

GeneNet: mapping the genetics of Ireland's native forests in a European context.

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Background

- Europe's native forests are natural banks of genetic diversity. "Conservation units" are designated in order to conserve unique "forest genetic resources" (FGR) in living stands.
- FGR determine the extent to which forests are buffered against environmental stresses, which are increasing due to climate change.
- The contribution of Ireland's native forests to overall European FGR has not been well studied.
- Ireland is a member of the **European Forest Genetic Resources Programme** (EUFORGEN), which was set up in 1994 to promote and share information about how to conserve Europe's FGR.
- EUFORGEN set up **EUFGIS**, a database which maps Europe's conservation units, of which 17 have been preliminarily selected in Ireland.

GeneNet

- GeneNet – a 2-year collaborative project between the National Botanic Gardens and Trinity College Dublin – aims to:
 - Update the EUFGIS database for Ireland with a more detailed geographic information system (GIS).
 - Genetically characterise the 17 EUFGIS sites along with a further 39 sites, with a focus on 'high-priority' species, including *Alnus glutinosa* (**Black Alder**), *Fraxinus excelsior* (**European Ash**), *Betula pubescens* (**Downy Birch**), *B. pendula* (**Silver Birch**), *Quercus petraea* (**Sessile Oak**), *Q. robur* (**Common Oak**) and *Pinus sylvestris* (**Scots Pine**).
- GeneNet will use medium- to high-throughput genotyping techniques to screen cpDNA and nDNA markers to investigate the genetic uniqueness and diversity of Ireland's native trees.

Results to date

- Almost 600 individuals spread across 19 native woodland sites have now been sampled (Fig. 1).
- High resolution melting (HRM) workflows have been successfully developed for medium-throughput screening of RFLPs for haplotype discovery (e.g., birch; Fig. 2).
- Mapping of these haplotypes reveals novel geographic structuring and site-specific structuring (e.g., birch; Fig. 3).
- Nuclear microsatellite and SNP markers have been selected to determine levels of gene flow and the effects of woodland fragmentation, as cpDNA markers may underestimate this.

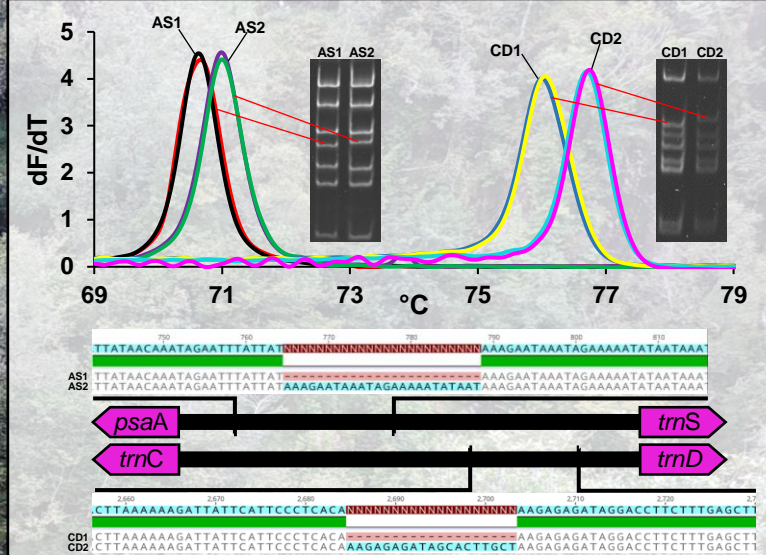


Fig. 2. (A) HRM profile of PCR-amplified cpDNA regions in *B. pubescens*. Shown are 24 (top) and 19 (bottom) bp indels which were originally identified by PCR-RFLP (wet lab gels shown).

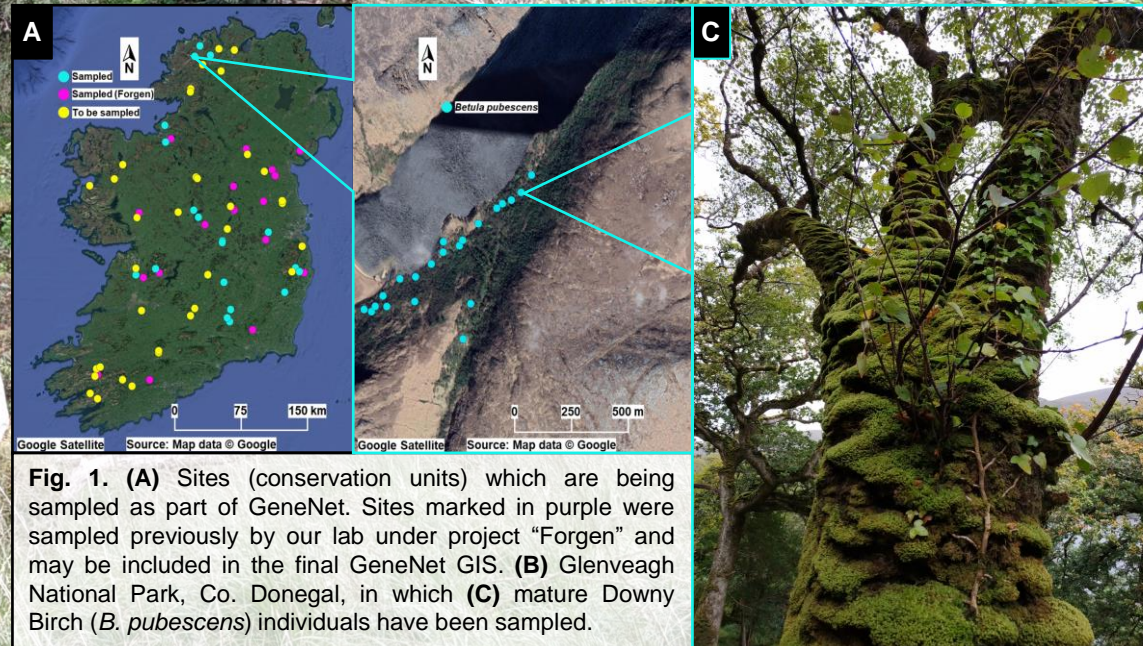


Fig. 1. (A) Sites (conservation units) which are being sampled as part of GeneNet. Sites marked in purple were sampled previously by our lab under project "Forgen" and may be included in the final GeneNet GIS. **(B)** Glenveagh National Park, Co. Donegal, in which **(C)** mature Downy Birch (*B. pubescens*) individuals have been sampled.

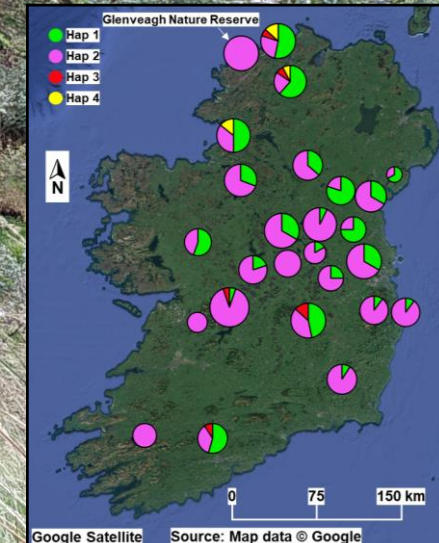


Fig. 3. Geographic distribution of the four birch haplotypes identified in this work ($G_{ST} = 0.262$). Pie chart size corresponds to sample size.