Department of Biotechnology
Indian Institute of Technology Kharagpur

Subject: Genetics (BT31009)/ Genetics and Genetic Engineering (BT31201)

END-Autumn Semester–2022 Examination **Full Marks: 50**
Date of Exam: **November 22, 2022 Tuesday** Time: **03 hours (2:00 PM – 5:00 PM)**
Number of students: 54 (2+52)

Instruction: ***This question paper has three parts- A, B and C. Answer Part-A, Part-B and Part-C separately on the single answer script. You may write Part-A/B/C first, followed by Part-B/C/A or C/A/B. Do not intermingle the Part-A, Part-B and Part-C. Answer all the components of one question in one designated place. Answer precisely to the point.***

Part-A (MKM): Total marks = 25

Note: ***Perform/show the rough works/calculations corresponding to each question number in the right-hand-side or in a separate page mentioning question number.***

Q1. (A) A dark female butterfly and a dark male butterfly were crossed. F_1 progeny analysis showed that all the male butterflies are dark, half of the female butterflies are light and the rest are dark. Explain the inheritance pattern of phenotypes with appropriate allele designation, considering the female and male butterflies are heterogametic and homogametic, respectively. ***[3]***

Q1. (B) Explain briefly the two types of sex determination systems in eukaryotic systems, citing appropriate examples. ***[1]***

Q2. (A) One pure line legume plant species producing long fruits and white flowers was crossed with another pure line of the same species producing short fruits and purple flowers. Upon selfing of F_1 progenies, the resulting F_2 progenies showed the following phenotypes:

long fruits with purple flowers	299
short fruits with purple flowers	101
long fruits with pink flowers	601
short fruits with pink flowers	199
long fruits with white flowers	301
short fruits with white flowers	99

(i) Establish logically the dominant-recessive relationship of the traits/phenotypes involved in the inheritance. **(ii)** Write the appropriate genotypes of the two pure parental lines used to generate the F_1 progenies. ***[2+1]***

Q2. (B) A selective crossing was performed in a given plant species between F_1 x F_1 individuals producing colored seed phenotype. It was noticed that among the total number of 160 F_2 progenies, 100 plants produced colored seeds and rest produced colorless seeds. **(i)** Determine whether the F_2 progeny phenotypes followed the expected ratio of 3:1 or 9:7 or 13:3 for colored seeds and colorless

seeds. **(ii)** Based upon your analysis of inheritance of this either monogenic or polygenic trait, arrange all the genotypes into two phenotypic classes. *[2+1]*

Q3. (A) The following progenies were obtained upon test-crossing the female *Drosophila* which is heterozygous for three linked recessive genes (controlling the respective traits)- ***e*** (ebony body), ***st*** (scarlet eyes) and ***ss*** (spineless bristles):

Spineless	65
Scarlet, spineless	10
Ebony, scarlet	68
Scarlet	368
Ebony, scarlet, spineless	78
Ebony, spineless	355
Ebony	08
Wild type	72

st ss e^+

st^+ ss^+ e

P': st ss^+ e^+

st^+ ss e

(i) Determine and draw the linkage map with the correct gene order and corresponding map distance. **(ii)** Calculate the coefficient of coincidence (COC) and interference (I) on the basis of the above findings. *[3+1]*

Q3. (B) In a plant species, the following F_2 progenies were obtained upon test-crossing the F_1 trihybrid having the phenotypes of tall height, green leaves and red fruits:

Dwarf, yellow leaves, white fruits	1246
Tall, yellow leaves, white fruits	176
Dwarf, green leaves, white fruits	84
Tall, green leaves, red fruits	1250
Dwarf, yellow leaves, red fruits	4
Tall, yellow leaves, red fruits	88
Dwarf, green leaves, red fruits	174
Tall, green leaves, white fruits	6

Considering the dwarf height, yellow leaves and white fruits are three recessive phenotypes with the corresponding alleles- ***d***, ***y*** and ***w***, respectively in this plant species,
(i) Determine and draw the genetic map with the correct gene order and corresponding map distance. **(ii)** Calculate the coefficient of coincidence (COC) and interference (I) on the basis of the above findings. *[3+1]*

Q3. (C) Write <u>at least four reasons</u> (in bullet points) to justify why the genetic map is not exactly correlated with the physical map. *[2]*

Q4. (A) A diploid animal species has 8 pairs of chromosomes, numbered as **1** (one) to **8** (eight). Consider meiotic nondisjunction can take place occasionally before gamete formation, and the resulting gametes subsequently undergo fertilization to develop zygotes, each having the following genetic makeup:

dyW

DYw

dyw

DYW

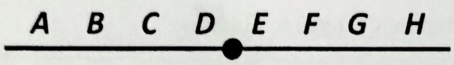
Comment on each of the zygote below (a) whether it is euploid or aneuploid; (b) mention the specific term to describe the individual's genetic makeup as accurately as possible. *[1 x 2 = 2]*

(i) **1111 2222 3333 4444 5555 6666 7777 8888**
(ii) **11 22 3 44 55 66 77 88**

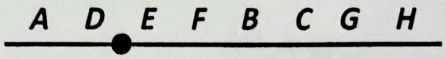
Q4. (B) Match column-I with column-II. *[0.5 x 4 = 2]*

Column-I	Column-II
1. Apple	a. Octaploid
2. Banana	b. Hexaploid
3. Strawberry	c. Tetraploid
4. Bread wheat	d. Triploid

Q4. (C) An organism is having a normal chromosome with the following gene order:



Name the specific type of chromosomal mutation depicted in each of the following the diagram: *[0.5 x 2 = 1]*

(i)


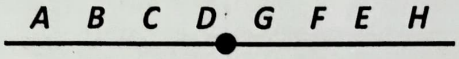
(ii)


Table: Chi-Square Probabilities

df	0.995	0.99	0.975	0.95	0.90	0.10	0.05	0.025	0.01	0.005
1	---	---	0.001	0.004	0.016	2.706	3.841	5.024	6.635	7.879
2	0.010	0.020	0.051	0.103	0.211	4.605	5.991	7.378	9.210	10.597
3	0.072	0.115	0.216	0.352	0.584	6.251	7.815	9.348	11.345	12.838
4	0.207	0.297	0.484	0.711	1.064	7.779	9.488	11.143	13.277	14.860
5	0.412	0.554	0.831	1.145	1.610	9.236	11.070	12.833	15.086	16.750
6	0.676	0.872	1.237	1.635	2.204	10.645	12.592	14.449	16.812	18.548
7	0.989	1.239	1.690	2.167	2.833	12.017	14.067	16.013	18.475	20.278
8	1.344	1.646	2.180	2.733	3.490	13.362	15.507	17.535	20.090	21.955

End of Part-A

Part-B (RD): Total marks = 12.5

Q5. (A) In order to cause a frameshift mutation, _____ must occur. *[1]*

a) The insertion of three nucleotides into the coding region
b) A missense mutation causing the insertion of a hydrophobic amino acid
c) A nonsense mutation leading to protein termination
d) One or two nucleotides must be inserted or deleted in the coding region

Q5. (B) Which of the following statements is true? *[1]*

a) Mutations are not heritable changes in the genome
b) The mutation occurs at a random basis within a genome
c) Recombination occurs when one part of chromosome breaks and joins with another chromosome
d) Transversions occur when Adenine changes to Guanine

Q5. (C) Consider a locus with two alleles, *A* and *a*. If the mutation rate from *A* to *a* is 0.86×10^{-3} and the mutation rate from *a* to *A* is 0.47×10^{-3}, what is the expected equilibrium frequency of *a*?

a) 0.65
b) 0.35
c) 0.55
d) 0.45

[1]

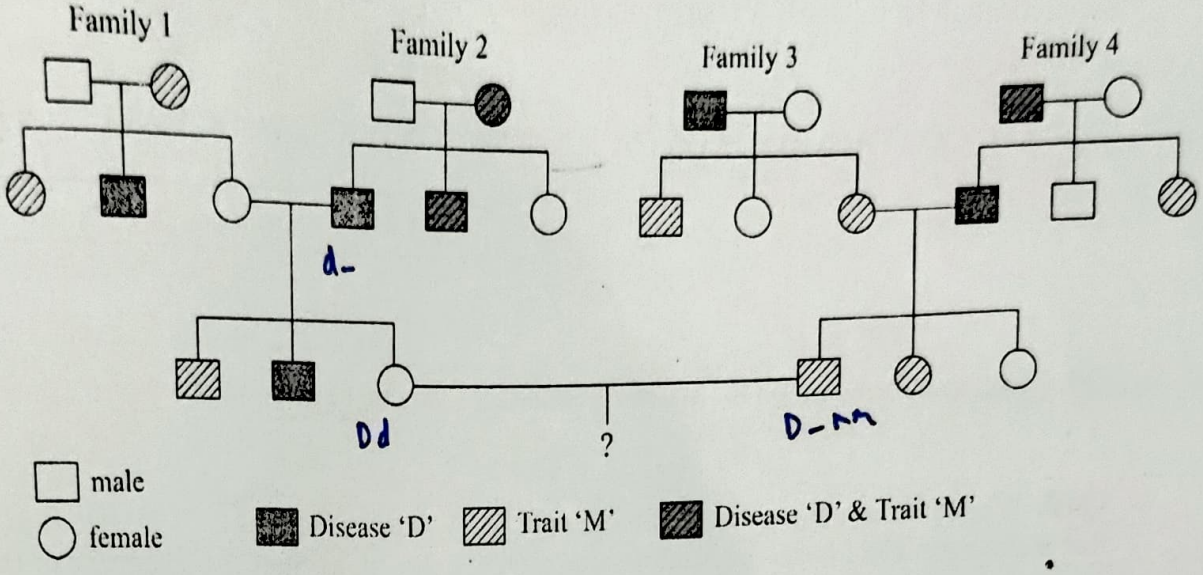
Q6. (A) Assume that a gene LDH has two alleles in a diploid yeast population – X and Y, in frequencies 0.6 and 0.4 respectively in generation 1. Also assume that the genotypes XX, YY, and XY have relative fitness values of 1, 0.5, and 0.8 respectively. Assuming effect of selection (but no mutation), calculate mean population fitness in generation 1 and calculate the allele frequencies in generation 2.

Q6. (B) Assume that allele X mutates to allele Y at a rate μ per generation. At what value of μ would the change in allele frequency of X due to selection be equal in magnitude to the change in allele frequency of X due to mutation from generation 1 to the next generation? *[2+2=4]*

Q6. (C) What do you understand by monosomy and trisomy? Explain trisomy 21 in this regard. *[1+0.5=1.5]*

Continued on the next page.....

Q7. Consider the family trees as shown below. The families are affected by one disease – disease 'D' and also show a trait 'M'. Disease D is caused by the allele 'd' of gene D and trait 'M' is caused by the allele 'm' of gene 'M'. Gene D and Gene M are not linked.



(A) Considering both disease 'D' and trait 'M' to be autosomal recessive, calculate the probability that the individual marked by '?' will have (i) disease 'D' (ii) trait 'M'

(B) Assume that the disease 'D' is X-linked recessive and trait 'M' is autosomal recessive. What is the probability that the individual marked by '?' will have (i) disease 'D' (ii) both disease 'D' and trait 'M', if this individual is male?

[2+2=4]

End of Part-B

Part-C (DS): Total marks = 12.5

Q8. Following sequence represents the coding strand of a gene. Design primers to mutate the tryptophan residue into alanine through site directed mutagenesis (codon chart provided). After the polymerization step, Dpn1, a restriction enzyme is also being used. Justify the necessity of Dpn1 enzyme in this process. ***[4+2]***

5' ATG CCG TAC GGA TCG ACA TGG CAA TCA GCC GAA GCA ATT CGA TAA 3'

Codon chart: Tryptophan- TGG, Alanine- GCG

Q9. Mention three common tools/strategies used for genetic engineering. ***[1.5]***

Q10. What are the unique features of *E. coli* BL21, BL21 (*DE3*) and BL21 (*DE3*) *pLysS* strains that make them ideal hosts for heterologous protein expression? State the advantage of BL21 (*DE3*) and BL21 (*DE3*) *pLysS* over BL21 as host strains for protein expression. ***[2+3]***