Name of the Student:_____
Max. Marks : 24 Marks **Time : 24 Minutes**

Q1.

Mycobacterium tuberculosis causes tuberculosis. The DNA of *M. tuberculosis* contains a direct repeat (DR) region. The DR region consists of 43 different, non-coding base sequences called spacers. Each spacer is found in a specific place in the DR region.
In different strains of *M. tuberculosis*, some of these spacers have been lost.

(a) (i) The DR region consists of non-coding base sequences.

What is meant by a non-coding base sequence?

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_____

(1)

(ii) Name the process by which the base sequence of a spacer is lost from a DR region.

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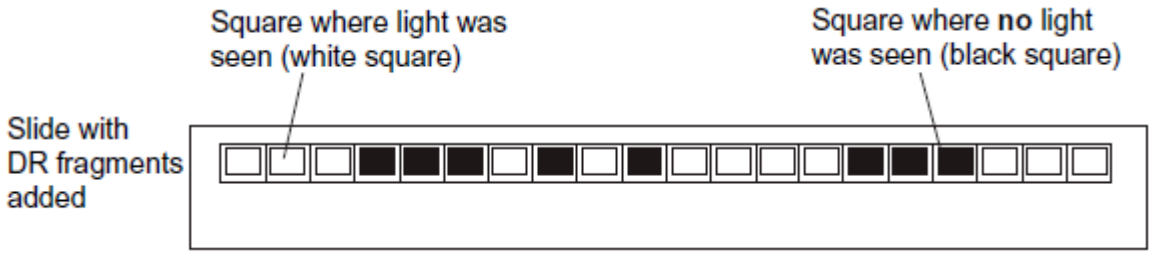
(1)

Scientists investigated the DR regions of different strains of *M. tuberculosis*. They produced a DNA probe for each of the 43 spacer sequences. Each probe was:

- labelled with a fluorescent marker that gave off light if the probe attached to its complementary spacer
- attached to a particular square on a slide.

They obtained samples of the DR region from each strain. These were cut into small single-stranded DNA fragments. The fragments from each strain were added to a slide with the DNA probes attached. The diagram below shows their results for one strain of *M. tuberculosis* with 20 of the probes.



(b) The scientists cloned the DR region DNA *in vitro* before testing for the presence of spacers.

Give the name of the method they used to clone the DNA *in vitro*.

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(1)

(c) Explain how the use of DNA probes produced the results in the diagram.

(3)

(d) Doctors can use the method with DNA probes to identify the specific strain of *M. tuberculosis* infecting a patient. This is very important when there is an outbreak of a number of cases of tuberculosis in a city.

Suggest and explain why it is important to be able to identify the specific strain of *M. tuberculosis* infecting a patient.

(2)
(Total 8 marks)

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Q2.

Imatinib is a drug used to treat a type of cancer that affects white blood cells. Scientists investigated the rate of uptake of imatinib by white blood cells. They measured the rate of uptake at 4°C and at 37°C.

Their results are shown in the table.

	Mean rate of uptake of imatinib into cells / µg per million cells per hour	
Concentration of imatinib outside cells / µmol dm^{-3}	**4°C**	**37°C**
0.5	4.0	10.5
1.0	10.7	32.5
5.0	40.4	420.5
10.0	51.9	794.6
50.0	249.9	3156.1
100.0	606.9	3173.0

(a) The scientists measured the rate of uptake of imatinib in µg per million cells per hour. Explain the advantage of using this unit of rate in this investigation.

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(2)

(b) Calculate the percentage increase in the mean rate of uptake of imatinib when the temperature is increased from 4°C to 37°C at a concentration of imatinib outside the cells of 1.0 µmol dm^{-3}.

Give your answer to one decimal place.

Answer _____

(2)

(c) Imatinib is taken up by blood cells by active transport.

(i) Explain how the data for the two different temperatures support this statement.

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(2)

(ii) Explain how the data for concentrations of imatinib outside the blood cells at 50 and 100 μmol dm^{-3} at 37°C support the statement that imatinib is taken up by active transport.

(2)
(Total 8 marks)

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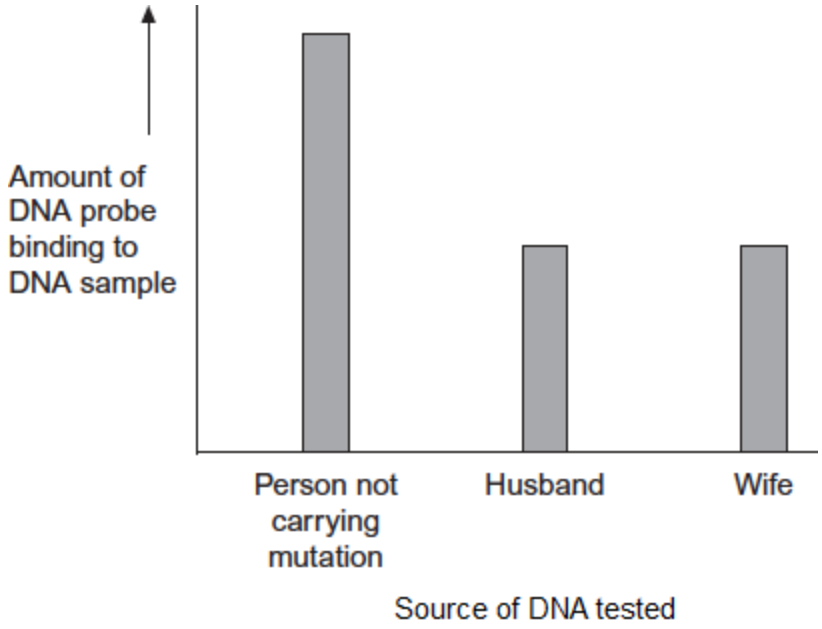
Q3.

A husband and wife wanted to know whether they were carriers of the mutated form of a gene. This mutation is a deletion that causes a serious inherited genetic disorder in people who are homozygous.

A geneticist took samples of DNA from the husband and the wife. He used a DNA probe to look for the deletion mutation. The DNA probe was specific to a particular base sequence in an exon in the gene. Exons are the coding sequences in a gene.

The geneticist compared the couple's DNA with that of a person known not to carry this mutation.

The chart shows the geneticist's results.



(a) The geneticist told the couple they were both carriers of the mutated gene. Explain how he reached this conclusion.

(3)

(b) The DNA probe the geneticist used was for an exon in the DNA, **not** an intron. Explain why.

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(3)

(c) To make the DNA probe, the geneticist had to find the base sequence of the normal gene. Once he had copies of the gene, what methods would he use to find the base sequence of the gene?

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(2)

(Total 8 marks)

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