Science-2 - Part-2 :

Assignment-1 :

NAGA MANOHAR
2021101128

① The conclusions that Charles Darwin made based on his observations during his voyage across Galapogas islands are :-

① In each island, there were unique birds, species and tortoises and no two islands had exactly the same kind of species, though similar to those found in the nearest island.

② The difference were related to the different environmental conditions that existed on each island.

② Natural Selection :- Darwin realised that the animals and plants that were best fit to their environment had a better chance of surviving and reproducing. Thus this lead to gradual evolution of species overtime.

③ Adaptation to the Environment :-
Darwin observed that the animals & plants on each island were adapted to environmental conditions of that Island only.
Ex :- the size & structure of beaks of birds were depending on the food available on that particular island.

and this happens by Natural selection

④ Darwin also concluded that all living beings on Earth shared a common ancestry. He believed that different species had evolved from a common ancestor over millions of years.

Natural selection (→) Survival of the Fittest

⑤ Individuals in a population exhibit variable triats i- variations

⑥ Many traits are heritable

⑦ Species adapt to their environment

⑧ Limited Resources

⑨ Competition for survival

(2)

RNA would have evolved first among the 3 (DNA, RNA, proteins).

Reasons behind the hypothesis:

(1) RNA is thought to have played a central role in the origin of life. The RNA world hypothesis proposes that RNA was first self replicating molecule on earth and that it served as the precursor to DNA and proteins

(2) RNA is capable of both storing genetic information and catalysing chemical reactions. Thus its more versatile when compared to DNA & protein which can only perform one of the 2 things.

(3) It's easier & simpler to synthesize the RNA. RNA could be synthesized by simple chemical reactions on the Early Earth.

(4) The genetic code is based on RNA suggesting the RNA was present before DNA or proteins

(5) We have evidence that RNA can be formed spontaneously from simple precursors, such as nucleotides in laboratory experiments simulating the conditions of the early Earth.

Thus RNA is likely evolved before DNA and Protein

③

Microbiome

There are trillions of microbes (microorganisms like bacterial, viruses and fungi) in our body, most or large part of them are in the small & large intestine

① It acts like an extra organ, helping us to digest molecules in our food that we couldn't break down ourselves, even can steal genes in order to help us digest exotic food.

② The Microbiome influences our health and behaviour

③ Generally in a healthy body the symbiotic & pathogenic microbes coexist peacefully, we become unhealthy when there is an imbalance

④ Metabolism :- The microbiome has been linked to metabolism and the regulation of weight, its disruption resulted in metabolic disorders like obesity

⑤ Skin health :- The microbiome on skin helps by protecting us from external pathogens.

⑥ Helps Immune System function (Gut microbes)
The microbiome helps to train and regulate the Immune system, which plays a key role in protecting body against infections & diseases.

- the gut microbes train the immune system
- immune system is vital in response to covid-19

⑦ Mental Health:

They may play a role in mental health, by the regulation of stress and anxiety.

- The diet that fits us is decided by the microbiome we have

Sulfite reducing microbes in gut — decide whether paracetamol is toxic to our liver or not.

(4)

(i) The first step is to divide the mRNA sequence into codons.

A codon is a sequence of three nucleotides that codes for a specific amino acid.

In this case codons are

Given =) 5' AUG GUG GCC UAU CAU UAG GGG CUU 3'

Codons :- AUG GUG GCC UAU CAU UAG GGG CUU

AUG - met (methionine)

GUG - val (valine)

GCC - Ala (Alanine)

UAU - Tyr (Tyrosine)

CAU - His (Histidine)

UAG - Stop codon

Here, UAG is the stop codon =) end of protien sequence

∴ polypeptide encoded by given mRNA sequence is

Met-Val-Ala-Tyr-His

(ii) The single base mutation at the twelfth base of the mRNA sequence changes U to A (U→A)

Thus the original codon UAU that coded for tyrosine is changed to UAA which is a stopcodon

New codons:

⇒ AUG GUG GCC UAA CAU UAG GGG CUU

AUG → Met
GUG → val
GCC → Ala
UAA → stop codon

Thus, new genetic code according to codon usage table is AUG-GUG-GCC-UAA (stopcode)

AUG - met (methionine)
GUG - val (valine)
GCC - Ala (Alanine)
UAA - Stop code

polypeptide sequence is Met-val-Ala

(iii)
if an extra 'C' were inserted between the third and fourth bases i.e., between G's then mRNA sequence will be

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

Met Arg Gly Leu Ser Leu Gly Ala

polypeptide sequence resulting from above mRNA sequence is

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

(5)

BamHI is a type II restriction endonuclease that is commonly used in molecular biology for cutting DNA.

It recognizes the palindrome sequence of 5'-GGATCC-3' and cleaves the DNA between 2G nucleotides.

Firstly, we need to analyse the SARS-CoV-2 genome sequence for the presence of BamHI recognition sites.

The SARS-CoV-2 genome is approximately 30kb in length and consists of single stranded RNA molecule.

The reference genome sequence for SARS-CoV-2 genome (NC-045512.2) doesn't contain any BamHI recognition sites.

Therefore,

BamHI cannot be directly used to cut the SARS-CoV-2 genome.

However, even if a BamHI recognition site were present within the SARS-CoV-2 genome, it may not be optimal choice for cutting the genome efficiently.

Because the SARS-CoV-2 genome is much longer and more complex than the typical plasmid or PCR product that restriction enzymes are commonly used to cut.

Additionally the genome contains regions of high GC content and secondary structures, which may make it difficult to efficiently cut with some restriction enzymes.

But we can use BamHI indirectly to study the SARS-CoV-2 genome,

Eg: Researchers could use BamHI to cut a plasmid vector that has a BamHI site, then insert a specific fragment of the SARS-CoV-2 genome into plasmid vector.

This modified plasmid could then be used as a tool to study the function of the SARS-CoV-2 genome fragment.

Hence,

BamHI is NOT a good restriction endonuclease for cutting the SARS-CoV-2.

But it can be used to study it indirectly.

(6)

BamH I: ------G|G A T C C------

BglII : ------A|G A T C T------

(i) No, the two enzymes will not necessarily result in the same number of fragments in a random DNA sequence.

As the No. and size of the fragments generated will depend on the specific DNA being cut, and whether the recognition sequences for these enzymes occur once (or) multiple times within the sequence.

Additionally, the distance between the recognition sites will also influence the size of the resulting fragments.

So, if a DNA sequence contains multiple recognition sites for BamHI (or) BglII, the enzyme will cleave the sequence at each site, resulting in more fragments than a sequence with only a single recognition site.

Conversely if the recognition sites are far from each other, larger fragments will be generated.

Therefore, the number and size of fragments produced by BamHI and BglII will depend on the DNA sequence being cut and the location of their recognition sites within that sequence.

(ii)
The advantage of having a pair of restriction enzymes (Rt's) (BamHI & BglII) is it allows for easier manipulation and ligation of DNA fragments.

Ent 2
If 2 different DNA sequences are cut with BamHI and BglII, the resulting fragments will have compatible sticky ends that can be easily ligated together.
This creates a "fusion product" that combines that two different DNA sequences into a single recombinant sequence.

This technique is known as restriction enzyme digestion and ligation, is commonly used in molecular biology research to clone and manipulate DNA sequences.

The use of restriction enzymes (RE's) that produce the same sticky ends simplifies the process of creating recombinant DNA sequences, as it allows for precise and efficient joining of DNA fragments

Furthermore, the use of different restriction enzymes with the same sticky ends provides flexibility and versatility in the cloning process, as different combinations of enzymes can be used to create a variety of recombinant DNA constructs. This is particularly useful when attempting to clone complex DNA sequences, as it allows for the creation of more complex constructs with greater precision and accuracy

Q2 consider the DNA sequence that contains 2 BamHI sites and 1 BglII site

5'-GATCCGATCCGATCTAGCTAGCTAGC-3'

① if we digest this sequence with only BamHI, we will obtain 3 fragments

5'-GATC-3', 5'-GGATC-3', 5'-GATCCGATCTAGCTAGC
TAGC-3'

(2) if we digest the same sequence with only BglII we will obtain 2 fragments

5'-GATC-3', 5'-GGATC-3' 5'-GATC-3' 5'TAGCTAGCTAGC
-3'

Here
2 BamHI sites are cut by BamHI, generating the first and third fragments and the BglII site is cut by BglII, generating the 4th fragment.

Thus, the advantage of using a double digestion is that it allows us to generate DNA fragments with defined ends that can be ligated to other fragments with complementary ends.

~~This is true~~

(7) cloning and PCR (polymerase chain Reaction) are two commonly used techniques for making copies of DNA. The following are the advantages and limitations of cloning over PCR is

Advantages:

(1) cloning can preserve epigenetic modifications such as DNA methylation, histone modification, which are important for regulating gene expression. PCR doesn't preserve epigenetic modifications.

(2) It can Amplify larger fragments of DNA than PCR. PCR is limited in the size of the DNA fragment that it can amplify, usual around 10kb.
But Cloning can amplify much larger fragments making it useful for generating large amounts of DNA.

(3) cloning can produce stable long term copies of DNA, which can be stored for a long time. This makes it useful where long-term storage is necessary like bio-technology and Genetic engineering.

Limitations:

① Time Consuming: It involves several steps, which include restriction enzyme digestion, ligation and transformation :) these can take several days to complete
But PCR can amplify the DNA in just few hours.

② It requires specialised equipments, such as bacterial culture system (which can be expensive and time consuming to set up).
whereas PCR requires a thermal cycler and some basic lab equipment.

③ Can Introduce Errors: into the amplified DNA such as mutations or rearrangements.
PCR is gives less errors compared to cloning.

Thus these are the advantages and limitations of cloning over PCR.