

Molecular Basis of Inheritance

RNA → In a few viruses only.

Base + sugar = Nucleoside

Nucleoside + P = Nucleotide

Polynucleotide

 $\} 3.49^\circ$


Strands: $A=T \times C \cong G$.

- Polynucleotide chain: \rightarrow Deoxyribose (-1'0')

3-Part 5: N-base + sugar + phosphate

Purine Pyrimidine

A. G.



N:1,3,7,4



N:1,3

- Dimers of $H_2A, H_2B, H_3 \times H_4$ makes histone octamers: wraps around 200bp DNA around it.

Chromatin

- Transforming Principle: Griffith (1928)

R-strain + Mice: **Survived**

Heat Killed S-strain: **Survived**

Heat Killed S-strain + R-strain: **Died**

- Hershey & chase experiment: unequivocal proof

**Do not enter
cell**

Enter the Cell

1. Should be able to replicate 2. Stable

3. Shall mutate slowly 4. Express itself

DNA is better!

Transc. Transl.
DNA → RNA → Protein

Replication

- Proved by Meselson & Stahl using N^{15}

(heavy isotope).

- By Taylor in Faba beans using radioactive ^{14}C

The diagram illustrates the first generation of DNA replication. A single green DNA molecule, labeled N^{15} , is shown on the left. An arrow points to the right, where two DNA molecules are produced. The top molecule is green and labeled N^{15} , and the bottom molecule is blue and labeled N^{14} . A second arrow points to the right, showing three DNA molecules: one green (N^{15}) and two blue (N^{14}).

Heavy Hybrid Hybrid & light

The diagram illustrates the process of DNA replication. A double-stranded DNA molecule is shown being unwound by a blue oval labeled 'Helicase'. The two resulting strands are the 'Leading strand' and the 'Lagging strand'. The leading strand is synthesized continuously towards the replication fork, indicated by a red arrow labeled 'primase' and a yellow arrow labeled 'polymerase'. The lagging strand is synthesized discontinuously away from the fork, with segments labeled 'Okazaki Fragment' connected by a green line. The 5' and 3' orientations of the strands are clearly marked throughout the diagram.

Helicase

→ primase

➤ **Leading strand**

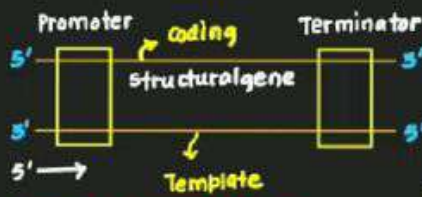
➤ **Lagging strand**

Fragment

Transcription: DNA to RNA by RNA polymerase

Transcriptional Unit

- Not both strands are transcribed
- Not complete DNA is transcribed



Bacterial transcription

- Polymerase binds at Promoter
- with σ : Initiation
- Alone: Elongation
- with ϕ : Termination
- Bacterial genes are polycistronic.

Eukaryotic Transcription

3-RNA polymerases & post transcriptional modifications

Pol. I: rRNA (28S, 18S, 5.8S)

Pol. II: mRNA (hnRNA)

Pol. III: tRNA, 5S rRNA, 5.8S rRNA

Genetic codes

Triplet: by George Gamow

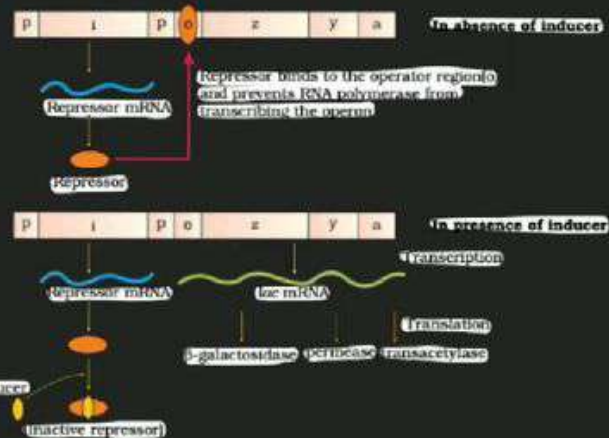
- out of 64 codons: 3 are stop codons: UAA, UGA, UAG
- AUG-start codon & methionine
- Almost universal
- Degenerate & unambiguous!



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

Translation: RNA to protein

- tRNA charging
- charged tRNA come to AUG; small ribosomal subunit binds to mRNA
- Mg^{2+} is required to connect both subunits of ribosomes.
- Amino acids are joined one by one & Ribozyme makes bonds b/w them
- At stop codon; release factor terminates the process.



Lac operon

Lactose
Many genes regulated by
Common promoter &
operator.

Human Genome Project: Megaproject (1984)

- 1990-2003
- Methodology & Whole genome sequencing
Expressed Sequence Tags
using Sanger's sequencing.

Goals	Results
<ul style="list-style-type: none"> • To complete sequencing of 3-billion bases & around 20-25K genes. • Storage, processing & retrieval of data. • Address ELSI. 	<ul style="list-style-type: none"> • 3.164 Billion bases • ~ 30000 genes (avg. size 3000 bp) (Dystrophin = 2.4 million bp) • < 2% content code for proteins • SNPs @ 14 lakh location • chr-1: 2468 genes; Y: 231 genes.

DNA Fingerprinting: By Alec Jeffery; based on VNTR [0.1-20Kb size]

- Important for solving paternity & crime cases.

