24PBSET1A01

SHRIMATHI DEVKUNVAR NANALAL BHATT VAISHNAV COLLEGE FOR WOMEN (AUTONOMOUS)

(Affiliated to the University of Madras and Re-accredited with 'A+' Grade by NAAC) Chromepet, Chennai - 600 044.

M.Sc.Biostatistics - END SEMESTER EXAMINATIONS - NOV' 2024 SEMESTER - I

24PBSET1A01 - Statistical Genetics

Total Duration: 2 Hrs. 30 Mins. Total Marks: 60

Section B

Answer any **SIX** questions $(6 \times 5 = 30 \text{ Marks})$

- 1. Illustrate the concept of genetic maps and explain their importance in studying heredity.
- 2. Explain gene frequency and relate it to population genetics, providing an example to show its significance.
- 3. Solve common statistical problems in human genetics and prepare a brief explanation of their implications.
- 4. Explain the concept of polygenic traits and describe their significance in genetics.
- 5. Show how the Chi-square test is applied to genetic data, and compute the expected results for a Mendelian ratio, providing an example to explain the process.
- 6. Apply the principles of linkage detection using back cross data and classify the key factors involved in estimating linkage.
- 7. Explain the concept of a multiple allelic system and describe its significance in genetics.
- 8. Determine the concept of heritability and explain its importance in genetics.

Section C

- I Answer any **TWO** questions $(2 \times 10 = 20 \text{ Marks})$
- 9. Elucidate different types of linkage and crossing-over, and predict their effects on genetic variation with relevant examples.
- 10. Classify various types of gene interactions and explain the expected outcomes in both monohybrid and dihybrid crosses.
- 11. Ascertain the principles of Hardy-Weinberg equilibrium and determine how they affect gene frequencies in a population, justifying your findings with examples.

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- 12. Prepare an analysis of human blood groups based on multiple allelic inheritance, predicting their evolutionary significance.
 - II Compulsory question $(1 \times 10 = 10 \text{ Marks})$
- 13. Analyse the different mating methods in genetics, contrasting their advantages and disadvantages for trait enhancement.
