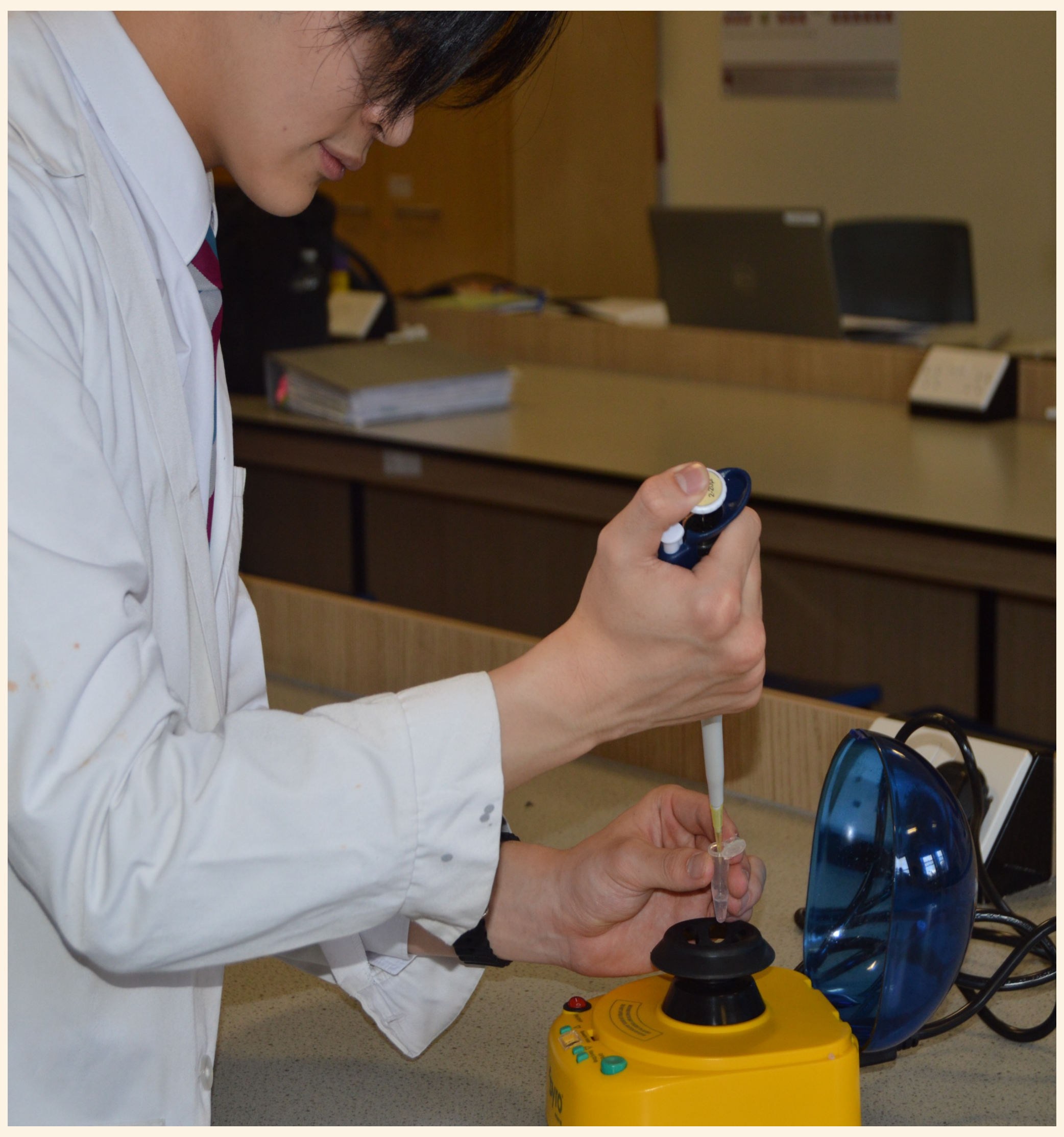
Emmanuel College

Centre for Bacterial Cell Biology, Newcastle University

Are all daffodils the same?

DNA sequencing

To study the difference between daffodil varieties, we used DNA sequencing, which is a technique used in the laboratory to work out which order the bases of DNA are arranged in. As the genetic code is degenerate, it can be used for all species, so it can help us to understand the function of genes alongside identifying and treating diseases, as well as trace species ancestry.
In this project, nanopore sequencing was used where DNA is analysed by passing individual molecules through nanopores embedded in a membrane. As they move through, they create a unique signal that can be used to determine the sequence of bases (A, T, G, C).



Nanopore sequencing
What makes nanopore sequencing special is the ability to read long stretches of genetic material in real time without needing chemical modification or amplification steps. It is faster and more adaptable than traditional sequencing methods.
It is also more efficient than the Sanger method which is highly accurate when sequencing short reads but is slower and less accurate sequencing long reads.
Nanopore sequencing uses have included pathogen identification, environmental studies and clinical diagnostics.

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