PRACHAND NEET

ONE SHOT

Botany

Molecular Basis of Inheritance

(Part- 2)

By –Archana Rathi Ma'am

PRACHAND SERIES

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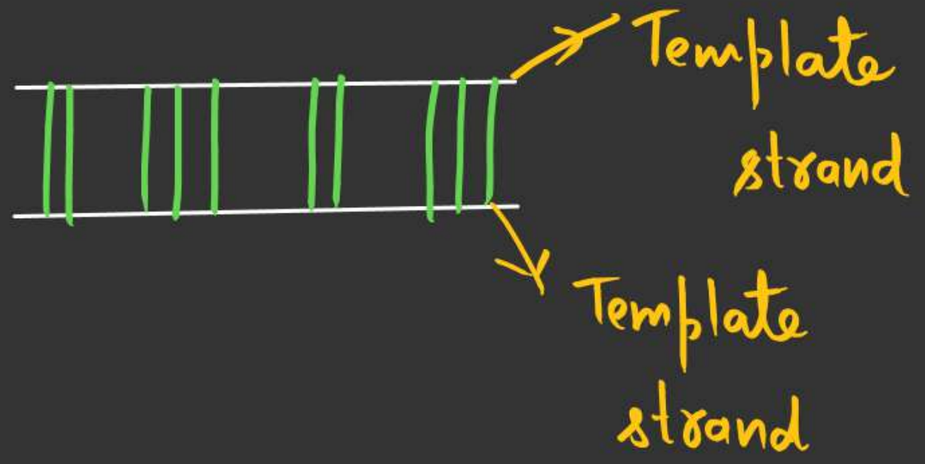
REPLICATION

Duplication of DNA where both strands of DNA act as Template strand



Site :

- Pro → Cytoplasm → During Binary fission
- EuK → Inside nucleus → During "S-phase" of Cell cycle

NOTE :

Entire length of DNA is replicated at the same time.

REPLISOME

(All the proteins & Enzymes together)

Topoisomerase

Releases the tension/supercoiling of DNA.

Helicase / Unwindase

Breaks H-bonds between (2) strands of DNA.

* ATP-dependent Enzyme

DNA polymerase

DNA-dependent

* DNA polymerase (Requires DNA template)
* Polymerizing activity

Arranges nucleotides and forms phosphodiester bond.

* Polymerises new DNA strand only in 5'-3' direction.
* In E.coli

DNA polymerase arranges

2,000 base pair/second

DNA polymerase

Cannot initiate the process.

Primase Enzyme → Forms RNA Primer

Has RNA polymerase activity

* Has initiating capacity

Has Free 3'-OH

DNA Ligase

(Molecular glue)

Joins DNA fragments

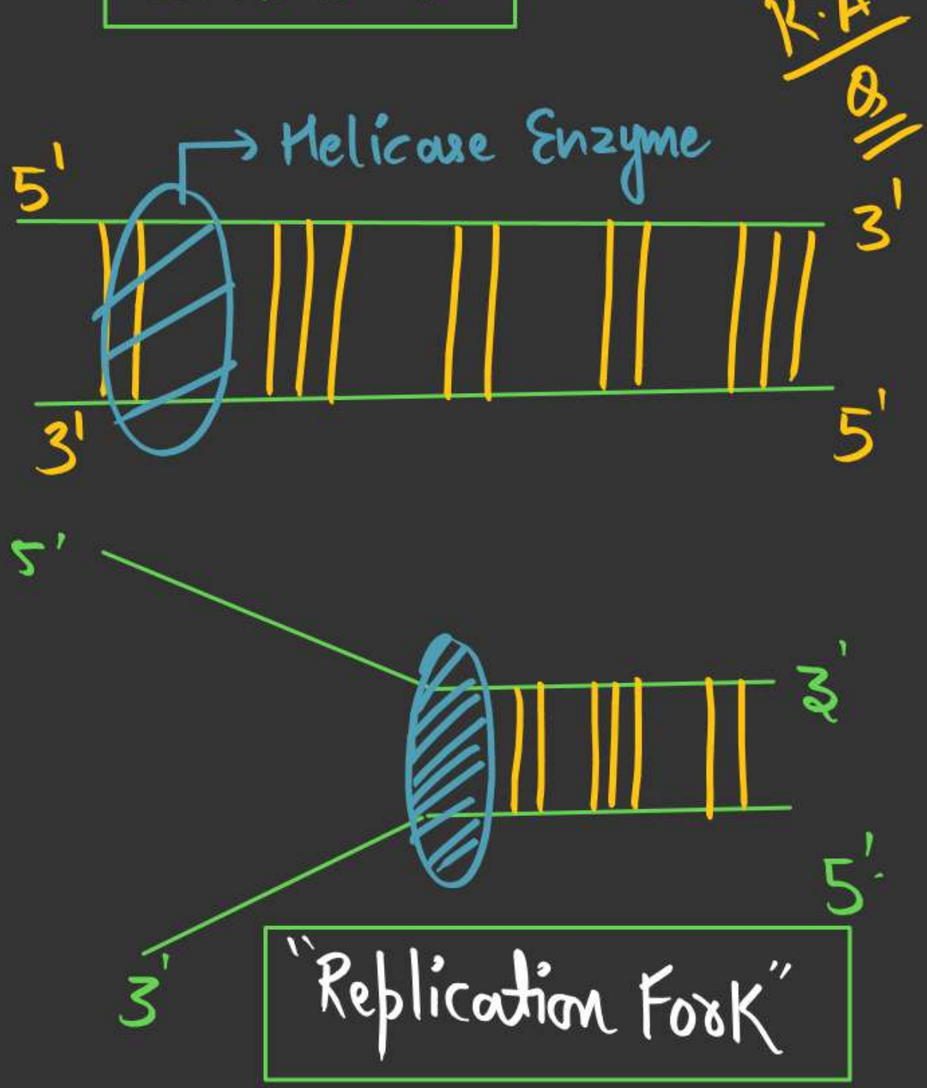
Process of Replication

- Initiation
- Elongation
- Termination

(a) Topoisomerase
Releases supercoiling

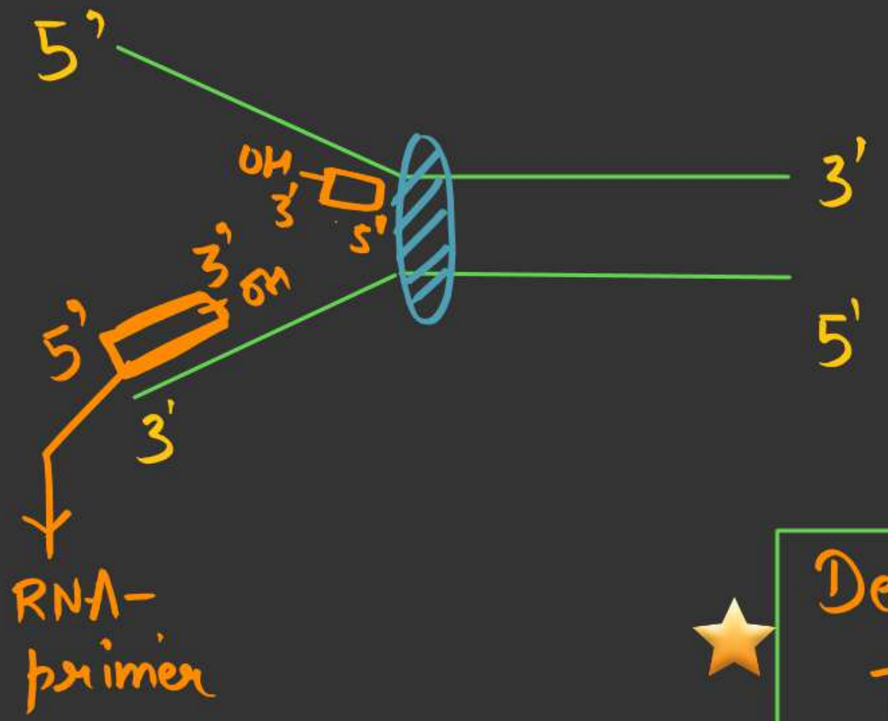
(b) Helicase
Enzyme

Initiation



Why Replication Fork is fork formed?

* Cell cannot provide enough energy to Helicase to open up whole DNA at the same time.



Activation | charging of nucleotides

deoxynucleoside monophosphate → deoxynucleoside triphosphate

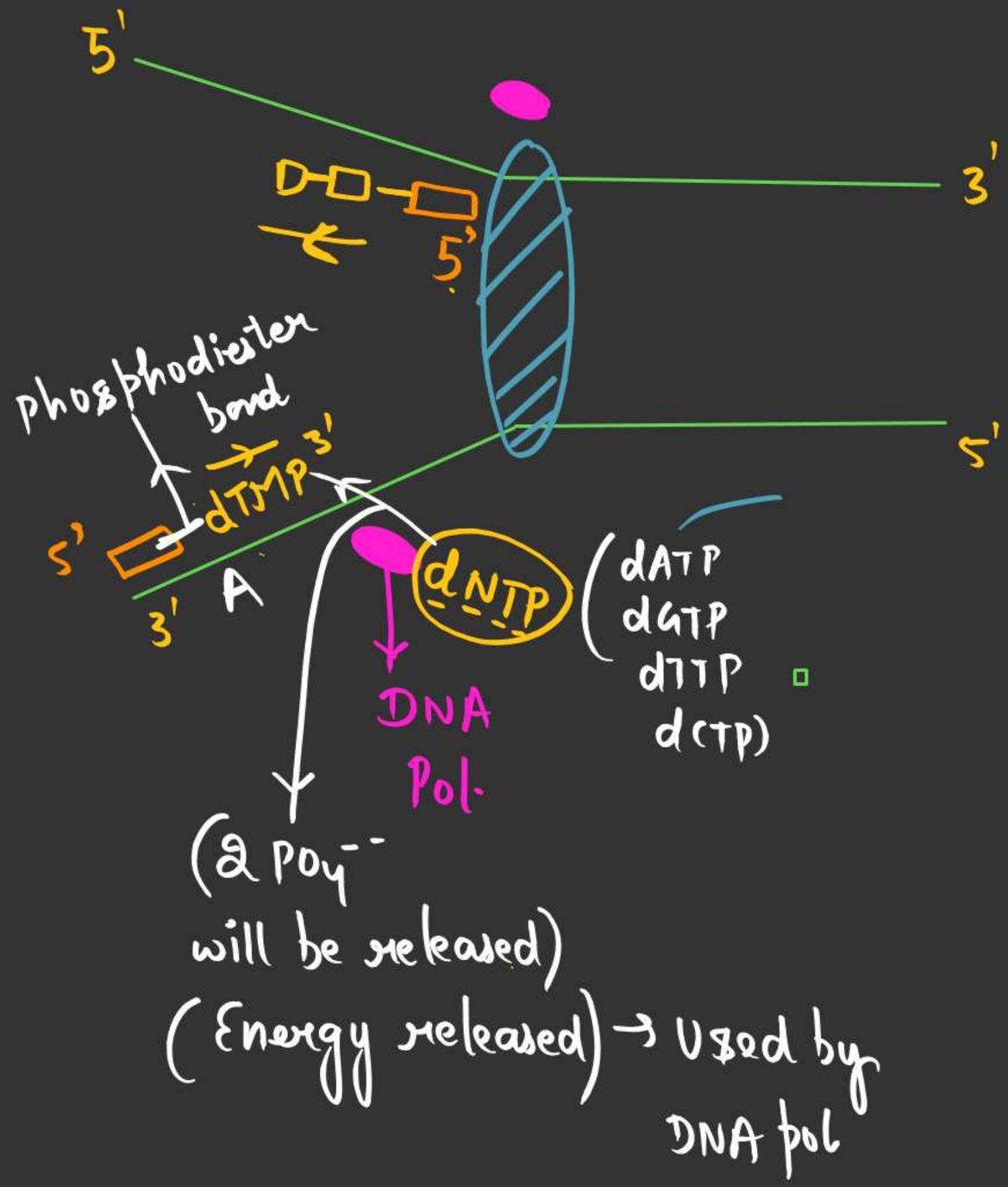
PYQ

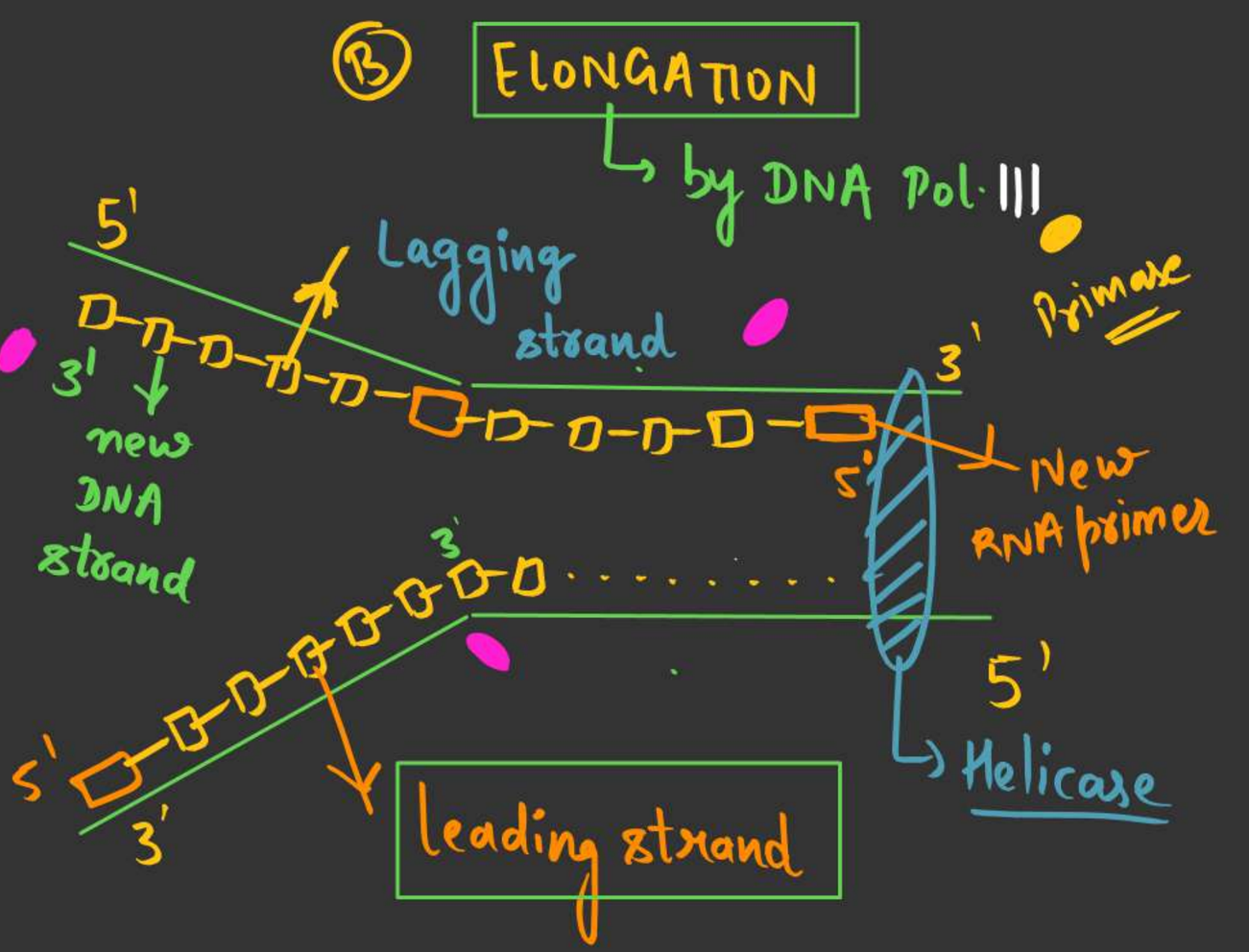
Deoxynucleoside Triphosphates

(Dual purpose)

- Act as Substrates for DNA polymerase
- Provide Energy for Polymerization.

- dAMP → dATP
- dCMP → dCTP
- dGMP → dGTP
- dTMP → dTTP


5'
3'
5'
5'
3'
Phosphodiester bond
dTTP
3'
5'
A
3'
dNTP
dATP
dGTP
dTTP
d(TP)
DNA Pol.
(2 PO_4^{--} will be released)
(Energy released) → Used by DNA pol


(B) ELONGATION
↳ by DNA Pol. III
5'
Lagging strand
Primase
3'
3'
new DNA strand
3'
5'
New RNA primer
3'
5'
5'
Helicase
5'
3'
leading strand

Questions:

Leading strand

★ Polarity → 5'-3'

★ Polarity of Template strand → 3'-5'
of leading strand

* Synthesised continuously

* Requires Single RNA Primer

Lagging strand

★ Polarity → 3'-5'

★ Template strand → 5'-3'

* Synthesised discontinuously in the form of Okazaki fragments
(later on joined by DNA ligase)

* Requires many RNA Primers

* DNA Replication
  - Semi-conservative
  - Semi-discontinuous → (R.A) 0//

★ a) DNA pol. polymerises only in 5'-3' direction ★

★ b) The two template strands of DNA are "Anti-parallel" ★

Activation of Nucleotides

Pyrophosphorylase

dAMP → dATP

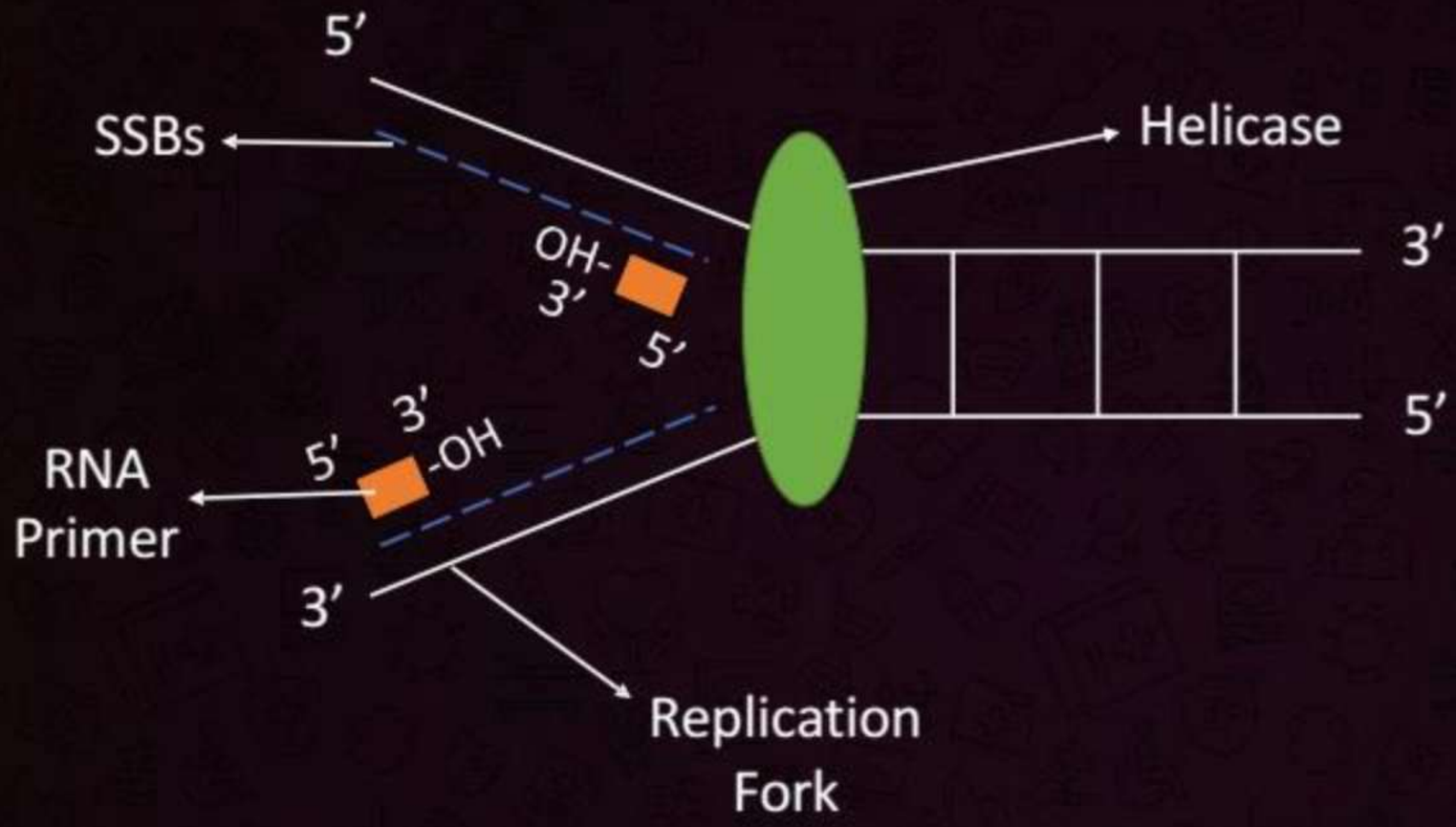
dGMP → dGTP

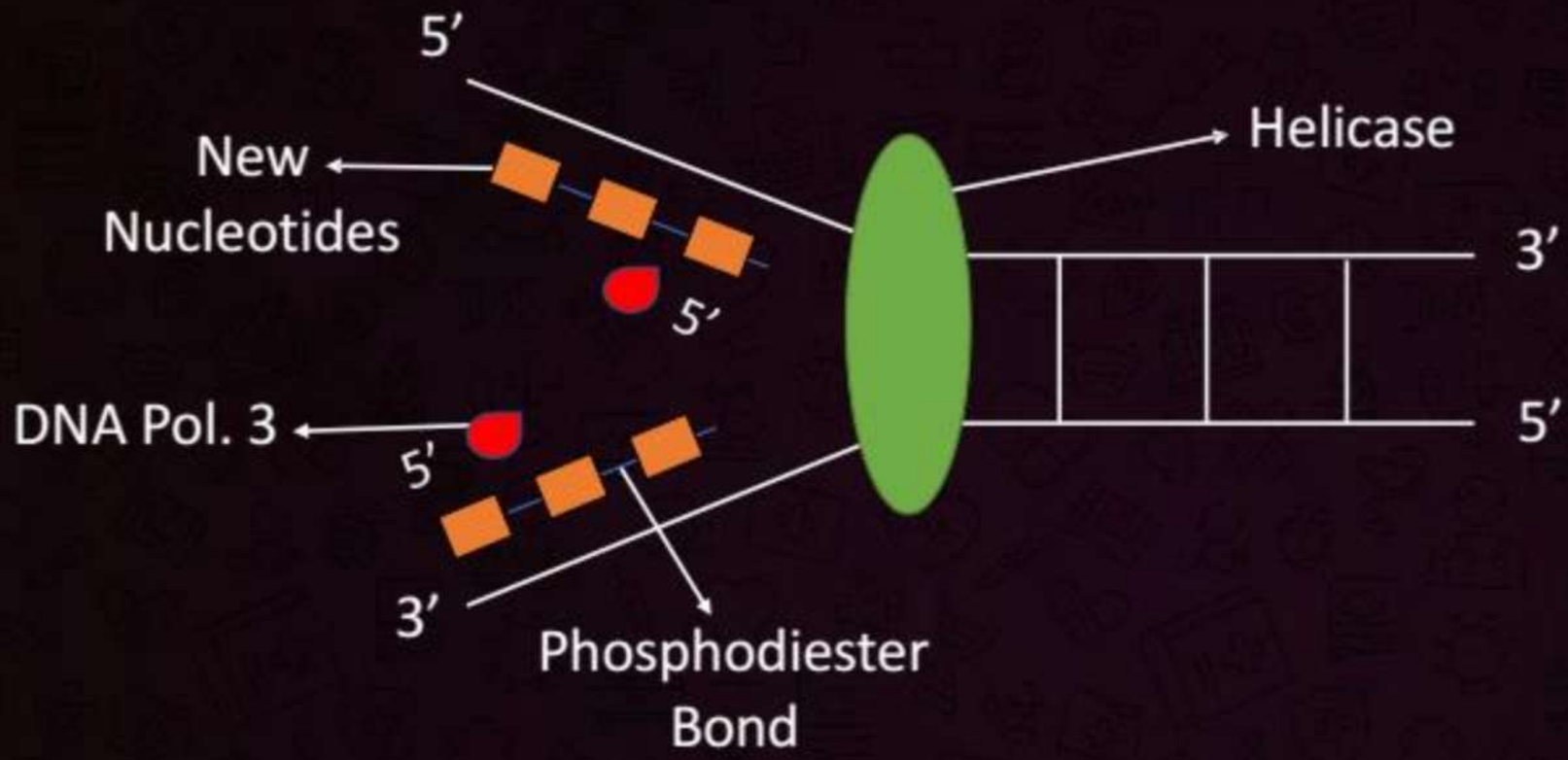
dCMP → dCTP

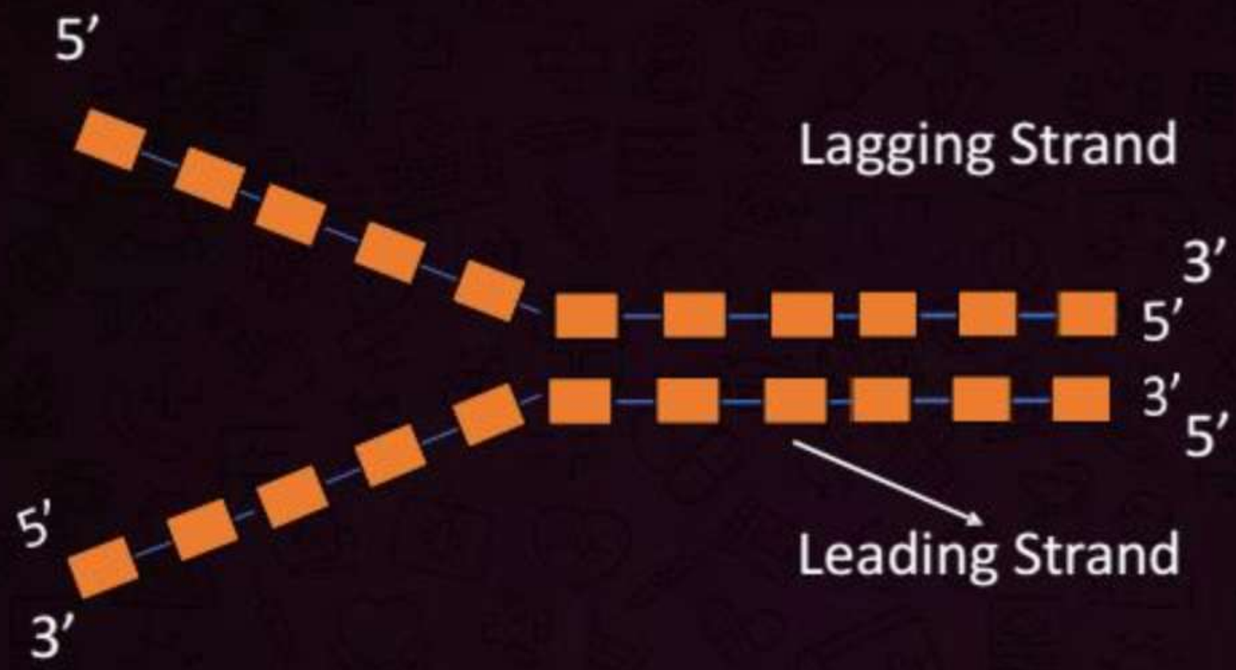
dTMP → dTTP

Inactive Nucleotide

Active Nucleotide


5′
SSBs
Helicase
OH-
3′
5′
3′
5′
3′
5′
-OH
RNA
Primer
3′
Replication
Fork


5′
New
Nucleotides
5′
Helicase
3′
5′
DNA Pol. 3
5′
3′
Phosphodiester
Bond


5′
Lagging Strand
3′
5′
3′
5′
5′
3′
Leading Strand

After both the new strands are synthesized on template strand.

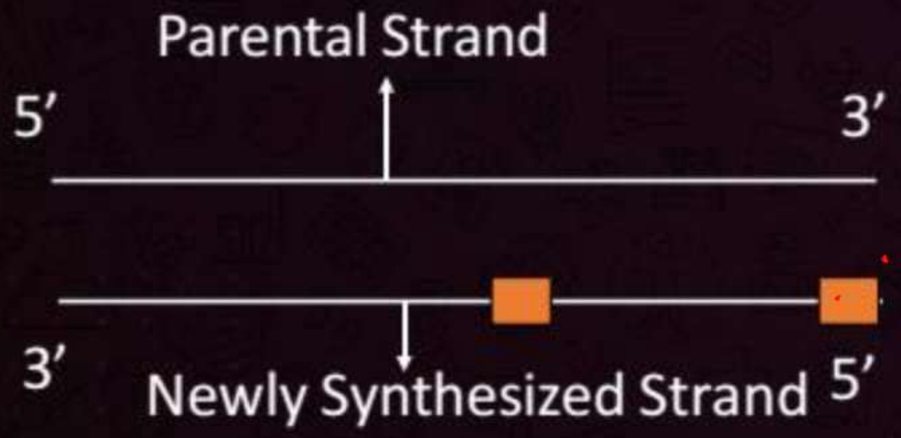
- Proof Reading is done by DNA Pol.1
- Removal of RNA Primer

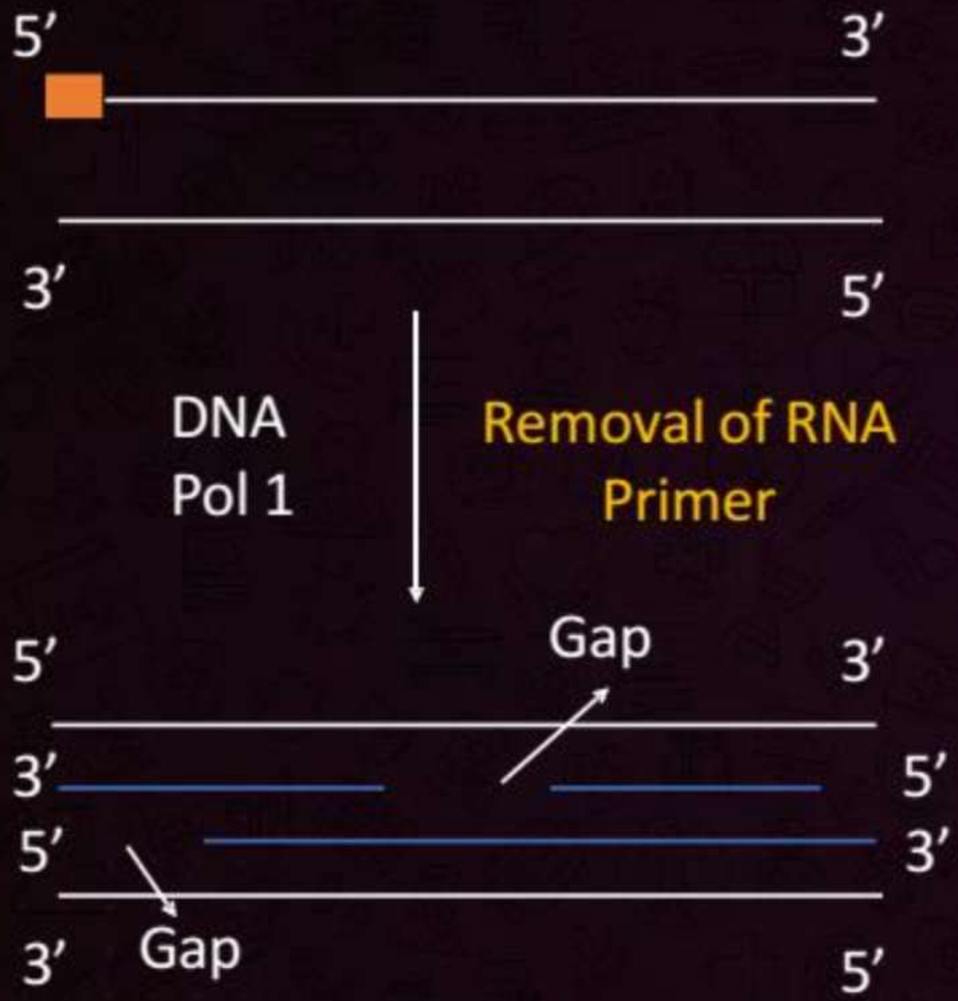
DNA Pol.

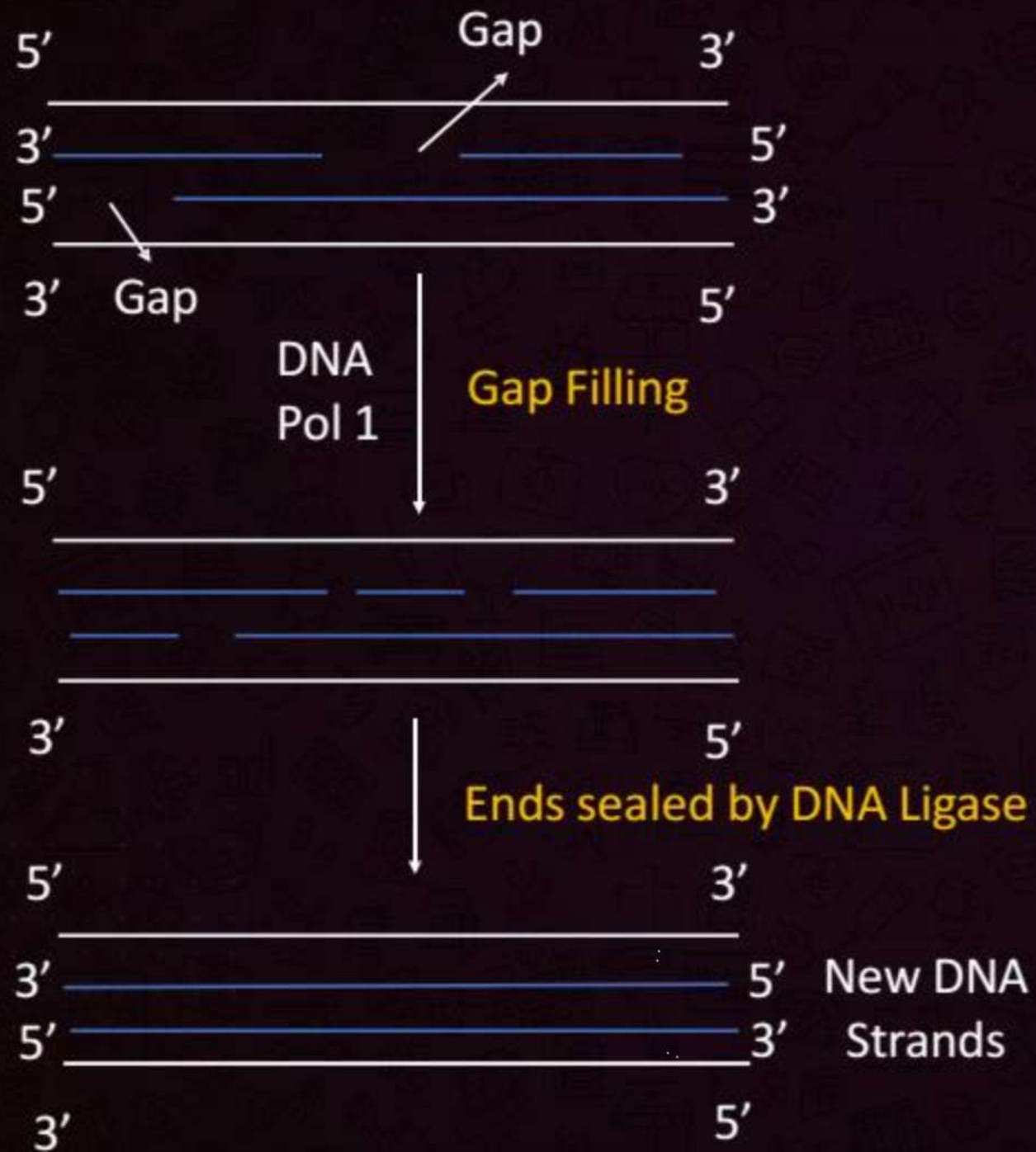
Pol. I

Pol. II

Pol. III




5′
3′
3′
5′
DNA
Pol 1
Removal of RNA
Primer
Gap
5′
3′
3′
5′
5′
3′
3′
Gap
5′


5′
Gap
3′
3′
5′
5′
3′
3′
Gap
5′
DNA
Pol 1
Gap Filling
5′
3′
3′
5′
Ends sealed by DNA Ligase
5′
3′
3′
5′
New DNA
Strands
5′
3′
3′
5′

Ori

* Origin of Replication
* A-T rich sequences
* Replication starts

Polyploidy

After Replication if a cells fails to divide, then polyploidy occurs.

Transcription

Copying of genetic information from one strand of DNA to m-RNA (RNA)

Site:

- Pro → cytoplasm
- Euk → Inside nucleus

Replication	Transcription
* Both DNA strands → Template	* One DNA strand → Template Polarity → 3'-5'
* Entire length of DNA participates	* Only a part of DNA participates (Gene)

Transcription

DNA ⟶ mRNA

DNA ⟶ t-RNA

DNA ⟶ r-RNA

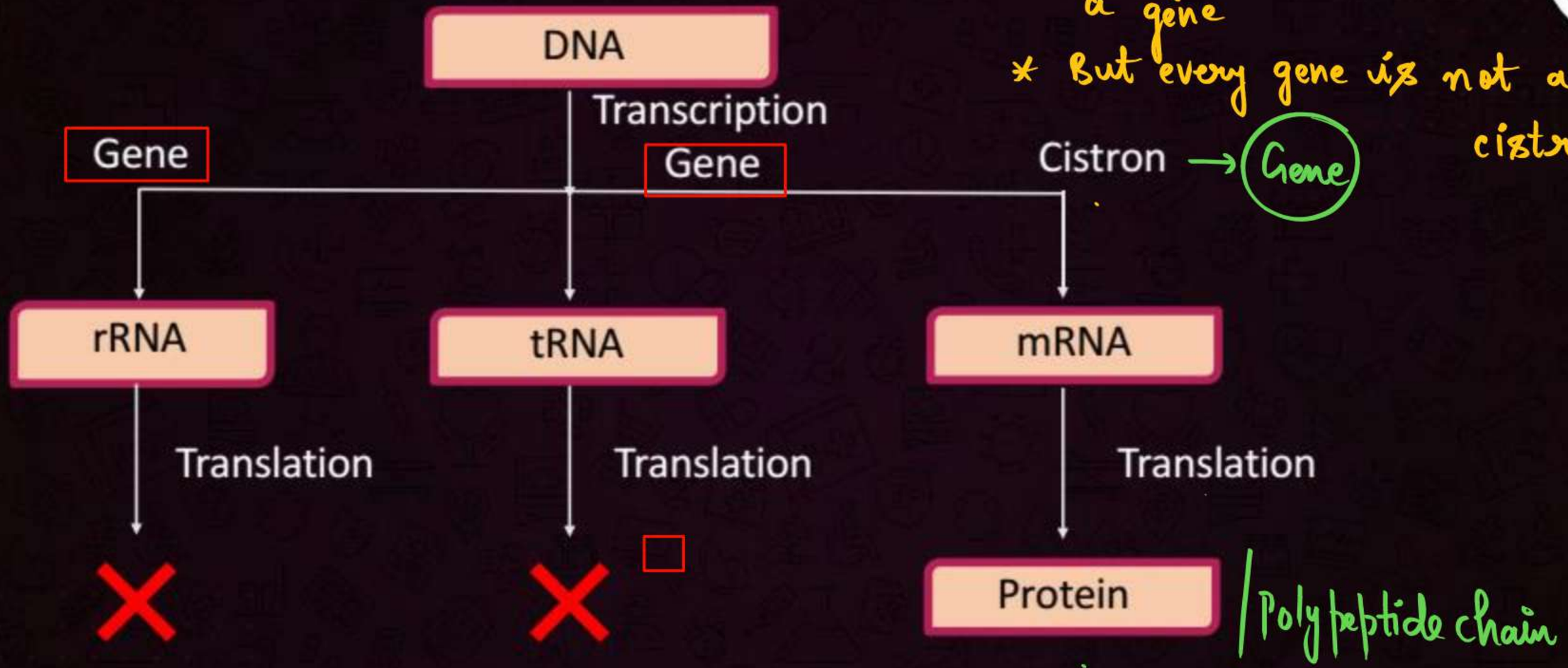
R.A

DNA → Both strands do not participate

If participated

* ds RNA (do not exist) would have formed

* If two-proteins would have formed then would have interacted



* Every cistron is a gene
* But every gene is not a cistron.

Cistron → Gene

Polypeptide chain

RNA Polymerase

* DNA-dependent RNA polymerase

* Also synthesizes RNA in 5'-3' direction

* ★ During Transcription ★

MB

RNA polymerase itself Breaks H-bonds

In Prokaryotes

only one type of RNA polymerase

In Prokaryotes

- Only one type of RNA polymerase is present.

Holoenzyme

Core Enzyme

- It helps in elongation of RNA on the template strand

σ - factor

- It initiates the process

In Eukaryotes

Imp PYQ

Three types of RNA polymerase is present.

RNA Pol. 1	RNA Pol. 2	RNA Pol. 3
➢ 28 srRNA ➢ 5.8 srRNA ➢ 18 srRNA	➢ Hn-RNA (Heterogenous nuclear RNA) ↓ (m-RNA)	➢ t- RNA ➢ 5sr RNA ➢ Sn RNA ➢ Sc RNA

Sn RNA (Small nuclear RNA)

Sc RNA (Small cytoplasmic RNA)

RNA Polymerase can synthesize only in 5'-3' direction.

Transcription Unit

Cistron

Promoter Site

Structural Gene

Terminator Site

Coding / Non-template strand / Sense strand

Polarity → 5'-3'

Template strand / Non-coding / Anti-sense

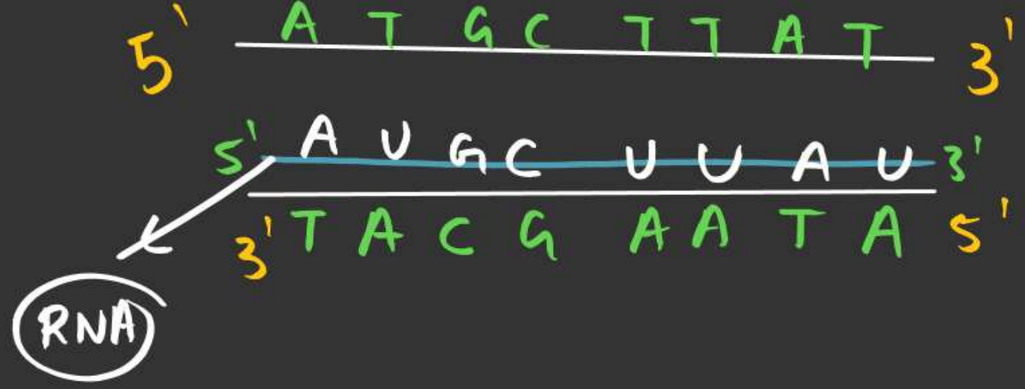
Polarity → 3'-5'

Coding strand

=

Frame of reference

Explained — Promoter, Terminater



The sequence of RNA

is similar as of

m-RNA (except thymine)

Promoter

* Towards 5'-end
* Upstream sequences
* RNA-polymerase binding site

Terminator

→ Towards 3'-end

→ Downstream sequence

→ Stops transcription.

Structural gene

↓

Actually codes for m-RNA

Cistron

Monocistron

Has information for formation of single polypeptide chain (Protein)

* Mostly Eukaryotes.

Polycistron

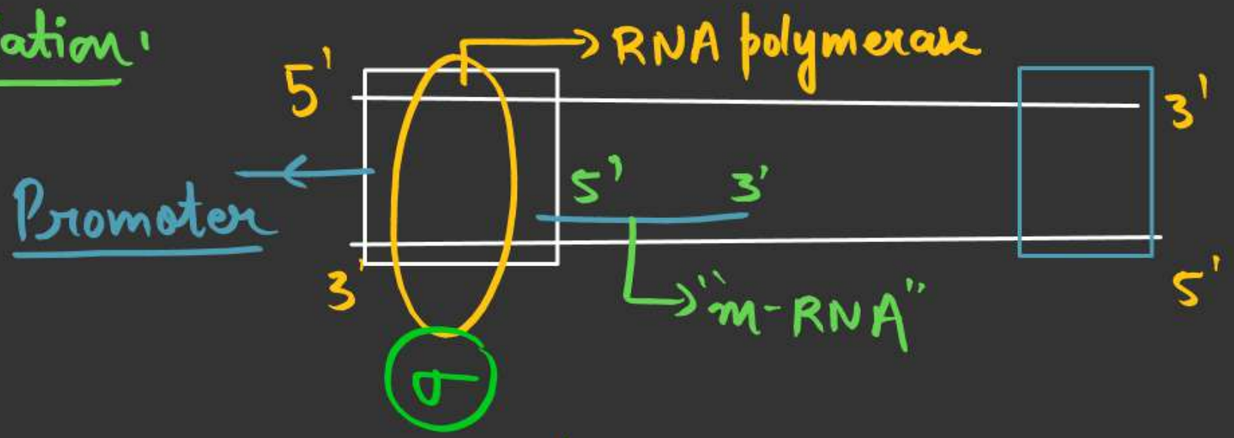
* Has information for more than one proteins

Ex → In prokaryotes (only)

Ex → operon

Transcription

Initiation:



Sigma-factor

Help in recognition of promoter sequence.

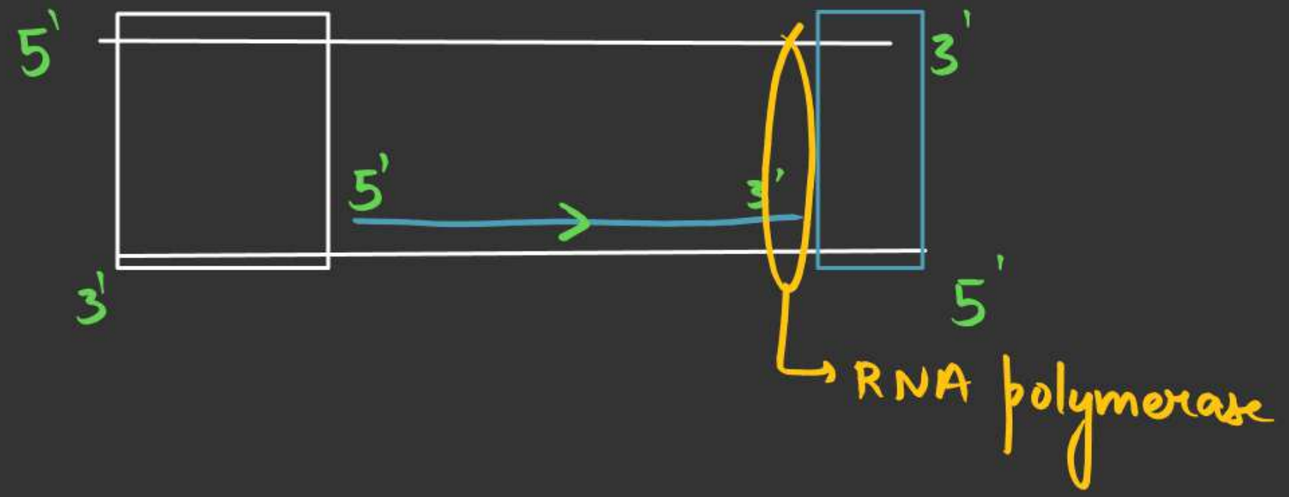
Once RNA starts to form →

σ factor

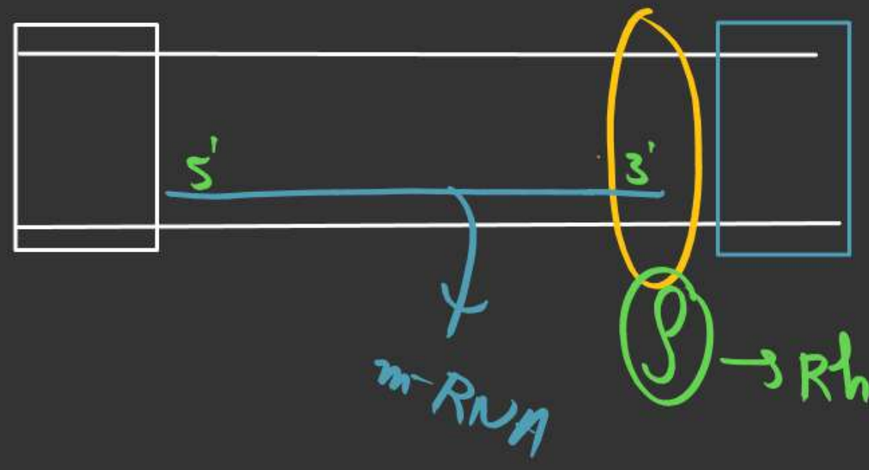
separates.

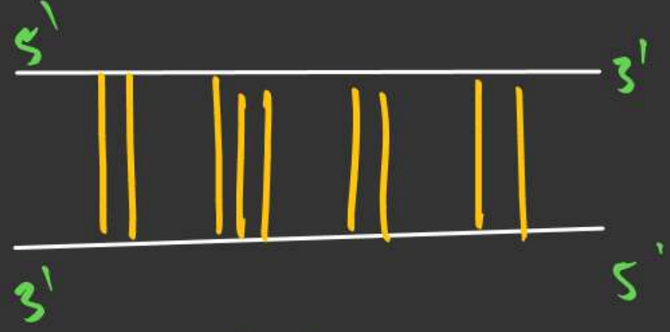
Elongation:

RNA polymerase



Termination:





DNA

5' 3'

m-RNA

In Bacteria

* Cytoplasm
* Needs no processing
* Ready for Translation.

In Eukaryotes

→ called as "Primary transcript" (hn-RNA)

(Inside nucleus)

* Not ready for Translation
* Requires **Processing**

Types of RNA

m-RNA	r-RNA	t-RNA
Messenger RNA/ Postman RNA/Carrier RNA / Template RNA	Ribosomal RNA	Transfer RNA/ Soluble RNA/Adapter molecule
It constitutes 5% of total RNA	It constitutes 80% of total RNA	It constitutes 15% of total RNA

m-RNA	r-RNA	t-RNA
Longest RNA	Smaller than mRNA	Smallest of all RNA
Least stable	Most stable	Stable
It carries information from DNA for polypeptide synthesis.	It has structural role & catalytic role	It carries amino acid from cytoplasm to mRNA during translation.

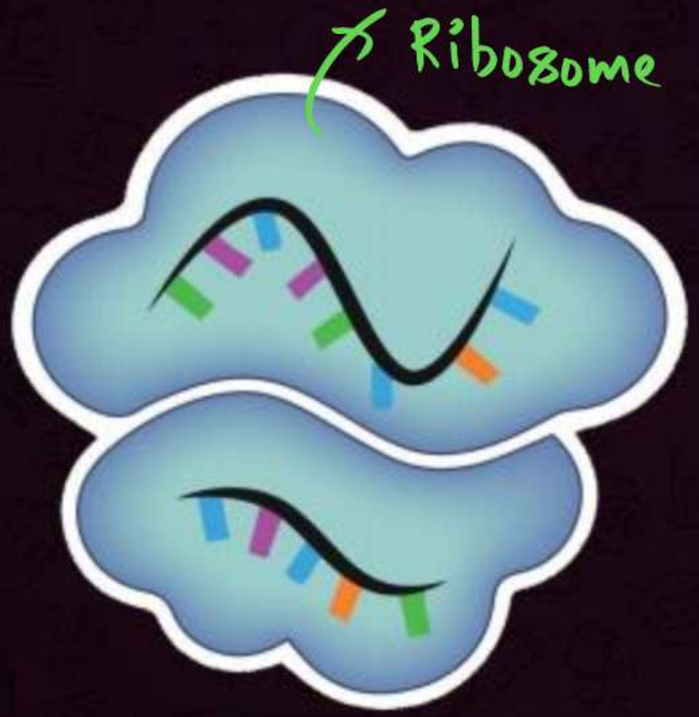
Forms Ribosome

Peptidyl transferase

m-RNA

r-RNA

t-RNA



RNA Processing

/ RNA maturation / PTM (Post Transcriptional Modification)

Occurs in nucleus and only in Eukaryotes.

hn-RNA $\xrightarrow[\text{PTM's}]{}$ m-RNA

- Capping
- Tailing
- Splicing

① Capping (CAP molecule at 5'-end)

CAP → 7-MG

[7-methyl Guanosine Triphosphate] (GTP)

② Tailing → 200-300 (ATPs)

or

POLYADENYLATION

Adenylate / Adenylic residues are added at 3'-end

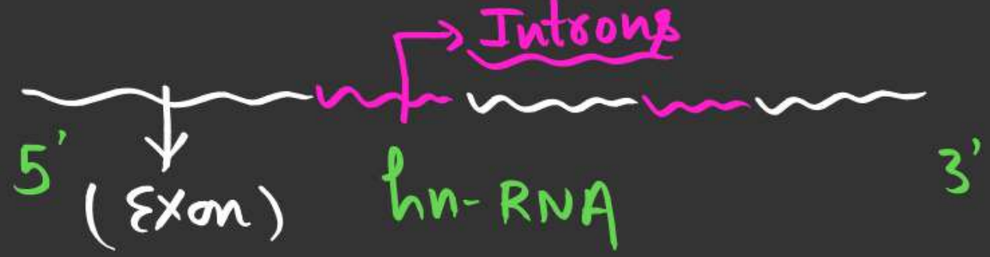
Done by

Poly A polymerase | Adenylate polymerase

Template independent Enzyme

(3) **Splicing**

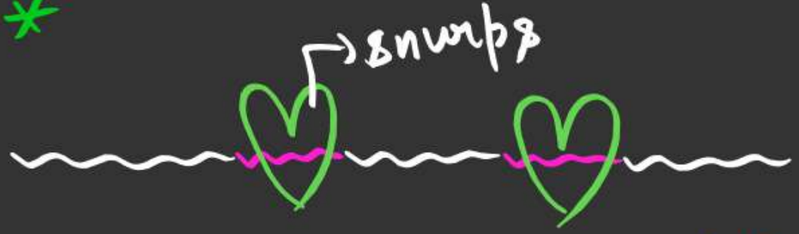
Removal of Introns from hn-RNA

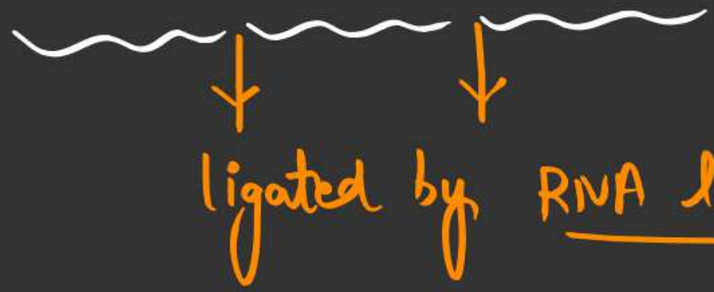


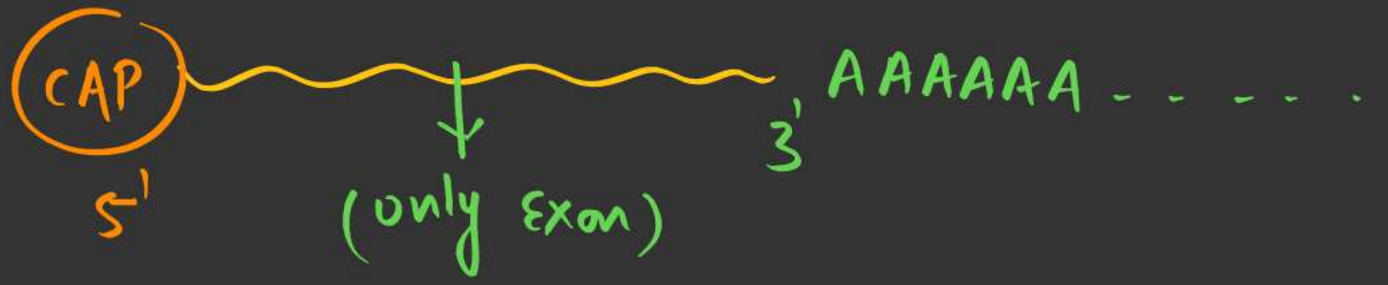
* Snurps | Sn RNPs

- Sn-RNA (Small nuclear RNA)
- Protein

*







Now it is called as m-RNA

Ready to be transported to cytoplasm for Translation.

"Split-Gene"

Split-gene Arrangement → only in Eukaryotes

Exon
(Coding part)

Introns
(Intervening sequences)
(Non-coding parts)

Introns < DNA, m-RNA

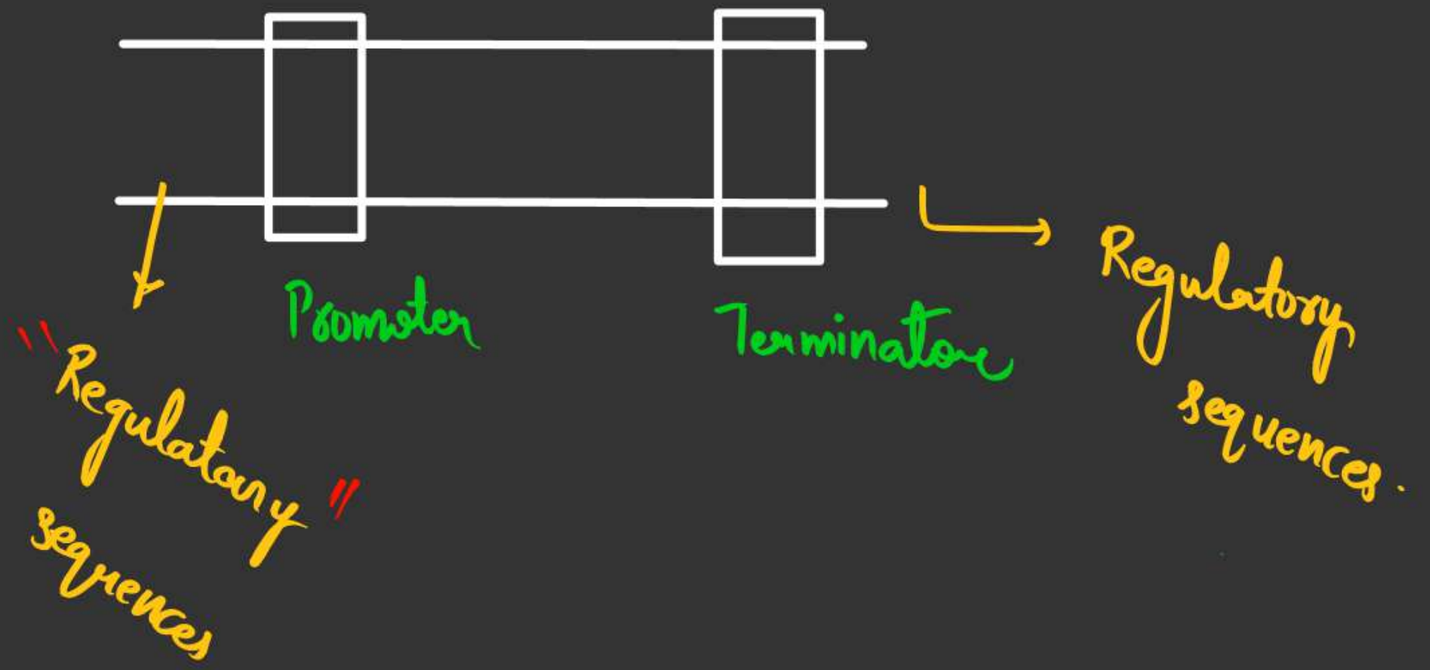
Introns → only in Eukaryotes

Introns are Absent in Prokaryotes

Important 3-lines

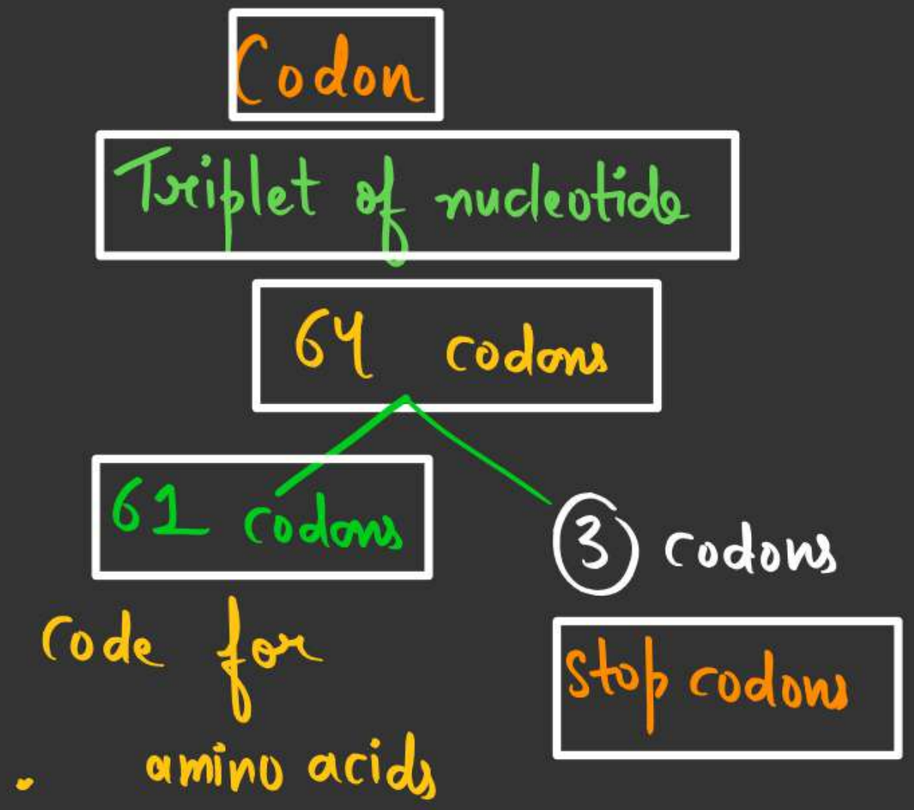
1. Split-gene arrangement is the ancient feature of genome.
2. **Presence of introns** is the Reminiscent of Antiquity
3. **Splicing** represents Dominance of RNA world.

Inheritance of a character is also affected by promoter and regulatory sequences of a structural gene. Hence, sometime the regulatory sequences are loosely defined as regulatory genes, even though these sequences do not code for any RNA or protein.



Genetic Code → Term → George Gamow

Inter-relationship between nucleotide sequences on DNA / m-RNA and amino-acid sequences on protein chain.



Decipher | Crack → Genetic Code

Nirenberg $ Matthaei

↓

Used only Homopolymers

Har-Gobind Singh Khurana

↓

Used both Homopolymers $ (Heteropolymers | Co-polymers)

✕

Nirenberg $ Har Gobind Singh Khurana

↓

Nobel Prize

* Synthetic m-RNA was formed.

By Severo-ochoa Enzyme / Polynucleotide phosphorylase

PYO = Imp

* works in DNA-template undependent manner

(Nirenberg) U U U U U U U U U U U U U U U

5' m-RNA 3'

m-RNA → (Homopolymer)

Translation

Phe Phe Phe Phe

UUU (Codon) → Phenylalanine (amino-acid)

Khurana

U C U C U C U C U C U C U C U C

Co-polymer

Characteristics of Genetic Code

Imp

Triplet nature

- Suggested by Gamow
  - $4^1 = 4$ ✗
  - $4^2 = 16$ ✗
  - $4^3 = 64$ ✓

Codons → AUG

UUU

- Proved by Nirenberg & Mathael

Universal

AUG - methionine

In all organisms.

- All the codons code for same amino acids in all organism.
- Exception – In mitochondrial DNA of mammals & Yeast, "UGA" codes for "Tryptophan" (otherwise it is stop codon). "AGG & AGA" – Stop codon (otherwise they code for for Arginine)
- UAA
  UAG
  AGG
  AGA

  Only in mitochondrial DNA of mammals & Yeast

AGA

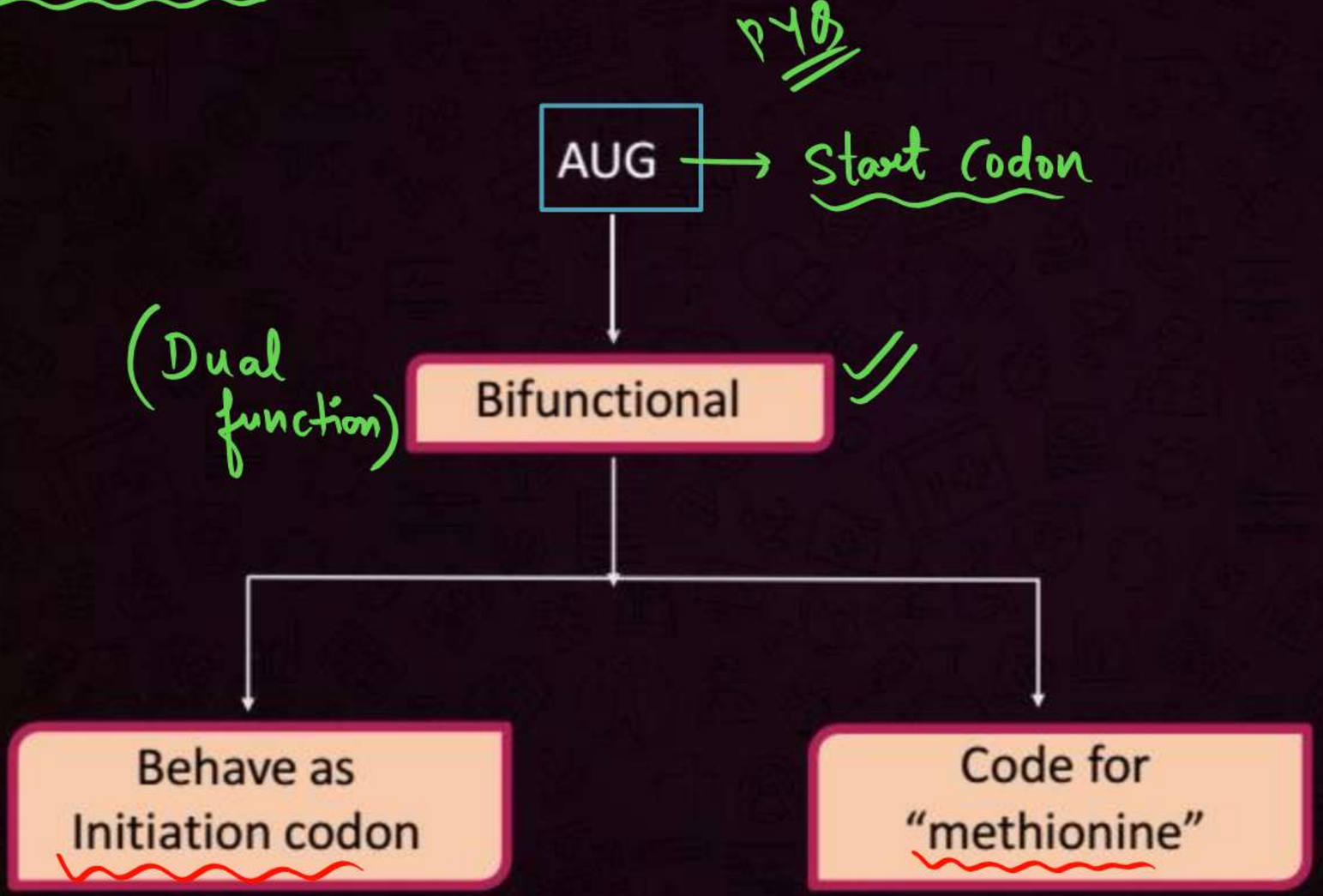
Stop codons / Termination Codons / Non-sense Codons

- Does not code for amino acids
  Also called termination codon.

- UAA = Ochre
  UAG = Amber
  UGA = Opal

8

Initiation codons



Non- ambiguous

(Clear) (Specific)

Each codon codes for a specific amino-acid.

Exception

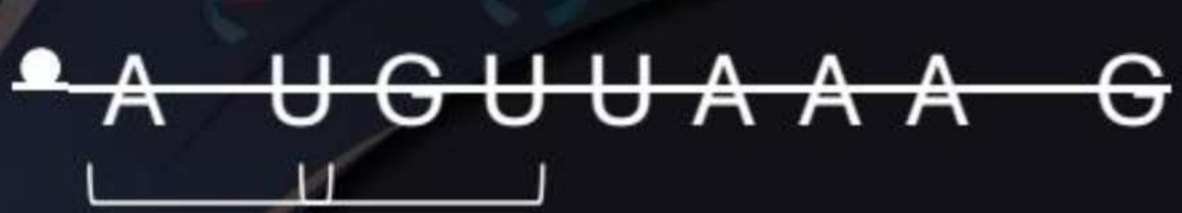
GUG is ambiguous

- Generally it codes for " Valine"
- When behaves as initiation codon(in prokaryotes) it codes for "methionine"

Commaless/Continuous

Punctuationless

Non-overlapping



Degenerate

One amino acid is coded by more than one codon.

Arginine (Amino-acid) → Coded by ⑥ codons

Serine → ⑥ codons

Non-degenerate

Exception:

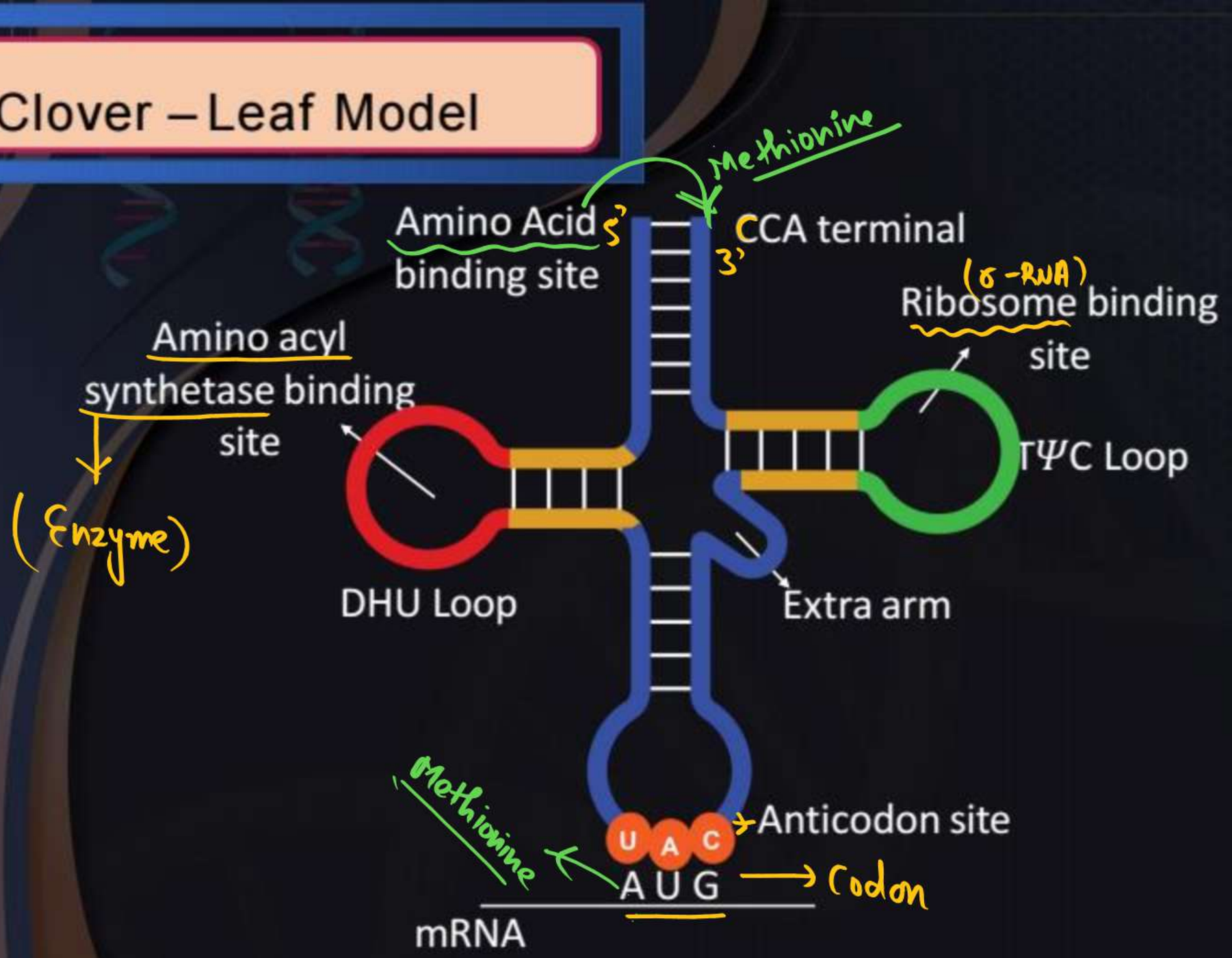
- Methionine — AUG
- Tryptophan — UGG

Structure of tRNA

Plant (Trifolium)

- Clover Leaf Model — 2-D Model
  - Given by "Halley"
- L shaped Model — 3-D Model
  - Given by "Kim & Klugs"

Clover – Leaf Model



t-RNA → Initially called as S-RNA
(Soluble RNA)

Later on:

Francis Crick → told that → t-RNA (Adapter molecule)

t-RNA → Understands Genetic Code on one hand

and can carry amino-acids on other hand.

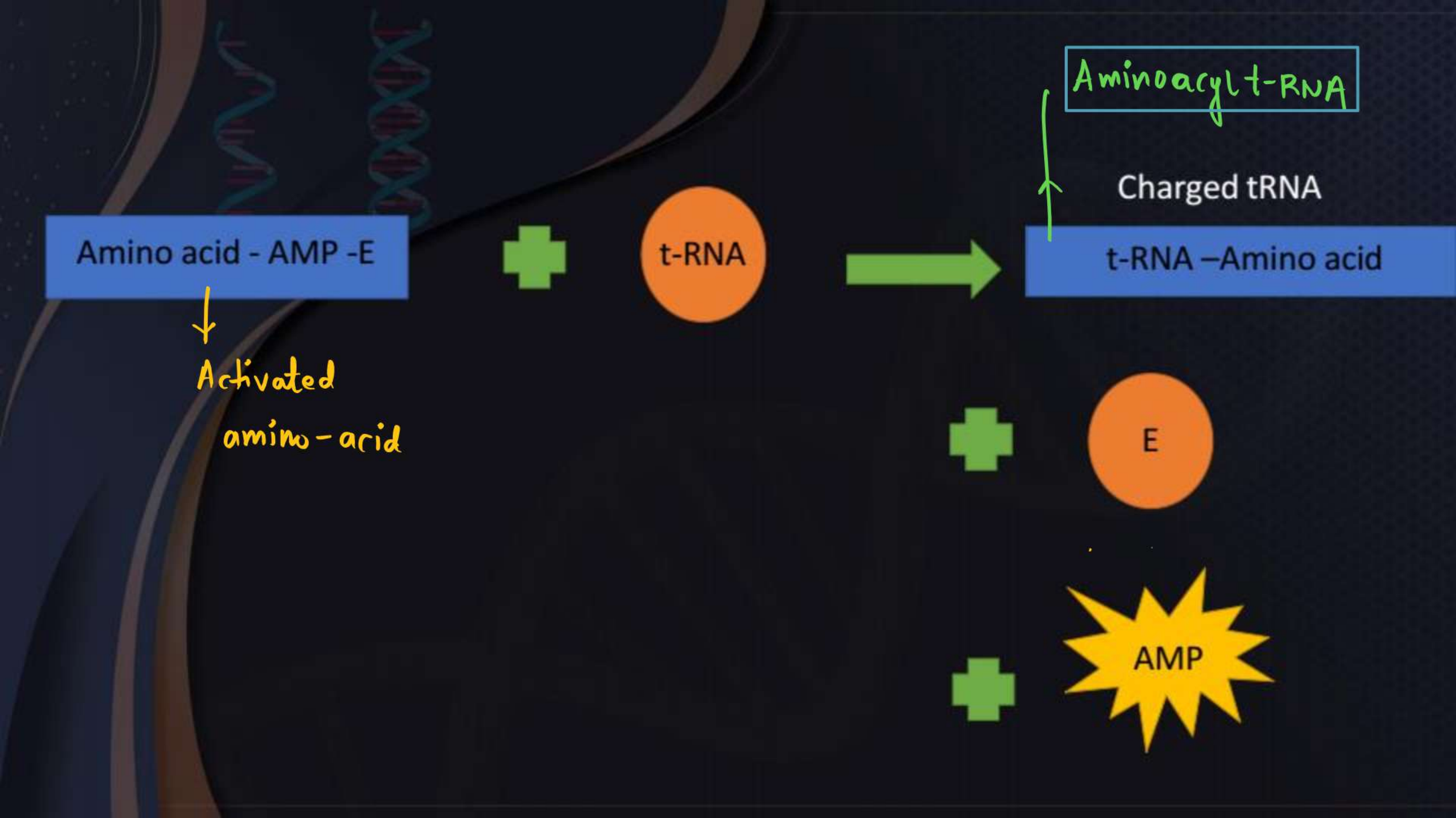
Translation

* Formation of protein chain on m-RNA

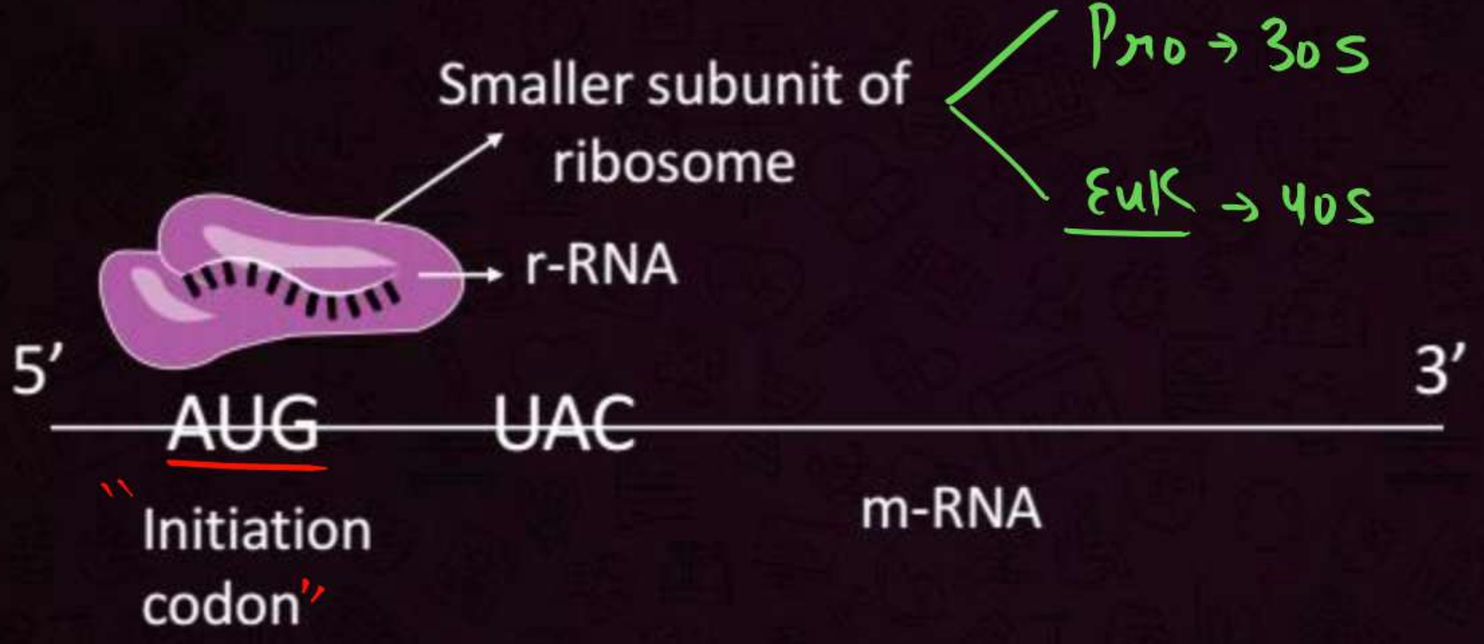
* Site
  - Pro → Cytoplasm
  - Euk → Cytoplasm

Initiation

[redacted]/Activation of amino acid


Aminoacyl t-RNA
Charged tRNA
Amino acid - AMP -E
t-RNA
t-RNA –Amino acid
Activated
amino-acid
E
AMP

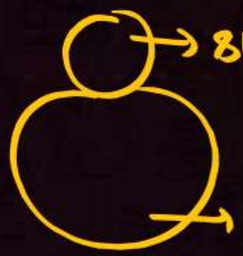
Binding of smaller subunit of ribosome to m -RNA



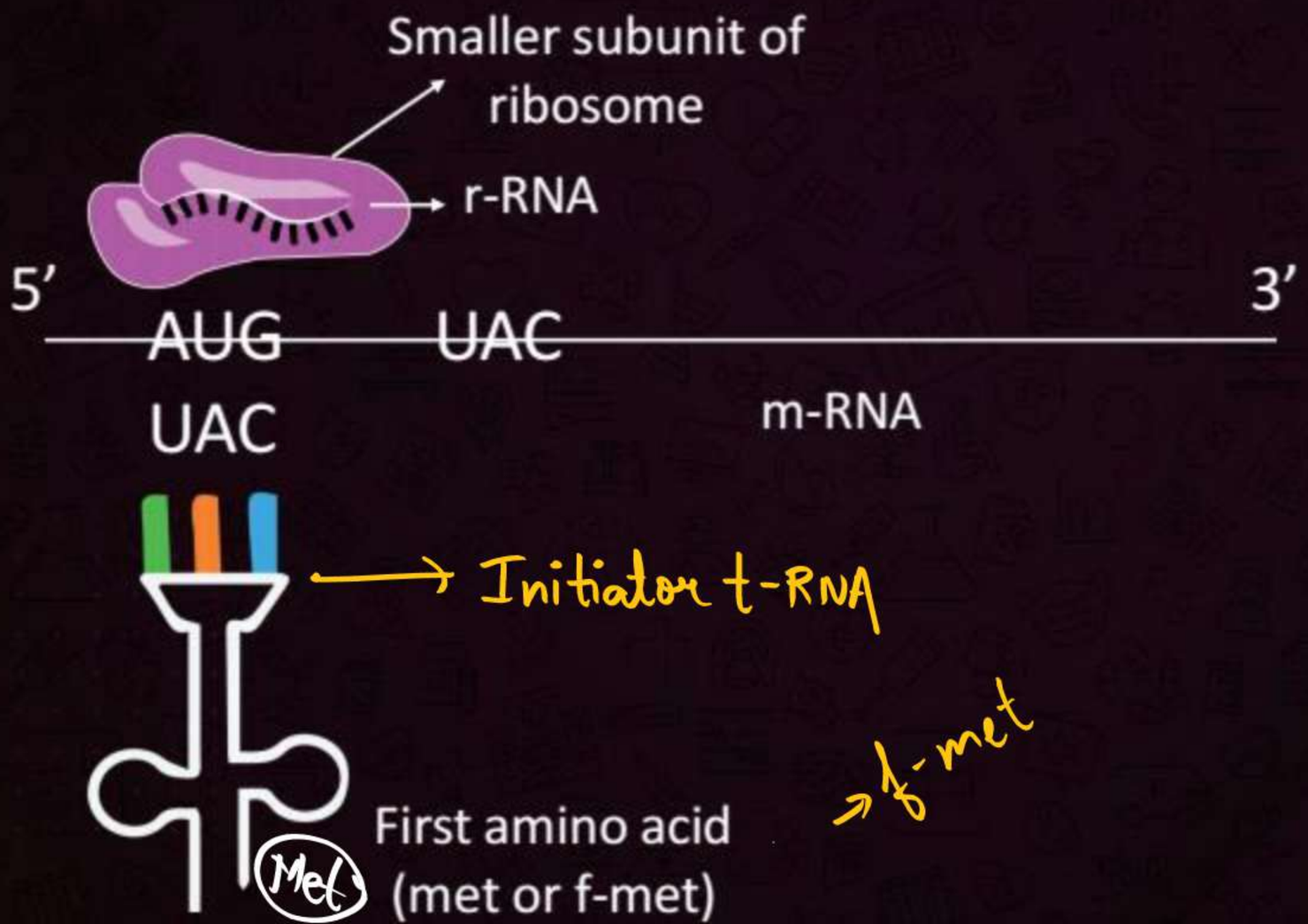
Pro → 30S

Euk → 40S

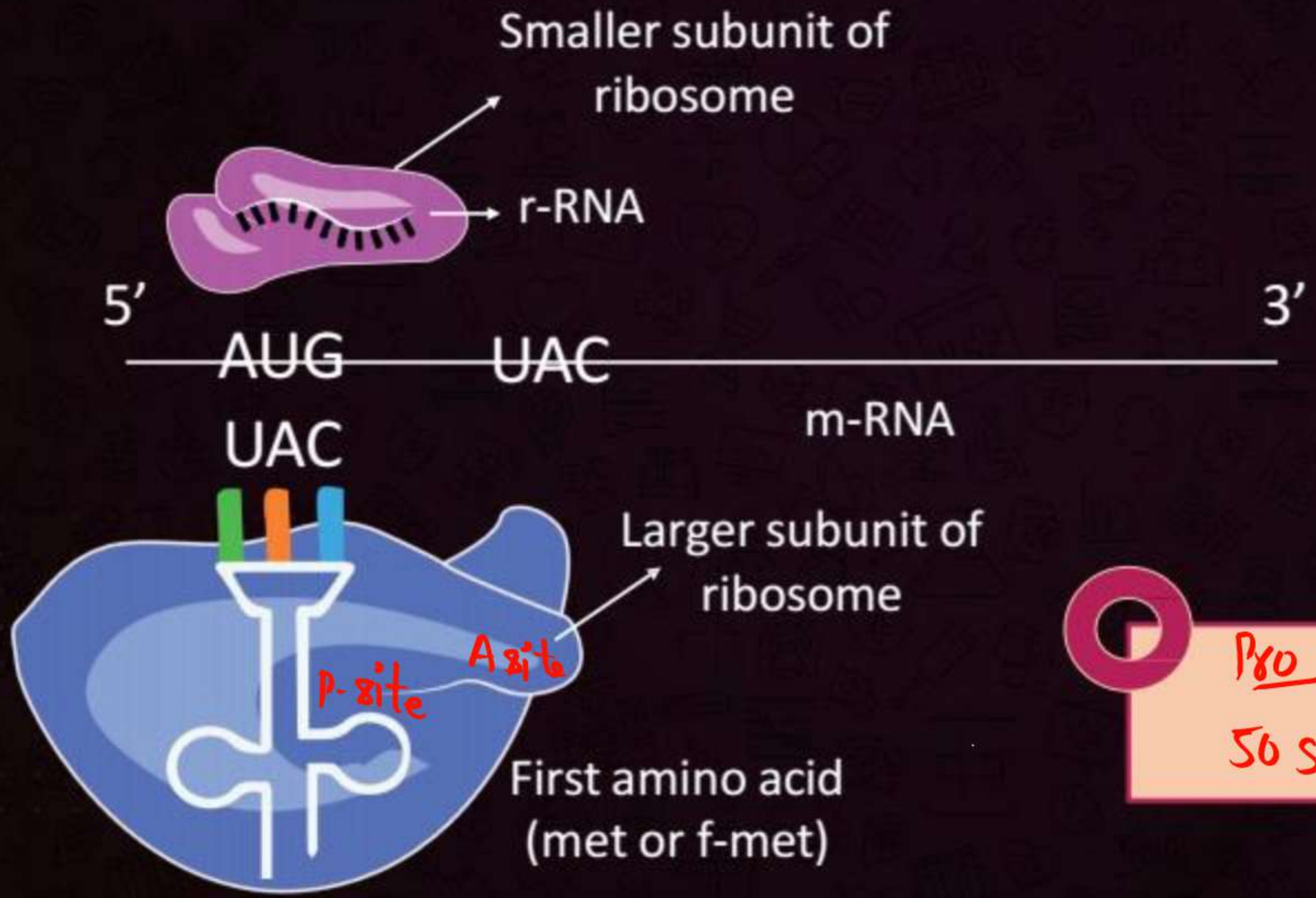
Ribosome



Binding of charged t-RNA to m -RNA



Binding of larger subunit of ribosome to m -RNA



Larger subunit

↓

2 sites

A-site

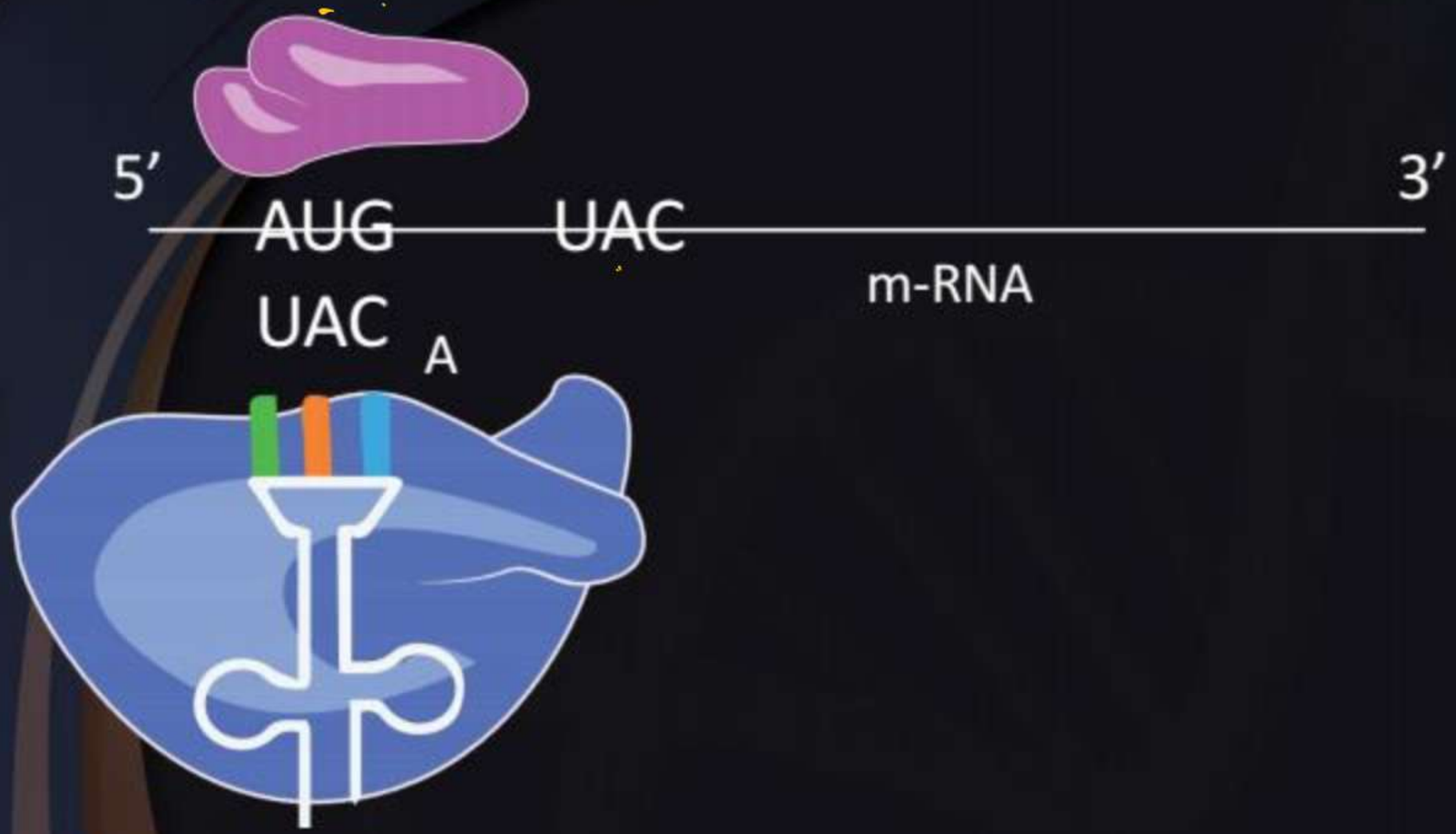
P-site

↓

Peptide bond formed

Pro	Euk
50 S	60 S

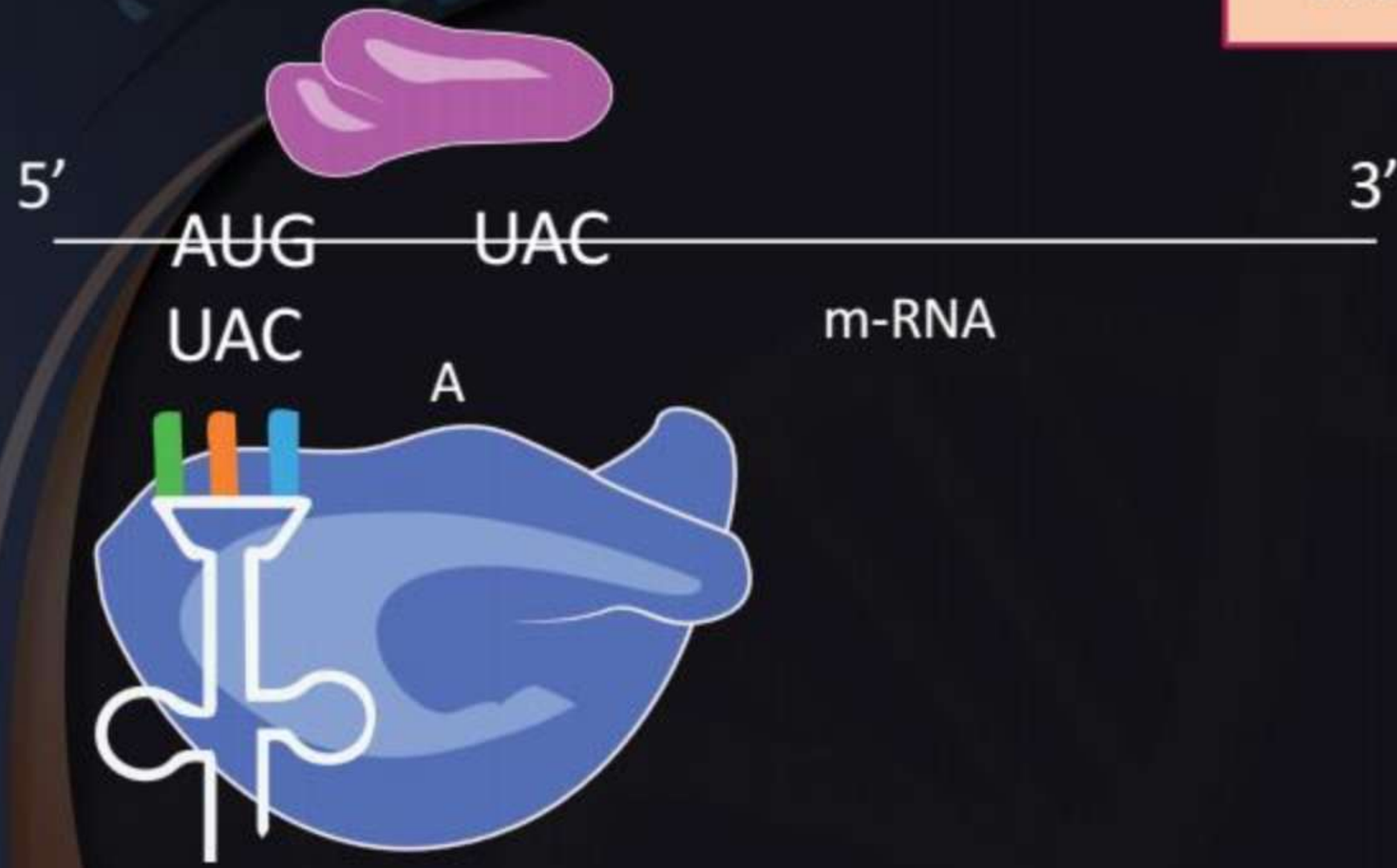
Elongation

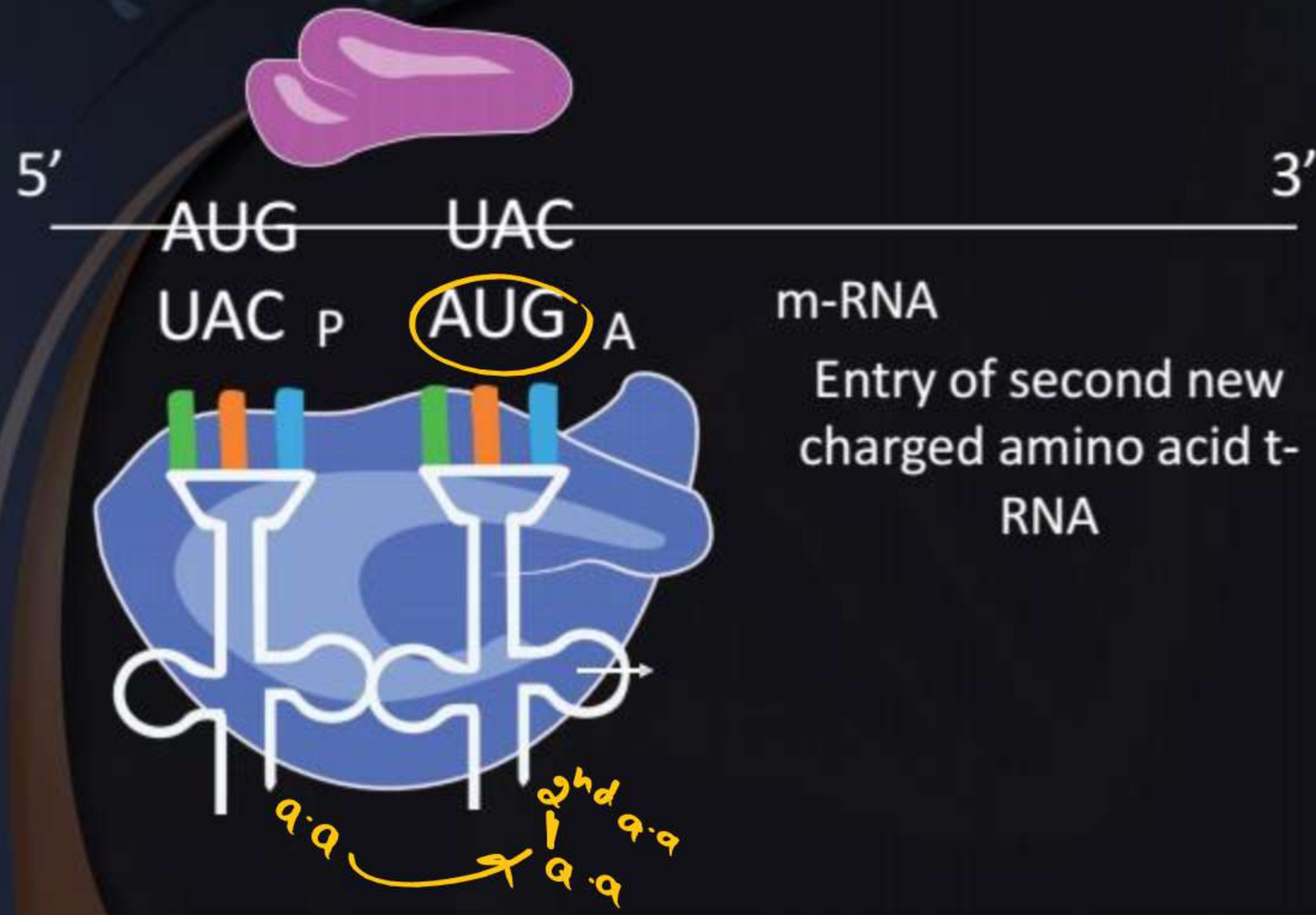


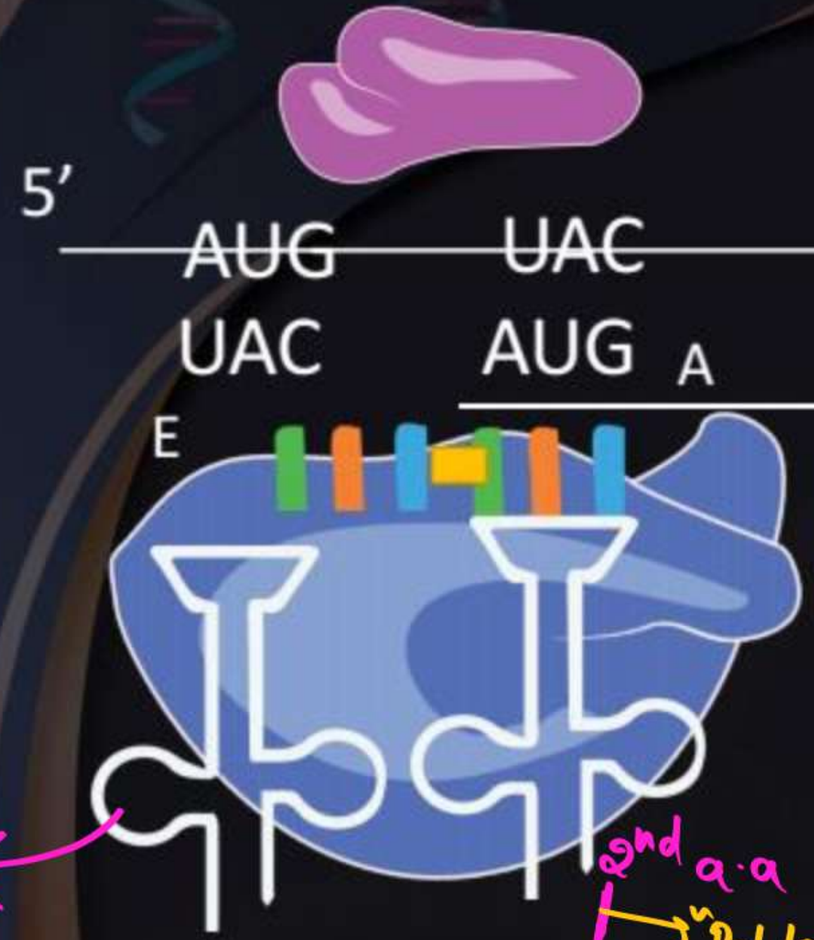
Translocation

of Ribozome on m-RNA

One GTP molecule is consumed




5’
3’
AUG
UAC
UAC P
AUG A
m-RNA
Entry of second new charged amino acid t-RNA
2nd



Peptide bond formation through

★ Peptidyl Transferase Enzyme ★

2nd a.a → "Peptide bond" ← 1st a.a

Imp

ProKaryotes

23S γ-RNA in larger subunit

(Peptidyl transferase)

EuK

larger subunit

★ 28S γRNA

(Peptidyl transferase)

Termination

There are no t-RNAs for stop-codon

Termination

Dissociation Factors dissociate the two subunits of ribosomes

5’ 3’

m-RNA

Polypeptide chain

If an m-RNA molecule has 810 nucleotides then calculate the number of amino acids by this m-RNA.

Q

3 nucleotides → (1) codon

810 " → $\frac{810}{3}$ = 270 codons

269 coding codon + 1 stop codon

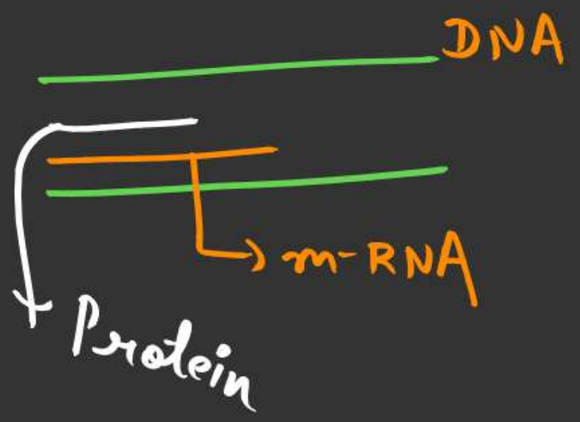
269 a.a

Regulation of Gene Expression

(Control)

Simple in Prokaryotes

* Imp — Initiation of Transcription is the Predominant site for Regulation.



* Imp — Transcription & Translation are Coupled in Bacteria

in same compartment (cytoplasm)

Complicated **Regulation of Gene Expression in Eukaryotes**

4 steps:

1. **Transcriptional level**: Formation of **primary transcript** (hn-RNA) (Nucleus)
2. **Processing**: Splicing of hn-RNA
3. Successful transfer of m-RNA to cytoplasm.
4. **Translation** (cytoplasm)

EX → **Embryo-development**

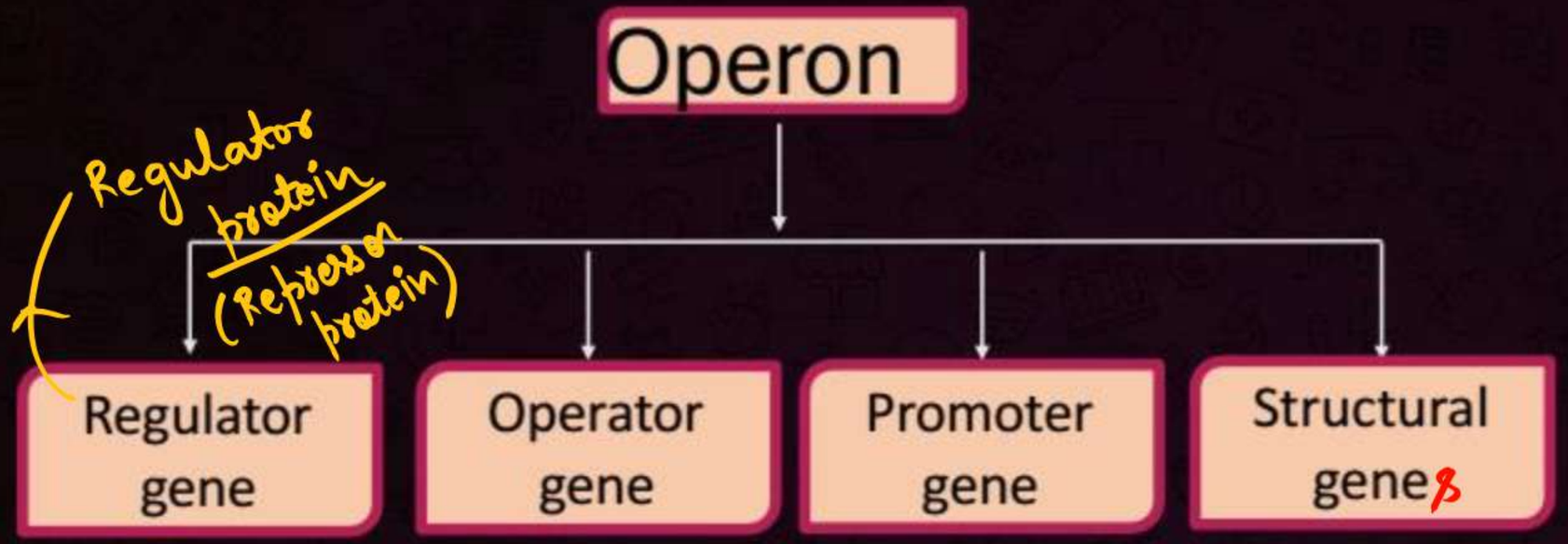
Jacob & Monod ← OPERON → only in ProKaryotes

DNA

* lac-operon
* try-operon
* his-operon

Segment of DNA → Has clusters of genes

→ Responsible for metabolism.



Inhibitor gene – synthesize regulation protein & controls activity of operator gene

Receives the products of regulation of gene

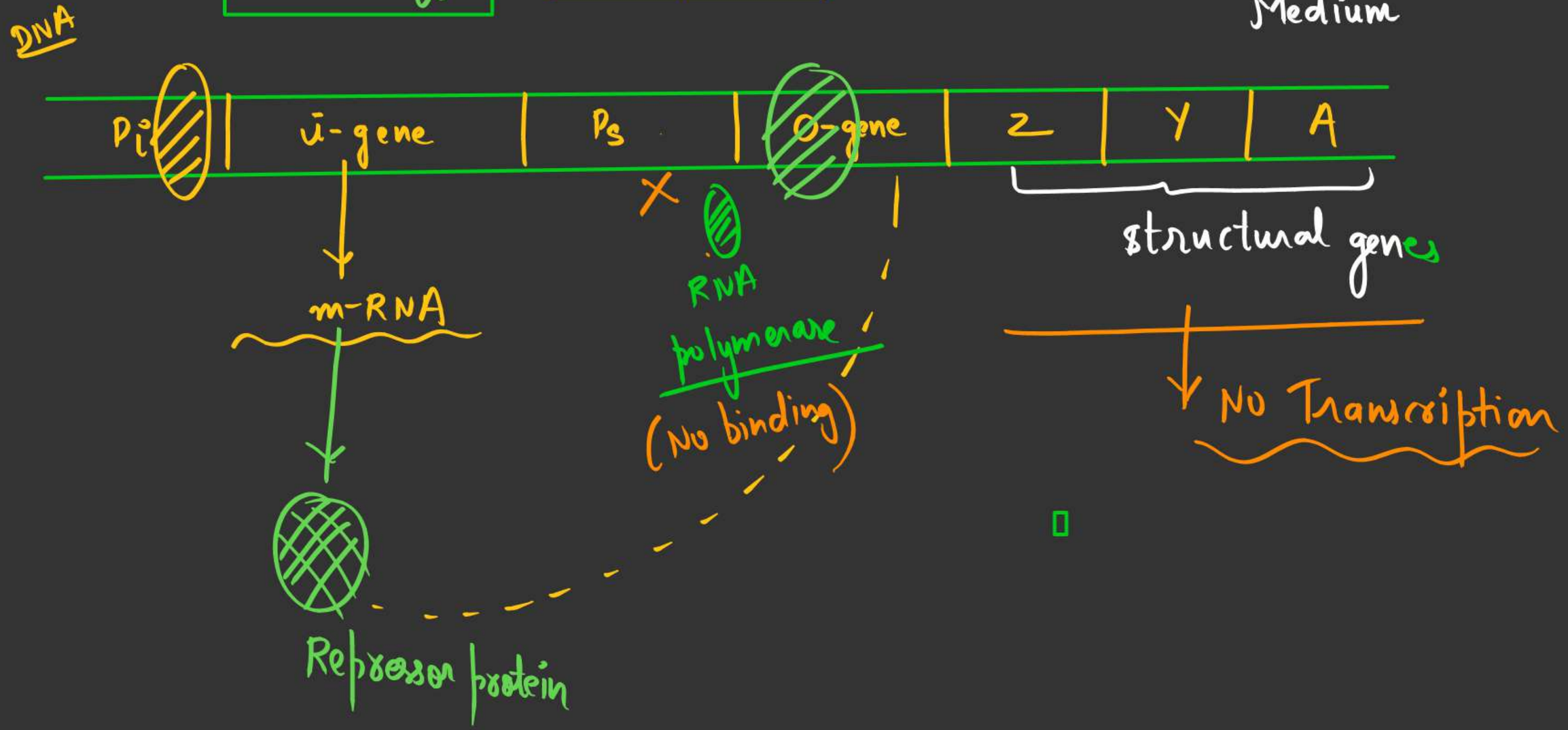
RNA Polymerase binding site

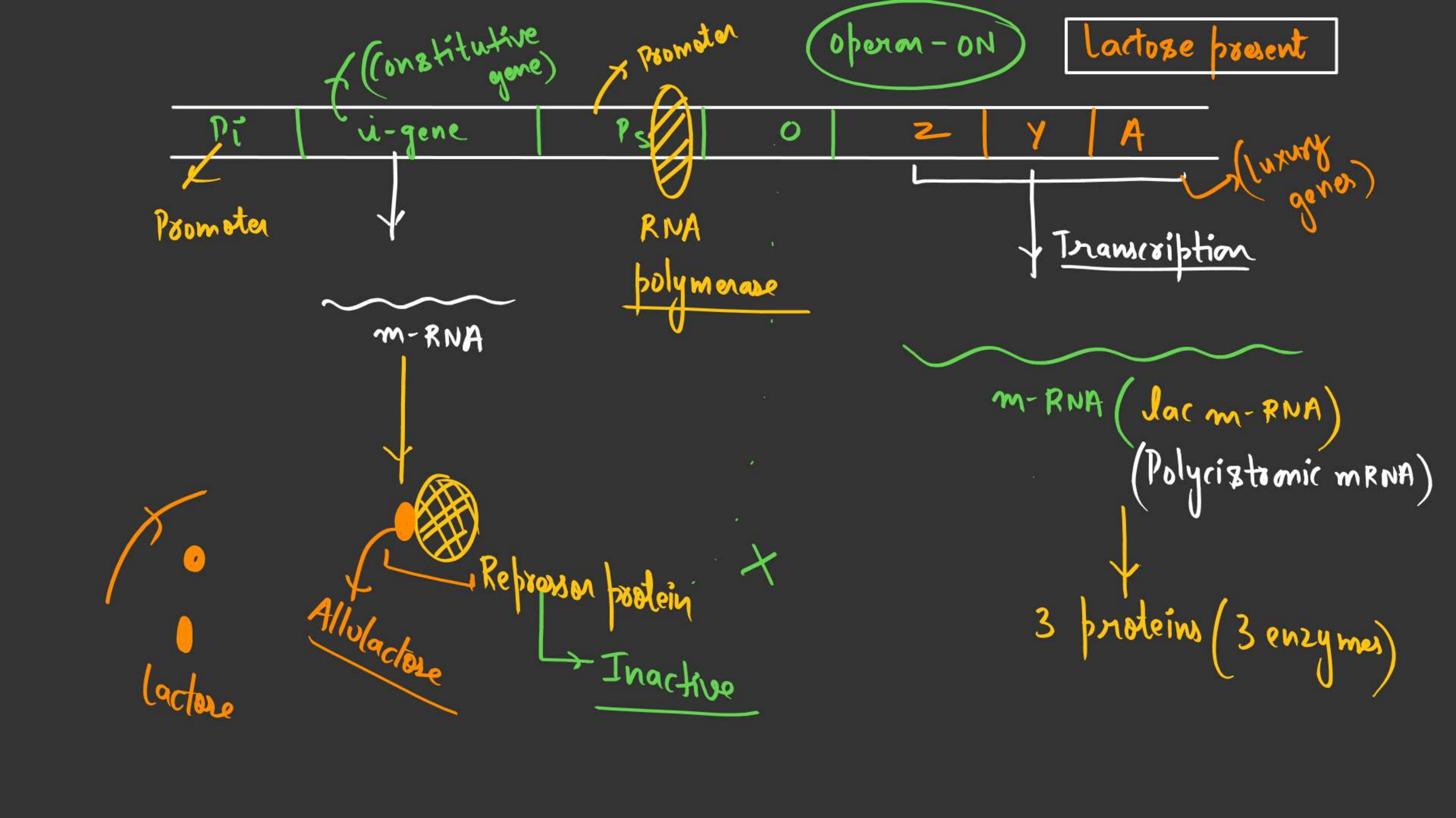
Responsible for protein synthesis → Metabolism

Operon - off

Lac-operon

1st case → lactose Absent in Medium




Operon - ON
Lactose present
(Constitutive gene)
Promoter
Pi
i-gene
Ps
O
Z
Y
A
(Luxury genes)
Promoter
RNA polymerase
Transcription
m-RNA
m-RNA (lac m-RNA)
(Polycistronic mRNA)
Repressor protein
Inactive
Allolactose
lactose
3 proteins (3 enzymes)

Z - gene

↓

β - galactosidase enzyme

Imp

Y - gene

↓

Permease enzyme

↓

Increases permeability

a - gene

↓

Transacetylase enzyme

lactose ⟶ Glucose + Galactose

lac-operon

→ Inducible operon ✓

Inducer → lactose ✓

→ Catabolism (Breakdown) ✓

→ under negative control ✓

↳ Repressor protein

also → under positive control (cAMP)

* little amount expression of operon is always there.

(little amount of Permease enzyme is always present).

HGP → 13 year (mega-project)

* 1990 → 2003

PYQ

* May 2006 → (chromosome 1) was the last to be sequenced.

America

US department of Energy

NIHS

Goals of HGP

Some of the important goals of HGP were as follows:

(i) Identify all the approximately 20,000-25,000 genes in human DNA;

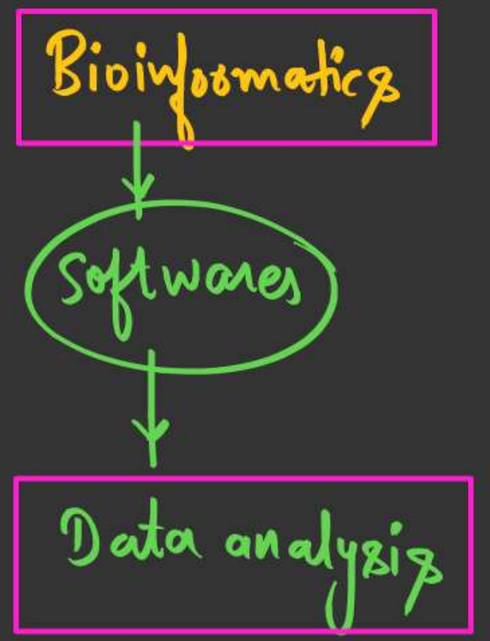
(ii) Determine the sequences of the 3 billion chemical base pairs that make up human DNA;

(iiii) Store this information in databases;

(iv) Improve tools for data analysis;

(v) Transfer related technologies to other sectors, such as industries;

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



Methodology

PYQ

EST's → Expressed Sequence Tags

Sequencing only those parts which are expressed as RNA

PYQ

Sequence Annotation

Sequencing whole genome later on coding & non-coding parts will be assigned.

Non-human organism

Genome Sequence

a) Bacteria

b) Yeast

c) Caenorhabditis (worm)

d) Drosophila (Fruit fly)

e) Rice (Plant)

f) Arabidopsis (Plant)

Process

1. DNA isolation
2. Fragments of DNA
   (Restriction Endonuclease)
3. Cloning
   (Millions of copies of each DNA fragment)

Cloning

- Vectors
  - BACs — Bacterial Artificial chromosomes
  - YACs — Yeast Artificial chromosomes
- Host-Cell
  - Yeast
  - E. coli

(9)

Sequencing

↓

By Sanger's technique

(Automated sequencing)

5.9.1 Salient Features of Human Genome

Some of the salient observations drawn from human genome project are as follows:

(i) The human genome contains 3164.7 million bp.

(ii) The average gene consists of 3000 bases, but sizes vary greatly, with the largest known human gene being dystrophin at 2.4 million bases.

(iii) The total number of genes is estimated at 30,000–much lower than previous estimates of 80,000 to 1,40,000 genes. Almost all (99.9 per cent) nucleotide bases are exactly the same in all people.

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

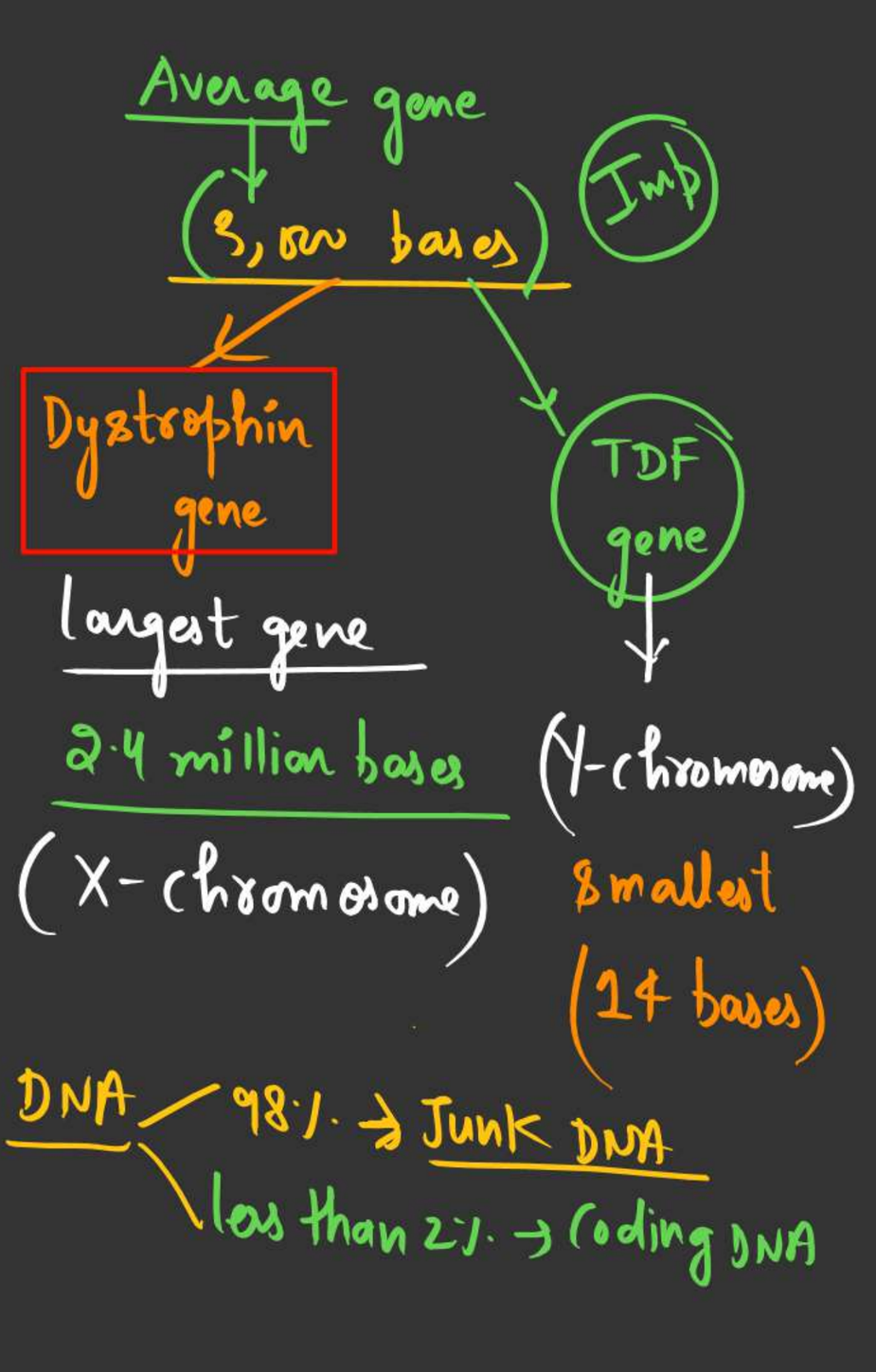
(v) Less than 2 per cent of the genome codes for proteins.

(vi) Repeated sequences make up very large portion of the human genome.

(vii) Repetitive sequences are stretches of DNA sequences that are repeated many times, sometimes hundred to thousand times. They are thought to have no direct coding functions, but they shed light on chromosome structure, dynamics and evolution.

(viii) Chromosome 1 has most genes (2968), and the Y has the fewest (231).

(ix) Scientists have identified about 1.4 million locations where single-base DNA differences (**SNPs – single nucleotide polymorphism**, pronounced as 'snips') occur in humans. This information promises to revolutionise the processes of finding chromosomal locations for disease-associated sequences and tracing human history.



Imp

Chromosome 1

↓

Largest chromosome

↓

2968 genes

Y-chromosome

↓

Smallest

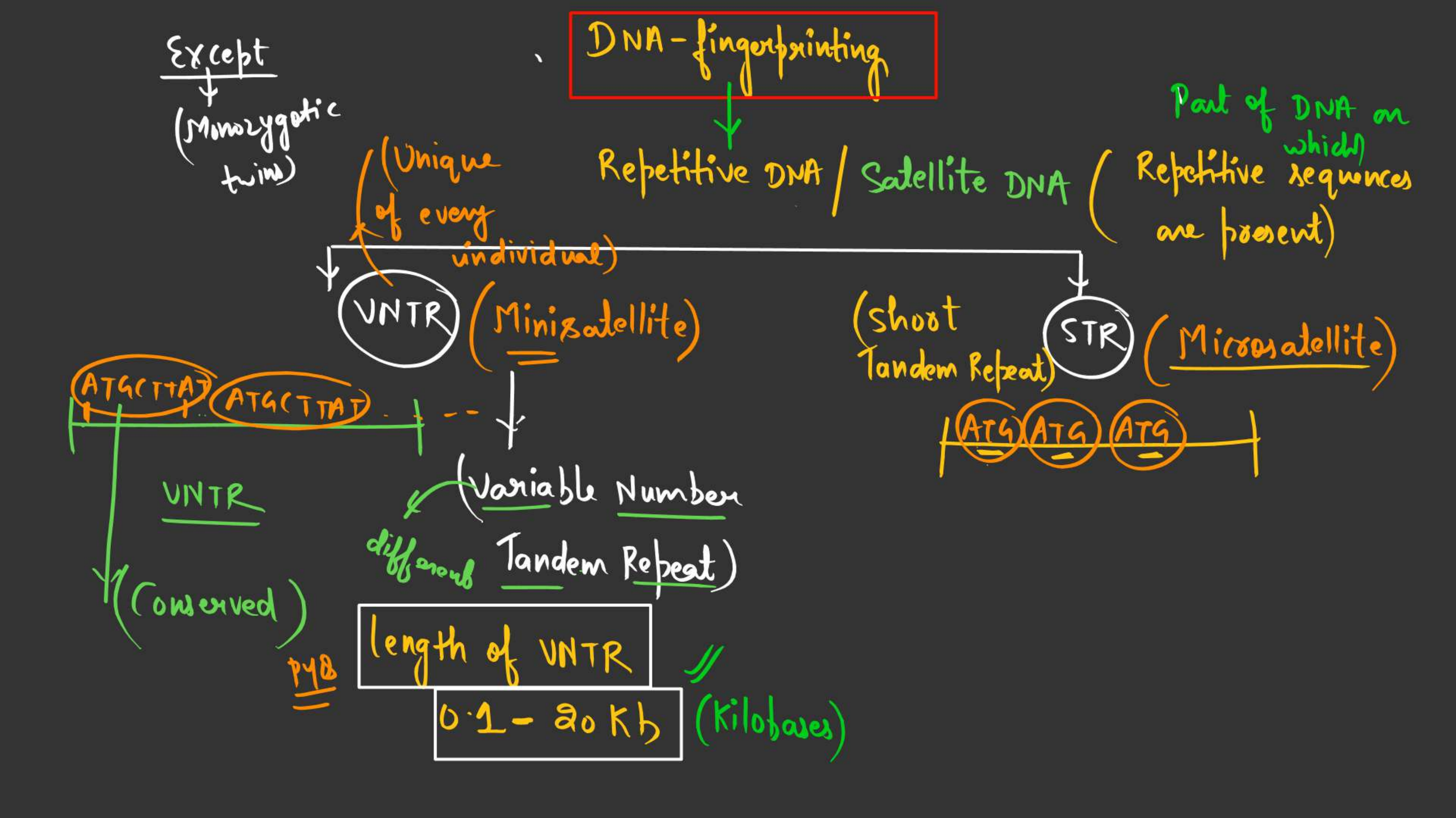
↓

(231 genes)

* Snips / SNPs → "Single Nucleotide Polymorphism"

↓

"1.4 million locations"


DNA-fingerprinting
Except
(Monozygotic twins)
Repetitive DNA / Satellite DNA
(Part of DNA on which Repetitive sequences are present)
(Unique of every individual)
VNTR
(Minisatellite)
STR
(Short Tandem Repeat)
(Microsatellite)
ATGCTTAT
ATGCTTTAT
ATG
ATG
ATG
VNTR
(Variable Number Tandem Repeat)
(different)
(conserved)
PYB
length of VNTR
0·1 - 20 Kb
(Kilobases)

All Humans

99.9 % → Similar

0.1 % → Different

0.1 % of 3×10^9 bps

3×10^6 bps

Coding parts - Non-coding parts → Repetitive DNA

DNA

Centrifugation

1st step → Isolation of DNA

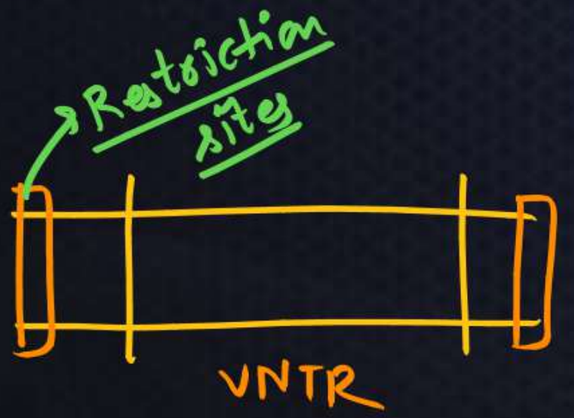
↓

(By enzymes)

Digestion of DNA

↳ Fragments of DNA

Process



DNA is cut by restriction endonuclease

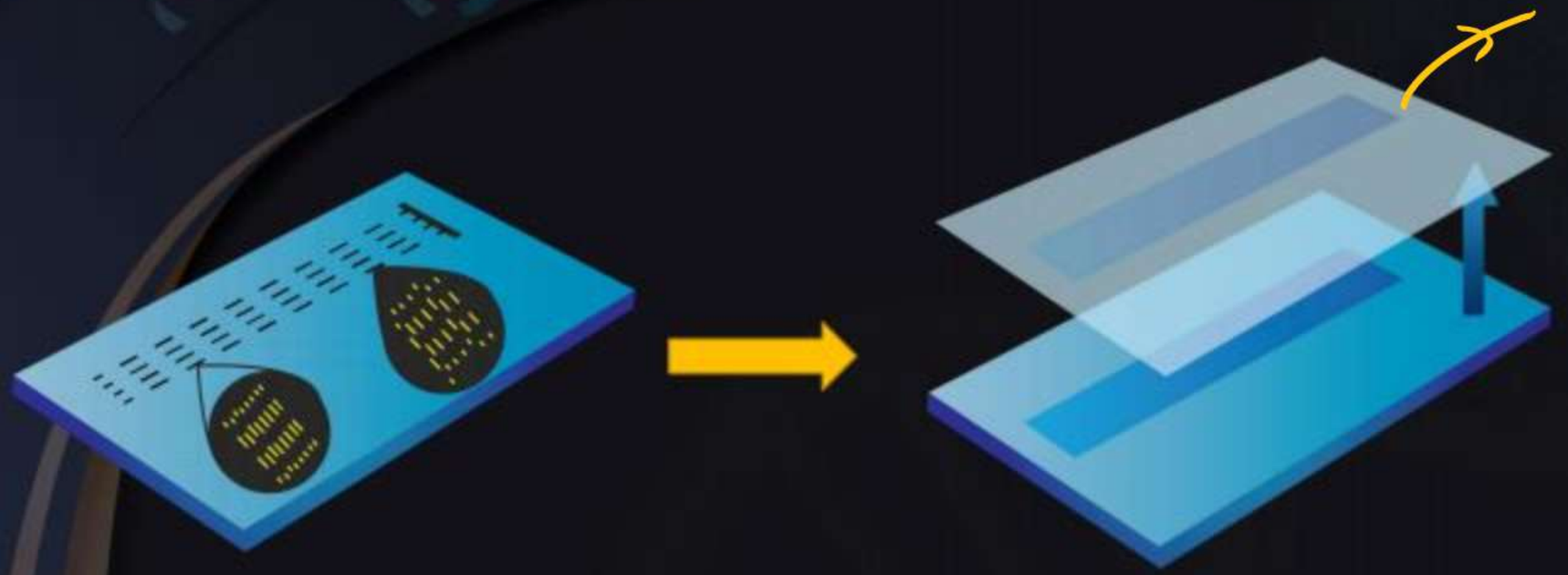
RFLP

Restriction Fragment length Polymorphism

Separation of DNA fragment by Gel Electrophoresis

The DNA fragments are separated into bands during electrophoresis in an agarose gel

Southern Blotting

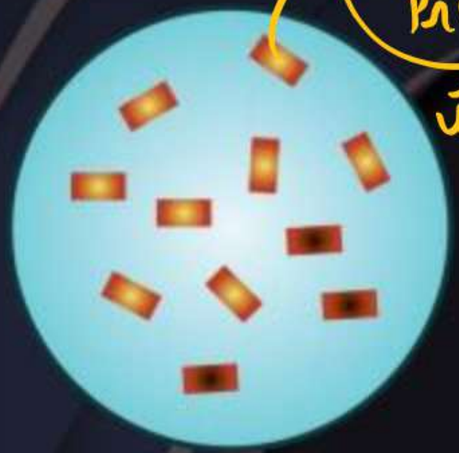


The DNA band pattern in the gel is transferred to a nylon membrane by a technique known as southern blotting

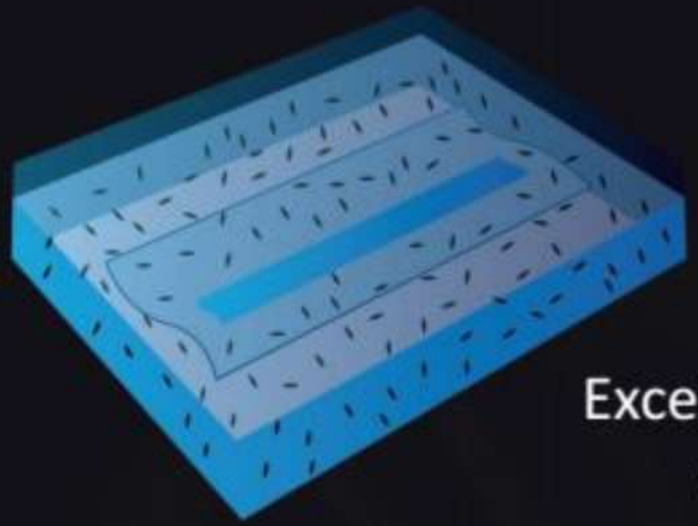
Radioactive Probing / Hybridisation

DNA VNTR Probe

ún (labs)



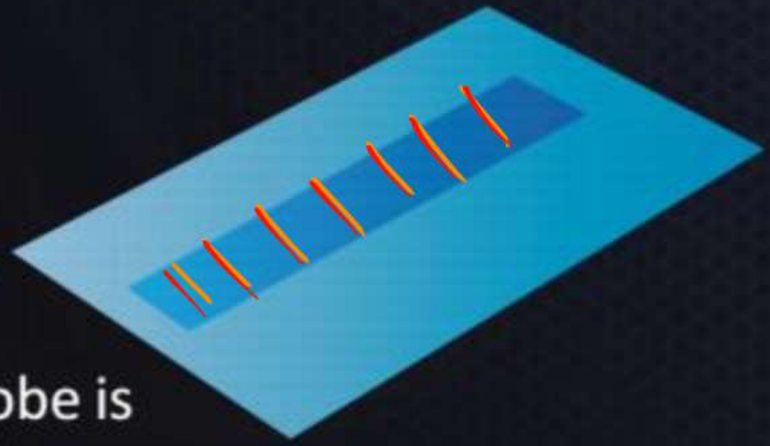
Radioactive DNA Probe is prepared



The DNA probe binds to specific DNA sequences on the membrane (Hybridisation)

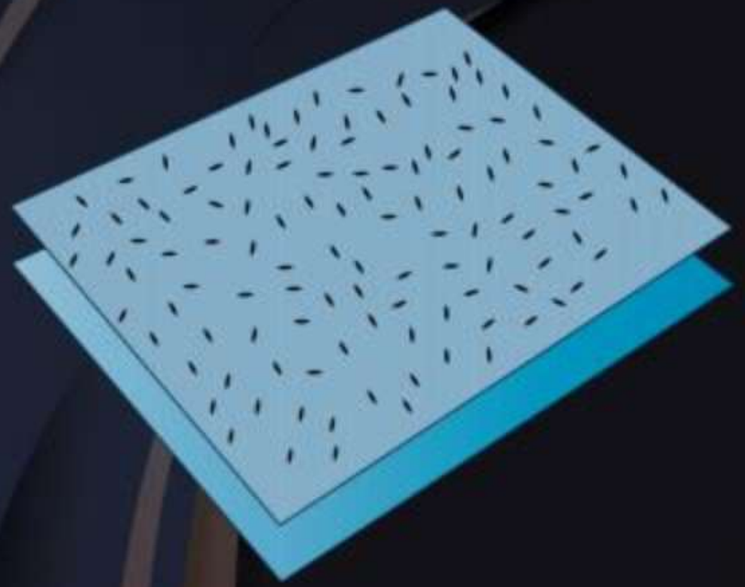
VNTR

Excess DNA probe is washed off



At this stage the radioactive probe is bound to the DNA pattern on the membrane

Detection by autoradiography

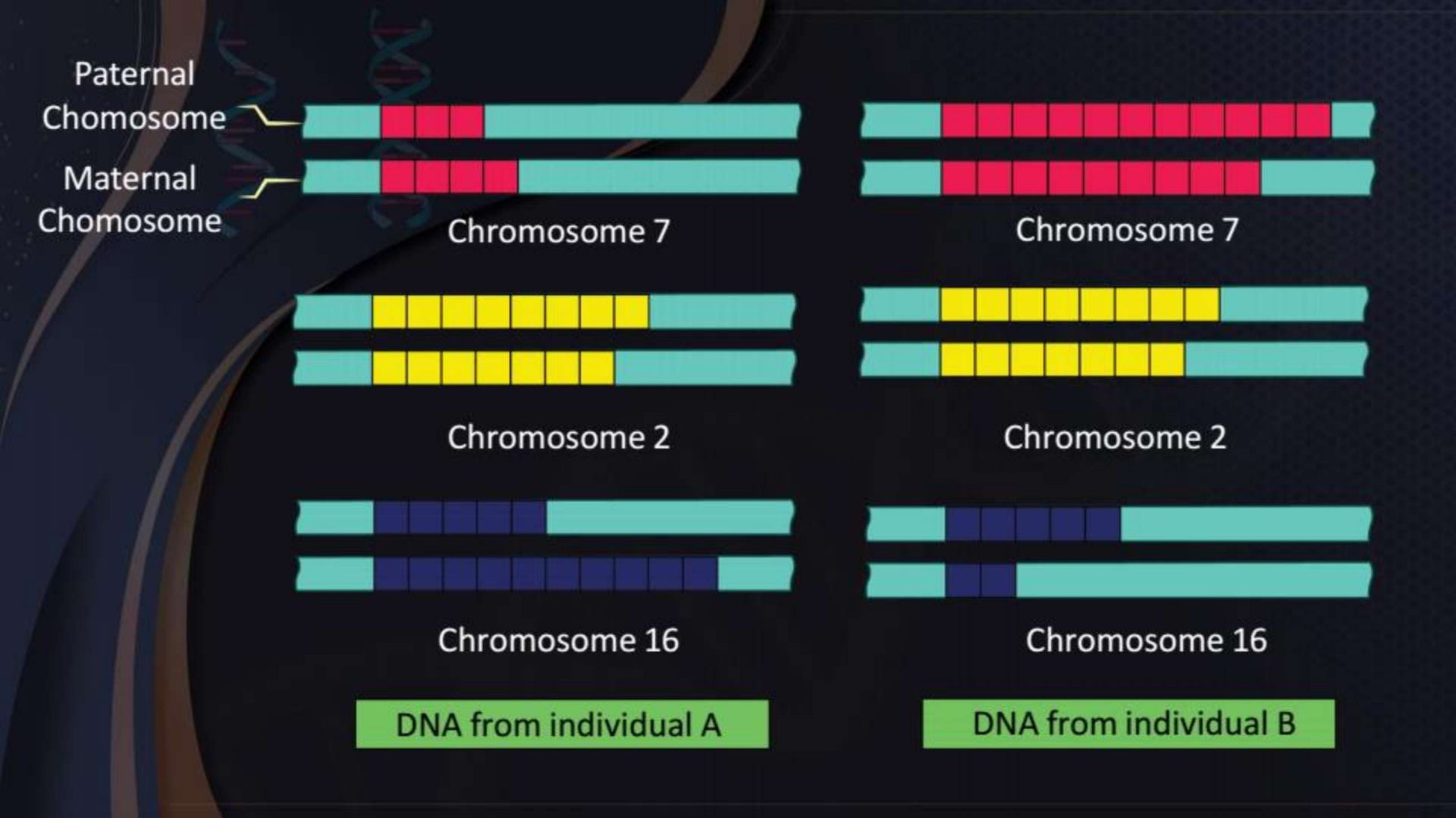


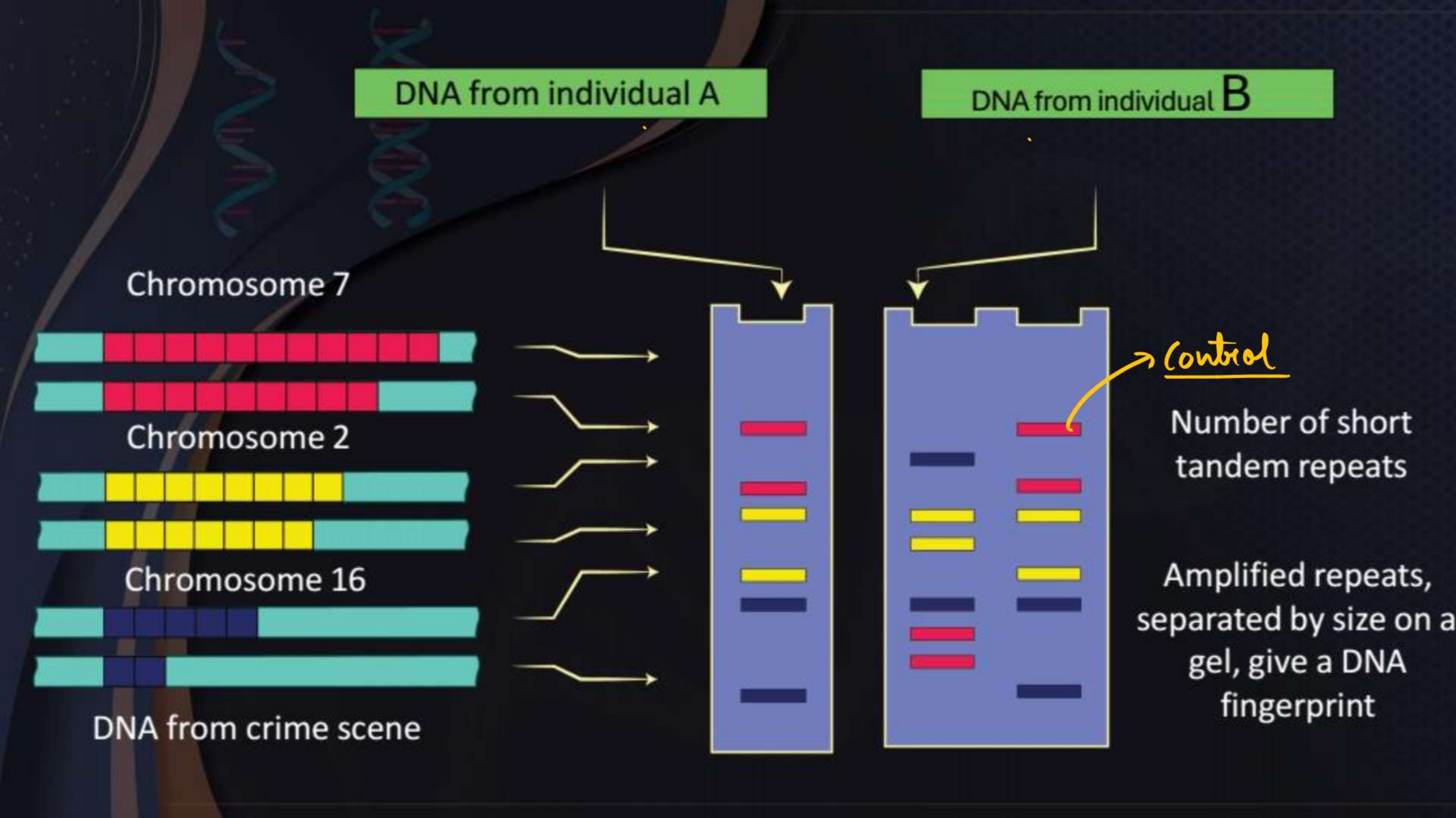
X-ray film is placed next to the membrane to detect the radioactive pattern

The X-ray film is developed to make visible the pattern of bands which is known as a DNA fingerprinting

Practical Applications

- Paternity-Maternity disputes
- Criminal identification and forensics
- Personal Identification
- Close relations of an intending immigrant

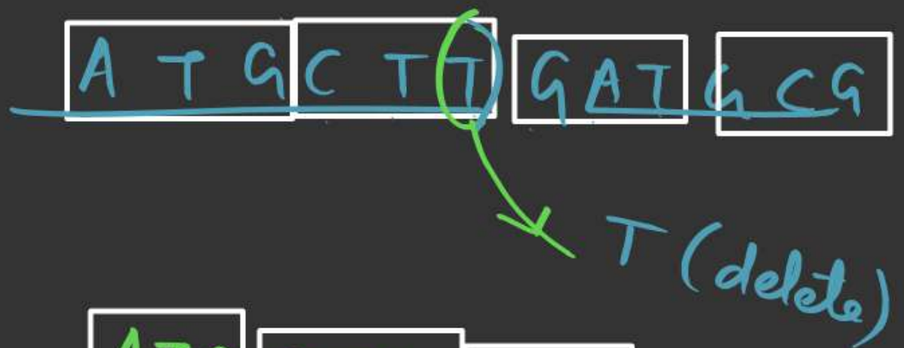

Paternal Chomosome
Maternal Chomosome
Chromosome 7
Chromosome 7
Chromosome 2
Chromosome 2
Chromosome 16
Chromosome 16
DNA from individual A
DNA from individual B

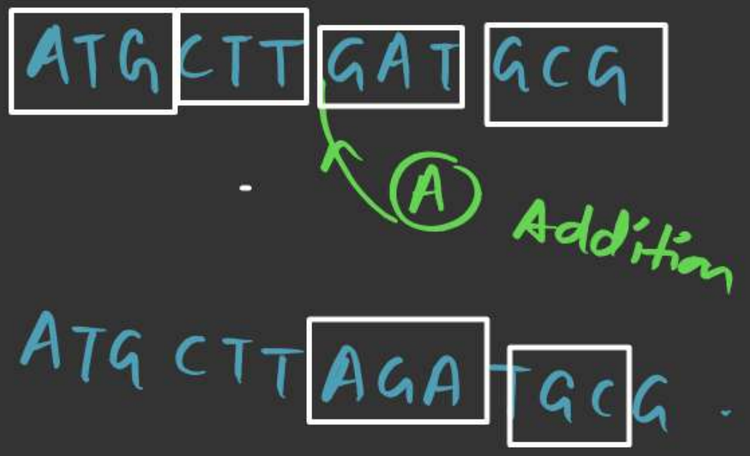

DNA from individual A
DNA from individual B
Chromosome 7
Chromosome 2
Chromosome 16
DNA from crime scene
Control
Number of short tandem repeats
Amplified repeats, separated by size on a gel, give a DNA fingerprint

Mutation

Frame-shift Mutation

- Addition
- Deletion





NOTE: If **whole codon** is added or deleted then mutation is there but not Frameshift mutation

Questions for Homework

For answers & Solutions

Uthaan Series

on Competitionwallah channel

QUESTION

Hallmark of the Watson and Crick three dimensional DNA model was based upon the findings of

1. Wilkins and Franklin
2. Erwin Chargaff
3. Hershey and Chase
4. Meselson and Stahl

QUESTION

Heterochromatin

1. Is transcriptionally active
2. Is densely packed
3. Replicated during early S-phase
4. Stains lightly

QUESTION

The number of glycosidic bonds associated with DNA of diploid human cell are

1. 6.6×10^9
2. $2 \times 6.6 \times 10^9$
3. 3.3×10^9
4. $3.3 \times 10^9 - 2$

QUESTION

Which of the following does not confer stability to the helical structure of DNA?

1. Phosphodiester bond
2. H-bond
3. N-glycosidic linkage
4. More than one option is correct

QUESTION

The biochemical nature of transforming principle was defined by

1. Griffith
2. Avery, Macleod, McCarty
3. Watson and Crick
4. Taylor

QUESTION

Which of the following acts as substrate as well as provide energy for DNA polymerisation?

1. Ribonucleoside
2. Deoxyribonucleoside
3. Ribonucleotide
4. Deoxyribonucleoside triphosphate

QUESTION

The mRNA of prokaryotes is

1. Polycistronic
2. Monocistronic
3. Formed by splicing of hnRNA
4. Carries genetic message to DNA

QUESTION

Capping in hnRNA is catalysed by

1. Poly A polymerase
2. SnRNA
3. Guanyl transferase
4. Catalytic RNA

QUESTION

Which of the following type of ribosomal RNA is not present in eukaryotic cytoplasm?

1. 18 S
2. 28 S
3. 5.8 S
4. 16 S

QUESTION

Which of the following codons is known as ochre?

1. UAG
2. UGA
3. UAA
4. UUU

QUESTION

Which of the following is an ambiguous codon?

1. AUG
2. GUG
3. UAG
4. GAG

QUESTION

Activation of amino acids during translation is done by

1. Peptidyl transferase
2. Aminoacyl-tRNA synthetase
3. Methionine
4. Initiation factors

QUESTION

How many structural genes are present in lac-operon of *E. coli*?

1. 4
2. 3
3. 2
4. 1

QUESTION

Select incorrectly matched pair

1. Lac z – Constitutive gene
2. Operator gene – Smallest gene of lac operon
3. Lac a - Transacetylase
4. Promotor gene – RNA polymerase

QUESTION

Sequencing the whole set of genome that contained all the coding and non-coding sequences and later assigning different regions in the sequence with functions is known as

1. Sequence annotation
2. PCR
3. Northern blot
4. Microarray

QUESTION

The last step of DNA fingerprinting is

1. Blotting
2. Autoradiography
3. Hybridisation
4. Isolation of desired DNA

QUESTION

In humans, the largest gene is present on

1. Chromosome-1
2. Y-chromosome
3. X-chromosome
4. Chromosome-7

QUESTION

TDF gene is the smallest gene in humans with

1. 231 bp
2. 14 bp
3. 2968 bp
4. 3000 bp

QUESTION

SNPs stands for

1. Single nucleoside polymorphism
2. Simple nucleotide polymorphism
3. Single nucleotide polymorphism
4. Simple nucleoside polymorphism

QUESTION

Find out the incorrect match.

1. UUU - Phenylalanine
2. UAG - Sense condon
3. GUG - Valine
4. UGG - Tryptophan

QUESTION

Mark the incorrect option w.r.t. lac operon

1. Is under positive as well as negative control
2. Controls catabolic pathway
3. Shows feed back repression
4. Discovered by Jacob and Monod

QUESTION

In *lac* operon, the *lac* mRNA

1. Has several initiation and termination codons
2. Forms four different enzymes
3. Is not transcribed in the presence of lactose
4. Is involved in an anabolic reaction

QUESTION

What is correct for bacterial transcription?

1. mRNA requires processing to become active
2. Translation can begin when mRNA is fully transcribed
3. Transcription and translation takes place in the same compartment
4. Rho factor initiates the process

QUESTION

In eukaryotes, RNA polymerase III catalyses the synthesis of

1. 5 S rRNA, tRNA & SnRNA
2. mRNA, HnRNA & SnRNA lo ajaeritaya
3. 28 S rRNA, 18 S rRNA & 5 S rRNA
4. All types of rRNA & tRNA

QUESTION

How many amino acids will be coded by the mRNA sequence - 5'CCCUCAUAGUCAUAC3' if a adenosine residue is inserted after 12th nucleotide?

1. Five amino acids
2. Six amino acids
3. Two amino acids
4. Three amino acids

QUESTION

The DNA strand showing replication using Okazaki fragments also shows

1. Continuous growth in 5' → 3' direction
2. Discontinuous growth on 5' → 3' parental strand
3. Discontinuous growth on 3' → 5' parental strand
4. Involvement of one primer only

QUESTION

Assertion: Sigma factor of RNA polymesase recognizes the start signal region in prokaryotes.
Reason: Promotor region lies at 5' of template strand.

1. Both Assertion & Reason are true and the Reason is a correct explanation of the Assertion.
2. Both Assertion & Reason are true but Reason is not a correct explanation of the Assertion.
3. Assertion is true but Reason is false.
4. Assertion is false but the Reason is true.

QUESTION

Assertion: Peptidyl transfer site is contributed by larger sub-unit of ribosome.
Reason: The enzyme peptidyl transferase is contributed by both 23S and 16S ribosomal sub-units.

1. Both Assertion & Reason are true and the Reason is a correct explanation of the Assertion.
2. Both Assertion & Reason are true but Reason is not a correct explanation of the Assertion.
3. Assertion is true but Reason is false.
4. Assertion is false but the Reason is true.

THANK YOU