

Assessing the genetic diversity of Southern England Douglas fir planted stands and how it is transferred to the offspring

Laura Guillardin(1), laura.quillardin@biology.ox.ac.uk, Prof. John MacKay(1) john.mackay@biology.ox.ac.uk, Dr Gary Kerr(2) gary.kerr@forestresearch.gov.uk
 1: Department of Biology - University of Oxford 2: UK Forest Research

WHY?



Climate Change
 Multi-purpose Forests
 Increase resilience

Continuous Cover Forestry transformation

Encourage natural regeneration

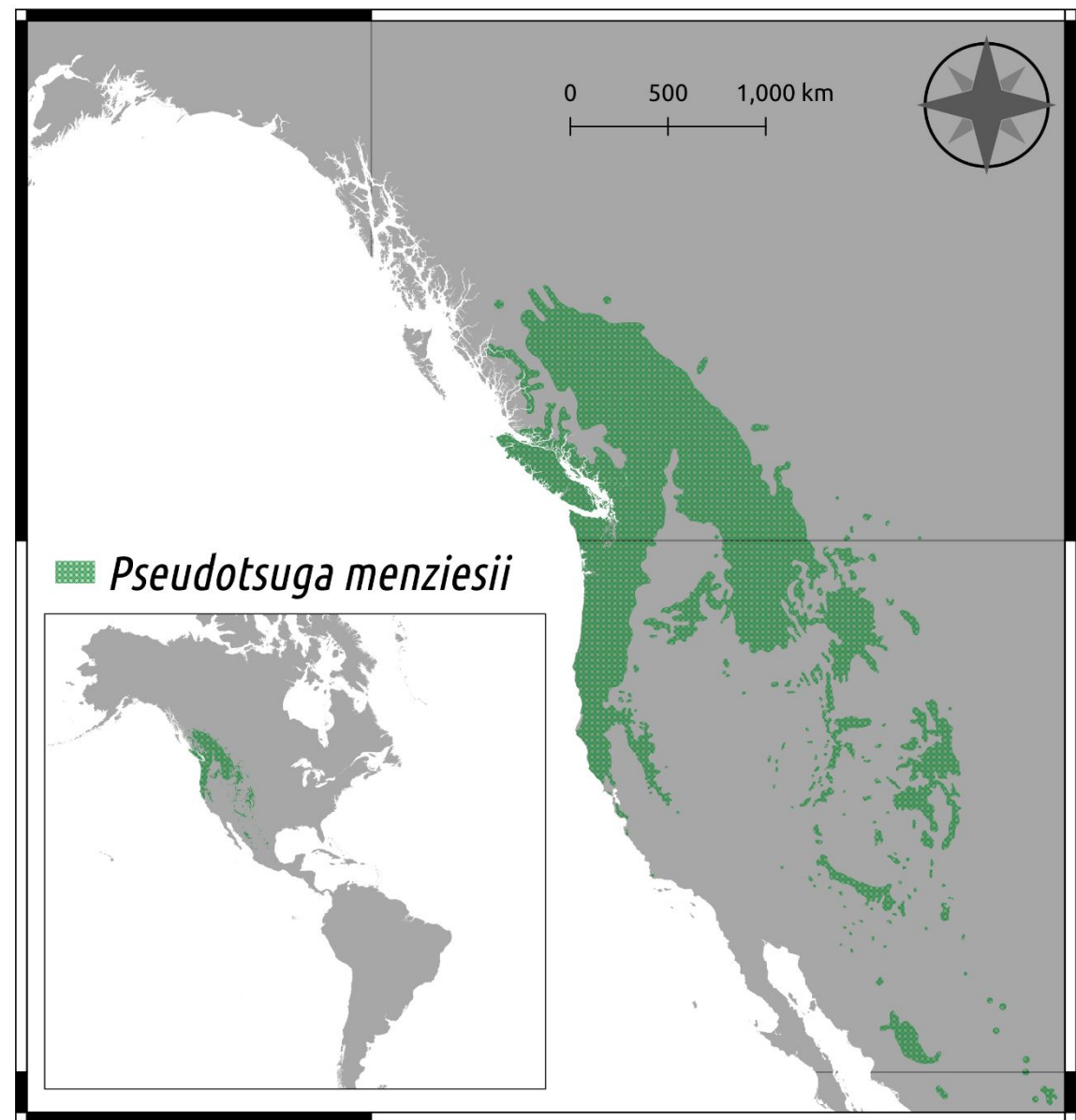
Hypothesis

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

Aim

Assess the genetic diversity (Gd) and its transmission across generations.

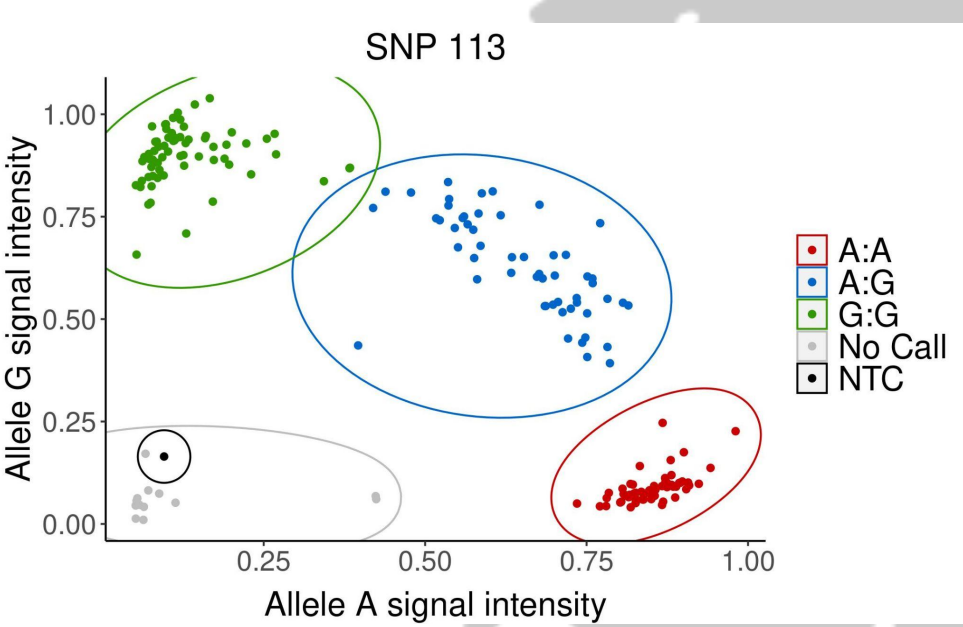
HOW?



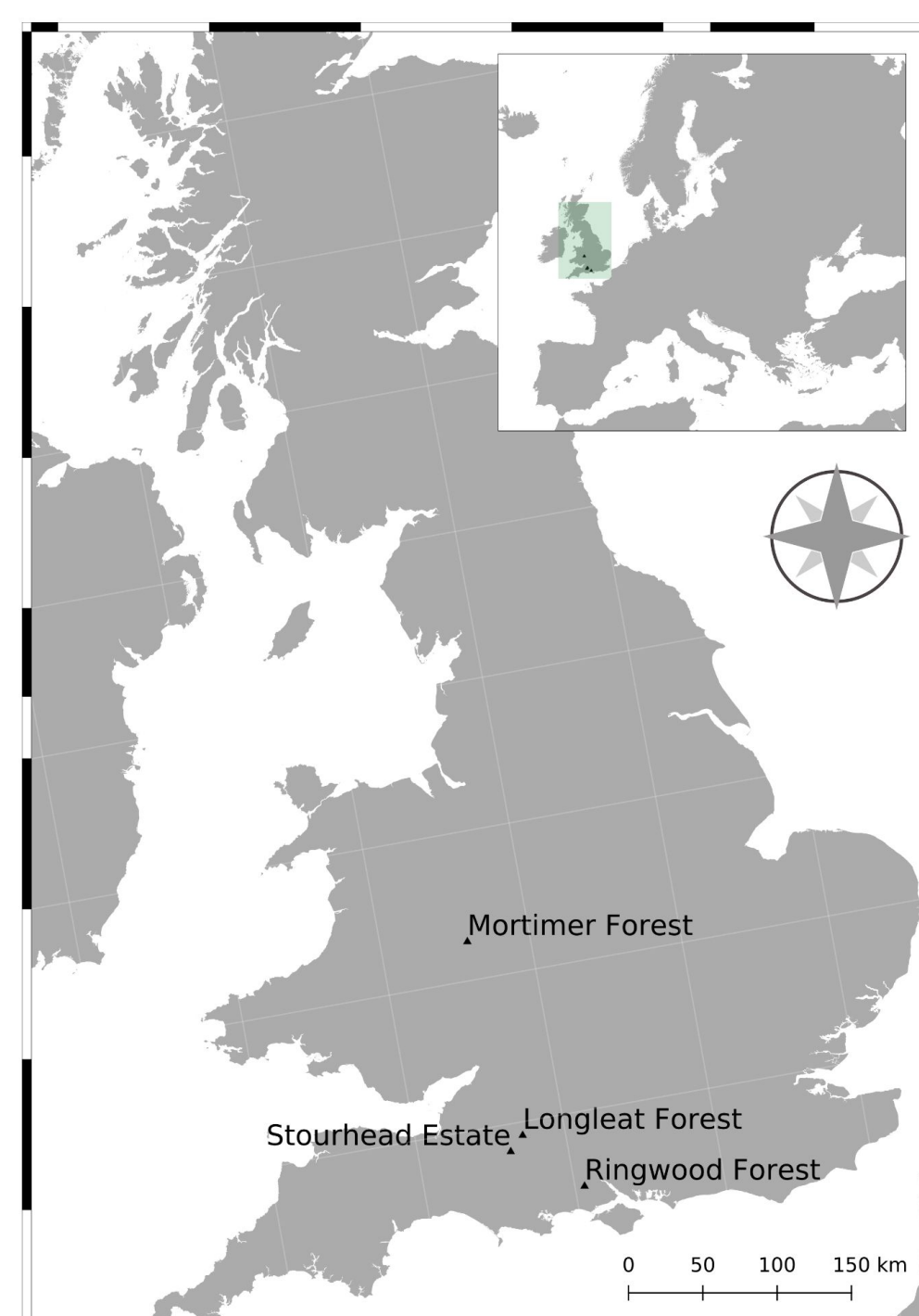
Sample leaves

Extract DNA

Genotyping



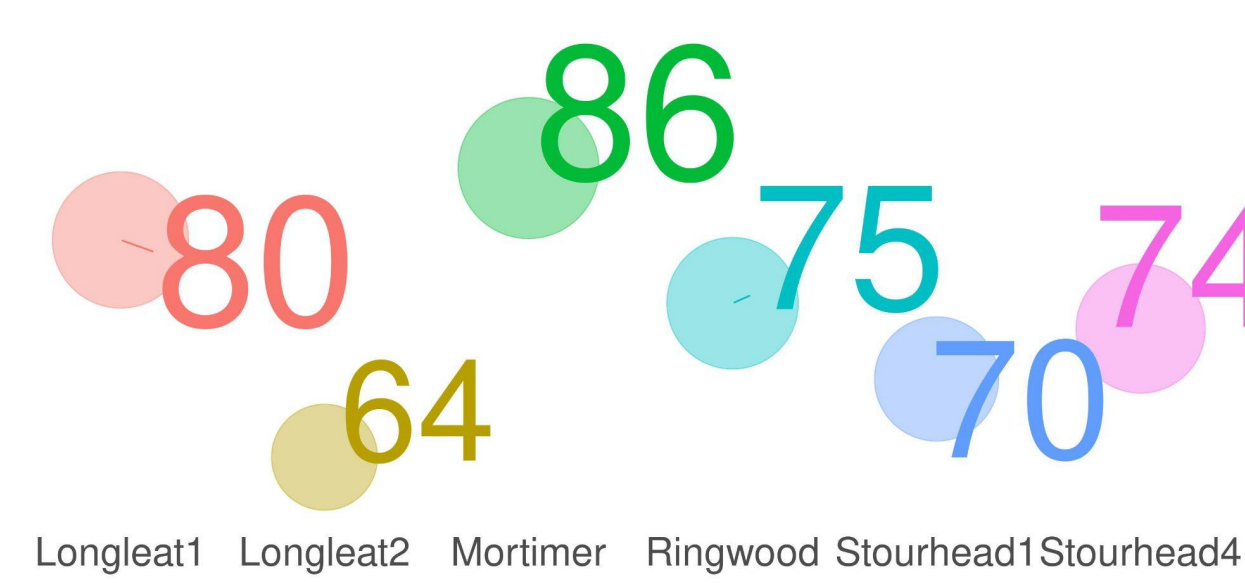
WHERE?



Site names:

- Longleat1 (Long1)
- Longleat2 (Long2)
- Mortimer (Mort)
- Ringwood (Ring)
- Stourhead1 (Stou1)
- Stourhead4 (Stou4)

Canopy density (CD) (%)



%CD higher in stands with lower species diversity levels: Long1 & Mort

LONGLEAT2 & STOURHEAD(1&4) SHOW HIGHER SPECIES DIVERSITY!

HOW DOES THE GENETIC DIVERSITY LOOK?

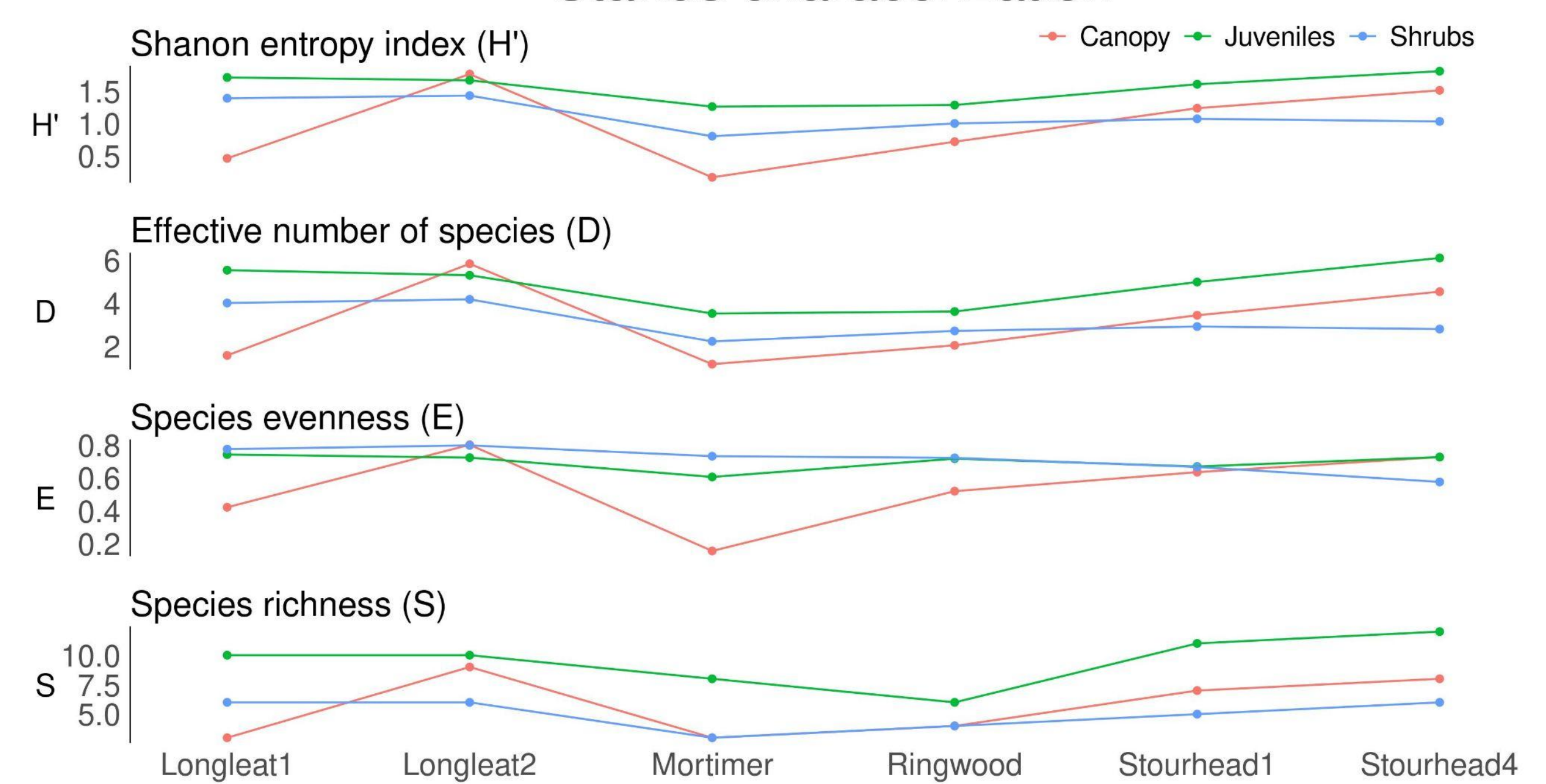
Effective population size is a genetic diversity indicator, $N_e > 500$ is considered to be the minimum to assure sufficient levels of genetic variation for adaptive capacity.

$N_e > 500$? ONLY IN: LONGLEAT2 (A&J) STOURHEAD4 (J)

Departure from HWE is due to evolutionary forces operating in the stands. HWE assumptions: no mutation, random mating, no gene flow, infinite population size, and no selection. Evolutionary forces: mutation, natural selection, genetic drift, and gene flow.

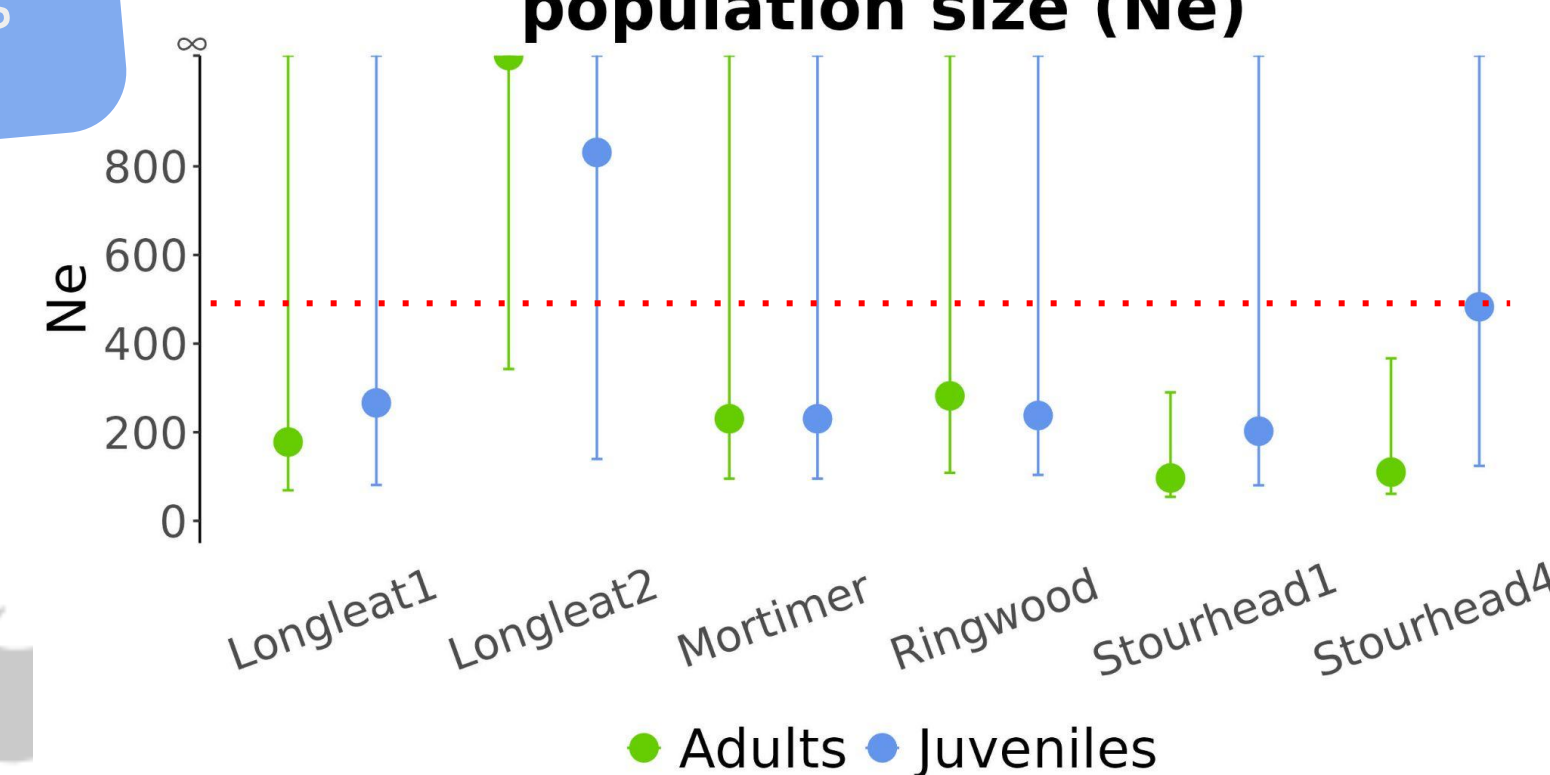
RESULTS

Stands characterization

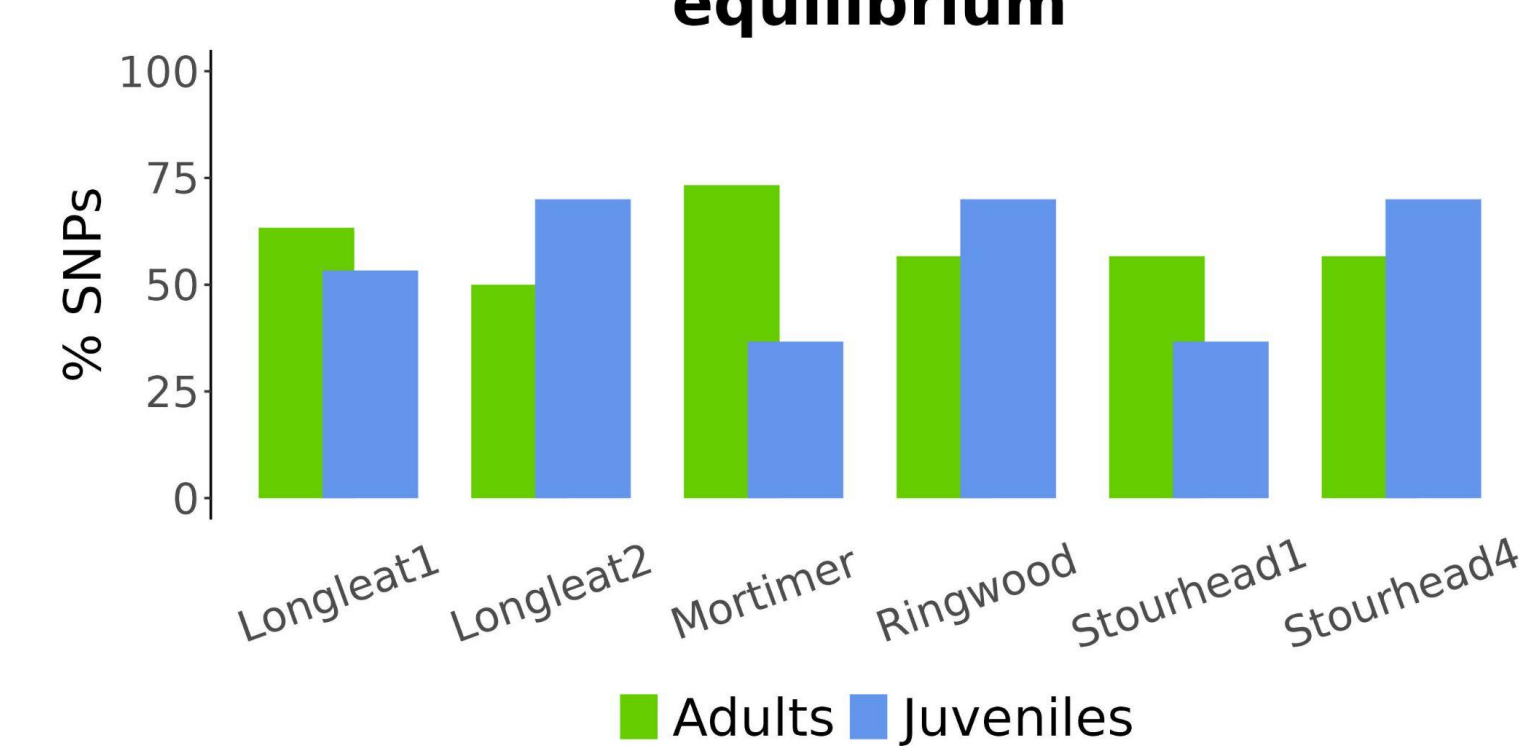


Juveniles appear to be the most diverse group throughout all the stands. Shrubs show highest diversity in Long1. Canopy diversity is high in Long2, Stou(1&4), very low in Long1 and Mort, intermediate in Ring.

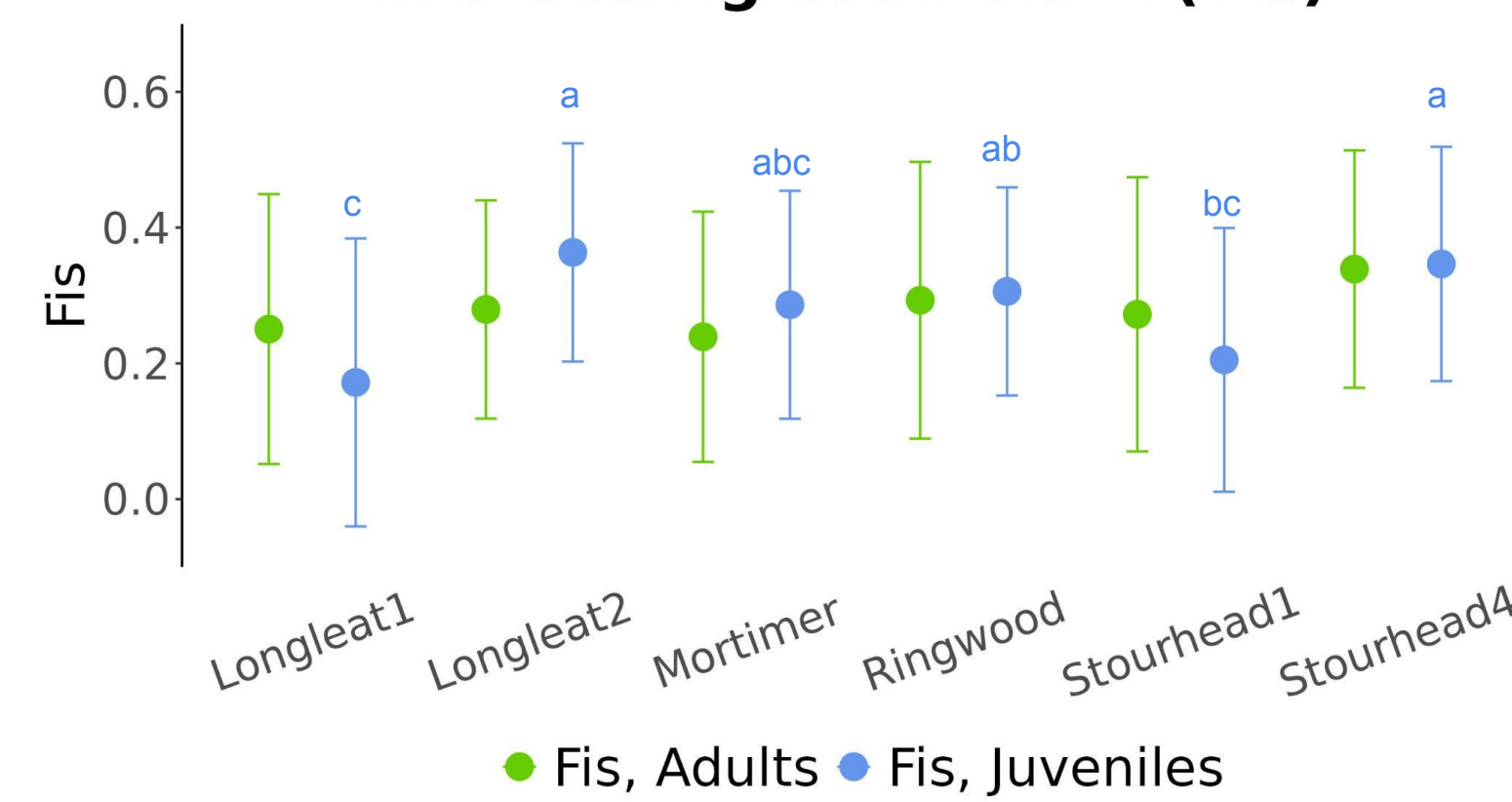
Estimated Effective population size (N_e)



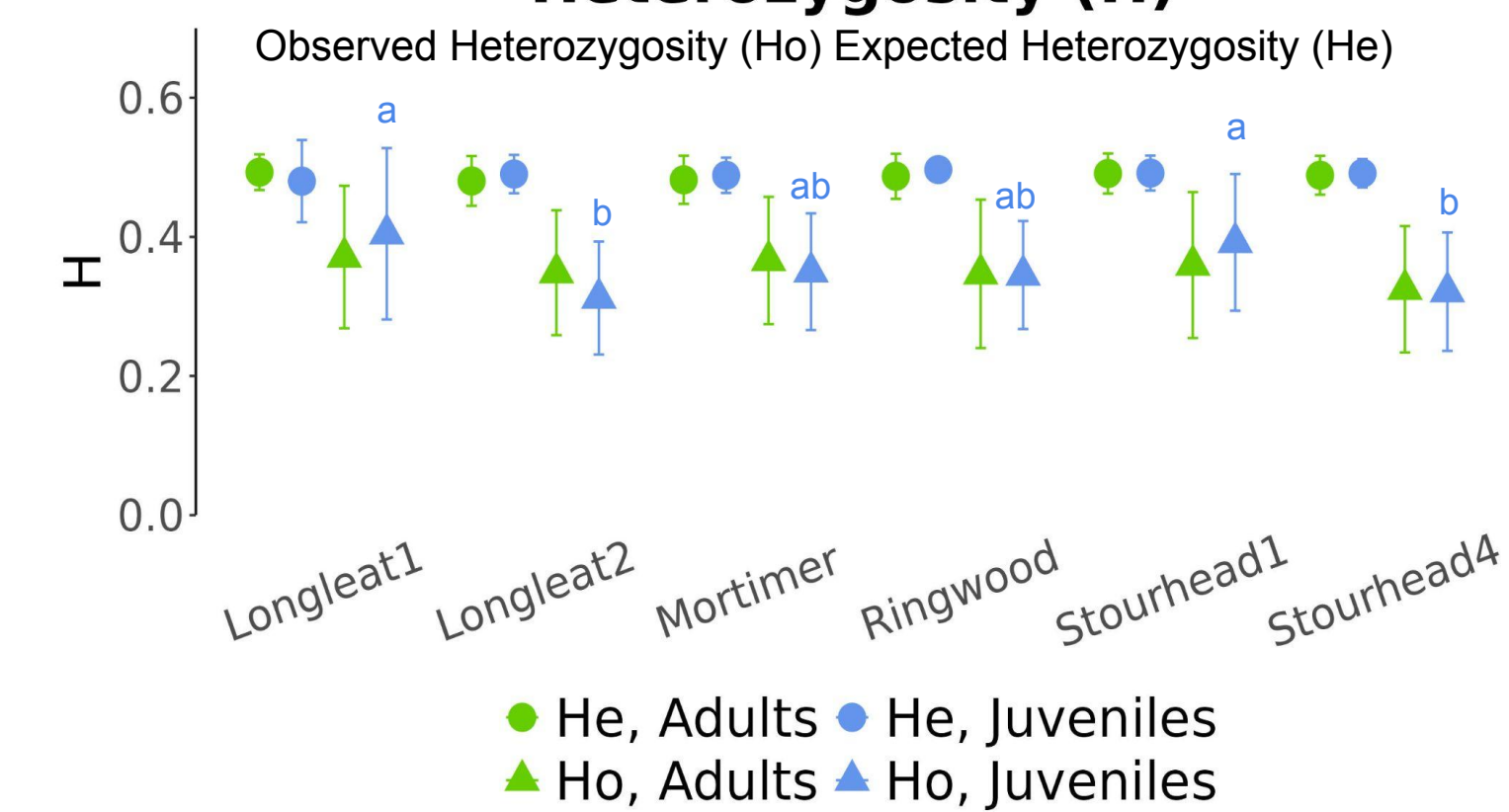
% SNPs under Hardy-Weinberg equilibrium



Inbreeding coefficient (F_{is})



Heterozygosity (H)



F_{is} levels are significantly different only among juveniles sites, Stou4 and Long2 show the highest levels and Long1 the lowest. Long1 and Stou1 juveniles' stands show the highest H_o levels. In contrary, Long2 juveniles exhibit the lowest H_o . H_o & H_e are not significantly different between adults and juveniles in any site. % SNPs that departure from HWE is highest in Mort and Ring juveniles stands.

Conclusions

Some of the stands that show the highest **species diversity** levels also exhibit the highest **genetic diversity** levels. The heterozygosity levels suggest relatively high genetic diversity across all the sites, additionally it **does not been shown to decrease** when the gene pool is transferred to the offspring. **Inbreeding ($F_{is} > 0$)** may be the cause of the lower H_o compared to H_e across all the sites, which may cause future increases in offspring homozygosity and lead to **reduced fitness**.

Next steps

- > To look at seed and plant sources used and to try to determine the provenance of the UK plantations by comparing them to provenance trial stands.
- > Investigate the same matter in a different species to examine if they follow the same pattern.