







The James Hutton Institute

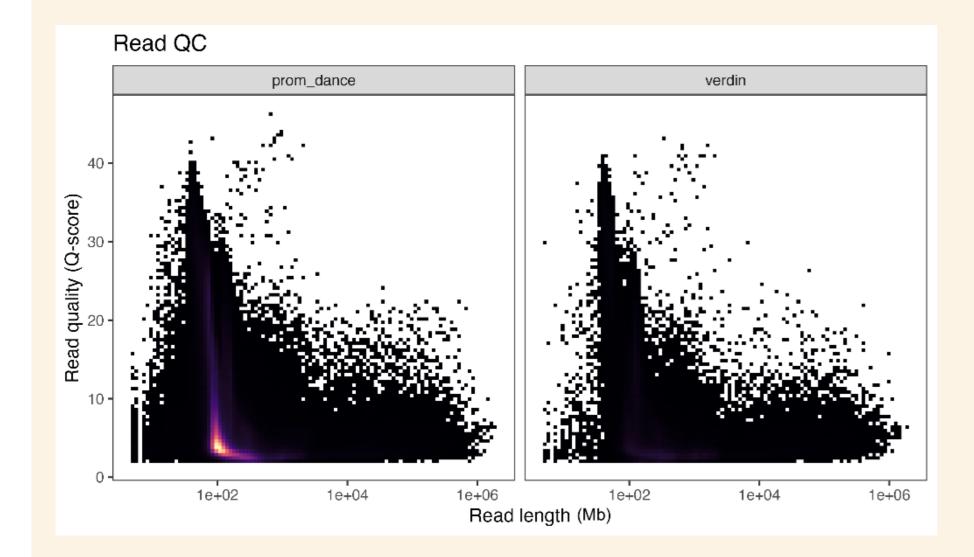
Are all the Daffodils the same?

Equipment used

Overview

Bentolab was used to assist with DNA isolation using the Qiagen DNeasy Plant Kit. An Oxford Nanopore MinION was used for DNA sequencing. This provided immediate data streaming and fragments of any length could be sequenced. This equipment is expensive and therefore a Partnership Grant from The Royal Society made access to this equipment possible for many schools.





Data produced

Data produced were the DNA length of each read and the average read quality. The quality of each read was determined and presented in Dorado software. A higher quality score (Q score) means a more accurate read.

To complete phylogenetic analysis, the chloroplast genome can be assembled to determine the history of the species by comparison to other chloroplast sequences.