Understandings:

1. Define clade.
- A clade is a <u>group that have evolved from a common ancestor</u>. The clade can be big or small depending on how you define a clade.

2. Explain how scientists can identify the members of a clade.
- How? Through sequences of genes! The target sequence is usually the genes producing proteins, such as haemoglobin, RNA, etc.

3. State that clades are a form of molecular clocks.
- The natural conclusion we reach is that <u>the longer the time period, the larger the difference there will be.</u> So when we compare two species and notice a large difference in genetic sequence, we can conclude that their common ancestor is very old or diverged very early.

4. Distinguish between analogous and homologous traits.
- Similarities can be either <u>analogous or homologous</u>.

Earlier we talked about the homologous and analogous structures. This is the same thing. Homologous structures are pentadactyl limbs. Analogous structures have convergent evolution so they have similar functions.

Human and eye and octopus eye have evolved independently but they have very similar <u>morphology</u> (form and structure).

5. Explain cladogram.
- Cladograms are tree diagrams that show the most likely path of divergence. As mentioned, clade classifications are almost always based on amino acid sequences.

Branching points are called nodes.
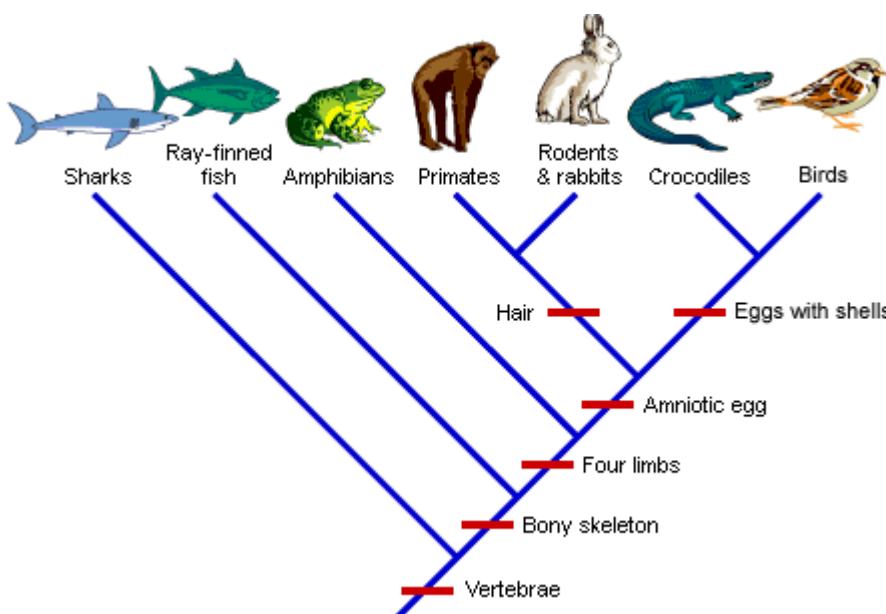
The red lines with description are the things that all species above have in common. So all have spinal cord, all except sharks have bony skeleton, all except sharks and fish have four limbs, etc.

6. State the problems of cladograms and how members are reclassified.

- So basically when we are constructing cladograms, we cannot take into account of all the variables of genetic sequence. We will probably have <u>different cladogram depending on what our analysing target is.</u>

However, cladograms are becoming more accurate as we move from morphology to computer based analysis of sequences.

Application and skills:

1. Understand the cladograms, including humans with other primates.
- Yes.

2. Explain how figwort family was reclassified with cladistics.
- From 1789, until recent years, we had classified the eighth largest angiosperm group <u>Scrophulariaceae</u> (I will not remember this in 10000 years), more commonly known as <u>figwort family</u> (this is better), into 1 group.

However, recent data compared chloroplast gene sequence and found that there were 5 distinct clades in that figwort family we thought of as 1 clade.

This is a real-life example of major reclassification.

3. Be able to analyse cladograms to deduce evolutionary relationships.
- Yes.

TOK:

1. A major step forward in the study of bacteria was the recognition in 1977 by Carl Woese that Archaea have a separate line of evolutionary descent from bacteria. Famous scientists, including Luria and Mayr, objected to his division of the prokaryotes. To what extent is conservatism in science desirable?