

DAVIS EXPEDITION FUND

REPORT ON EXPEDITION / PROJECT

Expedition/Project Title:	Points of interest inside the Sitka British breeding programme
Travel Dates:	10.6.-16.6. and 30.6 - 4.7. 2021
Location:	UK
Group Members:	Domen Finzgar
Aims:	Identification of additional sampling points that would give a better understanding about genetic diversity of Sitka spruce in Britain.

Outcome (a minimum of 500 words):-

Following the new reality regarding international travel, my initial plan to visit the natural populations of Sitka spruce on Haida Gwaii island has become unrealistic. Therefore, I have restructured my expedition to allow me a better understanding of both the technological and biological processes that are happening inside the Sitka British breeding programme.

Initially, the plan was to visit 2 clonal archives: Ledmore and Glencorse (both Scotland), 2 tree nurseries: Delamere (England) and Maelor (Wales), 3 continuous cover Sitka forests (Wales) and 3 even-aged plantations with possible natural population present (England and Wales). Out of initial selection, all sites were visited except Arecleoch plantation since it required a special permit for movement on wind farms. This plantation was then replaced with Sitka spruce's second most northern plantation in the UK (Hoy island). The expedition was split into two parts. Sites south of Edinburgh were visited in one go, and sites north of Edinburgh in another time period.

The primary outcomes of the expedition can be summarized in 5 points:

1. Inside all of the visited full-sib highly improved Sitka plantations, no natural regeneration was spotted. Sampling of the natural regeneration below full-sib plantations would be beneficial as a study on how feasible it is to transform such even-aged plantations to continuous cover woodlands without compromising genetic diversity.

Lack of natural regeneration might be a consequence of: a) plantations are planted relatively recently and are therefore still dense, not allowing regeneration below tightly closed canopy, and b) A lot of the trees did not yet reach sexual maturity.



Figure 1: Sites like were identified prior to the expedition based on expert opinions. I was looking for sites that had a disturbance (windfall) that would allow better light conditions for the regeneration to occur. Sadly, no regeneration cores were spotted.

- 2. There is plenty of natural regeneration emerging in the Welsh continuous cover forests.** These sites were planted in the 70s and 80s from seed sources of unknown provenances. I selected and visited 3 woodlands to learn how alternative management of Sitka forest would look like. Forests looked well and thriving. Three regeneration cores were selected and sampled to check its genetic diversity and determine the provenance of the seed source (no records in the management plans).



Figure 2: Plenty of natural regeneration below an opening in close-to-nature managed Sitka forests in Wales.

- 3. There are places in Scotland where conditions are too harsh for Sitka.** Experimental plots (planted by the Forestry Commission) on the Hoy island were in bad condition. The height of the trees was disproportionately low for their age due to the harsh winds. Plenty of trees were dying.



Figure 3: Sitka on Hoy

4. Clonal archives are well maintained and labelled

Clonal archives present the basis for any breeding programme. Genotypes of plus trees that constitute the breeding population are preserved in the archives, ready for collecting scions. All of the visited archives were well maintained and clearly labelled. Orientation inside the archive was easy and no mislabelled trees were observed. I have, however, collected a few genotypes across multiple sites for the purpose to confirm the clonality of these plus trees across various locations (and planting years)



Figure 4: Orientation through the clonal archives were never a problem with a printed map of genotypes planted in a grid system. (Photo taken in Glencourse)



Figure 5: Every cluster of clones is clearly marked with a pole and a label. Labels were all readable even though the sites were planted decades ago. (Photo from Ledmore, Scotland)

5. Tree nursery operations are well organized and aware of the importance of genetic diversity.

Samples from 2 nurseries were collected to check whether our genotyping method could be used as internal quality control for the nurseries. I was shown around their fields and polytunnels as well as testing sites.



Figure 6: Full-sib hedges of Sitka spruce at Maelor nursery.

CONCLUSIONS

The expedition provided me with plenty of new samples from the sites I would otherwise not be able to include in my PhD, for which I am incredibly grateful to the Davis Expedition Fund. Not only that, through the trip, I have made connections and discussions with forest managers, nursery managers, archive keepers. Seeing Sitka in a variety of settings gave me a much deeper insight into breeding programmes in general. It helped me realize the extent of Sitka's importance for British forestry.

Results from some of the samples collected during the expedition will already be presented in November 2021 at the "Introduction, Breeding, Propagation and Deployment of Pacific Northwest Conifers Around the World: 70 years of Progress Opportunities and Challenges." (see the page below for the photo from the book of abstracts)



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BREEDING PROGRAMS

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Born in Ljubljana [Slovenia], 1990. BSc and MSc in Forestry, University of Ljubljana. In pursuit of a PhD at the University of Edinburgh. After studying fungal communities on coarse woody debris in Slovenian virgin forests, I switched to forest genetics. I was a part of the LIFEENMON team at the Slovenian Forestry Institute for four years, developing a forest genetic monitoring system for European beech and Silver fir on a transect between Germany and Greece. Now, I am in my final year of a PhD project, focusing on the genetic diversity of Sitka spruce in Great Britain.

Genetic assessment of the Sitka spruce British breeding programme

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Sitka spruce (*Picea sitchensis* (Bong.) Carr) is a non-native forest tree species with great economic importance for forestry in Great Britain (GB). It is estimated that Sitka plantations contribute to around 51% of all GB woodland area. Every year more than 35 million Sitka trees are being restocked or used for new plantations. About 97% of all Sitka trees planted in GB come from the improved Sitka planting stock. Such stock originates from the home-produced supply from the Sitka spruce British breeding programme (The Programme): either vegetatively propagated material derived from controlled crosses of genetically superior parent clones or seeds sold to the nursery sector from a range of seed orchards based on grafted superior clones.

Since the beginning of The Programme in 1963, no systematic genetic assessment of the whole Programme was ever conducted. Nevertheless, such assessment would be of utmost importance for several reasons:

- It provides internal quality control for The Programme. For example, labelling mistakes could have been made when grafting superior plus trees inside different clonal archives in different years.
- It provides internal quality control for tree nurseries to help them improve their standard operational procedures.
- It identifies the extent of violation of the panmixia assumption inside the tree orchard and detects pollen contaminations.
- It can be used to measure the loss of genetic gain inside Sitka plantations due to the discrepancies between the management plan and the actual genetic composition of superior full-sib families.
- It can be used to compare genetic diversity in The Programme with the unimproved FRM from seed stands or Sitka natural populations.

Most importantly, a systematic genetic assessment would help us answer a simple but essential question: Is The Programme meeting our expectations and what could be done better?

Within a 3.5-year PhD project, different sites of The Programme were identified:

- IUFRO Farigaig provenance trial (natural population proxy);
- natural regeneration from the unimproved Sitka plantation;
- commercial Sitka plantation;
- tree nurseries;
- seed orchard and
- clonal archives.

Throughout the listed stages, more than 1200 DNA samples were collected. Furthermore, different phenological and demographical data were recorded in three growing seasons.

All samples were analysed with the same 12 microsatellite (SSR) markers, allowing direct comparisons of different sample sets. Additionally, a subset of samples was analysed using a Sequenom MassARRAY SNP genotyping platform.

This talk presents the extent of the project after the final growth season and the early results of some of the analyses made so far.

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Key words : Genetic diversity, microsatellites, SNP, seed orchard, full-sib families