

Knowledge gaps in the genetics of UK trees and shrubs

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Introduction

This report evaluates the knowledge gaps related to the genetics of UK trees and shrubs including those targeted by the UK National Tree Seed project. Risk assessments have been conducted by following a decision tree based on two essential considerations: 1. Sampling strategies to capture genetic diversity, 2. Selection of donors for successful re-introductions (Neaves, 2019).

During the assessment of the risks associated with sampling strategies and mixing, knowledge gaps have emerged, to a different extent for different target species.

Knowledge gap 1: Genetic diversity of UK populations

For most of the target species of the UKNTSP, studies related to the genetic diversity of British populations are either lacking or restricted to specific regions. When genetic studies have been conducted, they are usually focused on neutral genetic variation without information about the adaptive potential of the species. Despite providing useful information to assess historical processes such as demographic changes or gene flow (Holderegger et al., 2006), neutral genetic variation cannot be used to verify whether populations have the potential to be self-sustainable and not maladapted in the wild. Consequently, this is a critical lack of information when trying to set up a representative germplasm suitable for future re-introductions (Hamilton, 1994).

The shortage of studies about adaptive variation in wild populations is related to the relative ease of neutral markers over adaptive traits, both in terms of costs and time. As a precautionary measure for the lack of information about adaptive variation, the most common guidelines recommend collecting and using local seed for restoration. This is considered as the best approach for re-establishing populations with high fitness, with a lower risk of maladaptation and pollution of local gene pools (Mortlock, 2000; Potts et al., 2003; McKay et al., 2005; Broadhurst, 2008). However, it might not be appropriate for some species.

For the following species, information about genetic variation in the UK is lacking:

Acer campestre L., *Alnus glutinosa* (L.) Gaertn., *Berberis vulgaris* L., *Betula pendula* Roth. (incomplete information), *Betula pubescens* Ehrh. (incomplete information), *Buxus sempervirens* L., *Carpinus betulus* L., *Cornus sanguinea* L., *Corylus avellana* L. (incomplete information), *Crataegus laevigata* (Poir.) DC., *Crataegus monogyna* Jacq. (incomplete information), *Erica vagans* L., *Euonymus europaeus* L., *Frangula alnus* Mill. (incomplete information), *Ilex aquifolium* L., *Ligustrum vulgare* L., *Lonicera periclymenum* L., *Malus sylvestris* Mill. (incomplete information), *Prunus spinosa* L. (incomplete information), *Prunus padus* L., *Pyrus cordata* Desv., *Rhamnus cathartica* L., *Salix cinerea* L., *Salix pentandra* L., *Salix purpurea* L., *Salix repens* L., *Salix aurita* L., *Sambucus nigra* L., *Ulmus glabra* Huds., *Viburnum lantana* L., *Viburnum opulus* L.

In conclusion, more genetic research is necessary to fill the knowledge gaps related to British trees and shrubs. At least neutral variation should be investigated in British populations to understand which populations are genetically more diverse. Investigations of fragmented populations should be prioritised.

Knowledge gap 2: Taxonomic uncertainties/extent of hybridisation

Taxonomic uncertainties are reported for some of the target species of the UKNTSP (e.g., *Ulmus glabra*, *Malus sylvestris* and *Juniperus communis* L.). Some of them are related to the occurrence of different subspecies and to morphological/cytological variation among populations.

Hybridisation is frequent for several species targeted by the UKNTSP. In general, hybrid individuals are difficult to distinguish from their parental species. This may either lead to an incorrect sampling of the genetic diversity of parental species – in case the hybrids are sampled – or to an excessively precautionary approach in which representative genetic diversity is excluded from sampling. When introgression occurs, the problem is more exacerbated.

Issues related to the recognition of hybrid individuals were found for the following species:

Alnus glutinosa, *Betula* spp., *Corylus avellana*, *Crataegus* spp., *Ilex aquifolium*, *Malus sylvestris*, *Populus* spp., *Prunus spinosa*, *Pyrus cordata*, *Rubus idaeus* L., *Salix* spp., *Tilia* spp., *Ulmus glabra*, *Viburnum lantana*.

For some species, genetic markers able to discriminate among parental species are available (e.g., in *Populus*; Fossati et al., 2003). However, assessing the hybrid status of mother plants requires more resources as it implies preliminary genetic analysis of sampled mother trees.

Knowledge gap 3: Limits of the native distribution

Introduced populations are thought to be characterised by lower levels of genetic variation (Stone & Sunnucks, 1993; Fuentes-Utrilla et al., 2014). For many target species of the UKNTSP, boundaries between native and introduced populations are blurred by extensive gene flow (Sjölund et al., 2017). Consequently, a knowledge gap resides in the native status for some populations.

For the following species, the limits of the native distribution are unclear:

Acer campestre, *Berberis vulgaris*, *Buxus sempervirens*, *Carpinus betulus*, *Cornus sanguinea*, *Euonymus europaeus*, *Fagus sylvatica*, *Ilex aquifolium*, *Malus sylvestris*, *Pinus sylvestris*, *Populus nigra*, *Populus tremula* L., *Prunus avium*, *Prunus spinosa*, *Prunus padus*, *Rhamnus cathartica*, *Rubus idaeus*, *Salix pentandra*, *Salix purpurea*, *Salix caprea*, *Sambucus nigra*, *Taxus baccata*, *Tilia cordata*, *Tilia platyphyllos*, *Ulmus glabra*, *Viburnum lantana*.

In recent literature, genetic patterns due to human-mediated introductions have been detected (Fuentes-Utrilla et al., 2014; Sjölund et al., 2017), supporting the application of similar approaches for other target species.

Table 1: Summary of the knowledge gaps related to the species targeted by the UKNTSP.

	Genetic variation in British populations	Genetic variation in European populations	Adaptive variation in UK	Adaptive variation in Europe	Taxonomy and hybridisation	Limits of the native distribution
<i>Acer campestre</i>	✓		✓			✓
<i>Alnus glutinosa</i>	✓		✓		✓	
<i>Berberis vulgaris</i>	✓	✓	✓	✓		✓
<i>Betula pendula</i>	✓ (incomplete)		✓		✓	
<i>Betula pubescens</i>	✓ (incomplete)		✓		✓	
<i>Betula nana</i>			✓		✓	
<i>Buxus sempervirens</i>	✓		✓	✓		✓
<i>Carpinus betulus</i>	✓		✓	✓		✓
<i>Cornus sanguinea</i>	✓		✓			✓
<i>Corylus avellana</i>	✓ (incomplete)		✓		✓	
<i>Crataegus laevigata</i>	✓		✓	✓	✓	
<i>Crataegus monogyna</i>	✓ (incomplete)				✓	
<i>Erica vagans</i>	✓	✓	✓	✓		
<i>Euonymus europaeus</i>	✓	✓	✓	✓		✓
<i>Fagus sylvatica</i>			✓			✓
<i>Frangula alnus</i>	✓ (incomplete)		✓			
<i>Fraxinus excelsior</i>			✓			
<i>Ilex aquifolium</i>	✓		✓	✓		✓
<i>Juniperus communis</i>			✓	✓	✓	
<i>Ligustrum vulgare</i>	✓	✓	✓	✓		
<i>Lonicera periclymenum</i>	✓		✓	✓		
<i>Malus sylvestris</i>	✓		✓		✓	✓
<i>Pinus sylvestris</i>			✓			✓
<i>Populus nigra</i>			✓	✓	✓	✓
<i>Populus tremula</i>			✓		✓	✓
<i>Prunus avium</i>			✓	✓		✓
<i>Prunus spinosa</i>	✓ (incomplete)		✓	✓	✓	✓
<i>Prunus padus</i>	✓	✓	✓	✓		✓
<i>Pyrus cordata</i>	✓	✓	✓	✓	✓	
<i>Rhamnus cathartica</i>	✓	✓	✓			✓
<i>Rubus idaeus</i>			✓		✓	✓
<i>Salix cinerea</i>	✓	✓	✓	✓	✓	
<i>Salix pentandra</i>	✓	✓	✓		✓	✓
<i>Salix purpurea</i>	✓		✓	✓	✓	✓
<i>Salix repens</i>	✓	✓	✓	✓	✓	
<i>Salix aurita</i>	✓	✓	✓	✓	✓	
<i>Salix caprea</i>			✓	✓	✓	✓
<i>Sambucus nigra</i>	✓	✓	✓	✓		✓
<i>Taxus baccata</i>			✓	✓		✓
<i>Tilia cordata</i>			✓	✓	✓	✓
<i>Tilia platyphyllos</i>			✓	✓	✓	✓
<i>Ulmus glabra</i>	✓		✓	✓	✓	✓
<i>Viburnum lantana</i>	✓	✓	✓	✓	✓	✓
<i>Viburnum opulus</i>	✓	✓	✓	✓		

References

- Broadhurst LM, Lowe A, Coates DJ, Cunningham SA, McDonald M, Vesk PA, Yates C. 2008. Seed supply for broadscale restoration: maximizing evolutionary potential. *Evolutionary Applications*. **1**: 587-597.
- Fossati T, Grassi F, Sala F, Castiglione S. 2003. Molecular analysis of natural populations of *P. nigra* L., intermingled with cultivated hybrids. *Molecular Ecology*. **12**: 2033–2043
- Fuentes-Utrilla P, Venturas M, Hollingsworth PM, Squirrell J, Collada C, Stone GN, Gil L. 2014. Extending glacial refugia for a European tree: genetic markers show that Iberian populations of white elm are native relicts and not introductions. *Heredity*. **112**: 105.
- Hamilton MB. Ex situ conservation of wild plant species: time to reassess the genetic assumptions and implications of seed banks. *Conservation Biology*. **8**: 39-49.
- Holderegger R, Kamm U, Gugerli F. 2006. Adaptive vs. neutral genetic diversity: implications for landscape genetics. *Landscape Ecology*. **21**: 797-807.
- McKay JK, Christian CE, Harrison SP., Rice KJ. 2005. “How local is local?” – A review of practical and conceptual issues in the genetics of restoration. *Restoration Ecology*. **13**: 432-440.
- Mortlock W. 2000. Local seed for revegetation. Where will all that seed come from? *Ecological Management and Restoration*. **1**: 93-101.
- Neaves L. 2019. Genetic Diversity Action Plans: Capturing and re-introducing genetic diversity (species assessments). Preprints. 2019120176 (doi:10.20944/preprints201912.0176.v1)
- Potts BM, Barbour RC, Hingston AB, Vaillancourt RE. 2003. Genetic pollution of native eucalypt gene pools – identifying the risks. *Australian Journal of Botany*. **51**: 1-25.
- Sjölund MJ, González-Díaz P, Moreno-Villena JJ, Jump AS. 2017. Understanding the legacy of widespread population translocations on the post-glacial genetic structure of the European beech, *Fagus sylvatica* L. *Journal of Biogeography*. **44**: 2475-2487.
- Stone GN, Sunnucks P. 1993. Genetic consequences of an invasion through a patchy environment—the cynipid gallwasp *Andricus quercuscalicis* (Hymenoptera: Cynipidae). *Molecular Ecology*. **2**: 251-268.