Molecular Basis Of Inheritance

→ Means which molecules get inheritate from one G_1 to next G_2.

→ Further studies explain that Nucleic acid is the main genetic material for all types of living ~~origin~~ organism in which most of the animals having DNA as a genetic material and RNA is of very exceptional organism.

→ Nucleic acid was described and explain by Friedrich Miescher in (1868).

→ Friedrich Miescher given the term Nuclein for Nucleic acid.

→ Nucleic acid is made up of Nuclentide or Nucleotide is the polymer of Nucleic acid.

→ Term Nucleic acid was given by Altman.

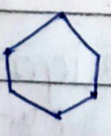
Nucleotide having trick of position –

(i) Nitrogenous Base
(ii) Pentose sugar
(iii) Phosphate

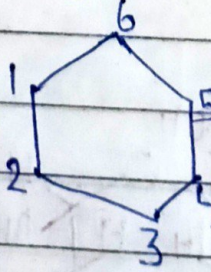
N-base is of two types –

(i) Pusine
→ It is made up of two types of ring.

(ii) Pyrimidine
→ It is made up of one type of ring.

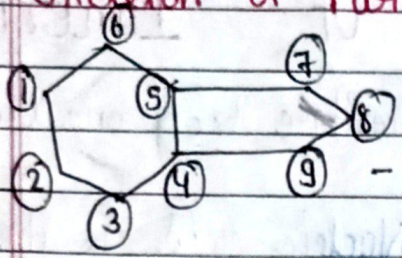
(i) Pyrimidine ring  6 atom

(ii) Imidazole ring  5 atom



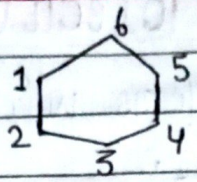
– Pyrimidine ring 6 atom

Skeleton of Purine



- 1, 3, 7, 9-N

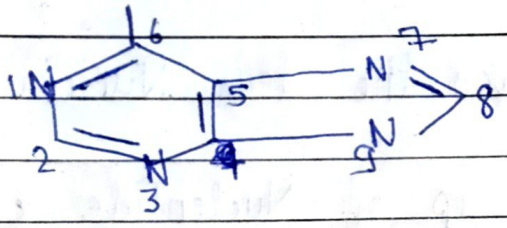
Skeleton of pyrimidine



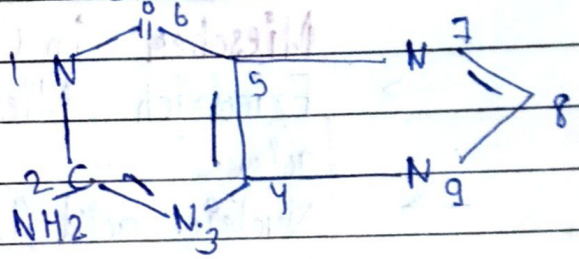
- 1 & 3 position having N.

Purine is of two types —

Adenine

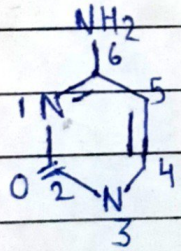


Guanine



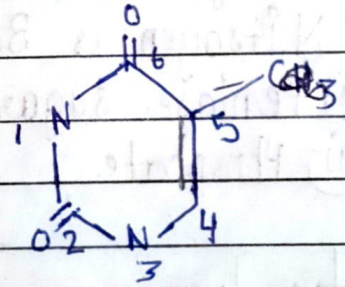
Pyrimidine is of three types —

Cytosine



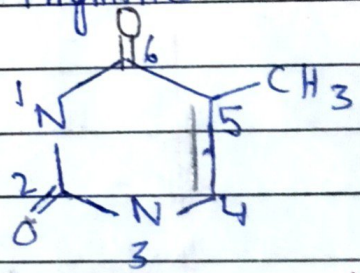
6-Amine, 2-oxidine Pyrimidine

Uracil



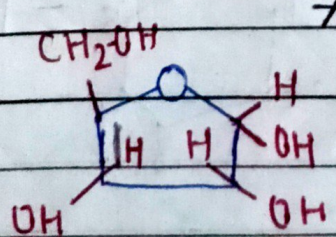
2,6-di oxidine pyrimidine

Thymine

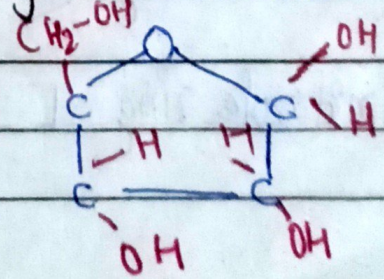


5-Methyl uracil
or
2-6 di oxidine
5-Methyl pyrimidine

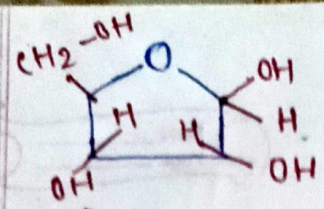
Pentose sugar (5 atom)



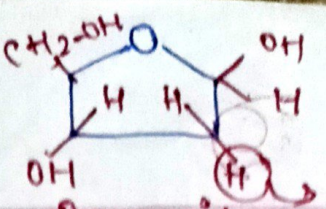
α-Ribose sugar



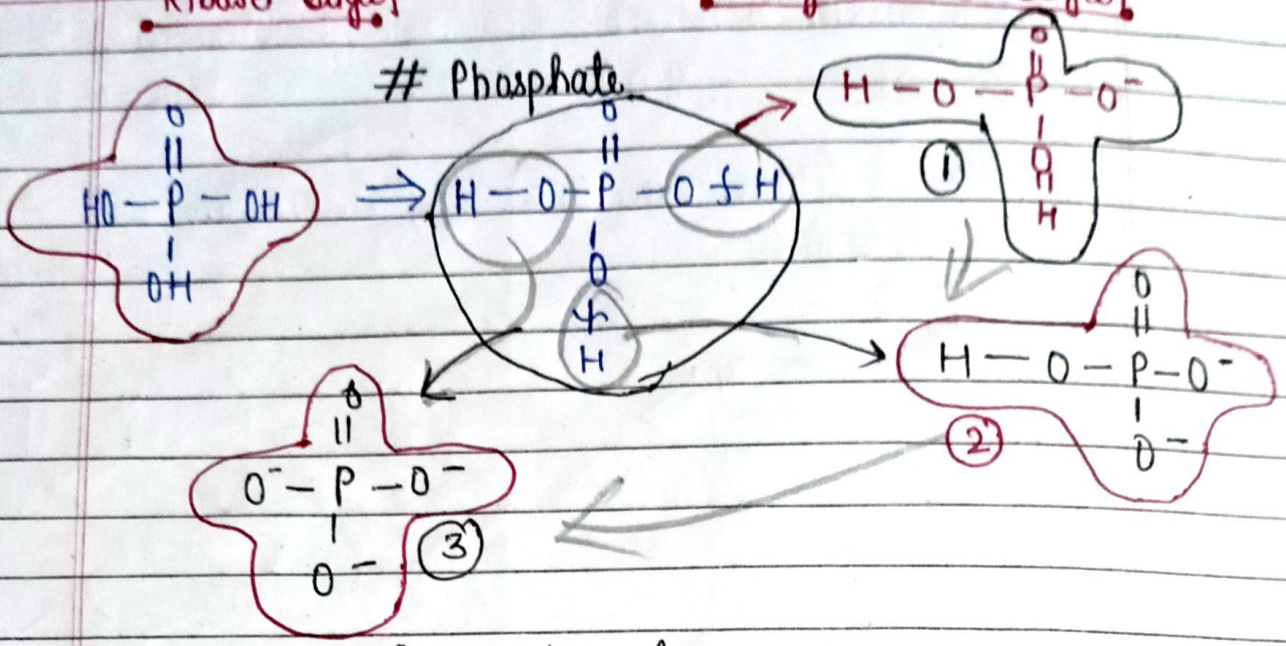
β-Ribose sugar



Ribose sugar



Deoxy ribose sugar



Nucleic acid is of two types –

	① DNA	② RNA
N-Base	A, T, G, C	A, U, G, C
Sugar	Deoxyribose sugar	Ribose sugar

→ Nitrogenous base + Sugar = Nucleotide

→ Nucleotide is basic structure.

→ When two or more nucleoside attached to each other then bond is used to form Glycosidic bond then this structure is called dinucleotide or polynucleoside

→ Nit. base + sugar + phosphate = Nucleotide

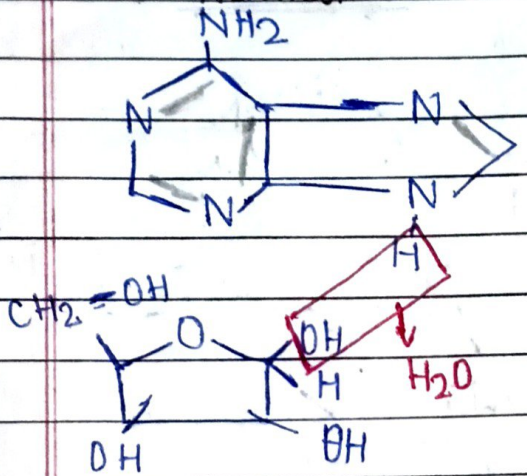
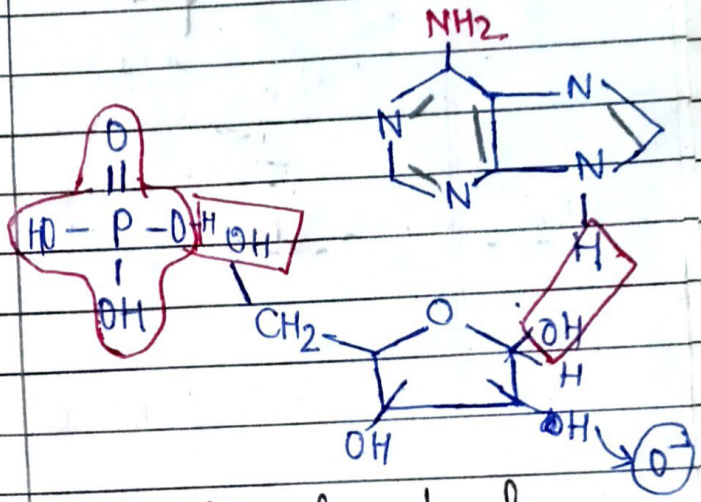
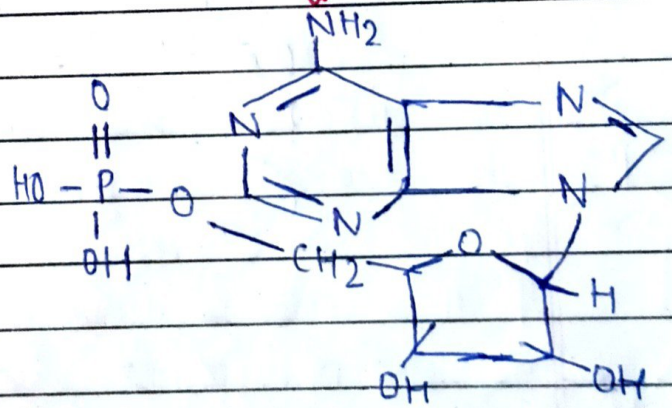
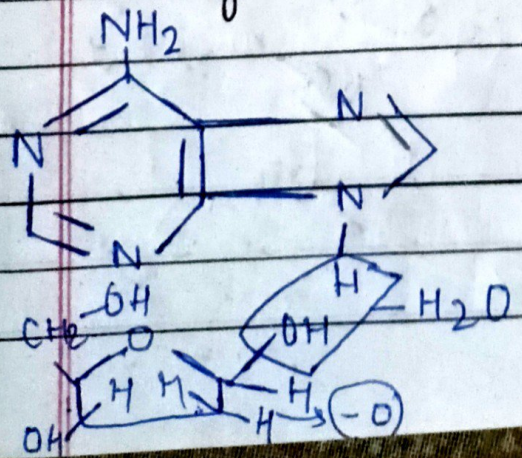
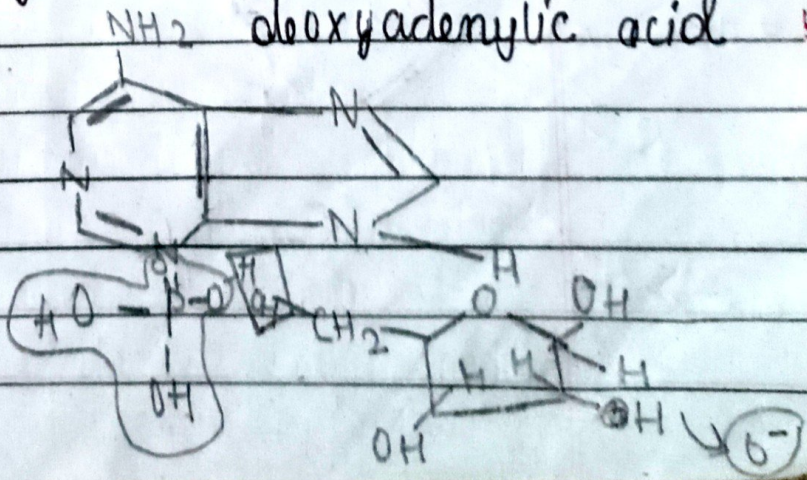
→ Nucleoside + phosphate = Nucleotide

→ Two or more nucleotide attached to each other then it is called dinucleotide or polynucleotide

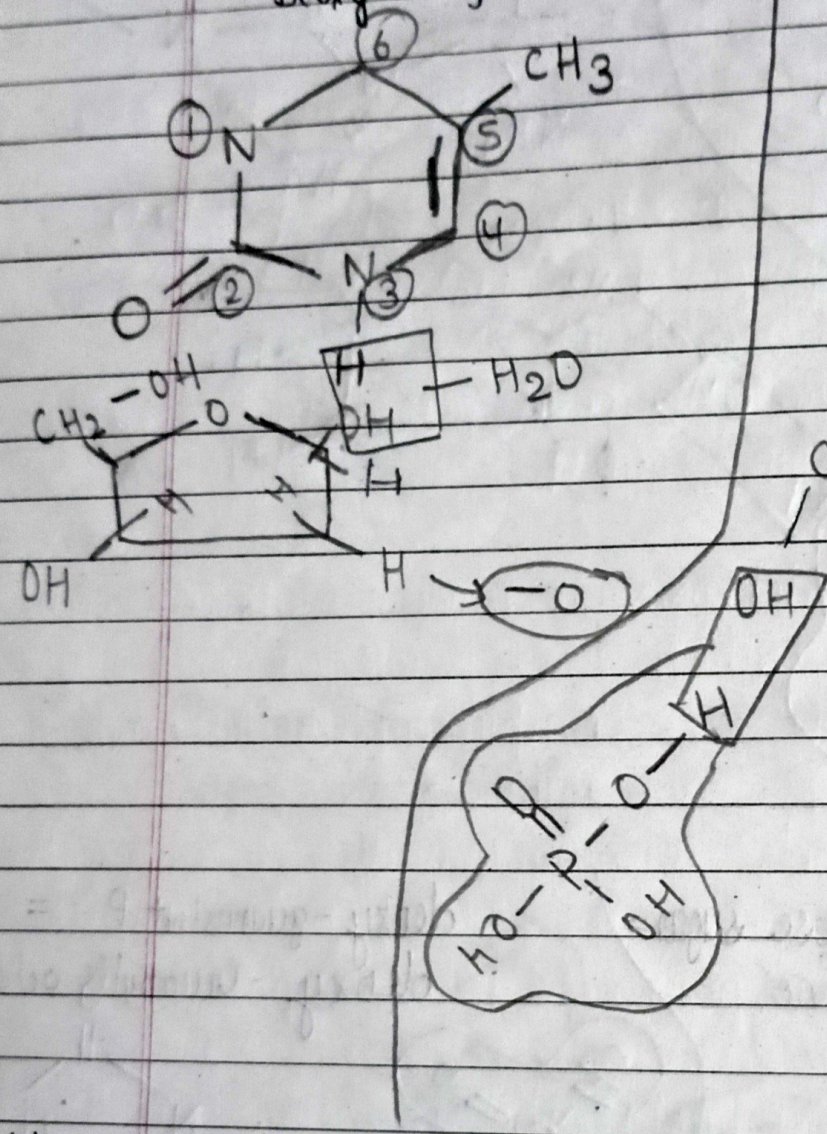
→ Phospho ester bond is used to form Nuclotide from Nucleoside with phosphate.

→ Nucleotide is acidic in nature due to presence of phosphate

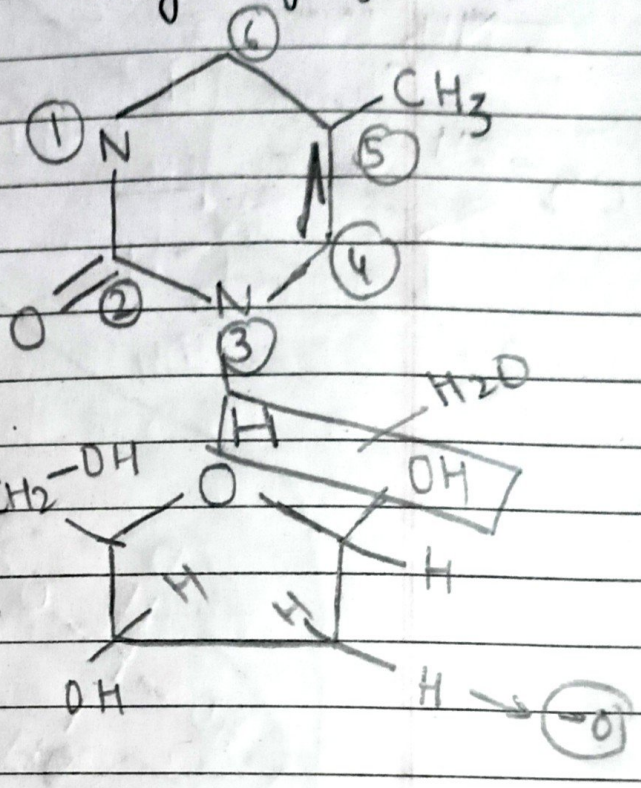
→ When many nucleotides attached to each other then it form Nucleic acid.

N- base	Nucleoside (N° base + Sugar)	Nucleotide (N° base + Sugar + P)
A	Adenine + Ribose sugar = Adenosine  1,9- Glycosidic bond	Adenosine + P = Adenylic Acid.  Phospho ester bond N - 1,9 - Glycosidic bond 
A	Adenine + deoxyribose sugar = Deoxy - adenosine 	deoxyadenosine + P = deoxyadenylic acid 

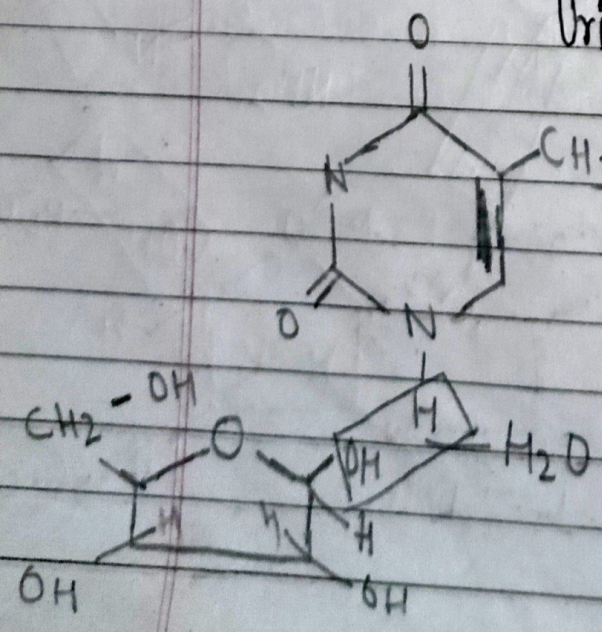
T Thymine + Deoxyribose sugar = Deoxy - thymioline



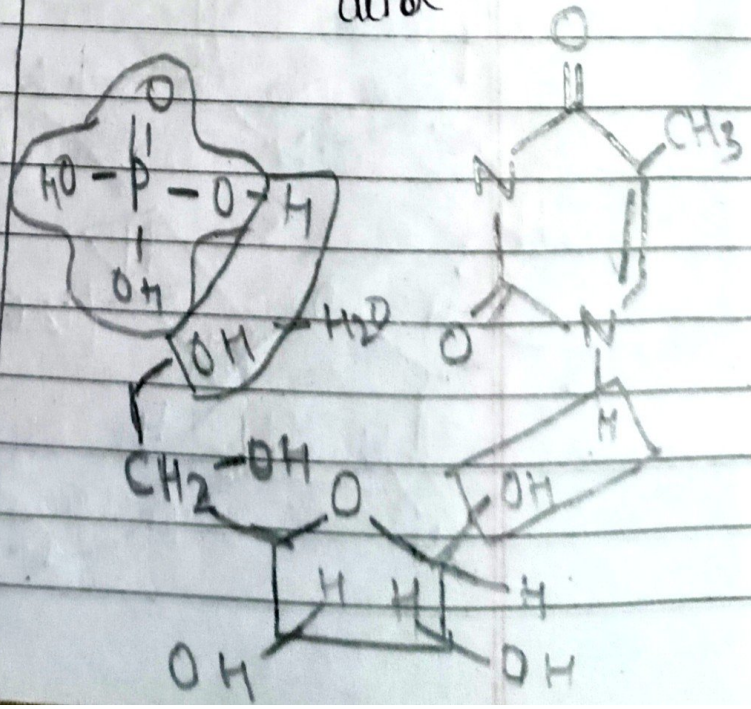
deoxy thymidine + P = deoxy- ~~deoxy~~ Thymidynlic acid



U Uracil + Ribose sugar = Uridine

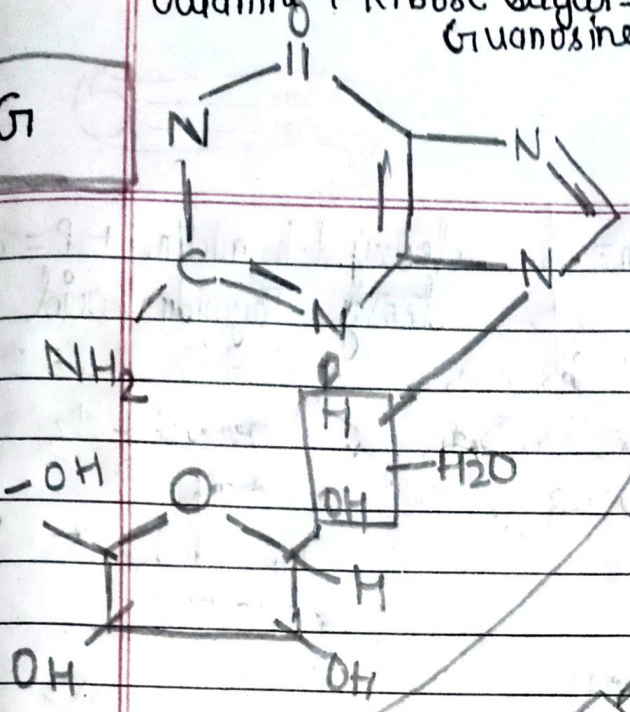


Uridine +P = Urinylic acid

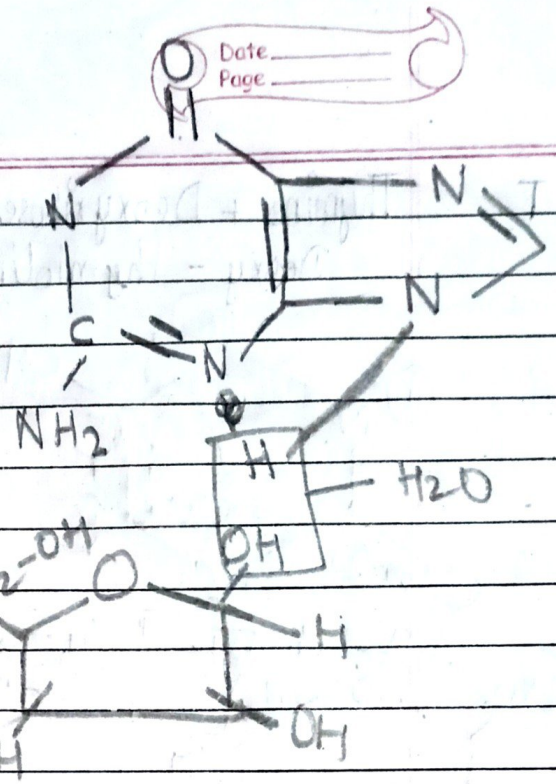


G

Guaning + Ribose sugar = Guanosine

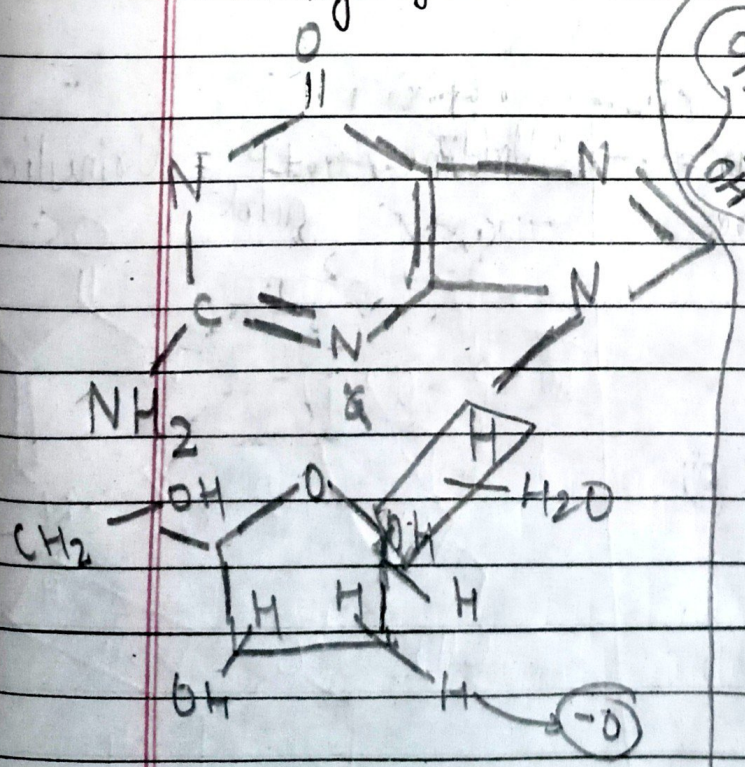


Guanosine + P = Guanylic acid

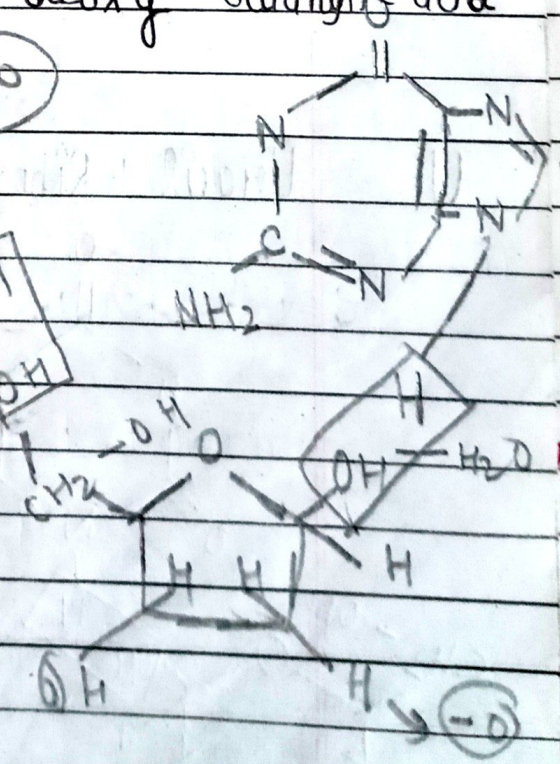


G

Guanine + deoxyribose sugar = deoxy - guanosine



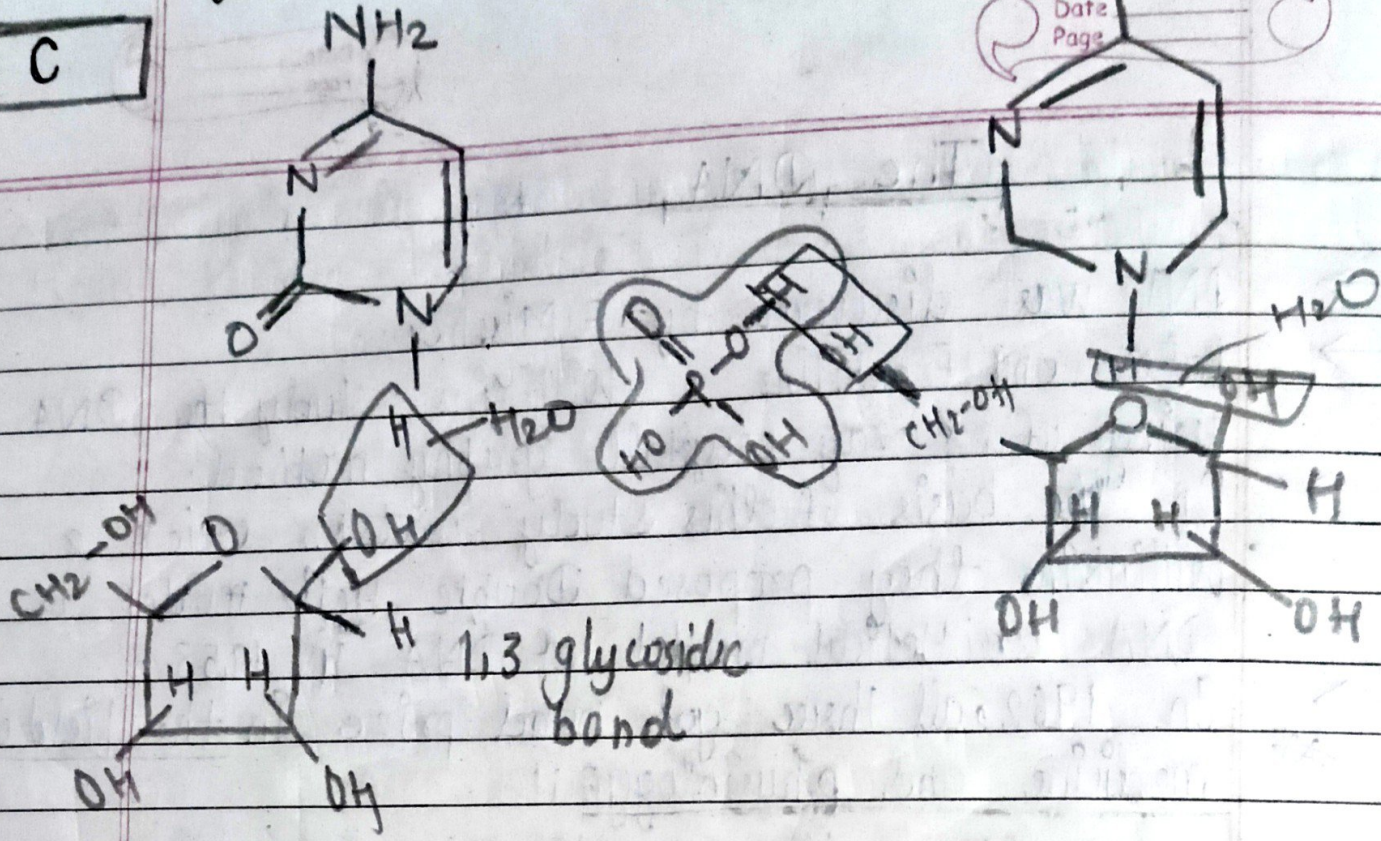
deoxy - guanosine + P = deoxy - Guanylic acid



C

Cytosine + Ribose sugar = Citidine

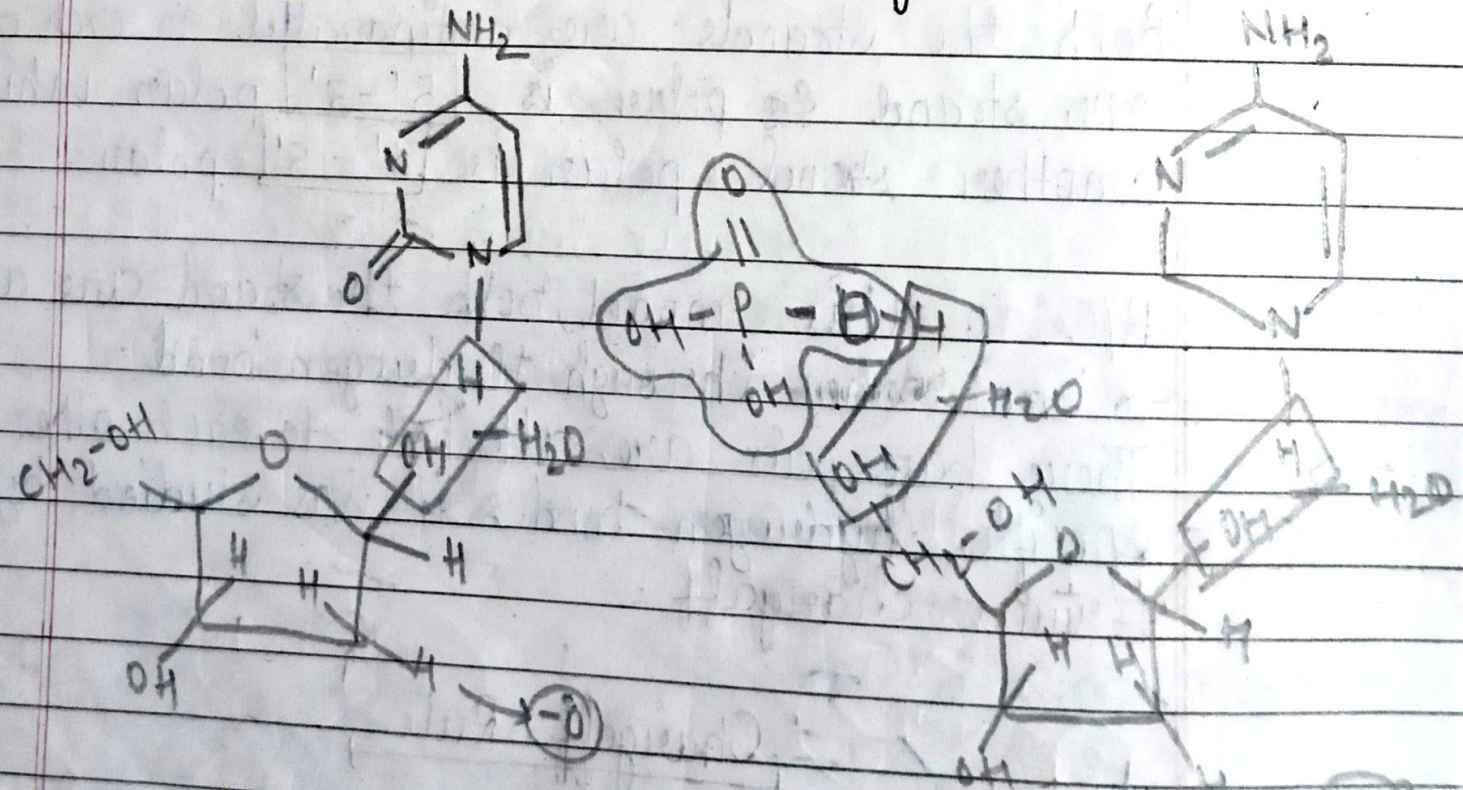
Citidine + P = Cytidylic acid



C

Citidine + deoxyribose sugar = deoxy-citidine

deoxy-citidine + P = deoxy-citidine acid



The DNA

→ DNA was discovered by F. Mischer.
→ Later on, Frankilins & Willikins study the DNA using of X-ray crystallo graphy method.
→ On the basis of this study watson crick & willinkins they proposed Double Helix model of DNA or Helical model of DNA in 1953.
→ In 1962, all three got nobel prize in the field of medicine and physiology.

→ A/C to this Model, DNA is made up of two poly nucleotide chain, which are arranged helically & both the strand are complimentary to each other. A – T and Cy – C.
→ Both the strands are antiparallel to each other one strand polar is 5'-3' polar while another strand polar is 3'-5' polar.

→ A/C to this model, both the strand are attached to each other through Hydrogen bond.
→ There base pair are attached to each other with specific hydrogen bond & it was studied by Erwin chargaff.

Chargaff Rule

→ It was given by Erwin chargaff.
→ A/C to, chargaff rule :—

(I) It is only applicable for DNA double strand.

(II) Purine = Pyrimidine i.e - A + G = C + T

i.e - A → T

G → C

(III) $\frac{A+G}{C+T} = 1$ → E coli = 0.92

Human = 1.52

(IV) A = T = double → H-bond

G ≡ C = triple → H-bond

Qn- If Adenine A = 30% of total DNA molecules what will be the % of Thymine, Cytosine and Guanine in it?

A = 30% i.e. A = T

30% = 30%

60% = 100 - 60 = 40%

G ≡ C

20% 20%

Qn- If Adenine A = 45% of total DNA molecules what will be the % of Thymine, Cytosine and Guanine in it?

A = 45% i.e - A = T

45% 45%

90% = 100 - 90 = 10%

∵ G ≡ C

5% 5%

Qn- If A = 60% of total DNA molecule ~~DNA~~ what will be the % of T, C = 60% & G in it.

→ A = T C ≡ G

60% 60% 60% 60%

120 120

140%

Configuration of DNA -

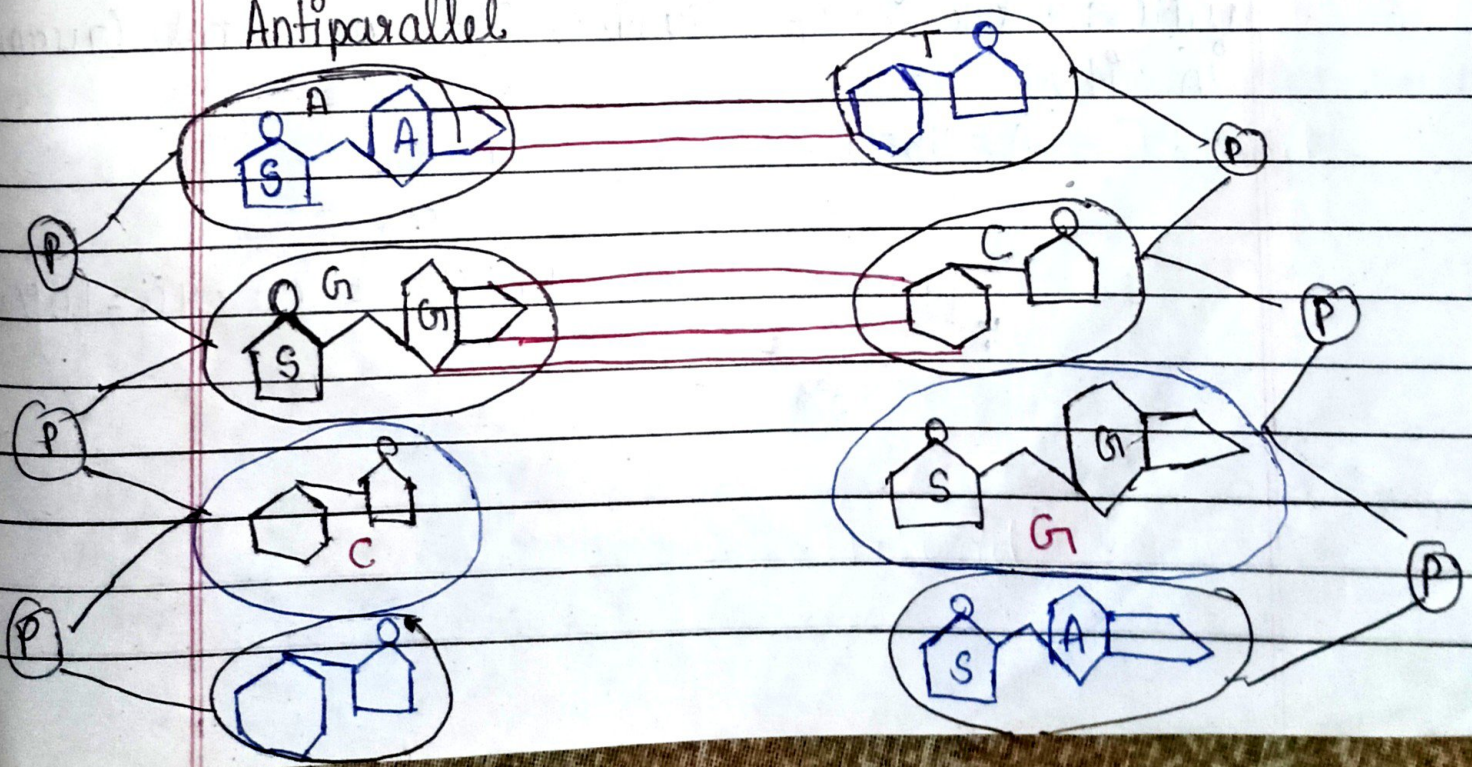
→ A/C. to double helix model, DNA structures is revolving ladder like structure, in which backbone of helix is formed by sugar & phosphate while step are formed by nitrogenous base.

Diameter of DNA is 20 Å.

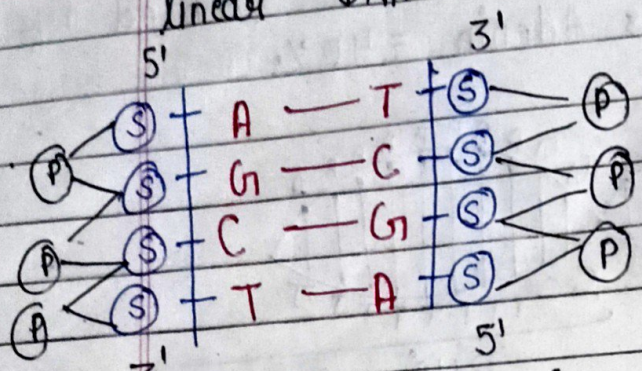
Length of one helix is equal to 34 Å.

→ In a single helix 10 base pair is ~~+~~nt.
Distance b/w two base pair is 3.4 Å.

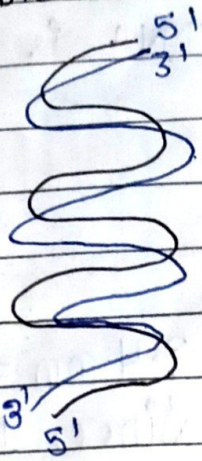
Antiparallel

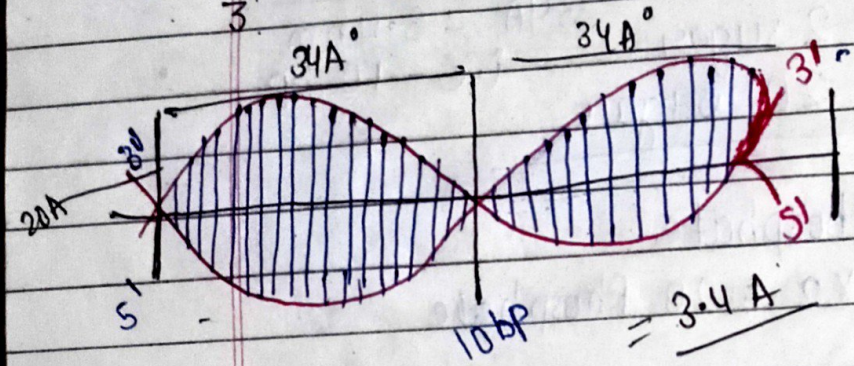


Linear DNA



Double helical



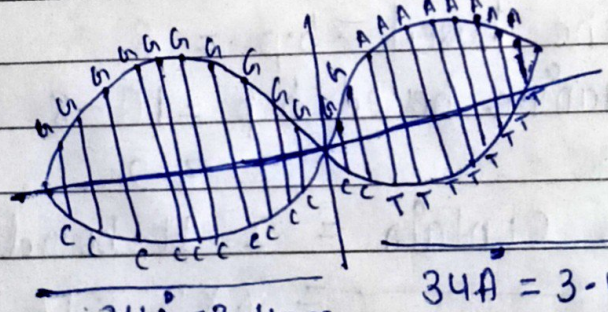


11-10-23

Find out the total sugar, Base pair (bP), Phosphate and H-bond if DNA is = 6.8 nm and Adenin = 20%.

→

34A° = 3.4 nm



34A° = 3.4nm

if adenine contain = 2 H bond

8A = 8 X 2 = 16 H

if 1(G) - 3 H bond

(12) G = 12X3 = 36 H-bond

So, total H bond = 16 + 36 = 52

34A° = 3.4nm i.e 10 bp

→ 6.8 nm = 20 bp

34A° = 3.4nm i.e. 10 b.p

Since, 1 bp = 2 sugar

20 bp = 20 X 2 = 40 sugar

1 bp = 2 Phosphate

20 bp = 20 X 2 = 40 phosphate

if A = 20%

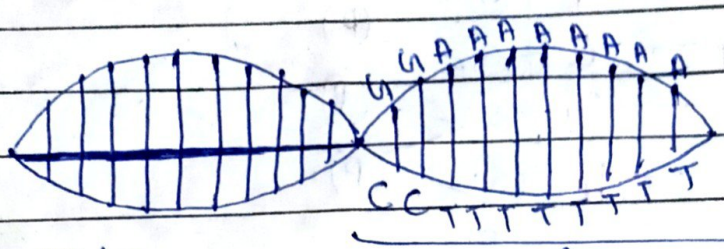
then 40 x 20/100 = 8

i.e. Adenin based b.p = 8

Guanine based b.p = 20 - 8 = 12

Qn- Find out the total sugar, BP, P & H bond if DNA is 3.4 nm & Adenin = 40%.

Sol^n -



3.4 nm = 10 bp
Since, 1 bp = 2 sugar
10 bp = 20 sugar

34Å = 3.4 nm
i.e 10 bp

1 bp = 2 Phosphate
10 bp = 10 x 2 = 20 Phosphate

if A = 40%
then, ~~40%~~ of $\frac{20 \times 40}{100} = 8$

i.e. Adenine based b.p = 8
then, Guanine based b.p = 10 - 8
= 2

if Adenine contain = 2 H-bond
8 (A) ——— = 8 x 2 = 16 H bond

if 1 G ⟶ 3 H bond
2 G ⟶ 2 x 3 = 6 H-bond

So, total H-bond = 16
6
22

22 H-bond

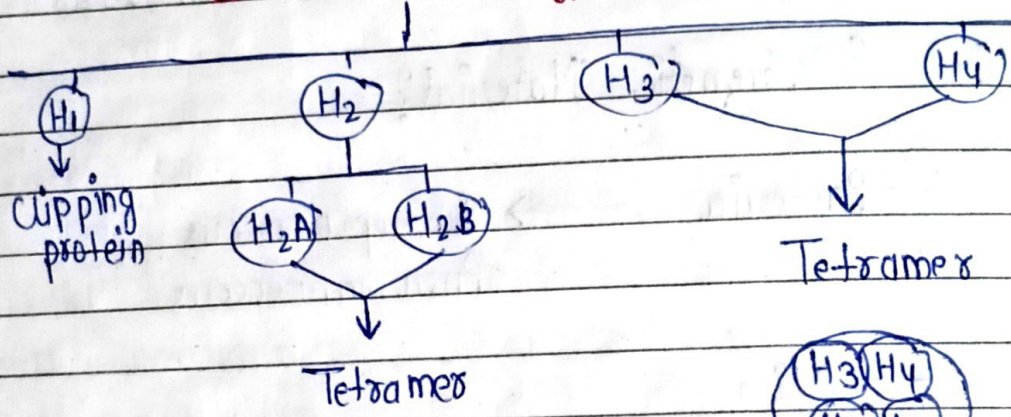
Packaging of DNA -

→ Through packaging of DNA we form chromatin

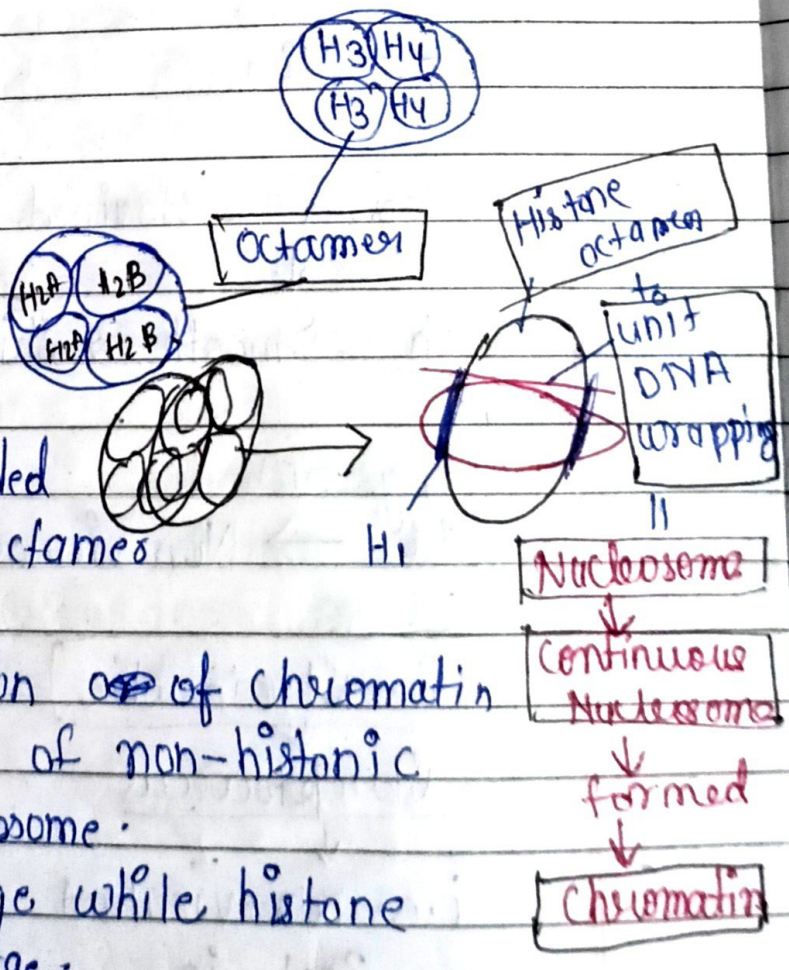
Chromatin = DNA + Histone protein

→ Histone protein - It is responsible for ordering and packaging.

It is of 4 types -



→ On histone octamer unit DNA rapp is called Nucleosome.



→ Nucleosome is a beeded structure in which octamer appear like bead.

→ continuous Successive condensation of chromatin fibre in the presence of non-histonic protein formed chromosome.

→ DNA is -vely charge while histone protein is +vely charge.

→ DNA is acidic in nature while Histone protein is base.

→ DNA is -ve and acidic is due to phosphate.
→ Histone protein is +vely charge and basic in nature due to 'HAL' complex.
(HAL = Histidine Argine lysine)

13.10.23

Transforming Principle -

Given by - Frederick Griffith in 1928.

→ What is Genetic Material?

organism
- Bacteria → Streptococcus Pneumanococcus
- Mice

→ R and S strained dy die.
↓ ↓
Rough and having no lipid → Non-virulant or Not disease causing.
Smooth & Shiny having more lipid → virulant i.e. Disease causing

R - Strain die
↓
~~Streptococcus~~
↓
i.e. non-virulant Bacteria
↓ inject
Mice
↓
live

S - Strain die
↓
~~Streptococcus~~
↓
i.e. virulant Bacteria
↓ inject
Mice
↓
Die

Heat Killed S-die

↓

Streptococcus

↓ inject

Mice

↓

Live

Heat Killed S-strain die

+

R Strain die

↓

Streptococcus

↓ inject

Mice

↓

Die

Conclusion –

(i) Bacteria – DNA having R-strain.

(ii) While S-strain was Heat Killed and Their DNA was Denatured.

⇓

DNA ≠ (R+S)

(iii) From heat killed S-strain something has transfer to R-strain and that cause death of mice due to Replication of New strained of Genetic material.

(iv) From this experiment, Griffith concluded something has transfer from heat Killed Sstrain to R strain But that was genetic material or not was conform.

Biochemical Characterization principle of Genetic Material -

Osteuald Avery, Colin Macleod and Maclyn McCarty in 1933-44.

(I) Heat Killed S-strain + R-strain Bacteria

Protease or proteinase → Inject → Mice → Die

Since, mice die that means Heat Killed S-strain to R-strain was not protein.

(II) Heat Killed S-strain + R-strain Bacteria

RNase Enzyme → Inject → Mice → Die

Since, Mice die that means from Heat-Killed S-strain to R-strain was not RNA.

(III) Heat Killed S-strain + R-strain Bacteria

DNAase → Inject → Mice → live

Since mice live that means from Heat killed S-strain → to R-strained DNA was transferred - but after digesting that DNA it not get transfered & Replicated.

i.e. Genetic material is DNA.

Conclusion – (i) After biochemical characterization by Macarty, Avery and Macleod we can say that DNA & RNA both can act as genetic material (ii) DNA is a stable & better for storage of genetic information. (iii) While RNA is better for expression of genetic material.

Hershey and Chase Experiment for confirmation of DNA is Genetic Material –

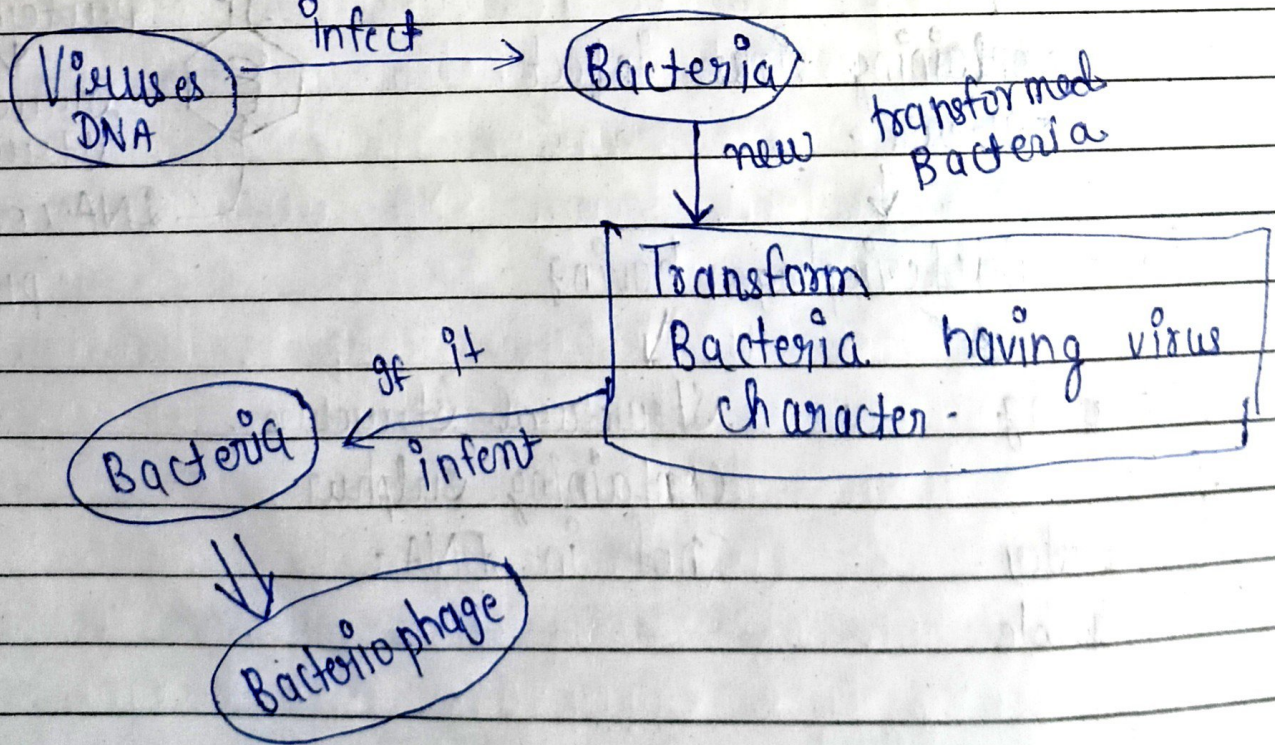
Bacteria
Virus
Bacteriophage } used organisms.

→ Viruses are smaller than Bacteria.
→ So, can infect the Bacteria.

Bacteriophage formation –

Viruses
~~DNA~~

When a viruses infect to bacteria a transformed bacteria is formed having virus DNA is tnt, and if transform bacteria infect to a fresh bacteria then bacteriophage form.



Protein

Contain = Sulphur

Normal

Isotopes → Atomic no. same but mass no. different.

S^{32} (16) | S^{35} (16)

diff. — same

Virus grow Sulphur containing protein are cystein and methionine

Sulphur – isotopes

↓

containing virus Infect Bacteria.

↓

i.e – Bacteriophage having

↓

Structural structure containing sulphur not in DNA.

↓

② Blending

water soluble

DNA

Contain – Phosphorus

Normal

Isotopes

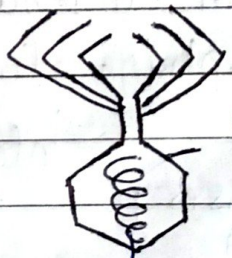
P^{31} (15) | P^{32} (15)

diff. — same

Virus grown Normal

Virus → Bacteria

– In bacteriophage



↓

protein (capsid)

↓

Structural structure

DNA contain Phosphorus

Phosphorus – Isotopes
↓
containing virus infect Bacteria.
↓
i.e. Bacteriophage having
↙
② Blending → DNA containing isotopes phosphorus
→ Not in structural structure
water soluble
③ Centrifugation.

→ Both phosphorus isotopes & sulphur isotopes containing virus infect to bacteriophage.
→ Bacteriophage blended so that their structural structure isolated out and we can analysi then & we found that only structural structure having sulphur containing protein.
→ After centrifugation it clear DNA containg material don't have sulphur isotopes.
→ In DNA material, Only phosphorus isotopes is found not Sulphur isotopes found.
→ It conclude that DNA is a genetic material.

Properties of genetic material –

If we compare DNA with RNA we can say ~~that~~ molecules

④ Molecules that behaves as genetic material must fulfill following criteria –

(i) Should be able to generates its copy i.e. replication.

(ii) Chemically and structurally stable.

(iii) That have scope to change its their structure for better representation (+ve mutations) molecule should be able to expression in terms of mendelian characteristic

27.10.23

RNA WORLD

RNA world was discovered by Leslie orgel (a chemist)
Through RNA world we able to known that RNA is genetic material.
Various life processes like metabolism, translation, splicing all evolved around RNA.
RNA can act as genetic material as well as catalyst or enzyme.
DNA evolved from RNA with some chemical modification like —

(i) Methyl group is added as 5th position of ~~thymine to form uracil~~ Uracil to form thymine.

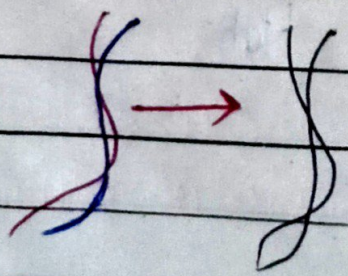
(ii) An oxygen is remove from 2nd position of ~~deoxy~~ribose sugar to form deoxyribose sugar and also become double strand to resist changing.

Replication –

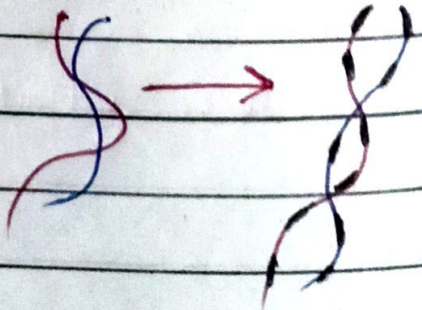
Again copy ⇒ Duplication

→ Duplication of DNA is called Replication.
→ DNA duplication occur due to semiconservative mode for DNA Replication.
→ Semi-conservative mode of DNA Replication is most excepted model.
→ A/C to this model, every Replicated DNA consist of one new strand and another old strand DNA.
→ Replication of DNA occur in S-phase of interphase.
→ Before, semi-conservative mode of DNA replication two model was also proposed that was conservati and Disruptive.
→ Both the mode of replication was rejected only semi-conservative mode of DNA replication exepted.
→ A/C to conservative mode of DNA replication new DNA is form is totally different from its parent DNA i.e. DNA to DNA formation takes place but denovo (totally new form).
→ A/C to disruptive mode of DNA replication new DNA is form from parent DNA in alternate segmentation form.

Conservative



Disruptive



→ Our DNA is replicated through semi-conservative mode of DNA replication & it is experimentally proven by Matthew Messelson and Franklin stahl (1958).

Semi-conservative Mode of DNA replication—

→ Organism – Bacteria (E. coli)

→ Environment – NH_4Cl

↓ use of

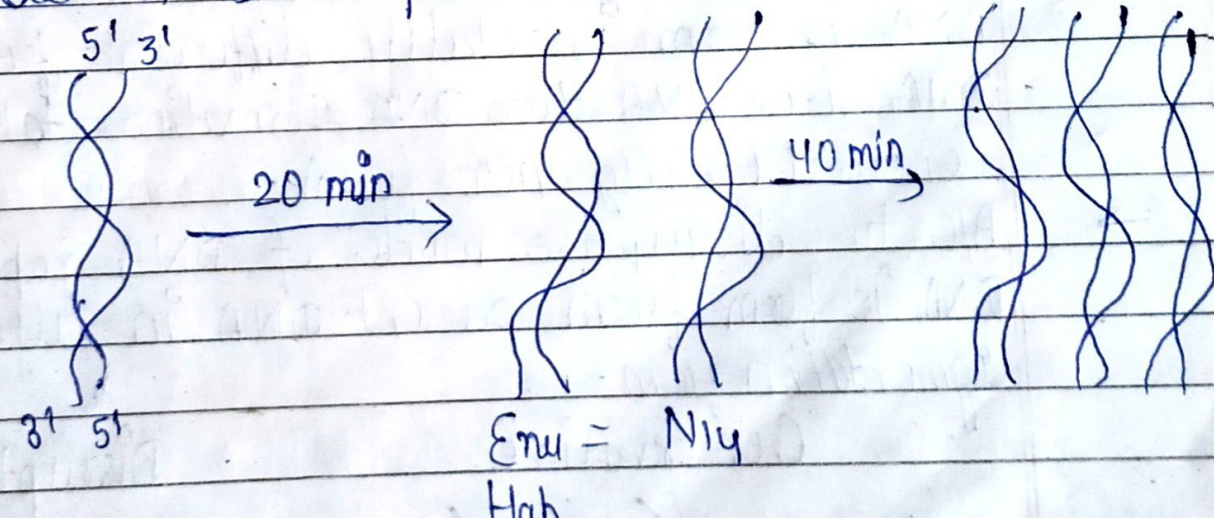
Isotopes of Nitrogen

N → N_7^{14} — Normal

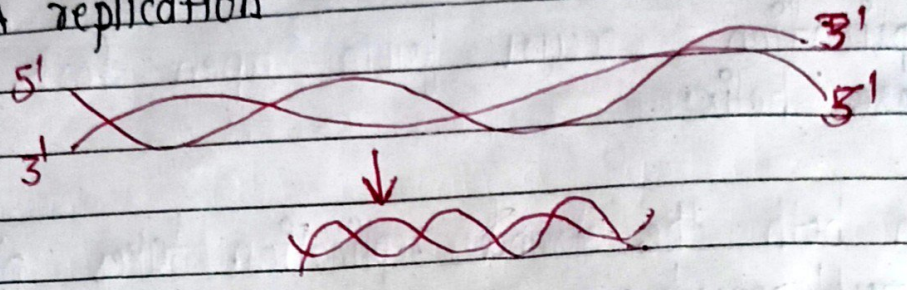
↓

N_7^{15} – Isotopes

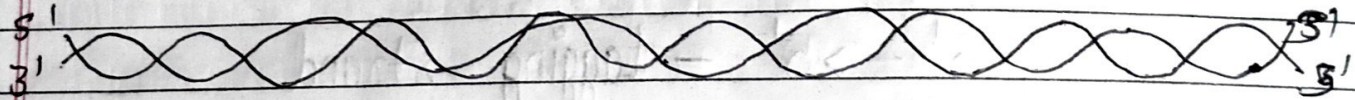
Melson and that experiment – Semi-conservative mode of DNA replication.



DNA replication —

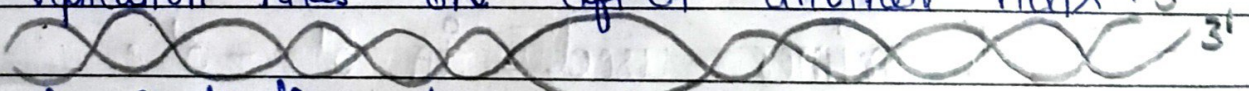


DNA replication always occur from 5'→3'.
DNA replication not all helix removed out simultaneously.
DNA replication takes one after another helix.
In replication bubble replication fork formed.



During DNA replication not all helix removed out simultaneously.

DNA replication takes one after another helix.



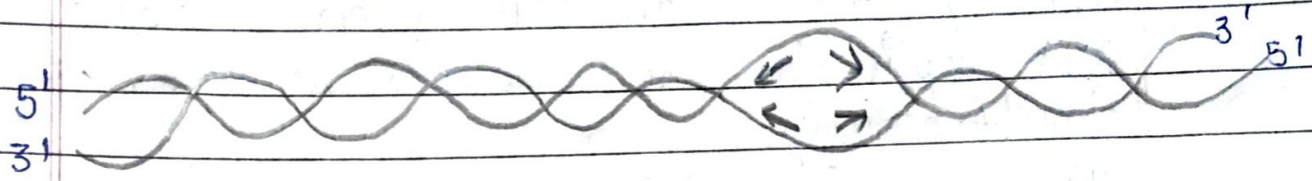
→ Due to Replication fork ori-site.

→ Replication fork is of y-shape origination or imitation site.

→ In bacteria (prokaryote) only one ori-site formed.
→ In eukaryote multiple many ori-site formed.

→ Replication occurs from open fork to close helix.

→ In both the strand replication takes place simultaneously.



5' → 3' – leading strand

3' → 5' – Lagging strand

↓

Many fragment

↓

Okaraki fragment

→ 1 primer used in 5' – 3'.

→ While in 3'-5' strand many primer are used.

01.11.22

DNA replication completed into two steps -
(i) Unwinding
(ii) Synthesis of new strand of DNA.

(i) Unwinding - separation of both the strand of DNA.
It occur at a specific site i.e. called origination or ori or inisiation site.
since, unwinding is a energeticcally process it required heavy energy so, DNA replication occur at small fragment i.e. bubble that turn into replication fork.

(ii) Synthesis of new strand of DNA - First of all, All RNA primer synthesise in 5' to 3' direction.
After synthesis of new DNA strand RNA primer disappear.
During DNA replication deoxyribo nucleoside triphosphate has dual function.
(i) It acts as substrate.
(ii) It provide energy for DNA replication.

Enzymes -
Tools and Technique -

(i) DNA dependent DNA polymerase
(ii) Topo isomerase (Eukaryote)
(iii) DNA gyrase. (Prokaryote)
(iv) Helicase.
(v) Helix disestablising protein.
(vi) RNA primar or RNA polymerase.
(vii) Exonuclease.
(viii) DNA ligase

ii) DNA polymerase — It acts as DNA templates and polymerise the synthesis of new strand i.e complementary to old strand.

→ This enzyme is very efficient.

→ Since, In E.coli having 4.5×10^6 Base pair replication completed within 18 min i.e. 2000 Base pair per sec. with highly accuracy, mistakes lead to mutation.

→ In prokaryote three type of polymerase is used —

(i) DNA polymerase I
(ii) DNA polymerase II
(iii) DNA polymerase III

DNA polymerase I — RNA primer ~~and~~ removing and adding okazaki fragment in single unit.

DNA polymerase II - Correcting enzyme.
DNA polymerase III - Synthesing enzyme.

→ In eukaryote 5 type of DNA polymerase is used —

(I) DNA polymerase α
(II) DNA polymerase β
(III) DNA polymerase γ
(IV) DNA polymerase δ
(V) DNA polymerase ε

(ii) Topoisomerase - used in to cut and separate the DNA strand.

eukaryote - At a time it works on single strand of DNA thats why it is also called single strand specific.
That is topoisomerase prevent from super coiling ~~prevention~~ of DNA.

(iii) DNA gyrase - It has similar function like topoisomerase.

(iv) Helicase - It breaks hydrogen bond b/w both the strand of DNA & separate them completely.

(v) Helix disestablising protein - Prevent from re-helixing of DNA.

(vi) RNA primers - is used for inisiation or starting point or triggered or insiator.

(vii) Exonuclease - is used for cutting of RNA primer & to proced. for adding of okazaki fragment with the help of DNA ligase in single strand.

(viii) DNA ligase - is used to add sigment of DNA.

hnRNA – hetero nuclear RNA
SnRNA – short nuclear RNA
mi-rRNA – Micro nuclear RNA

03.11.23

Date
Page

Transcription

is the process in which copying of genetic material from one strand of DNA get converted into RNA.

→ In early time, transcription process was analysis described by central dogma (A independent institution for molecular ~~inhancement~~ structure inhancement committee)

→ A/C to central dogma that is transcription (DNA to RNA formation takes place in uni-directional not bi-direction) & there respective enzyme are transcripted (-ase)

→ Transcriptase included RNA polymerase I
RNA polymerase II
RNA polymerase III

RNA polymerase I	formed "rRNA" (except 5 rRNA)
RNA polymerase II	formed mRNA & hnRNA
RNA polymerase III	formed 5s rRNA, mi-rRNA, SnRNA

→ A/C to new rule of transcription —

(i) Transcription can take place in bi-direction i.e. from DNA to RNA & RNA to DNA.

(ii) From DNA to RNA formation is called transcription.

(iii) From RNA to DNA formation is called Reverse transcription and there respective enzyme is called reverse transcriptase.

Enzyme in transcription –

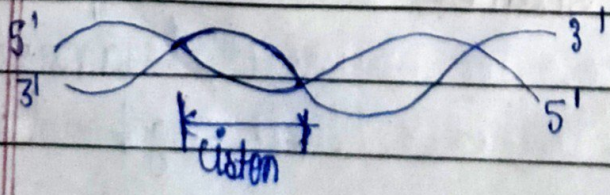
→ RNA primer never used in transcription.
Instead of RNA primer RNA polymerase I is used.

#

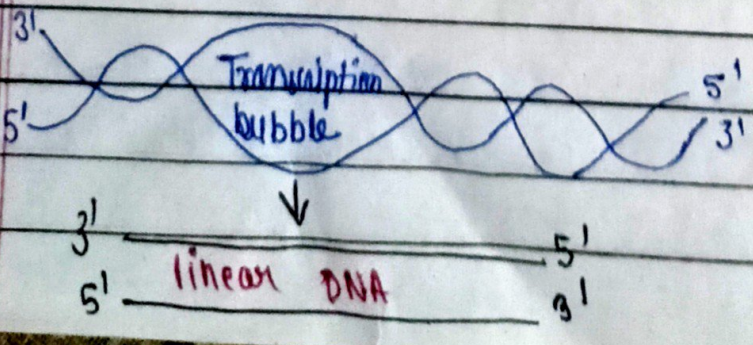
RNA polymerase I formed "rRNA" (except 5 rRNA)
RNA polymerase II formed mRNA & hnRNA
RNA polymerase III formed 5s rRNA, mi-rRNA, SnRNA, tRNA

mRNA	tRNA	rRNA
Act as templet.	being required amino acid	form peptide bond.

→ Transcription always takes from 5' → 3'
→ while DNA segment read out from 3' → 5'
→ DNA segment that takes part in transcription is called "Cistron".
→ whole DNA of transcription is called Structural DNA.
→ 1st of all bubble is formed i.e. called transcription bubble.
→ In whole DNA ~~and~~ strand transcription can't takes place simultaneously.
→ Transcription takes place in single strand only (i.e. 5' → 3') Since, RNA is formed.



– Structural gene / DNA



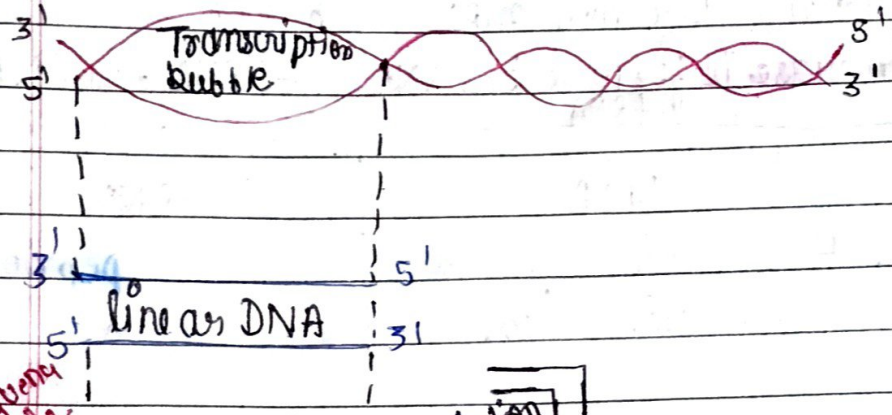
→ mRNA formed in single strand.

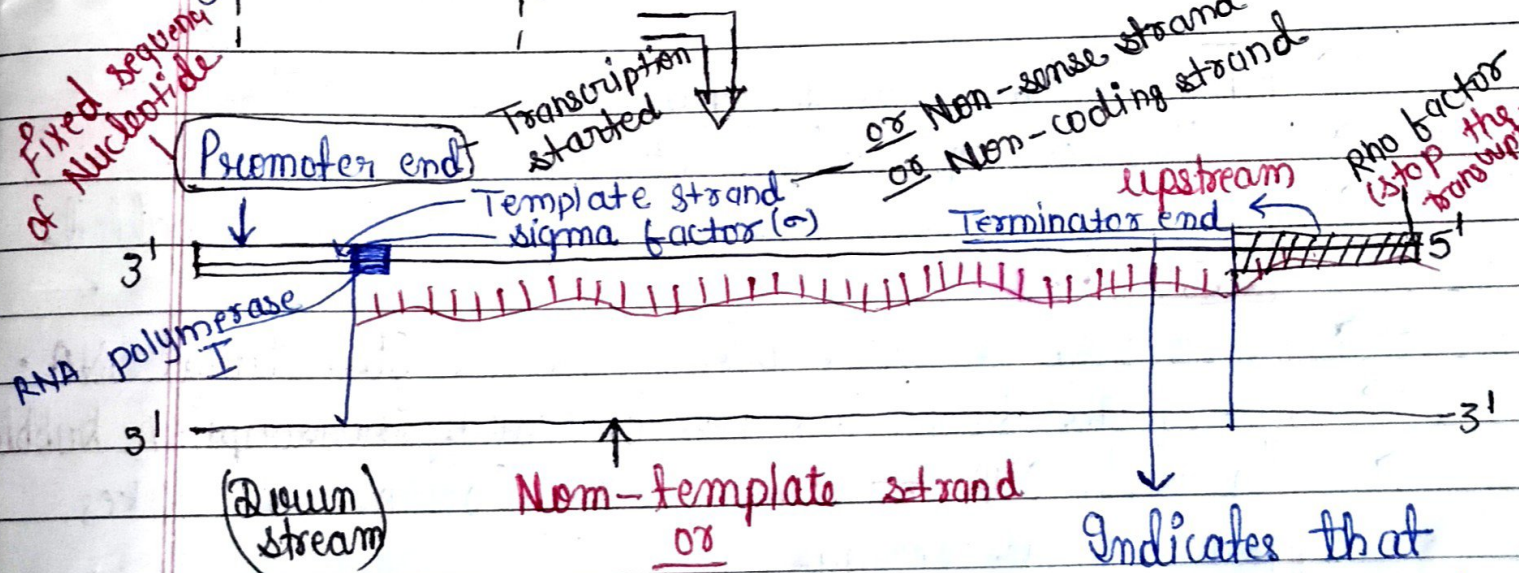
→ RNA - primer not used in transcription.

↳ Equivalent enzyme is RNA polymerase I.

Process –

1st of all bubble is formed i.e. transcription bubble.





Non-template strand
or
Coding strand
or
Sense strand

Indicates that transcription is about to finish So, speed of transcription get lower.

→ Template strand is reference for mRNA formation.
→ RNA polymerase are single strand specific.

Prokaryote - DNA ⟶ mRNA
Eukaryote - DNA → hnRNA → mRNA

Terminator synthesized during transcription while promoter not.

Transcription completed into three step -

① Initiation -

→ During transcription DNA formed two end 1st one is called promotor end or initiation end while other is called terminator end or stopping end.

→ From promoter end transcription started while terminator end transcription stop.

→ There is factor called σ-factor get attached with RNA polymerase I then promoter end transcription started.

→ And promoter end cut the DNA one strand with the help of RNA polymerase enzyme to separate both strand.

→ Out of two DNA strand only one have polarity i.e 3' — 5' end take part in transcription and this is called template strand or Non-coding strand or Non-sense strand.

→ Transcription started from 5'end to 3'end.
→ Transcription process used Ribonucleoside tri-phosphate (ATP, GTP, CTP, TTP) as substrate.

(ii) Elongation -

→ RNA polymerase enzyme establish phospho-diester bond ~~stablish phospho diester bond~~ b/w nucleotide to form complete strand i.e. elongation.

(iii) Termination -

→ At the end, a factor called Rho is ~~+nt~~ that indicate the ~~stoping~~ of transcription process.

→ At terminator side DNA ~~+nt~~ in Palendromic sequence. (ex- MIAMI (ulta-seedha).

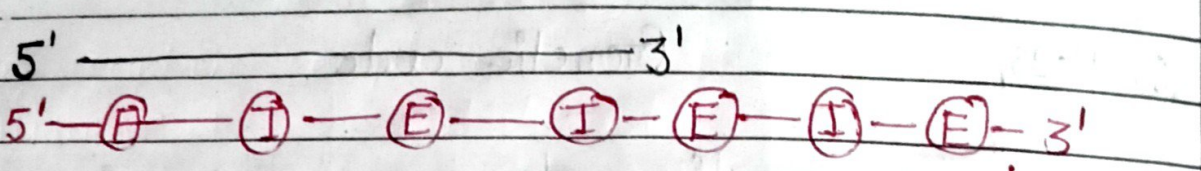
In prokaryotes, mRNA formed from DNA i.e. only functional part ~~+nt~~ or formed during transcription.

While in eukaryote, in transcription process, DNA to hnRNA formed & then ~~DNA~~ hnRNA to mRNA finally formed.

In eukaryotes, non-functional & functional part formed in hnRNA.

mRNA splicing or mRNA maturation or mRNA promotion —

→ mRNA splicing only occur in eukaryotes.
→ mRNA splicing occur in formation of mRNA from hnRNA except two protein —
Interferon
Histone protein

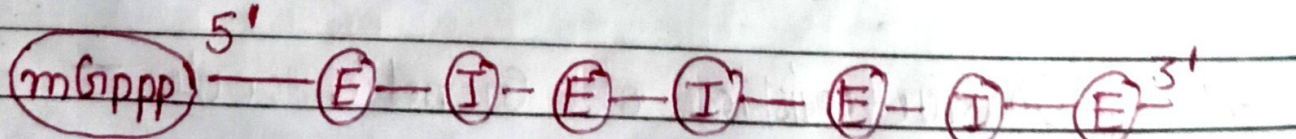


Exon (E) = Functional part
Intron (I) = Non-functional part

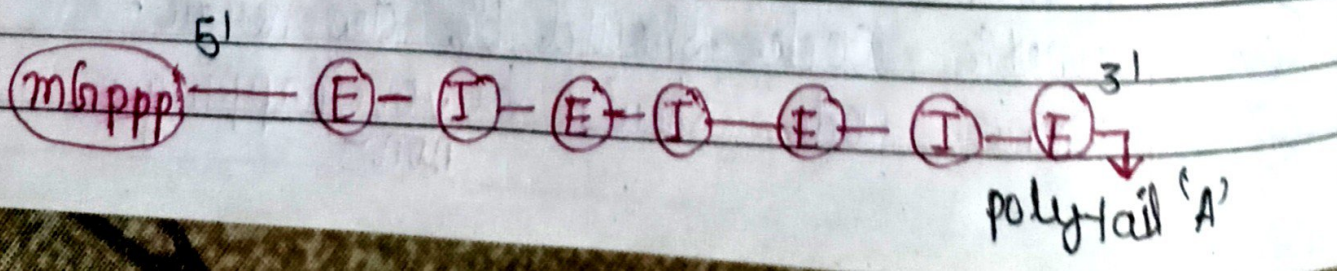
→ DNA having functional and Non-functional part = Split gene

1. Capping 2. Tailing 3. Exit of Intron

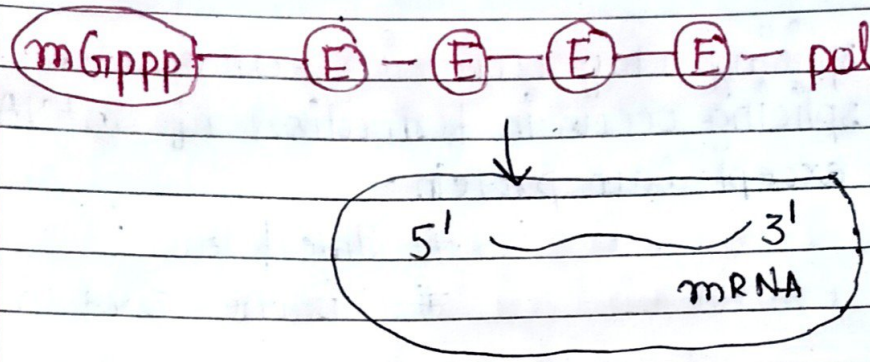
1. Capping – Adding of Methyle guanine triphosphate (m7Gppp) at 5' end of hnRNA.



2. Tailing – Adenylic acid (200-300) are attached at 3' end of hnRNA.



3. Exit of Intron – Removal of Non-functional part i.e. intron.



08.11.23, Genetic code –

→ Term genetic code was given by George Gamow.
→ Genetic code discovered by – Nirenberg
– Mithai
– H.G. Khorana

→ The relationship b/w nucleotide sequence of mRNA and Amino acid having sequence of protein or polypeptide chain is called genetic code.

→ Codon is the sequence of three specific Nucleotide of mRNA which code for particular amino acid

Characteristic of Genetic code –

(i) Genetic code are triplet in nature.
(ii) Genetic code are universal.
(iii) Genetic code unambiguous (error free)
(iv) Genetic code should be degenerate.
(v) Genetic code should be non-overlapping.

(VI) Genetic code should be comma less (No special character).

(VII) Genetic code having dual nature like AUG.

(VIII) Genetic code would be ~~triplet~~ in nature that was experimentally given by George Gamow.

Types of Genetic code - x^n

Here $x = 4$ type of nucleotide

n = may be no. of nucleotide in a codon.

(I) ex - If ~~singlet~~ codon is singlet $4^1 = 4$ Not fulfill our amino acid Requirement.

(II) If codon is doublet $4^2 = 4 \times 4 = 16$ only represent 16 A.A not fulfill our A.A Requirement.

(III) If codon is triplet $4^3 = 4 \times 4 \times 4 = 64$ ~~only that~~ fulfill our 20 AA requirement to represent. ~~that~~

*Non-functional

	A	U	G	C	
A	AAA AAU AAG AAC	AUA AUU *AUG AUC	AGA AGU AGG AGC	ACA ACU ACG ACC	A U G C
U	*UAA UAU *UAG UAC	UUA UUU UUG UUC	*UGA UGU UGG UGC	UCA UCU UCG UCC	A U G C
G	GAA GAU GAG GAC	GUA GUU GUG GUC	GGA GGU GGG GGC	GCA GCU GCG GCC	A U G C
C	CAA CAU CAG CAC	CUA CUU CUG CUC	CGA CGU CGG CGC	CCA CCU CCG CCC	A U G C

→ Genetic code is degenerative since one A.A can be coded by more than one codon except two amino acid.

(i) Tryptophan
(ii) Methionin

→ Genetic code is non-overlapping since, one nucleotide is the consituent of only one codon not any other codon.

UAG - Amber
UAA - Ochre
UGA - OPAL
= STOP codon

→ Starting codon AUG.

Type of RNA —

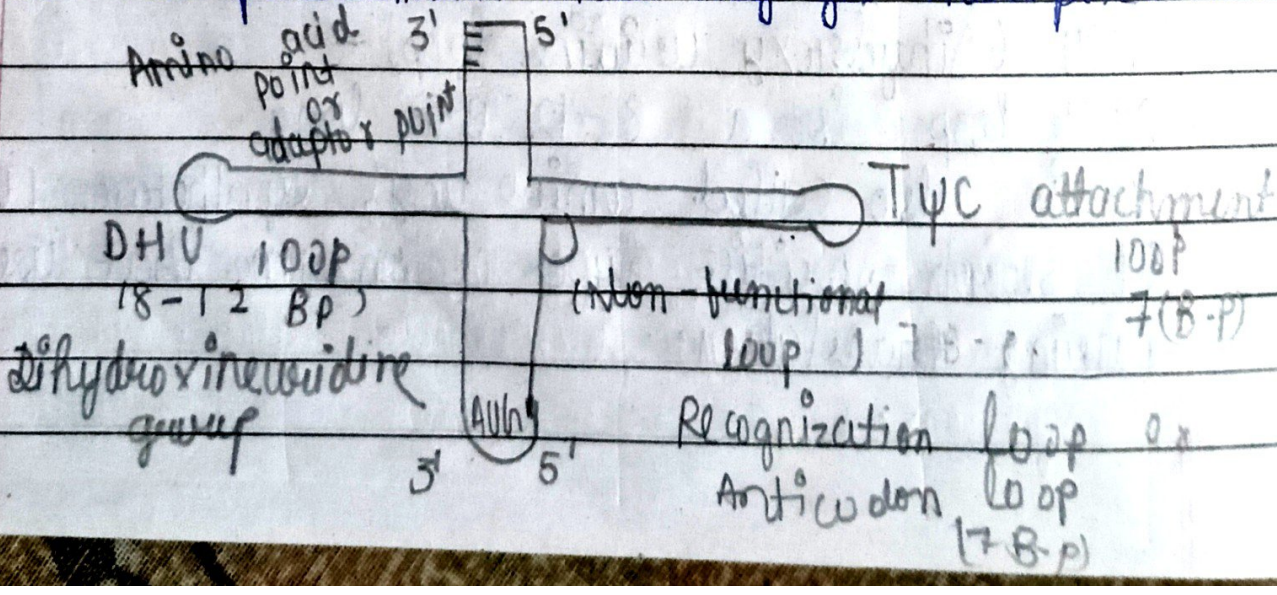
(i) rRNA
(ii) mRNA
(iii) tRNA

(i) rRNA - is the most abundant RNA found 80% of total RNA. It is insoluble and most stable. It is formed by nucleolus except 5'S RNA i.e. formed outside the Nucleolous in chromatin fibre. It is found in Ribosome that help in protein synthesis to attached mRNA & tRNA with ribosome.

(II) mRNA - ~~was~~ discovered by Jacob & Monard.
→ It is least stable RNA.
→ It is found only 1 to 5% total RNA.
→ It is synthesis during transcription process from DNA.
#→ It acts as templet strand for translation or protein synthesis.

(III) tRNA - It is found 10 to 15% total RNA.
→ It is soluble RNA.
→ It is also called adaptor RNA since, it help in transfer of A.A from ribosome for protein synthesis.
→ It is smallest RNA i.e made up of only 80 nucleotide.
→ It is of single type i.e 45 type.

Structure of tRNA -
It having two types of model —
(I) Clover leaf model (2-D) (II) L-shape model (3-D)
→ We have to study Clover leaf model.
→ Clover leaf model - was proposed by Robert Holley along with him Nerienberg, H.G. Kohrana also include.
→ For this predominant model they got nobel prize in 1968.



→ tRNA is a single strand RNA.
→ At 3' polar end of tRNA activated amino acid is attached.
→ Activated amino acid is formed when energy and enzymes are loaded with amino acid.
→ Activated amino acid attached with 3' end of tRNA since, carboxylic group is not.

TΨC loop / Attachment loop -
→ It is of 7 B.P
→ It helps in attachment of tRNA with largen subunit of ribosomes.

Recognizing loop -
→ It is of 7 B.P
→ At their loop 3-nucleotide sequence specific type is not, which is complementary to mRNA that is called anticodon or NODUC.
→ This loop help in recognize the specific amino acid so also called recognization loop.
→ specific amino acid on the basic of anticodon.
→ Gi type of tRNA can found specific amino acid from cytoplasm of cell.

DHU (Dihydroxy uridine loop) -
→ DHU loop is a 8-12 B.P long.
→ It is also called amino acyl synthetase loop.
→ It search specific type of enzyme that uses during translation.

Amino acid /Adapter point -

→ From this point specific type of amino acid got entered into translation process.

How to use amino acid -

→ Two step use to use amino acid -

① Activation of amino acid

or

Aminoacylation

Amino acid + ATP $\xrightarrow[\text{synthetase}]{\text{Aminoacyle}}$ Aminoacyl - AMP - Enzyme complex.

② Charging of Amino acid -

Amino acyl - AMP - E complex + tRNA → Aminoacyl AMP + tRNA

Charged A.A = Aminoacyle + tRNA

Translation - It is a process in which protein synthesis takes place.

→ The sequence of amino acid in a polypeptide chain formed protein that determine by sequence of codon (template on mRNA).

→ Formation of peptide bond required energy so translation is in active process.

→ After charging tRNA it move toward ribosome

→ When two charged tRNA comes closer to each other on P-site the formation of peptide bond

occur with the help of rRNA using enzyme peptidyle transfer.

→ When mRNA encounted with smaller subunit of ribosome then process of translation started.

→ At large subunit 3 site is thd -
(i) Amino acyl site
(ii) Peptidyl site
(iii) Exit site

→ Translation completed into 3-step -
(i) Initiation (ii) Elongation (iii) Termination

→ Charged tRNA attach with layer subunits of ribosome A/C to codon of mRNA.

→ During initiation a site is empty.

→ When two charged tRNA comes closer to each other on p site then formation of ~~each other on~~ peptide bond occur with the help of rRNA using enzyme peptidyl transferase.

→ The enzyme peptidyl transferase help in synthesis of peptide bond.

→ In prokaryote 16's rRNA act as enzyme peptidyle transferase.

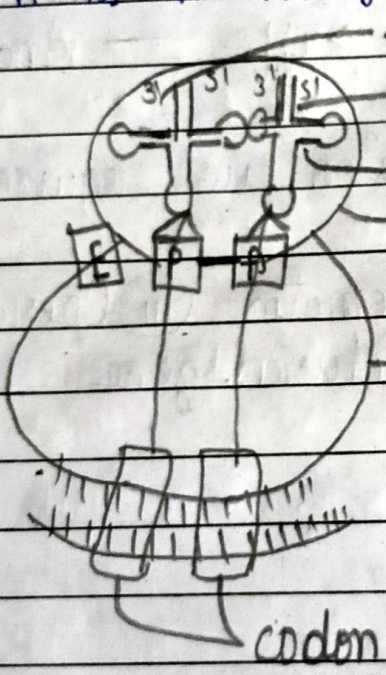
Elongation - formation of peptide bond b/w amino acid due to which polypeptide chain form it is called elongation.

Termination – When stop codon (UAG, UAA, UGA) comes on mRNA then process of translation stop it is called translation.

UTR (Untranslated region) –

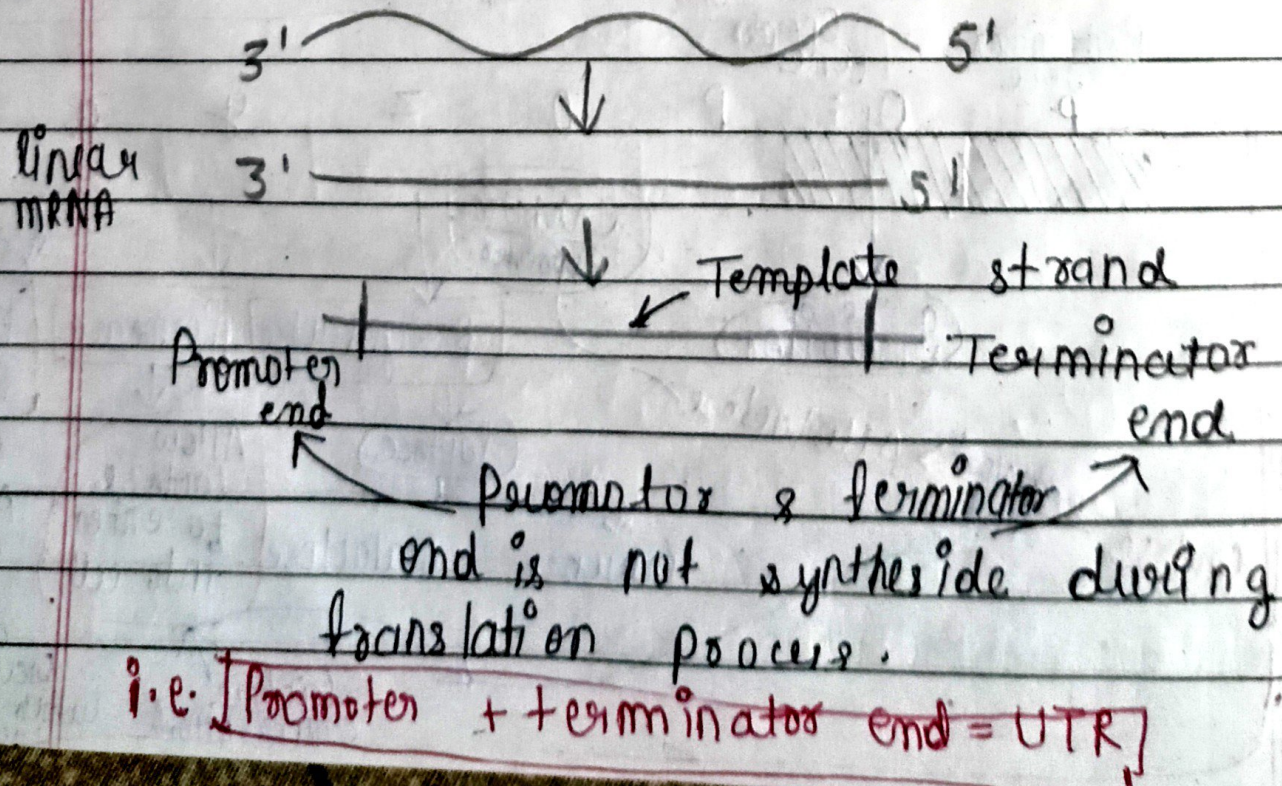
→ At both side of mRNA before start and after end stop codon their are certain region which do not take part in translation process.

→ UTR is necessary for efficient translation process.



peptide bond formed with the help of rRNA using enzyme peptidyl transferase.

$AA_1 + AA_2 + AA_3 + \dots AA_n$



Promotor & terminator end is not synthesize during translation process.

i.e. Promoter + terminator end = UTR

Gene expression – is a demand of body or cell through which gene get revolut regulated.

→ Gene regulation was given by Francois Jacob and Jacque Monod, in E.coli bacteria.

→ Gene regulation is performed by two types of enzyme –

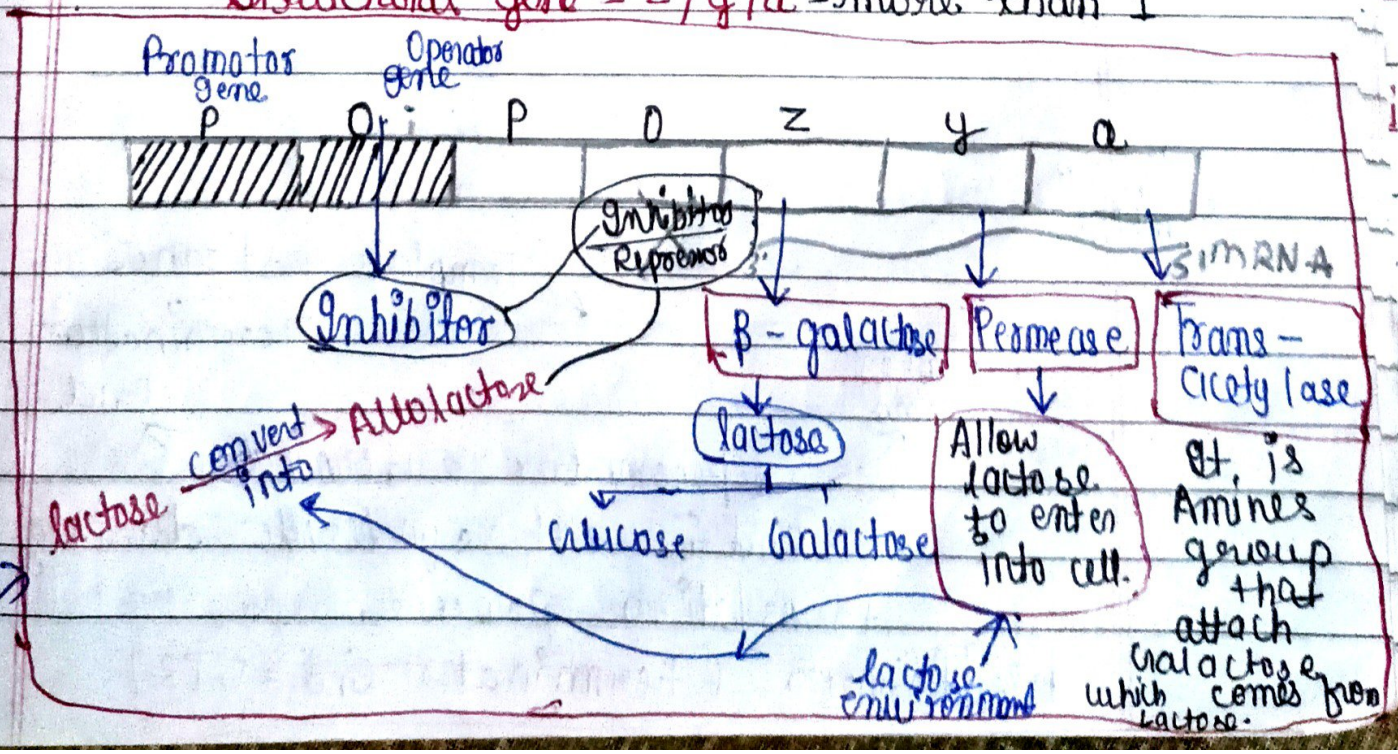
(I) Inducer — off → ON — catabolic
(II) Repressor — ON → off — Anabolic

To regulate gene expression we require four diff. type of gene –

(I) Regulator (II) Promotor (III) Operator
(IV) Structural gene

i.e.

Regulator / Repressor – i = 1
Promotor – P = 1
Operator = O = 1
Structural gene = z / y / a = more than 1



→ Lac operon concept activated in environment where lactose is +nt and glucose is -nt.

→ In this senerio, lactose digestion gene expression should be regulate.

→ When lactose comes in bacterial environment due to little secretion of permease, cause transportation of lactose inside bacterial cell wall, that convert into Allolactose. lactose.

→ When lactose is +nt in environment and influence of permease large amount of lactose get entered into bacterial cell.

→ Due to lactose +nt bacterial cell have to break lactose into glucose and galactose.

→ First of all, Allolactose bind the inhibitor so, transacetylase also activated and it ~~binds~~ regulate translation process & accumulate Non-digesting galactose.

DNA Fingerprinting

DNA fingerprinting was discovered by Allec Jeffrey so, also called father of DNA Fingerprinting.

Indian father of DNA fingerprinting is —

(i) Lal jee singh
(ii) V.K. Kasyap.

→ DNA fingerprinting is use to compare two diff. individual DNA sequence.

→ Human genome contain 3.3×10^9 B.p.

→ 99.9% human having same DNA or similar DNA i.e. .1% variation occur in all human DNA sequence.

→ Out of this less than 2% DNA can code for protein synthesis in human.

→ More than 98% DNA is non-functional in human, i.e. unable to code for protein synthesis i.e called Satellite DNA or junk DNA.

Junk DNA is of two types —

(i) Mini satellite → (15-60 Bp) variation

(ii) Micro satellite → (1-13 Bp) variation
Single Nucleotide protein (SNP)

→ Satellite DNA get classified into two part due to mutation.

→ Mini satellite is also called Variable number Tendum Repeat). (VNTR)

→ Since, no. of Tendum repeat varies from individuals to individuals.

→ Satellite DNA or Junk DNA or VNTR is the basis of DNA fingerprinting.

NOTE - VNTR is basic of Human genome project.

Process of DNA fingerprinting —

(i) Collect the sample (like - blood, nail, hair, follicles, mucus, semen, saliva etc.)

(ii) Cell Isolated to find out lysis process to find out DNA.

(iii) DNA is ppted out through chilled ethanol (min. 1 mg is required for DNA fingerprinting). (If less than 1mg DNA is ~~int~~ then multiplied using PCR (Polymer chain rk^.))

(iv) Cut the DNA ~~fragment~~ into small fragment REE (Restriction Endo Nuclease)

(v) All the DNA arranged lengthwise for using gel electrophoresis method.

(vi) DNA fragment is shifted into alkaline solution since, having multiple nuclease enzyme which component dissolve the one strand of DNA.

(vii) This DNA sequence shifted on Nitro cellulose paper through southern blotting method.

(viii) Radioactive single strand DNA that form complement & Anti-parallel DNA i.e called Probe

Application of DNA fingerprinting -

(i) Forensic purpose for criminal case investigation.

(ii) Find out Mutation.

(iii) To detect patternity.

Human Genome Project (HGP)

→ Start - 1990
End - 2003 (Not Yet end)

→ HGP is also called Mega project since it duration was 13 yrs.

→ In human being approxiametly 3×10^9 bp.

→ ~~Cost~~ Expense estimation - per BP = 3$
Total estimated expense - 9 Billione $ (Dollar).

→ HGP approach started on new branch of Biology i.e called Biojnformetics.

→ HGP was insiated by - Wellcom trust of Britain
- US department of energy
- National institute of health.

→ Other participated country was Japan, France, Germany, china and other countries.

Goal of HGP -

(i) Identify all the gene in human being approx. 20-25 thousands.

(ii) Determine the sequence of 3 billion chemical bp i.e. used for human DNA.
(iii) Store this information in Database.
(iv) Improve tools for data analysis.
(v) Transfer related techniques to other sector such as industries based on.
(vi) Address the ethical, legal and social issues (ELSI) that may arise from the project.

Methodologies:-
Two Methodologies used —

EST
(Expressed sequence TAGs)
→ is focus on that genome that are responsible for expressed RNA for protein synthesis.

SA
(Sequence Annotation)
→ means it synthesized and sequenced intire DNA i.e. functional as well as non-functional both.

Processure —

(i) Isolate the DNA from cell using lysising enzyme.
(ii) Convert it into Random sequence using RFE.
(iii) Clone it with suitable host using BAC or YAC for amplification purcess. (Use the no.).
(iv) Now, fragments are sequential using auto DNA model based on Sendrick & Sanger method.
(v) Sequenced are arranged based on overlapping reason.

(vi) Alignment of sequence using computer programming.

→ First sequence of chromosome was completed in 2006 i.e called Chromosome I.

Salient feature of HGP ——

(ii) HG contain 3164.7 million bp.
(iii) Average gene contain 3000 bases but it may varies upto 2.4 million bp (Dystrophin protein having 2.4 million bp).
(iv) Total no. of estimated genes are 30,000 but we had expected 80,000 to 1,40,000 genes.
(v) 50% gene function are unknown.
(vi) Less than 2% of genome codes for protein.
(vii) Repeated sequences make up very large portion of human genome.
(viii) Repeated sequence work as dynamically and reason for evolution (i.e variation in character).
(viii) Chr. I has most genes (2968) and the Y gene has the fewest (231).
(ix) In HGP work on more than 1.4 million location on genome where we analysie on the basis of SNPs (Single Nucleotide polymorphism) i.e helpful for particular disease analysis & Human Health History.