TM252141A

Reg. No :.....

Name :.....

MASTER'S DEGREE (C.S.S) EXAMINATION, MARCH 2025

2020, 2021, 2022, 2023 ADMISSIONS SUPPLEMENTARY

SEMESTER II - CORE COURSE ZOOLOGY

ZO2C07TM20 - Genetics and Bioinformatics

Time : 3 Hours **Maximum Weight : 30**

Part A

I. Answer any Eight questions. Each question carries 1 weight **(8x1=8)**

1. What is the principle of segregation? Why is it important?
2. Differentiate incomplete dominance and co-dominance.
3. Write a brief description about Nucleosomes.
4. Write a short note on eukaryotic chromosome.
5. What is semiconservative replication?
6. Tabulate the different components required for replication in bacterial cell.
7. Define Lod Score.
8. Differentiate between gene frequency and allelic frequency.
9. Discuss the functions and features of Biological databases.
10. Define Proteomics. Discuss the importance of proteomics in research.

Part B

II. Answer any Six questions. Each question carries 2 weight **(6x2=12)**

11. What does Mendel's monohybrid crosses reveal?
12. Explain renaturation kinetics and its significance.
13. Explain the concept of dominant epistasis with a suitable example.
14. What are the different chromosomal rearrangements? How do they contribute towards mutations?
15. Enlist the consequences of defects in DNA repair mechanisms. Mention 3 examples with explanations.
16. Write a short note on Huntington's disease.
17. Explain the inheritance pattern of Autosomal Dominant traits. Give examples.
18. Write a description on Composite databases with examples.

Part C

III. Answer any Two questions. Each question carries 5 weight **(2x5=10)**

19. Explain the different allelic and non-allelic interactions with suitable examples. Drive the ratios and justify that they are modifications of normal mendelian monohybrid and dihybrid ratios.
20. Write an elaborate essay on nature of transposable elements and different mechanisms of transposition and its regulation.
21. What is mutagenesis? Explain the different types of mutations and the molecular mechanisms in mutation.
22. Discuss the different methods that are used for obtaining phylogenetically useful information from different sequences.