BIRLA INSTITUTE OF TECHNOLOGY AND SCIENCE, PILANI
Second Semester 2017-18
BIO F243 (GENETICS)
Comprehensive Examination

Total Marks=80M **Total Time: 3.0 Hrs.** **03.04.2018**

Question paper is divided into two parts. Attempt Part-A & B in separate answer book.

Part-A [40 Marks]

1. In a cross of *Limnea,* the snail contributing the egg wasdextral, but of unknown genotype. Both the genotype and the phenotype of other snail are unknown. All F_1 offspring exhibited dextral coiling. Ten of the F_1 snails were allowed to undergo self fertilization. One-half produced only dextrally coiled offspring, whereas the other half produced only sinistrally coiled offspring. What were the genotypes of the original parents? **[8.0 M]**

2. Parents ABC / abc X abc / abc

   Map : a_____10_____b_____20_____c
   Interference: 40%
   Given the above information, determine the kinds and frequencies of progeny genotype and phenotypes. **[8.0 M]**

3. (a) How is F' factors are formed? What role do they pay in bacterial gene transfer? **[4.0 M]**
   (b) The *Cro* gene is mutated in bacteriophage lambda. What effect it would generate on phage cycle when this infects a new host? **[4.0 M]**

4. A gram negative bacteria contains an operon which is responsible for the production of an enzyme needed to form a theoretical amino acid ceplon (cpl). The *cpl* operon is regulated by a separate gene, R, deletion of which causes loss of enzyme synthesis. In the absence of cpl, the enzyme is made. Mutations in the operator gene result in repression regardless of the presence of cpl. Is the operon under positive or negative control? Propose a model for (a) repression of the genes in the presence of cpl in wild-type cells and (b) the O^- mutations. **[8.0 M]**

5. (a) Six mutations are known to belong to three cistrons. From the results of the complementation test, determine which mutants are in the same cistron.

1	**2**	**3**	**4**	**5**	**6**	
0	+	+				**1**
	0		+	+		**2**
		0	+	0		**3**
			0		+	4
				0	+	5
					0	6

+ = complementation
0 = non complementation
Blank = not tested

[4.0 M]

(b) A non- lytic response usually is observed in lysogenic (λ)*E. coli* cells when conjugated with non-lysogenic Hfr donar or in cross between Hfr (λ) X F^- (λ). The donated prophage is almost never inherited by the recombinants. Lysis is very anomalous in crosses of Hfr (λ) X F^-. Explain these observations. **[4.0 M]**

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Part-B [40 Marks]

Q1. a) How is the function of a protein encoded by an oncogene different from that of the proto- oncogene? Tumor-suppressor genes are also called recessive oncogenes. Why? **4M**

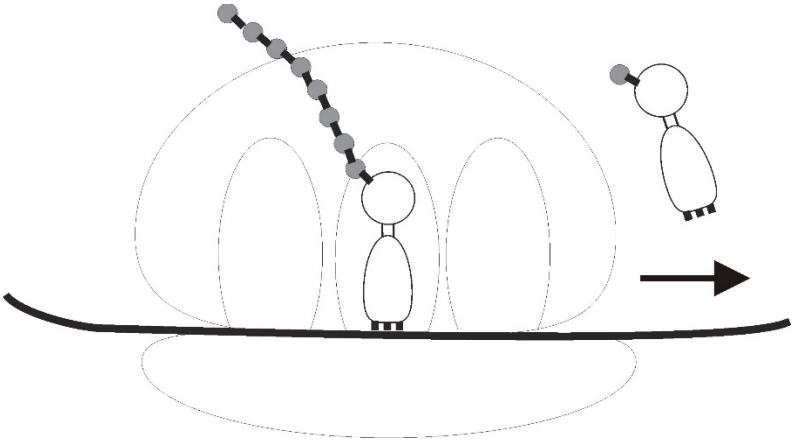
b) Five cell types are described below. Identify the normal version of Gene M, N, O, P or Ras as either a tumor suppressor gene or a proto-oncogene and give the phenotype of the cell that carries the two alleles described above. Choose transformed (i.e., has characteristics of a cancer cell) or NOT transformed. Justify **8M**

Cell	Affected Gene	Normal function of protein	Allele 1	Allele 2
1	Gene E	Protein E is a S phase cyclin	A mutation in promoter enabling cyclin expressing at all stages of cell cycle	Wild type
2	Gene F	Protein F prevents exit from G1 phase	A non-sense mutation that replaces the fourth codon with a stop codon	A deletion of entire gene
3	Gene G	Protein G stimulates apoptosis when activated	A mutation resulting in constitutively active protein P	A deletion of entire gene
4	Gene H	Protein H turns on a signal cascade that promotes cell cycle	A loss of function mutation	Wild type

Q2. During mismatch repair using the Mut system: **2+2=4M**

a) why is it necessary to distinguish between the template strand and the newly made daughter strand?
b) how is this distinguishing between the template strand and the newly made daughter strand accomplished?

Q3. In the given diagram, label the three tRNA sites, codons and anticodons, peptide and mRNA. List the sequence of events that will occur when the in-coming tRNA sets into its binding site. Redraw the diagram as it will appear immediately after the next peptide bond is formed. **6M**



Q4. In a Drosophila salivary chromosome, the bands have a sequence of 1 2 3 4 5 6 7 8. The homologue with which this chromosome is synapsed has a sequence of 1 2 3 6 5 4 7 8. What kind of chromosome change has occurred? Draw the synapsed chromosomes and the gametes formed **4M**

Q5. Diagrammatically represent the formation of initiation complex in eukaryotic transcription. What causes the release of RNA polymerase from the initiation complex during Eukaryotic transcription? **3+2=5M**

Q6. a) What is the role of geminin in DNA replication in eukaryotes **2M**

b) Differentiate between permissive and non-permissive model for termination of replication with the help of diagram **4M**

Q7. Working with an animal cell culture system, a student created random point mutations in the genes for the RNA polymerases. Individual cells with RNA polymerase mutations were isolated and used to generate a cell line that expressed that particular mutation. The levels of different RNAs expressed in each of the cell lines are given below. Which type of RNA polymerase (I, II, or II) appears to be mutated in each one of the cell lines. Explain. **3M**

Cell Line	RNA expression (%) relative to unmutated cells			
	Hexose kinase	U4 snRNA	18S rRNA	Tyrosine tRNA
Unmutated cells	100	100	100	100
Cell line A	100	30	98	40
Cell line B	20	90	100	95
Cell line C	98	96	43	100