Scoping multi-species genotyping for genome-environment association study

Project overview

UK woodlands need to adapt to a warming climate, which may disrupt existing patterns of local adaptation. We need to make careful choices about the sources of seeds in order to plant resilient woodlands. To do this, we need to understand the genetic basis of adaptation within tree species.

The aim of this project was to identify genetic variations in collections of UK birch and alder seeds that are associated with possible adaptations to different local environments. It is the largest study to date using seed germinated from the UK National Tree Seed Project (UKNTSP) – a programme led by Kew to establish a genetically representative seed collection of the UK's native trees and shrubs for long-term conservation and research.

Over 1,000 seeds from UK native birch and alder trees collected by the UKNTSP and held at Kew's Millennium Seed Bank (MSB) were germinated and grown, and their whole genomes sequenced.

Key outputs

- Good-quality whole genome sequence data was obtained from the UK birch and alder trees used in this study.
- Whole genome sequences have been made publicly available on the National Center for Biotechnology Information (NCBI) Sequence Read Archive under BioProject accession PRJNA825844.
- 98 million single nucleotide genetic variants were discovered in UK downy birch, 50 million in silver birch and 37 million in dwarf birch.. In alder, 43 million variants were found.

Ongoing and future work

We are now carrying out genome-environment association (GEA) studies, which analyse the genomes of trees for genetic variations that correlate with climatic differences, as part of a new project "Understanding the genetic basis of silver birch adaptation to local environments and disease" under the Centre for Forest Protection's 2022–2025 research plan and one of our internships.