7 **Questions: Mutability and Repair of DNA** November 2021

1) The DNA sequence of a gene from three independently isolated mutants is given here. Using this information, what is the most likely sequence of the wild-type gene in this region? Reason your answer.

mutant 1	ACCGTAATCGACTGGTAAACTTTGCGCG
mutant 2	ACCGTAGTCGACCGGTAAACTTTGCGCG
mutant 3	ACCGTAGTCGACTGGTTAACTTTGCGCG

ACCGTAGTCGACTGGTTAAACTTTGCGCG

2) When a particular mutagen identified by the Ames test is injected into mice, it causes the appearance of many tumors, showing that this substance is carcinogenic. 致癌. When cells from these tumors are injected into other mice not exposed to the mutagen, almost all of the new mice develop tumors. However, when mice carrying mutagen-induced tumors are mated to unexposed mice, virtually all of the progeny are tumor free. Why can the tumor be transferred horizontally (by injecting cells) but not vertically (from one generation to the next)?

The mutation are in somatic cells not in germ cells

3) When the *his*$^-$ *Salmonella* strain used in the Ames test is exposed to substance X, no *his* revertants are seen. If, however, rat liver supernatant is added to the cells along with substance X, revertants do occur. Is substance X a potential carcinogen for human cells? Explain.

Yes. The rat liver supernatant contains enzymes that convert substance X to a mutagen and hist revertants occur.

Our liver contain similar enzymes that process various substances, converting them into other forms that cause mutation and can ledd to cancer.

4) The following is a list of mutational changes. For each of the specific mutations described, indicate which of the terms at the end applies, either as a description of the mutation or as a possible cause. More than one term from the list can apply to each statement at the end.

1. an A–T base pair in the wild-type gene is changed to a G–C pair a, b, z.
2. an A–T base pair is changed to a T–A pair b, c
3. the sequence AAGCTTATCG is changed to AAGCTATCG f, i
4. the sequence AAGCTTATCG is changed to AAGCTTTATCG g, i
5. the sequence AACGTTATCG is changed to AATGTTATCG a, b, z
6. the sequence AACGTCACACACACATCG is changed to AACGTCACATCG f, h, k
7. the gene map in a given chromosome arm is changed from *bog-rad-fox1-fox2-try-duf* (where *fox1* and *fox2* are highly homologous, recently diverged genes) to *bog-rad-fox1-fox3-fox2-try- duf* (where *fox3* is a new gene with one end similar to *fox1* and the other similar to *fox2*) g, k
8. the gene map in a chromosome is changed from *bog-rad-fox1-fox2-try-duf* to *bog-rad-fox2-fox1-try-duf* d, h
9. the gene map in a given chromosome is changed from *bog-rad-fox1-fox2-try-duf* to *bog-rad-fox1-mel-qui-txu-sqm* e, f, g, h

pair with: a. transition, b. base substitution, c. transversion, d. inversion, e. translocation, f. deletion, g. insertion, h. X-ray irradiation, i. intercalator, k. unequal crossing-over

2. deanimation

large deletion

5) Over a period of several years, a large hospital kept track of the number of births of babies displaying the trait achondroplasia. Achondroplasia is a very rare autosomal dominant condition resulting in dwarfism with abnormal body proportions. After 120,000 births, it was noted that there had been 27 babies born with achondroplasia. One physician was interested in determining how many of these dwarf babies result from new mutations and whether the apparent mutation rate in his area was higher than normal. He looked up the families of the 27 dwarf births and discovered that 4 of the dwarf babies had a dwarf parent. What is the apparent mutation rate of the achondroplasia gene in this population? Is it unusually high or low?

27-4=23 mutant gametes

of 240,000 gametes

freq: $\frac{23}{240,000}$ → 9.6×10^{-5}

$\frac{23}{1 \text{ in}}$

higher than normal

(mouse about $2 \sim 12 \times 10^{-6}$