Science-2 ROMICA RAISINGHANI
Assignment-3 2021101053

Ans1) Charles Darwin's observations due to natural selection.
during his voyages to Galapagos Islands helped him develop his theory of evolution by natural selection. Some of his conclusions were:

1) Species change over time:
Darwin observed that the finches and tortoises on the different islands had unique traits that were adapted to their particular environments. He realized that these traits had evolved over time in response to different ecological conditions.

2) Natural selection is the mechanism of evolution:
Darwin proposed that the environment selects for certain traits that confer a survival or reproductive advantage. Individuals with these traits are more likely to survive and pass on their genes to the next generation, leading to the gradual evolution of new species.

3) Common ancestry:
Darwin observed that many species on the Galapagos Islands resembled species on the South American mainland, but with adaptations to their island habitats. He concluded that these species had descended from a common ancestor and had diverged over time

4) Variation within species:
Darwin observed that there was considerable variation within populations of the same species, and that this variation provided the raw material for natural selection to act upon.

Ans2) It is believed that RNA is the most likely biopolymer to have evolved first. There are several reasons to support this hypothesis:

1) RNA is capable of both storing genetic information and catalyzing chemical reactions. This dual function suggests that RNA could have been the first self-replicating molecule capable of directing its own replication and catalyzing the synthesis of other macromolecules.

2) RNA is simpler than DNA and proteins, both in terms of chemical structure and synthesis. RNA can be synthesized in a laboratory under conditions that mimic prebiotic Earth, using simple building blocks such as nucleotides and ribose.

3) RNA is found in all living organisms, indicating its essential role in the evolution of life. Additionally, RNA is a critical component of many biological processes, including protein synthesis

and regulation of gene expression.

4) Studies have shown that RNA can undergo spontaneous self-assembly, forming complex structures such as ribozymes and ribosomes. These structures are essential for many cellular processes, including translation of genetic information into proteins.

Ans3) Microbiome refers to the collection of microorganisms, including bacteria, viruses, fungi and other microbes that live in and on our body. The microbiome plays many important roles in our health and well-being including:

1) Digestion: Microbiome helps to break down food and extract nutrients from it, which can help us to maintain a healthy weight and prevent nutrient deficiencies.

2) Immune function: Microbiome helps to train and regulate our immune system, which can help to protect us from infectious diseases.

3) Brain function: Microbiome has been linked to a variety of brain-related functions, including mood, cognition and behaviour.

4) Protection against pathogens: Microbiome helps to prevent harmful bacteria and other pathogens from taking up residence in our body.

5) Synthesis of vitamins and other important molecules: Some microbes in the microbiome can produce vitamins and other molecules that are important for our health.

6) Regulation of inflammation: Microbiome can help to regulate inflammation in our body, which is important for preventing chronic diseases such as heart attacks, diabetes and cancer.

Overall, the microbiome plays a critical role in maintaining our health and wellbeing and disruptions to the microbiome have been linked to a variety of health problems.

Ans4)

i) The mRNA sequence can be translated into a polypeptide by using the genetic code. Each group of three nucleotides, called a codon, specifies a particular amino acid or a stop signal. Here is the translation of the given mRNA sequence into a polypeptide:

5' AUG GUG GCC UAU CAU UAG GGG CUU 3'

Met Val Ala Tyr His * Gly Leu

The start codon AUG specifies the amino acid methionine (Met), which is usually the first amino acid in a polypeptide.

The next codon, GUG, specifies the amino acid Valine (Val).

The third codon, GCC, specifies the amino acid Alanine (Ala).

The fourth codon, UAU, specifies the amino acid Tyrosine (Tyr).

The fifth codon, CAU, specifies the amino acid Histidine (His)

The sixth codon, UAG, ~~specifies~~ is a stop codon, which signals the end of the polypeptide

The last codon, GGG, specifies the amino acid Glycine (Gly), which will not be included in the final polypeptide because it comes after the stop codon.

Therefore, the amino acid sequence of the polypeptide encoded by the given mRNA sequence is Met - Val - Ala - Tyr - His.

subsequent codons, causing a frameshift mutation. The remaining codons are now read in a different frame, leading to a different amino acid sequence. The new polypeptide sequence is :

Met - Val - Ala - Leu - Ser - Leu - Gly - Ala

Therefore, the insertion of an extra C between the third and fourth bases of the mRNA sequence causes a frameshift mutation and alters the amino acid sequence of the resulting polypeptide.

ii) If we replace U with A we get the following sequence :

5' AUG GUG GCC UAA CAU UAG GGG CUU 3'

Therefore, let us now divide it into triplets as follows :

5' AUG - GUG - GCC - UAA - CAU - UAG - GGG - CUU 3'

Now, we replace the triplets with the amino acids using the codon table as follows :

AUG → Met
GUG → Val
GCC → Ala
UAA → stop codon
CAU → His
UAG → stop codon
GGG → Gly
CUU → Leu

Therefore, the amino acid sequence is :

Met - Val - Ala

Thus, UAA forms a stop codon that does not specify any amino acid and signals the termination of translation. As a result, the polypeptide chain being synthesized would be terminated.

iii) The new sequence formed after inserting an extra C between the third and fourth bases is as follows :

5' AUG C GUG GCC UAU GAU UAG GGG UUU 3'

Let us divide the above sequence into triplets :

5' AUG - CGU - GGC - CUA - UCA - UUA - GGG - GCU - U 3'

Let us replace the triplets with amino acids with the help of codon table :

AUG → Met
CGU → Arg
GGC → Gly
CUA → Leu
UCA → Ser
UUA → Leu
GGG → Gly
GCU → Ala

the amino acid sequence is as follows:

Met-Arg-Gly-Leu-Ser-Leu-Gly-Ala

The change of a singe nucleotide in the ~~codon~~ therefore, the insertion of an extra C between the third and fourth bases of the mRNA sequence causes a frameshift mutation and alters the amino acid sequence of the resulting polypeptide.

Ans 5) BamHI is not a good endonuclease for cutting the SARS-CoV-2 genome. Here are the reasons:

1) BamHI is a type II restriction endonuclease that recognizes and cuts the DNA sequence GGATCC. This sequence occurs infrequently in the SARS-CoV-2 genome, with only two occurrences in the entire genome.

2) Restriction endonucleases are used to cut DNA at specific locations to create fragments that can be analyzed or manipulated. Since BamHI is not a good match for the SARS-CoV-2 genome, it would not produce many fragments that are useful for analysis.

3) The SARS-CoV-2 genome is very large, consisting of about 30,000 base pairs. A restriction endonuclease that recognizes a sequence that occurs infrequently in the genome would not be efficient for cutting the genome into manageable fragments.

4) There are other restriction endonucleases that are better suited for cutting the SARS-CoV-2 genome. For example, enzymes such as BstUI and MluI recognize and cut more frequently occurring DNA sequence in the genome, making them more efficient for fragmenting the genome.

Therefore, while BamHI is a useful enzyme in many applications, it is not a good choice for cutting the SARS-CoV-2 genome.

Ans 6)

i) No, the two enzymes will not result in the same number of fragments. This is due to the fact that both the enzymes recognize different DNA sequences and will cut the DNA at different locations.

BamH I recognizes the sequence "GGATCC" and cuts between the two G's, creating "sticky ends" that has "G" on one strand and "C" on other strand. Bgl II recognizes the sequence "AGATCT" and cuts between the two A's, creating sticky ends with an "A" on one strand and "T" on other strand. Therefore, the two enzyme will produce different fragments with different sizes when used on a random DNA sequence.

ii) The advantage of having a pair of restriction enzymes like BamH I and Bgl II, which recognize different DNA sequences but leave the same sticky ends, is that they can be used together in a cloning strategy to insert a foreign DNA fragment into a plasmid vector.

For example, if we have a plasmid vector with a BamH I site and a foreign DNA fragment with a Bgl II site, we can use both enzymes to create complementary sticky ends that will anneal to each other and ligate the foreign DNA fragment into the plasmid vector. This strategy is called a "blunt-end-ligation" and it allows for precise control over the orientation and location of the foreign DNA fragment within the plasmid vector.

Alternatively, if we have a plasmid vector with a BamH I site and a foreign DNA fragment with a BamH I site, we can use the Bgl II enzyme to create a complementary sticky end that will anneal to the BamH I site on the plasmid vector, allowing for ligation of the foreign DNA fragment into the plasmid vector. This strategy is called a "sticky-end-ligation" and it allows for high efficiency and specificity of cloning.

Ans 7) - Cloning and PCR are both techniques used to make copies of DNA, but they differ in their methodology and applications. Here are the advantages and limitations of cloning over PCR:

Advantages:

1) Cloning can produce large quantities of DNA, while PCR is limited to a certain amount of DNA that can be amplified.

2) Cloning can produce longer DNA fragments than PCR, which is limited to fragments of upto a few kilobases in length.

3) Cloning can produce DNA that is free of errors, while PCR can introduce errors into the amplified DNA.

4) Cloning can be used to express the cloned DNA in a host organism, allowing for the production of large quantities of proteins or other products.

5) Cloning can be used to create multiple copies of a DNA sequence that is difficult to amplify by PCR.

Limitations:

1) Cloning can be time-consuming and requires specialized equipment and expertise.

2) Cloning may require the use of vectors or other cloning agents, which can introduce their own biases or limitations.

3) Cloning may not be suitable for certain applications, such as amplifying DNA from very small samples or from degraded or ancient DNA.

4) Cloning can introduce mutations or changes in the original DNA sequence, particularly during the cloning process itself.

5) Cloning can be relatively expensive compared to PCR, particularly for large-scale production of DNA.