

Generating data for a genome-wide association study on acute oak decline

Project overview

Acute oak decline (AOD) is a complex disease affecting thousands of UK oak trees, many of which die every year. It is associated with multiple risk factors including bacterial infection, insect pests, soil health, drought, waterlogging and other environmental stresses. Affected trees can die very rapidly and evidence suggests that climate change could lead to more frequent and severe oak declines, creating an urgent cause for concern.

The aim of this study was to identify genetic factors contributing to AOD susceptibility in UK oak populations, which is crucial for developing effective strategies to mitigate the impacts of this devastating disease.

We carried out a genome-wide association study (GWAS) to search for genetic variations in oak trees that are associated with AOD. This involved sampling 700 British oak trees across 23 sites, most of which were prevalent with AOD but also included control sites that were either close to, or far away from, areas affected by AOD.

Observations related to the health of the tree (e.g. canopy transparency, number of beetle (*Agilus biguttatus*) exit holes, and number of bleeds) were recorded for each individual. The whole genome of each tree was then sequenced and the resulting data was added to a data set of 458 previously sequenced oak genomes and analysed to look for correlations between genetic variations and susceptibility or resistance to AOD.

Key findings

- This project represents a step forward in unravelling the genetic factors contributing to AOD in UK oak populations.
- The study did not identify genetic factors which are significantly associated with AOD, but there were promising weak associations.
- For example, one of the genetic variants is close to a candidate gene related to aluminium tolerance, which is interesting because high soil aluminium has been associated with AOD.
- Other candidate genes identified have possible involvement with insect, bacterial or stress responses that could affect oak tree susceptibility to AOD.

- An increase in sample size could potentially increase statistical power and reveal significant associations.
- All genome sequence data from this project has been uploaded to the National Center for Biotechnology Information (NCBI) public database under BioProject accession [PRJNA816149](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA816149).

Ongoing and future work

This work is being expanded under a new project titled, "[Assessing Genetic Susceptibility to Acute Oak Decline](#)" as part of the Centre for Forest Protection's 2022–2025 research plan. This new project aims to sequence 400 more genomes from six additional UK sites, and to look for genetic variations associated with environmental differences.

The continuation of this research will contribute to a more comprehensive understanding of acute oak decline susceptibility and help to inform tree planting and breeding programmes to establish more resilient oak woodlands.