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3 (Sem-4/CBCS) BOT HC 1

2025

BOTANY

(Honours Core)

Paper : BOT-HC-4016

(Molecular Biology)

Full Marks : 60

Time : Three hours

***The figures in the margin indicate
full marks for the questions.***

1. Give short answers of the following : 1×7=7
- (a) What is gene silencing ?
 - (b) Define nucleosome.
 - (c) Who proposed the Central Dogma theory ?
 - (d) What is alternative splicing ?
 - (e) Which genetic code is called as start codon ?

- (f) Name the bond which is formed between t-RNA and amino acid.
- (g) Which type of RNA polymerase synthesizes mRNA in eukaryotes ?

2. Answer the following questions briefly :

2×4=8

- (a) Distinguish between exon and intron.
- (b) What do you mean by Okazaki fragments ?
- (c) "Genetic Code is degenerate." Justify the statement.
- (d) What are the differences between constitutive and facultative heterochromatin ?

3. Answer **any three** of the following questions :

5×3=15

- (a) Discuss the role of different enzymes in DNA replication.
- (b) Is mitochondrial inheritance part of Mendelian inheritance ? Mention the salient features of mitochondrial DNA.
- (c) Write the properties of genetic code.

- (d) Distinguish between purine and pyrimidine.

- (e) Write the salient features of Watson and Crick model of DNA.

4. Answer the following questions : (**any three**)

10×3=30

- (a) Describe the mechanism of protein synthesis in prokaryotes. Point out the role of different RNAs in this process.
7+3=10
- (b) Give a comparative account on the Trp operon and Lac operon for the metabolism of tryptophan and lactose in bacteria.
- (c) Give a detailed note on the chief antibiotics which inhibit protein synthesis. How is transcription regulated ?
5+5=10
- (d) Discuss the role of Griffith and Avery in establishing the fact that 'DNA is a genetic material'.
5+5=10
- (e) Why is semi-conservative mode of DNA replication essential for genetic stability ? With labelled diagram, describe semi-conservative replication process of DNA.
3+7=10

(f) Write an account on the following :

5×2=10

(i) Structure of prokaryotic RNA polymerase

(ii) Charging of t-RNA during translation