FREE EDITION · NOTES + 3 SAMPLE MCQS

CUET · BIOLOGY · CLASS XII · CODE 304

Molecular Basis of Inheritance

CUET unit: Genetics and Evolution → Molecular Basis of Inheritance

By **UniDrill** · NCERT-grounded study material

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📌 Snapshot

- Establishes DNA as the universal genetic material, its double-helix structure (Watson-Crick, 1953) and the rules of base pairing (A=T, G≡C) that govern replication, transcription and translation.
- Walks through the classical experiments — Griffith (transforming principle), Avery-MacLeod-McCarty (DNA is the transforming principle), Hershey-Chase (32P/35S blender) and Meselson-Stahl (semi-conservative replication) — every one of which is a CUET favourite.
- Develops the Central Dogma (DNA -> RNA -> Protein), the genetic code (triplet, degenerate, near-universal, with AUG as initiator and UAA/UAG/UGA as stops), and the lac operon as the model of prokaryotic gene regulation.
- Closes with two "big-science" themes that CUET routinely tests: the Human Genome Project (1990-2003; ~3.1 x 10^9 bp; ~30,000 genes; chr 1 has most, Y the fewest) and DNA Fingerprinting (Alec Jeffreys, VNTRs, satellite DNA, forensic and paternity applications).
- Highest-weight chapter in CUET Biology — questions test numerical recall (0.34 nm, 3.4 nm, 10 bp/turn, 2000 bp/sec), scientist–experiment matching, and operon component identification.

📖 Detailed Notes

2.1 Core concepts

- DNA is a long polymer of deoxyribonucleotides; length is measured in nucleotides/ base pairs. phiX174 = 5386 nt, lambda phage = 48,502 bp, E. coli = 4.6 x 10^6 bp, haploid human DNA = 3.3 x 10^9 bp (NCERT §5.1, p. 80).
- A nucleotide = nitrogenous base + pentose sugar (deoxyribose in DNA, ribose in RNA) + phosphate. Purines = Adenine, Guanine; Pyrimidines = Cytosine, Thymine (DNA) / Uracil (RNA). Base + sugar = nucleoside; +phosphate (at 5'-C) = nucleotide. Nucleotides link via 3'-5' phosphodiester bonds (NCERT §5.1.1, p. 80).
- Friedrich Meischer (1869) first isolated DNA from nucleus and called it 'Nuclein'; Watson and Crick (1953) proposed the Double Helix using Wilkins-Franklin X-ray data and Chargaff's rule (A/T = G/C = 1) (NCERT §5.1.1, p. 81).
- Salient features of B-DNA double helix: two anti-parallel chains (5'->3' paired with 3'->5'); A=T (2 H-bonds), G=C (3 H-bonds); right-handed; pitch (per turn) = 3.4 nm; ~10

bp/turn; rise per bp = 0.34 nm; base-pair stacking stabilises the helix (NCERT §5.1.1, pp. 81-82).

- Central Dogma (Francis Crick): genetic information flows DNA -> RNA -> Protein; in some viruses the flow is reversed (RNA -> DNA, reverse transcription) (NCERT §5.1.1, p. 82).
- DNA packaging: prokaryotes hold negatively-charged DNA with positively-charged proteins in a region called the **nucleoid** as large loops. Eukaryotes use basic histones (rich in lysine + arginine); 8 histones form a **histone octamer** around which ~200 bp of DNA wraps to form a **nucleosome**. Nucleosomes are the repeating unit of **chromatin** ("beads-on-string" under EM) -> chromatin fibres -> metaphase chromosomes; higher-order packaging needs **Non-histone Chromosomal (NHC) proteins**. **Euchromatin** = loosely packed, light-staining, transcriptionally active; **Heterochromatin** = densely packed, dark-staining, inactive (NCERT §5.1.2, pp. 83-84).
- Search for genetic material — **Griffith (1928)** worked on Streptococcus pneumoniae: live S (smooth, virulent) killed mice; live R (rough) did not; heat-killed S alone did not; heat-killed S + live R -> mice died and live S was recovered -> "transforming principle" transferred genetic material (NCERT §5.2, pp. 84-85).
- **Avery, MacLeod & McCarty (1933-44)** purified biochemicals from heat-killed S; only DNA caused transformation; proteases and RNases did not block transformation, but DNase did — concluded DNA is the hereditary material (NCERT §5.2, p. 85).
- **Hershey-Chase (1952)** used T2 bacteriophages grown on 32P (labels DNA) and 35S (labels protein); after infection of E. coli, the blender removed phage coats and centrifugation separated cells from coats. Only 32P (DNA) entered bacteria; 35S (protein) stayed outside -> DNA is the genetic material (NCERT §5.2.1, pp. 85-86).
- Criteria a genetic material must fulfill: (i) replication, (ii) chemical/structural stability, (iii) scope for slow change (mutation), (iv) ability to express as Mendelian characters. DNA wins on stability (no 2'-OH; thymine instead of uracil; double-stranded with repair). RNA, however, evolved first and mutates faster (NCERT §5.2.2, p. 87).
- **RNA World** — RNA was the first genetic material; it served as both genetic material and catalyst (ribozymes catalyse splicing, peptide-bond formation). DNA evolved from RNA with chemical modifications that made it more stable (NCERT §5.3, p. 88).
- **Replication is semi-conservative** — proposed by Watson & Crick (1953). Proved by **Meselson and Stahl (1958)** in E. coli grown in 15NH4Cl, then shifted to 14NH4Cl. After one generation (20 min) DNA was of hybrid density; after two generations (40 min) hybrid + light in equal amounts. Taylor et al. (1958) proved the same in Vicia faba using radioactive thymidine (NCERT §5.4 & §5.4.1, pp. 88-90).
- Replication enzymes — main enzyme is DNA-dependent **DNA polymerase**; E. coli (4.6 x 10^6 bp) replicates in ~18 min -> average rate ~ 2000 bp/sec. dNTPs serve dual roles (substrate + energy from terminal phosphates). Replication happens at the

replication fork; polymerase synthesises only in **5'->3'**, so the 3'->5' template strand is copied **continuously** and the 5'->3' template strand is copied **discontinuously** (Okazaki-style fragments joined by **DNA ligase**). Replication begins at the **origin of replication**; in eukaryotes it happens during S-phase (NCERT §5.4.2, pp. 90-91).

- **Transcription** copies one DNA strand (3'->5' = template strand) into RNA following A-U pairing; the other DNA strand (5'->3') is the **coding strand** (same sequence as RNA except T for U). A transcription unit = Promoter + Structural gene + Terminator. Promoter is upstream (5'-end of coding strand) and binds RNA polymerase; terminator is downstream (3'-end) (NCERT §5.5 & §5.5.1, pp. 91-92).
- A **cistron** = DNA segment coding for a polypeptide. Eukaryotic structural genes are **monocistronic** and **split** (exons + introns); prokaryotic structural genes are **polycistronic** and continuous. Exons appear in mature RNA; introns are removed by **splicing** (NCERT §5.5.2, p. 93).
- Bacteria have a single DNA-dependent RNA polymerase that makes all RNAs; it needs **sigma factor** for initiation and **rho factor** for termination. Eukaryotes have three nuclear RNA polymerases: **RNA Pol I -> rRNAs (28S, 18S, 5.8S)**; **RNA Pol II -> hnRNA (mRNA precursor)**; **RNA Pol III -> tRNA, 5S rRNA, snRNAs**. hnRNA is processed by **splicing**, **5'-capping** (methyl-guanosine triphosphate added) and **3'-tailing** (200-300 adenylate residues, template-independent) (NCERT §5.5.3, pp. 93-95).
- **Genetic code** is triplet (Gamow's proposition; 4^3 = 64 codons). 61 code for amino acids; 3 are stop (UAA, UAG, UGA). Properties: **triplet, degenerate** (multiple codons per amino acid), **contiguous (no punctuation), nearly universal** (exceptions in mitochondrial & some protozoan codons), **unambiguous** (one codon -> one amino acid). **AUG** has dual function — Methionine + initiator (NCERT §5.6, pp. 95-96).
- Code was deciphered using Khorana's chemically synthesised RNAs (homopolymers/copolymers), Nirenberg's cell-free protein-synthesis system, and Ochoa's polynucleotide phosphorylase (NCERT §5.6, p. 96).
- Point mutation example — sickle-cell anaemia (single bp change -> glutamate replaced by valine in beta-globin). Insertion/deletion of bases not in multiples of 3 = **frameshift mutation**; insertion/deletion of 3 or multiples leaves reading frame intact (NCERT §5.6.1, pp. 97-98).
- **tRNA = adapter molecule** (Crick's postulate); has an **anticodon loop** (reads codon) and an **amino-acid acceptor end** (binds amino acid). Specific tRNAs for each amino acid; a separate **initiator tRNA**; no tRNA for stop codons. Secondary structure = clover-leaf; actual 3-D = inverted L (NCERT §5.6.2, p. 98).
- **Translation** — amino acids polymerise via peptide bonds to make polypeptides. First, amino acids are activated (ATP) and attached to cognate tRNA = **charging/aminoacylation of tRNA**. **Ribosome** = rRNA + ~80 proteins; in inactive state = large + small subunits. 23S rRNA in bacteria acts as the peptidyl-transferase

ribozyme. mRNA has 5' and 3' **UTRs** (untranslated regions, flanking start/stop codons) needed for efficient translation. Initiation begins when ribosome binds mRNA at AUG; elongation adds amino acids per codon-anticodon pairing; a **release factor** binds stop codon to terminate (NCERT §5.7, pp. 98-99).

- **Regulation of gene expression** — in eukaryotes can occur at (i) transcriptional, (ii) processing/splicing, (iii) mRNA transport, (iv) translational levels. In prokaryotes, **transcription-initiation** is the dominant control point; regulatory proteins act as activators (+) or repressors (-) via **operator** sequences (NCERT §5.8, pp. 99-100).
- lac **operon** (Jacob & Monod) — polycistronic structural genes (**z**, **y**, **a**) regulated by one common promoter (p), one operator (o) and one regulatory gene (**i** — for "inhibitor"). **z** -> beta-galactosidase (hydrolyses lactose -> glucose + galactose); **y** -> permease (increases cell permeability to beta-galactosides); **a** -> transacetylase. Inducer = **lactose / allolactose**. In absence of lactose, the i-gene product (repressor) binds operator and blocks RNA polymerase. In presence of lactose, repressor binds inducer -> inactive -> RNA polymerase transcribes z, y, a. Negative regulation; positive regulation also exists (not detailed). Glucose and galactose are NOT inducers (NCERT §5.8.1, pp. 100-101).
- **Human Genome Project (HGP)** — launched 1990, completed 2003; 13-year mega-project coordinated by US Dept. of Energy + NIH, with Wellcome Trust (UK), Japan, France, Germany, China. Cost estimate at start: ~US $9 billion (US$3 per bp x 3 x 10^9 bp). Closely linked to growth of **Bioinformatics**. Goals included identifying ~20,000-25,000 human genes, sequencing ~3 x 10^9 bp, building databases, tool development, technology transfer and addressing **ELSI** (ethical, legal, social issues) (NCERT §5.9, pp. 102-103).
- HGP methodology — two approaches: **Expressed Sequence Tags (ESTs)** identified RNA-expressed genes; **Sequence Annotation** sequenced the entire genome and later assigned functions. Total DNA was fragmented, cloned into **BAC** (bacterial artificial chromosomes) or **YAC** (yeast artificial chromosomes), then sequenced on automated sequencers using **Frederick Sanger's** method. Chromosome 1 was the last sequenced (May 2006); 24 human chromosomes = 22 autosomes + X + Y (NCERT §5.9, p. 103).
- Salient HGP findings — human genome = **3164.7 million bp**; average gene ~ 3000 bp; largest gene = **dystrophin (2.4 million bp)**; total genes estimated at **~30,000** (much less than earlier 80,000-1,40,000); 99.9% of bases identical across humans; functions unknown for >50% genes; <2% of genome codes for proteins; repeat sequences make up a large portion. **Chromosome 1 has the most genes (2968), Y has the fewest (231)**. ~1.4 million **SNPs (Single Nucleotide Polymorphisms — "snips")** identified (NCERT §5.9.1, p. 104).
- **DNA Fingerprinting** — developed by **Alec Jeffreys**; identifies polymorphisms in **repetitive DNA** sequences. Bulk genomic DNA + small density peaks = **satellite DNA**, classified by base composition, segment length and repeat number into micro-satellites, mini-satellites etc. These don't code for proteins but show high

polymorphism. The probe used = **Variable Number of Tandem Repeats (VNTR)** — a mini-satellite repeated in tandem; VNTR size varies from 0.1 to 20 kb. Steps: (i) isolation of DNA, (ii) restriction digestion, (iii) electrophoresis, (iv) Southern blotting to nitrocellulose/nylon, (v) hybridisation with labelled VNTR probe, (vi) autoradiography. Same in all tissues of one person, but unique between individuals (except identical twins). Sensitivity enhanced by PCR. Applications: forensic science, paternity testing, population/genetic diversity studies (NCERT §5.10, pp. 105-107).

2.2 Definitions to memorise

Term	Definition	Page
Nucleoside	Nitrogenous base + pentose sugar (linked by N-glycosidic bond)	80
Nucleotide	Nucleoside + phosphate (linked at 5'-C by phosphoester bond)	80
Chargaff's rule	In dsDNA, A/T = G/C = 1	81
Nucleosome	~200 bp of DNA wrapped around a histone octamer	83
Euchromatin / Heterochromatin	Loosely-packed transcriptionally active / Densely-packed inactive chromatin	84
Transforming principle	Substance (DNA) that transferred virulence from heat-killed S to live R bacteria	85
Semi-conservative replication	Each daughter DNA has one parental + one newly synthesised strand	88
Replication fork	Small Y-shaped opening of DNA where replication occurs	90
Origin of replication	Specific DNA region where replication initiates	90
Template strand	DNA strand (3'->5') read by RNA polymerase during transcription	92
Coding strand	DNA strand (5'->3') with same sequence as RNA (except T for U); not transcribed	92
Cistron	Segment of DNA coding for a polypeptide	93
Exon / Intron	Coding (retained in mature RNA) / Non-coding intervening sequence (spliced out)	93
Capping	Addition of methyl-guanosine triphosphate to 5'-end of hnRNA	95
Tailing	Template-independent addition of 200-300 adenylate residues to 3'-end	95
Degenerate code	One amino acid coded by more than one codon	96
Frameshift mutation	Insertion/deletion of bases not in multiples of 3, altering the reading frame	97

Term	Definition	Page
Charging of tRNA (aminoacylation)	ATP-dependent activation and linking of amino acid to its tRNA	98
Ribozyme	RNA molecule with catalytic activity (e.g., 23S rRNA in bacteria)	99
Operon	Cluster of structural genes under common promoter/ operator regulation (mostly bacteria)	100
Inducer	Molecule (e.g., lactose/allolactose) that inactivates a repressor and switches on operon	101
Bioinformatics	Computational discipline that grew with HGP for data storage, retrieval, analysis	102
BAC / YAC	Bacterial / Yeast Artificial Chromosomes used as cloning vectors in HGP	103
SNP	Single Nucleotide Polymorphism (~1.4 million identified in humans)	104
Satellite DNA	Repetitive non-coding DNA appearing as small peaks in density gradient	105
VNTR	Variable Number of Tandem Repeats — mini-satellite used as DNA fingerprinting probe	106

2.3 Diagrams / processes to remember

- **Figure 5.1 / 5.2 (pp. 80, 82)** — Polynucleotide chain & double-stranded DNA with 5' phosphate, 3' hydroxyl, sugar-phosphate backbone, A-T (2 H-bonds), G-C (3 H-bonds).
- **Figure 5.3 (p. 82)** — DNA double helix (right-handed, base pairs stacked, sugar-phosphate backbone outside).
- **Figure 5.4a/b (p. 83)** — Nucleosome (DNA around histone octamer + H1) and EM "beads-on-string" chromatin.
- **Figure 5.5 (p. 86)** — Hershey-Chase experiment (32P enters bacteria; 35S stays in supernatant after blending + centrifugation).
- **Figure 5.6 (p. 88)** — Watson-Crick semi-conservative replication model.
- **Figure 5.7 (p. 89)** — Meselson-Stahl CsCl gradient showing heavy / hybrid / light DNA at 0 / 20 / 40 min.
- **Figure 5.8 (p. 91)** — Replication fork: continuous (5'->3' on 3'->5' template) vs discontinuous (Okazaki-style) synthesis.
- **Figure 5.9 (p. 92)** — Transcription unit: Promoter – Structural gene – Terminator (with coding/template strands).
- **Figure 5.10 (p. 93)** — Bacterial transcription: Initiation (sigma), Elongation, Termination (rho).

- **Figure 5.11 (p. 94)** — Eukaryotic transcription with capping (m-G-ppp), splicing of introns, polyadenylation (poly-A tail).
- **Table 5.1 (p. 96)** — Codon checker-board for all 64 codons.
- **Figure 5.12 (p. 98)** — tRNA clover-leaf with anticodon loop and amino-acid acceptor end.
- **Figure 5.13 (p. 99)** — Translation on ribosome (mRNA, tRNAs, growing polypeptide).
- **Figure 5.14 (p. 101)** — lac operon in absence vs presence of inducer.
- **Figure 5.15 (p. 103)** — HGP workflow (cell -> chromosome -> DNA -> automated sequencer -> computer alignment).
- **Figure 5.16 (p. 107)** — DNA fingerprinting via VNTR copy number, restriction digestion, electrophoresis, autoradiography.

2.4 Common confusions / NTA trap points

- A-T has **2** hydrogen bonds, G-C has **3** — NTA loves to flip these.
- Pitch (per full turn) = **3.4 nm**; rise per bp = **0.34 nm**; bp/turn = **10**. Don't mix up "pitch" with "distance between adjacent bp".
- **Coding strand** = the one NOT transcribed (5'->3', same as mRNA except T->U). **Template strand** = the one read by RNA pol (3'->5'). Most students reverse these.
- i gene of lac operon means "inhibitor", NOT "inducer". The repressor itself is constitutively expressed.
- Inducer for lac operon = **lactose / allolactose only**; glucose and galactose CANNOT induce it.
- RNA Pol I -> rRNA (28S, 18S, 5.8S); RNA Pol II -> hnRNA/mRNA; RNA Pol III -> tRNA, 5S rRNA, snRNA. The "II makes mRNA" mapping is the most trapped fact.
- Hershey-Chase used **32P (DNA)** and **35S (protein)** — NOT 14N or 15N (that was Meselson-Stahl).
- Human genome = ~**3 x 10^9 bp** total / **3.3 x 10^9** haploid / **6.6 x 10^9** diploid / **3164.7 million bp** per HGP findings — pay attention to which figure the stem asks for.
- Chr 1 has **most** genes (2968), **Y** has **fewest** (231) — students often guess "X" for fewest.

🎯 Practice MCQs

Q1. What is the distance between two consecutive base pairs in the B-form of DNA double helix as described by Watson and Crick?

A. 3.4 nm

B. 0.34 nm

C. 34 nm

D. 0.034 nm

Q2. The haploid content of human DNA is approximately:

A. 4.6 x 10^6 bp

B. 48,502 bp

C. 3.3 x 10^9 bp

D. 5386 bp

Q3. A typical nucleosome contains how many base pairs of DNA wrapped around a histone octamer?

A. 100 bp

B. 146 bp

C. 200 bp

D. 250 bp

📊 PYQ Alignment

This is one of the highest-weight chapters in CUET Biology, typically generating ~20-22 questions across PYQ papers (2023-25). Frequently tested patterns include: numerical recall of DNA dimensions (0.34 nm rise / 3.4 nm pitch / 10 bp per turn), scientist-experiment matching (Griffith, Hershey-Chase, Meselson-Stahl, Jacob-Monod, Jeffreys,

Khorana, Nirenberg), genetic code properties (triplet, degenerate, universal, UAA/UAG/UGA stops, AUG start), eukaryotic RNA-polymerase assignments (I -> rRNA, II -> hnRNA, III -> tRNA/5S/snRNA), lac operon gene-product mapping (i/z/y/a -> repressor/beta-gal/permease/transacetylase), and Human Genome Project facts (3.1 x 10^9 bp, ~30,000 genes, Chr 1 most genes / Y fewest, dystrophin largest, BAC/YAC, Sanger sequencing).

CUET 2025 — Actual PYQs from this chapter

Q.9 (CUET 2025) The process of copying genetic information from one strand of DNA into RNA is termed as:

- A) Replication
- B) Translation
- C) Transcription
- D) Regulation

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

Q.13 (CUET 2025) Which of the following is not associated with transcription in bacteria?

- A) Rho factor
- B) Methyl guanosine triphosphate
- C) Sigma factor
- D) DNA-dependent RNA polymerase

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

Q.16 (CUET 2025) Match gene name with encoded enzyme. Gene Encodes (A) ‘i’ (i) Permease (B) ‘z’ (ii) Repressor (C) ‘y’ (iii) Transace tylase (D) ‘a’ (iv) β-galacto sidase

- A) [option not extracted — see source]
- B) [option not extracted — see source]
- C) [option not extracted — see source]
- D) [option not extracted — see source]

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

Q.34 (CUET 2025) If double-stranded DNA has 15% adenine, percent of cytosine will be:

- A) 15%
- B) 30%
- C) 35%
- D) 85%

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

CUET 2024 — Actual PYQs from this chapter

Q.11 (CUET 2024) Which statements are incorrect with respect to nucleotides? (A) Purines and pyrimidines are nitrogenous bases (B) Nucleotides are non-enzymatic molecules (C) Phosphate group linked to 5′ C by phosphoester bond (D) RNA has additional –OH at 2′ position (E) Thymine is a pyrimidine Options given.

- A) [option not extracted — see source]
- B) [option not extracted — see source]
- C) [option not extracted — see source]
- D) [option not extracted — see source]

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

Q.13 (CUET 2024) Nucleosome is associated with _____ molecules of histones.

- A) Four
- B) Nine
- C) Two
- D) Eight

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

Q.14 (CUET 2024) Select correct observations from Human Genome Project. Statements A–E given.

- A) [option not extracted — see source]
- B) [option not extracted — see source]
- C) [option not extracted — see source]
- D) [option not extracted — see source]

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

CUET 2023 — Actual PYQs from this chapter

Q.9 (CUET 2023) Arrange the steps of Griffith's experiment in correct order: (A) S strain injected → mice died (B) Heat-killed S strain injected → mice lived (C) R strain injected → mice lived (D) Heat-killed S strain + R strain injected → mice died

- A) A, B, C, D
- B) B, A, C, D
- C) B, C, D, A
- D) A, C, B, D

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

Q.12 (CUET 2023) Identify the statements true for RNA: (A) RNA acts as genetic material for some viruses. (B) RNA functions as adaptor molecule. (C) RNA has hexose sugar backbone. (D) RNA acts as catalyst in some cases.

- A) A, B and C only
- B) A, B and D only
- C) B, C and D only
- D) A, C and D only

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key

Q.13 (CUET 2023) Match List-I with List-II List-I (A) Ribosome (B) Histone (C) DNA polymerase (D) RNA polymerase List-II (I) Replication (II) Transcription (III) Translation (IV) Nucleosome

- A) A-IV, B-III, C-II, D-IV
- B) A-III, B-I, C-II, D-IV
- C) A-I, B-III, C-IV, D-II
- D) A-III, B-IV, C-I, D-II

Tests: aligns with §2 (replication / transcription / translation machinery) Answer: Not in extracted key — verify against official NTA key

Q.14 (CUET 2023) In DNA, N-glycosidic linkage is present between:

- A) Pentose sugar and phosphate group
- B) Nitrogenous base and pentose sugar
- C) Two nitrogenous bases
- D) Two pentose sugars

Tests: aligns with §2 (molecular biology of the gene) Answer: Not in extracted key — verify against official NTA key