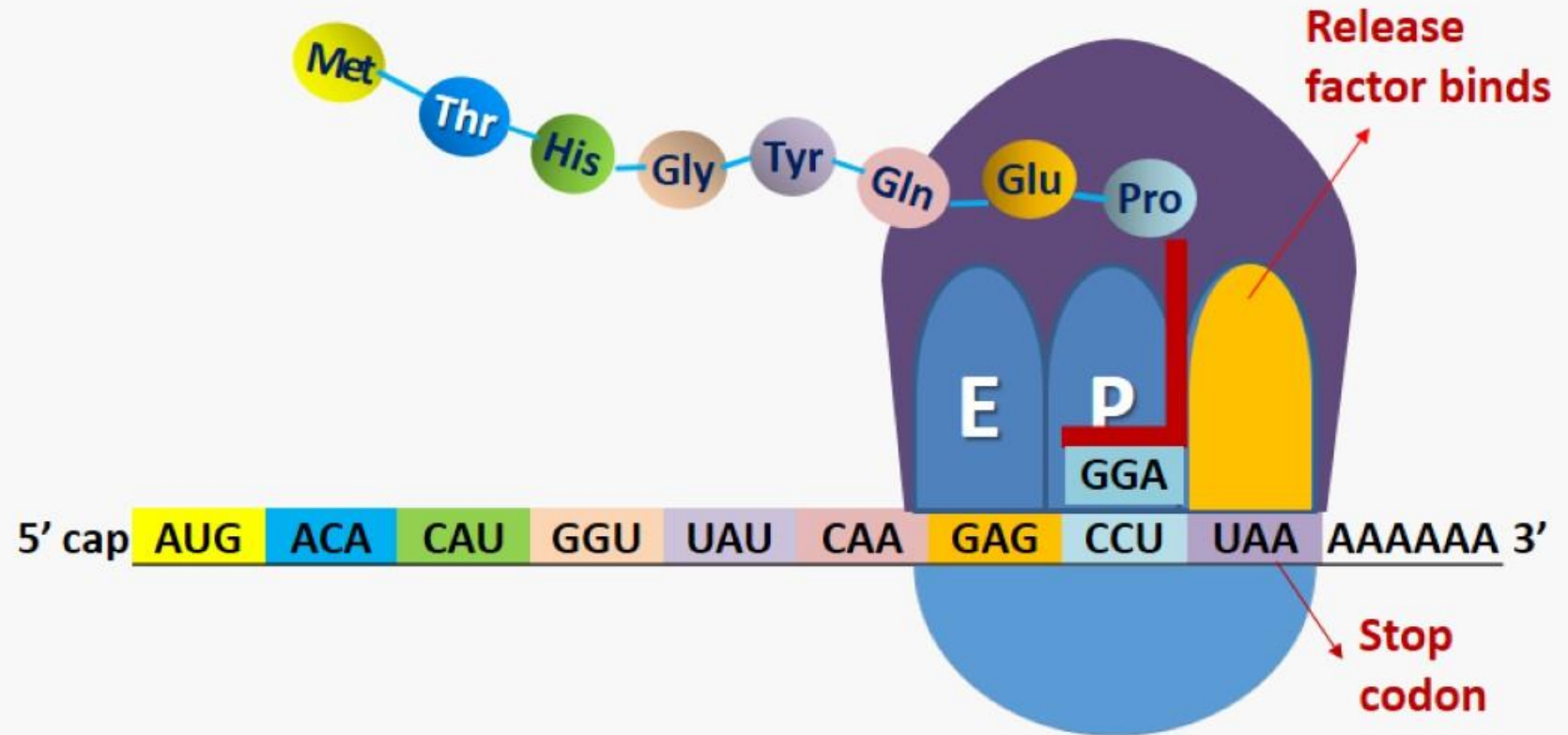


TRANSLATION IN ACTION

5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'
mRNA

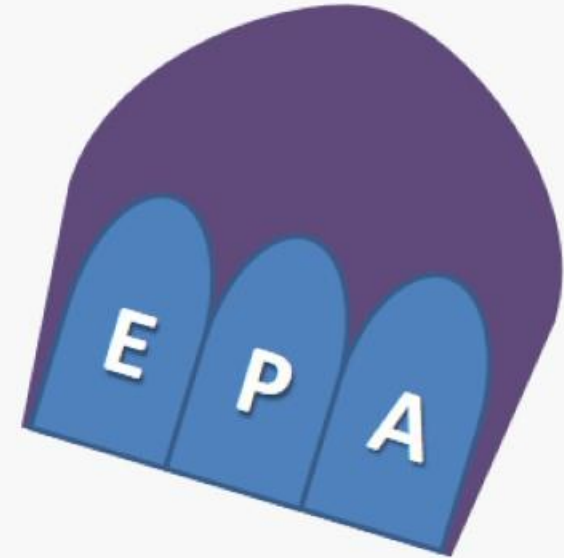
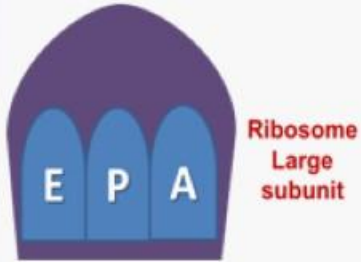


3. Termination



TRANSLATION IN ACTION

5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'
mRNA



5' cap AUG ACA CAU GGU UAU CAA GAG CCU UAA AAAAAA 3'





REGULATION OF GENE EXPRESSION

REGULATION OF GENE EXPRESSION

- In eukaryotes, gene expression occurs by following levels:

1. Transcriptional level (formation of primary transcript).

2. Processing level (splicing, capping etc.).

3. Transport of mRNA from nucleus to the cytoplasm.

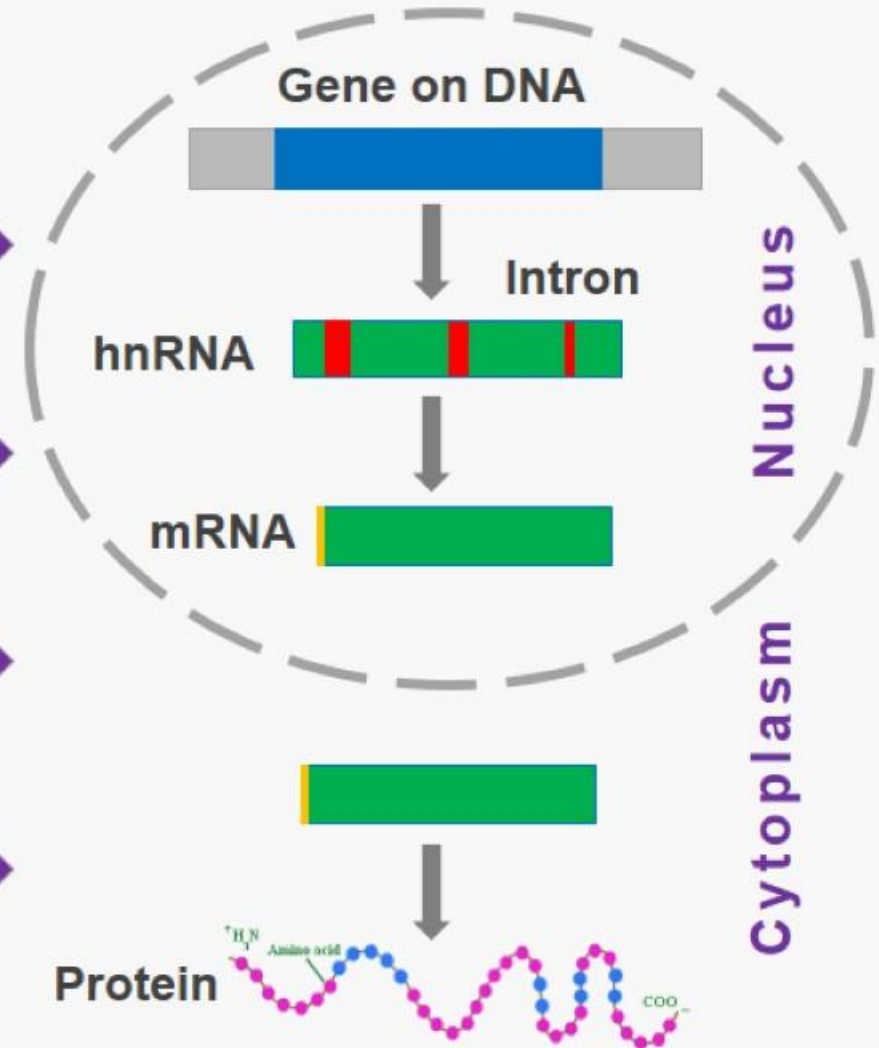
4. Translational level (formation of a polypeptide).

Transcriptional level

Processing level

mRNA transport

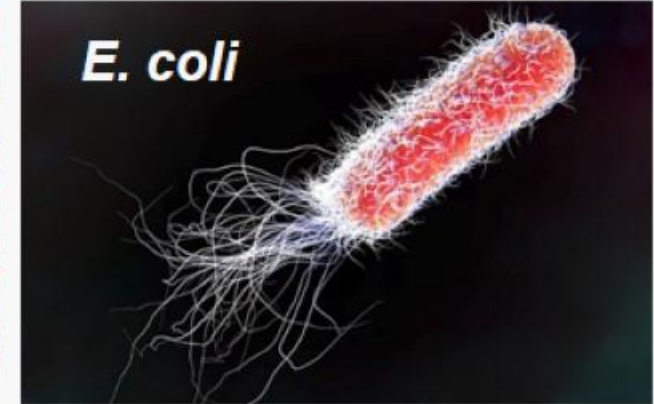
Translational level



REGULATION OF GENE EXPRESSION

The **metabolic, physiological and environmental conditions** regulate the gene expression. E.g.

- ✓ In *E. coli*, the **beta-galactosidase** enzyme hydrolyses **lactose** into galactose and 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 expression of several set of genes.



REGULATION OF GENE EXPRESSION

- 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**.

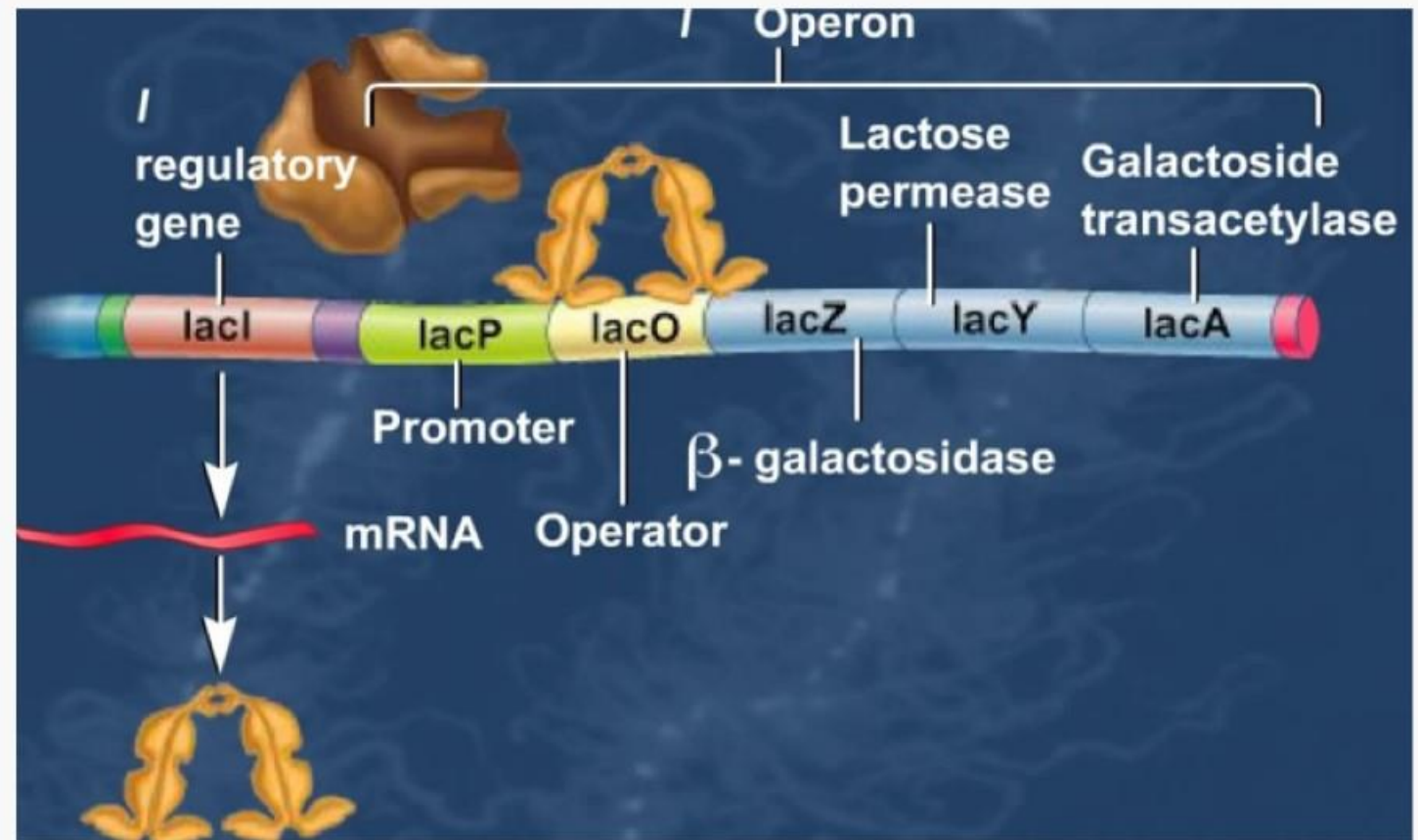


E. Coli growth medium

REGULATION OF GENE EXPRESSION

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.



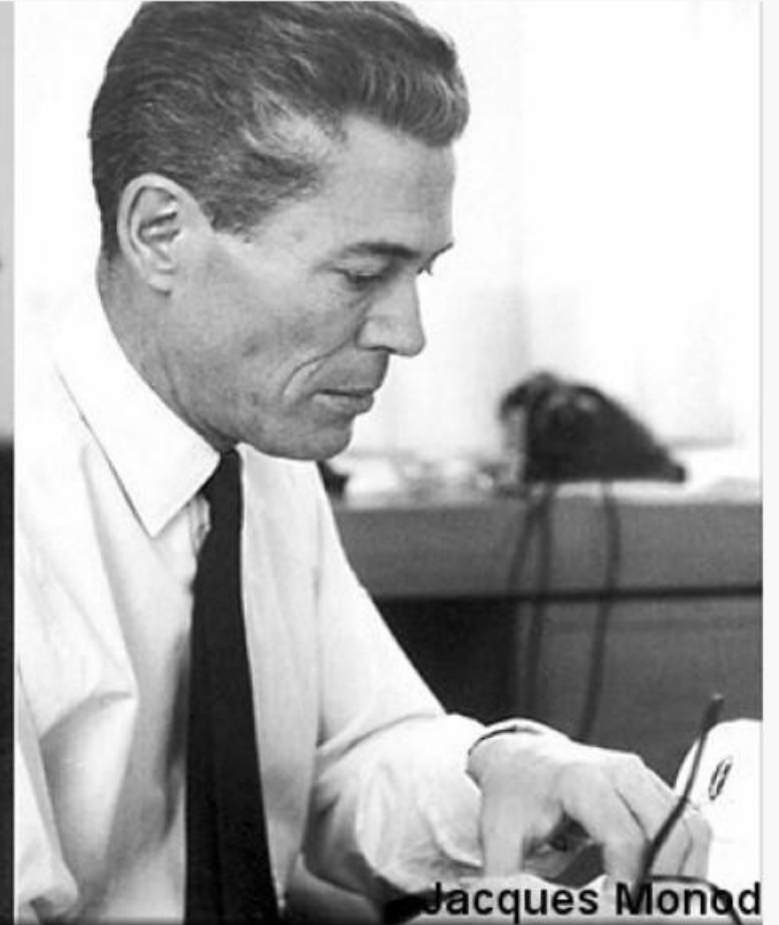
REGULATION OF GENE EXPRESSION

LAC OPERON

- Lac operon is the operon controlling **lactose metabolism**.
- It is proposed by **Francois Jacob & Jacque Monod**.



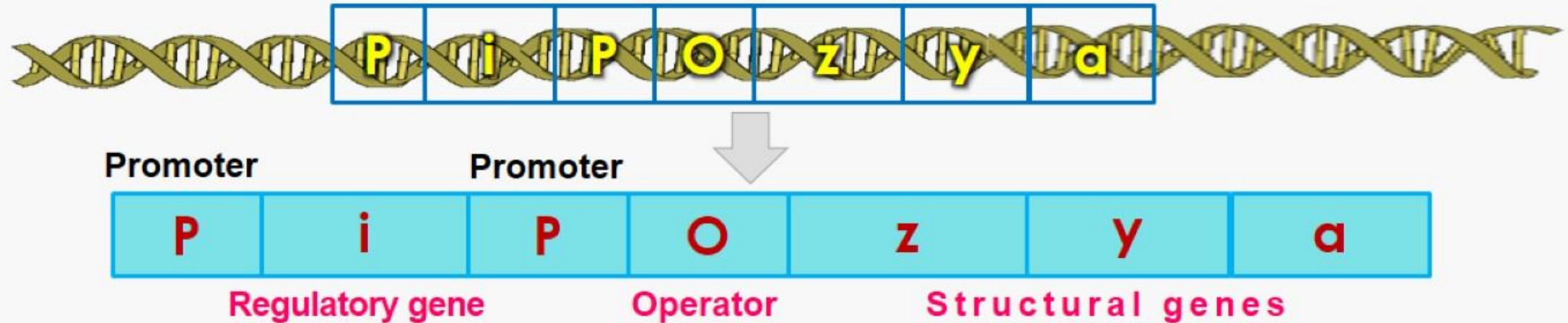
François Jacob



Jacques Monod

REGULATION OF GENE EXPRESSION

LAC OPERON



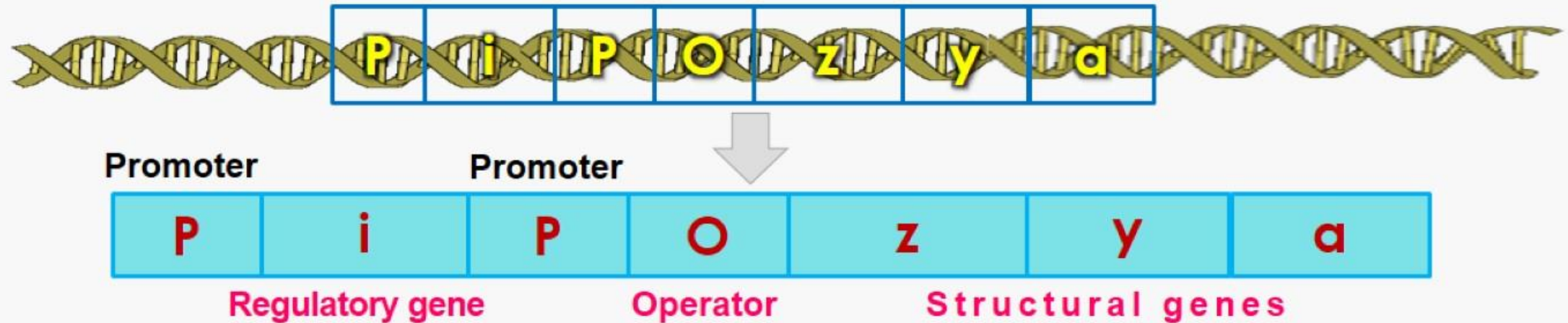
Lac operon consists of

- a. **A regulatory or inhibitor (i) gene:** Codes for repressor protein.
- b. **3 structural genes:** z gene, y gene and a gene.
- c. **An Operator region.**

Genes in the operon function together in the same or related metabolic pathway.

REGULATION OF GENE EXPRESSION

LAC OPERON



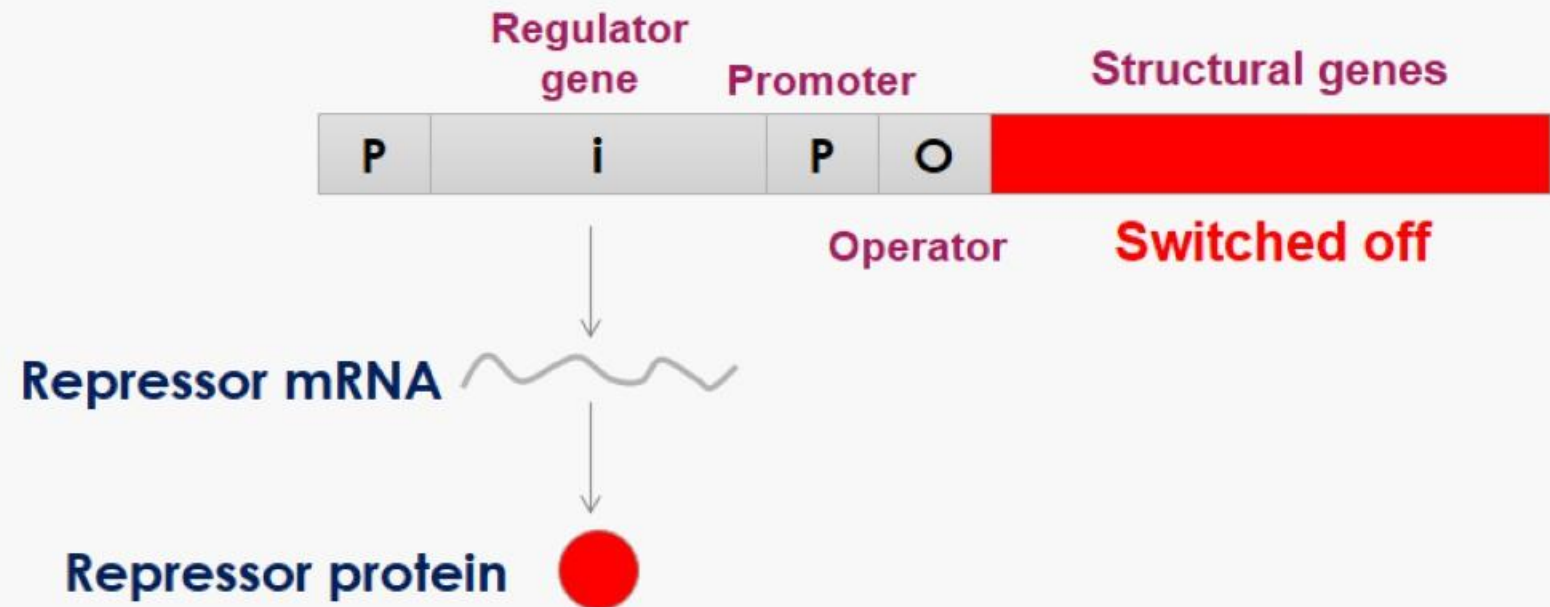
Role of structural genes:

- i. **z gene:** Codes for *β galactosidase*. It hydrolyzes lactose to galactose & glucose.
- ii. **y gene:** Codes for *permease*. It increases permeability of the cell to β -galactosides (lactose).
- iii. **a gene:** Codes for a *transacetylase*.

REGULATION OF GENE EXPRESSION

LAC OPERON

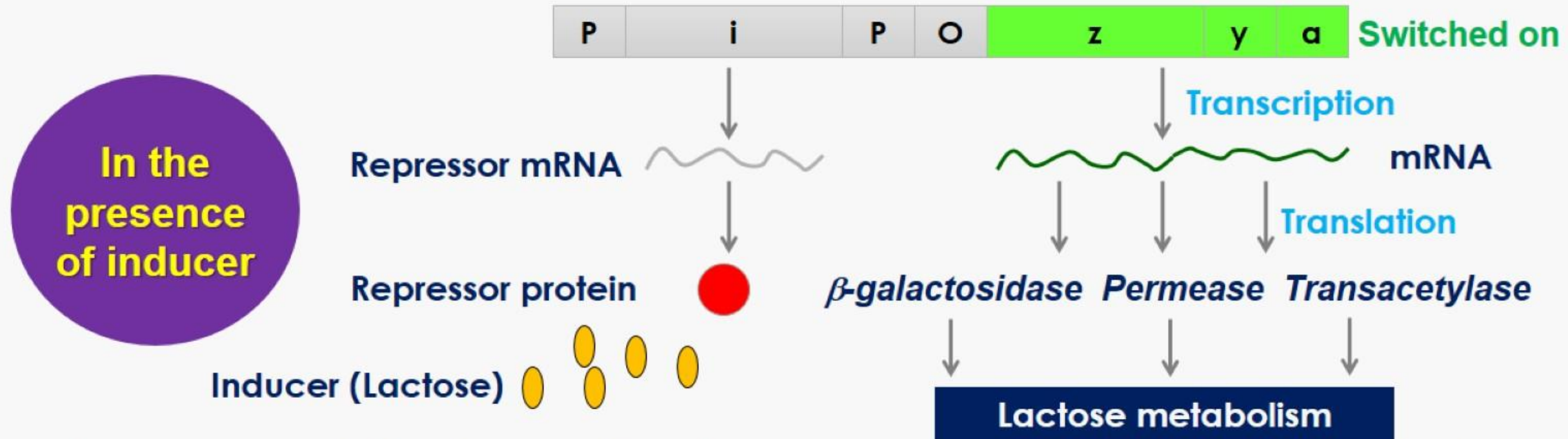
In the
absence
of inducer



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

REGULATION OF GENE EXPRESSION

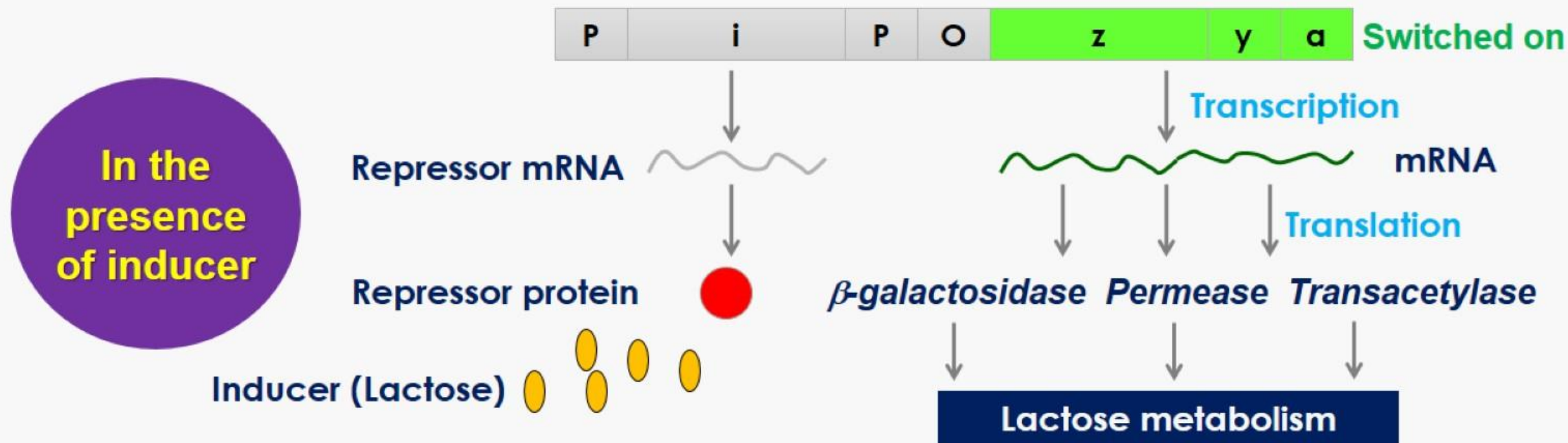
LAC OPERON



- 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. The operator region becomes free and induces the *RNA polymerase* to bind with promoter gene. Then transcription starts.

REGULATION OF GENE EXPRESSION

LAC OPERON



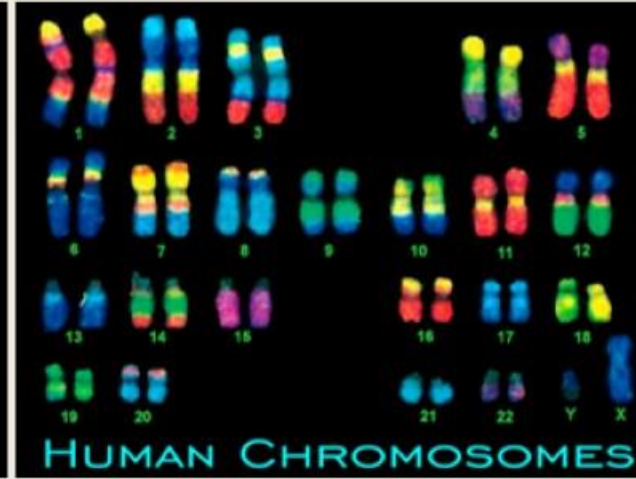
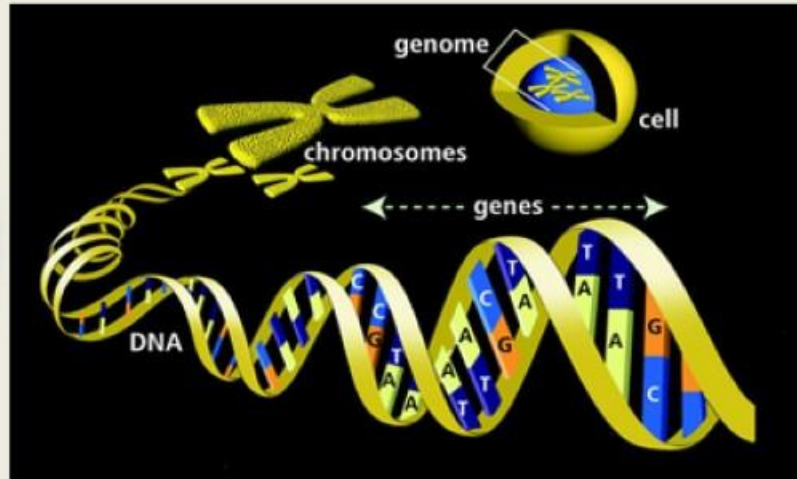
- Glucose or galactose cannot act as inducers for lac operon.
- Regulation of lac operon by repressor is called **negative regulation**.
- Lac operon is under control of positive regulation as well.



HUMAN GENOME PROJECT (HGP)



HUMAN GENOME PROJECT (HGP)

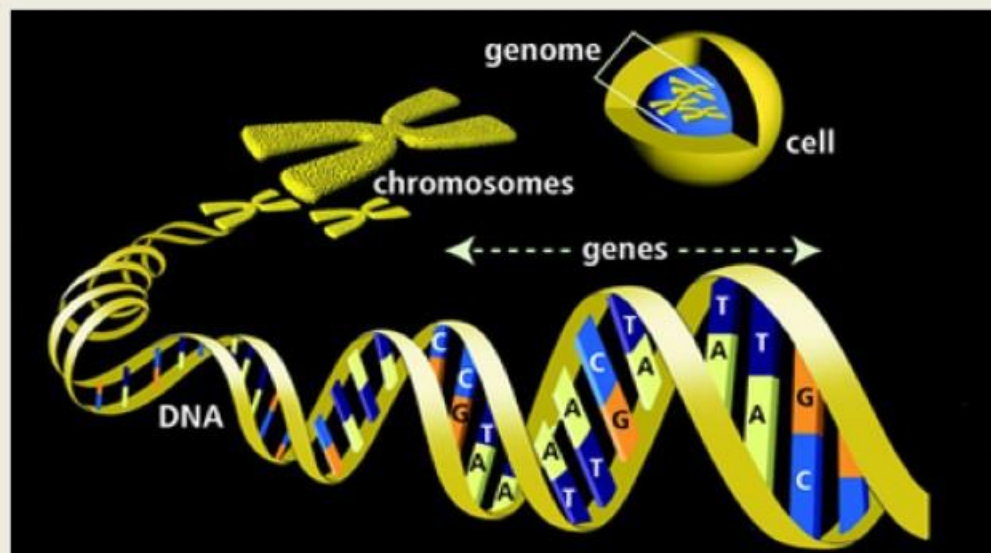


- The entire **DNA in the haploid set of chromosomes** of an organism is called a **Genome**.
- In Human genome, DNA is packed in 23 chromosomes.
- Human genome contains about **3×10^9 bp**.
- **Human Genome Project** (1990-2003) was the first mega project for the sequencing of nucleotides and mapping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

HUMAN GENOME PROJECT (HGP)

GOALS OF HGP

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✓ Identify all the estimated **genes** in human DNA.

✓ **Sequencing** of 3 billion chemical **base pairs** of human DNA.

✓ Store this information in **databases**.

✓ Improve tools for **data analysis**.

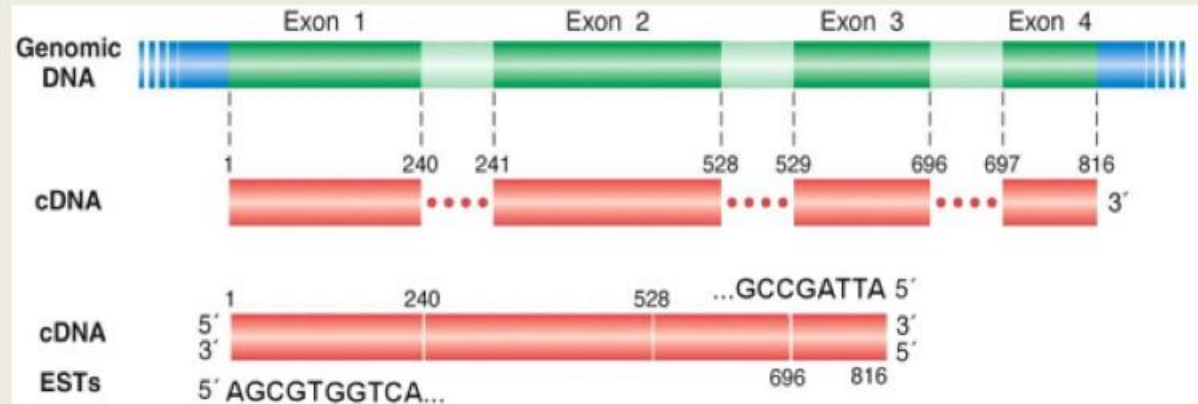
✓ **Transfer** related technologies to other sectors.

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

It involves 2 major approaches.

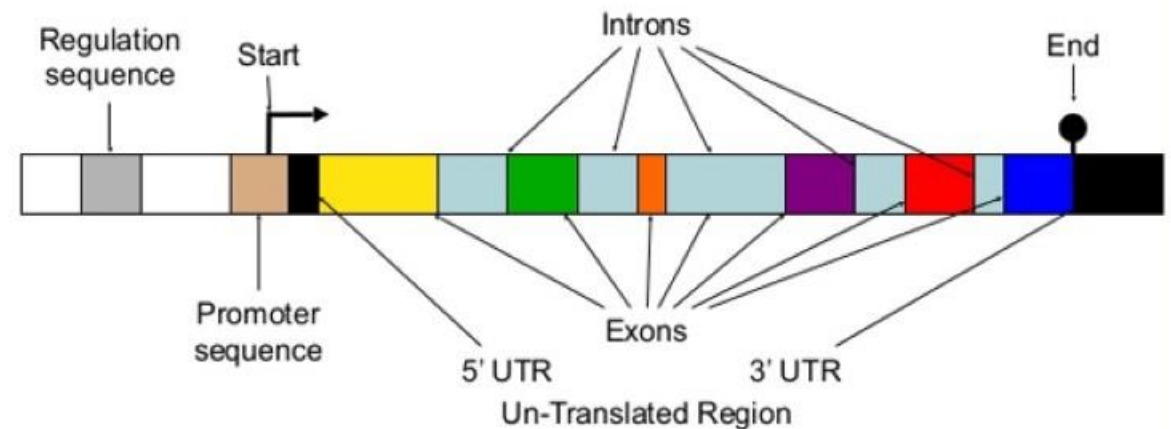
1. Expressed Sequence Tags (ESTs)

Focused on identifying all the genes that are expressed as RNA.



2. Sequence annotation

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



HUMAN GENOME PROJECT (HGP)

PROCEDURE

Isolate DNA from a cell

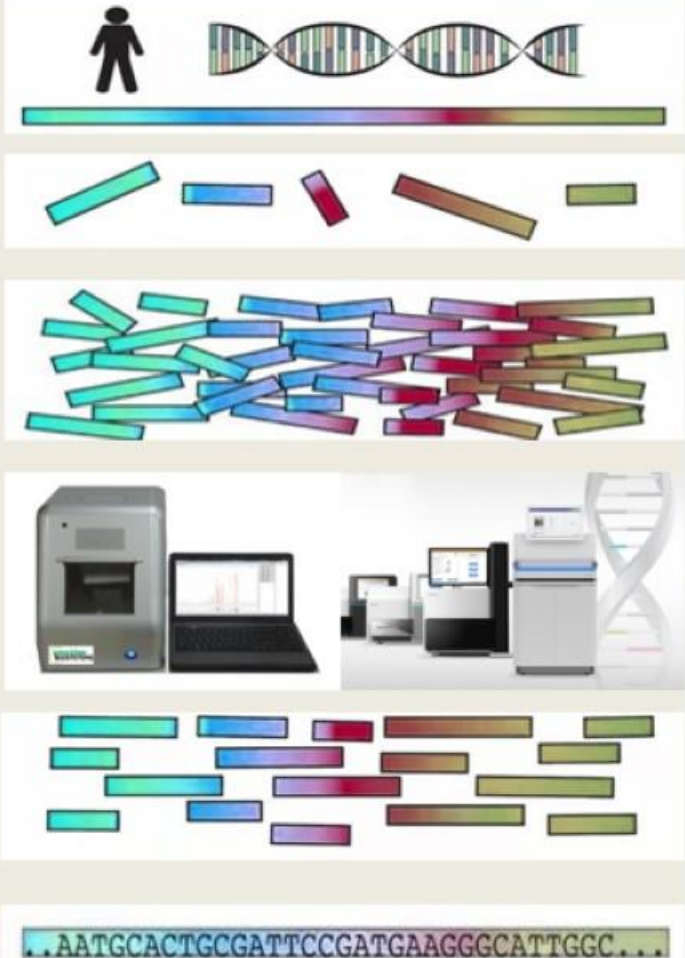
Convert into random fragments

Clone in a host (bacteria & yeast) using vectors (e.g. BAC & YAC) for amplification

Sequencing of fragments using Automated DNA sequencers (using Frederick Sanger method)

Arrange the sequences based on overlapping regions

Alignment of sequences using computer programs.



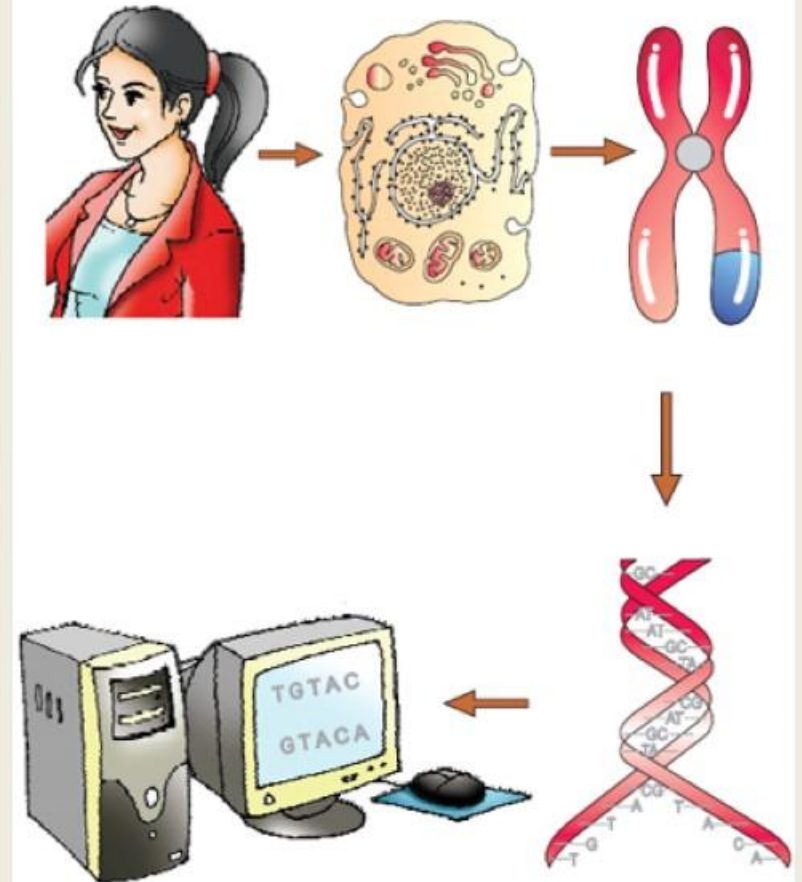
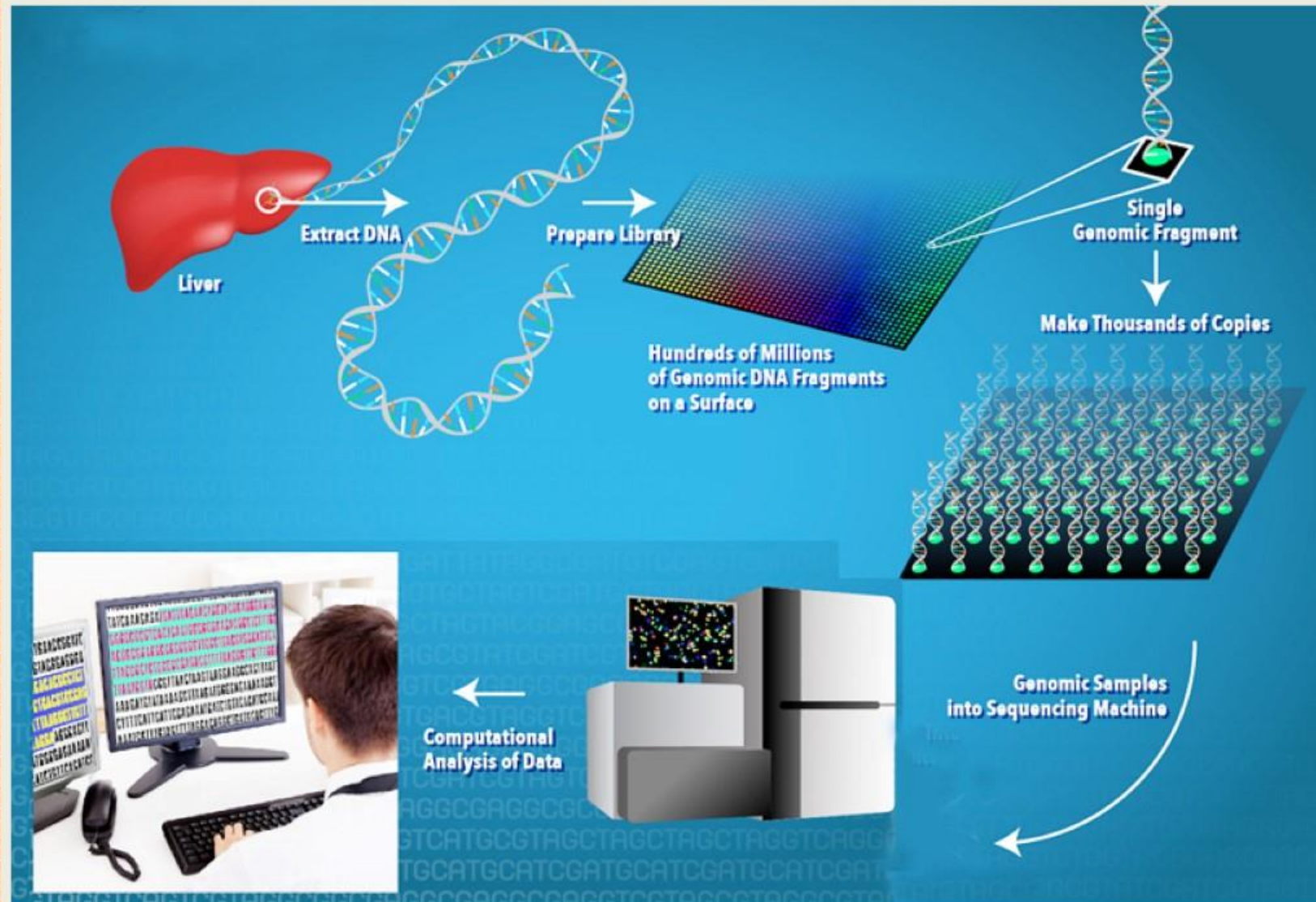
BAC= Bacterial Artificial Chromosomes

YAC= Yeast Artificial Chromosomes

HUMAN GENOME PROJECT (HGP)

PROCEDURE

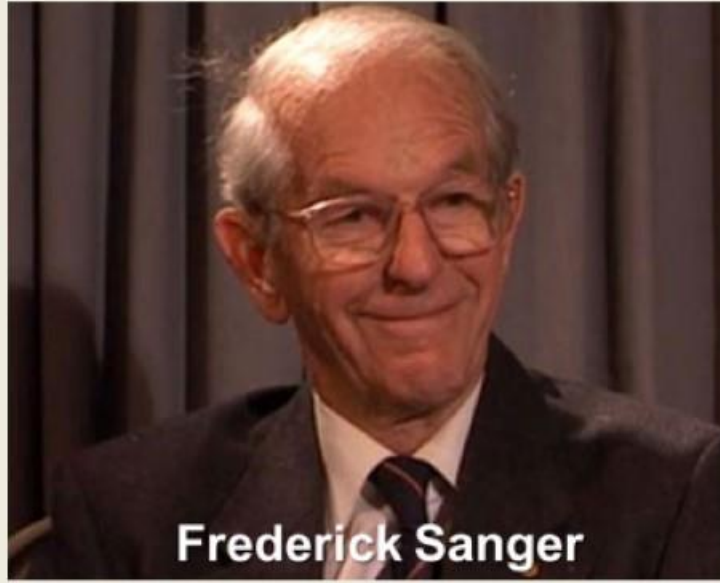
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HUMAN GENOME PROJECT (HGP)



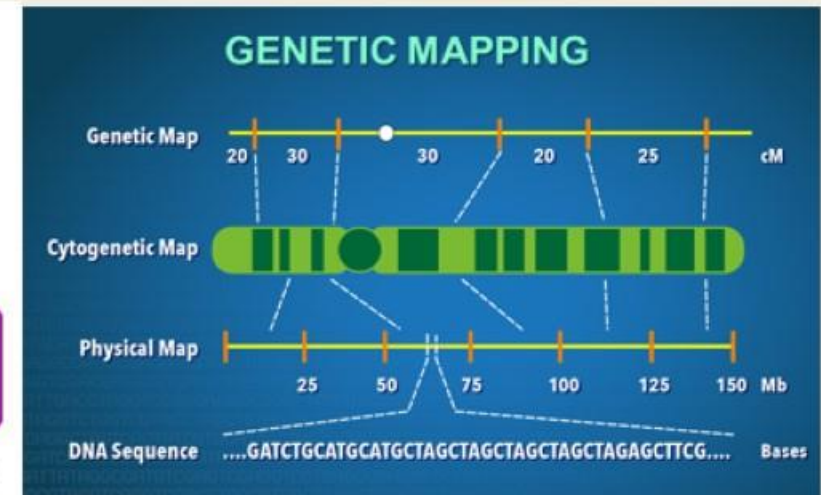
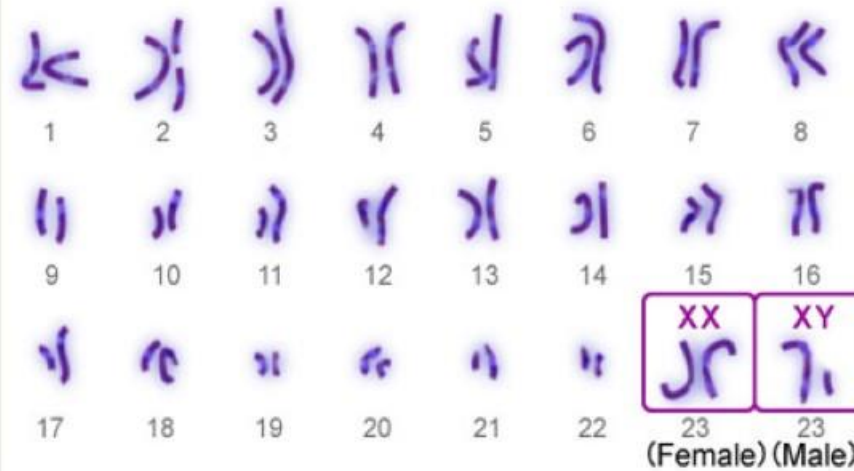
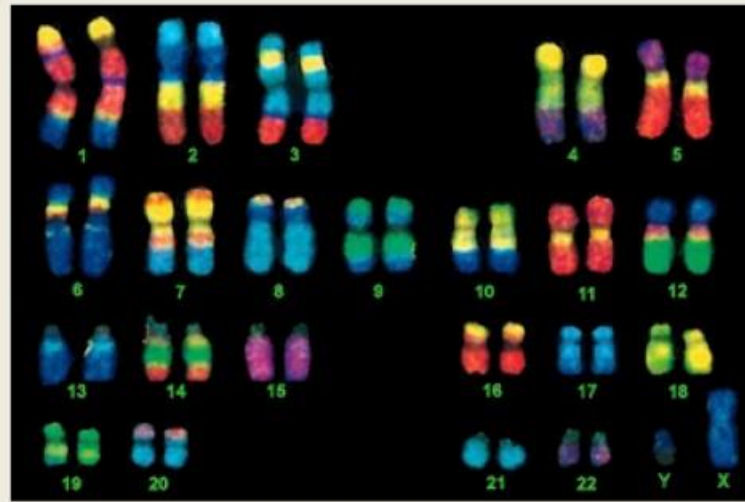
Frederick Sanger



- Sanger has also developed method for **sequencing of amino acids** in proteins.
- DNA is converted to random fragments as there are technical limitations in sequencing very long pieces of DNA.
- HGP was closely associated with **Bioinformatics**.
- **Bioinformatics**: Application of computer science and information technology to the field of biology & medicine.



HUMAN GENOME PROJECT (HGP)



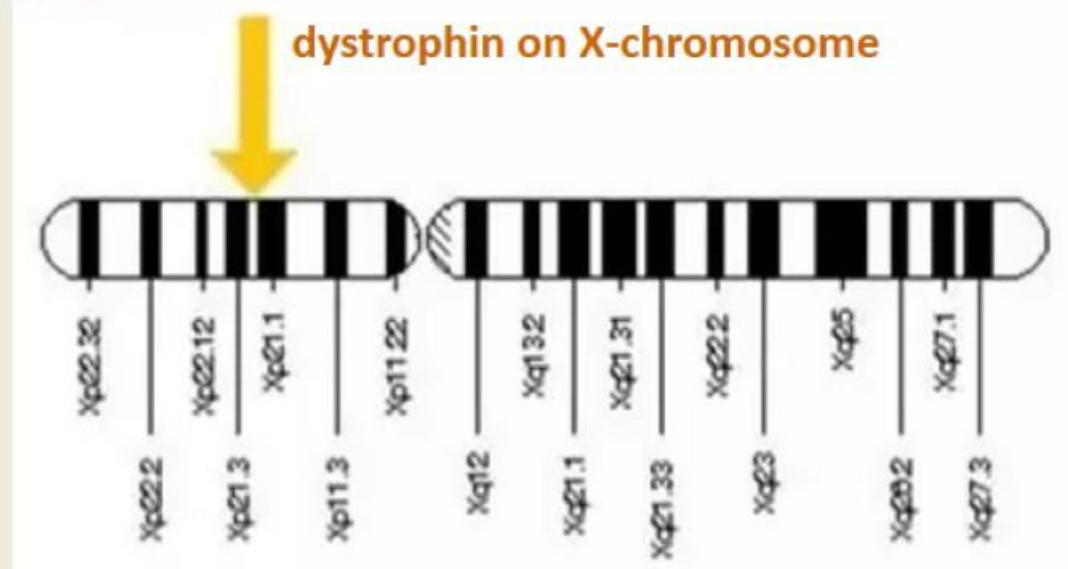
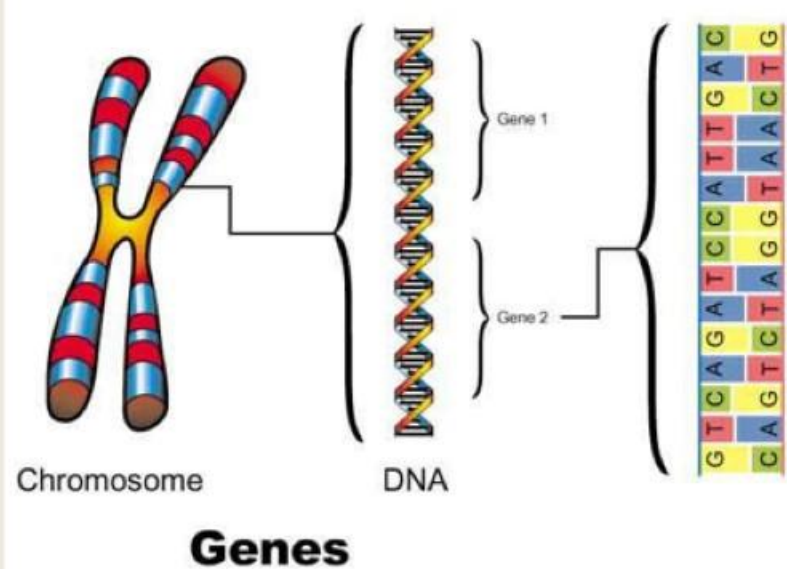
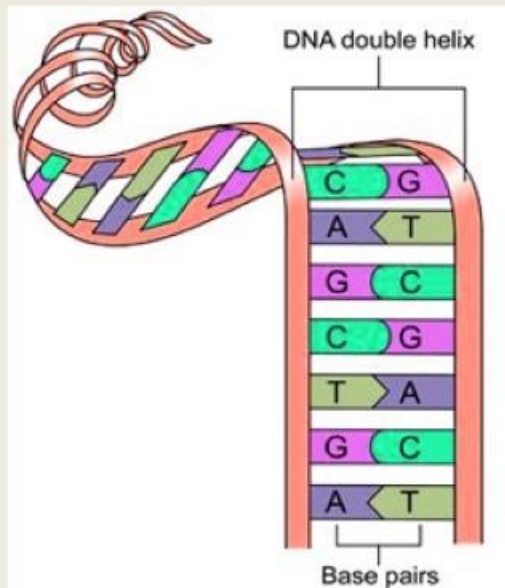
- Of the 24 chromosomes (22 autosomes and X & Y), the last sequenced one is **chromosome 1** (May 2006).
- Genetic and physical maps on the genome were generated using information on polymorphism of **restriction endonuclease** recognition sites and some **repetitive DNA sequences (microsatellites)**.
- DNA sequencing also have been done in bacteria, yeast, ***Caenorhabditis elegans*** (a free living non-pathogenic nematode), *Drosophila*, plants (rice & Arabidopsis), etc.



HUMAN GENOME PROJECT (HGP)

SALIENT FEATURES OF HUMAN GENOME

1. Human genome contains **3164.7 million** nucleotide bases.
2. Total number of genes= about **30,000**.
3. Average gene consists of **3000 bases**, but sizes vary. Largest known human gene (**dystrophin on X-chromosome**) contains **2.4 million bases**.

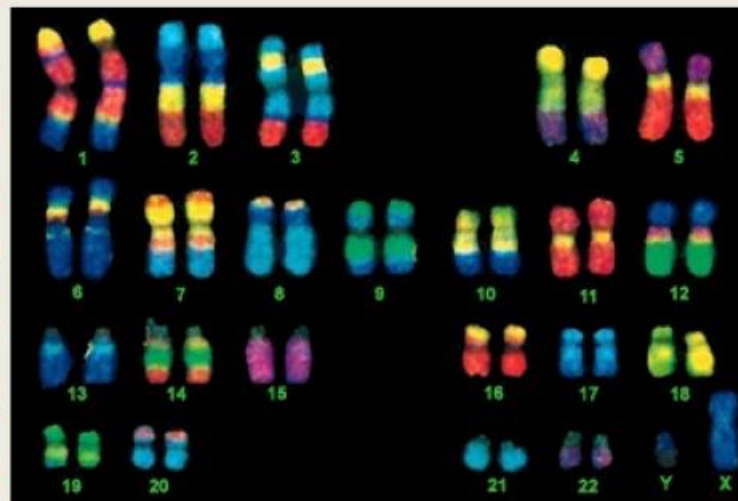




HUMAN GENOME PROJECT (HGP)

SALIENT FEATURES OF HUMAN GENOME

4. **99.9%** nucleotide bases are same in all people. Only **0.1%** (3×10^6 bp) difference makes every individual unique.
5. Functions of over 50% of discovered genes are unknown.
6. **Chromosome I** has most genes (**2968**) and **Y** has the fewest (**231**).
7. Less than **2%** of the genome codes for proteins.





HUMAN GENOME PROJECT (HGP)

SALIENT FEATURES OF HUMAN GENOME

8. 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.
9. About **1.4 million** locations have single-base DNA differences. They are called **SNPs (Single nucleotide polymorphism or 'snips')**. This helps to find chromosomal locations for disease-associated sequences and tracing human history.

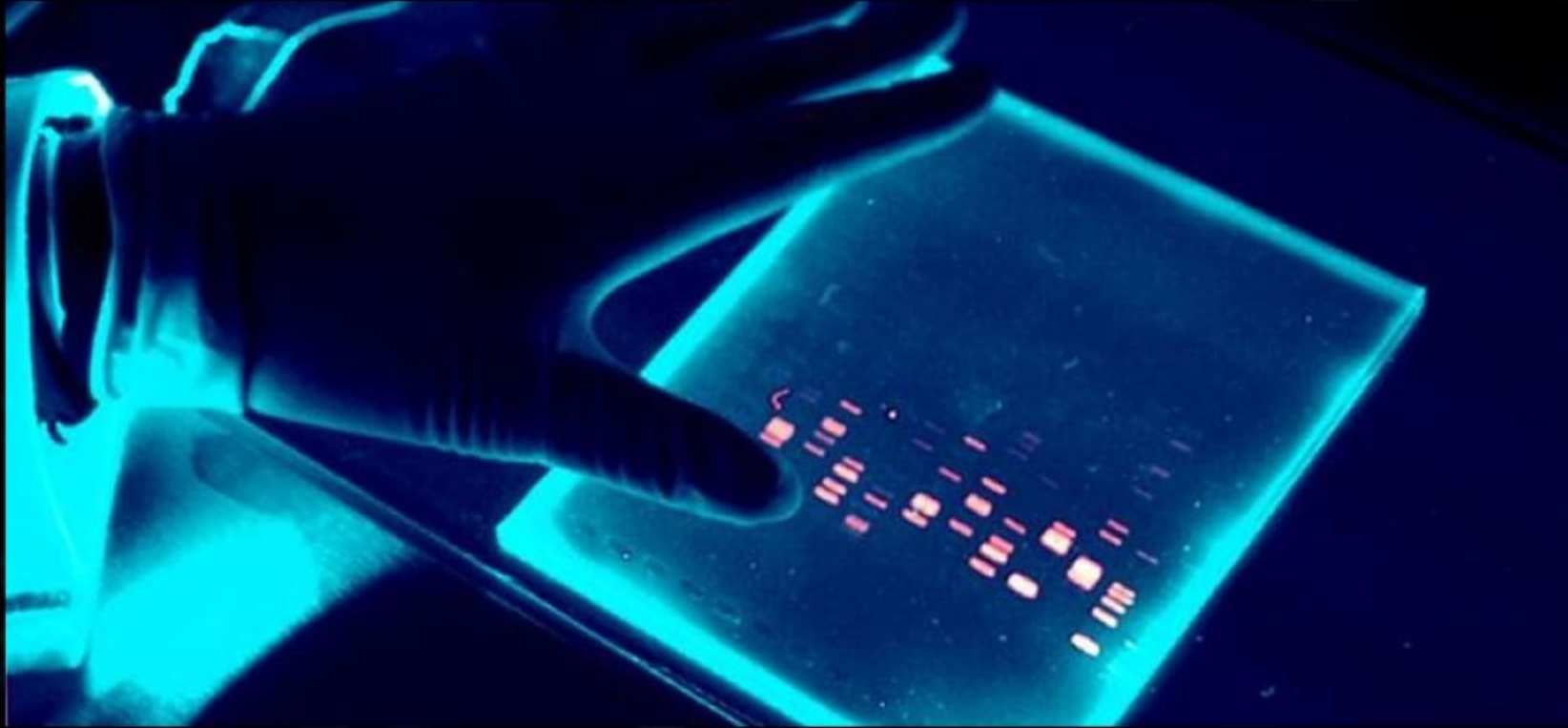
bankofbiology.com



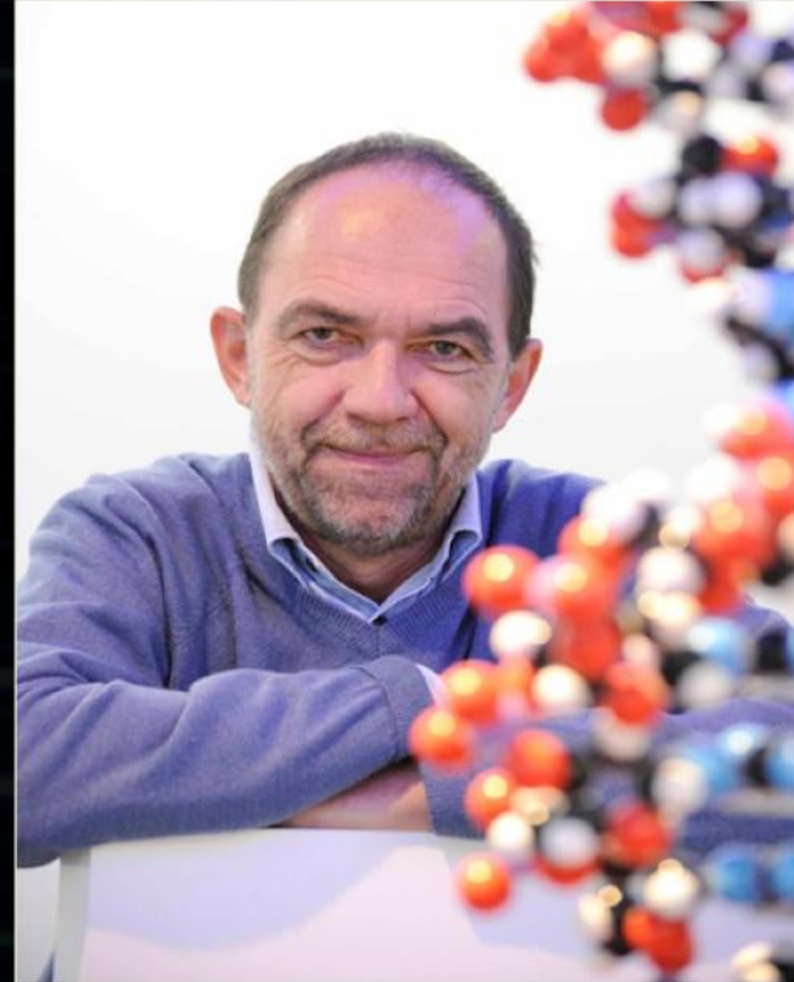


DNA FINGERPRINTING (DNA PROFILING)

DNA FINGERPRINTING (DNA PROFILING)



- It is the technique to identify the similarities and differences of the DNA fragments of 2 individuals.
- Developed by **Alec Jeffreys (1985)**.



Alec Jeffreys

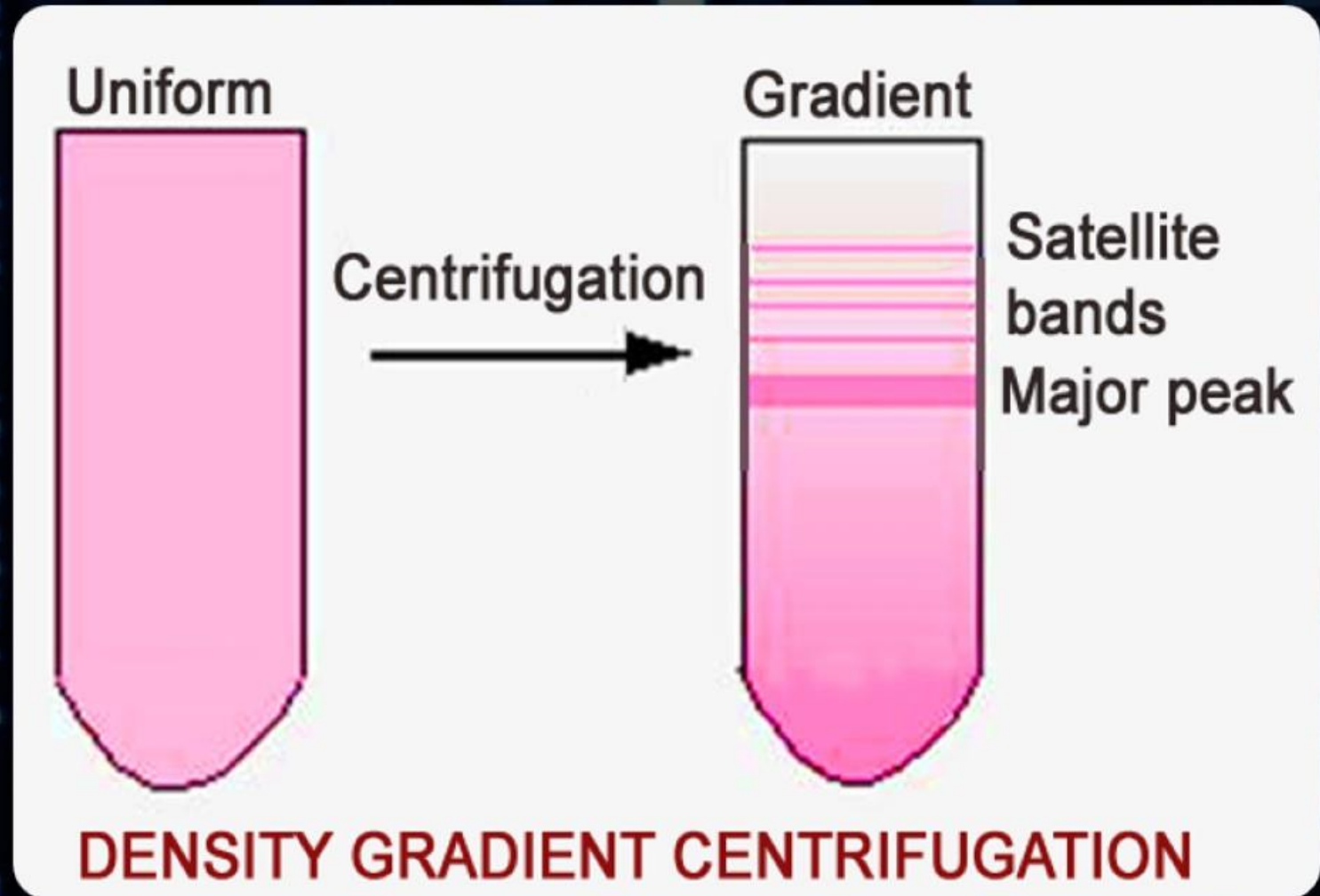
DNA FINGERPRINTING: BASIS

- DNA carries some non-coding **repetitive sequences**.
- Number of repeats is specific from person to person. E.g.



DNA FINGERPRINTING: BASIS

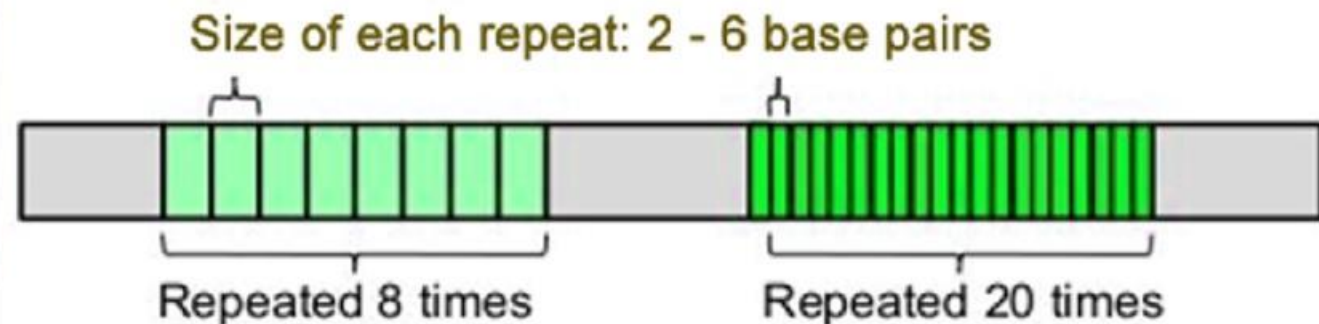
- **Repetitive DNA** can be separated from **bulk genomic DNA** as different peaks during **density gradient centrifugation**.
- The **bulk DNA** forms a **major peak** and the small peaks are called **satellite DNA**.



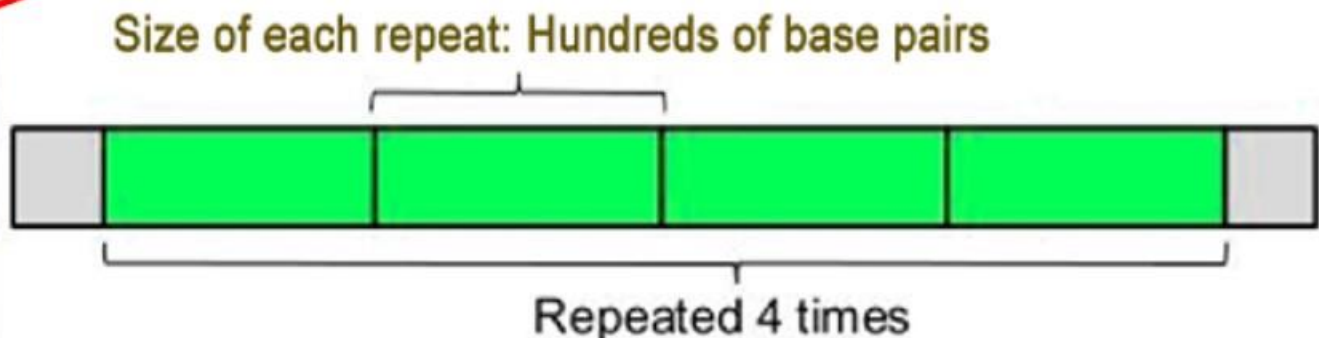
DNA FINGERPRINTING: BASIS

- 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.
- A DNA sequence which is tandemly repeated in many copy numbers is called **variable number tandem repeats (VNTR)**.
- VNTR belongs to **mini-satellite DNA**.

Microsatellite: Short Tandem Repeats (STR)



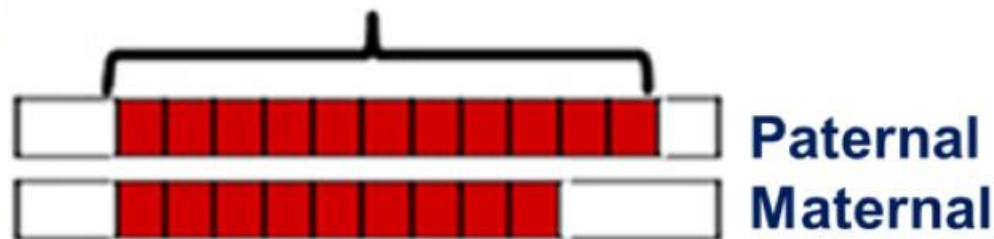
Minisatellite: VNTR



DNA FINGERPRINTING: BASIS

- In a person, copy number varies in each chromosome.
- Two alleles (paternal & maternal) of a chromosome also contain different copy numbers of VNTR.

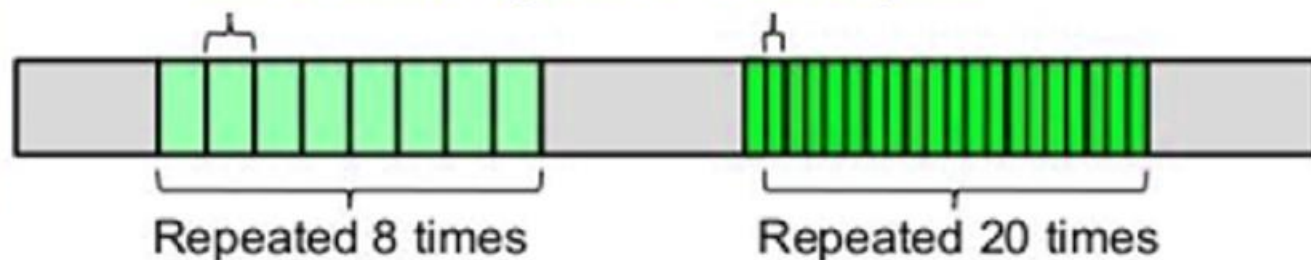
Copy number of VNTR



2 alleles of a chromosome

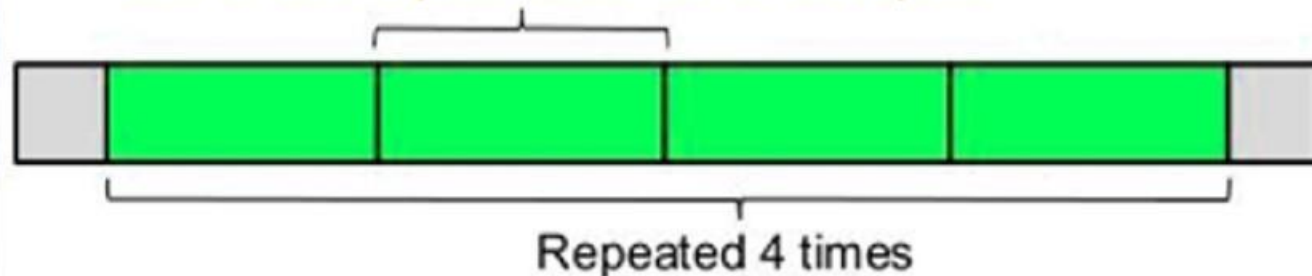
Microsatellite: Short Tandem Repeats (STR)

Size of each repeat: 2 - 6 base pairs



Minisatellite: VNTR

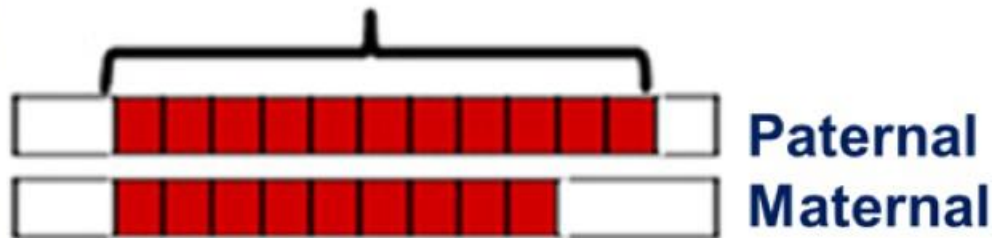
Size of each repeat: Hundreds of base pairs



DNA FINGERPRINTING: BASIS

- VNTR is specific from person to person.
- The size of VNTR varies from **0.1 to 20 kb (kilobase)**.

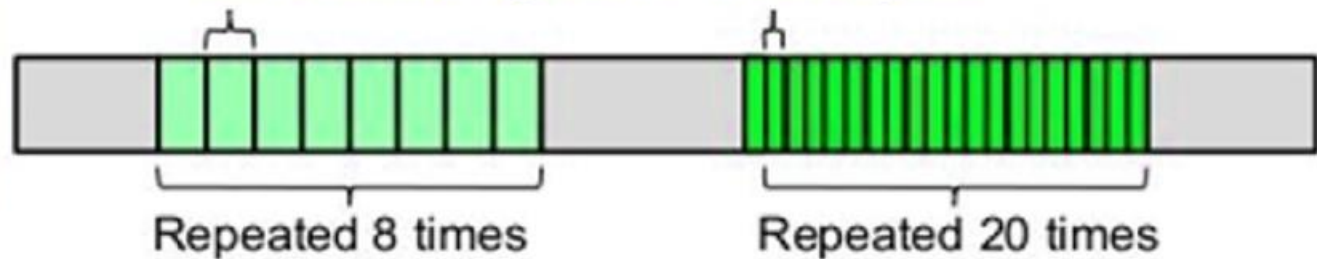
Copy number of VNTR



2 alleles of a chromosome

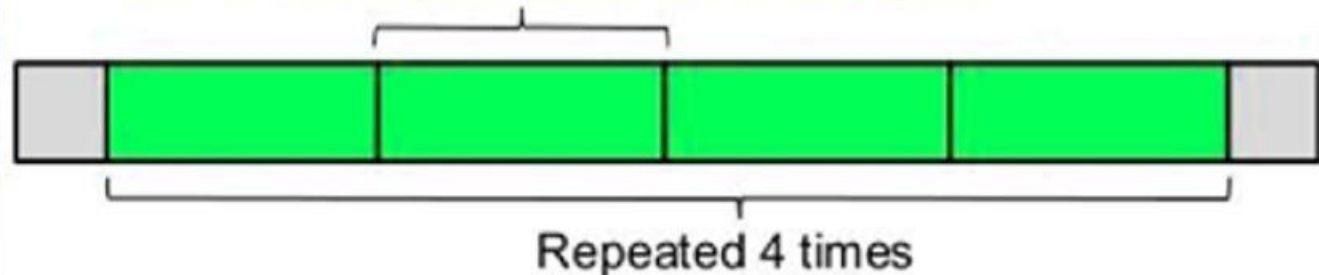
Microsatellite: Short Tandem Repeats (STR)

Size of each repeat: 2 - 6 base pairs



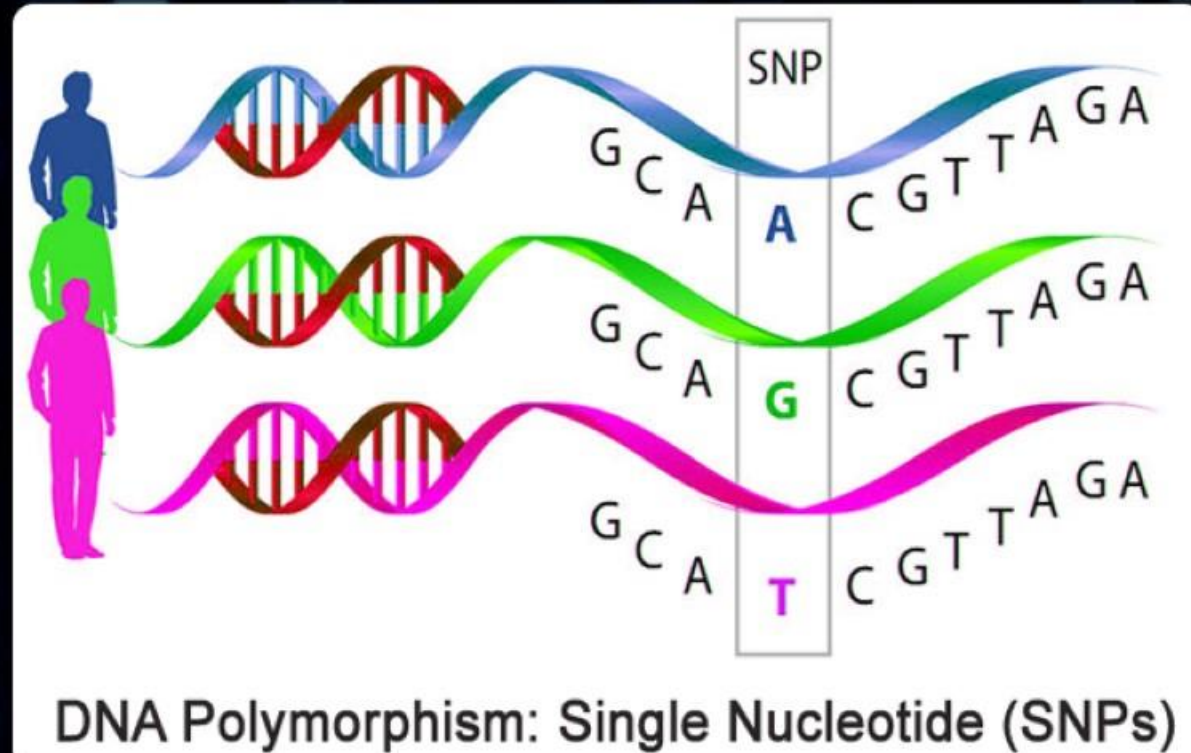
Minisatellite: VNTR

Size of each repeat: Hundreds of base pairs



DNA FINGERPRINTING: BASIS

- 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 affect an individual's reproductive ability.
- These mutations accumulate generation to generation causing polymorphism.



Polymorphisms have great role in evolution & speciation.

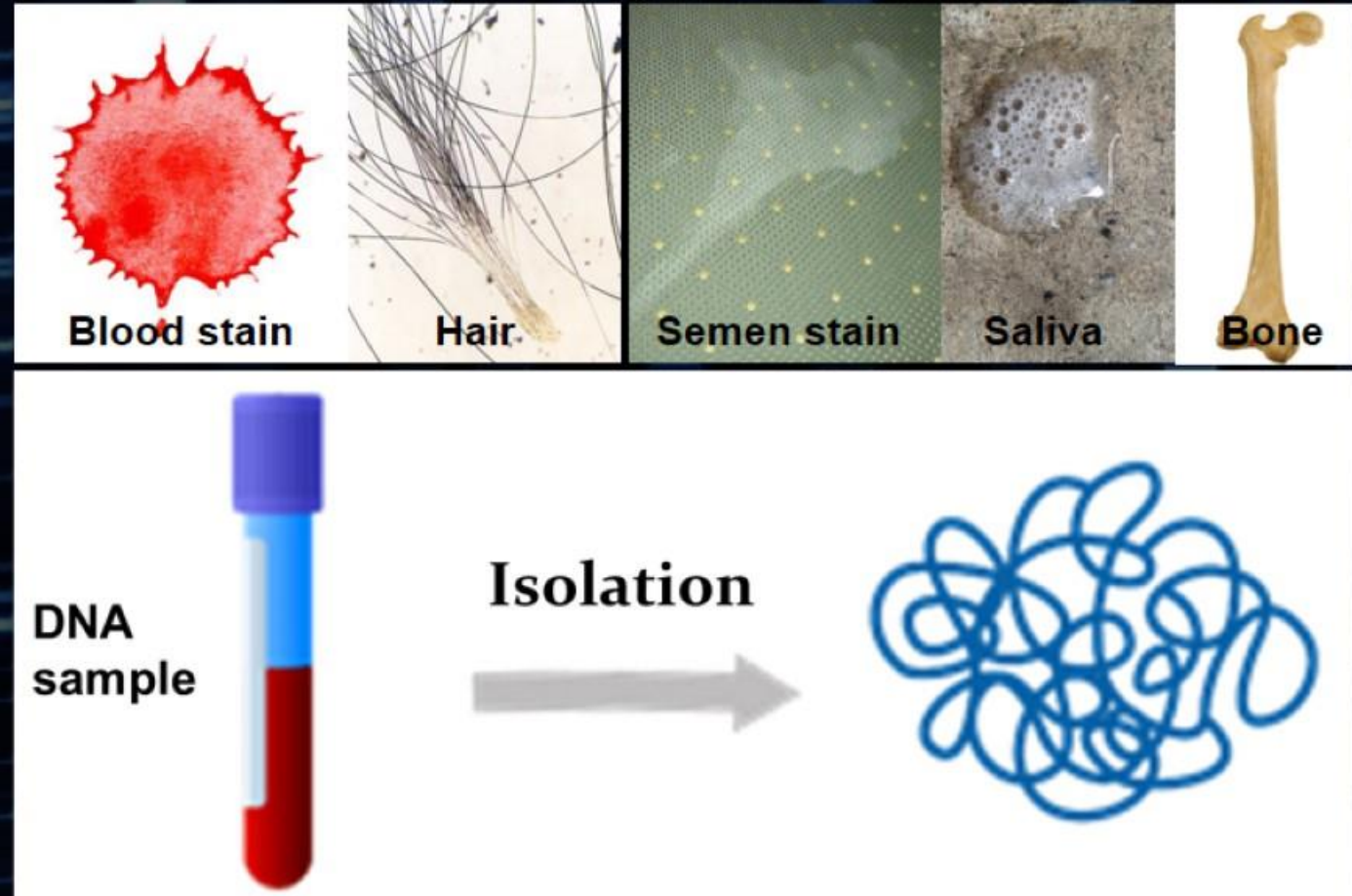
DNA FINGERPRINTING: STEPS

SOUTHERN BLOTTING TECHNIQUE

1

Isolation of DNA

(from any cells or blood stains, semen stains, saliva, hair roots, bone, skin etc.).



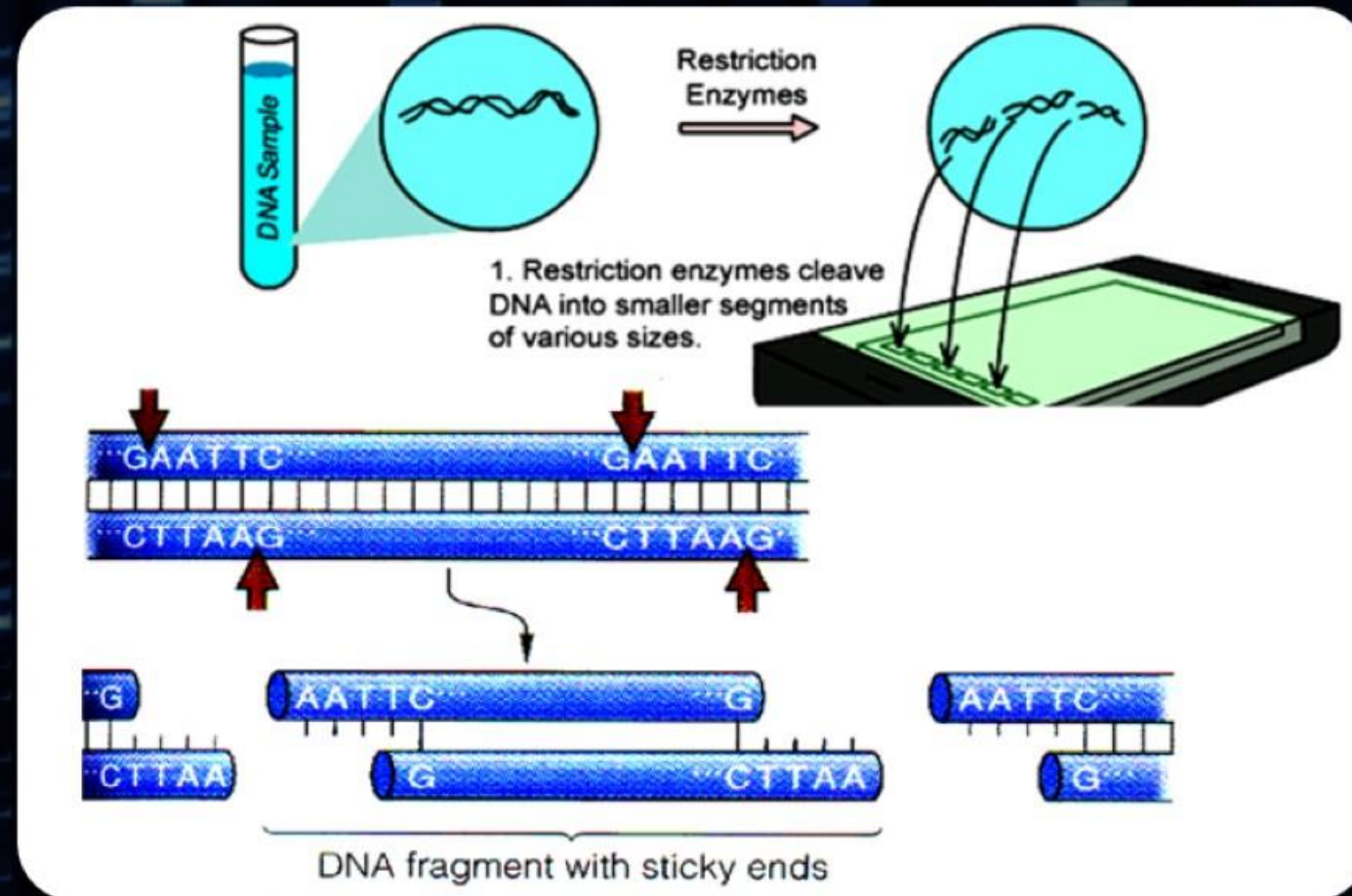
DNA FINGERPRINTING: STEPS

SOUTHERN BLOTTING TECHNIQUE

2

Digestion of DNA

By restriction endonucleases.



DNA FINGERPRINTING: STEPS

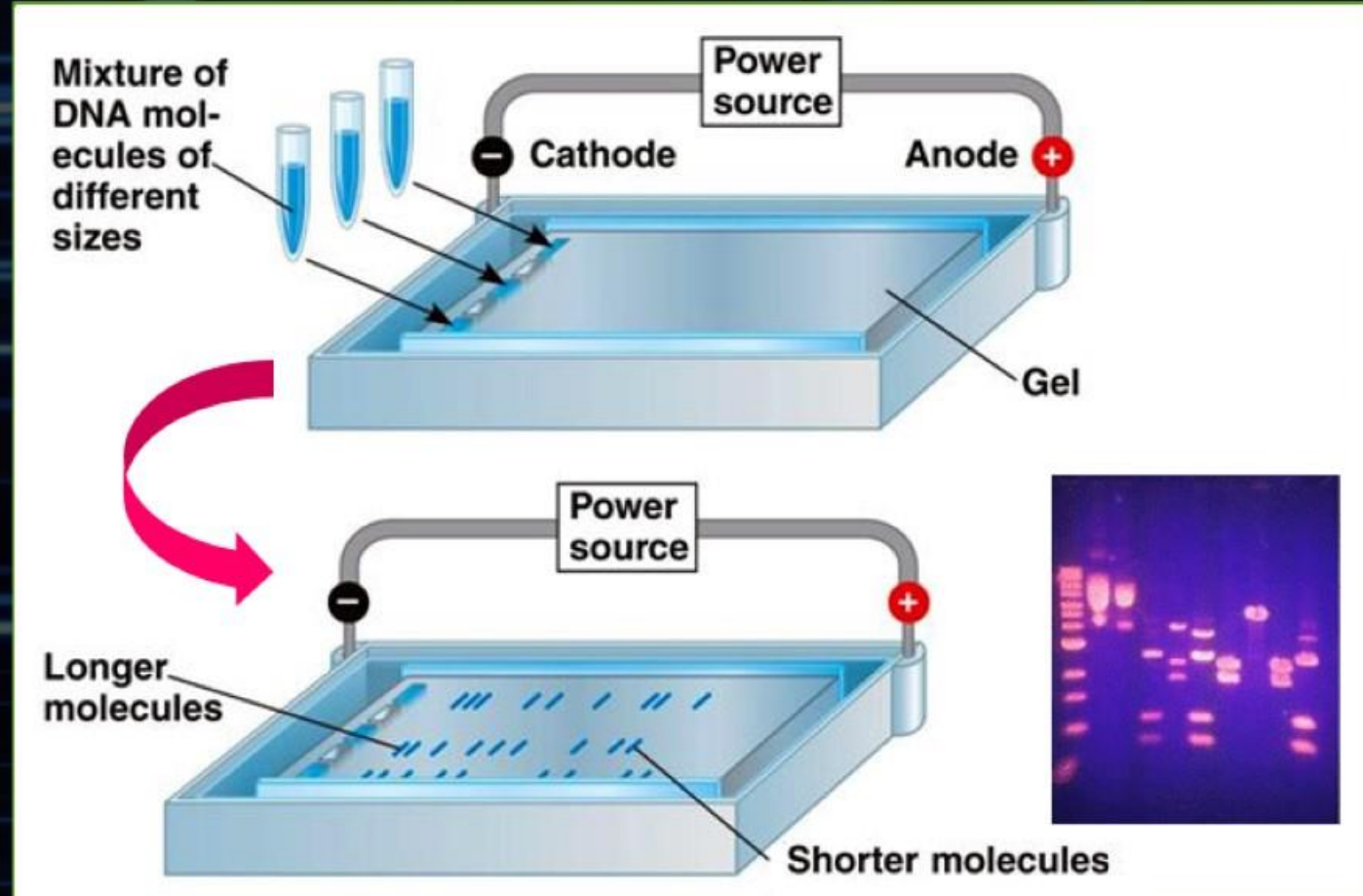
SOUTHERN BLOTTING TECHNIQUE

3

Separation of DNA fragments

By gel electrophoresis.

Then treat the DNA fragments with alkali solution (NaOH) to denature DNA bonds in the gel into single strands.

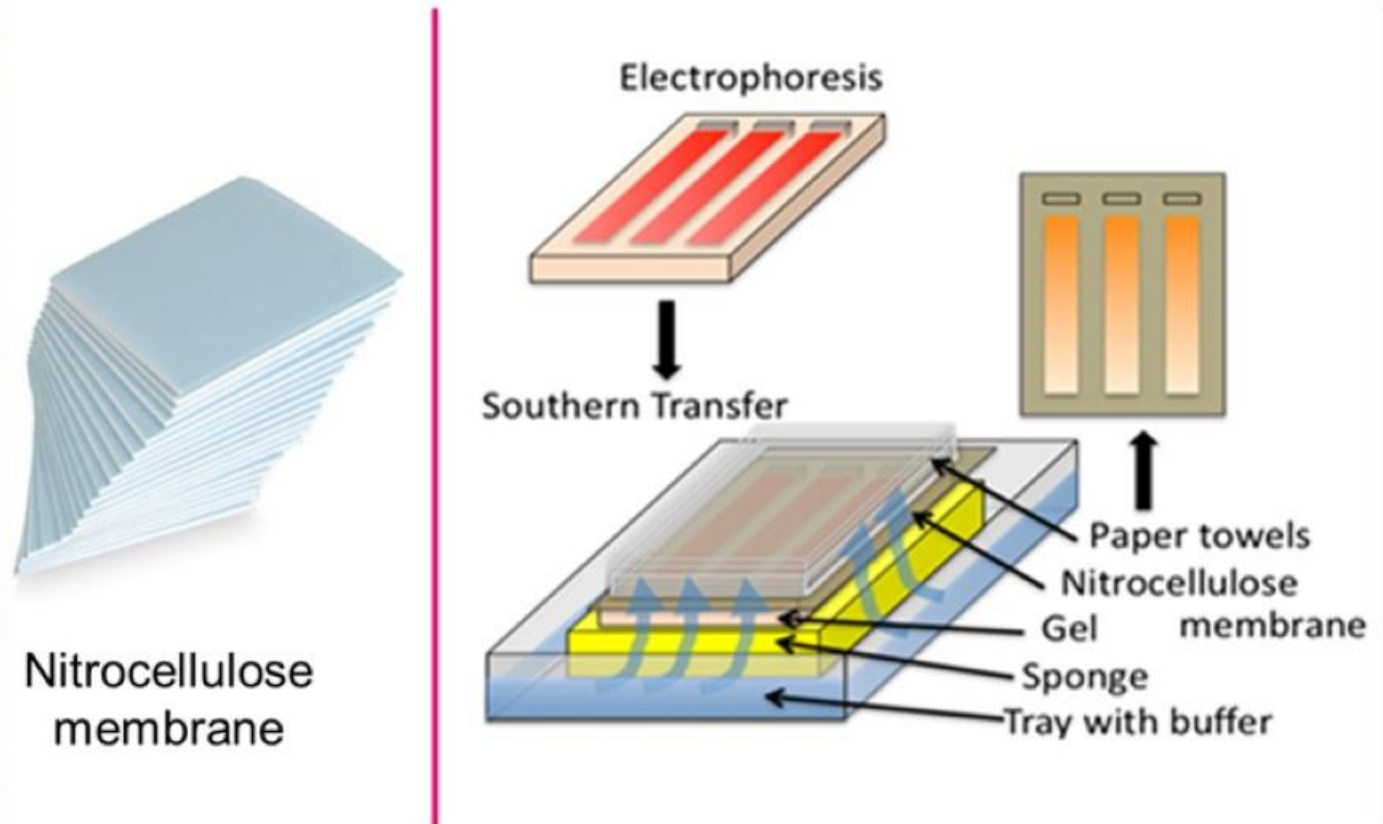


DNA FINGERPRINTING: STEPS

SOUTHERN BLOTTING TECHNIQUE

4

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



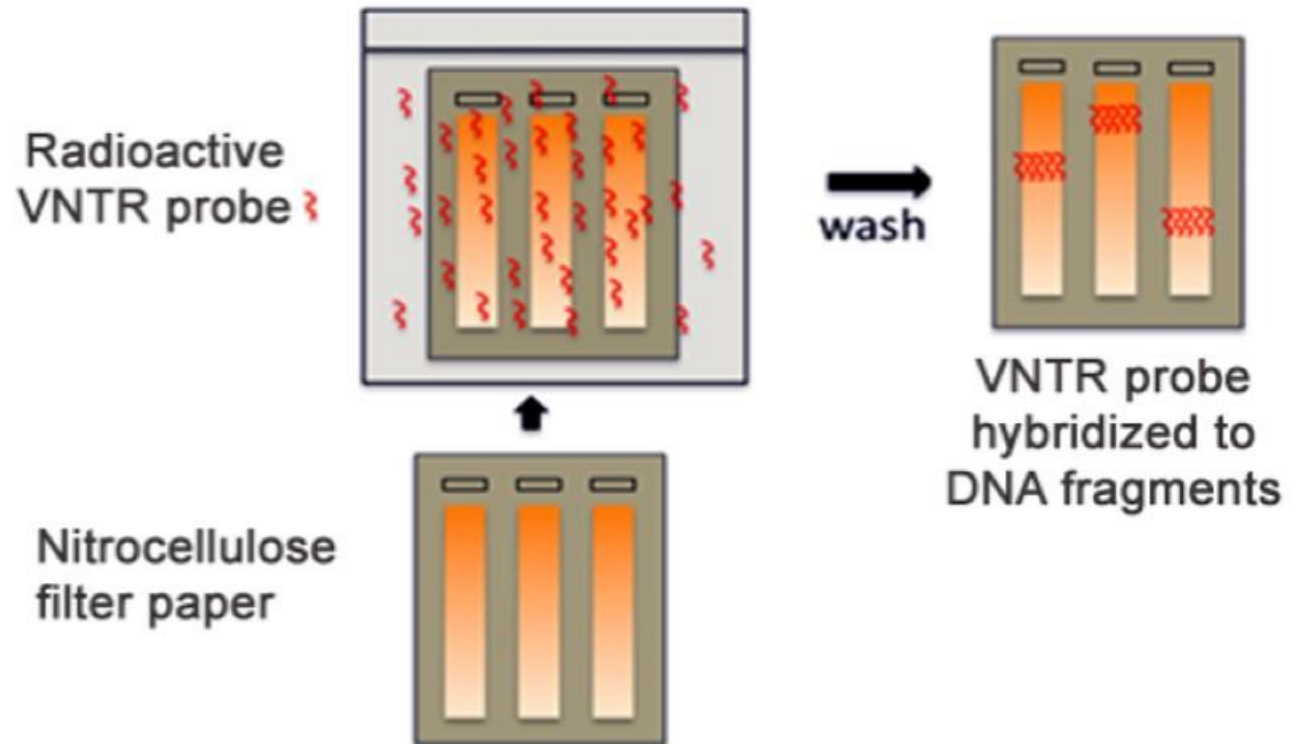
DNA FINGERPRINTING: STEPS

SOUTHERN BLOTTING TECHNIQUE

5

Hybridization using radioactive labelled VNTR probe.

*(Place the nitrocellulose filter paper in a solution of radioactive labeled single stranded DNA probe. DNA probe binds with the complimentary sequences of the DNA fragment on the membrane to form a **hybridized DNA**).*



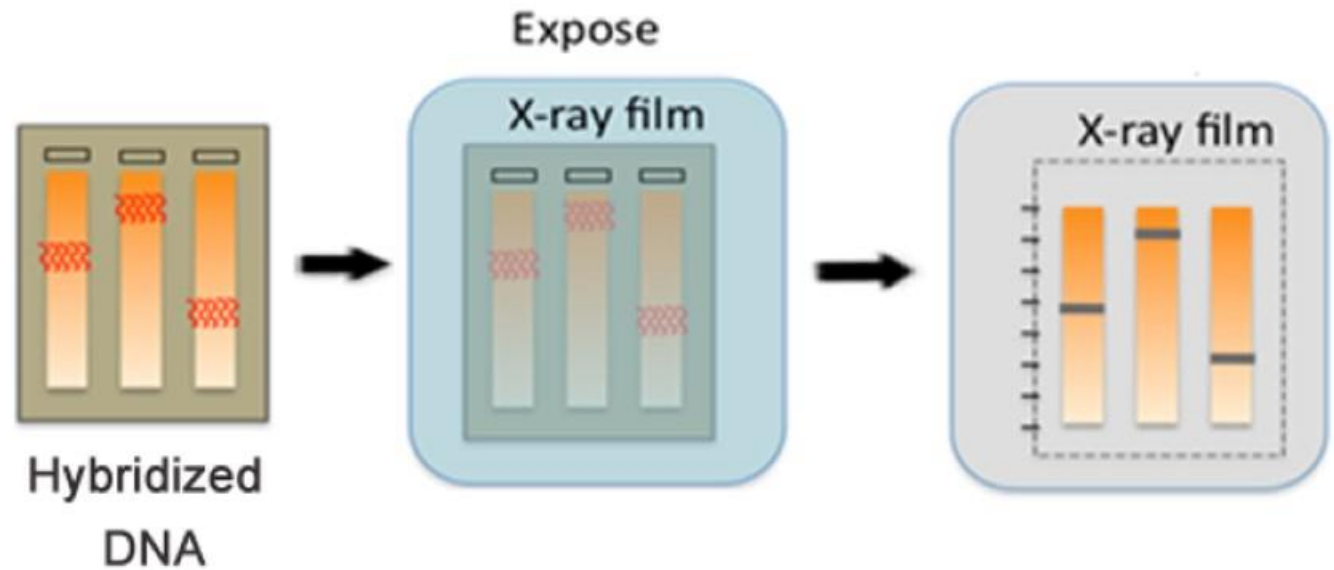
DNA FINGERPRINTING: STEPS

SOUTHERN BLOTTING TECHNIQUE

6

Detection of hybridized DNA by **Autoradiography**.

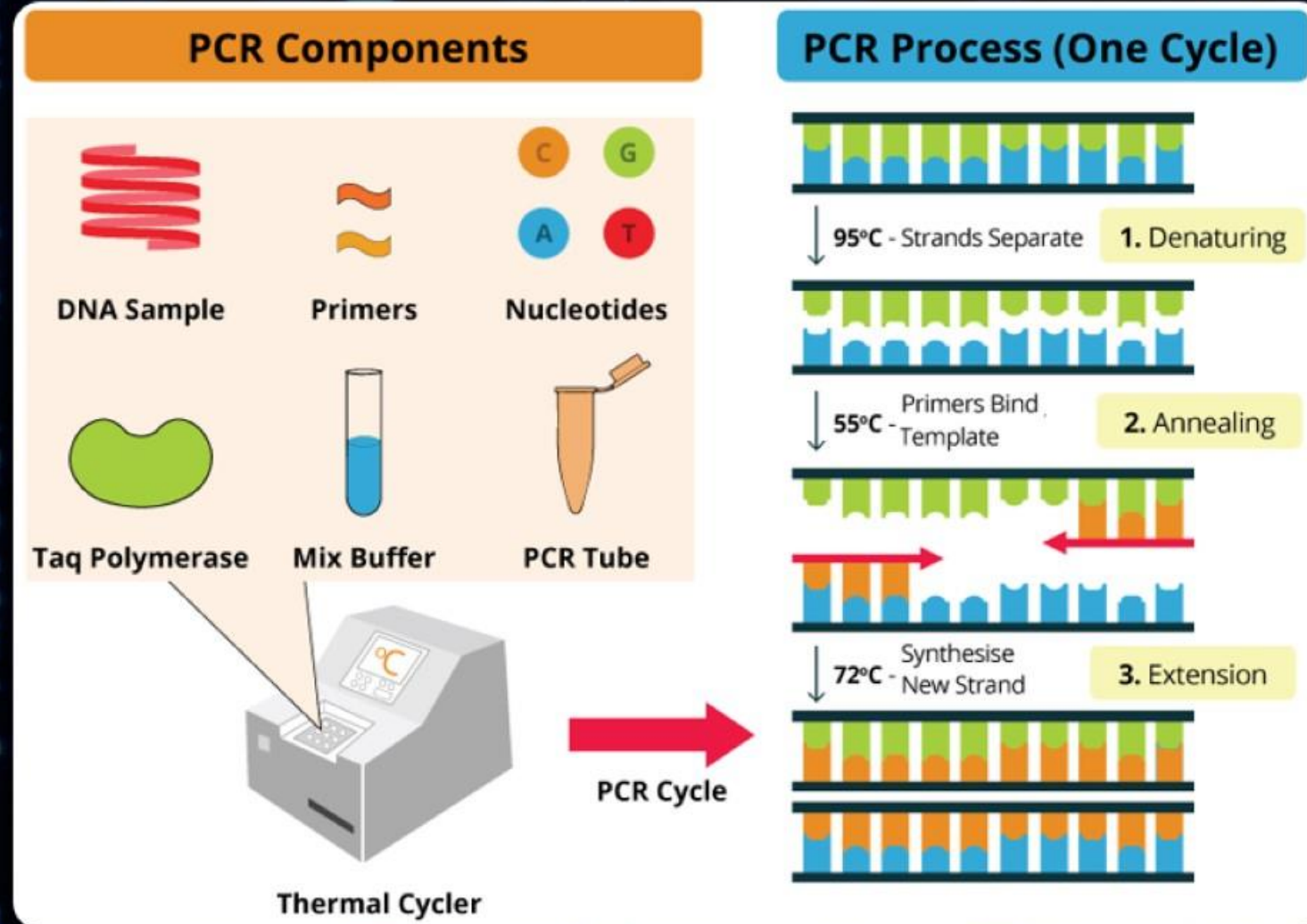
(Hybridized DNA is photographed on to an X-ray film).



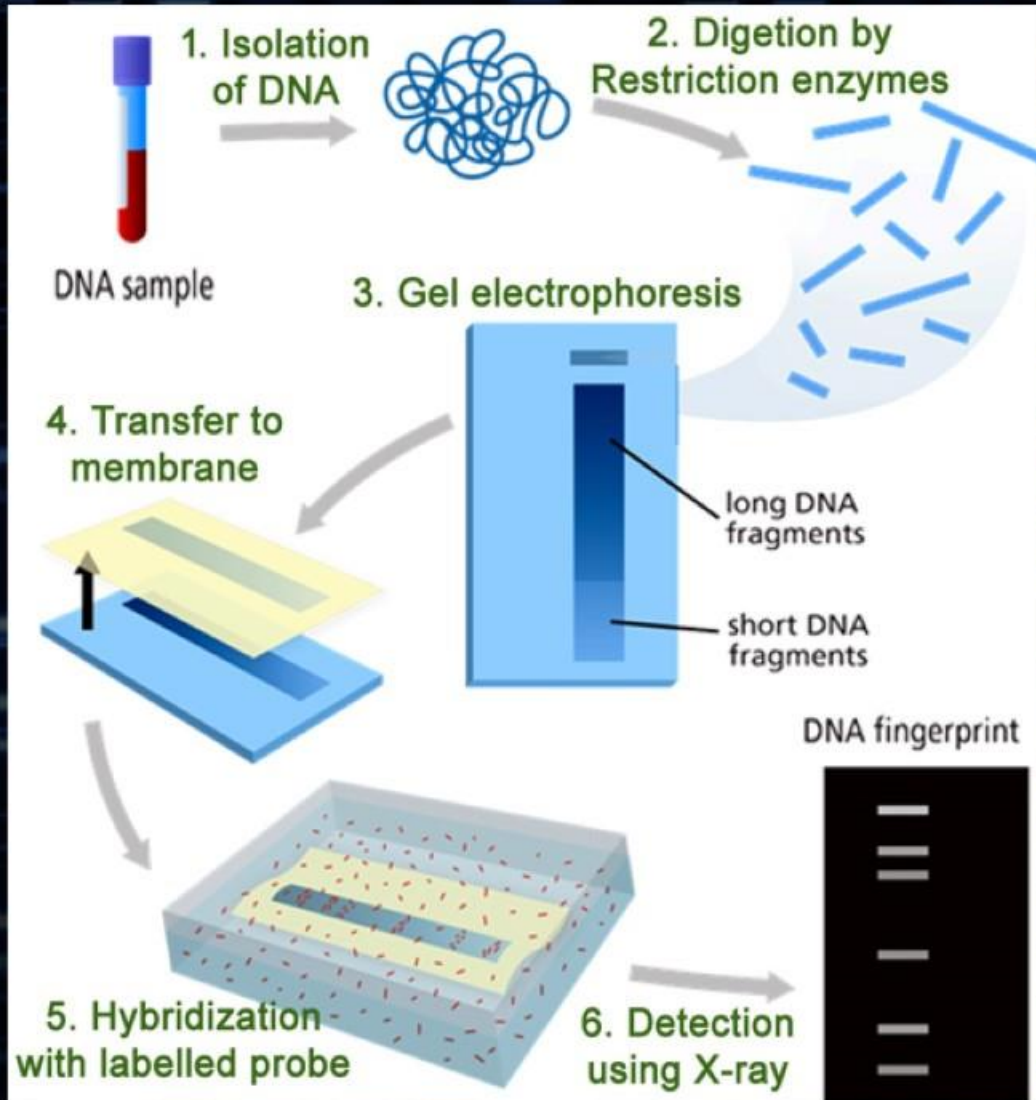
The autoradiogram gives an image in the form of dark & light bands. It is called **DNA fingerprint**.

DNA FINGERPRINTING (DNA PROFILING)

- DNA fingerprint differs in everyone except in **monozygotic (identical) twins**.
- The sensitivity of the technique can be increased by use of **polymerase chain reaction (PCR)**. Therefore, DNA from a single cell is enough for DNA fingerprinting.



DNA FINGERPRINTING: AT A GLANCE



1. Isolation of DNA.

2. Digestion of DNA by restriction endonucleases.

3. Separation of DNA fragments by gel electrophoresis.

4. Transferring DNA fragments to synthetic membranes.

5. Hybridization using radioactive labelled VNTR probe.

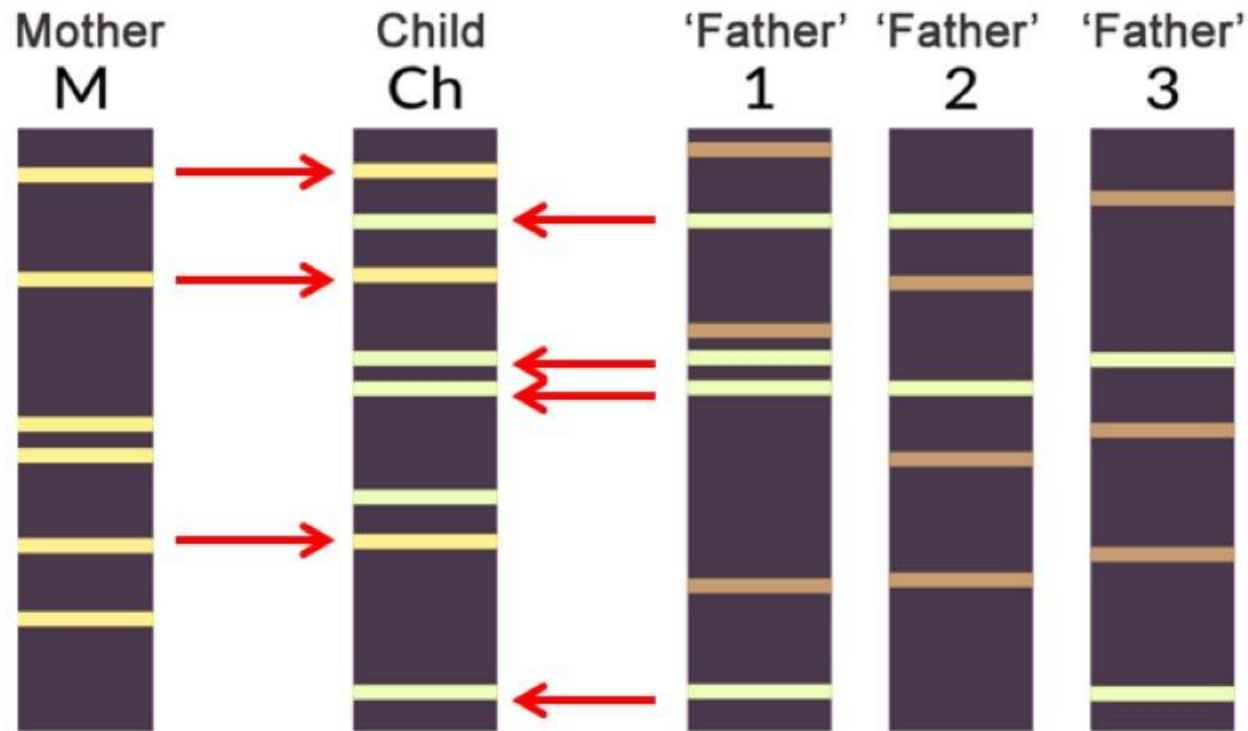
6. Detection of hybridized DNA by autoradiography.

DNA FINGERPRINTING: APPLICATIONS



- 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.

DNA FINGERPRINTING: APPLICATIONS



Solving paternity using DNA fingerprinting

Here, person 1 is likely to be the father of child

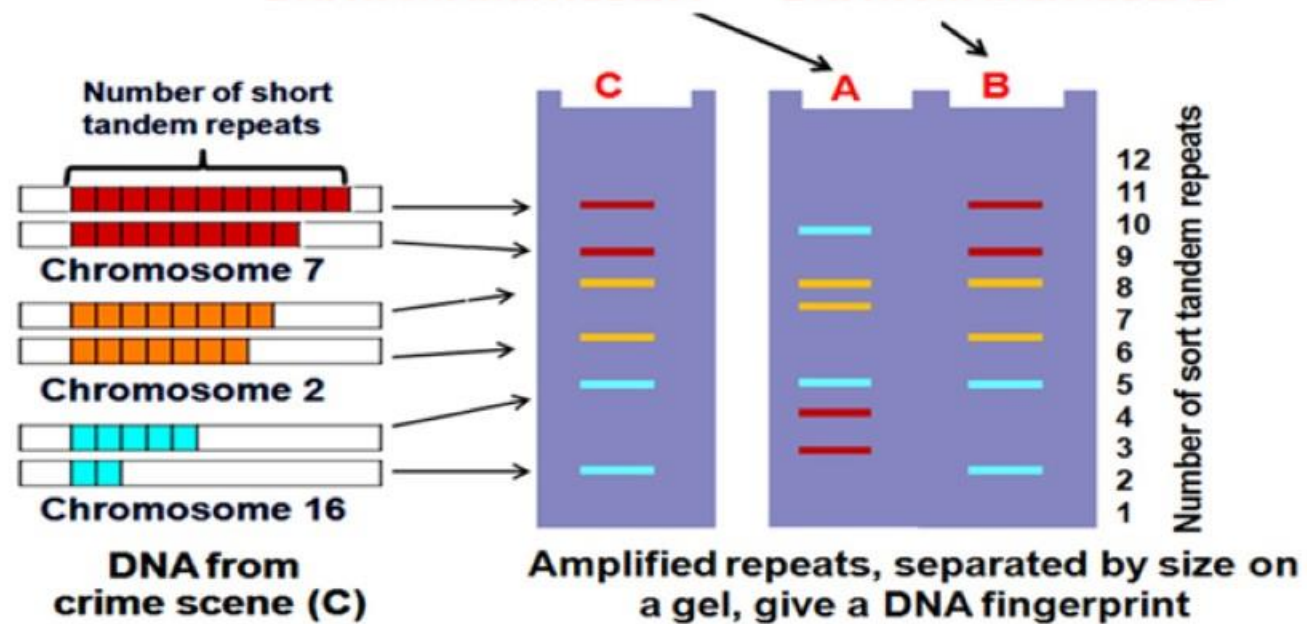
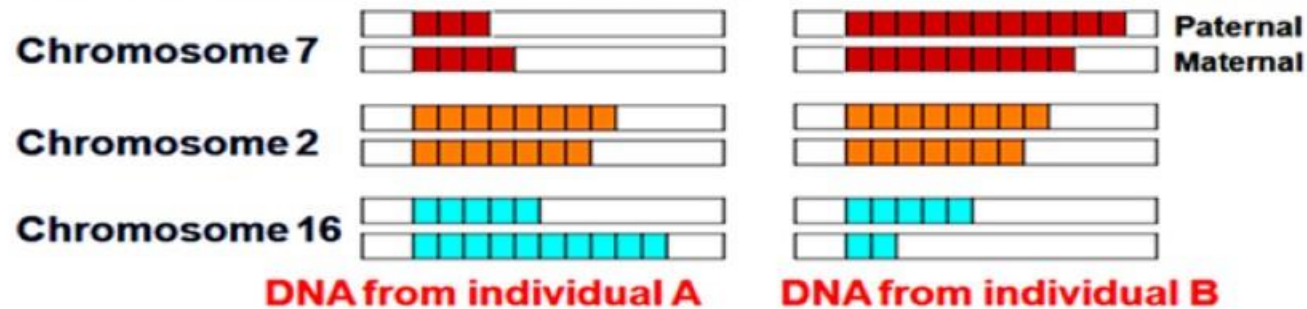
- Forensic tool to solve paternity, rape, murder etc.

- For the diagnosis of genetic diseases.

- To determine phylogenetic status of animals.

- To determine population and genetic diversities.

DNA FINGERPRINTING: APPLICATIONS



■ 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.

Solving a crime with the help of DNA fingerprinting