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CHAPTER NOTES

Molecular Basis of Inheritance Class 12 Notes — CBSE Biology Chapter 6

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Molecular Basis of Inheritance Class 12 Notes — CBSE Biology Chapter 6

Chapter 6 — **Molecular Basis of Inheritance** — is the molecular genetics chapter covering DNA structure, replication, transcription, translation, gene regulation, and the Human Genome Project. This carries **10-12 marks** — one of the highest-weightage chapters in Biology. Master DNA replication, central dogma, and the lac operon.

Key Concepts

DNA Structure (Watson-Crick Model)

Double helix: Two antiparallel polynucleotide strands ($5' \rightarrow 3'$ and $3' \rightarrow 5'$)

Base pairing: A=T (2 H-bonds), G=C (3 H-bonds) → Chargaff's rule: A=T, G=C

Sugar-phosphate backbone: Deoxyribose sugar + phosphodiester bonds

Pitch: 3.4 nm per turn; 10 bp per turn; each bp = 0.34 nm apart

Diameter: 2 nm; Right-handed helix

DNA Replication

Semiconservative (proved by Meselson and Stahl, 1958 using *E. coli* + $^{15}\text{N}/^{14}\text{N}$)

Key enzymes:

Helicase → unwinds double helix

SSB proteins → stabilise single strands

Primase → synthesises RNA primer

DNA Polymerase III → adds nucleotides ($5' \rightarrow 3'$ only)

DNA Polymerase I → removes RNA primer, fills gaps

Ligase → joins Okazaki fragments

Leading strand: Continuous synthesis ($5' \rightarrow 3'$ towards replication fork)

Lagging strand: Discontinuous (Okazaki fragments, $5' \rightarrow 3'$ away from fork)

Central Dogma

DNA → (Transcription) mRNA → (Translation) Protein

Transcription (DNA → mRNA)

Template strand: 3'→5' (read by RNA polymerase)

Coding/sense strand: 5'→3' (same sequence as mRNA, except T→U)

RNA polymerase synthesises mRNA in 5'→3' direction

In prokaryotes: single RNA polymerase

In eukaryotes: RNA Pol I (rRNA), RNA Pol II (mRNA), RNA Pol III (tRNA)

Post-transcriptional processing (eukaryotes):

Capping (5' cap) + Polyadenylation (3' poly-A tail) + Splicing (remove introns, join exons)

Genetic Code

Property	Details
Triplet	3 bases = 1 codon = 1 amino acid
Degenerate	More than one codon for most amino acids (61 sense codons for 20 amino acids)
Universal	Same code in almost all organisms
Non-overlapping	Codons read sequentially without overlap
Non-ambiguous	One codon codes for only one amino acid
Start codon	AUG (methionine) — initiates translation
Stop codons	UAA, UAG, UGA — terminate translation

Translation (mRNA → Protein)

Occurs on **ribosomes**. tRNA brings amino acids.

Steps:

1. **Initiation:** Small ribosomal subunit + mRNA + initiator tRNA (with Met) → start at AUG
2. **Elongation:** Aminoacyl-tRNA enters A-site → peptide bond formed → ribosome translocates
3. **Termination:** Stop codon (UAA/UAG/UGA) → release factor → polypeptide released

Regulation of Gene Expression — Lac Operon

Jacob and Monod model (*E. coli*):

Structural genes: lacZ, lacY, lacA (encode β -galactosidase, permease, transacetylase)

Promoter: RNA polymerase binds here

Operator: Repressor protein binds here

Regulator gene (i): produces repressor

Without lactose: Repressor binds to operator → blocks transcription → genes OFF

With lactose: Lactose (inducer) binds to repressor → repressor falls off → RNA polymerase transcribes → genes ON

This is an **inducible operon** (switched on by inducer).

Human Genome Project (HGP)

- 1990-2003, coordinated by NIH (USA) and Wellcome Trust (UK)
- Total human genome: ~3.2 billion base pairs
- ~20,000-25,000 genes (only ~2% of genome codes for proteins)
- Chromosome 1 has most genes; Y chromosome has fewest
- Used BAC and YAC vectors; Sanger's method and shotgun sequencing

DNA Fingerprinting

Based on **VNTRs (Variable Number Tandem Repeats)** — unique to each individual

Steps: Isolation → Restriction digestion → Gel electrophoresis → Southern blotting →

Hybridisation with probe → Autoradiography

Applications: paternity testing, forensics, immigration disputes

Solved Examples

Example 1

Q: The sequence of one strand of DNA is 3'-ATGCATGCATGC-5'. Write the mRNA sequence.

Solution: mRNA is synthesised using the template (3'→5') strand. mRNA = 5'-UACGUACGUACG-3' (complementary, with U replacing T).

Example 2

Q: Explain why the lac operon is called an inducible operon.

Solution: The lac operon is normally switched OFF (repressor blocks operator). It is switched ON only when **lactose (inducer)** is present — lactose binds to repressor, changes its shape, repressor detaches from operator, allowing transcription. Since it needs an inducer to turn on, it's called an **inducible operon**.

Important Questions

3 Mark

1. Describe the semiconservative nature of DNA replication.
2. What is the central dogma? Draw a flow chart.
3. Explain the regulation of lac operon in E. coli.

5 Mark

1. Describe the process of translation with a diagram.
2. Explain the Watson-Crick model of DNA. How did Meselson and Stahl prove semiconservative replication?

Quick Revision Points

- DNA: double helix, antiparallel, A=T (2 H-bonds), G≡C (3 H-bonds), 3.4 nm pitch
- Replication: semiconservative (Meselson-Stahl); leading (continuous) + lagging (Okazaki fragments)
- Transcription: template 3'→5'; RNA Pol II makes mRNA in eukaryotes
- Genetic code: 64 codons (61 sense + 3 stop); AUG = start; degenerate, universal

- Translation: initiation (AUG) → elongation → termination (UAA/UAG/UGA)
- Lac operon: inducible; lactose = inducer; repressor blocks operator when no lactose
- HGP: 3.2 billion bp, ~20,000 genes, 2% coding
- DNA fingerprinting: VNTRs, Southern blotting, used in forensics

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