Biotechnology and Evolution

Name \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ mark \_\_\_\_\_/49

When Darwin put forward his theory of natural selection and Evolutions his main sources of evidence were Comparative anatomy, the fossil record, biogeography, variation in species and similarities within Genera. Since then other methods have been developed to support his theories. Comparative studies of DNA and proteins provide additional evidence for evolutions. Genomic information enables the construction of Phylogenetic trees.

Biotechnological techniques are needed for this. The main techniques to be looked at in this topic will be: PCR, the use of Bacterial enzymes and Gel electrophoresis to facilitate DNA sequencing of genomes.

When Homo sapiens first migrated out of Africa around 60,000 years ago at least two other species of hominid existed in Europe and Asia: Neanderthals and Denisovans. As Homo sapiens migrated through Eurasia, they met the Neanderthals and interbred. According to one theory, Neanderthals, Denisovans, and all modern humans are descended from the ancient human Homo heidelbergensis. Between 300,000 to 400,000 years ago, an ancestral group of H. heidelbergensis left Africa and then split shortly after. One branch ventured north-westward into West Asia and Europe and became the Neanderthals. The other branch moved east, becoming Denisovans. By 130,000 years ago H. heidelbergensis in Africa had become Homo sapiens.

Studying the evolutionary relationship between these different groups has been done a in a number of ways. Comparative genomics is one such method.

Homo sapiens are still alive and well all over the world so there is a huge source of DNA to sample and the Homo sapiens genome was sequenced in 2003. Neanderthals and Denisovans however died out many thousand years ago. For Denisovans the only trace found is a single finger bone and two teeth, but those fragments have been enough to sequence the whole Denisovan genome and compare their DNA to Neanderthals and Modern Homo sapiens.

So how are scientists able to sequence the whole genome of long extinct species?

To do this a number of biotechnology methods are use.

In this assignment you will research a number of biotechnology methods used to gather and compare genomic information.

1.

|  |  |  |  |
| --- | --- | --- | --- |
| Word | Definition | Mark | Mark scored |
| Genome |  | 1 |  |
| Biotechnology |  | 1 |  |
| Comparative genomics |  | 1 |  |
| Phylogenetic tree |  | 1 |  |

# 2. Draw the potential phylogenetic tree suggested in the articles above for Homo heidelbergensis, Homo sapiens, *Homo neanderthalensis and Denisovans.*

# *(1 mark)*

# 3. (a) Remains of the human species, Homo floresiensis have been found on the Island of Flores, Indonesia. They lived from about 100,000 years till 50,000 years ago. Why at the time of writing (2016) are scientists not able to accurately place Homo floresiensis on a human ancestral phylogenetic tree with regard to Homo heidelbergensis, Homo sapiens, Homo neanderthalensis and Denisovans?

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# *(1 mark)*

# *b. What evidence is there that humans interbred with Neanderthals?*

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1. marks)

# *4.* Two of the important enzymes used in this area of science are Restriction enzymes and DNA ligase. Complete the table below for these two enzymes.

|  |  |  |
| --- | --- | --- |
| Word | Function | Mark |
| Restriction enzymes |  | 2 |
| DNA ligase |  | 1 |

***5.*** The **Polymerase Chain Reaction** (PCR) has been very helpful in the study of the genome of human ancestors.

1. What is the PCR process?

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1. marks)

(b) In simple point form explain the steps involved in PCR.

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(6 marks)

6. One method of comparing DNA from one person to another, or from one species to another DNA profiling. This is made possible by DNA Gel Electrophoresis. In point form explain how this process occurs.

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**(8 marks)**

**7**. How has bioinformatics helped process the data collected when comparing species genomes?

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(2 mark)

8. Another method used to compare the genomes of different species is the use of Endogenous retroviruses (ERVs). What are ERVs and how can they be used to compare different genomes?

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(3 marks)

9. Not only Nuclear DNA is used in comparing genomes. Mitochondrial DNA can also be used?

a. Give a theory on why mitochondria have their own DNA.

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(2 mark)

1. Which gamete is most likely to be the source of mitochondria found in the zygote?

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(1 mark)

1. Why can mtDNA be used to compare genetic relationships between different groups.

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(3 marks)

10. The first analysis of mitochondrial DNA (mtDNA) from Neanderthals was published in 1997. A second one was carried out 2000. What were the sources of the DNA and what did both show?

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(5 marks)

11. Another area of biotechnology that can be used in comparing the genetic relatedness of different groups is protein sequences. Proteins are made up of sequences of amino acids. By sequencing the amino acids of specific proteins and then comparing these sequences from one species to another the genetic relatedness can be studied. Two closely related species will have similar amino acid sequences in specific proteins.

A. what are ubiquitous proteins and why do researches use them when studying evolution?

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1. marks)

b. Cytochrome C is a protein often used in studying evolution. Why is it such a useful protein when studying evolution?

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(2marks)

1. The table below shows a comparison of difference in Cytochrome C between different species. Use it to form a list of the organisms going from most closely genetically related to least.

|  |  |
| --- | --- |
| Two organism | Difference between species with regard to amino acid sequence in Cytochrome C |
| Human and cauliflower | 44 |
| Cauliflower and parsnip | 13 |
| Cauliflower and Chimpanzee | 44 |
| Garden snail and chimpanzee | 29 |
| Human and Chimpanzee | 0 |
| Garden snail and human | 29 |

(1 mark)

**References** (at least 3)

(3 marks)