



Trinity College Dublin

Coláiste na Tríonóide, Baile Átha Cliath

The University of Dublin

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Genetics of Plus Tree Oaks & Progeny

Genetic characterisation of Oak (*Quercus* spp.) for breeding and conservation

Project supervisors:

- Dr Trevor Hodkinson
- Dr Colin Kelleher
- Dr Jo Clark

Project funded by **Future Trees Trust** and **Forest Genetics Resources Trust (FGRT)** Ireland.



Department
for Environment
Food & Rural Affairs

Project Aims

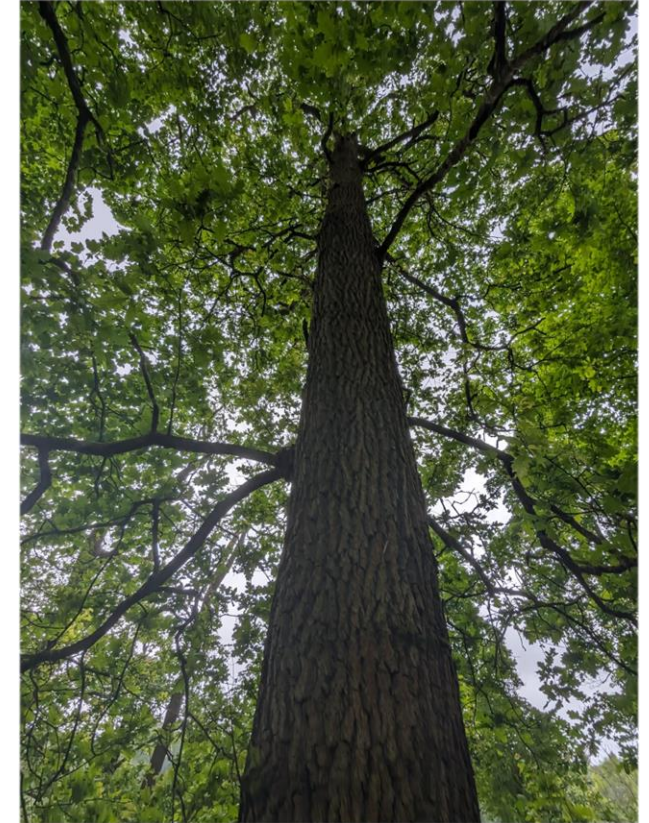
- **Identify potential introgression** within the Plus tree collection through genetic analysis.
- **Quantify the genetic diversity** within the Plus tree collection.
- **Assess the parentage** and identity of progeny sibling families.



Plus Tree Progeny showing good stem straightness Ballyhae Rathluirc Co. Cork Ireland.



Quercus petraea leaf , Ballyhae Rathluirc Co. Cork Ireland.

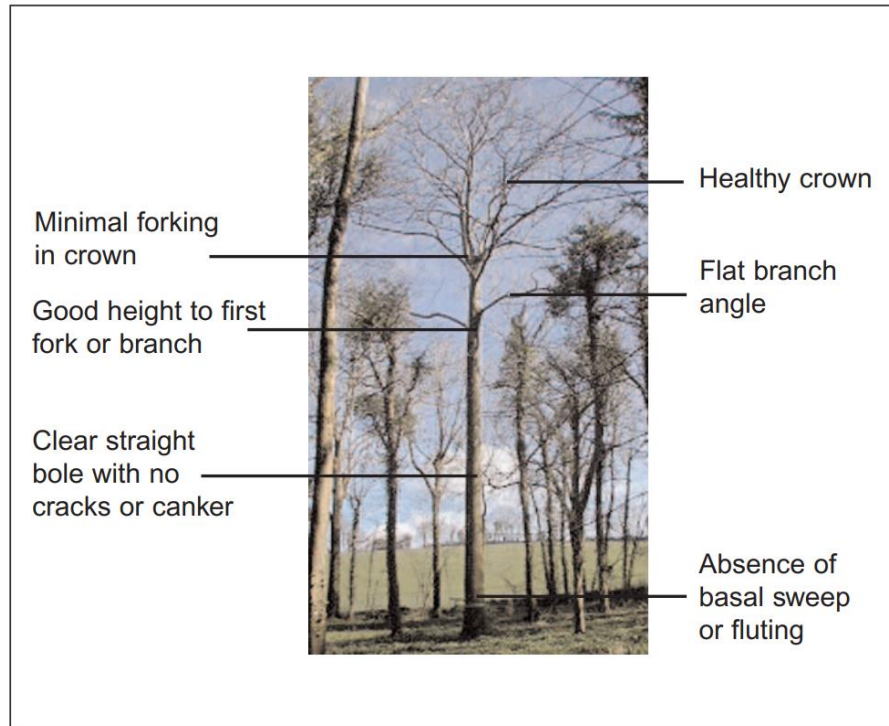


High quality *Quercus robur* Ariundle Oakwood National Nature Reserve Scotland.

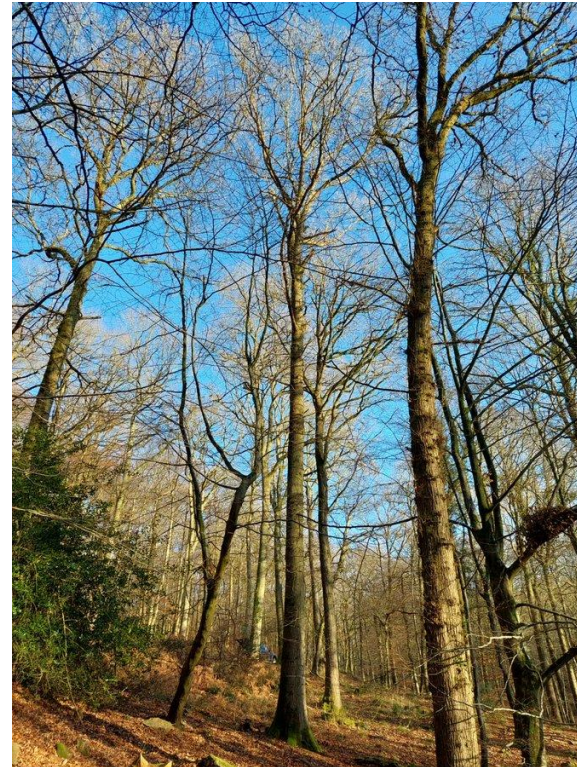
What are plus trees?

Traits selected for in Oak plus tree classification and breeding

- Dominant in the stand
- Tree form (straightness)
- Stem quality (absence of defects)
- Crown health (well distributed and able to sustain future growth)
- Branch free stem (self pruning)



Clark, J. & Wilson, T. (2005)



Plus tree at Forest of Dean Gloucestershire, England

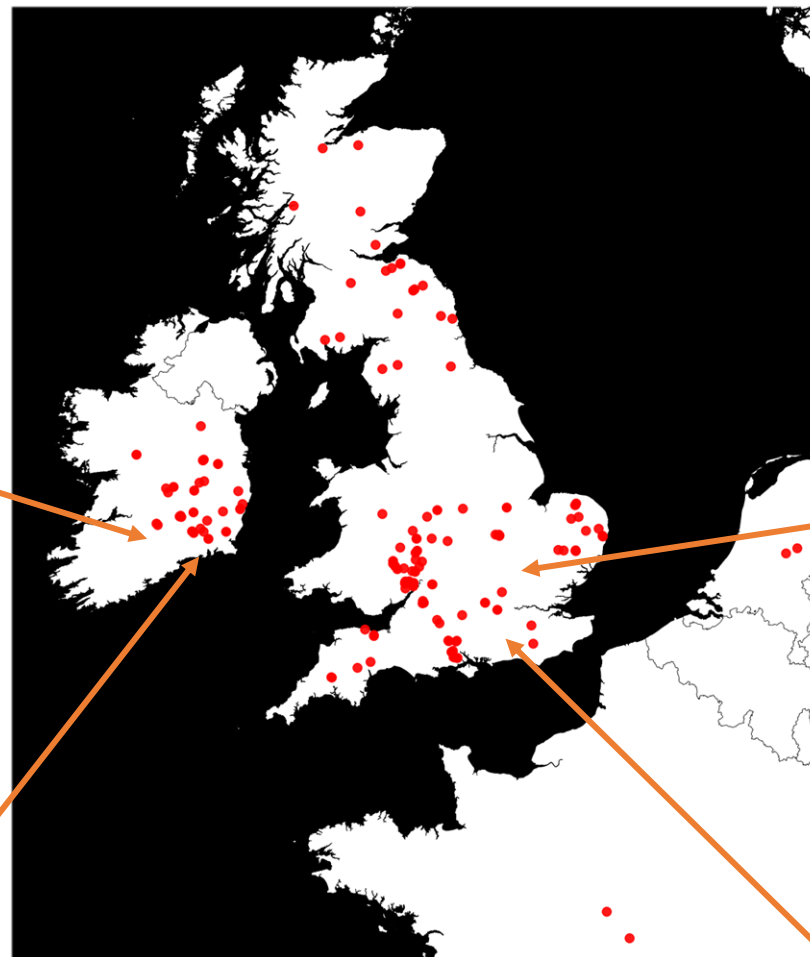


Quercus robur on the road of the Ferry in Tarbert county Kerry

Plus tree source locations and archives



Progeny trial Charleville Ireland



Red points are source of one potential plus tree



Progeny trial Little Wittenham UK



Tree Archive JFK arboretum co. Wexford Ireland

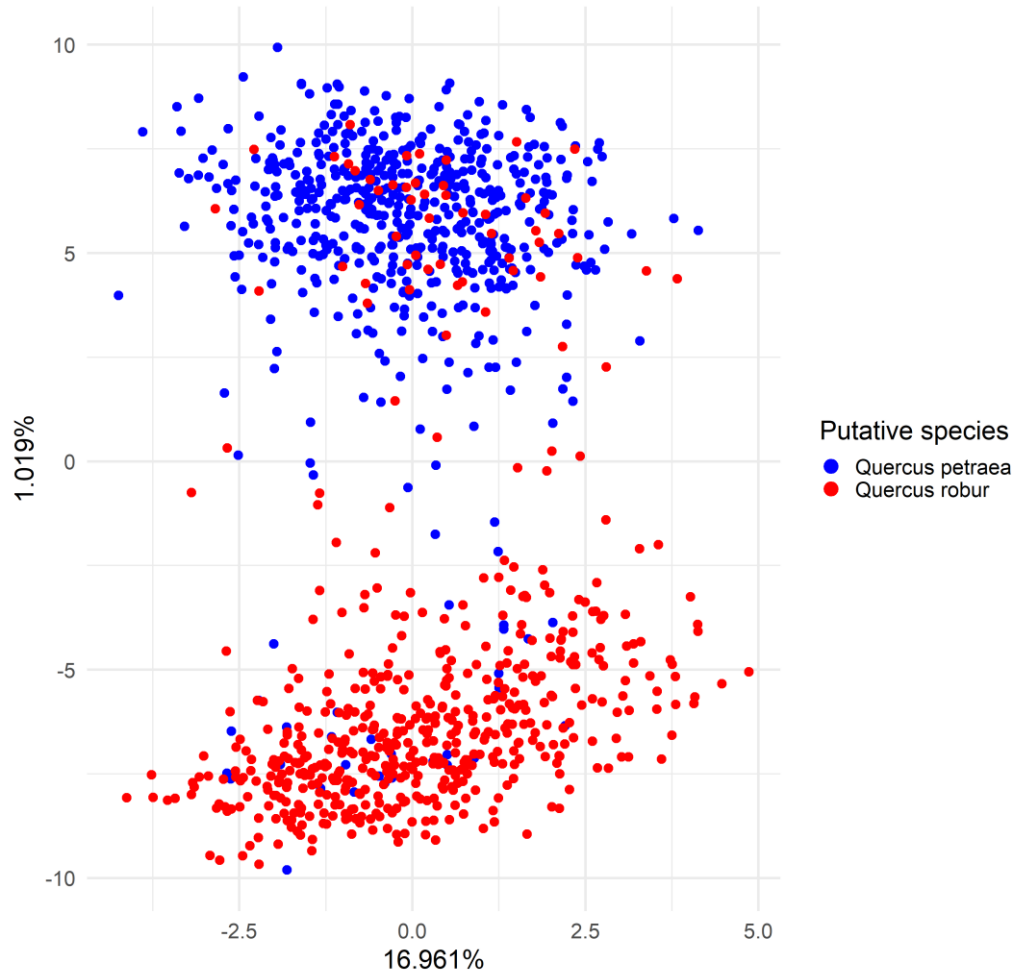


Tree Archive Backhouse woods Kent UK

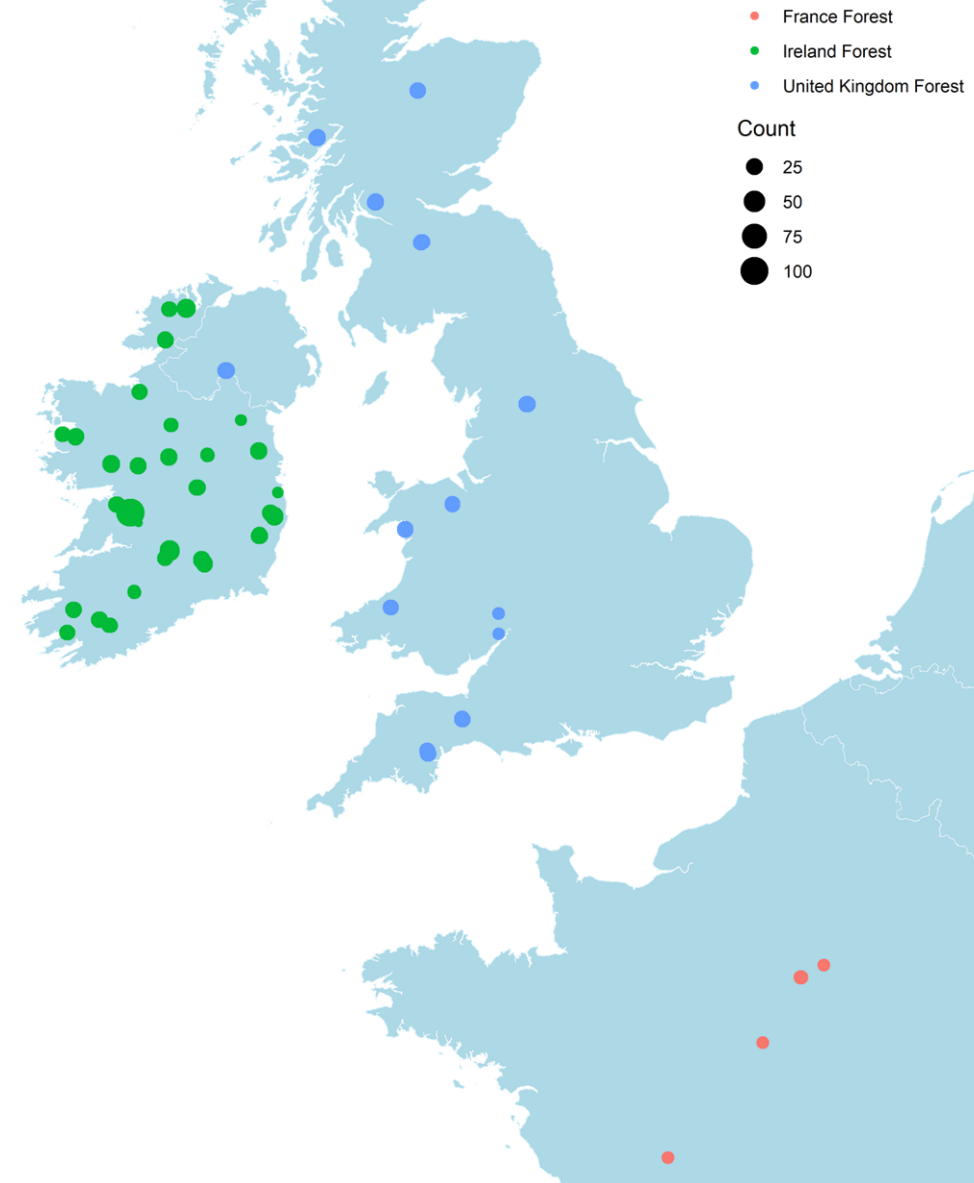
Species Assignment

All individual trees will cluster into two species groupings.

PCA plot of 412 nuclear SNPs for 1365 Samples

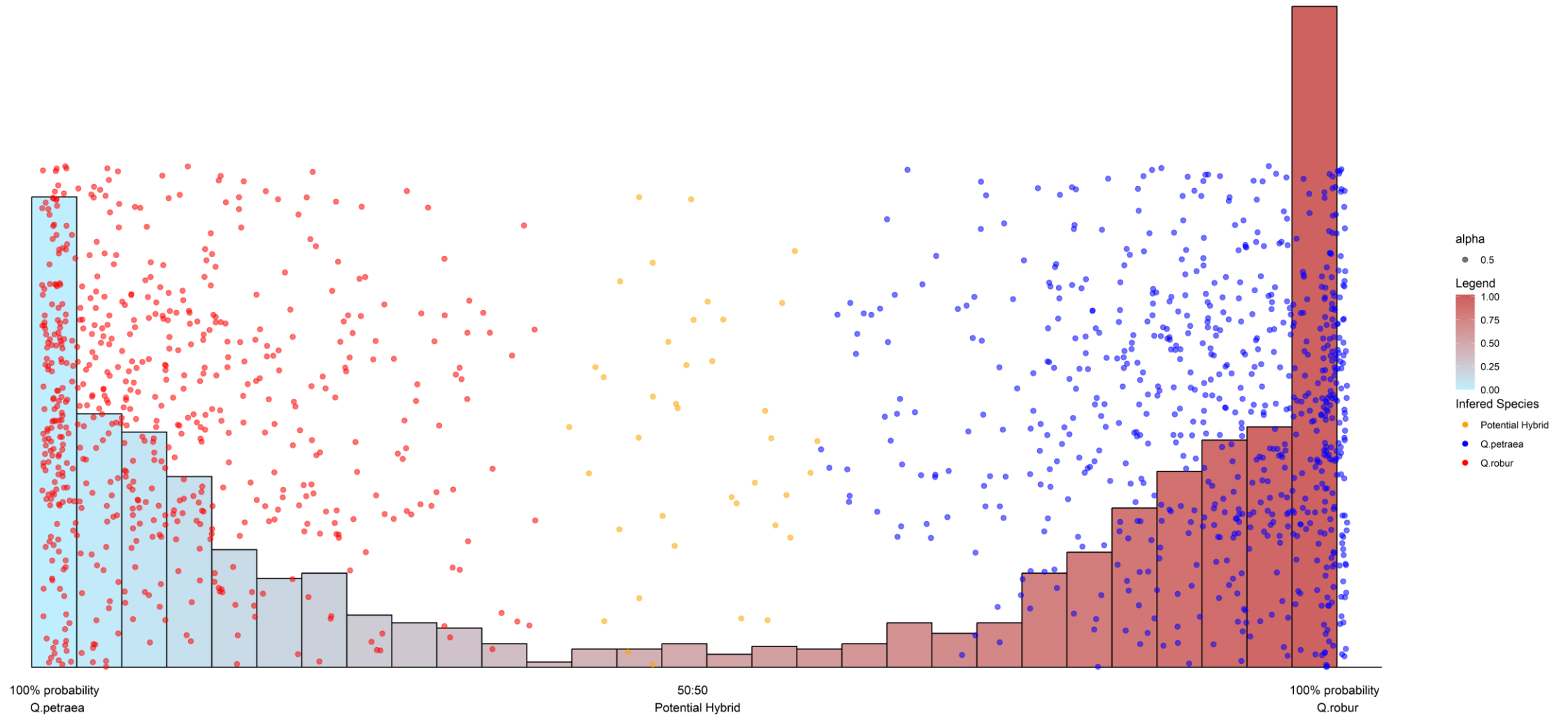


Reference data across the Plus tree climate/growing range.

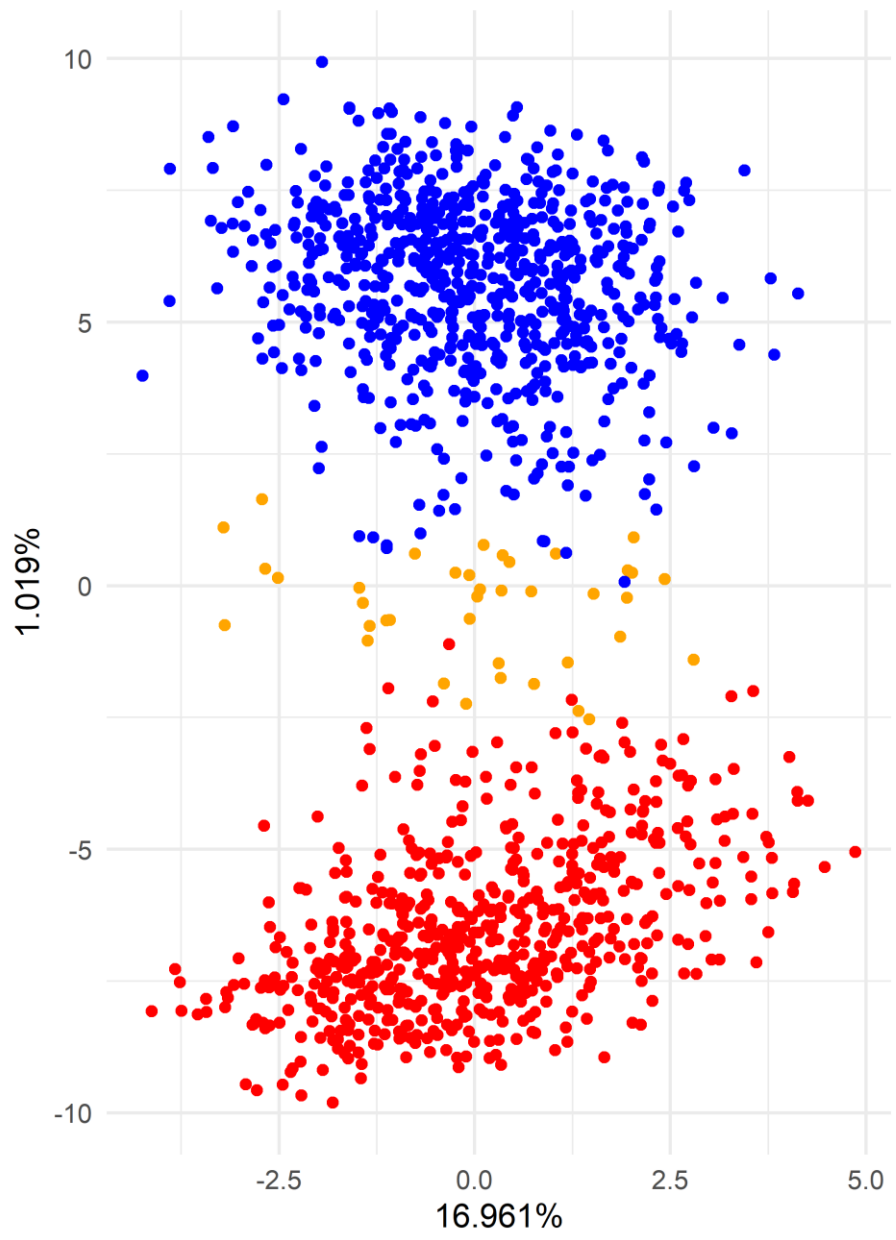


sNMF (Sparse Non-negative Matrix Factorization) species assignment probability.

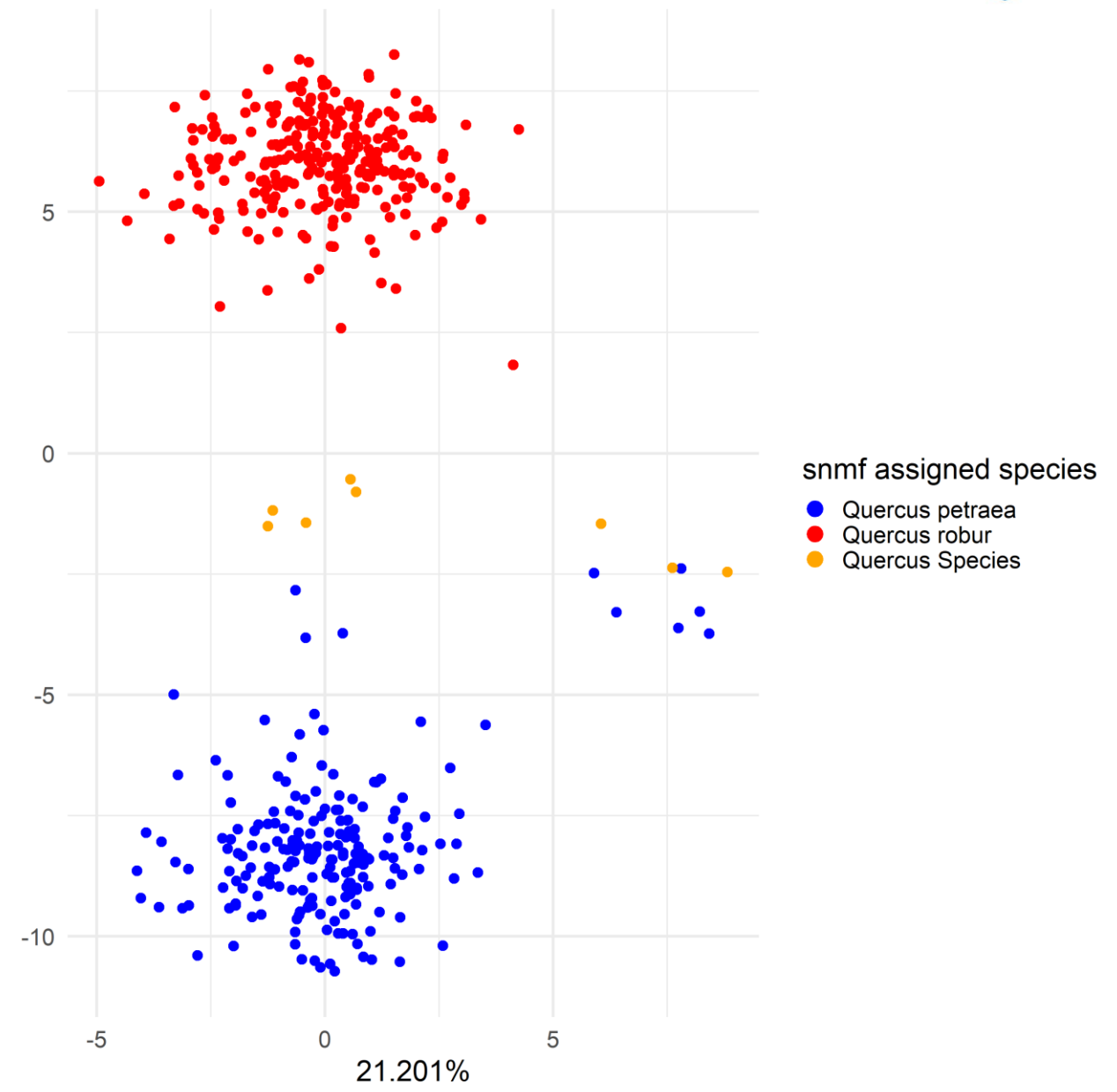
Probability of belonging to *Q.petraea* or *Q.robur*



PCA plot of 412 nuclear SNPs for 1365 Samples



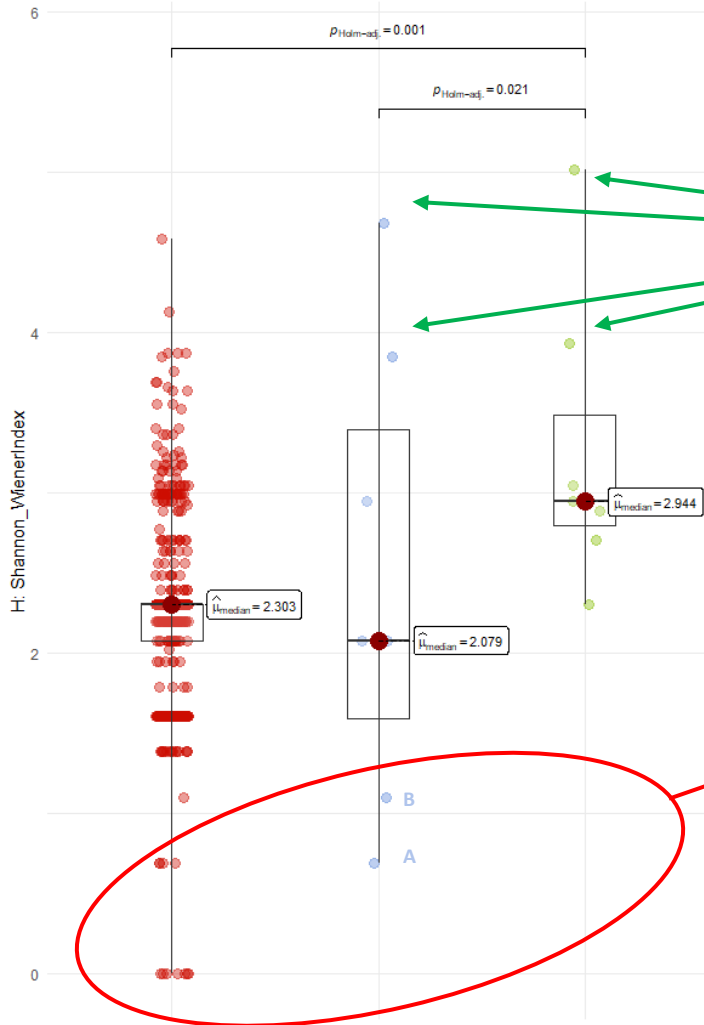
PCA plot of 412 nuclear SNPs for 480 Samples



Varied levels of genotype richness and evenness across plus trees & progeny

H: Shannon_Wiener Index by Population

$\chi^2_{Kruskal-Wallis}(2) = 12.371, p = 0.002, \hat{\epsilon}^2_{ordinal} = 0.020, CI_{99\%} [0.010, 1.000], n_{obs} = 616$

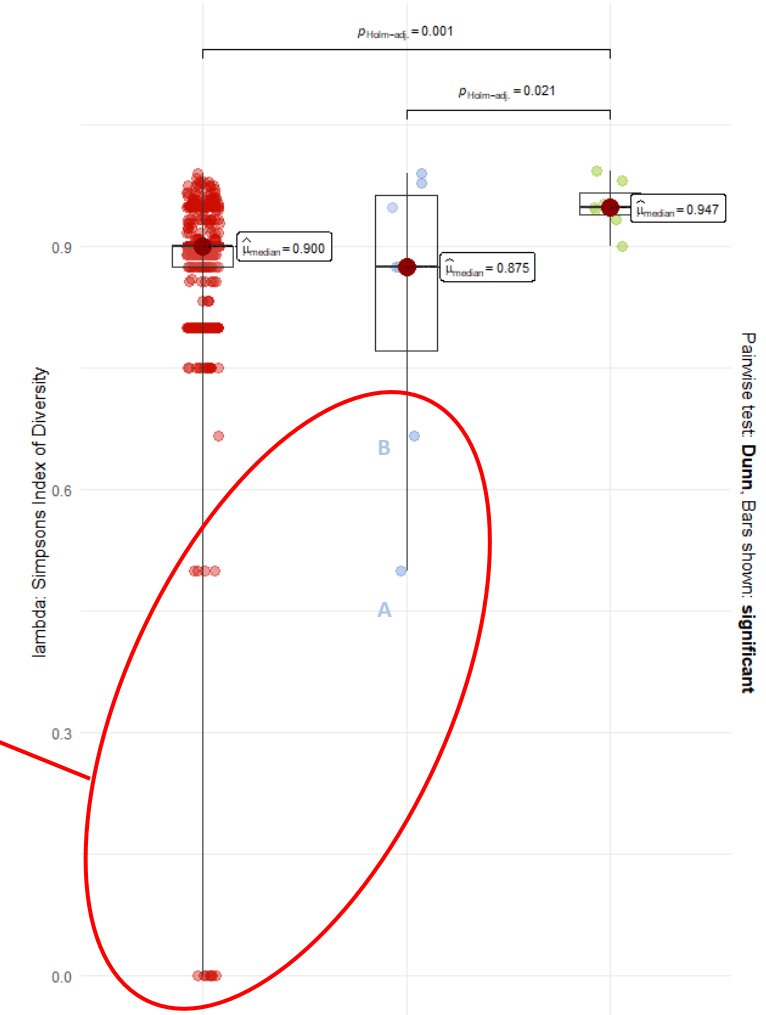


Many unique genotypes with high genetic diversity.

reduced diversity and dominance of few genotypes.

lambda: Simpsons Index of Diversity by Population

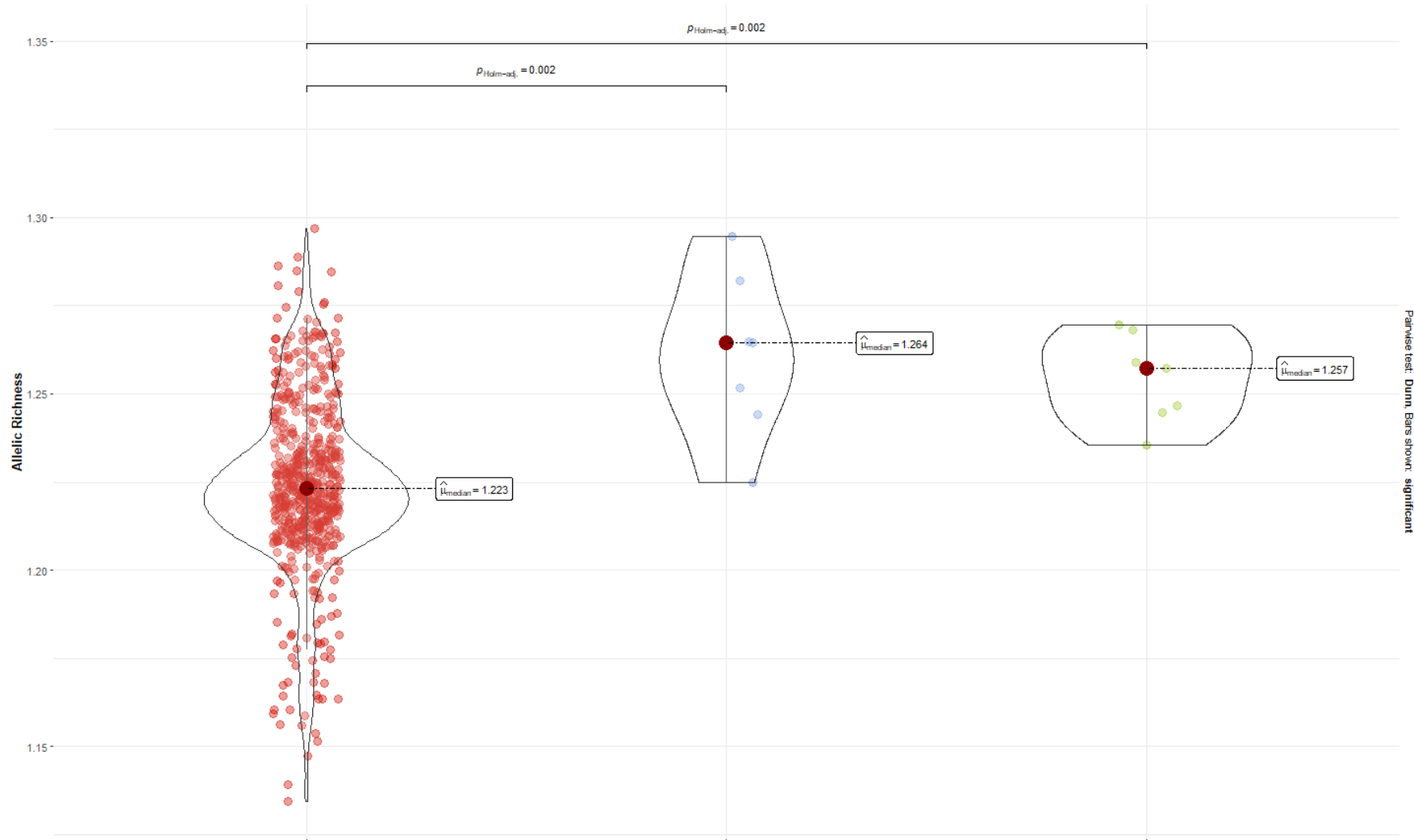
$\chi^2_{Kruskal-Wallis}(2) = 12.371, p = 0.002, \hat{\epsilon}^2_{ordinal} = 0.020, CI_{99\%} [0.009, 1.000], n_{obs} = 616$



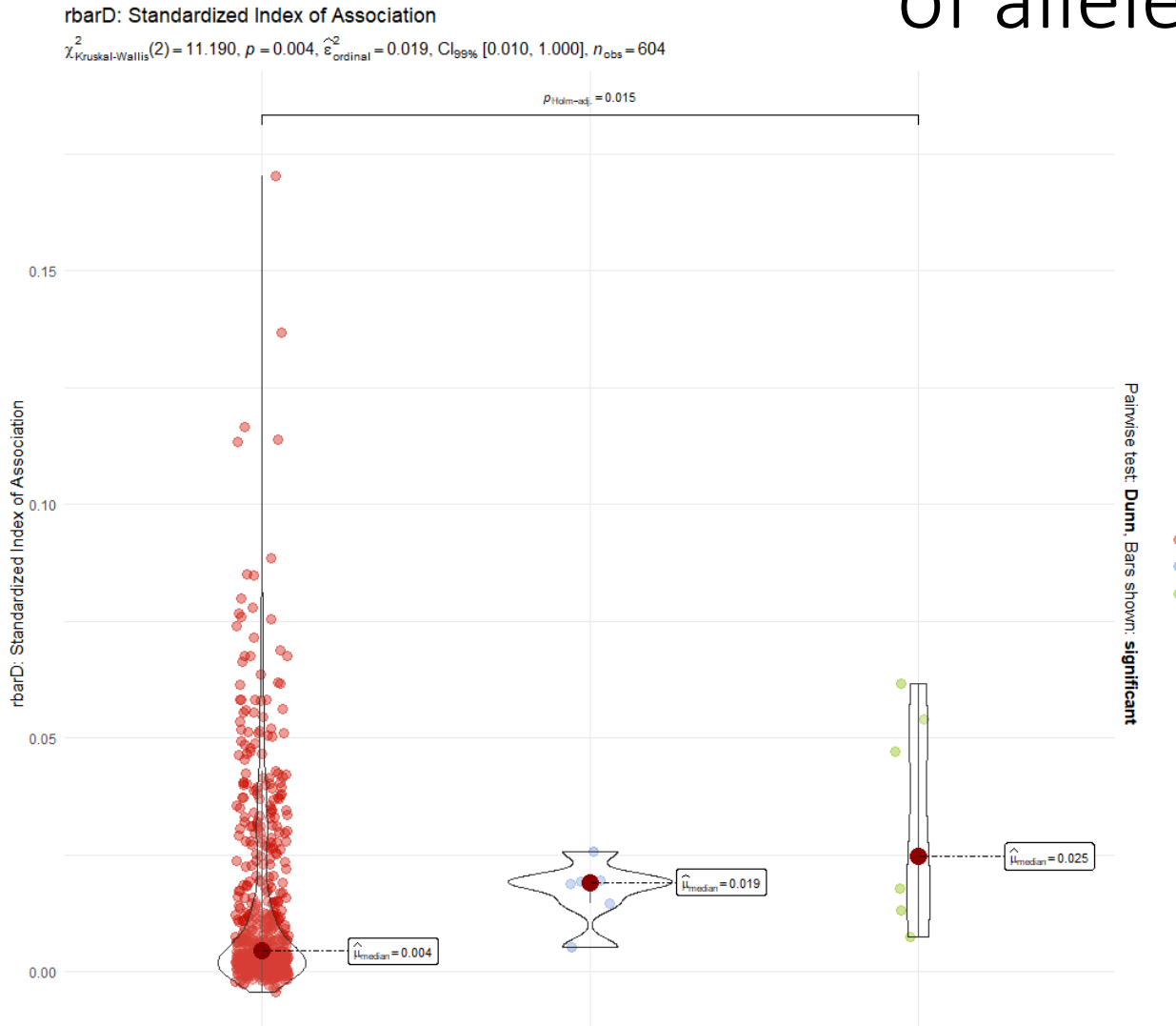
Plus Tree & Progeny show significantly **higher Allelic richness** when compared to the reference datasets.

Allelic Richness by Population

$\chi^2_{Kruskal-Wallis}(2) = 23.351, p = 8.499e-06, \hat{\epsilon}^2_{ordinal} = 0.038, CI_{99\%} [0.022, 1.000], n_{obs} = 616$



Plus tree progeny indicate **non-random** association of alleles.

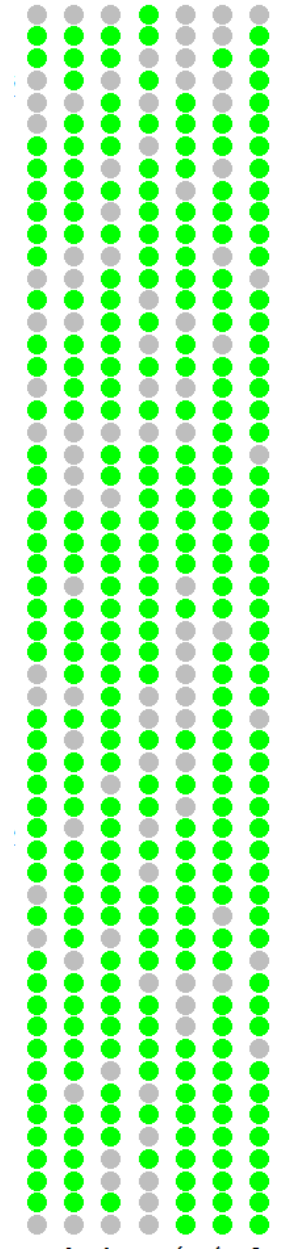


- Non-random association of alleles may indicate clonal reproduction or strong selection as expected with progeny tree seed collection.
- Indicates potential of population sub structure.
- Values near 0 Suggest **random association** of alleles, typical of sexually reproducing populations or random selection.
- Plus trees are within the expected distribution of the reference forest population.

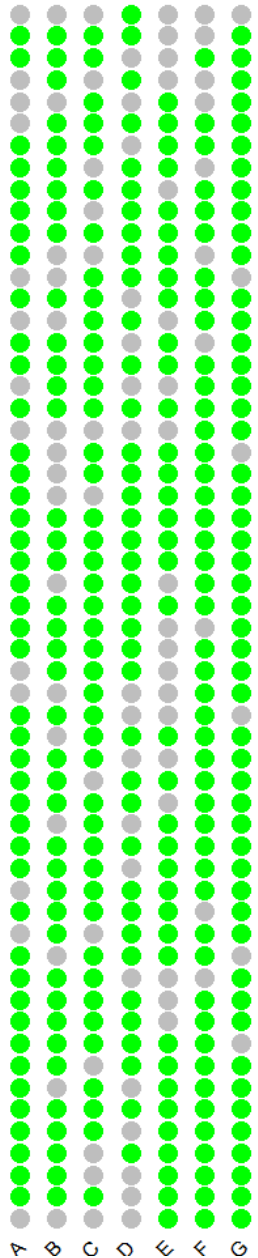
Parentage and identity of progeny sibling families.

Progeny Forest
56 families * 39 blocks

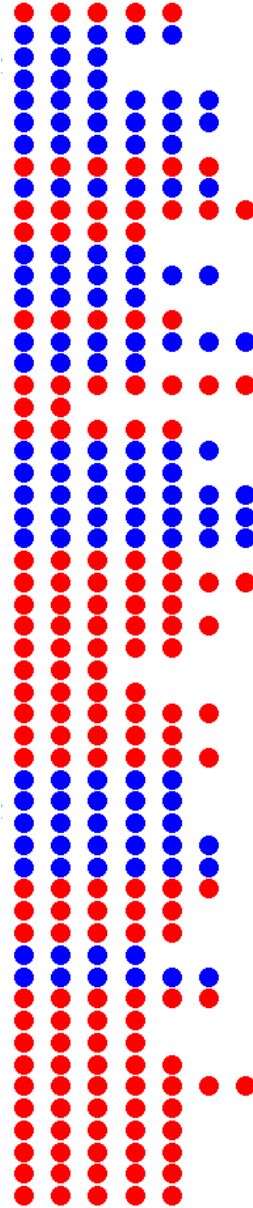
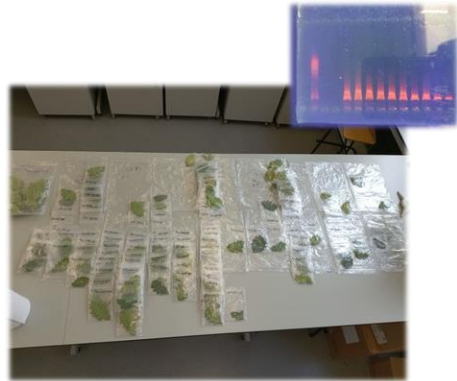
69 m



Are their hybrids or misassigned species identities in the progeny demonstration line?

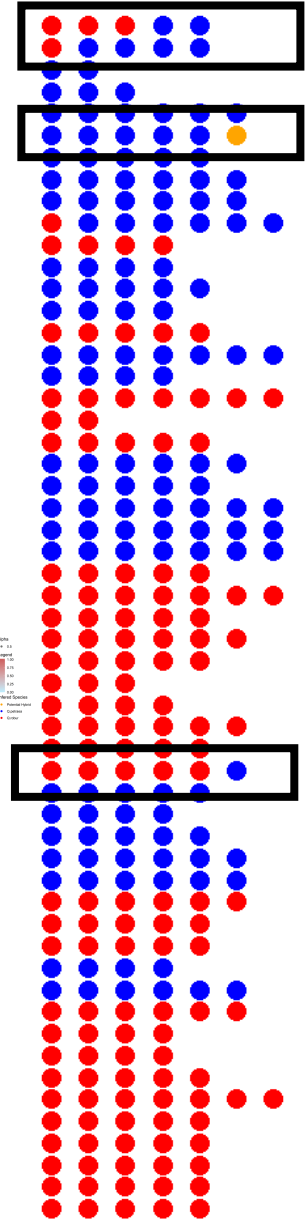
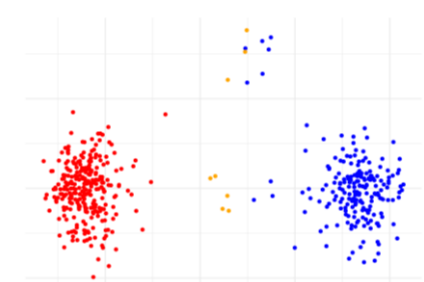
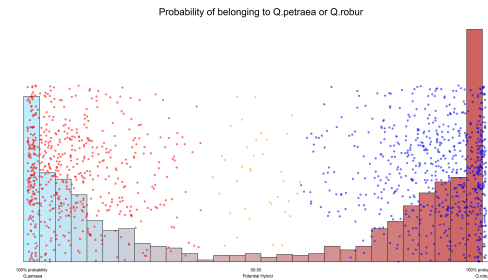


Sampling and SNP sequencing.

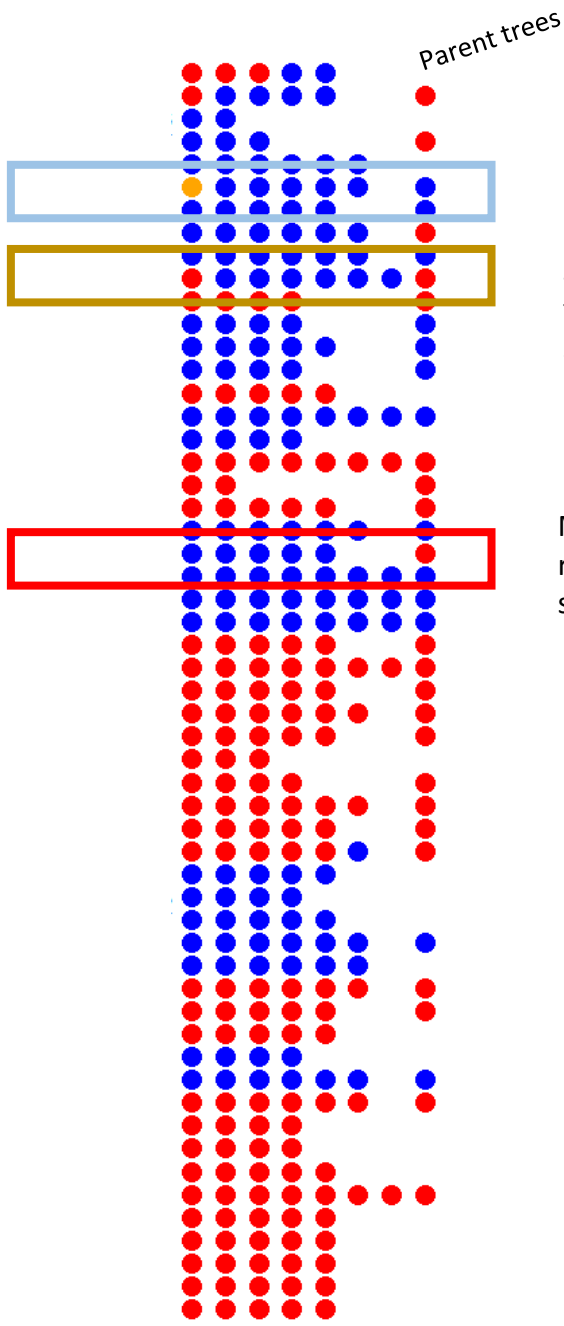


- *Quercus petraea*
- *Quercus robur*
- *Quercus robur x petraea*

Species assignment using sNMF



Can we confirm species assignment using tSNE clustering?

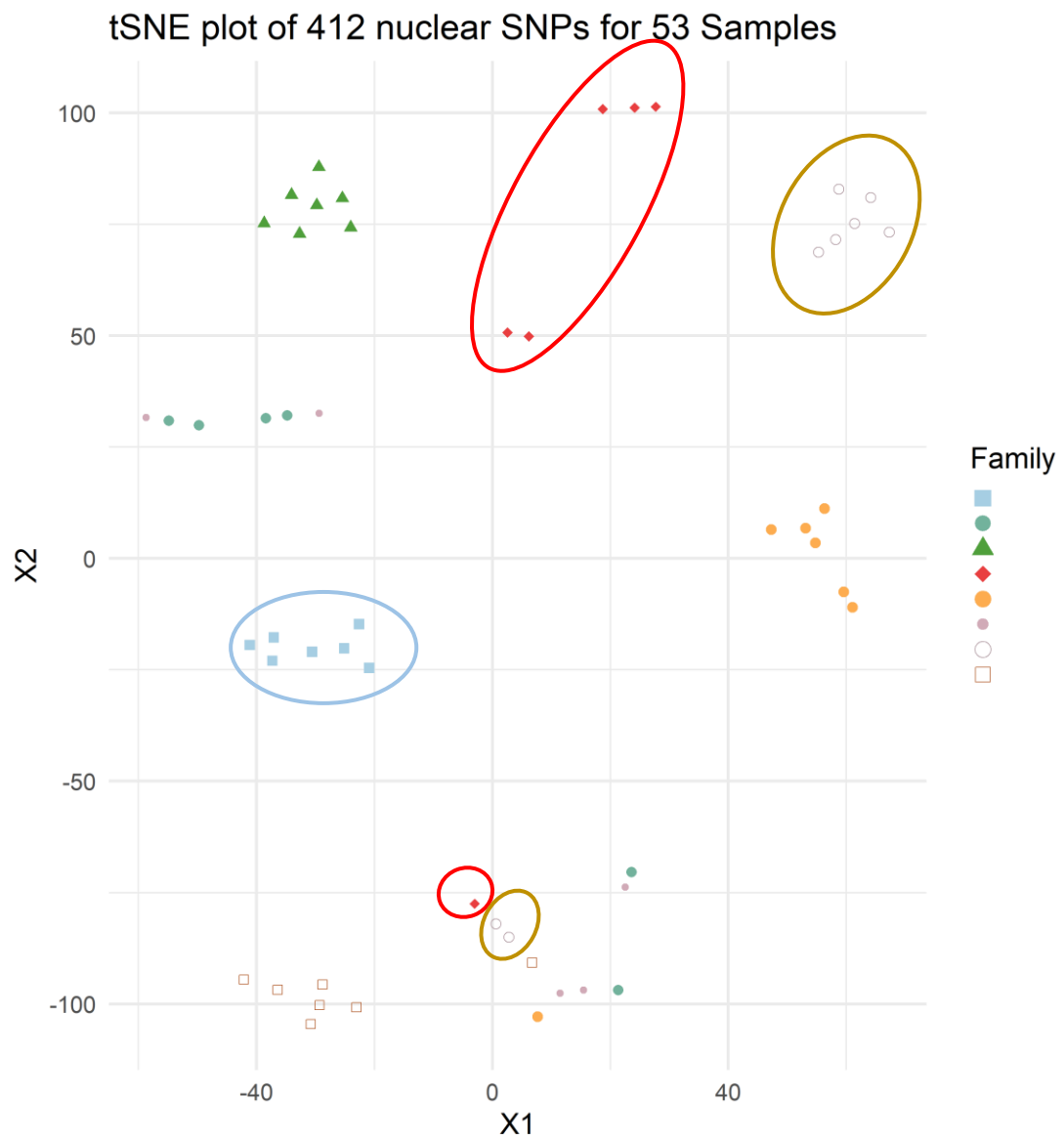


Potential F1 hybrid

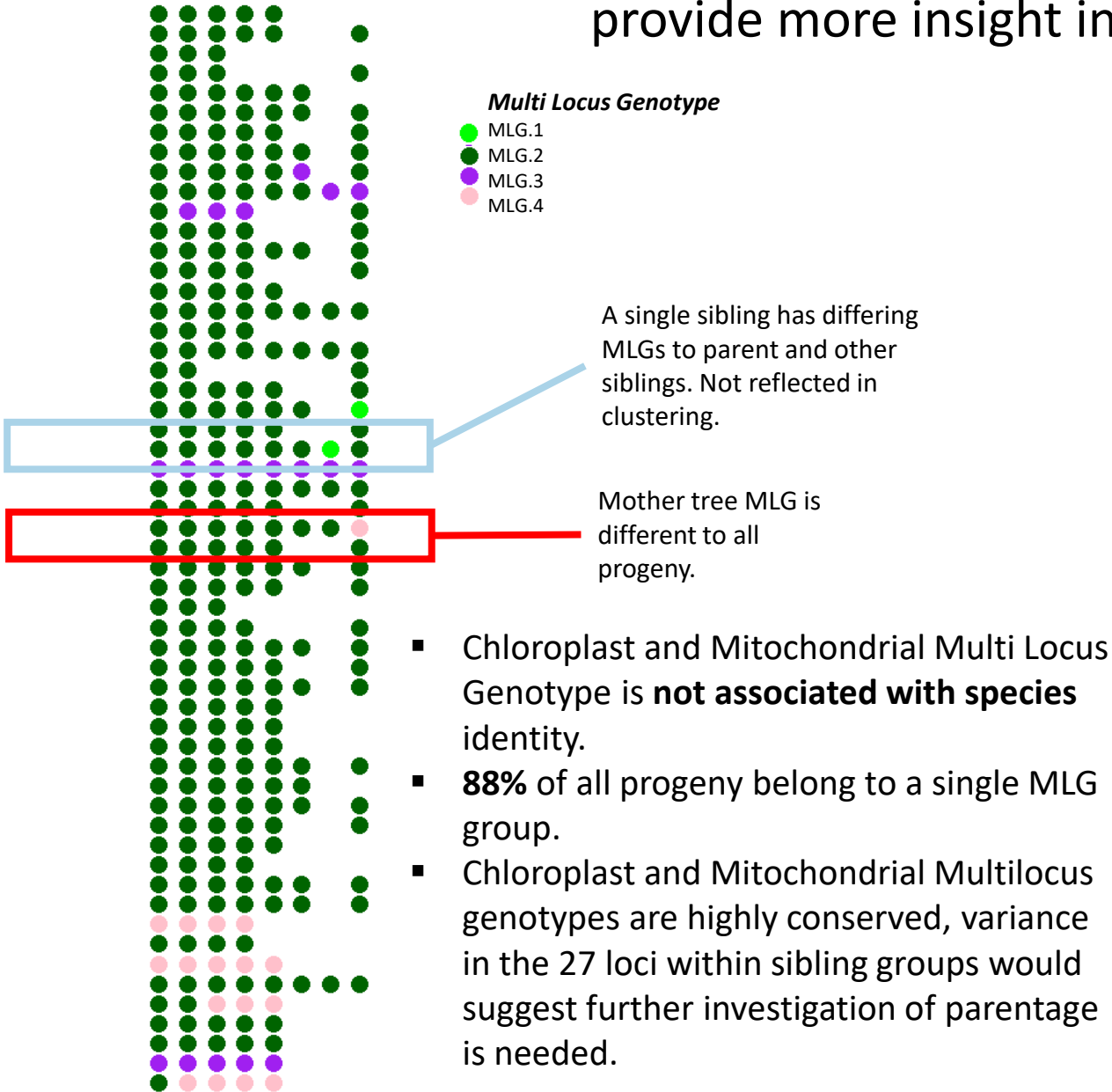
Six siblings entirely different from mother tree and one sibling

Mother tree clustering near *robur* and potential substructures in sibling groups

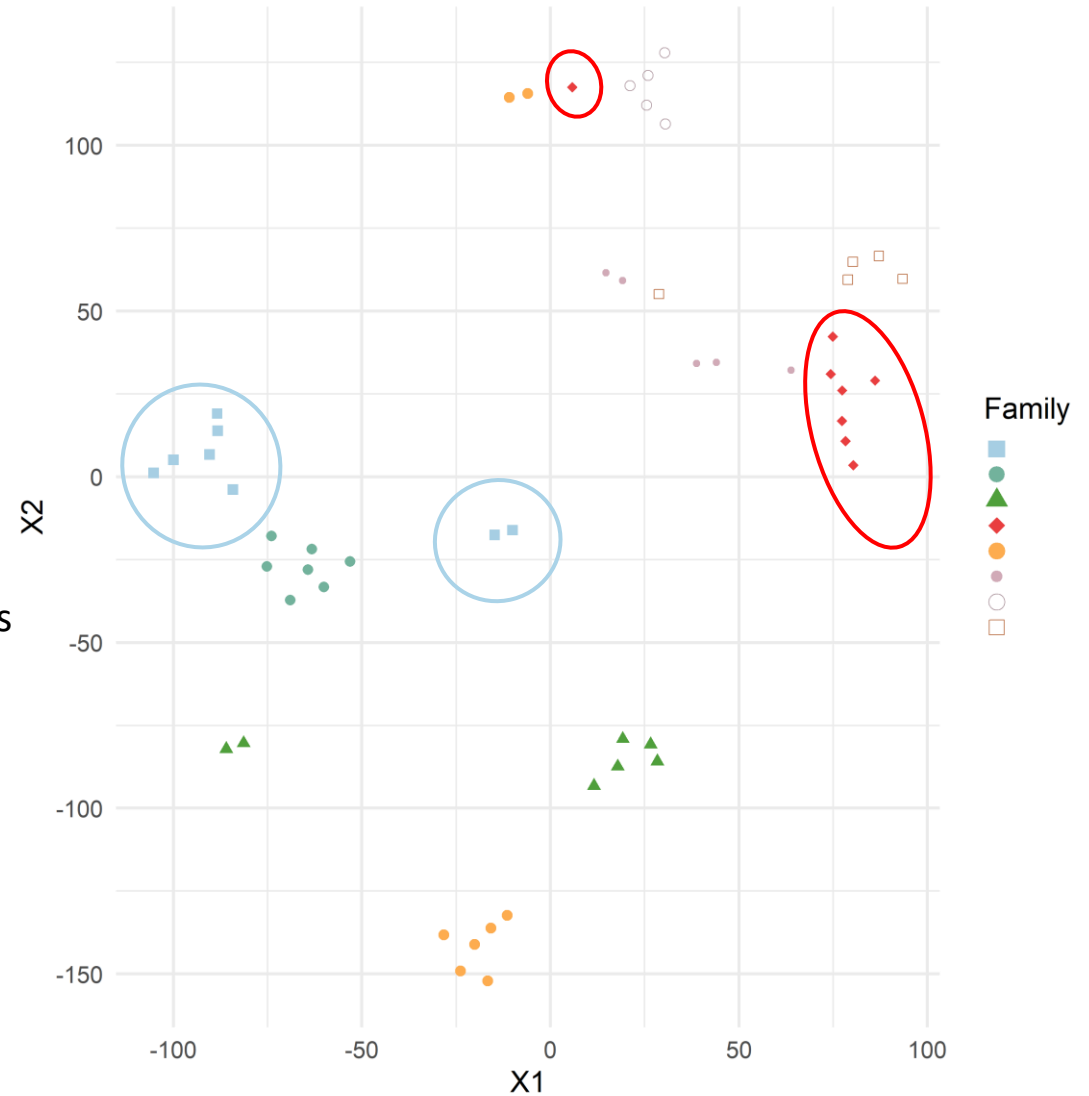
- *Quercus petraea*
- *Quercus robur*
- *Quercus robur x petraea*



Can Chloroplast and Mitochondrial Multilocus genotypes provide more insight into parentage?



tSNE plot of 412 nuclear SNPs for 53 Samples



Further work

- Assess the influence of other *Quercus* species on our collection.
- Homing in on the effect of population substructures on genetic diversity metrics.
- Increase the resolution of the Chloroplast and Mitochondrial Multi Locus Genotypes.
- Fully explain the relationships within each sibling group using nuclear genotypes.
 - Can leaf morphology give some insight into this?