University of Oxford
Department of Biology

Genetics behind the Continuous Cover Forestry approach - do UK plantations hold enough genetic diversity to face environmental changes?

IX International Symposium SRUK/CERU
Laura Guillardin
02/07/2022

Department of BIOLOGY

UNIVERSITY OF OXFORD

Background

CHALLENGES IN THE 21st-CENTURY FOREST MANAGEMENT

Climate change

Extreme temperatures

Species switch

Pests & diseases

Drought & Fires

Multi-purpose forests

Timber production

Biodiversity

Landscape

Public access, safety and recreation

Water quality and flooding risk

Carbon management – both in the soil and in standing timber

Cultural values – including archaeology, history and community interest

Continuous Cover Forestry approach

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The Continuous Cover Forestry Challenge

Even-aged **plantations**

First stages of irregular stands

Irregular, mixed stand

The planted trees in UK forests used **in CCF** may **not hold** enough **genetic diversity** to face the current and future disturbances.

We aim to assess the **diversity** in the **gene pool** and study its transmission to **offspring**

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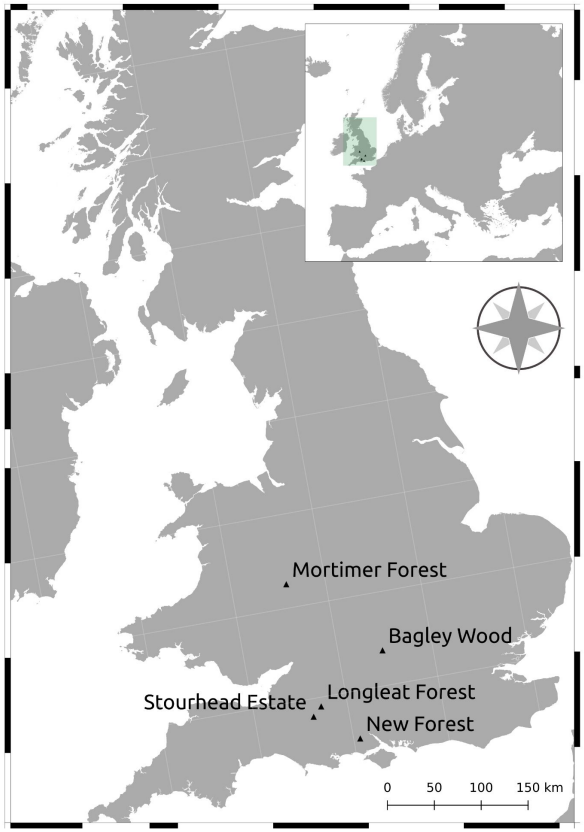
UK study sites (5) and genotyping method

Study sites and Species



Pseudotsuga menziesii

Thuja plicata

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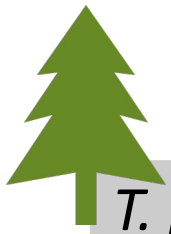
Genotyping method & SNP discovery pre-step

P. menziesii

Genotyping

FLUIDIGM

- 158 SNPs tested, 72 selected; 28K database (Howe *et al.* 2020)
- SNP type assay (Fluidigm) - Allele-specific PCR



T. plicata

Genotyping by Sequencing (GBS)

- 80 redcedars chosen from the different sites
- Molecular marker discovery

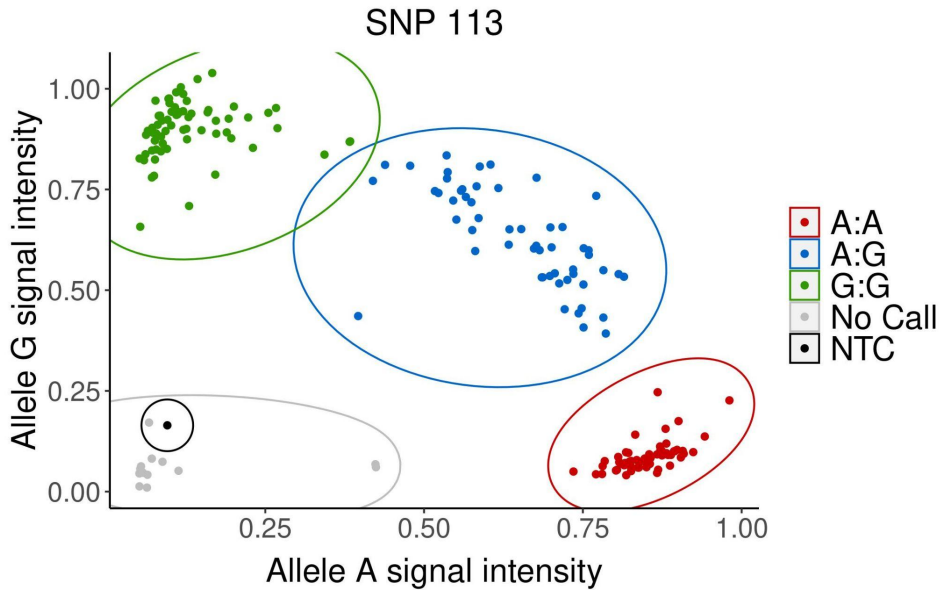
Genotyping

FLUIDIGM

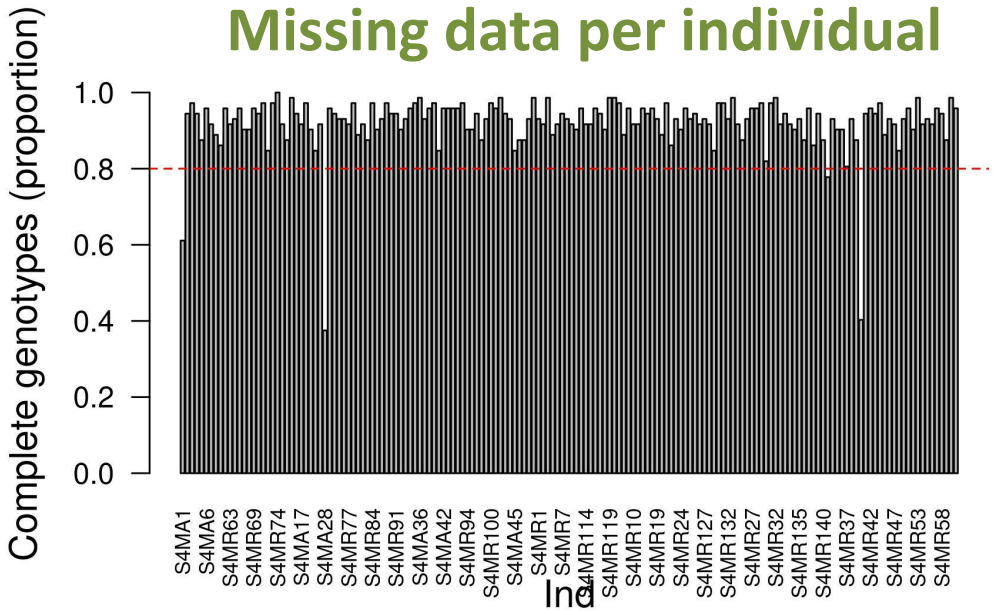
- SNP type assay (Fluidigm) - Allele-specific PCR

Assay development and quality control: 72 SNPs

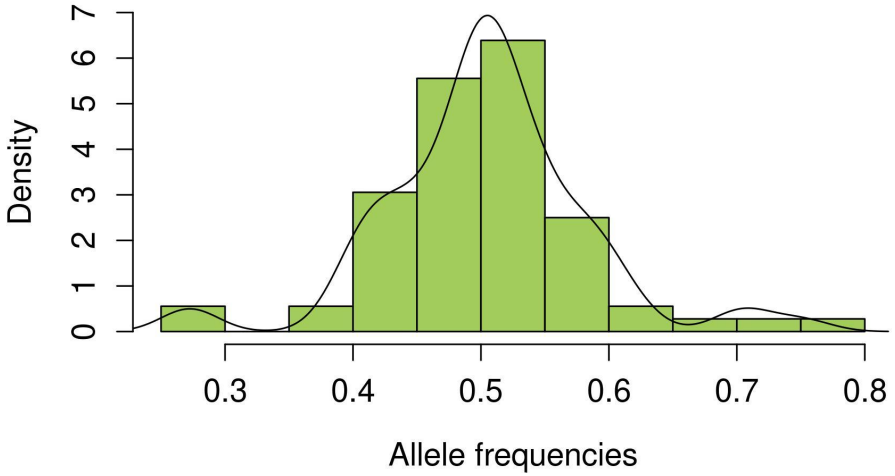
P. menziesii



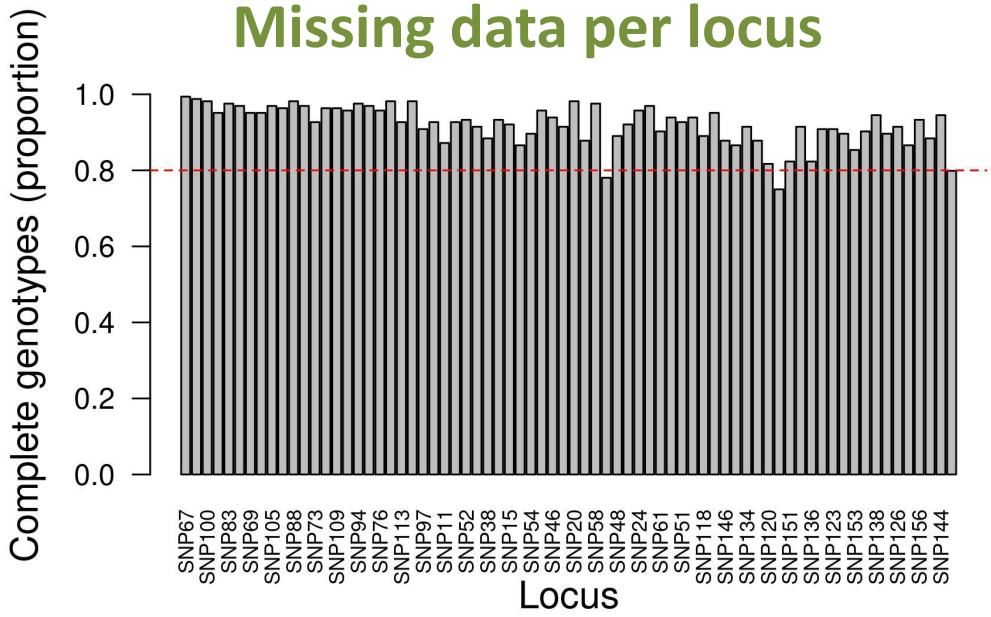
Missing data per individual



Distribution of allele frequencies



Missing data per locus



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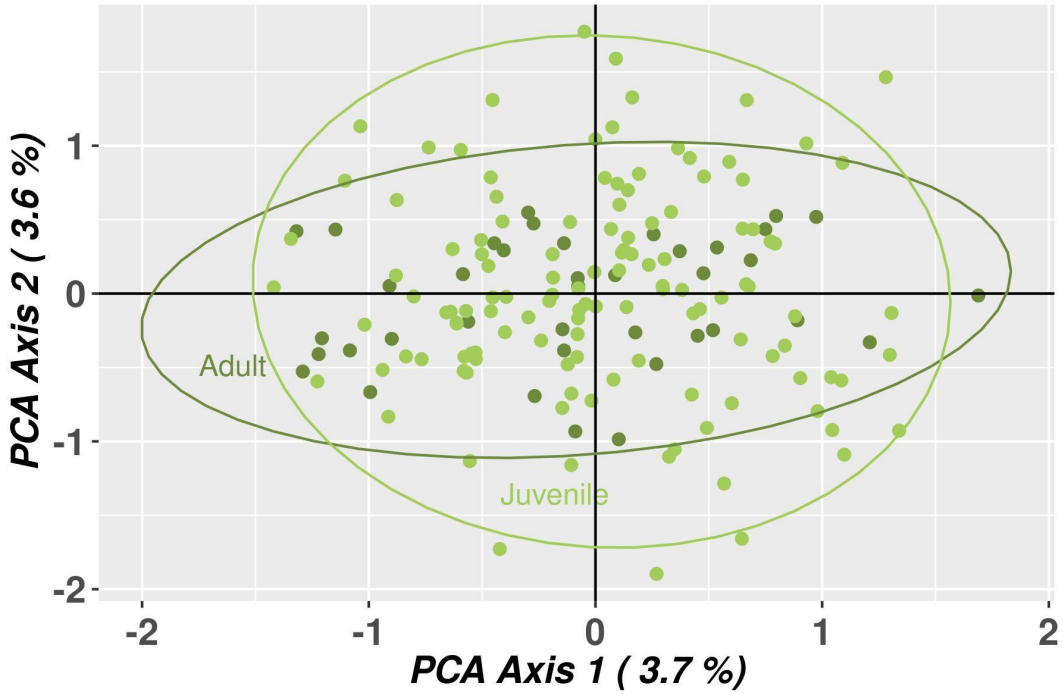
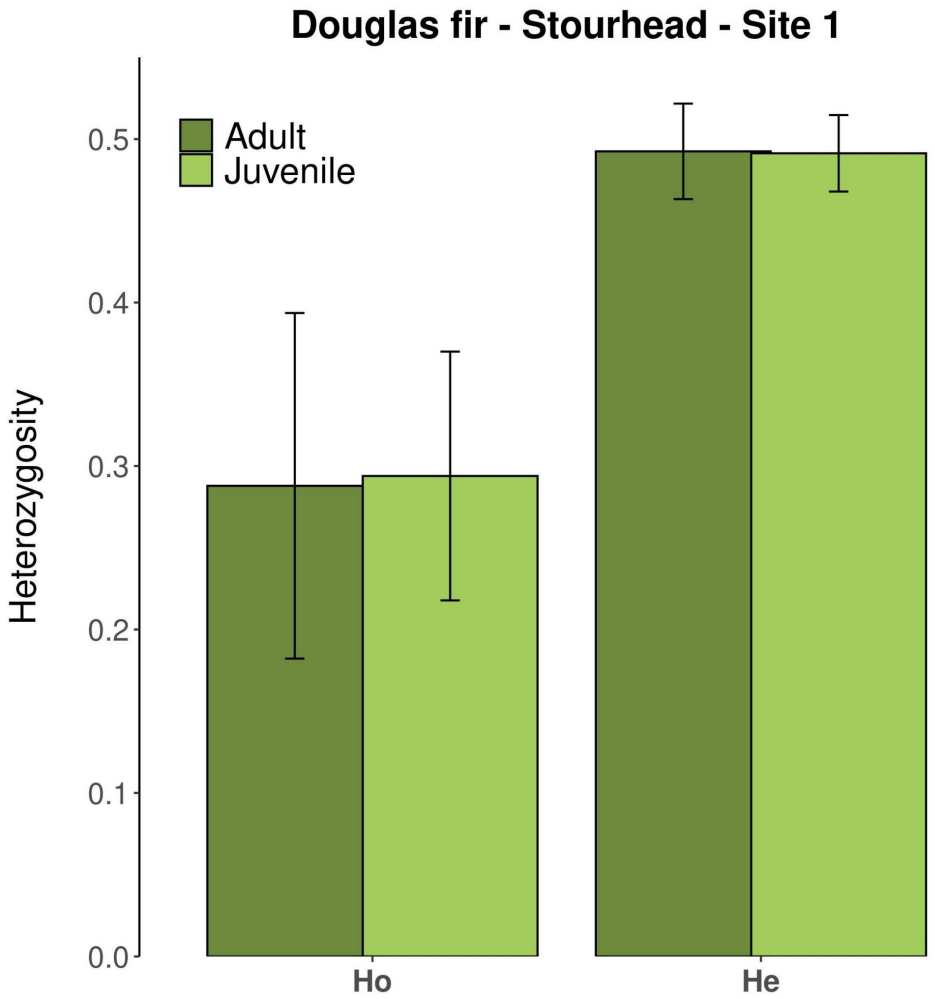
Preliminary population genetic results

P. menziesii

PCA (Principal components analysis)



Genetic diversity (GD)



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Preliminary population genetic results GBS

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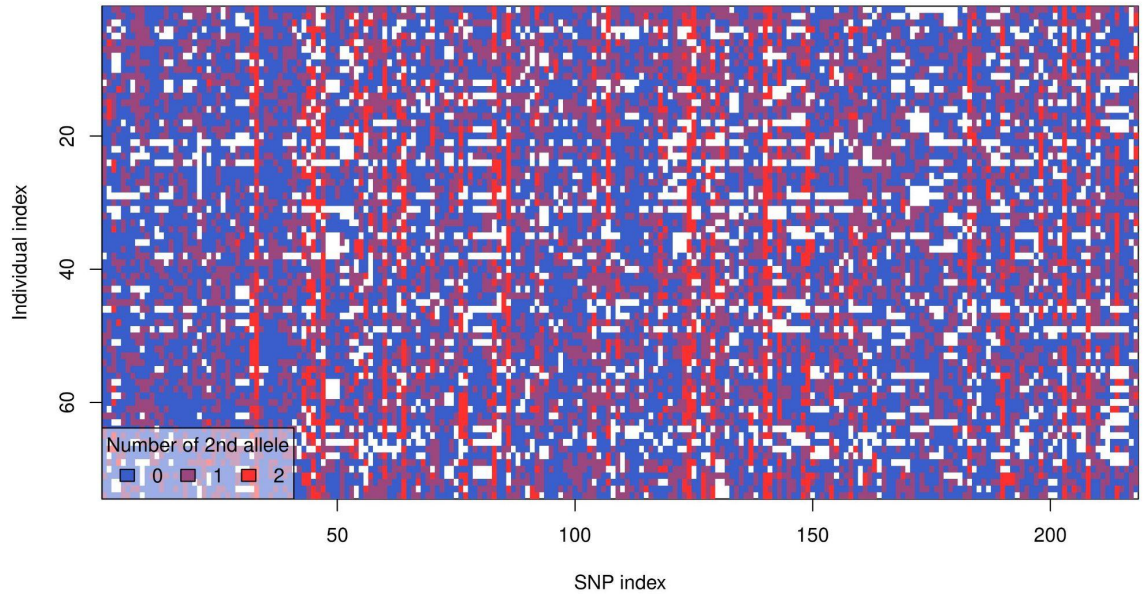
Missing data per individual and loci



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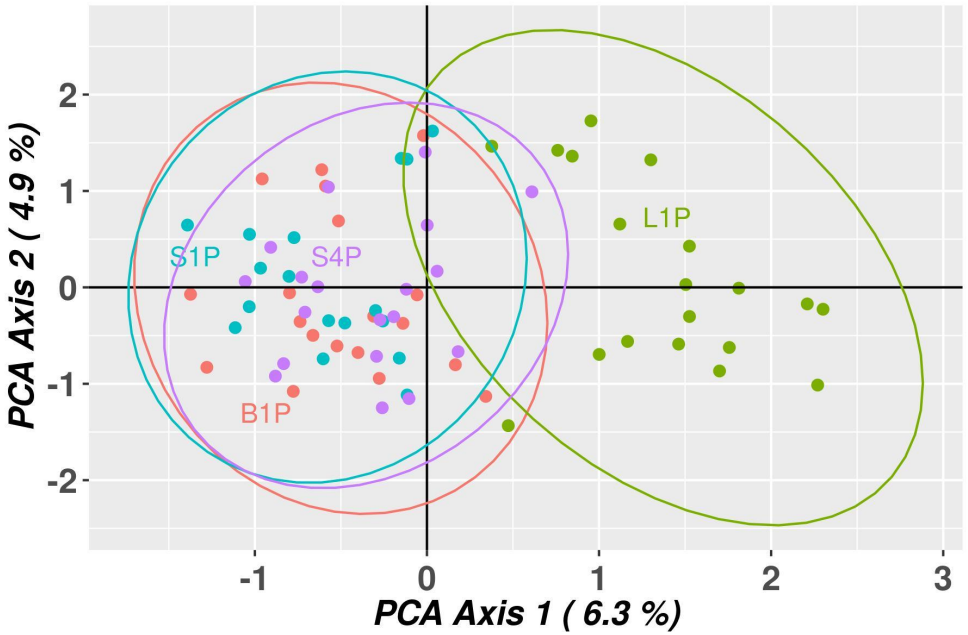
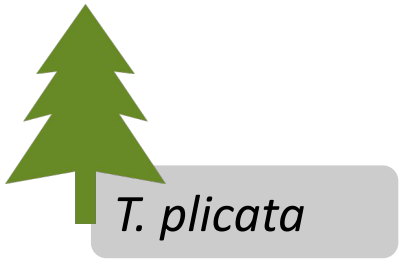


NEXT STEPS

P. menziesii

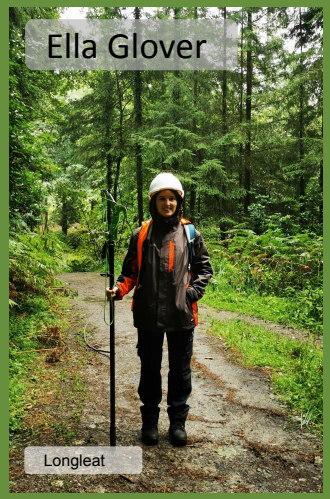
- Genotype the rest of the sites
- Look at different SNPs set scenarios
- Measure GD per site and strata



T. plicata

- Genotyping by Sequencing (GBS)
- Select the SNPs for downstream analysis
- Genotype the rest of the sites
- Measure GD per site and strata

ACKNOWLEDGMENTS



Dr Gary Kerr

Oxford-John Oldacre Graduate Scholarship

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