

18BB1451

M. Tech. EXAMINATION, 2020

(Second Semester)

(C Scheme) (Re-appear)

(BIO-TECHNOLOGY)

BT502C

Genomics and Proteomics

Time : 2½ Hours]

[Maximum Marks : 75

Before answering the question-paper candidates should ensure that they have been supplied to correct and complete question-paper. No complaint, in this regard, will be entertained after the examination.

Note : Attempt *Four* questions in all. All questions carry equal marks.

1. (a) Give a comparative account of the following :
 - (i) Structural organization of prokaryotic and eukaryotic genomes.
 - (ii) Distribution and arrangement of different features in a prokaryotic and eukaryotic genome.
- (b) Distinguish between the terms 'genetic map' and 'physical map'. Giving the details of a few genetic markers based upon the principle of linkage analysis, explain, how linkage analysis is used to construct genetic maps ?
2. (a) Describe the constitution of the two major eukaryotic organelle genomes. How is it different from nuclear genomes ?
- (b) With the help of examples of each, contrast the role of restriction endonucleases in genetic and physical mapping techniques.

- (c) Describe, how FISH is used to construct a physical map, including the modifications used to increase the sensitivity of this technique ?
3. (a) Demonstrate the strengths and limitations of the shotgun, whole-genome shotgun and clone contig methods of genome sequencing. Illustrate, how these have been applied in whole genome sequencing of prokaryotic and eukaryotic genomes ?
- (b) Determine and show the basis of ORF scanning and explain, why it is not always successful in locating genes in eukaryotic genomes ? Predict the modifications that could help its successful application in eukaryotic genomes.
4. (a) Illustrate the significance and give a detailed outline of various computational and experimental techniques used for functional annotation of eukaryotic genomes.
- (b) Demonstrate, how SAGE and MPSS can be applied for transcriptome analysis.
5. (a) Outline the various steps involved in protein expression analysis. Justify the use of electrophoretic and spectrometry techniques in protein profiling and protein identification.
- (b) Evaluate and compare the methods that aid in assessing physical and functional interactions between pairs and groups of proteins.
6. (a) Illustrate, how protein-protein interactions can be inferred using phage-display and yeast two-hybrid systems ?
- (b) Recommend and critically evaluate the different techniques that can be used to assess protein expression analysis.
7. (a) Enlist and explain a few practical examples where genomic and proteomic studies have been used for bringing improvement in agronomic traits.
- (b) Demonstrate the use of genomic and proteomic tools in high throughput screening in genome for drug discovery and identification of gene targets.

8. (a) Describe, how the advancements in genomics and proteomics have revolutionized the field of medical biotechnology ? Discuss a few relevant examples.
- (b) Demonstate, how genomic and proteomic studies can be applied in pharmacogenomics and personalized medicine ?
9. Explain the following :
- (a) STS mapping
 - (b) RACE for mapping of ends of transcripts
 - (c) Chain-termination DNA sequencing
 - (d) Affinity purification for analysis of protein complexes
 - (e) Comparative genomics