Trinity College Dublin
Coláiste na Tríonóide, Baile Átha Cliath
The University of Dublin

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

Project supervisors:

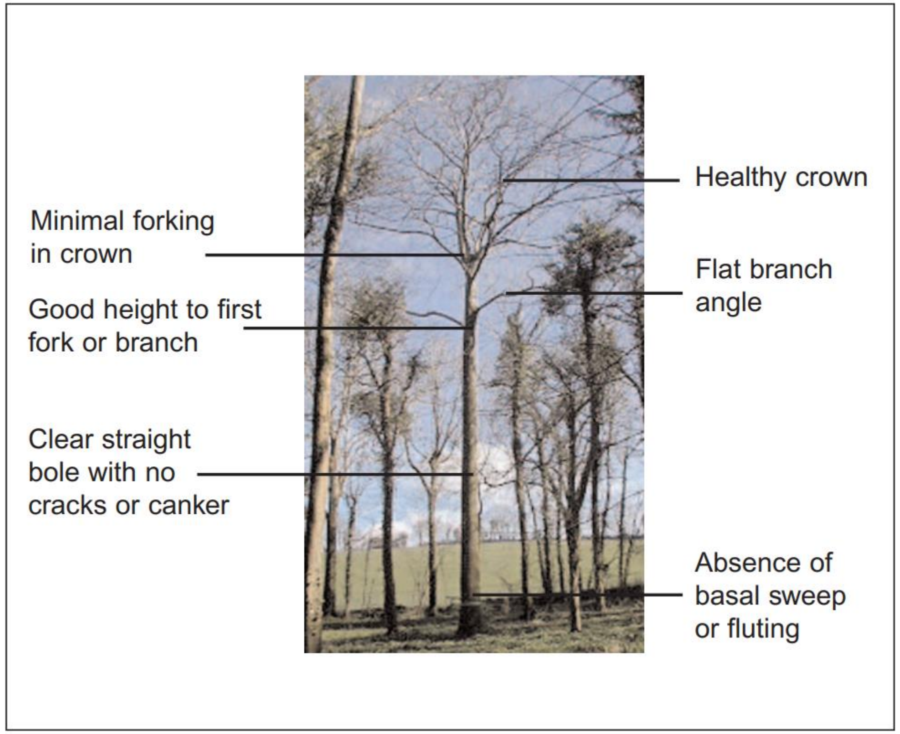
- Dr Trevor Hodkinson
- Dr Colin Kelleher
- Dr Jo Clark

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

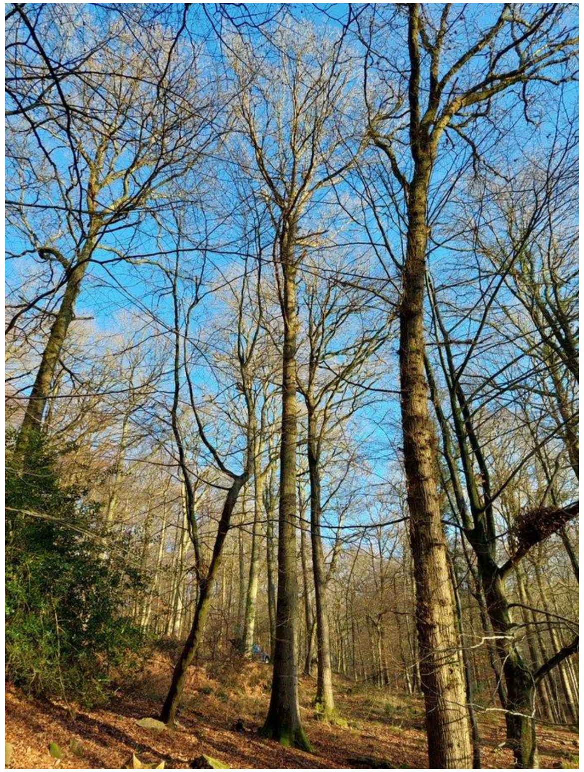
What are plus trees?

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)



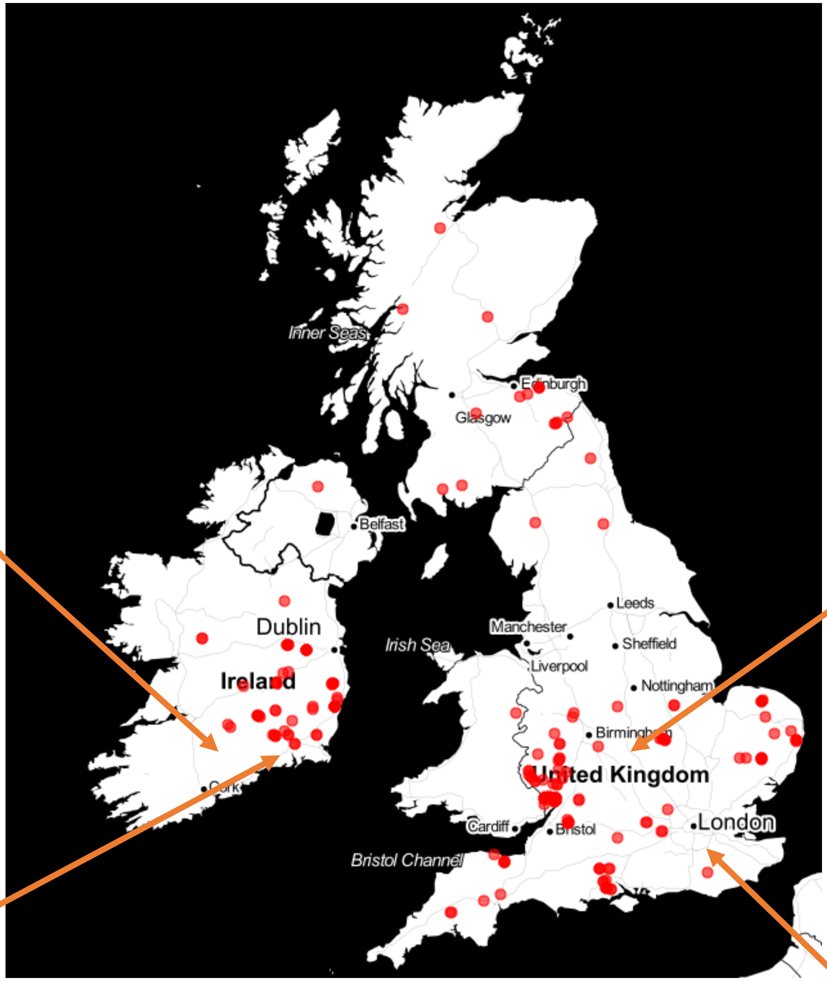
Plus tree at Forest of Dean Gloucestershire, England

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

Where are the Plus trees now?

Progeny trial Charleville Ireland

Tree Archive JFK arboretum co. Wexford Ireland



Red points are source of one potential plus tree

Progeny trial Little Wittenham UK

Tree Archive Backhouse woods Kent UK

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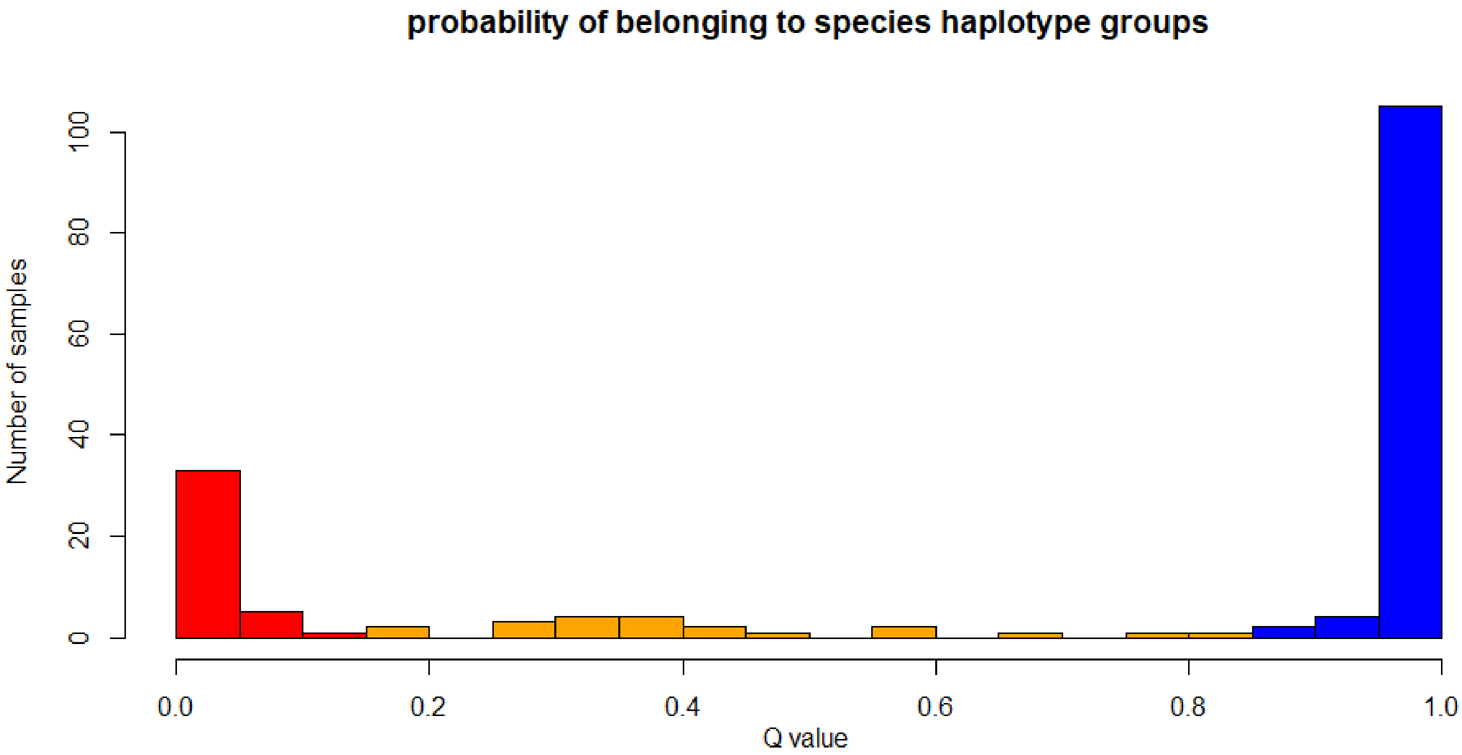
Project Aims

- Identify using genomic markers the true species of each individual tree in addition to the classification of any hybrids within the collection.
- Quantify the genetic variance seen within the collection and compare to native regional populations and to populations abroad.
- Identify morphological leaf features associated with the plus tree collection.
- Identification of plus tree associated SNPs

Structural analysis for species classification

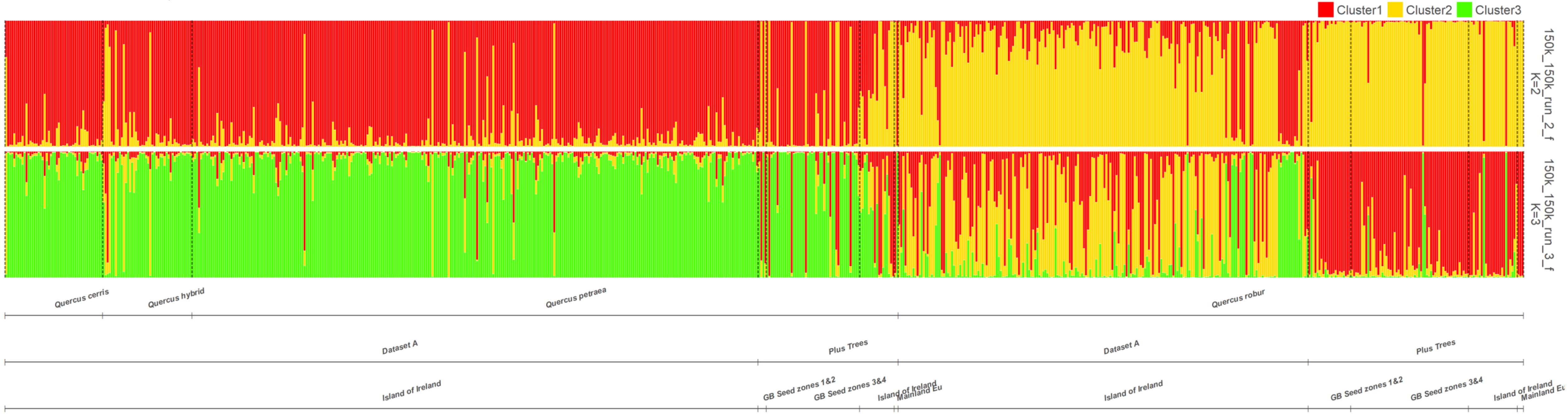
- We would expect highly distinct peaks with gradual declines with little to no hybrids.
- Potential reflection of selection bias
- Potential of genetic hybrids



Q. petraea (Red) Hybrids (Orange) Q. robur (Blue)

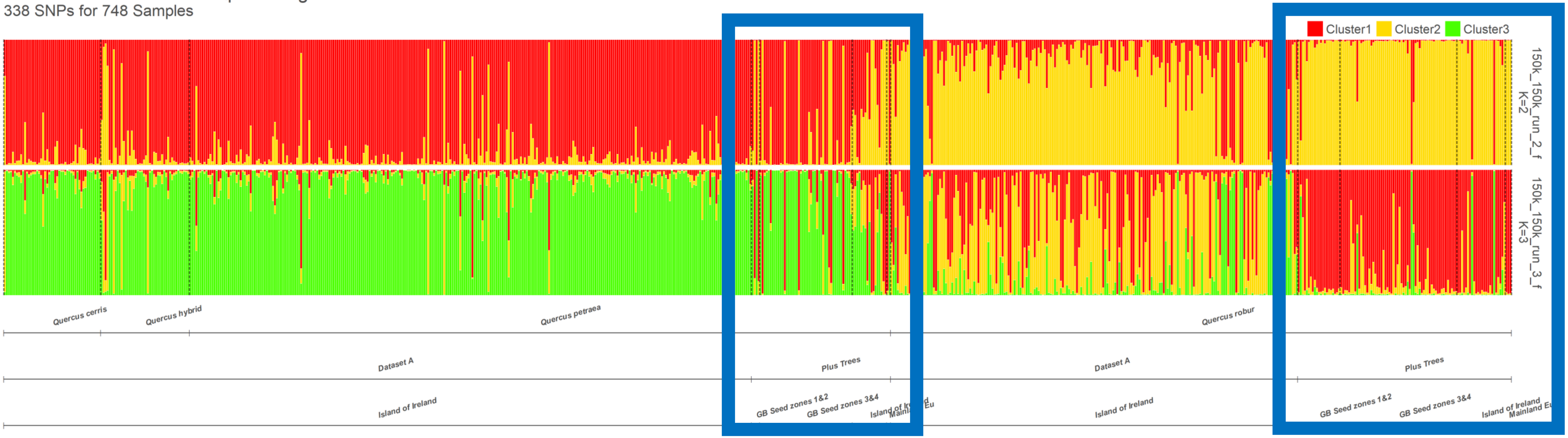
STRUCTURE admixture Qplot using K = 2-3.

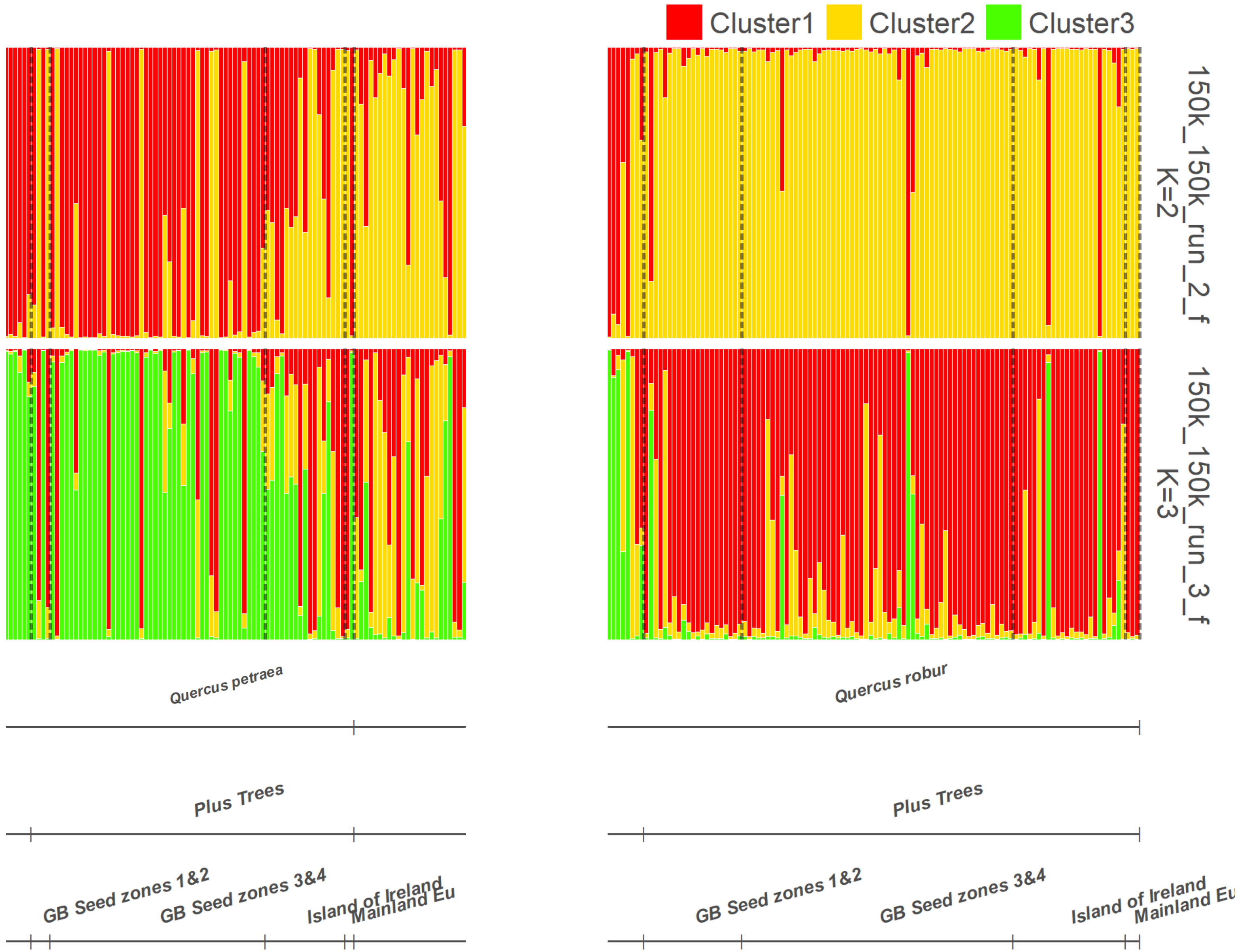
338 SNPs for 748 Samples

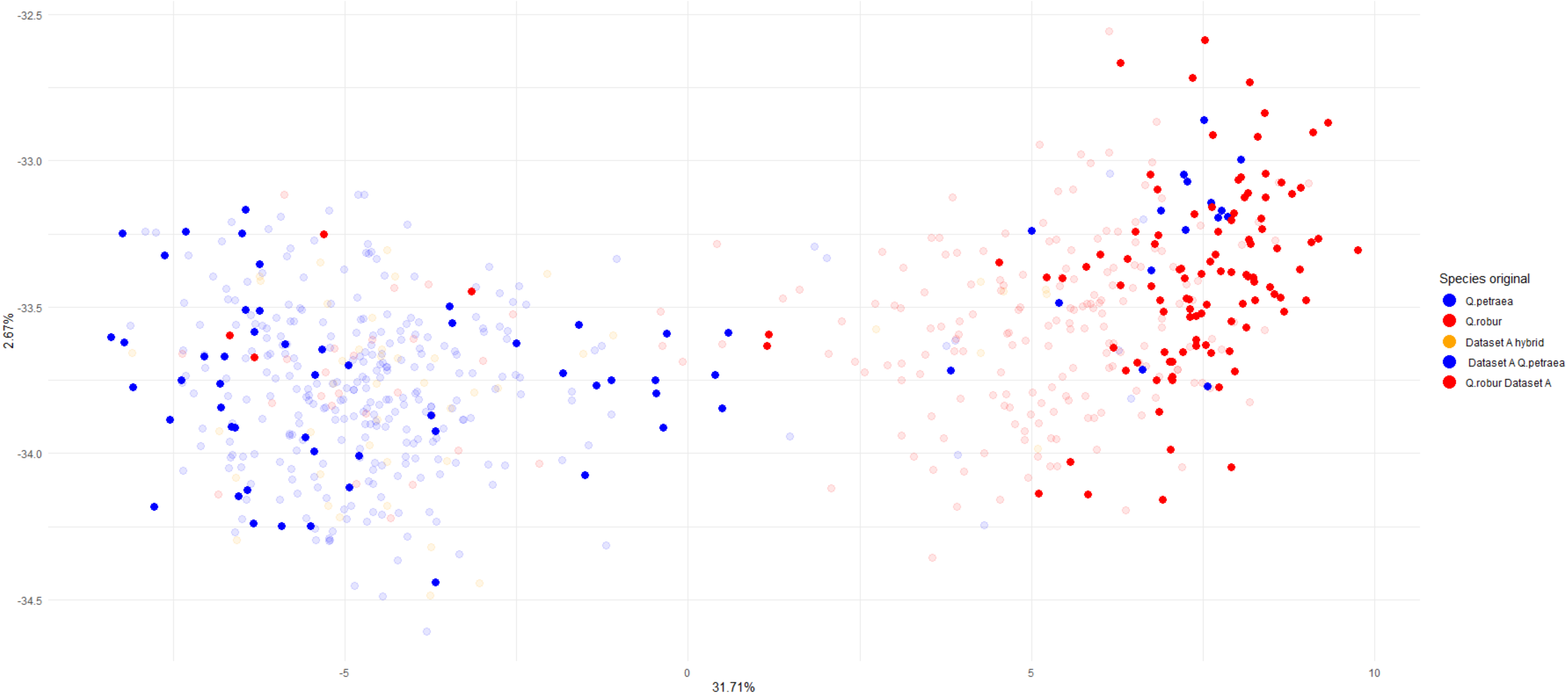


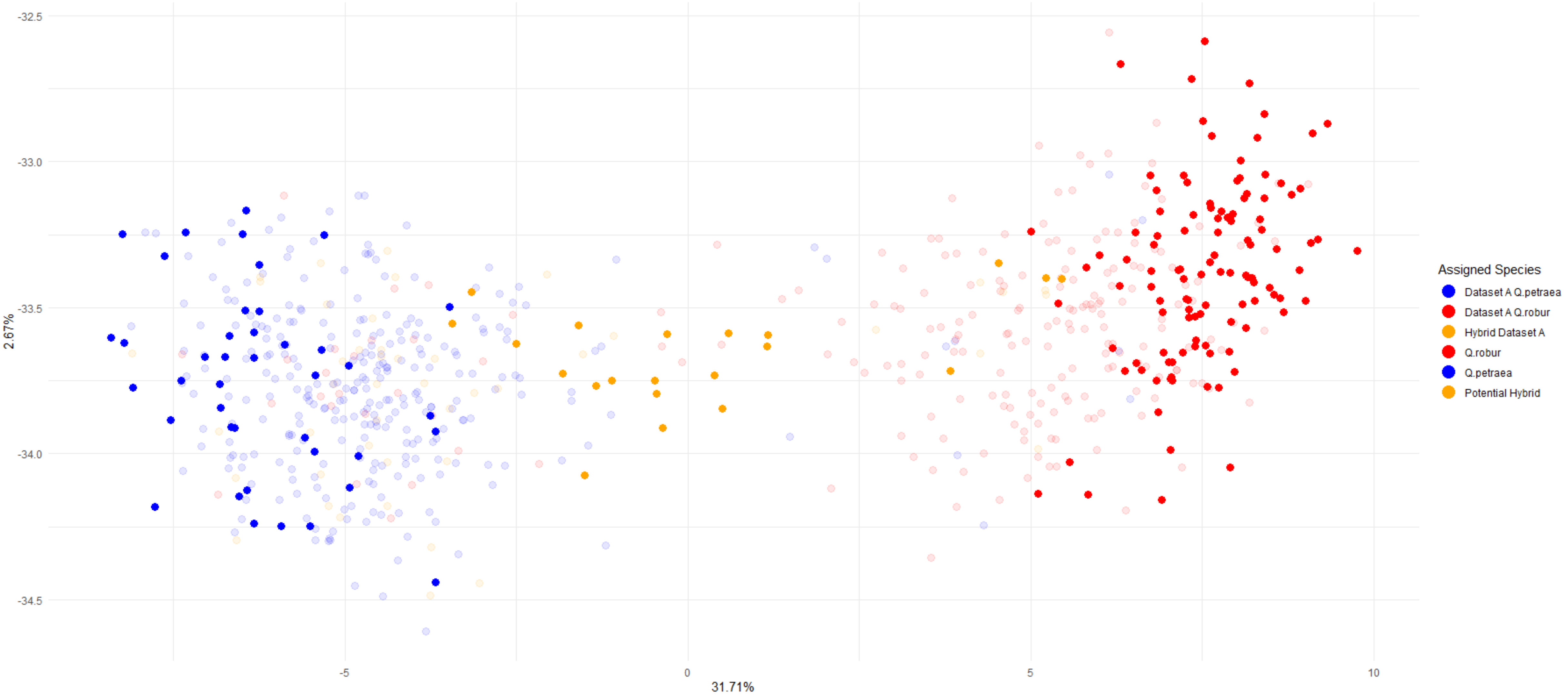
Data courtesy of Dr Sam Belton

STRUCTURE admixture Qplot using K = 2-3.
338 SNPs for 748 Samples




Cluster1
Cluster2
Cluster3
150k_150k_run_2_f
K=2
150k_150k_run_3_f
K=3
Quercus petraea
Quercus robur
Plus Trees
Plus Trees
GB Seed zones 1&2
GB Seed zones 3&4
Island of Ireland
Mainland Eu
GB Seed zones 1&2
GB Seed zones 3&4
Island of Ireland
Mainland Eu


-32.5
-33.0
-33.5
-34.0
-34.5
2.67%
-5
0
5
10
31.71%
Species original
Q.petraea
Q.robur
Dataset A hybrid
Dataset A Q.petraea
Q.robur Dataset A


-32.5
-33.0
-33.5
-34.0
-34.5
2.67%
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0
5
10
31.71%
Assigned Species
Dataset A Q.petraea
Dataset A Q.robur
Hybrid Dataset A
Q.robur
Q.petraea
Potential Hybrid

- Across all three analysis approaches species assignment where in agreement for **79.68%** of samples.
- When we remove samples with a missingness greater than 30% **113 *Q.robur* , 41 *Q.petraea* and 21 potential hybrids.**
- **12** F1 potential hybrids originally assigned 10 *Q.petraea* 2 *Q.robur*,
- **5** F2 potential *Q.petraea* backcross hybrid (qpe403024,qpe403036, qpe405001, qpeIRE010, qro202001)
- **4** F2 potential *Q.robur* backcrosses hybrid (qpeIRE030, qro108001, qroIRE017, qroIRE031).

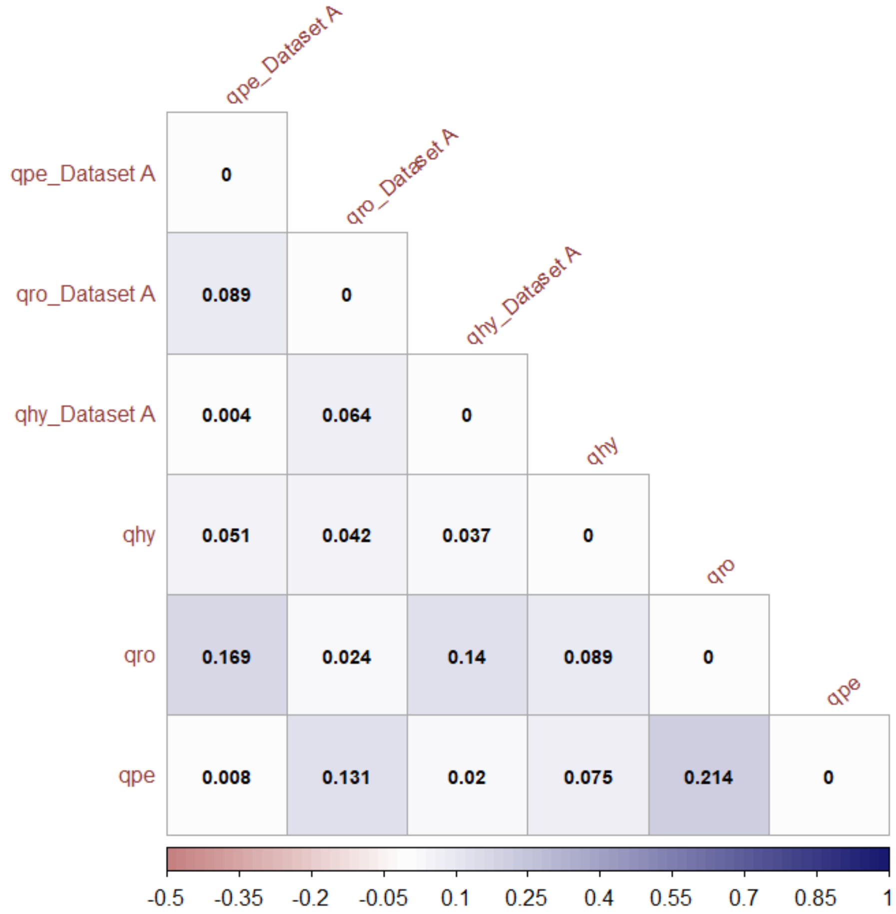
		Original		
		Q.petraea	*Q.robur*	Total
Assigned	*Q.petraea*	**38**	**3**	41
	Q.robur	**16**	**97**	113
	Potential hybrid	**15**	**6**	21
	Total	69	106	175

Allelic richness

	Plus trees			Dataset A (Island or Ireland)		
Species	**qro**	**qpe**	**qhy**	**qro**	**qpe**	**qhy**
N trees	113	41	21	203	280	45
Total sum of Alleles	680.95	677.13	676.23	703.13	690.96	694.66
Mean Allelic Richness	1.782	1.772	1.770	1.840	1.808	1.818

Genetic Distance

Heatmap of Fst between species and datasets
Fst are calculated using Nei (87) equations for Fst

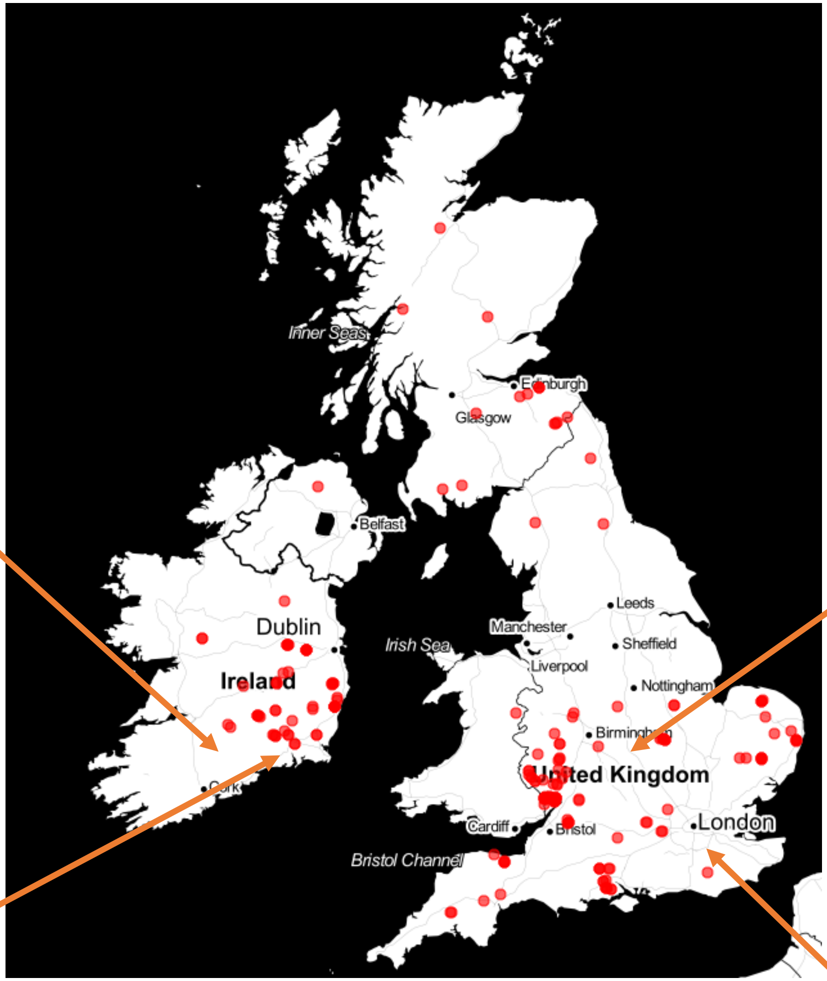


	qpe_Dataset A	qro_Dataset A	qhy_Dataset A	qhy	qro	qpe
qpe_Dataset A	0					
qro_Dataset A	0.089	0				
qhy_Dataset A	0.004	0.064	0			
qhy	0.051	0.042	0.037	0		
qro	0.169	0.024	0.14	0.089	0	
qpe	0.008	0.131	0.02	0.075	0.214	0

Next Steps

Progeny trial Charleville Ireland

Tree Archive JFK arboretum co. Wexford Ireland



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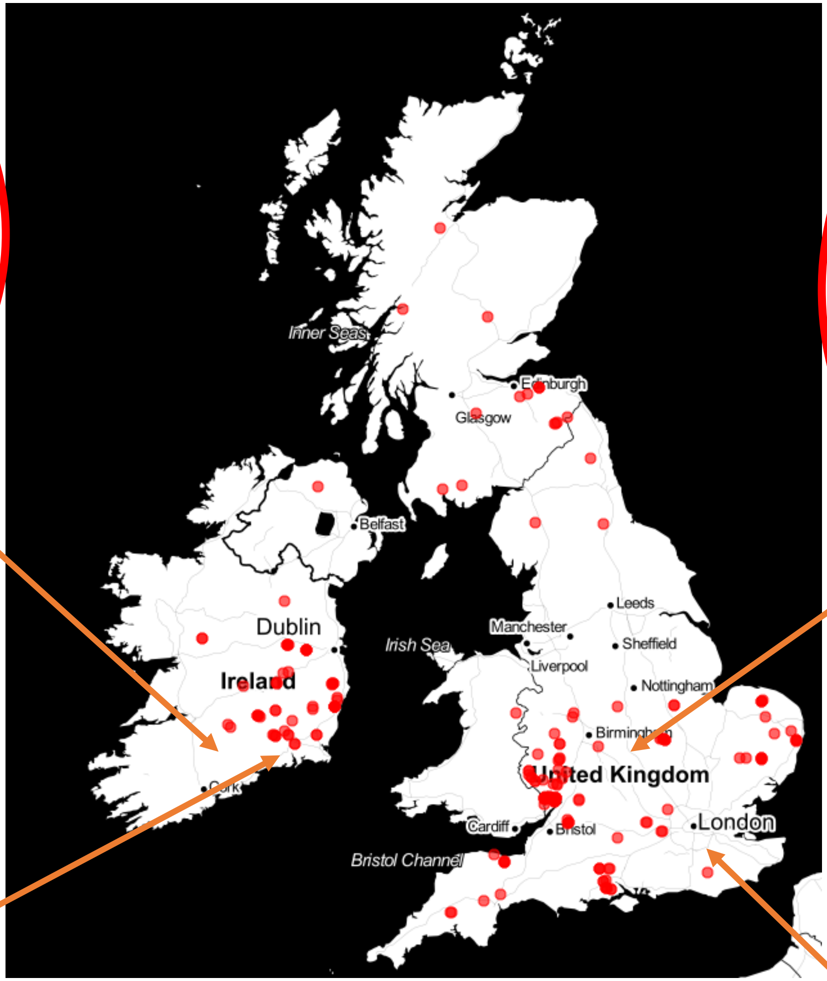

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Sampling Progeny Demonstration line

- Collected and in the process of sequencing 288 progeny tree samples in order to examine the parentage and exogenous gene flow within the progeny trial trees.
- 56 unique accessions (31 *Q.robur* 24 *Q.petraea*)
- Irish trees under-represented in demonstration line. (4%)
- Trees originating from the Netherlands (18%) and France(9%) over-represented.

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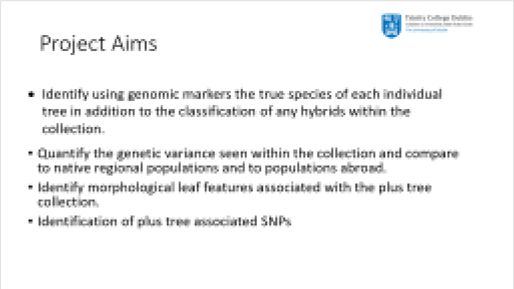

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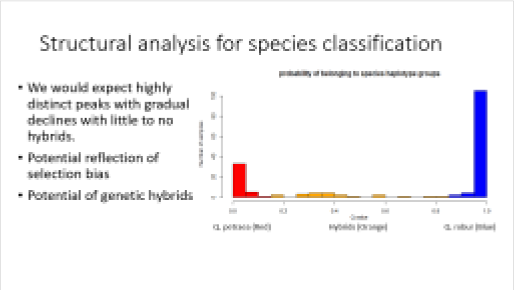

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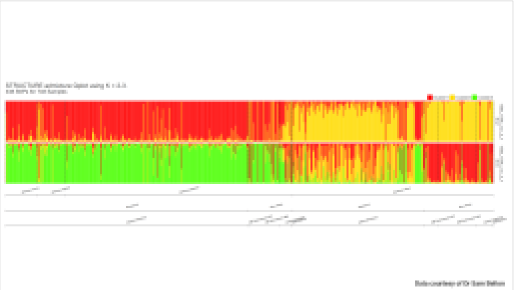

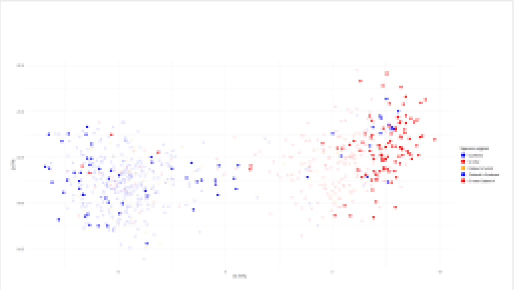

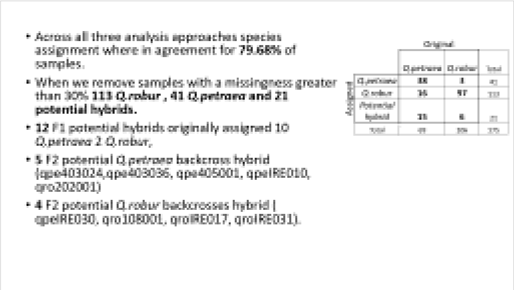

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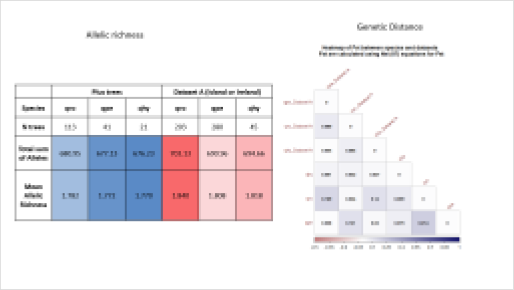
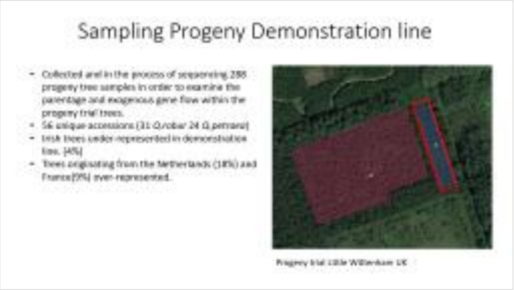
	Total	[illegible]	[illegible]	[illegible]



Allelic richness

Genetic Distance

Next Steps



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