

**M.Sc. 1st Semester Examination, 2024**

**ZOOLOGY**

*( Cytogenetics )*

**PAPER – ZOOL-108**

*Full Marks : 25*

*Time : 1 hour*

**Answer all questions**

*The figures in the right hand margin indicate marks*

*Candidates are required to give their answers in their own words as far as practicable*

**GROUP – A**

- 1. Answer any two questions from the following :**
- 2 × 2**
- (a) Two X-linked mutations in Drosophila, white ivory and white apricot cause the eyes to be ivory and apricot colored**

*( Turn Over )*

respectively. When hemizygous white ivory males are crossed with homozygous white apricot females, the female progeny (trans-heterozygote) have light-apricot colored eyes. Are the white ivory and white apricot mutations in the same gene or different genes ?

- (b) Assuming that Hardy-Weinberg equilibrium has been established, what are the frequencies of heterozygote ( $Gm^{*+}/Gm^{*-}$ ) in the following Swedish population where  $Gm^{*+}$  is dominant over  $Gm^{*-}$  :

<u>No Tested</u>	<u>No Phenotypes</u>	
	$Gm^{*+}$	$Gm^{*-}$
160	108	52

- (c) Why do we call Rous sarcoma virus (RSV) a retrovirus ? How can RSV be transmitted from chicken to human ?

1 + 1

- (d) Order che A, che B, eda and sup D from the following data :

<u>Markers</u>	<u>% Cotransduction</u>
che A- eda	15
che A- sup D	7
che B- eda	48
che B- sup D	2
eda- sup D	0

### GROUP - B

2. Answer any *two* questions from the following :

- (a) In a London population of cats, Searle scored both males and females for the yellow genotype and found the following :

	<u>Numbers</u>		
	<u>+/+</u>	<u>+/y</u>	<u>y/y</u>
Females :	277	54	7
Males (hemizygous) :	311		42

What are the gene frequencies in this population ? Is this population in Hardy-Weinberg equilibrium ?

- (b) Determine the order and cotransduction frequency of *trp-pyr* and *trp-qts* from a three factor transduction error :-

Donor        *trp*<sup>+</sup> *pyr*<sup>+</sup> *qts*  
Recipient   *trp*   *pyr*   *qts*<sup>+</sup>

<u>Unselected Markers</u>	<u>Number</u>
<i>pyr</i> <sup>+</sup> <i>qts</i> <sup>+</sup>	22
<i>pyr</i> <sup>+</sup> <i>qts</i>	10
<i>pyr</i> <i>qts</i> <sup>+</sup>	68
<i>pyr</i> <i>qts</i>	0

- (c) You are studying a bacteriophage and trying to determine how many genes are required for the phage to infect and lyse the host bacterium. You have eight mutants, all of which are unable to lyse a particular host bacterium. You performed pairwise infections with each of the mutant strains and got the following results.

( 5 )

“+” = pair of phage lysed bacterium,  
“-” = pair of phage failed to lyse bacterium.

	M1	M2	M3	M4	M5	M6	M7	M8	wt
M1	-	+	+	-	-	+	+	+	+
M2		-	+	+	+	+	+	+	+
M3			-	+	+	-	-	-	+
M4				-	-	+	+	+	+
M5					-	+	+	+	+
M6						-	-	-	+
M7							-	-	+
M8								-	+
wt									+

Determine the complementation groups and how many genes have you identified.

(d) Elucidate the role of p53 in the cellular response to DNA damage.

## GROUP - C

3. Answer any *one* question from the following :

8 × 1

(a) Hutt collected the following data from the families of Cornell University veterinary students :

<u>Mating</u>	<u>No. of Couples</u>	<u>No. of offspring</u>	
		Tasters	Non tasters
taster × taster	250	654	76
taster × non taster	150	354	205
non taster × non taster	<u>100</u>	7(?)	98
	500		

Calculate whether this population is in equilibrium with respect to genotypic frequencies.

(b) (i) Five different rII deletion strains of phage T4 were tested for recombination by pairwise crossing in E.coli B.

( 7 )

The following results were obtained, where + = r<sup>+</sup> recombinant produced and 0 = no r<sup>+</sup> recombinants produced.

	A	B	C	D	E
E	0	+	0	+	0
D	0	0	0	0	
C	0	0	0		
B	+	0			
A	0				

Draw a deletion map compatible with these data.

(ii) Seven different point mutants (1-7) of phage T4 were tested for recombination crosses in E.coli B with five deletion strains described above, where + = r<sup>+</sup> recombinants produced and 0 = no r<sup>+</sup> recombinant produced.

( 8 )

	A	B	C	D	E
1	0	+	0	+	+
2	+	0	0	+	+
3	0	+	0	+	0
4	+	+	0	+	0
5	+	0	0	0	+
6	0	+	0	0	+
7	+	+	0	0	+

In which regions of the map can you place the seven point mutations ?

[ Internal Assessment — 5 Marks ]

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