Ch 5 · Molecular Basis of Inheritance

अध्याय 5 · वंशागति का आणविक आधार

Class 12 Biology · NCERT based · English + हिंदी · ✍️ revision notes

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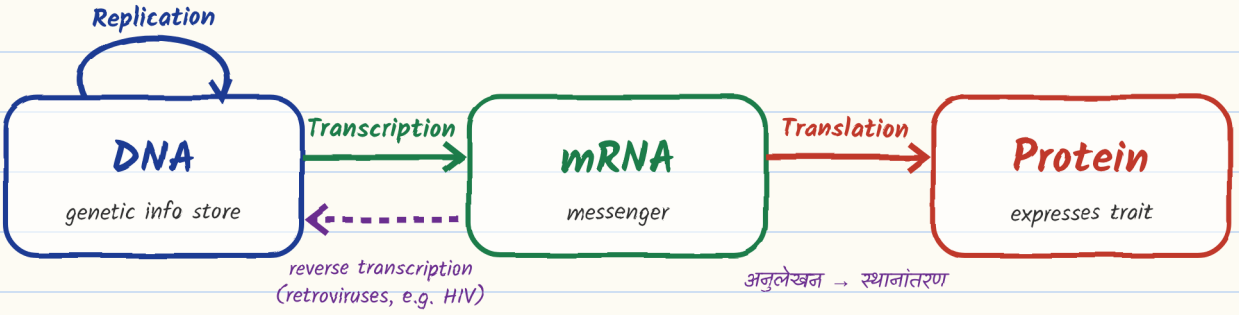
Central Dogma · केंद्रीय सिद्धांत (Francis Crick)



Infographic: Central dogma of molecular biology

1. The DNA / डीएनए

DNA = long polymer of **deoxyribonucleotides**. Length is defined by number of nucleotides / base pairs (bp).

Organism	DNA length
Bacteriophage φ×174	5386 nucleotides
Bacteriophage lambda (λ)	48,502 bp
Escherichia coli	4.6×10^6 bp
Human (haploid)	3.3×10^9 bp

(a) Structure of polynucleotide chain पॉलीन्यूक्लियोटाइड शृंखला

- Nucleotide = **nitrogenous base** + **pentose sugar** + **phosphate group**.
- Bases: **Purines** (प्यूरीन) – Adenine (A), Guanine (G); **Pyrimidines** (पिरिमिडीन) – Cytosine (C), Thymine (T, in DNA), Uracil (U, in RNA). Thymine = **5-methyl uracil**.
- Sugar: **deoxyribose** in DNA, **ribose** in RNA (RNA has extra **2′-OH**).
- Base + sugar (via N-glycosidic linkage at 1′C) = **nucleoside**. e.g. adenosine, deoxyadenosine.
- Nucleoside + phosphate (via phosphoester linkage at 5′-OH) = **nucleotide**.
- Two nucleotides join by 3′→5′ phosphodiester linkage → dinucleotide → polynucleotide.
- Polynucleotide has a free phosphate at **5′ end** and free OH at **3′ end**. Backbone = sugar + phosphate; bases project out.

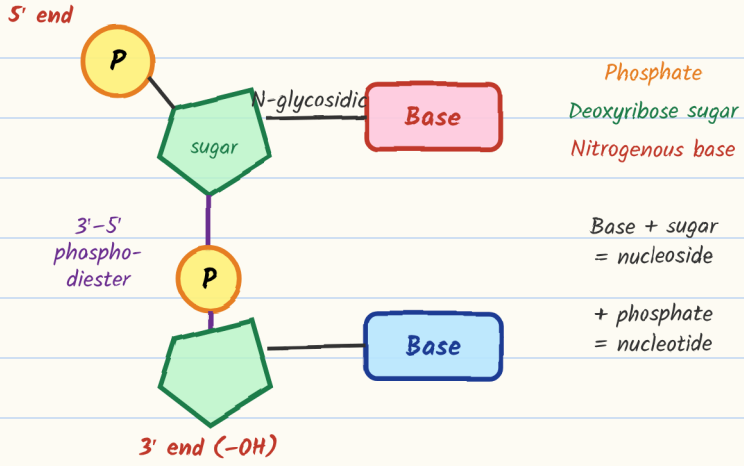
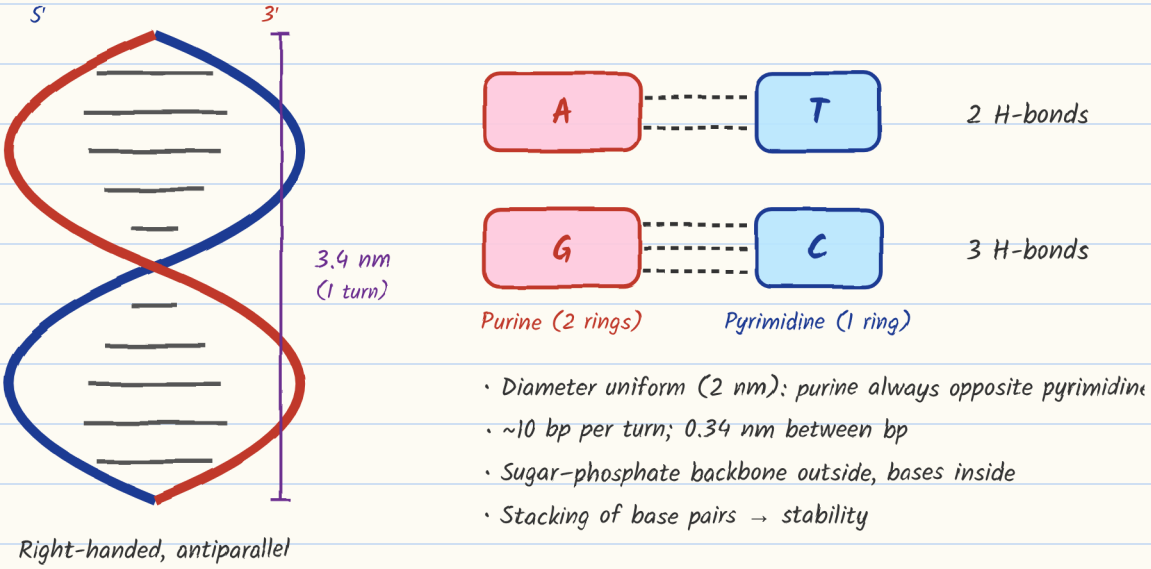


Fig: A polynucleotide chain (dinucleotide) · पॉलीन्यूक्लियोटाइड शृंखला

(b) Double helix model द्विकुंडलिनी मॉडल

- **Friedrich Meischer (1869)** – first identified DNA as acidic substance in nucleus = "**Nuclein**".
- **Maurice Wilkins & Rosalind Franklin** – X-ray diffraction data.
- **James Watson & Francis Crick (1953)** – proposed double helix model.
- **Erwin Chargaff** – in dsDNA, A = T and G = C; ratio (A+G)/(T+C) = 1 (Chargaff's rule).



Infographic: DNA double helix & complementary base pairing · पूरक क्षार युग्मन

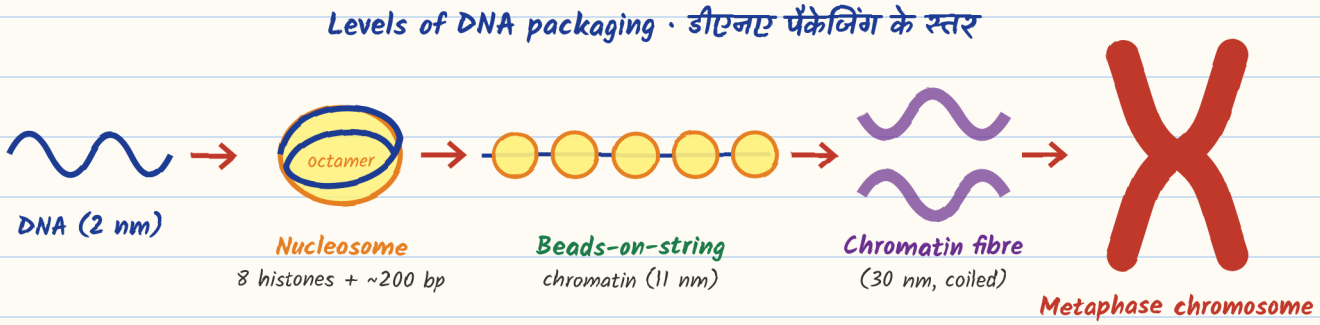
Salient features of double helix (द्विकुंडलिनी की मुख्य विशेषताएँ):

1. Made of **two polynucleotide chains**; backbone = sugar–phosphate, bases project inside.
2. Two chains have anti-parallel polarity (one 5′ → 3′, other 3′ → 5′).
3. Bases of two strands paired by **H-bonds**: **A=T (2)**, **G≡C (3)**. Purine always pairs with pyrimidine → uniform distance.
4. Two chains coiled in a right-handed fashion. **Pitch = 3.4 nm**, **~10 bp per turn**, distance between bp = **0.34 nm**.
5. Plane of one base pair stacks over the other → additional stability (besides H-bonds).

📌 **Numerical favourite:** If DNA has 20% A → T = 20%, G = C = 30% (Chargaff). Total length of human DNA = 6.6×10^9 bp × 0.34×10^{-9} m/bp = **2.2 m**.

(c) Packaging of DNA helix डीएनए कुंडलिनी का पैकेजिंग

- 2.2 m of DNA must fit in a nucleus of about **10^{-6} m** → needs packaging.
- **Prokaryotes** (e.g. *E. coli*): no defined nucleus; DNA (–ve) held with some +ve proteins in a region called **nucleoid**, organised in large loops.
- **Eukaryotes**: positively charged basic proteins = histones (rich in basic amino acids **lysine & arginine**).
- 8 histone molecules = **histone octamer**. –ve DNA wraps around +ve octamer → nucleosome (न्यूक्लियोसोम). Typical nucleosome has **200 bp** of DNA.
- Repeating nucleosomes → **chromatin** = "**beads-on-string**" structure (under electron microscope).
- Chromatin → packaged into **chromatin fibres** → further coiled & condensed at metaphase → **chromosomes**. Higher-level packaging needs **NHC (non-histone chromosomal) proteins**.



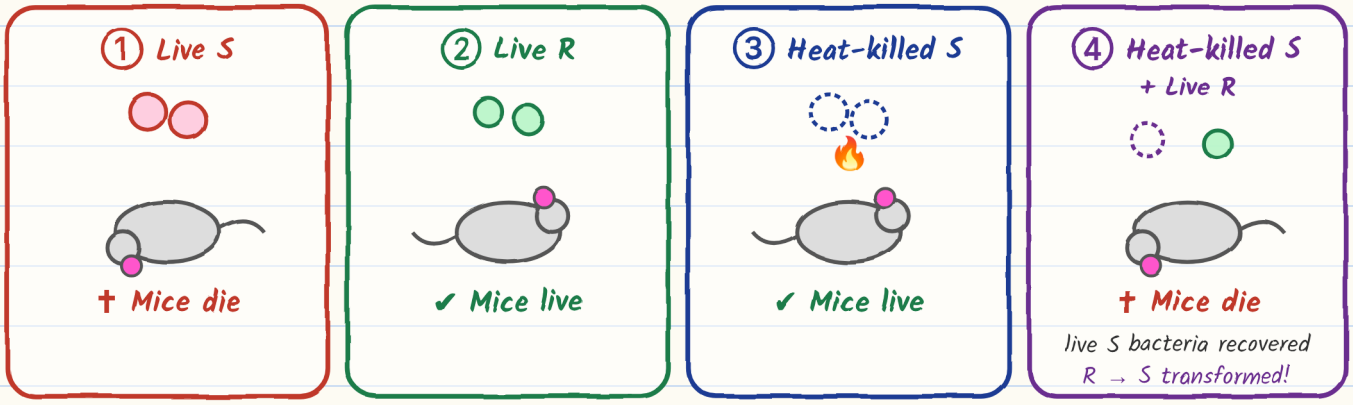
Infographic: DNA → nucleosome → chromatin → chromosome

Euchromatin (सुगुणसूत्रिका)	Heterochromatin (विषमगुणसूत्रिका)
Loosely packed	Densely packed
Stains **light**	Stains **dark**
Transcriptionally active	Inactive

2. Search for Genetic Material / आनुवंशिक पदार्थ की खोज

(a) Transforming principle – Griffith (1928) रूपांतरण सिद्धांत

Bacterium Streptococcus pneumoniae (causes pneumonia). ***S strain*** *– smooth, shiny colonies,* ***mucous (polysaccharide) coat***, ***virulent***. ***R strain*** *– rough colonies, no coat,* ***non-virulent***.



Infographic: Griffith's experiment · ग्रिफिथ का प्रयोग

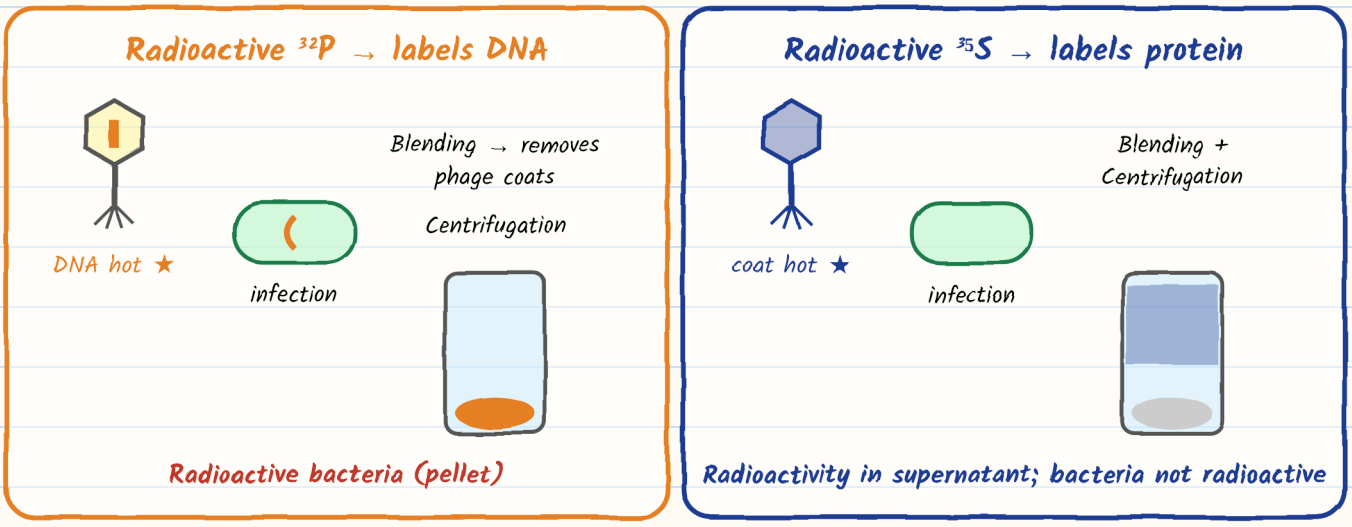
Conclusion: *R strain was* ***transformed*** *by some "transforming principle" from heat-killed S strain → R synthesised smooth coat & became virulent. Must be due to transfer of genetic material. Biochemical nature not identified.*

(b) Biochemical characterisation – Avery, MacLeod & McCarty (1933–44)

- *Purified biochemicals (proteins, DNA, RNA) from heat-killed S cells.*
- ***Protein-digesting enzymes (proteases)*** *&* ***RNases*** *did not affect transformation.*

- DNase inhibited transformation → **DNA is the hereditary material.**
- But not all biologists were convinced.

(c) Hershey–Chase experiment (1952) हर्शे-चेस प्रयोग – unequivocal proof



Infographic: Hershey–Chase experiment with bacteriophage

- Grew some viruses (bacteriophages) on medium with **radioactive phosphorus (^{32}P)**, others with **radioactive sulphur (^{35}S)**.
- DNA contains P but no S; protein contains S but no P.
- Bacteria infected with ^{32}P phage were radioactive; with ^{35}S phage were not → DNA (not protein) enters bacteria from virus → **DNA is the genetic material.**

3. Properties of Genetic Material / आनुवंशिक पदार्थ के गुण

DNA is the predominant genetic material; **RNA** is genetic material in some viruses (e.g. TMV, QB bacteriophage).

A molecule that can act as genetic material must:

1. Be able to generate its **replica** (replication).
2. Be **chemically & structurally stable.**
3. Provide scope for **slow changes (mutation)** required for evolution.
4. Be able to **express itself** as "Mendelian characters".

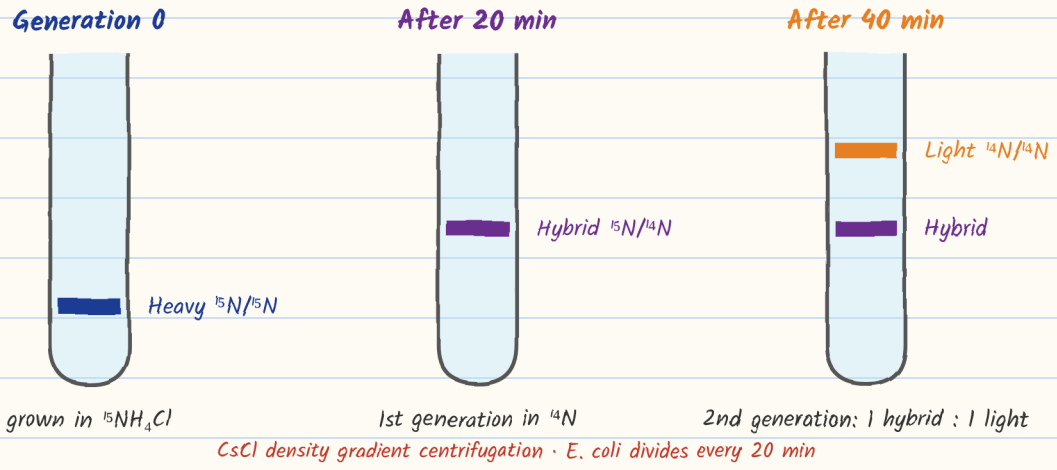
DNA – better for storage	RNA – better for transmission/expression
No 2′-OH → less reactive, more **stable**	2′-OH present → reactive, labile, easily degradable; acts as **catalyst**
Has **thymine** (more stable than uracil)	Has **uracil**
Double-stranded, complementary → repair possible	Mutates faster → RNA viruses have shorter life span, evolve faster
Depends on RNA for protein synthesis	Can directly code for protein synthesis

📌 **RNA World** (आरएनए संसार): **RNA was the first genetic material**. Essential life processes (metabolism, translation, splicing) evolved around RNA. RNA acted both as genetic material & catalyst (**ribozymes**). Being reactive & unstable, DNA evolved from RNA with chemical modifications that make it more stable.

4. Replication / प्रतिकृतीयन

- Watson & Crick proposed semiconservative replication: two strands separate, each acts as template; each new DNA has **one parental (old) + one new** strand.

Meselson & Stahl experiment (1958) मेसेल्सन-स्टाल प्रयोग



Infographic: Proof of semiconservative replication · अर्धसंरक्षी प्रतिकृतीयन का प्रमाण

- Grew *E. coli* in medium with $^{15}NH_4Cl$ (heavy isotope) for many generations → ^{15}N incorporated in DNA → **heavy DNA**.
- Transferred cells to medium with normal $^{14}NH_4Cl$; took samples at intervals; separated DNA by CsCl density gradient centrifugation.
- After **20 min** (one generation): all DNA **hybrid/intermediate**. After **40 min** (two generations): equal **hybrid & light** DNA.

- Similar experiment on ***Vicia faba*** (faba beans) by **Taylor & colleagues (1958)** using radioactive thymidine → chromosomes also replicate semiconservatively.

Machinery & enzymes प्रतिकृतीयन तंत्र व एंजाइम

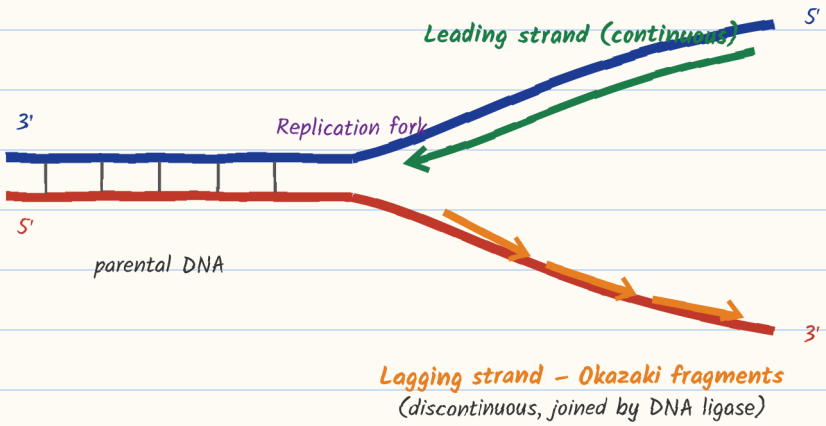


Fig: Replication fork · प्रतिकृतीयन द्विशाख

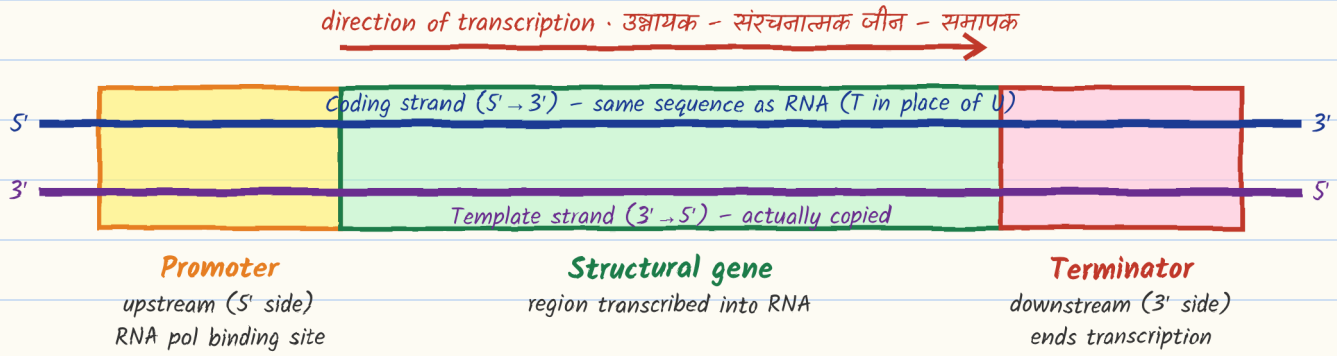
- Main enzyme: DNA-dependent DNA polymerase – uses DNA template to catalyse polymerisation of deoxynucleotides.
- Very fast: *E. coli* (4.6×10^6 bp) completes replication in **38 minutes** → average rate **~2000 bp/second**. Also highly accurate.
- **Deoxyribonucleoside triphosphates** (dNTPs) serve **dual purpose**: act as substrates + provide energy for polymerisation (two terminal phosphates).
- DNA strands can't be fully opened at once (high energy) → replication happens within a small opening = replication fork.
- DNA polymerase polymerises **only in 5′→3′ direction**. So:
  - Template with **3′→5′** polarity → **continuous** replication (leading strand).
  - Template with **5′→3′** polarity → **discontinuous** replication (lagging strand) → fragments (**Okazaki fragments**) joined by DNA ligase.
- Replication starts at a definite region = **origin of replication (ori)** – that's why vectors need an ori in rDNA technology.
- In eukaryotes, replication occurs in **S-phase**. Failure in cell division after replication → **polyploidy**.

5. Transcription / अनुलेखन

Process of copying genetic information from **one strand of DNA into RNA**. Adenine pairs with **uracil** instead of thymine.

📌 **Why only one strand is transcribed? (2M)** ① If both strands code, two different RNAs → two different proteins from one segment → complicates genetic information transfer. ② The two RNAs would be complementary → form **double-stranded RNA** → prevent translation; transcription would be futile.

(a) Transcription unit अनुलेखन इकाई



Infographic: Schematic structure of a transcription unit

- 3 regions: **Promoter** (उन्नायक), **Structural gene** (संरचनात्मक जीन), **Terminator** (समापक).
- RNA polymerase also catalyses polymerisation only in **5′→3′** direction → template strand has 3′→5′ polarity.
- Promoter = DNA sequence providing binding site for RNA polymerase; its presence defines template & coding strands.
- Sometimes **regulatory sequences** also present further upstream/downstream of promoter.

(b) Transcription unit & the gene जीन

- **Gene** = functional unit of inheritance. **Cistron** = segment of DNA coding for a **polypeptide**.
- **Monocistronic** structural genes – mostly in **eukaryotes**. **Polycistronic** – mostly in **bacteria/prokaryotes**.
- In eukaryotes, genes are split genes: coding sequences = **exons** (व्यक्तेक) (appear in mature/processed RNA); interrupted by **introns** (अव्यक्तेक) (intervening sequences, not in mature RNA).

(c) Types of RNA आरएनए के प्रकार

RNA	Role
mRNA (messenger)	Provides the **template** for translation
tRNA (transfer)	Brings **amino acids** & reads the genetic code (adapter)
rRNA (ribosomal)	**Structural & catalytic** role during translation

(d) Process of transcription in bacteria

Initiation
RNA pol + σ (sigma) factor binds promoter

→

Elongation
uses NTPs, follows complementarity rule

→

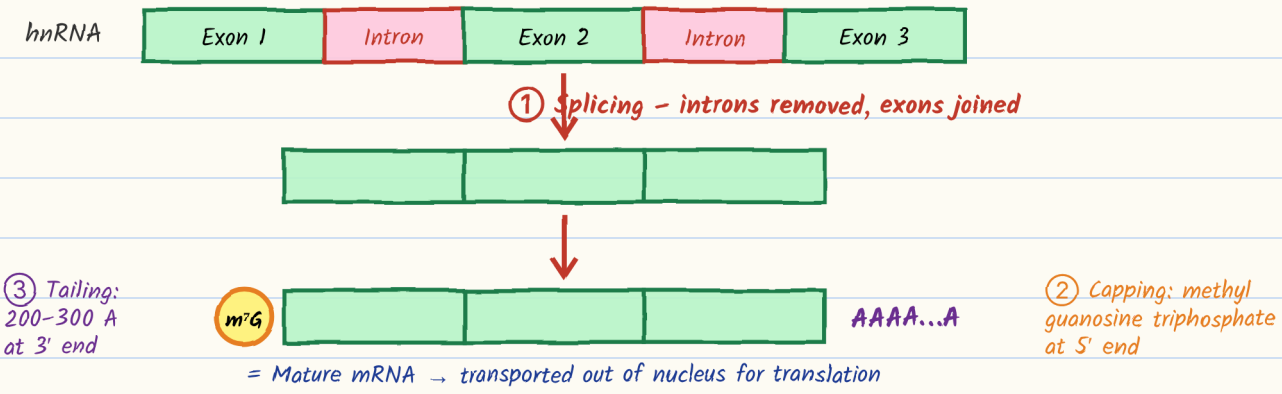
Termination
ρ (rho) factor at terminator; RNA pol & RNA released

- Bacteria have a **single DNA-dependent RNA polymerase** that transcribes all types of RNA.
- RNA polymerase can only catalyse elongation; it associates transiently with **σ (initiation)** and **ρ (termination)** factors.
- In bacteria, mRNA needs no processing; transcription & translation occur in the **same compartment** (no nuclear membrane) → translation can begin even before mRNA is fully transcribed (coupled).

(e) Transcription in eukaryotes – extra complexities

RNA polymerase	Transcribes
RNA pol I	rRNAs – **28S, 18S, 5.8S**
RNA pol II	Precursor of mRNA = hnRNA (heterogeneous nuclear RNA)
RNA pol III	**tRNA, 5S rRNA, snRNAs** (small nuclear RNAs)

Post-transcriptional processing of hnRNA · hnRNA का प्रक्रमण



Infographic: Splicing, capping and tailing · समबंधन, कैपिंग व टेलिंग

- **Splicing** (समबंधन) – introns removed & exons joined in a defined order.
- **Capping** – unusual nucleotide **methyl guanosine triphosphate** added to **5′ end** of hnRNA.
- **Tailing** – adenylate residues (**200–300**) added at **3′ end** in a **template-independent** manner.
- Split genes & introns represent probably an **ancient feature** of the genome; splicing reflects dominance of the **RNA world**.

6. Genetic Code / आनुवंशिक कूट

- **George Gamow** (physicist): 4 bases code for 20 amino acids → code should be a combination of **3 bases** ($4^3 = 64$ **codons**).
- **Har Gobind Khorana** – chemical method for synthesising RNA molecules with defined combination of bases (homopolymers & copolymers) → instrumental in deciphering code.
- **Marshall Nirenberg** – **cell-free system** for protein synthesis → finally helped decipher the code.
- **Severo Ochoa** enzyme (**polynucleotide phosphorylase**) – helped polymerise RNA with defined sequences in a template-independent manner (enzymatic synthesis of RNA).

The genetic code (mRNA codons) · आनुवंशिक कूट तालिका

1st ↓ / 2nd →	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
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
A	AUU Ile AUC Ile AUA Ile **AUG Met/Start**	ACU Thr ACC Thr ACA Thr ACG Thr	AAU Asn AAC Asn AAA Lys AAG Lys	AGU Ser AGC Ser AGA Arg AGG Arg
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

Salient features of genetic code (आनुवंशिक कूट की विशेषताएँ):

1. **Triplet**: 61 codons code for amino acids; 3 codons – UAA, UAG, UGA – are stop codons (don't code any amino acid).
2. **Unambiguous & specific**: one codon codes for only **one** amino acid.
3. **Degenerate** (अपहासित): some amino acids coded by more than one codon.
4. Read in mRNA in a **contiguous** fashion – **no punctuations** (commaless).
5. **Nearly universal**: e.g. UUU codes for Phenylalanine (Phe) from bacteria to humans. Exceptions: mitochondrial codons & some protozoans.
6. AUG has dual functions: codes for **Methionine (Met)** and acts as **initiator (start) codon**.

Mutations & genetic code उत्परिवर्तन व कूट

- **Point mutation**: sickle-cell anaemia – change of single base in β-globin gene → **GAG** → **GUG** → Glu → Val.
- **Frameshift mutations** (फ्रेमशिफ्ट): insertion or deletion of **one or two bases** changes the **reading frame** from the point of insertion/deletion.

- Insertion/deletion of **three bases (or multiples)** → inserts/deletes one (or more) codon → one or more amino acids added/removed, **reading frame unaltered** from that point onwards.

> **Example (NCERT):** RAM HAS RED CAP
> +B insertion → RAM HAS **BRE DCA P** (frame shifted ✖)
> +BIG (3 letters) → RAM HAS **BIG** RED CAP (frame intact ✔)
> Delete R → RAM HAS EDC AP (frame shifted ✖)

tRNA – the adapter molecule tRNA – अनुकूलक अणु

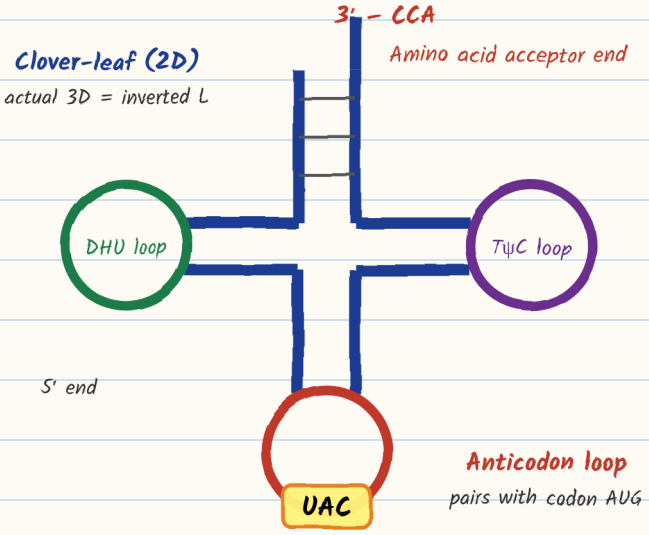


Fig: tRNA – clover leaf model · tRNA का पत्ती जैसा मॉडल

- **Francis Crick** postulated an **adapter molecule** that would read the code and link to amino acids → tRNA (earlier called **sRNA** – soluble RNA).
- Has an **anticodon loop** (bases complementary to codon) and an **amino acid acceptor end** (binds amino acid).
- tRNAs are **specific** for each amino acid. Specific tRNA for initiation = **initiator tRNA**. No tRNAs for stop codons.
- 2D: **clover-leaf**; 3D: compact **inverted L** shape.

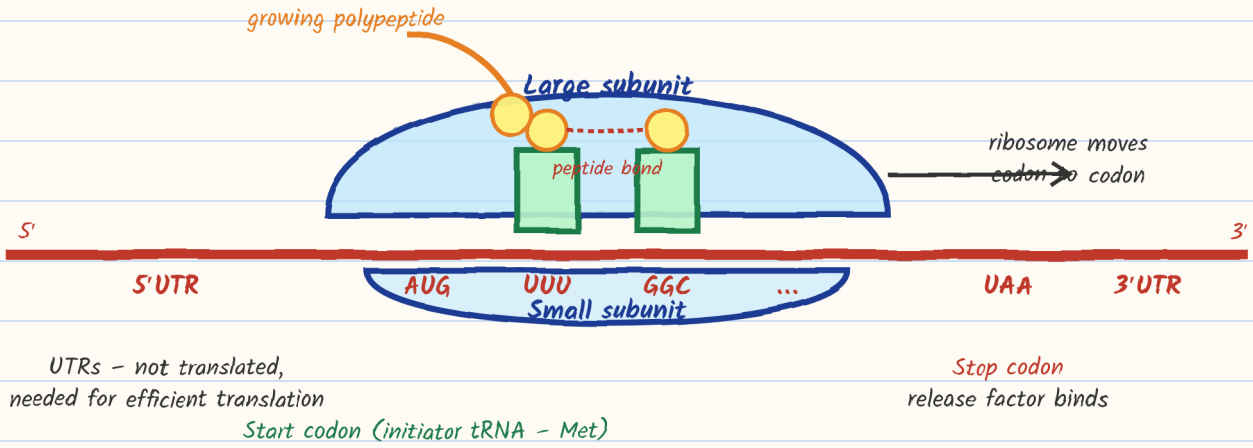
7. Translation / स्थानांतरण (अनुवादन)

Process of **polymerisation of amino acids** to form a polypeptide; order & sequence defined by sequence of bases in mRNA. Amino acids joined by **peptide bond** (needs energy).

Steps चरण

1. **Charging / aminoacylation of tRNA** (tRNA का आवेशन): amino acids activated in presence of **ATP** and linked to their cognate tRNA. If two charged tRNAs come close → peptide bond formation is energetically favourable (needs catalyst).

2. **Ribosome** = cellular factory for protein synthesis: **structural RNAs + ~80 proteins**. In inactive state, two subunits (large + small). When small subunit encounters mRNA → translation begins.
3. Large subunit has **two sites** for subsequent amino acids to bind, close enough for peptide bond formation.
4. **Ribosome also acts as catalyst**: 23S rRNA in bacteria is the enzyme (**ribozyme**) for peptide bond formation.



Infographic: Translation on ribosome · राइबोसोम पर स्थानांतरण

Stage	What happens
Initiation (प्रारंभन)	Ribosome binds mRNA at **start codon (AUG)**, recognised only by **initiator tRNA**.
Elongation (दीर्घीकरण)	Complexes of amino acid + tRNA sequentially bind to appropriate codon by base pairing with tRNA anticodon. Ribosome moves from codon to codon along mRNA; amino acids added one by one → polypeptide.
Termination (समापन)	**Release factor** binds to **stop codon** → translation terminates, polypeptide released from ribosome.

UTRs (untranslated regions) – additional sequences on mRNA not translated: at **5′ end (before start codon)** and **3′ end (after stop codon)**; required for efficient translation.

8. Regulation of Gene Expression / जीन अभिव्यक्ति का नियमन

In eukaryotes regulation can be at 4 levels: ① **transcriptional** (formation of primary transcript), ② **processing** (regulation of splicing), ③ **transport of mRNA** from nucleus to cytoplasm, ④ **translational**.

- Genes are expressed to perform a function; metabolic, physiological or environmental conditions regulate expression. e.g. *E. coli* makes **β-galactosidase** (hydrolyses lactose → galactose + glucose) only when lactose is the carbon source.

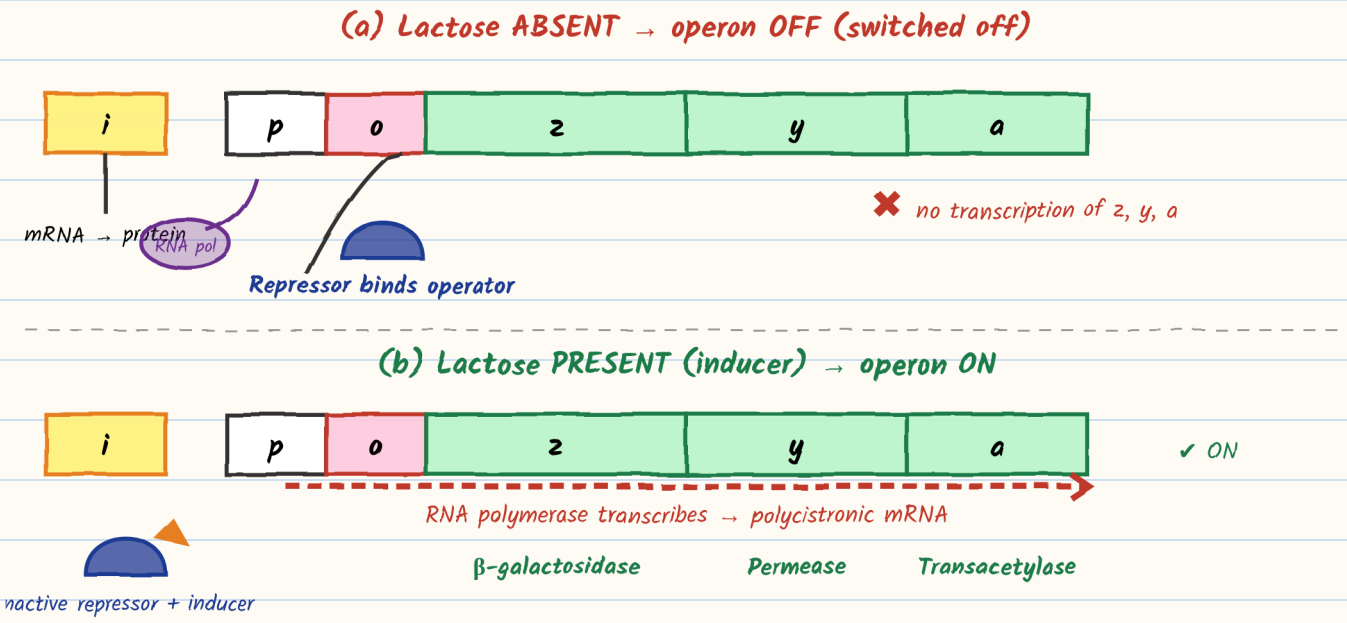
- In prokaryotes, control of **rate of transcriptional initiation** is the predominant site. Accessibility of promoter is regulated by interaction of proteins with **operators** (sequences adjacent to promoter).
- Each **operon** has its specific operator & repressor. e.g. **lac** operon, **trp** operon, ara operon, his operon, val operon.

Lac operon (Jacob & Monod) लैक प्रचालेक

Operon = polycistronic structural gene regulated by a common promoter & regulatory genes.

Elucidated by geneticist **François Jacob** & biochemist **Jacques Monod**.

Gene	Product / Role
i (inhibitor) – regulatory gene	Codes for **repressor** of lac operon (constitutively expressed)
p – promoter	RNA polymerase binding site
o – operator	Repressor binding site
z	β-galactosidase – hydrolysis of lactose → galactose + glucose
y	Permease – increases permeability of cell to β-galactosides
a	Transacetylase



Infographic: Lac operon – switched off vs switched on · लैक प्रचालेक

- **Lactose** = substrate for β-galactosidase and also the inducer (प्रेरक). A very low level of lac operon expression is always present so that permease lets lactose enter.
- **Absence of inducer**: repressor (from i gene) binds **operator** → prevents RNA polymerase from transcribing.
- **Presence of inducer** (lactose or allolactose): inducer binds repressor → repressor **inactivated** → can't bind operator → RNA polymerase accesses promoter → **transcription proceeds**.

- Regulation by repressor = negative regulation. Lac operon can also be under positive control.

9. Human Genome Project (HGP) / मानव जीनोम परियोजना

- Mega project launched in 1990, completed in 2003; **~3 × 10^9 bp**.
- Cost ≈ **US $3 per bp** → **~9 billion US dollars**.
- Data storage: would need **3300 books** of 1000 pages each (1000 letters/page). Rapid field of **bioinformatics** emerged.
- Coordinated by **US Department of Energy & National Institute of Health (NIH)**; **Wellcome Trust (UK)** major partner; Japan, France, Germany, China also contributed.
- Sequence of **chromosome 1** completed last, in **May 2006**.

Goals of HGP लक्ष्य

1. Identify all the approximately **20,000–25,000 genes** in human DNA.
2. Determine the sequences of the **3 billion chemical base pairs**.
3. Store information in **databases**.
4. Improve tools for data analysis.
5. Transfer related technologies to other sectors (e.g. industries).
6. Address the **ELSI** – ethical, legal & social issues.

Methodologies विधियाँ

Expressed Sequence Tags (ESTs)	Sequence Annotation
Identify all genes that are **expressed as RNA**	**Blind** sequencing of whole genome (coding + non-coding), later assign functions

Isolate total DNA → Break into random small fragments →
Clone in host using vectors – **BAC** & **YAC** →
Sequence with **automated DNA sequencers** (Sanger's method) →
Arrange using overlapping regions (computer programs) →
Annotate & assign to chromosomes

BAC = bacterial artificial chromosome; YAC = yeast artificial chromosome. Sequencing method developed by **Frederick Sanger**.

Salient features of human genome (मुख्य विशेषताएँ):

1. Contains **3164.7 million** nucleotide bases.
2. Average gene has **3000 bases**; largest known gene = dystrophin with **2.4 million bases**.
3. Total number of genes estimated at **30,000** (much lower than earlier estimate of 80,000–1,40,000).
4. 99.9% nucleotide bases are exactly the **same in all people**.
5. Functions unknown for **over 50%** of discovered genes.
6. Less than 2% of genome codes for proteins.
7. **Repeated sequences** make up a very large portion of the genome (thought to have no direct coding function, but shed light on chromosome structure, dynamics & evolution).
8. **Chromosome 1** has most genes (**2968**); **Y** has fewest (**231**).
9. ~**1.4 million** locations of single-base DNA differences = **SNPs** ("snips" – single nucleotide polymorphism).

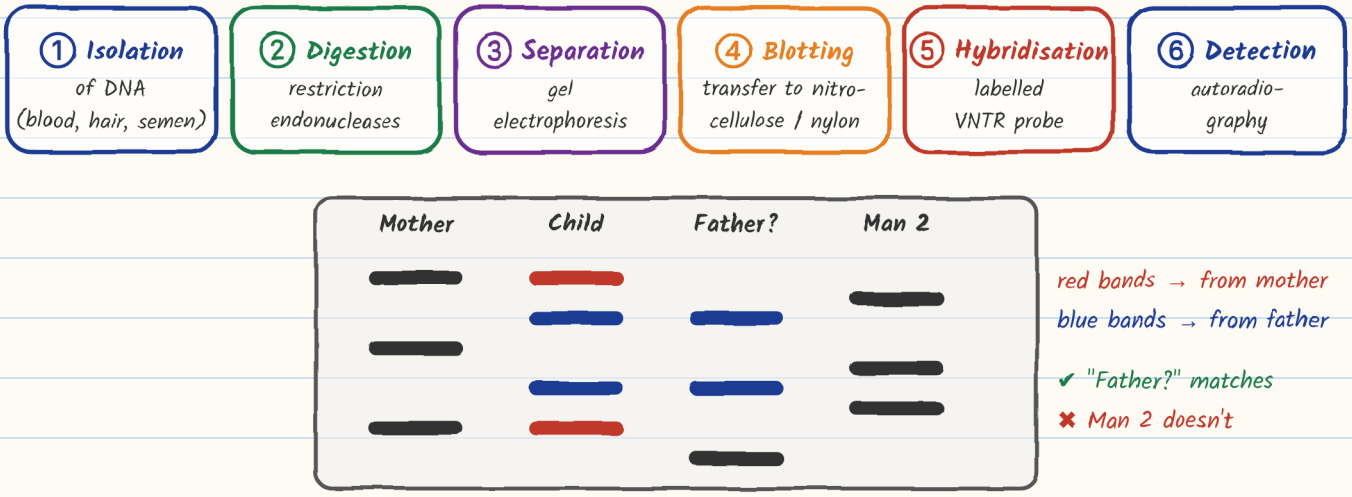
Applications: understanding disease & treatment, studying biological systems; sequencing of model organisms – bacteria, yeast, *Caenorhabditis elegans*, *Drosophila*, rice, *Arabidopsis*, etc.

10. DNA Fingerprinting / डीएनए अंगुलिछापी

- 99.9% bp same in all humans; differences in DNA sequence make each individual unique.
- **DNA fingerprinting** = quick way to compare DNA sequences of two individuals by identifying differences in specific regions called repetitive DNA.
- Technique developed by Alec Jeffreys.

Repetitive / satellite DNA अनुषंगी डीएनए

- Small stretch of DNA repeated many times.
- In **density gradient centrifugation**, bulk genomic DNA forms a **major peak**; other small peaks = satellite DNA.
- Classified as **micro-satellites, mini-satellites** etc. based on base composition (A:T rich or G:C rich), length of segment & number of repetitive units.
- Normally **do not code** for proteins, but show high degree of **polymorphism** → basis of DNA fingerprinting.
- Polymorphism (variation at genetic level) arises due to mutations; inheritable mutations observed at high frequency (>0.01) in population = **DNA polymorphism**.
- Jeffreys used VNTR (Variable Number of Tandem Repeats) – a satellite DNA – as **probe**. VNTR size varies **0.1 to 20 kb**; copy number varies from chromosome to chromosome & individual to individual.



Infographic: DNA fingerprinting steps & paternity test band pattern

- After hybridisation with VNTR probe, autoradiogram gives bands of differing sizes → characteristic pattern for each individual.
- Every individual has a unique pattern, except **monozygotic (identical) twins**.
- Sensitivity increased by **PCR** – DNA from a **single cell** is enough.
- **Applications**: (1) **forensic science** (identify criminals), (2) **paternity/maternity disputes**, (3) determining **population & genetic diversities**.

⚡ Quick Revision / त्वरित पुनरावृत्ति

Scientist	Contribution
Friedrich Meischer (1869)	Discovered "Nuclein" (DNA)
Wilkins & Franklin	X-ray diffraction of DNA
Watson & Crick (1953)	Double helix model
Erwin Chargaff	A = T, G = C
Francis Crick	Central dogma, adapter hypothesis
Frederick Griffith (1928)	Transforming principle
Avery, MacLeod & McCarty	DNA is the transforming principle
Hershey & Chase (1952)	DNA is genetic material (bacteriophage)
Meselson & Stahl (1958)	Semiconservative replication (E. coli, ^{15}N)
Taylor et al. (1958)	Semiconservative replication in Vicia faba
George Gamow	Triplet code proposal
Har Gobind Khorana	Chemical synthesis of RNA – decoding
Marshall Nirenberg	Cell-free protein synthesis
Severo Ochoa	Polynucleotide phosphorylase
Jacob & Monod	Lac operon
Frederick Sanger	DNA sequencing method
Alec Jeffreys	DNA fingerprinting

Number to remember	Value
Pitch of helix / bp per turn / distance between bp	3.4 nm / 10 / 0.34 nm
Human DNA length (diploid)	6.6×10^9 bp ≈ 2.2 m
DNA per nucleosome	~200 bp
E. coli replication	38 min, ~2000 bp/s
Codons / sense / stop	64 / 61 / 3
Poly-A tail	200–300 adenylates
HGP	1990–2003, $3/bp, 3164.7 million bp
Genes (HGP estimate)	~30,000; Chr 1 – 2968; Y – 231
SNPs	1.4 million
VNTR size	0.1 – 20 kb

⭐ Exam Corner / परीक्षा उपयोगी प्रश्न

1-Mark Questions (1M)

Q1. Name the linkage that joins a nitrogenous base to pentose sugar. / नाइट्रोजनी क्षारक व शर्करा के बीच बंध?

→ N-glycosidic linkage.

Q2. Histones are rich in which amino acids?

→ Lysine and arginine (basic, positively charged).

Q3. Which radioactive isotope labels protein in the Hershey–Chase experiment?

→ ^{35}S (sulphur).

Q4. Name the enzyme that joins Okazaki fragments.

→ DNA ligase.

Q5. Which RNA polymerase transcribes tRNA in eukaryotes?

→ RNA polymerase III.

Q6. Which codon has a dual function?

→ AUG – codes for methionine & acts as start codon.

Q7. Which rRNA acts as a ribozyme in bacteria?

→ 23S rRNA.

Q8. What is the inducer of lac operon?

→ Lactose (allolactose).

2/3-Mark Questions (2–3M)

Q9. A DNA segment has 30% cytosine. Find the % of the other bases.

→ G = 30%, A = T = 20% each (Chargaff's rule).

Q10. Why is DNA a better genetic material than RNA?

→ No 2'-OH → less reactive, stable; thymine instead of uracil; double-stranded with complementary repair; RNA mutates faster.

Q11. Differentiate euchromatin and heterochromatin.

→ Loose/light/active vs dense/dark/inactive.

Q12. Why is replication continuous on one strand and discontinuous on the other?

→ DNA polymerase works only 5'→3'; template 3'→5' → continuous; template 5'→3' → Okazaki fragments joined by ligase.

Q13. Name the 3 processing steps of hnRNA in eukaryotes.

→ Splicing, capping (5' m^7G), tailing (3' poly-A).

Q14. Explain frameshift mutation with an example.

→ Insertion/deletion of 1 or 2 bases shifts reading frame (RAM HAS RED CAP example); 3 bases keep frame.

Q15. Why does the Hershey–Chase experiment prove DNA is genetic material?

→ Only ^{32}P (DNA) entered bacteria; ^{35}S (protein) remained outside in supernatant.

Q16. What are VNTRs? How are they used in DNA fingerprinting?

→ Satellite DNA with variable tandem repeats (0.1–20 kb); used as probes → unique band patterns.

5-Mark Questions SM ★★★

Q17. Describe the Meselson–Stahl experiment. What did it prove?

→ ^{15}N → ^{14}N, CsCl gradient, hybrid at 20 min, hybrid + light at 40 min → semiconservative replication.

Q18. Explain the lac operon with labelled diagrams (in presence and absence of inducer).

→ i, p, o, z, y, a genes; repressor; inducer; negative regulation.

Q19. Describe the process of transcription in bacteria. How is it different in eukaryotes?

→ Transcription unit; σ & ρ factors; single RNA pol vs 3 RNA pols; split genes; hnRNA processing.

Q20. List the goals and salient features of the Human Genome Project.

→ 6 goals + 9 features (see box).

Q21. Explain the steps of DNA fingerprinting and give its applications.

→ Isolation → digestion → electrophoresis → blotting → hybridisation (VNTR probe) → autoradiography; forensics, paternity, diversity.

✏ Diagrams to practise / अभ्यास हेतु चित्र:

1. Polynucleotide chain ⭐
2. DNA double helix
3. Nucleosome
4. Meselson–Stahl experiment
5. Replication fork
6. Transcription unit ⭐
7. Splicing/processing of hnRNA
8. tRNA clover leaf ⭐
9. Translation
10. Lac operon ⭐
11. DNA fingerprinting (schematic)

🎯 **Last-minute tips:** Always mark **5′ and 3′ ends** in diagrams · Write isotope symbols correctly (^{32}P, ^{35}S, ^{15}N) · In lac operon, clearly say "repressor binds **operator**" (not promoter) · Remember stop codons: **U Are Away, U Are Gone, U Go Away** (UAA, UAG, UGA).

~ All the best! / शुभकामनाएँ! ~