

Class 11 · Biotechnology · Unit III

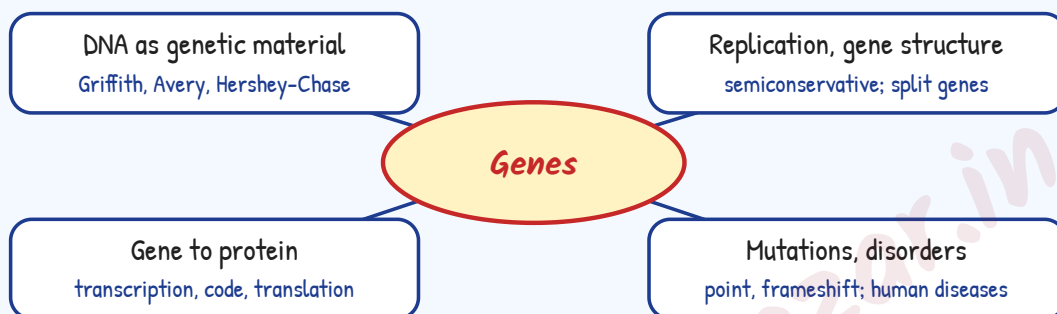
Chapter 5

Genes and Genomes: Structure and Function

DNA
|
RNA
|
Protein
central dogma

CBSE Biotechnology (045) syllabus 2026–27 · Unit III Genetics and Molecular Biology =
20 marks of 70

Chapter map



What is inside

1. Concept notes with diagrams and tables
2. Important textbook questions, fully solved
3. Exam-pattern questions (CBSE 045), fully solved
4. Practice A–G with a case study, 20 MCQs, 6 A–R, answers, summary

Colour code used

red = key term green = definition

purple = sub-heading black = explanation

★ **Exam tip:** Learn the three classic experiments, Meselson–Stahl, enzymes of replication, properties of the genetic code, steps of transcription and translation, and types of mutation with one disorder each.

Based on the CBSE Biotechnology syllabus 2026–27 and the CBSE textbook. All answers written by us.

5.1 Discovery of DNA as genetic material ★★★

Griffith (1928)	Streptococcus pneumoniae: heat-killed virulent S (smooth) + live harmless R (rough) injected into mice killed them; live S cells recovered. A " transforming principle " passed from dead S to live R
Avery, MacLeod, McCarty (1944)	purified the transforming principle; DNase destroyed transformation, but protease and RNase did not: it is DNA
Hershey and Chase (1952)	T2 phage labelled with ³²P (DNA) or ³⁵S (protein) infected E. coli; after blending and centrifuging, ³²P entered the bacteria , ³⁵S stayed outside: DNA is the genetic material

RNA is the genetic material in some viruses (TMV, HIV).

5.2 DNA replication ★★★

Semiconservative: each new DNA has one old (parental) strand and one new strand. Proved by **Meselson and Stahl**

(1958): E. coli grown in ¹⁵N then moved to ¹⁴N; CsCl density-gradient centrifugation gave hybrid (¹⁵N/¹⁴N) DNA after one generation, and hybrid + light after two.

helicase	unwinds the double helix at the origin (replication fork)
SSB proteins, topoisomerase	keep strands apart; relieve supercoiling
primase	makes a short RNA primer
DNA polymerase (III in E. coli)	adds nucleotides only 5'→3' to a 3'-OH
DNA polymerase I	removes primers and fills gaps
DNA ligase	joins the fragments

Leading strand: made continuously; **lagging strand**: made discontinuously as **Okazaki fragments**, later joined by ligase.

5.3 Fine structure of the gene ★★★

A gene is a segment of DNA that codes for a functional product (polypeptide or RNA). **Seymour Benzer** (T4 rII locus) divided the gene into the **cistron** (unit of function), **recon** (unit of recombination) and **muton** (unit of mutation, as small as one base pair).

Split genes (eukaryotes): coding **exons** interrupted by non-coding **introns** (Sharp and Roberts, 1977). Prokaryotic genes are usually continuous and may be grouped in **operons**. A gene has a **promoter** (where RNA polymerase binds), the coding region, and a **terminator**.

5.4 From gene to protein ★★★

Central dogma (Crick): DNA → (transcription) → RNA → (translation) → protein; DNA replicates itself. **Reverse transcription** (RNA → DNA) occurs in retroviruses.

Transcription

1. **initiation**: RNA polymerase (with sigma factor in bacteria) binds the **promoter**; DNA unwinds
2. **elongation**: RNA made **5'→3'** using the **template (antisense) strand**; U pairs with A
3. **termination** at the terminator (rho-dependent or independent)

Eukaryotic processing of hnRNA to mRNA: **5' cap** (methyl-G), **3' poly-A tail**, **splicing** (introns removed, exons joined).

Eukaryotes have RNA polymerases I (rRNA), II (mRNA), III (tRNA).

5.5 The genetic code ★★★

Deciphered by **Nirenberg, Matthaei, Khorana** (and Holley); Nobel 1968.

- **triplet**: three bases (codon) = one amino acid; **64** codons
- **61** sense codons; **3** stop codons: **UAA, UAG, UGA**
- **AUG** = start codon and methionine
- **degenerate**: most amino acids have more than one codon
- **unambiguous**: one codon → one amino acid
- **non-overlapping** and **comma-less**; read 5' → 3'
- nearly **universal** (exceptions in mitochondria)

5.6 Translation ★★★

Takes place on **ribosomes** (70S in prokaryotes; 80S in eukaryotes). **Charging**: aminoacyl-tRNA synthetase attaches each amino acid to its tRNA (uses ATP). **tRNA** has an **anticodon** that pairs with the mRNA codon.

1. **initiation**: small subunit binds mRNA; initiator tRNA (Met) pairs with **AUG**; large subunit joins (P site)
2. **elongation**: next aminoacyl-tRNA enters the A site; **peptidyl transferase** (rRNA) forms a peptide bond; ribosome **translocates** one codon
3. **termination**: a stop codon is reached; release factors free the polypeptide

Several ribosomes on one mRNA form a **polysome**.

5.7 Mutations ★★★

A mutation is a sudden heritable change in the DNA sequence. Causes: errors in replication; **mutagens**: UV (thymine dimers), X-rays, chemicals (nitrous acid, base analogues like 5-bromouracil).

point (substitution)	one base replaced: transition (purine ↔ purine) or transversion (purine ↔ pyrimidine)
silent	codon changes but same amino acid
missense	different amino acid (sickle cell: GAG → GTG, Glu → Val)
nonsense	codon becomes a stop codon; short protein
frameshift	insertion or deletion of bases (not in threes) shifts the reading frame
chromosomal	deletion, duplication, inversion, translocation; aneuploidy

5.8 Human genetic disorders ★★★

sickle cell anaemia	autosomal recessive; Glu → Val at beta-globin position 6
thalassaemia	autosomal recessive; reduced alpha or beta globin
phenylketonuria	autosomal recessive; no phenylalanine hydroxylase; phenylalanine builds up, harming the brain
haemophilia	X-linked recessive ; clotting factor VIII or IX missing; mostly males
cystic fibrosis	autosomal recessive; CFTR chloride channel defect
Down syndrome	trisomy 21 (47 chromosomes)
Turner syndrome	45, XO female
Klinefelter syndrome	47, XXY male

Exam-style · 1 mark Hershey and Chase labelled protein with: (A) ^{32}P (B) ^{35}S (C) ^{15}N (D) ^{14}C [1]

Ans. (B) ^{35}S (proteins contain sulphur; DNA does not)

Exam-style · 2 marks Write the mRNA and polypeptide for the template strand 3' TAC GGA ACT 5'. [2]

Ans. mRNA: 5' AUG CCU UGA 3'. Polypeptide: **Met-Pro**, then UGA is a stop codon.

Exam-style · 3 marks Explain the Meselson-Stahl experiment. [3]

Ans. E. coli grown for many generations in $^{15}\text{NH}_4\text{Cl}$ (heavy DNA) was moved to ^{14}N medium. DNA was separated by **CsCl density-gradient centrifugation**. After one generation all DNA was of **intermediate (hybrid)** density; after two, half hybrid and half light. This proves **semiconservative** replication.

Exam-style · 5 marks Explain the properties of the genetic code. [5]

Ans. Triplet (64 codons); 61 code amino acids and 3 are stops (UAA, UAG, UGA); AUG is the start (Met); degenerate; unambiguous; non-overlapping and comma-less; nearly universal; read 5' $\rightarrow$ 3' in a fixed frame.

Textbook: Why is the lagging strand made in fragments?

Ans. DNA polymerase works only 5' $\rightarrow$ 3'. On the strand running 5' $\rightarrow$ 3' towards the fork, synthesis must go away from the fork, so it is made in short Okazaki fragments, each with its own primer, joined later by ligase.

Practice set Exam-style

A. Fill in: 1. Griffith worked with _____ pneumoniae. 2. Okazaki fragments form on the _____ strand. 3. The start codon is _____.

B. True or false: 1. Introns are present in mature mRNA. 2. Haemophilia is X-linked. 3. A deletion of 3 bases always causes a frameshift.

D/E: 1. Distinguish transition and transversion. 2. Describe processing of hnRNA. **G. HOTS:** Why does a frameshift near the start of a gene usually destroy the protein?

Case study: A child has pale skin, musty-smelling urine and developmental delay; blood shows high phenylalanine. (i) Disorder? (ii) Enzyme missing? (iii) Pattern of inheritance? (iv) Management? [4]

Answers

A. 1. Streptococcus 2. lagging 3. AUG **B.** 1. F 2. T 3. F (it removes one amino acid but keeps the frame) **D/E.** 1. transition: purine to purine or pyrimidine to pyrimidine; transversion: purine to pyrimidine or vice versa 2. 5' cap, 3' poly-A tail, splicing out introns **G.** all codons after it are read wrongly, giving wrong amino acids and usually an early stop codon **Case.** (i) phenylketonuria (ii) phenylalanine hydroxylase (iii) autosomal recessive (iv) low-phenylalanine diet from birth (newborn screening)

20 MCQs

1. Transforming principle was found by:

(A) Sanger (B) Watson (C) Griffith (D) Morgan

3. Hershey-Chase used:

(A) M13 (B) TMV (C) lambda (D) T2 phage

2. Transforming principle was identified as DNA by:

(A) Avery, MacLeod, McCarty (B) Hershey and Chase (C) Meselson and Stahl (D) Crick

4. Semiconservative replication was proved by:

(A) Griffith (B) Meselson and Stahl (C) Benzer (D) Khorana

5. Heavy isotope used by Meselson and Stahl:

(A) ^{35}S (B) ^{15}N (C) ^{32}P (D) ^{14}C

6. Enzyme that unwinds DNA:

(A) polymerase I (B) ligase (C) primase (D) helicase

7. Primers in replication are made of:

(A) RNA (B) DNA (C) protein (D) lipid

8. Okazaki fragments are joined by:

(A) primase (B) helicase (C) DNA ligase (D) RNase

9. Unit of function in Benzer's terms:

(A) codon (B) muton (C) recon (D) cistron

10. Non-coding sequences in split genes:

(A) exons (B) introns (C) promoters (D) codons

11. RNA polymerase binds the:

(A) ribosome (B) terminator (C) promoter (D) intron

12. Number of codons:

(A) 64 (B) 61 (C) 20 (D) 3

13. A stop codon:

(A) AUG (B) UAA (C) GUG (D) UUU

1 (C) · 2 (A) · 3 (D) · 4 (B) · 5 (B) · 6 (D) · 7 (A) · 8 (C) · 9 (D) · 10 (B) · 11 (C) · 12 (A) · 13 (B) · 14 (C) · 15 (D) · 16 (A) · 17 (A) · 18 (D) · 19 (B) · 20 (C)

14. Code has more than one codon per amino acid; it is:

(A) overlapping (B) ambiguous (C) degenerate (D) universal only

15. Peptide bond formation is catalysed by:

(A) primase (B) helicase (C) ligase (D) peptidyl transferase (rRNA)

16. tRNA pairs with mRNA through its:

(A) anticodon (B) amino acid arm (C) cap (D) poly-A

17. Sickle cell mutation is a:

(A) missense mutation (B) nonsense mutation (C) frameshift (D) silent mutation

18. Down syndrome is:

(A) trisomy 18 (B) XO (C) XXY (D) trisomy 21

19. Haemophilia is:

(A) autosomal dominant (B) X-linked recessive (C) Y-linked (D) mitochondrial

20. Klinefelter syndrome karyotype:

(A) 47, +21 (B) 45, XO (C) 47, XXY (D) 46, XX

Assertion-Reason (6)

(A) Both true, R explains A. (B) Both true, R does not explain A. (C) A true, R false. (D) A false, R true.

1. A: The lagging strand is made discontinuously. R: DNA polymerase works only $5' \rightarrow 3'$.

2. A: ^{35}S stayed outside bacteria in Hershey-Chase. R: Phage protein coats do not enter the bacterium.

3. A: Mature eukaryotic mRNA contains introns. R: Splicing removes exons.

4. A: The genetic code is ambiguous. R: The genetic code is degenerate.

5. A: A nonsense mutation shortens the protein. R: It creates a premature stop codon.

6. A: DNA replication is semiconservative. R: Haemophilia is X-linked.

Key: 1 (A) · 2 (A) · 3 (D) · 4 (D) · 5 (A) · 6 (B)

Last-night summary

- Griffith 1928, Avery et al. 1944, Hershey-Chase 1952 (^{32}P in, ^{35}S out).
- Replication: semiconservative (Meselson-Stahl 1958); helicase, primase, pol III, pol I, ligase; leading v lagging (Okazaki).
- Gene: cistron, recon, muton (Benzer); exons, introns; promoter, terminator.

- Transcription: initiation, elongation, termination; cap, tail, splicing. Code: triplet, 64, AUG, 3 stops, degenerate, universal.
- Translation: charging, initiation, elongation (peptidyl transferase), termination.
- Mutations: transition, transversion, silent, missense, nonsense, frameshift. Disorders: sickle cell, thalassaemia, PKU, haemophilia, CF, Down, Turner, Klinefelter.

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