



GENETIC effects of applying Continuous Cover Forestry in non-native conifer UK populations

Laura Guillardin, University of Oxford

Prof. John MacKay, University of Oxford
Dr Gary Kerr, UK Forest Research



WHY?

Climate Change

Multi-purpose
Forests

Increase resilience

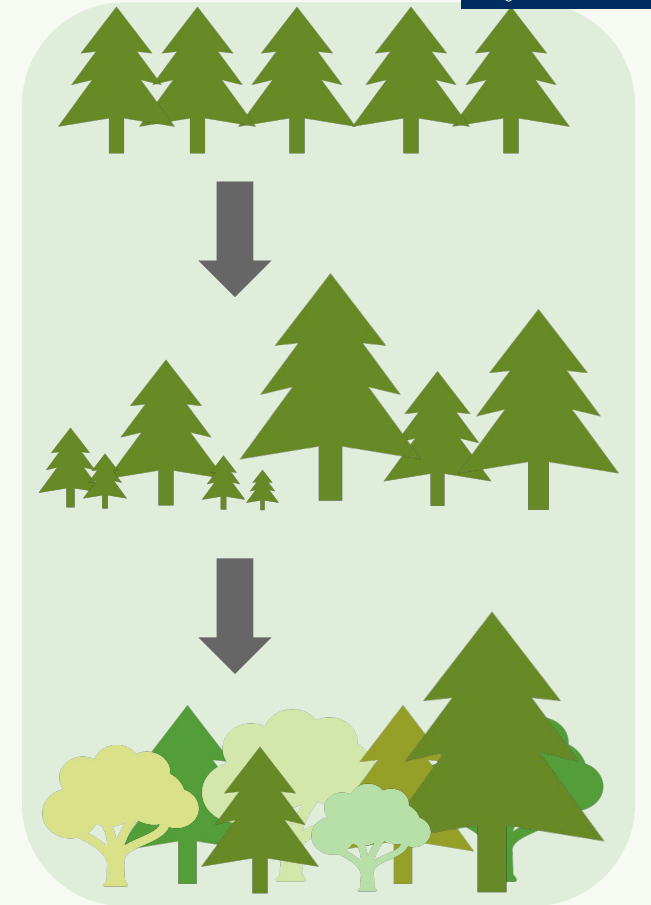
CCF approach:

Ecosystem management

Rely on **natural regeneration**
and disturbances

Work with site limitations

Irregular stand structure and a
mixture of ages and species





Hypothesis

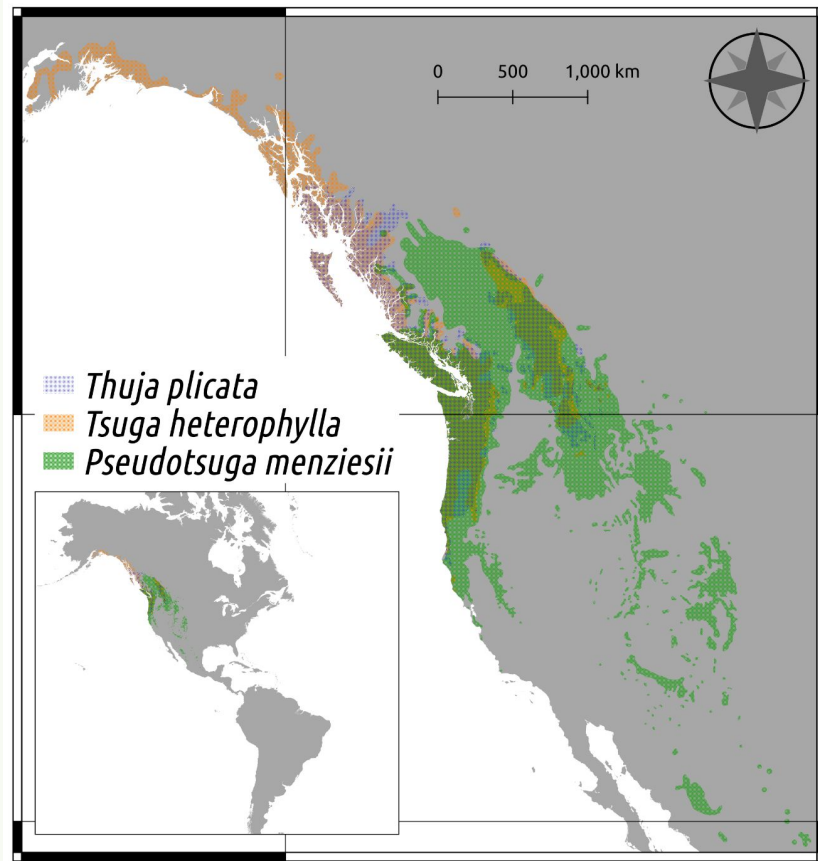


The planted trees that composed the UK forests may not hold enough genetic diversity to face the current and future disturbances.

So, how the gene pool is being transmitted to the offspring?

Study Species and UK sites

Species Natural distribution:



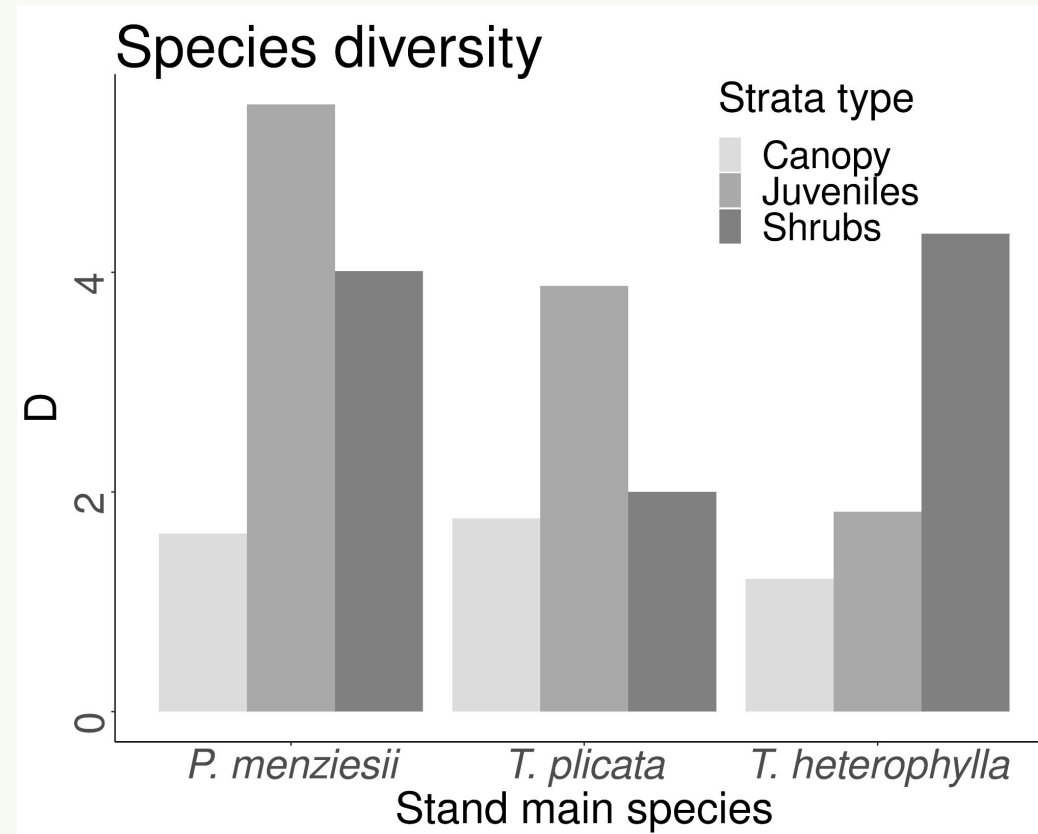
Study sites:





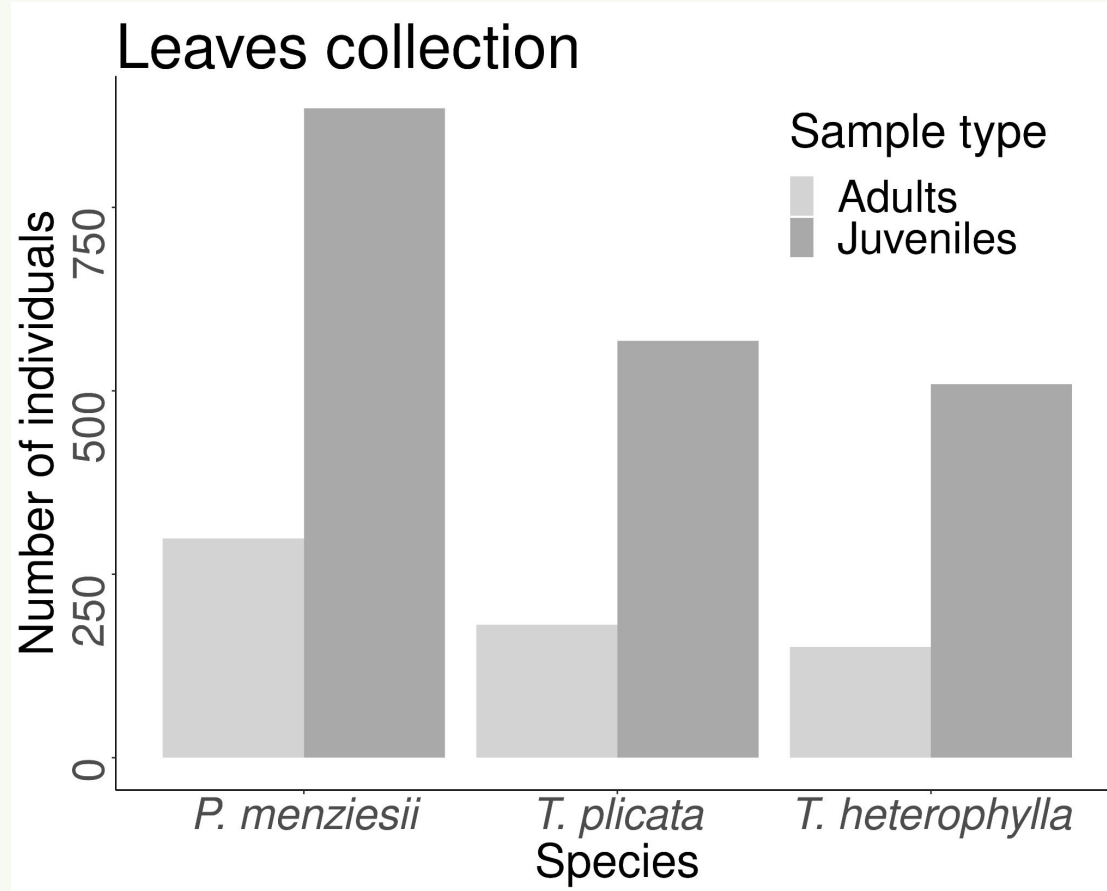
Sites characterization

Aim: To investigate the stands CCF stage of transformation



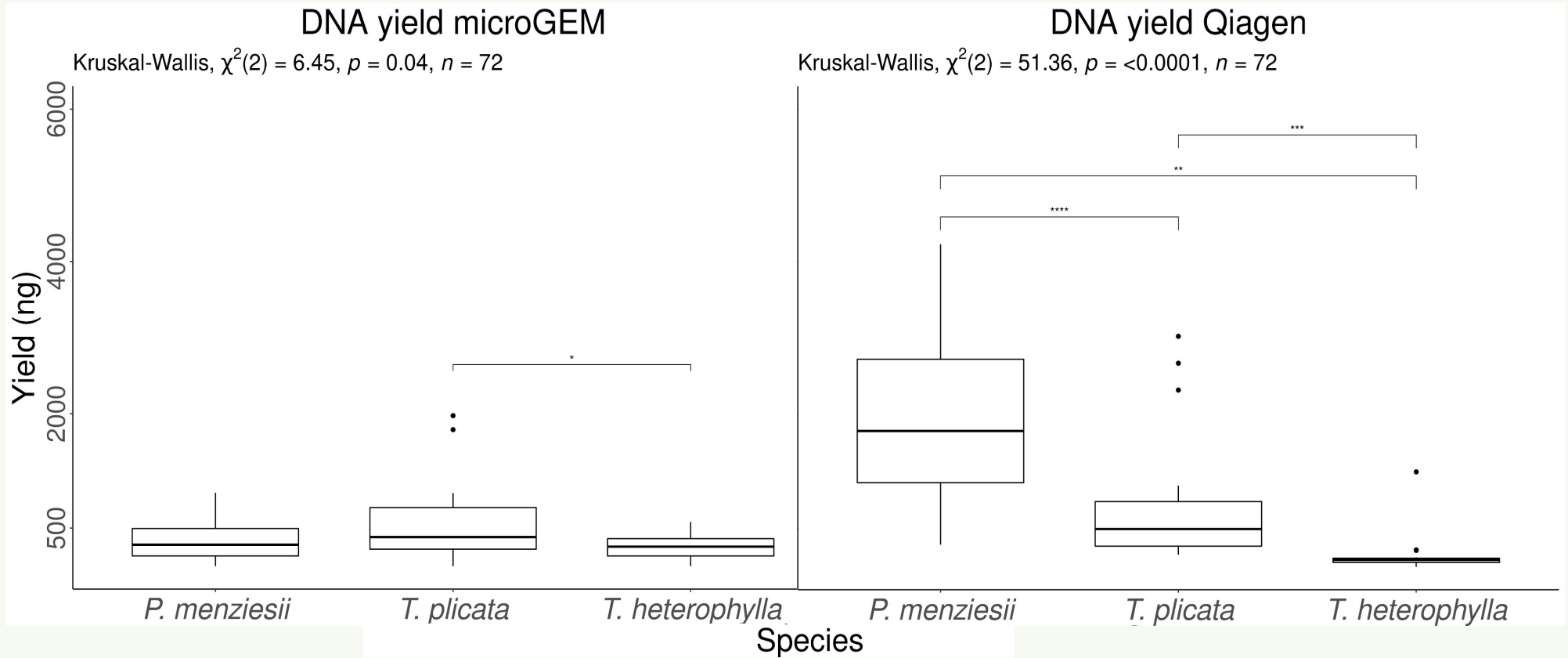


Tissue sampling





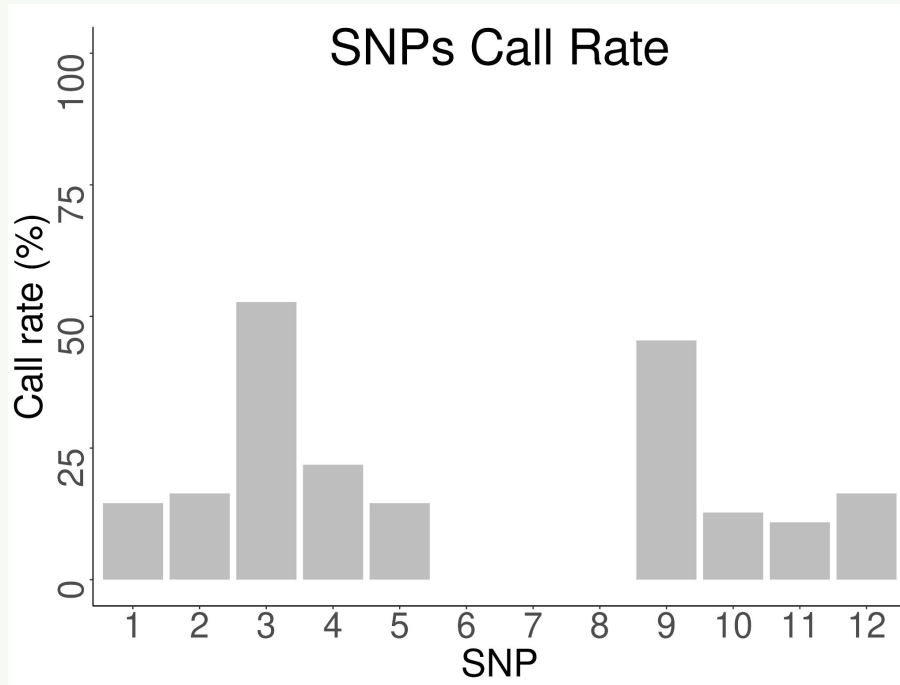
DNA extraction





Genotyping

For *P. menziesii* there is a database of 28k SNPs available (Howe et al., 2020)



Fluidigm genotyping platform steps:

D3 software to design assays
(from SNP sequences)

Genomic DNA
pre-amplification

Allele-specific PCR
(Juno)

Detect SNPs
intensity (Biomark)

References:

Howe, G. T., Jayawickrama, K., Kolpak, S. E., Kling, J., Trappe, M., Hipkins, V., ... McEvoy, S. (2020). An Axiom SNP genotyping array for Douglas-fir. *BMC Genomics*, 21(1), 9. <https://doi.org/10.1186/s12864-019-6383-9>

2021 FOREST GENETICS

CFGGA/WFGA STUDENT AND POSTDOC SYMPOSIUM



Any Questions?

laura.guillardin@plants.ox.ac.uk / @LGuillardin