4.7 INVESTIGATING DIVERSITY

- **DNA and mRNA base sequence**
  - Gene technology allows us to read the base sequence of DNA and mRNA
  - Can compare how similar the base sequences are between species
    - More similar DNA = more closely related in evolutionary history
  - As mRNA sequences are complementary to DNA, we can also read the mRNA to ascertain how closely related species are
- **Observable characteristics**
  - As observable features are determined by DNA and proteins, it is a useful way of seeing similarities and differences
  - Most observable features are polygenic – coded for by more than one gene
    - Tend to vary continuously, so difficult to distinguish
  - Observable features can be changed by the environment, so not reflective of DNA differences
- **Proteins**
  - The amino acid sequence of a protein is determined by mRNA, which in turn in determined by DNA
  - Similar sequences of amino acids indicate more closely related species
- **Quantitative measurements of variation**
  - Inter- and intra-specific variation
  - Data collection
    - Mean and standard deviation
      - Large standard deviation = large variation
    - Normal distribution curves
  - Sampling
    - Random sampling reduces sampling bias
    - Large sample size to reduce chance
      - Statistical analysis to see if the results were the result of chance

AQA