

Branch - **APPLIED MICROBIOLOGY**
GENETICS & GENETIC ENGINEERING

Time: Three Hours

Maximum: 75 Marks

SECTION-A (10 Marks)Answer **ALL** questions**ALL** questions carry **EQUAL** marks

(10 × 1 = 10)

Module No.	Question No.	Question	K Level	CO
1	1	A phenotype that is expressed only when the individual has two copies of the allele is (i) Dominant (ii) Recessive (iii) Codominant (iv) Incomplete	K1	CO1
	2	When does the same genotype result in different degrees of phenotypic expression? (i) Penetrance (ii) Expressivity (iii) Pleiotrophy (iv) Epistasis	K2	CO1
2	3	_____ protein is essential for the formation of the holiday junction during homologous recombination (i) RecA (ii) RuvC (iii) DNA Ligase (iv) SSB	K1	CO2
	4	In bacterial conjugation, Hfr strain is characterised by (i) Free F plasmid (ii) Integrated F plasmid (iii) Lack of F factor (iv) RNA-based transfer	K2	CO2
3	5	The <i>loxP</i> - <i>Cre</i> system is primarily used for _____ genetic event (i) Transposition (ii) Site-specific recombination (iii) DNA Repair (iv) RNA Splicing	K1	CO3
	6	"Petite mutant" in yeast genetic depicts (i) High growth rate (ii) Deficiency in respiratory metabolism (iii) Resistance to phages (iv) Ability to fix nitrogen	K2	CO3
4	7	Enzyme to remove phosphate groups from the 5' ends of DNA to prevent self-ligation (i) Polymerase (ii) Alkaline phosphatase (iii) Methylase (iv) Helicase	K1	CO4
	8	Primary advantage of Phagemid vector over a standard plasmid vector (i) Larger insert size (ii) Ability to produce single-stranded DNA (iii) Lower metabolic load (iv) Higher copy number	K2	CO4
5	9	"SAGE" in transcriptomics stands for (i) Simple Analysis of Gene Elements (ii) Serial Analysis of Gene Expression (iii) Systematic Analysis of Genome Entities (iv) Standard Assay for Gene Evaluation	K1	CO5
	10	In the Maxam-Gilbert method of sequencing, _____ is used to cleave the DNA (i) Dideoxynucleotides (ii) Chemical modification and cleavage (iii) DNA Polymerase (iv) Fluorescent dyes	K2	CO5

Cont...

Module No.	Question No.	Question	K Level	CO
1	11.a.	Illustrate the extensions of Mendelian principles with specific focus on how pleiotropy and epistasis.	K2	CO1
	(OR)			
	11.b.	Compare and contrast the molecular basis of Nucleotide Excision Repair (NER) and Base Excision Repair (BER).		
2	12.a.	Analyze the molecular differences between conjugation models in bacteria.	K4	CO2
	(OR)			
	12.b.	Examine the role of RecA and RuvABC proteins in the Double Strand Break Repair model of recombination.		
3	13.a.	Differentiate between the lytic and lysogenic cycles of Phage Lambda, focusing on the regulatory roles of cI and Cro proteins.	K4	CO3
	(OR)			
	13.b.	Analyze the genetic requirements and molecular mechanisms of transposition in bacterial Class II transposons.		
4	14.a.	Evaluate the criteria for selecting an appropriate high capacity vector (Cosmid vs. YAC) when constructing a genomic library for a complex organism.	K5	CO4
	(OR)			
	14.b.	Justify the use of cDNA libraries over genomic libraries for the study of eukaryotic gene expression.		
5	15.a.	Design a workflow for the expression of Bacillus and other host for cloning other than <i>E. coli</i> .	K6	CO5
	(OR)			
	15.b.	Formulate a comparative strategy using Next Generation Sequencing (NGS) to identify SNPs in two different bacterial strains.		

SECTION -C (30 Marks)

Answer ANY THREE questions

ALL questions carry EQUAL Marks

(3 × 10 = 30)

Module No.	Question No.	Question	K Level	CO
1	16	Describe the various types of chromosomal mutations (deletion, duplication, inversion, translocation) and their genetic implications.	K2	CO1
2	17	Analyze the process of gene transfer by conjugation, distinguishing between F ⁺ , F ⁻ , Hfr, and F' transfer mechanisms.	K4	CO2
3	18	Examine the regulation of gene expression in the lysogenic phase of Phage Lambda, focusing on the roles of cI, cII, and cIII proteins.	K4	CO3
4	19	Appraise the steps and enzymes involved in the construction and screening of a cDNA library.	K5	CO4
5	20	Create a comparative analysis of DNA sequencing methods, highlighting the shift from traditional Sanger sequencing to Whole Genome Shotgun sequencing.	K6	CO5

Z-Z-Z END