BIO 201: Genetics and Evolution
First Mid-Semester Examination, 12th September 2019
Total Marks: 28, Time: 1 Hour
Please write genotypes, reasons for your answers where ever necessary

1. a. For questions 1a and 1b, please give reasons for your answer.
The following mRNA codon key is needed to answer the next two questions:
GCC Alanine, AAU Asparagine, CCU Proline, GGA Glycine, UGG Tryptophan, UGA"Stop" (no amino acid), GAA Glutamic acid, GAG Glutamic acid, AGG Arginine, CCC Proline, CAU Histidine.

The following DNA sequence (coding strand) occurs near the middle of the coding region of a gene.
DNA50 55 60 65 5'—A A TG A A T G G G A G C C T G A A G G A G —3'
The corresponding mRNA sequence is shown below. The first triplet of nucleotides AAU is in frame for coding, and encodes Asparagine as the codon table above indicates.
mRNA50 55 60 65 5'—A A UG A A U G G G A G C C U G A A G G A G —3'

Which of the following DNA mutations is almost certain to result in a shorter than normal mRNA? (2)
a) A→G at position 50 b) G→A at position 53 c) C→A at position 58 d) None of the above

Substitutions in DNA do not change the length of the corresponding mRNA. The corresponding mRNA only contains the mutated base pair at the mutation site.

1. b. For the same DNA sequence, which of the following DNA mutations is almost certain to result in a shorter-than-normal *protein*? (2)
a) T→C at position 59 b) A→G at position 61 c) Insertion of a G after the G at position 54 d) None of the above

m-RNA: 5'-AAU GAA UGG GAG CCU GAA GGA G -3'
(50 over GAA, 55 over GAG, 60 over GAA)

Protein: 

after insertion of G after the G at position 54 :-

m-RNA: 5'- AAU GAA UGG GGA GCC UGA AGGAG -3'
(50 over GAA, 55 over GGA)

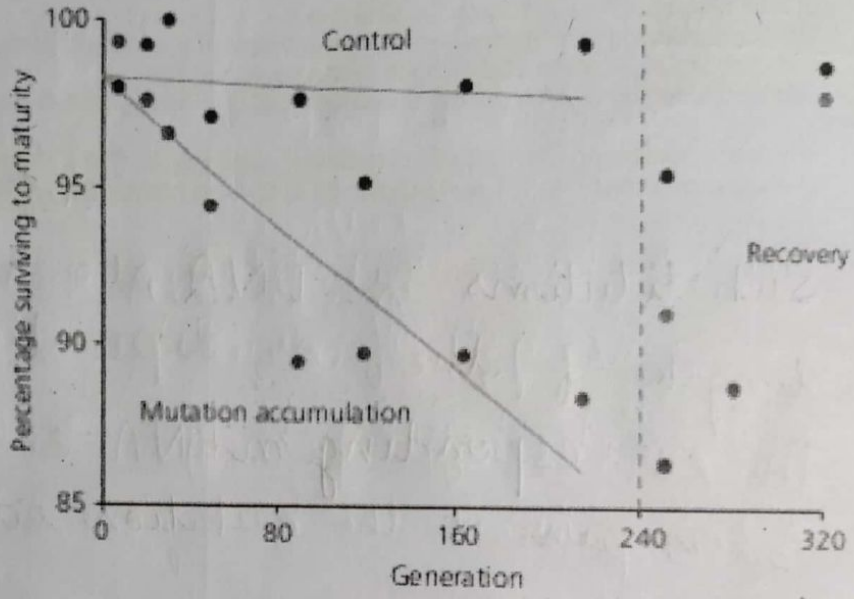
Protein: 
Stop codon

1

2. Denver et al (2004) conducted a mutation accumulation experiment with 72 lines of *C. elegans*. The mutation accumulation lines were propagated each generation with a single worm. The control populations were always maintained with a large number of individuals. The results are summarised in the figure below. Percentage surviving to maturity is a measure of fitness. (a) Since mutations are random and should be occuring in the control populations as well, why did the average fitness of the control population not decline over the first 240 generations? (b) After generation 240, mutation accumulation lines were maintained like control populations. The fitness of the mutation accumulation lines then improved between 240-320 generations. How can we explain this result?

(2 +2 = 4)

Caenorhabditis elegans



a) Mutations are random and occur at a low rate per base per generation. Mutations can be beneficial, deleterious or neutral. Most mutations are expected to be deleterious. Few are expected to be beneficial. In a large population, when random mutations occur in a few individuals and reduce their fitness, the low fitness individuals have to compete with the non-mutated, high fitness individuals. Therefore, in the long run, the low fitness individuals are eliminated and average fitness does not decline.

b) When mutation accumulation lines are maintained as large populations, random mutations will very rarely create individuals with increased fitness. These individuals will out compete the other low fitness individuals in the population. Hence, average fitness will increase.

3. Calico cats have large patches of colored fur. Tortoiseshell cats have very small color patches. Both these phenotypes are supposed to be because of random X chromosome inactivation (also called Lyonisation). Explain the difference between the two phenotypes based on the age of onset of Lyonization (is it early or late during embryonic development). (3)

- A gene having two alleles - A and a controls coat color.
  X^AX^A, X^AX^a → orange fur ; X^aX^a → Black fur
  [O → inactivated X-chromosome]
- Lyonisation being random for each embryonic cell; any given cell of embryo would end up as X^AO or X^aO.
- Once an embryonic cell decides to inactivate a particular X, all its progeny cells will inactivate the same X.
- All the skin tissues that arise from an embryonic cell having X^AO express orange fur while those arising from embryonic cells having X^aO express black fur.
- Larger patches of colored fur (in calico cats) may be caused by slightly earlier lyonisation during embryonic development. (The earlier the inactivation, the larger the patch of skin derived from each Lyonised progenitor embryonic cell).

4. If two black mice are crossed, ten black and three white mice result.
a. Which allele is dominant?
b. Which allele is recessive?
c. What are the genotypes of the parents? (1+1+2= 4)

BB , Bb → black bb → White

a) B allele for Black coat colour is dominant.

b) b allele for white coat colour is recessive.

c) Genotypis of parents :- Bb & Bb.

P_o :- Bb × Bb

↓

F_1 :- BB : Bb : bb

1 : 2 : 1

Black white

Black : White = 10 : 3 ~ 3 : 1

5. Two short-eared pigs are mated. In the progeny, three have no ears, seven have short ears, and four have long ears. Explain these results by diagramming the cross. (3)

S is dominant over s.

SS → long ears
Ss → Short ears
ss → no ears

P_0 :- Ss (Short) × Ss (Short)

↓

F_1 :- SS : Ss : ss
long ears : Short ears : no ears

Theoretical :- 1 : 2 : 1

Experimental :- 4 : 7 : 3

~ 1 : 2 : 1

6. A particular variety of corn has a gene for kernel color and a gene for height with the following phenotypes:
CC, Cc: purple kernels
cc: white kernels
TT: tall stem
Tt: medium height stem
tt: dwarf stem
Give the proportions of genotypes and phenotypes produced if a dihybrid plant is selfed. (4)

P_0 :- CCTT × cctt

↓

F_1 :- CcTt

Selfing of F_1 :- CcTt × CcTt

↓

F_2 :-

Genotypic Proportions

1 – CC TT – Purple, Tall
2 – CC Tt – Purple, Med.
1 – CC tt – Purple, dwarf
2 – Cc TT – Purple, Tall
4 – Cc Tt – Purple, Med.
2 – Cc tt – Purple, dwarf
1 – cc TT – White, Tall
2 – cc Tt – White, Med.
1 – cc tt – White, dwarf

Phenotypic Proportions :-

Purple, Tall : Purple, Med. :
Purple, dwarf : White, Tall :
White, med : White, dwarf

⇓

3 : 6 : 3 : 1 : 2 : 1

7. Based on the following Drosophila crosses, explain the genetic basis for each trait and determine the genotypes of all individuals:
white-eyed, dark-bodied female X red-eyed, tan-bodied male
F 1 : females are all red-eyed, tan-bodied; males are all white-eyed, tan-bodied
F 2 : 27 red-eyed, tan-bodied
24 white-eyed, tan-bodied
9 red-eyed, dark-bodied
7 white-eyed, dark-bodied
(No differences between males and females in the F 2 generation.) (6)

Eye Colour

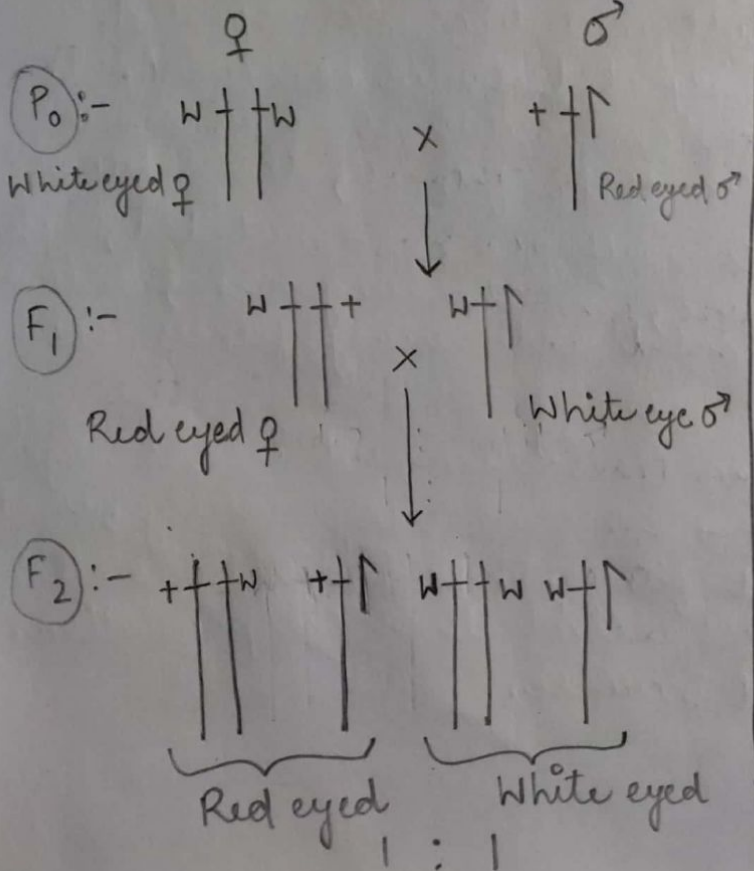
$F_1 \rightarrow$ Red : white = 1 : 1

$F_2 \rightarrow$ Red : White = (27+9) : (24+7)
= 36 : 31
~ 1 : 1

In the F_1, all the ♂ have same eye-colour as their mother.

X-linked

+ → Red w → white
+ is dominant over w.



Body colour

$F_1 \rightarrow$ all tan bodied

$F_2 \rightarrow$ tan : dark = (27+24) : (9+7)
= 51 : 16
~ 3 : 1

Autosome-linked

T → Tan t → dark
T is dominant over t.