Biotechnology and Evolution

When Darwin put forward his theories 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 (genomic and Mitochondrial) and proteins provide additional evidence for evolutions. Genomic information enables the construction of Phylogenetic trees showing evolutionary relationships between groups.

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 our modern human ancestors migrated through Eurasia, they encountered the Neanderthals and interbred. Because of this, a small amount of Neanderthal DNA was introduced into the modern human gene pool.

According to one theory, Neanderthals, Denisovans, and all modern humans are all 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 northwestward 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. Our modern human ancestors did not begin their own exodus from Africa until about 60,000 years ago, when they expanded into Eurasia and encountered their ancient cousins.

Studying the evolutionary relationshoip 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 sapien genome was sequenced in 2003. Neanderthals and Denisovans however died out many thousand years ago. Denisovans. The only trace that we have found, however, 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 sapines.

So how are scienctists able to sequence the whole genome of long extinct speices?

To do this a number of biotechnology methods are use.

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

1.

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

# 2. Draw a potential phylogenetic tree for Homo heidelbergensis, Homo sapiens, *Homo neanderthalensis and Denisovans.*

# *(1 mark)*

# 3. 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 ancestoral phylogenetic tree with regard to Homo heidelbergensis, Homo sapiens, *Homo neanderthalensis and Denisovans.*

# *(1 mark)*

# *4. Two of the more important enzymes in this area of science are Restriction enzymes and DNA ligase.*

# *Complete the table bellow for these two enzymes.*

|  |  |
| --- | --- |
| Word | Function |
| Restriction enzymes |  |
| DNA ligase |  |

# (2 marks)

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

1. What is PCR?

The **Polymerase Chain Reaction** (PCR) is a fast and inexpensive technique used to "amplify" - copy - small segments of DNA.

1. mark)

-In simple point form explain the steps involved in PCR.

-The sample is heated (1)so the DNA denatures (unwinds) (1)into two pieces of single-stranded DNA.

-The enzyme **DNA polymerase** is added. (1)

-Copies of the 4 different nucleotide bases (A, T, C, G) are added.(1)

-The mixtures is cooled and the DNA polymerase builds two new strands of DNA, using the original strands as templates. (1)

-The cycle of denaturing and synthesizing new DNA is repeated as many as 30 or 40 times, leading to more than one billion exact copies of the original DNA segment.(1)

(6 marks)

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

**DNA cut into fragments using restriction enzymes.(1)**

**A layer of agar gel is set up.(1)**

**One end of the gel has a positive charge and the other has negative charge.(1)**

**The DNA fragments are placed at the negative end of the gel.(1)**

**DNA has a negative charge, so the fragments are pulled through the gel towards the positive end.(1)**

**Short fragment move farther and fastest through the gel. As result shorter fragments end up nearer the positive end of the gel and longer fragments end up closer to the negative end.(1)**

**This causes bands of DNA in the gel. Separated due to difference in length.(1)**

**Dye (often fluorescent) can be used to dhow the banding clearer.(1)**

**(8 marks)**

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

**Allows us to compare lots of information about different genomes using maths and computer modelling.**

**(1 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?**

**(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 won DNA.

(1 mark)

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

(1 mark)

1. Why can mtDNA be used to compare genetic relationships between different grousp.
2. marks)

10. 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 studdeid. Two closely related species will have similar amino acid sequeinces in specific proteins.

a. what are ubiquitous proteisn and why do researches use them when studying evolution?

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1. marks)

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

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(2marks)

1. The table below show a comparision 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 in amino acid sequence in cytochrome C |
| Human 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)