

2021
Zoology
Paper: ZCT-104
Genetics
Full Marks: 50

The figures in the margin indicate full marks

Candidates are required to give their answers in their own words as far as practicable.

*Answer **any Four** questions*

Q1.a) Define sequence homology.

- b) Describe the process of homologous recombination in eukaryotes with proper illustrations.
- c) Comment on the input given by Meselson and Radding on homologous recombination.
- d) Outline the functions of recombination in a cell.

2+5+3+2.5=12.5

Q2. a) Mention salient features of genomic imprinting in mammal.

- b) Design an experiment to show the contributions of maternal and paternal genome are not equivalent in zygote.
- c) Comment on role of lncRNA in regulation of genomic imprinting.

3.5+ 5+ 4=12.5

Q3.a) Explain how DNA double-strand breaks are amended.

- b) How are UV-induced Pyrimidine dimers repaired through Photoreactivation?
- c) Write the cause and symptoms of Xeroderma pigmentosum and Fanconi anemia.

5+4+3.5=12.5

Q.4. a) State the molecular features of MSL2 and MOF in *Drosophila melanogaster*.

- b) Comment on roX1 and roX2 RNA in *Drosophila* dosage compensation.

(4+4.5) + (2+2) =12.5

Q5.a) Explain the process of meiotic recombination in humans with a suitable illustration.

- b) Do you agree that the “Synaptonemal complex forms as a consequence of recombination”? Substantiate your answer with proper proof.
- c) List the protein components of the Synaptonemal complex in mammals.

5.5+4+3.5=12.5

Q6.a) Comment on histone arginine methylation and lysine methylation on gene functioning.
b) Define histone code and reader-writer complex. $(4+4)+(2+2.5)=12.5$

Q7.a) Outline the process of salvage pathway for purine synthesis with proper diagram.
b) What is HAT medium? Why HAT medium is used in hybrid selection.
c) Describe how monoclonal antibody is produced. $4.5+(1+3)+4=12.5$

Q8. a) Briefly describe how XIST initiate formation of silencing complex.
b) Tabulate different long non-coding RNA that regulate XIST transcription.
c) Comment on a model that describes how some genes escape dosage compensation $5+5+2.5=12.5$