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M.Sc. (IVth Semester) Examination, 2020

ZOOLOGY

**(Genomics, Metagenomics and
Epigenetics Genomics)**

Time Allowed : Three Hours

Maximum Marks : 70

SECTION - A

Note : Attempt any ten questions. Each question carries one mark. **10×1=10**

Q. 1. Objective type :

- (1) C-value in genome represents _____.
- (2) The first completed genome sequencing project is of _____.
- (3) Variation between individuals due to single base changes is called as _____.
- (4) DNA sequencing followed by genome annotation are steps of _____.

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(2)

- (5) Genes involved in the same metabolic pathway tend to be clustered among phylogenetically diverse organisms. (True/False).
- (6) Which of the following information sequence comparisons do not provide ?
 - (a) Gene relationships
 - (b) Function history
 - (c) Evolutionary history
 - (d) Gene locations
- (7) Which of the following is not a gene expression database ?
 - (a) GenBank
 - (b) Flyview
 - (c) SeedGenes
 - (d) BodyMap

(3)

(8) Which of the following is the correct order of organization of genetic material from smallest to largest ?

- (a) Genome, chromosoem, gene, nucleotide
- (b) Nucleotide, gene, chromosome, genome
- (c) Gene, nucleotide, chromosome, genome
- (d) Chromosome, genome, nucleotide, gene

(9) Which of the following is used to construct a genetic map of a chromosome ?

- (a) Recombination frequencies
- (b) Banding patterns of chromosomes
- (c) Molecular distances separating sites on a DNA fragment
- (d) Restriction endonuclease sites

(4)

(10) Tandem repeats that are extremely valuable in the creation of high density maps of eukaryotic chromosomes are known as :

- (a) RFLP
- (b) EST
- (c) Microsatellites
- (d) SNPs

(11) Which of the following procedures is a variation on FISH and has been used for comparative genome analysis ?

- (a) Chromosome painting
- (b) Chromosome walking
- (c) Recombination mapping
- (d) Chromosome jumping

(5)

(12) Fluorescent in situ hybridization (FISH)

requires :

- (a) Dideoxynucleotides
- (b) Labeled probe
- (c) DNA polymerase
- (d) None of the above

SECTION - B

Note : Attempt any five questions. Each question carries
2 marks. **5×2=10**

Q. 2. Very short answer type (25-30 words) :

- (1) Differentiate physical and genetic map.
- (2) What is SINE ?
- (3) What is high-throughput sequencing ?
- (4) Name tools used for protein-protein interaction.
- (5) What is pairwise alignment ?

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(6)

- (6) What is base calling ? How sequence accuracy can be measured ?
- (7) What is organellar genome ?

SECTION - C

Note : Attempt any five questions. Each question carries
4 marks. **5×4=20**

Q. 3. Short answer type (250 words) :

- (1) Write a note on application of microarray for gene expression profiling.
- (2) Explain the strategies for sequencing the entire genome of an organism.
- (3) What is C-value paradox ? How genome complexity and DNA content are interrelated ?
- (4) Explain insertional mutagenesis by citing suitable examples.

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(7)

- (5) What is bioinformatics ? Give its application in various fields.
- (6) How SNPs can be used as molecular marker for genome mapping ?
- (7) Biological databases are the source of scientific information. Justify.

SECTION - D

Note : Attempt any three questions. Each question carries 10 marks. **3×10=30**

Q. 3. Essay type (more than 500 words) :

- (1) Describe how automated DNA sequencing has revolutionarised the study of human genome project.
- (2) What are LINEs and SINEs ? How can LINEs and SINEs lead to human disease ?

(8)

- (3) Why are eukaryotic genome larger ? Do complex organisms have larger genomes ? Briefly explain about cot curve.
- (4) Write a note on protein evolution by exon shuffling ?

