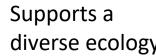
## Using genomics to help breed better oaks

Eamonn Cooper

## Why breed better Oak

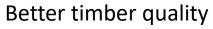
diverse ecology





Disease and pest resistance







Increase in Oak populations





## Why breed better Oak

Supports a diverse ecology

Better timber quality



All factors will serve to future proof Oak against the ongoing threats of Climate Change and Human interests

Increase in Oak populations





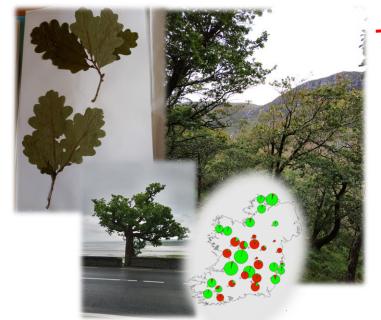
Disease and pest resistance





# How do we do this? Selected Plus Trees





Informed approach to selecting the best trees and traits for breeding.

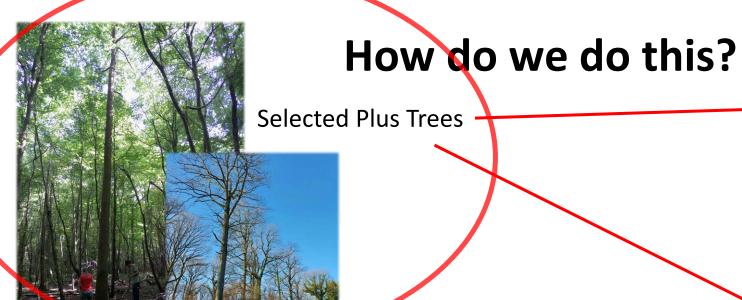


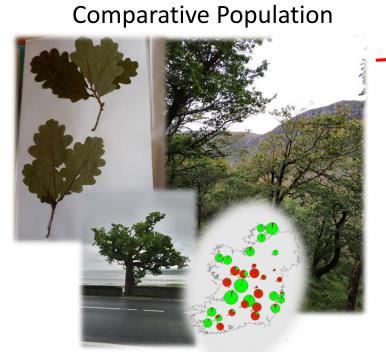


**Genetic Testing** 









Informed approach to selecting the best trees to be breeding from.





**Genetic Testing** 

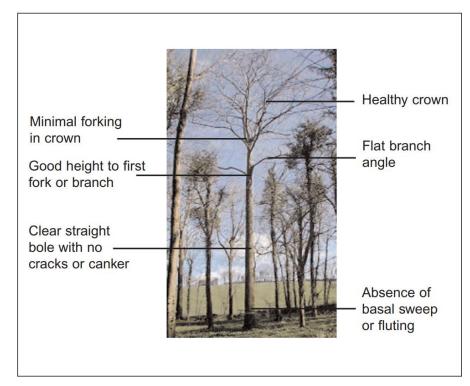




### What are plus trees?

#### 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



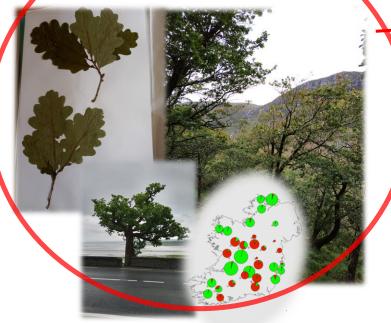
*Q.robur* on the road of the Ferry in Tarbert county Kerry



## How do we do this?

Selected Plus Trees





Informed approach to selecting the best trees to be breeding from.





**Genetic Testing** 

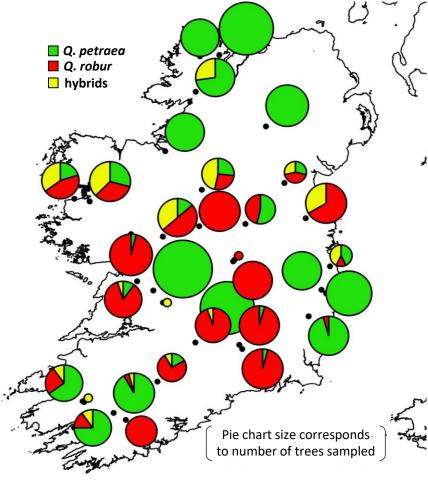




#### **GeneNet project**

- Two-year project funded by DAFM to map the genetic diversity of several native Irish tree species one of which is oak.
- 682 individual trees sampled
  - 380 Q. petraea
  - 242 Q. robur
  - 60 putative hybrids
- Spread across 30 populations
  - Roughly 20 trees per population.
  - Sites mainly owned by Coillte, and NPWS (remaining owned by other state bodies or privately owned).
  - Three specimen trees ("King Oak", "Royal Oak" and "Brian Boru Oak").





**Species composition** 





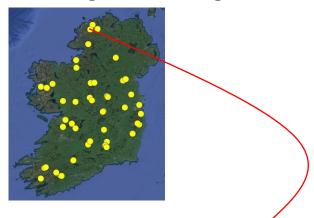
### Derrygorry, Co. Monaghan

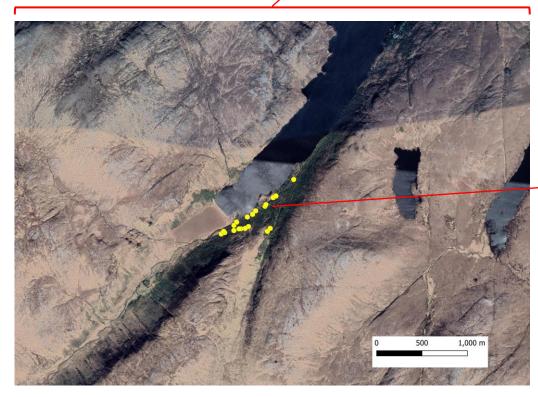






### Glenveagh, Co. Donegal







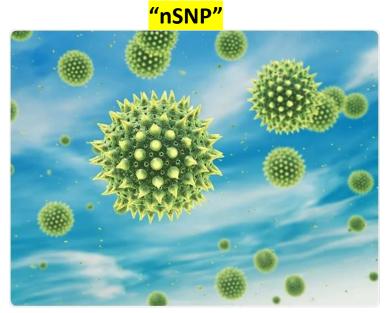




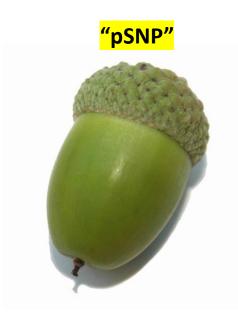
#### **Genetic analysis**



- Allows us to assess the levels of diversity contained within our native oak forests
- Analysis involves a focus on:
  - 1. Contemporary gene flow (via pollen) between individual trees and forest sites.
  - 2. Historic 'post-glacial' migration of oak (via seed) i.e., where does our oak come from?
- Although the oak genome has recently been sequenced, it is not practical to study the whole genome of each tree, so we use "genetic markers".
- Genetic markers are regions of an organism's genome which are variable here, we look at over 400 different genetic markers for oak this number offers very good resolution!
- Two types of genetic markers that we need to understand:



Contemporary gene flow



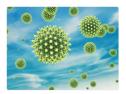
Historic species migration since Ireland's last ice age





#### **Genetic analysis**

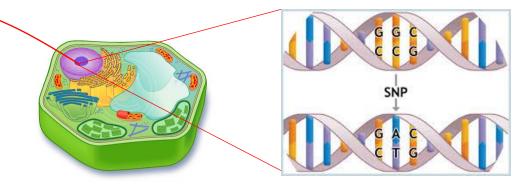
Variation at 412 <u>n</u>uclear <u>Single</u>
 <u>N</u>ucleotide <u>P</u>olymorphisms (nSNPs) analysed.

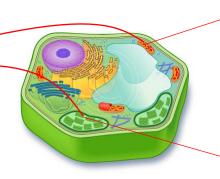


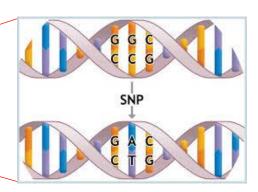
- Codominant markers, affected by sexual recombination, and higher mutation rate.
- Variation therefore more recent in time.
- Geographic variation often reflects pollen-mediated gene flow.
- Variation at 29 <u>p</u>lastid (chloroplast + mitochondria) <u>Single Nucleotide</u>
   <u>Polymorphisms</u> (pSNPs) analysed.



- Lower mutation rate, no sexual recombination, maternal inheritance (chloroplast).
- Variation therefore more ancient.
- Geographic variation often reflects seed-mediated gene flow.
- Variation at 441 SNP loci spread across three genomes.
  - nSNP data for 504 trees (>25% null allele cut-off)
  - pSNP data for 656 trees (>25% null allele cut-off)



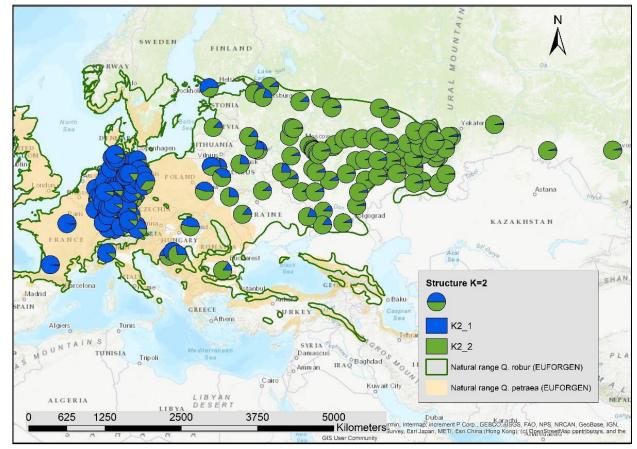


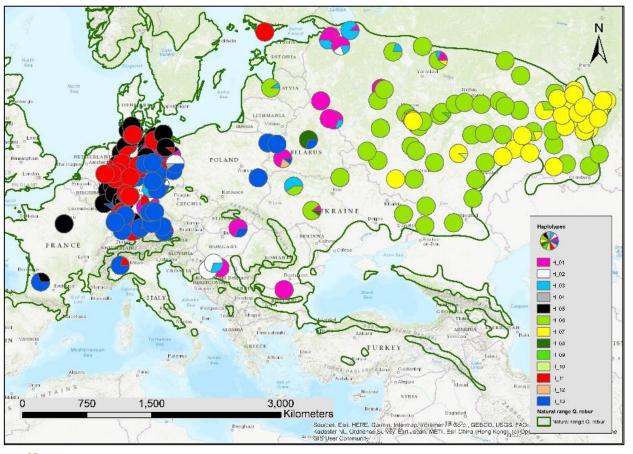




#### **Genetic analysis – why these markers?**

(Degen et al. (2021), Forests, 12: 1425)







nSNP markers show a clear east-west division, with a central hybridisation zone in between. (Degen et al. (2021), Forests, 12: 1425)



pSNP loci show a more historic picture of oak in Europe (i.e., its post-glacial recolonisation history). (Degen et al. (2021), Forests, 12: 1425)





#### **Genetic analysis – our final data**

- DNA extracted from a total of 664 trees and shipped to LGC Genomics in Berlin.
- Genotype-by-sequencing ("SeqSNP") performed, with **404 out of 441** SNPs being variable (*i.e.*, informative) in our samples.





	nSNP	pSNP
All		
Q. robur		
Q. petraea		
Hybrids		

24% (160 trees) had more than 25% of null alleles – these will be discarded ahead of all analyses.

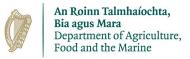




Genetic analysis – what questions about breeding population can be addressed with these SNP markers/ loci and our data?

- Is the total genetic diversity of our breeding populations the same as (or close to the level of) our native stands? Implications for adaptability.
- Have our breeding populations captured all native haplotypes?
   Can some be added?
- Do any of our native populations contain unique sub-population structure? Should seed from such populations be collected?
- To what extent are non-native germplasm represented in our breeding populations?











**Degen, B.**; Yanbaev, Y.; Mader, M.; Ianbaev, R.; Bakhtina, S.; Schroeder, H.; Blanc-Jolivet, C. Impact of Gene Flow and Introgression on the Range Wide Genetic Structure of *Quercus robur* (L.) in Europe. *Forests* **2021**, *12*, 1425. https://doi.org/10.3390/f12101425

Quine, Christopher & Atkinson, Nick & Denman, Sandra & Desprez-Loustau, Marie & Jackson, Robert & Kirby, Keith. (2019). An assessment of the current evidence on oak health in the UK, identification of evidence gaps and prioritisation of research needs: Action Oak Knowledge review.

(https://www.researchgate.net/publication/341986922 An assessment of the curr ent evidence on oak health in the UK identification of evidence gaps and prio ritisation of research needs Action Oak Knowledge review)

Clark, J. & Wilson, T. (2005) The importance of plus-tree selection in the improvement of hardwoods. Quarterly Journal of Forestry. 99(1): 45-50. (PDF) The importance of plus-tree selection in the improvement of hardwoods. (researchgate.net)





