15. *(a)* What is the function of electron multiplier in mass spectrometry? 2

(b) What is surface-enhanced laser desorption ionization (SELDI)? 2

(c) What is the basic principle of separation of proteins in 2D-GEL electrophoresis? 1

16. *(a)* What are molecular ions, fragment ions and base peak in mass spectrometric analysis? 1×3=3

(b) How does quadrupole analyze the mass of a peptide in a mass spectrometry? 2

★★★

MASTER OF SCIENCE EXAMINATION, 2024

(2nd Year, 1st Semester)

BIOTECHNOLOGY

PAPER : BT/PG/332T

(Genomics and Proteomics)

Time : *Two Hours* *Full Marks* : 40

GROUP—A

Answer Question **1** and ***any five*** questions from the rest taking at least **one** question from each Part :

1. Answer ***any five*** questions : 5×1=5

(i) State the law of "Independent Assortment" as proposed by Mendel. What is its condition?

(ii) State the difference between mechanisms of incomplete dominance and co-dominance at the molecular level.

(iii) What is "LOD" score? Mention its application in genetics?

(iv) What is "genetic suppression"? Provide an example of intergenic suppression.

(v) What do you mean by "counter selection" method? In yeast genetics, which chemical is frequently used in counter selection procedure?

(vi) What is "tetrad"? Which unique attribute of tetrad is extremely useful to geneticists to study meiotic recombination?

(vii) What do you mean by "one-step-gene-replacement" procedure?

(viii) What is Tiled Microarray technique? What is the benefit of this technique over the conventional microarray?

(ix) Explain how the use of "barcode" helps in multiplexing during the library preparation for RNA sequencing.

(x) Explain what is "ribodepletion". In which process, ribodepletion is carried out?

PART—I

2. *(a)* Provide a cytological evidence that crossing-over during meiosis involves physical breakage and rejoining of chromosome arms. 2

(b) Sickle cell anemia is a recessive genetic disease caused due to a point mutation in the 6^{th} codon abolishing one of the *Msp*II endonuclease digestion sites present in

GROUP—B

(Answer ***any two*** questions, each carry **5** marks, Total **10**)

12. *(a)* What is the important feature of tryptic digestion in proteomics? 2

(b) What are the basic components required for a mass spectrometry? 3

13. *(a)* Briefly describe the electrospray and chemical ionization methods in mass spectrometry. 3

(b) Tryptic digest of a heptapeptide (composed of 3 lysine, 2 alanine, 1 tyrosine and 1 phenylalanine) yielded tri and tetrapeptide. Based on the above information, write down the probable sequence of the heptapeptide. 2

14. *(a)* Following is the amino acid sequence, subjected to tryptic digestion for mass spectrometric analysis. Write down the different peptide fragments that you would get after tryptic digestion. 2

RLVEVALGKIGGGANTRGYEVALVNTKFWMC
SMVALPGMSWFRH

(b) Explain briefly the basis of MALDI-TOF for the analysis of proteins. 3

transcription factor that can activate multiple genes in response to growth I presence of high copper sulphate. Suggest an experimental approach to identify *(i)* potential binding sites of these target genes in the genome (at the genome-wide scale) and *(ii)* prove if the protein truly binds DNA. 3+2=5

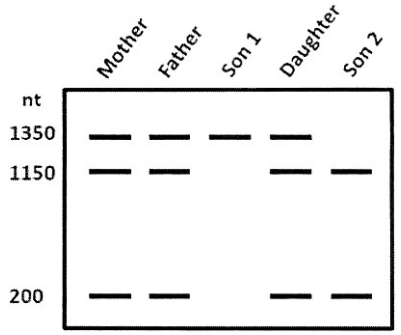
10. *(a)* What is the role of index sequence present in the flanking oligonucleotides in an Illumina workflow? 1

(b) You want to determine the total pool of "antisense" transcripts that become stabilized (increased) in yeast *Saccharomyces cerevisiae*, when it is grown in presence of a metal ion in the medium with respect to the absence of that metal ion. Which technique will be appropriate to find out the answer of this question? Since, you are looking to determine the anti-sense transcripts, what specific step you must carry out when designing your experiment? 4

11. *(a)* What do you mean by "clustering" in the microarray data analysis? Briefly explain why and how clustering is carried out during microarray data analysis. 1

(b) Briefly outline the pipeline involved in RNA Sequencing technology. You may present a workflow diagram of RNA sequencing technique without any description of individual steps within small boxes. 4

β-globin gene. *Msp*II digested DNA from a normal person gives two bands, 1150 bp and 200 bp in β-globin gene. The *Msp*II digestion pattern of β-globin gene from the blood samples from the members of a family is given below :



Explain the *Msp*II digestion data and provide the genotype (with respect to Sickle cell anemia) of each of the family members. 3

3. *(a)* In *Drosophila*, vestigial wings and ebony colour are due to two separate recessive genes. The dominant alleles are normal (long) wings and normal (gray) body colour. What type of offspring would you expect from a cross between a homozygous vestigial ebony female and a normal double homozygous (long-winged, gray-bodied) male? If the F1 flies are allowed to breed among themselves what types of offspring would you expect in the F2? Show complete genotype and phenotype of both generations. 3

(b) In *Drosophila*, the allele for white eyes is sex-linked and recessive to the wild-type allele, red eyes. When white-eyed males were crossed with red-eyed females, the FI progeny consisted of 433 red-eyed females and 420 red-eyed males. The F2 progeny showed the following results:

Red-eyed males 105

Red-eyed females 204

White-eyed males 96

White-eyed females 0

Do these data fit the appropriate genetic hypothesis? 2

4. *(a)* Following phenotypic data were obtained from a test cross progeny in *Drosophila melanogaster* :

	Phenotypes			**Number**
1.	+	m	+	218
2.	w	+	f	236
3.	+	+	f	168
4.	w	m	+	178
5.	+	m	f	95
6.	W	+	+	101
7.	+	+	+	3
8.	W	m	f	1
			Total	1000

Construct a genetic map. 3

8. *(a)* You are performing a complementation experiment as part of a genetic screen to isolate a mutation that destroys the ability of a yeast strain to process/trim 5.8S ribosomal RNA, which you named *rrp* (ribosomal RNA processing) mutation. You have isolated one mutation called *rrp1-1* and you crossed this strain to a $RRP1^{+}$ strain. After isolating the diploid and sporulation you noticed a 3 : 1 segregation pattern of the mutant *rrp1-1* allele. What is the most likely conclusion of this experiment? 2

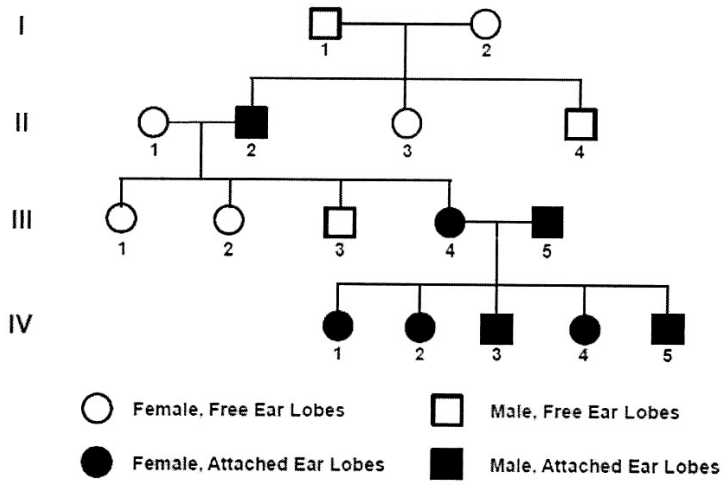
(b) A temperature sensitive mutation is a conditional lethal mutation where the yeast strain carrying the mutation grows fine at normal temperature of 25 °C, but cannot grow at high temperature of 37 °C. You are planning to isolate a temperature-sensitive mutation. What temperature would you prefer to carry out mutagenesis, screening and selection procedure? Explain with reasons. 3

PART—III

9. You identified a new protein in *Saccharomyces cerevisiae*. A preliminary bioinformatic analysis is indicating that this protein could be a transcription factor, because it has a putative leucin zipper domain (which can potentially bind DNA) and a stretch of polyglutamine (PolyQ) towards the c-terminal end of the primary sequence. You think from available experimental evidence that this protein might serve as a

(b) With 10% recombination between genes *a* and *h*, 15% recombination between genes *h* and *c*, the order being *a h c*, and a coefficient of coincidence value of 1.0, calculate the expected gametic frequencies in an individual with the genotype *Aa Bh Cc*. 2

5. The following is a pedigree of ear lobe shape in human beings :



(i) State which pattern of inheritance for this trait is consistent with this pedigree. Give reasons.

(ii) Using the first letter of the alphabet, give the genotype of each of the following persons : I-1, II-1 and III-4

(iii) No ancestry information is available for II-1. How do you justify the assignment of her genotype? 5

PART—II

6. *(a)* With the help of boxed flow chart, briefly describe the experimental outline of Beadle and Tatum's experiment with *Neurospora crassa* (No detailed description is necessary). Which important genetic principle was initially proposed from this experiment? 3

(b) Mention how the mating type is determined in baker's yeast. Which genetic determinant/ element is involved in this process and which fundamental molecular process is involved in this process? 2

7. *(a)* Explain what do you mean by "complementation group". In an attempt to identify the genes involved in leucine biosynthesis in *Neurospora* you have initially mutagenized a wild type strain by methyl methane sulphonate. Initially you have obtained 745 strains who failed to grow on minimal media lacking leucine, but all of them have grown fine on rich YPD medium. Outline an approach how you would ascertain if all 745 leucine-auxotrophic mutant strains belong to one class. If not, how you would classify them experimentally using systematic genetic analysis? 4

(b) Mention two advantages of using *Saccharomyces cerevisiae* as a genetic tool. 1