Scotland's Biodiversity Progress to 2020 Aichi Targets

Aichi Target 13 – Genetic Diversity Maintained – Supplementary Report 2020

Scottish Natural Heritage
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Contributors

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* Contributed equally

Contents

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AICHI TARGET 13 – GENETIC DIVERSITY MAINTAINED

By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species, is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity.

This report covers wild species of socio-economic importance. It complements the assessment of cultivated plants, and farmed and domesticated animals, and their wild relatives, which can be found in the main body of the report.

Methodology

As there is no agreed national list of species of socio-economic and/or cultural value for Scotland, we developed a set of criteria for selecting species. These include:

- Species prioritised for conservation value
- Species identified as being culturally important
- Species providing important ecosystem services
- Game species
- Species collected for food or medicine

Using these criteria, we selected 26 species for initial assessment. For each species, we produced a Genetic Scorecard, outlining:

- Relevant genetic conservation issues for the species in question
- The importance of its genetic diversity on an international scale
- An evaluation of the genetic risks facing *in situ* populations
- A statement of confidence in the assessment
- The degree to which representation in *ex situ* collections mitigate against genetic diversity loss (further explanation of these maps is provided in Section 4).
- An overall 'traffic light' score of genetic risks and whether current conservation actions are effective

Using 2010 as a baseline reference point, the approach assesses contemporary genetic issues, and likely future issues during a 25-year window from the point of assessment.

For quantification of levels of risk, we adopted the following framework:

- *Negligible:* No obviously detectable genetic problems occurring or expected over the next 25 years.
- *Moderate:* Moderate genetic problems occurring or expected over the next 25 years; e.g.:
    - Moderate loss of populations that are likely to contain unique diversity (e.g., resulting in losses of up to 25% of important genetic types / distinct populations);
    - Clearly observable fitness problems in up to 25% of populations due to low genetic variation and subsequent inbreeding depression;
    - Marked and clearly observable loss of genetic integrity by hybridisation at up to 25% of populations;
    - Severe restrictions on regeneration/recruitment/reproduction in many or most populations of long-lived species limiting evolutionary change in the immediate future.

- *Serious*: Serious genetic problems occurring or expected over the next 25 years; e.g.:
    - Severe loss of populations that are likely to contain unique diversity (e.g., resulting in losses of > 25% of important genetic types / distinct populations);
    - Loss of any highly divergent endemic lineages that are globally unique;
    - Strong, clearly observable fitness problems in >25% of populations due to low genetic variation and subsequent inbreeding depression;
    - Marked and clearly observable loss of genetic integrity by hybridisation at >25% of populations.

The assessment is based on expert opinion, using direct genetic data, where available, combined with information on species biology, abundance and distribution. Where no direct genetic data are available, the genetic risk assessment is based on species biology, abundance and distribution.

For quantification of uncertainty in the production of the genetic scorecards, we use the approach adopted for the UK Biodiversity Climate Change Impacts Report Card (Figure 1). This combines the level of agreement among experts and the amount and type of available evidence. The overall confidence level is governed by the lowest score for *either* expert agreement or evidence availability.

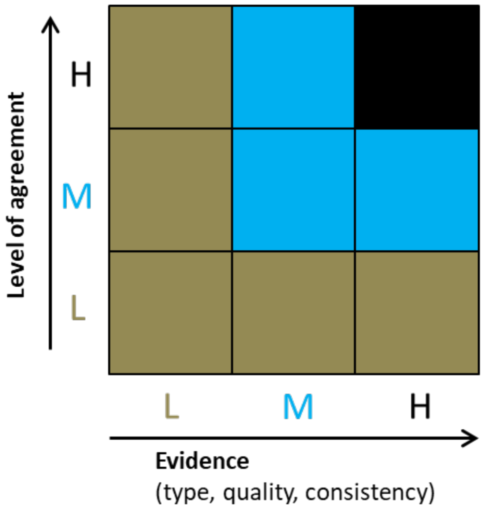


Figure 1. Summary of confidence levels used for genetic risk assessment.

We classify whether current management actions are appropriate and effective for mitigating any current or imminent genetic problems. This is articulated via a 4-point scale:

- Mitigation not required
    - The current status of the species is stable with negligible genetic risks
- Mitigation effective
    - Although there is a risk to genetic diversity, current measures are considered to be effective and sufficient to improve the situation
- Mitigation not effective
    - There is a recognised risk to genetic diversity and current mitigation are not considered to be effective or sufficient
- Mitigation not in place
    - There is a recognised risk to genetic diversity and mitigation is not in place

Full details of the methodology are presented in in Hollingsworth *et al.* (2019) Conserving Genetic Diversity: Development of a national approach for addressing Aichi Biodiversity Target 13 that includes wild species. SEFARI & SNH.

Scottish distribution maps presented in the Scorecards for each species use data from the National Biodiversity Network, showing Scottish records since 1992 unless otherwise stated.

Summary of findings

Twenty-six species of socio-economic and/or cultural importance were assessed in this report, ranging from extremely rare species of high national conservation importance, through to widespread dominant species that provide important functional ecosystem services. Table 1 summarises the genetic risk scores for each species and the primary pressures associated with any genetic risks.

Of the 26 species assessed in this report:

- 14 species were classed as being at negligible genetic risk
- Eight species were classed as being at moderate risk, with effective mitigation in place for five of these
- Four species were classed as being at risk of severe genetic problems

Serious risk species

Of the four species classified as being at serious risk, two (Scottish wildcat and ash) are primarily threatened by non-native species. In the case of the Scottish wildcat, the primary threat is extinction-by-hybridisation from feral domestic cats, with the small number of remaining pure Scottish wildcats being vulnerable to further loss of genetic integrity. In the case of ash, although there are millions of ash trees still present in the UK, there is a serious risk of genetic diversity loss due to large-scale mortality from the introduced ash-dieback pathogen, and the potential for further pressures from the introduced emerald ash borer. For both Scottish wildcat and ash, despite extensive mitigating actions being undertaken, the scale of threat means that the risks to their genetic diversity remain serious.

In the case of the great-yellow bumblebee, land-use change leading to sub-optimal habitat management has resulted in population declines, and this, coupled with the short-life cycle of the species, creates a risk of further rapid decline in genetic diversity. Likewise, the freshwater pearl mussel is experiencing continued population declines with the associated risk of genetic diversity loss.

Moderate risk species

Many of the species at moderate risk of genetic problems are relatively widespread species facing acute pressures from pests/pathogens and/or non-native species. For instance, closely related non-native species are a source of pressure for both the British bluebell and the red squirrel, farmed salmon is a pressure for Atlantic salmon, and risks of population declines due to pests and pathogens are important for Scots pine, Atlantic salmon, sea trout/brown trout, red grouse and red squirrel. The primary threat to the woolly willow in contrast, is its rarity, occurring in just 12 populations, many with very few individuals, with only the longevity of individual bushes acting as a buffer against immediate serious genetic diversity loss.

Of the eight species classed as being at moderate risk, effective mitigation is not in place for sea trout/brown trout and Atlantic salmon, or for the Scottish bluebell.

Negligible risk species

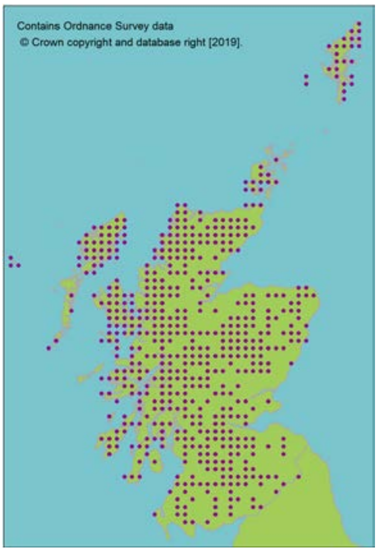
Species scored as having low levels of genetic risk were often species that are common. Two of the categories (ecosystem service provision, food/medicine) were dominated by widespread species with negligible genetic risks, reflecting in part the criteria used for selection. For instance, species providing important ecosystem services were selected based on high levels of land cover. Likewise, the species of importance for food/medicine were selected based on reported high frequency of use by foragers. These selection criteria resulted in the inclusion of extremely common species in the assessment, and their abundance is in turn associated with negligible genetic risks (abundance acts as a considerable buffer against genetic diversity problems). However, it is noteworthy that risks of genetic diversity loss can still occur in abundant species, as illustrated by the serious risk score for ash.

Table 1. Selected Scottish species of socio-economic and/or cultural value species

	Selection criteria					Taxonomic group	Risk and response	Confidence	Types of threat associated with moderate/ serious genetic risks	Page No.
	Conservation	Culturally Important	Ecosystem Services	Food/ Medicines	Game					
Papillose bog-moss *Sphagnum papillosum*			■			Bryophyte	Negligible risk Mitigation not required	Med	n/a	8
Scots pine *Pinus sylvestris*		■				Vascular plant	Moderate risk Mitigation effective	High	Pathogens, regeneration limitation	10
Raspberry *Rubus idaeus*				■		Vascular plant	Negligible risk Mitigation not required	High	n/a	12
Oak *Quercus* spp.		■				Vascular plant	Negligible risk Mitigation effective	High	n/a	14
Woolly willow *Salix lanata*	■					Vascular plant	Moderate risk Mitigation effective	High	Small isolated populations, regeneration limitation	16
Heather *Calluna vulgaris*		■	■			Vascular plant	Negligible risk Mitigation not required	High	n/a	18
Blaeberry *Vaccinium myrtillus*				■		Vascular plant	Negligible risk Mitigation not required	Med	n/a	20
British bluebell *Hyacinthoides non-scripta*		■				Vascular plant	Moderate risk Mitigation effective	High	Hybridisation & competition with non-native species	22
Harebell/Scottish bluebell *Campanula rotundifolia*		■				Vascular plant	Moderate risk Mitigation not in place	Med	Population declines due to pollution	26
European ash *Fraxinus excelsior*		■				Vascular plant	Serious risk Mitigation not effective	High	Pests/pathogens	30
Elderberry *Sambucus nigra*				■		Vascular plant	Negligible risk Mitigation not required	Med	n/a	34
Yorkshire fog *Holcus lanatus*			■			Vascular plant	Negligible risk Mitigation not required	Med	n/a	36
Purple moor-grass *Molinia caerulea*			■			Vascular plant	Negligible risk Mitigation not required	Med	n/a	38

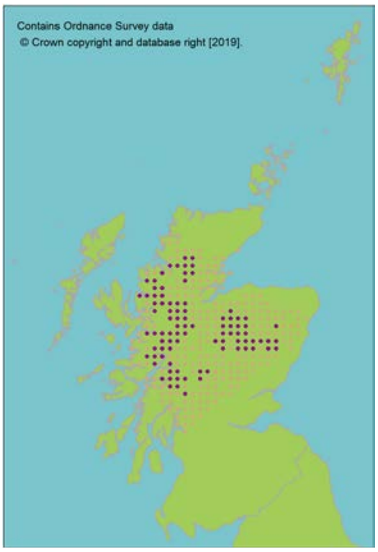
Hazel gloves *Hypocreopsis rhododendri*	■					Fungus	Negligible risk Mitigation effective	High	n/a	40
Chanterelle *Cantharellus cibarius*				■		Fungus	Negligible risk Mitigation not required	Med	n/a	42
Freshwater pearl mussel *Margaritifera margaritifera*	■					Mollusc	Serious risk Mitigation not effective	Med	Population declines due to pollution, exploitation and climate change	44
Great yellow bumblebee *Bombus distinguendus*	■					Insect	Serious risk Mitigation not effective	Low	Population declines associated with habitat loss, climate change	46
Sea trout/brown trout *Salmo trutta*					■	Fish	Moderate risk Mitigation not in place	Low	Pests/pathogens, hybridisation with non-native species, climate change, pollution	48
Atlantic salmon *Salmo salar*		■			■	Fish	Moderate risk Mitigation not effective	High	Pest/parasites, hybridisation with farmed stock, climate change, pollution	52
Common frog *Rana temporaria*				■		Amphibian	Negligible risk Mitigation not required	High	n/a	54
Golden eagle *Aquila chrysaetos*		■				Bird	Negligible risk Mitigation effective	High	n/a	56
Red grouse *Lagopus lagopus*					■	Bird	Moderate risk Mitigation effective	High	Pests/pathogens, population declines associated with habitat loss	58
Red squirrel *Sciurus vulgaris*		■				Mammal	Moderate risk Mitigation effective	Med	Pests/pathogens, hybridisation & competition with non-native species	60
Scottish wildcat *Felis silvestris*	■					Mammal	Serious risk Mitigation not effective	High	Hybridisation with non-native species	62
Red deer *Cervus elaphus*		■			■	Mammal	Negligible risk Mitigation not required	High	n/a	64
Roe deer *Capreolus capreolus*					■	Mammal	Negligible risk Mitigation not required	High	n/a	66

Species reports

<table>
<tr><td>Scientific name</td><td><i>Sphagnum papillosum</i></td><td>Common Name</td><td>Papillose bog-moss</td></tr>
<tr><td>GB IUCN Category</td><td>LC</td><td>T13 Status</td><td>Negligible risk
Mitigation not required</td></tr>
<tr><td colspan="3"></td><td>
</td></tr>
<tr><td rowspan="3">Context</td><td>Background</td><td colspan="2">Mat-forming widely distributed dioecious moss; the most common bog moss in cool-temperate Eurasia, and an indicator of good habitat quality due to low tolerance of pollution and shade (Blockeel <i>et al</i>., 2014). Also widespread in wet grassland, heath and other wet peaty habitats (Atherton <i>et al</i>., 2010). This single species is the main component of most peat deposits (Blockeel <i>et al</i>., 2014) and therefore crucial for carbon storage. It is uniformly polyploid across the circumboreal zone (Karlin <i>et al</i>., 2010). Globally, <i>Sphagnum</i> distribution is expected to contract due to climate warming (Bragazza, 2008; Gallego-Sala <i>et al</i>., 2013).</td></tr>
<tr><td>Current threats</td><td colspan="2">Most bogs in the UK have been substantially modified by artificial drainage, afforestation, overgrazing, burning, erosion and pollution (Bragg & Tallis, 2001). Climate and management are predicted to result in increased erosion over parts of the UK (Li <i>et al</i>., 2016), and over 50% of bog habitats currently exceed nitrogen critical loads leading to preferential growth of more competitive grasses and direct toxicity (APIS, 2019a).</td></tr>
<tr><td>Contribution of Scottish population to total species diversity</td><td colspan="2">No evidence for divergent genetic lineages being present in Scotland.</td></tr>
<tr><td></td><td>Diversity loss: population declines</td><td colspan="2">Despite ongoing population declines, the overall abundance of the species suggests any imminent loss of genetic diversity will be negligible.</td></tr>
</table>

<table>
<tr><td rowspan="4">Genetic risks</td><td>Diversity loss: functional variation</td><td colspan="5">Acidification during the Industrial Revolution resulted in historical loss of <i>S. papillosum</i> from parts of England which may have involved past loss of adaptive variation (Blockeel <i>et al</i>., 2014). However, no direct evidence of historical losses from Scotland, and no overall evidence of loss of functional/adaptive variation.</td></tr>
<tr><td>Diversity loss: divergent lineages</td><td colspan="5">Negligible risk (no evidence for divergent lineages in Scotland).</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">None known.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Turnover rates in these long-lived species are poorly known. Sexual reproduction is common and experiments in cultivation suggest spores are easy to obtain and grow (Gaudig <i>et al</i>., 2014).</td></tr>
<tr><td rowspan="9">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (a very abundant and widespread species despite many ongoing risks from habitat loss and degradation).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">Medium (assessment based on good distribution and ecological data supported by direct data on most aspects of species’ distribution and management requirements, but lacking direct genetic data).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Some material is held in <i>ex situ</i> cultivation for both micropropagation and experimental farming techniques (Caporn <i>et al</i>., 2018; Gaudig <i>et al</i>., 2014). No structured sampling to-date to represent <i>S. papilosum</i> in spore banks.</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Raised bog and blanket bogs are conservation priority habitats under EU habitats directives (92/43/EEC) and UK government supports phasing out peat in cultivation. Restoration of peatlands is an ongoing activity, and although hydrologic conditions can successfully be restored, vegetation recovery depends on additional factors (topography and climate).</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td>X</td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation not required</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Limited immediate genetic concerns due to the shear abundance of the species. Pollution and climate change may, in the future, lead to population declines that create genetic problems, but in the immediate future the risk is low.</td></tr>
<tr><td>Assessor</td><td colspan="5">Rebecca Yahr, Royal Botanic Garden Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Aline Finger, Royal Botanic Garden Edinburgh
Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Pinus sylvestris*	**Common Name**	Scots pine
GB IUCN Category	LC	**T13 Status**	Moderate risk Mitigation effective



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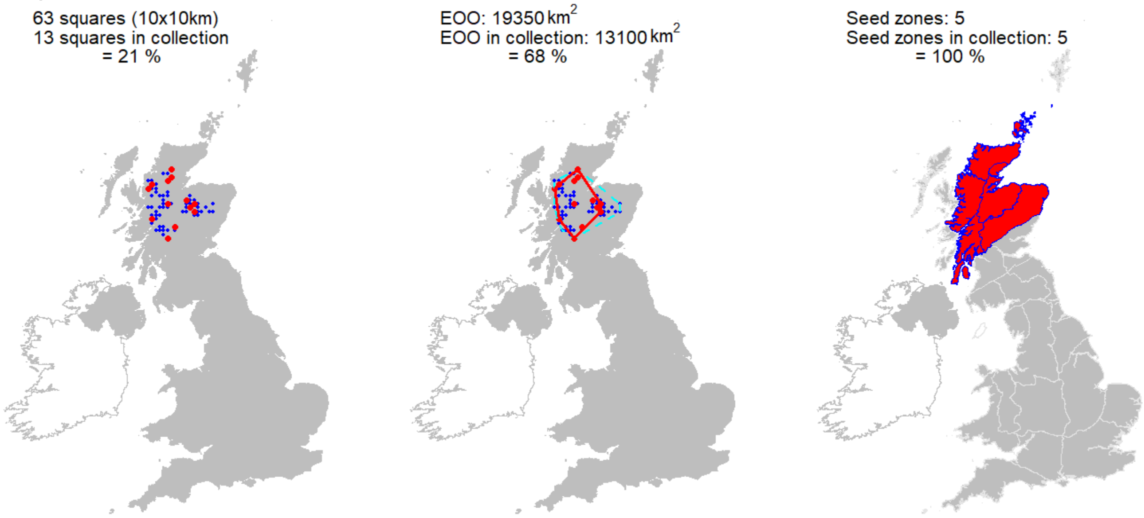
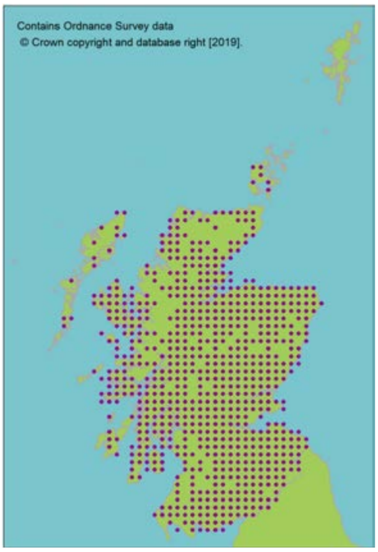
Context	**Background**	Hermaphrodite, wind pollinated, widely distributed tree. Present in 84 natural stands, often small and fragmented (dark circles on map, light circles are plantations). Natural stands represent only 10% of trees in Scotland. Genetic marker studies show large amounts of neutral genetic diversity. Some evidence of adaptive differentiation in Scotland from west to east (Salmela, 2011; Donnelly *et al*., 2018).
	Current threats	Plant pathogens represent the major emerging threat (*Dothistroma septosporum* races introduced on Corsican and lodgepole pine) (Piotrowska *et al*., 2018).
	Contribution of Scottish population to total species diversity	Molecular evidence for putative separate lineage in north western Scotland, although nuclear markers indicate very low differentiation, even from continental Europe (Ennos *et al*., 1997). Scotland does, however, contain a uniquely oceanic adapted population (Ennos *et al*., 1997; Donnelly *et al*., 2018).
Genetic risks	**Diversity loss: population declines**	Multiple small populations with no regeneration coupled with a biased age-structure towards older trees compromises the sustainability of many populations. However, there is limited risk of imminent genetic diversity loss due to high levels of standing variation in adult trees (assuming no catastrophic population losses due to pathogens).
	Diversity loss: functional variation	The general persistence of the species across its range in Scotland is not threatened, which minimises likely loss of adaptive variation. There are risks to loss of high elevation populations across its range which may lead to some loss of adaptive variation.
	Diversity loss: divergent lineages	Limited divergence from European populations precludes loss of major divergent lineages. The most genetically distinct populations are in the north west of Scotland around Shieldaig. These populations are not currently threatened.
	Hybridisation/ introgression	Buffer zones in which planting of non-local seed is prohibited around existing native stands limit risk to loss of integrity from exotic stands.

<table>
<tr><td></td><td>**Low turnover/ constraints on adaptive opportunities**</td><td colspan="5">Deer grazing is a major limitation on turnover and regeneration, but the risk is mitigated in c. 20% of populations where active management is in place.</td></tr>
<tr><td rowspan="9">**Cumulative risk summary**</td><td>***In situ* genetic threat level**</td><td colspan="5">Moderate (in the face of emerging pathogen threats, major limitations to regeneration present a moderate risk of genetic variation loss and constraints to adaptation).</td></tr>
<tr><td>**Confidence in *in situ* threat level**</td><td colspan="5">High (assessment based on good demographic data and direct data on genetic variation, population differentiation and biology).</td></tr>
<tr><td>***Ex situ* representation**</td><td colspan="5">Seeds from 13 10km squares held at the Millennium Seed Bank, including all 5 UK ‘standard’ tree seed zones in which native stands occur, with 68% *ex situ* coverage of its wild extent of occurrence.</td></tr>
<tr><td colspan="6">Representation in seed bank collection

 </td></tr>
<tr><td rowspan="3">**Current conservation actions**</td><td colspan="5">Grazing controls at c. 20% of sites promote regeneration providing adaptive opportunities. Establishment of Gene Conservation Unit at Beinn Eighe National Nature Reserve safeguards some variation.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td>X</td><td>X</td><td></td></tr>
<tr><td>**Overall T13 status**</td><td colspan="5">Moderate risk; Mitigation effective</td></tr>
<tr><td>**Overall T13 status explanation**</td><td colspan="5">Despite the fragmented nature and small size of many populations, longevity of individual trees minimises imminent loss of genetic diversity. Management to promote regeneration supports some ongoing evolutionary processes, and wide representation of all seed zones in seed banks likely catches main adaptive variation.</td></tr>
<tr><td></td><td>**Assessor**</td><td colspan="5">Richard Ennos, University of Edinburgh</td></tr>
<tr><td></td><td>**Reviewer**</td><td colspan="5">Stephen Cavers, Centre for Ecology and Hydrology
Peter Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Rubus idaeus*	**Common Name**	Raspberry
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation not required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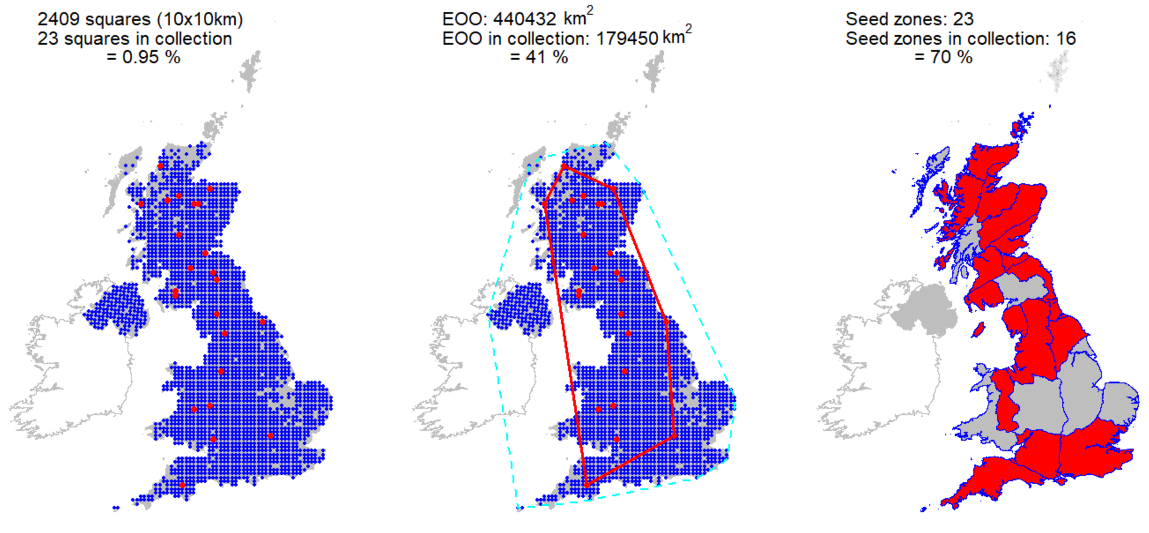
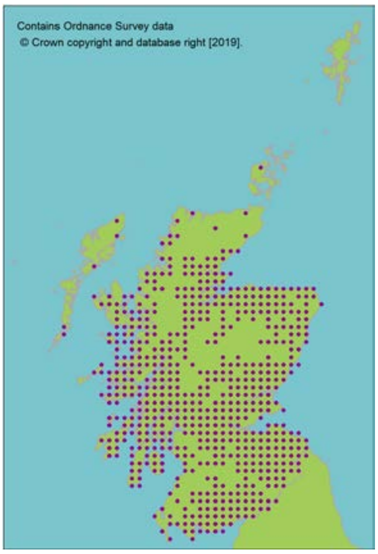
Context	**Background**	Widespread woody perennial reproducing via seed and suckering. Raspberry is native to Europe and Asia, and is found throughout Scotland, including the Northern Isles where the species is considered to be introduced. Raspberry is widely cultivated both as a commercial crop and for domestic use.
	Current threats	Hybridisation has been recorded in the UK with other *Rubus* species. Introgression between domestic cultivars and wild raspberry has been recorded. Genetic diversity has been reduced in domesticated populations (Haskell, 1960; Graham & McNicol, 1995). In Tayside wild populations remain more diverse than cultivated plants (Graham, Marshall & Squire, 2003).
	Contribution of Scottish population to total species diversity	With a wide distribution within temperate Europe and Asia, and predominantly sexual reproduction, the Scottish population of raspberry is likely to make a small contribution to the global species diversity.
Genetic risks	**Diversity loss: population declines**	Scrub clearance is likely to have led to localised reductions in populations, but given the remaining abundance and distribution of the species, any diversity losses are likely to be minimal.
	Diversity loss: functional variation	There is some evidence for adaptive differences between populations (e.g., populations at high altitudes can have later bud-burst and shorter growth than other populations; Jennings, 1964). However, there is no evidence of declines that are leading to a marked loss of populations containing unique adaptive variants.
	Diversity loss: divergent lineages	Considered negligible risk.

<table>
<tr><td></td><td>Hybridisation/ introgression</td><td colspan="5">Low risk. Hybridisation has been recorded between raspberry and other <i>Rubus</i> species, but although gene flow occurs, it is infrequent and localised (Lusby & McNicol, 1995). Despite several decades of potential exposure to commercial clones in Tayside, gene flow between wild populations and cultivars is low (Graham <i>et al.</i>, 2003).</td></tr>
<tr><td></td><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">No evidence for constraints on reproduction.</td></tr>
<tr><td rowspan="9">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (extremely widespread species, limited threat from hybridisation).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (direct genetic data available, abundant species).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">The Millennium Seed Bank has collections from 23 10 km squares, from widely distributed localities in the UK, including comprehensive coverage of Scotland. Many commercial cultivars grown in Scotland.</td></tr>
<tr><td colspan="6">
</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Promotion of pollinator-friendly management provides an opportunity for lowland populations of raspberry to increase.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk: Mitigation not required</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">The widespread distribution and low level of introgression with domestic cultivars indicate that the Scottish raspberry population is genetically healthy with no evidence for genetic problems.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Iain Macdonald, Scottish Natural Heritage</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Angus Hannah, BSBI
Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Quercus robur* *Quercus petraea* complex	**Common Name**	Oak (English oak & sessile oak)
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation effective



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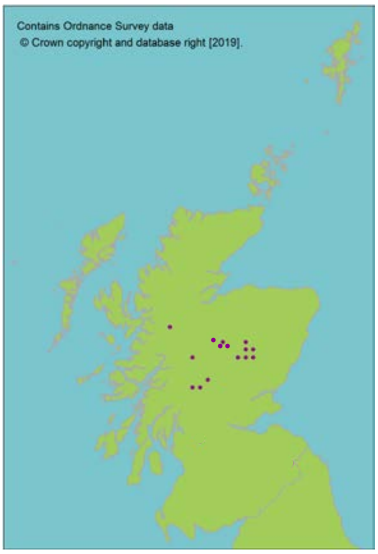
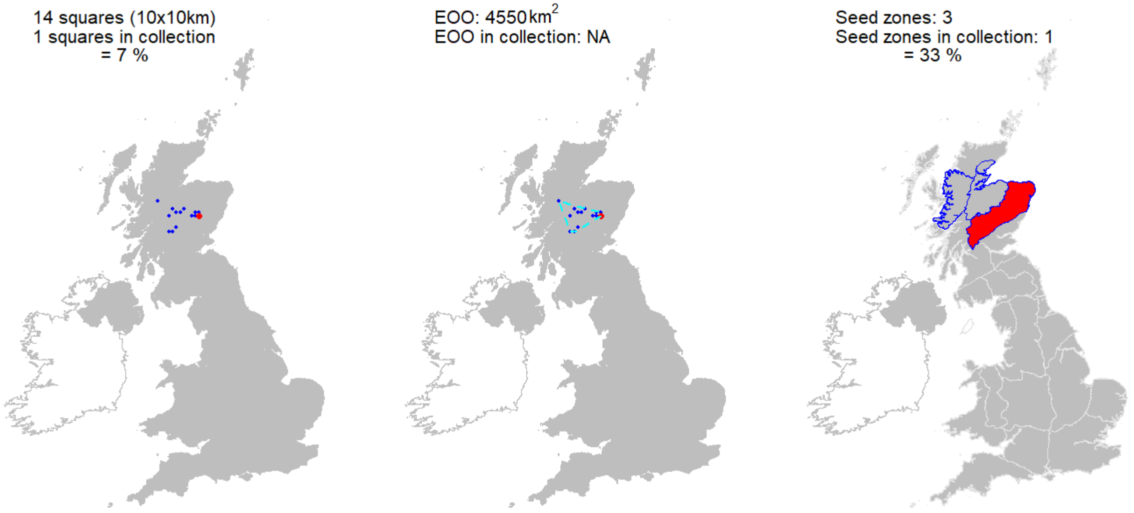
Context	**Background**	Hermaphrodite, wind-pollinated and bird-dispersed (jay, *Garrulus glandarius*), widely distributed tree. Present in both natural populations and in current and former plantations, the latter often established historically for charcoal and bark production under coppice management. In the west of Scotland, the oaks are keystone species within the Atlantic rainforests. The two species regularly hybridise in Scotland (Gerber *et al*., 2014). Genetic marker studies show colonisation exclusively from an Iberian refugium (Cottrell *et al.*, 2002), and that populations retain large amounts of neutral genetic diversity at nuclear loci. There is evidence of adaptive differentiation in the UK on a north-south axis (Wilkinson *et al*., 2017).
	Current threats	A syndrome of ill health in principally older oak populations in the UK has been dubbed 'oak decline', but this appears to be a problem associated with ageing trees located in inappropriate habitats. Many woodlands throughout Scotland lack regeneration due to high browsing pressure.
	Contribution of Scottish population to total species diversity	Scottish populations share their postglacial origins with oaks in Spain and France and show little differentiation for neutral markers (Cottrell *et al*., 2002). Scottish populations show evidence of adaptation to shorter growing seasons compared to populations from elsewhere in the distribution.
Genetic risks	**Diversity loss: population declines**	There is limited risk of imminent genetic diversity loss due to high levels of standing variation in adult trees. However, if the problem of lack of natural regeneration is not solved long-term losses due to inability to adapt to future environments are likely.
	Diversity loss: functional variation	The general persistence of the species complex across its range in Scotland is not threatened, which minimises likely loss of adaptive variation.

<table>
<tr><td rowspan="3"></td><td>Diversity loss: divergent lineages</td><td colspan="5">Limited divergence from European populations in Spain and France precludes loss of major divergent lineages.</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">Hybridisation between the two oak species is a natural and common phenomenon in Scotland. Despite high levels of hybridisation, the integrity of the individual species remains.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Lack of regeneration in existing oakwoods has long been a problem. Overgrazing by deer and livestock is an important contributor. However, lack of recognition of the role of jays in facilitating regeneration in other areas of the landscape e.g. birchwoods means that grazing protection measures have often not been well targeted (Worrell <i>et al</i>., 2014).</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (major limitations to regeneration pose no immediate threat, but may lead to loss of diversity in the long term if not addressed).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (detailed genetic and demographic data available).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Oak is not currently represented in seed banks, as it is ‘recalcitrant’. Acorns are sensitive to desiccation, so they cannot be stored in conventional seed bank conditions of low humidity and temperature. A project at Kew is working to develop cryopreservation techniques and storage protocols to bank recalcitrant seeds. Our native oaks are represented in many botanic gardens and arboreta, including the Royal Botanic Gardens Edinburgh.</td></tr>
<tr><td rowspan="3">Current conservation action</td><td colspan="5">The key management intervention is management to promote regeneration.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Longevity of individual trees minimises imminent loss of genetic diversity. Management to promote regeneration supports some ongoing evolutionary processes. Proactive work to understand potential impact from pathogens also underway.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Richard Ennos, University of Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Jeanette Hall, Scottish Natural Heritage
Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

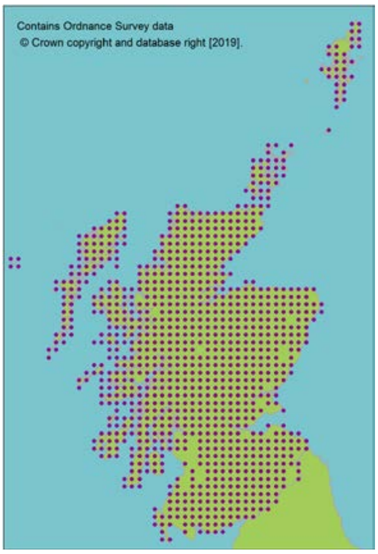
Scientific name	*Salix lanata*	**Common Name**	Woolly willow
GB IUCN Category	VU	**T13 Status**	Moderate risk Mitigation effective



Context	**Background**	Perennial dioecious shrub occurring in 14 10 km squares in Scotland; only two sites exceed 200 individuals and three sites contain only a single sex. Capable of local clonal spread, but most individual bushes are unique genotypes consistent with a primarily sexual reproduction. Considered to be previously more widespread (Marriott *et al*., 2016). Population genetic studies show low population differentiation and little correlation between population size and genetic diversity consistent with the longevity of individual bushes acting to retard rates of genetic erosion in small populations (Scottish Montane Willow Group, 2005).
	Current threats	Primary threat is grazing, restricting the species to steep crags and cliffs at most sites.
	Contribution of Scottish population to total species diversity	The species is common elsewhere in its range and there is no expectation of divergent endemic genetic lineages in Scotland, although the populations may be adapted to the local environment.
Genetic risks	**Diversity loss: population declines**	Populations are small, fragmented and isolated but existing evidence shows low population differentiation and limited evidence for genetic diversity loss: individual plant longevity ameliorates short term risks.
	Diversity loss: functional variation	No immediate risk to functional variation from population declines. Populations occupy relatively similar environmental conditions, minimising likelihood of unique adaptive variants.
	Diversity loss: divergent lineages	Limited risk as no evidence for phylogenetically divergent lineages present in Scotland.
	Hybridisation/ introgression	The species co-exists with hybridising species, and inter-specific hybrids are recorded at several sites. However, genetic marker data give no evidence for extinction-by-hybridisation risk (Forrest, 2006).

<table>
<tr><td></td><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Regeneration is considered a limiting factor due to grazing limiting flower production coupled with poor seedling establishment (Scottish Montane Willow Group, 2005). This will limit levels of adaptive change.</td></tr>
<tr><td rowspan="9">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Moderate (small fragmented populations of hybridising species present genetic risks, mitigated by the longevity of individual plants).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (assessment based on good demographic data and direct data on genetic variation, population differentiation and hybridisation).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Two accessions from one 10 km square held at the Millennium Seed Bank, resulting in partial coverage of Scotland; further collections being sourced. Additional representation in the Royal Botanic Garden Edinburgh living collection of 31 accessions from six Scottish populations.</td></tr>
<tr><td colspan="6">Representation in seed bank collection
 </td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Restoration underway at four sites, involving seed and cutting collection, <i>ex situ</i> propagation, and translocation to reinforce extant populations. Grazing controls in place at most important populations.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td>X</td><td>X</td><td>X</td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Moderate risk; Mitigation effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Despite the small population sizes and fragmented nature of the species range, conservation interventions have halted declines, there is representation in <i>ex situ</i> collections, and restoration interventions are increasing numbers of individuals <i>in situ</i>.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Rob Ogden, University of Edinburgh</td></tr>
</table>

Scientific name	*Calluna vulgaris*	**Common Name**	Heather
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation not required



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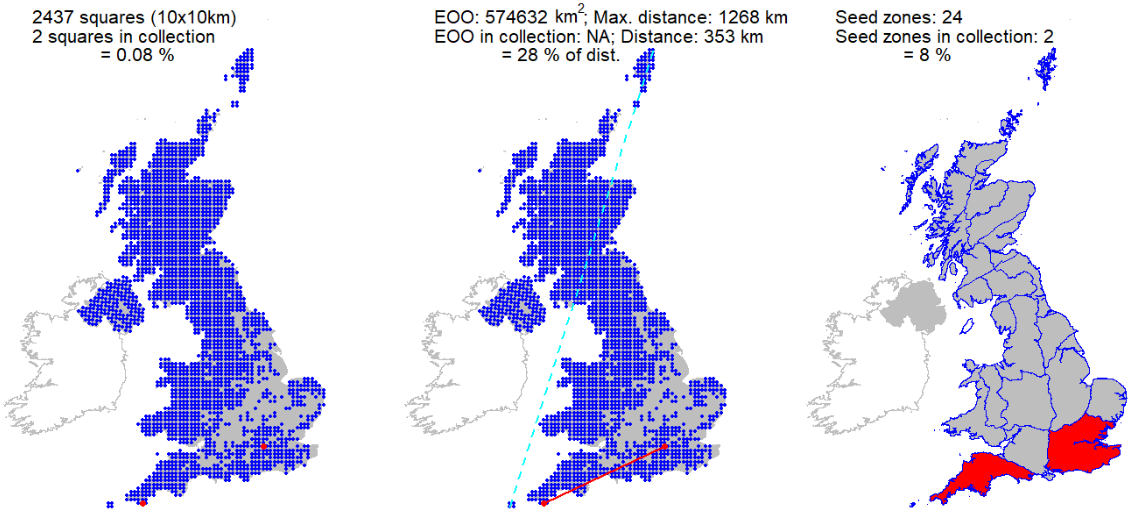
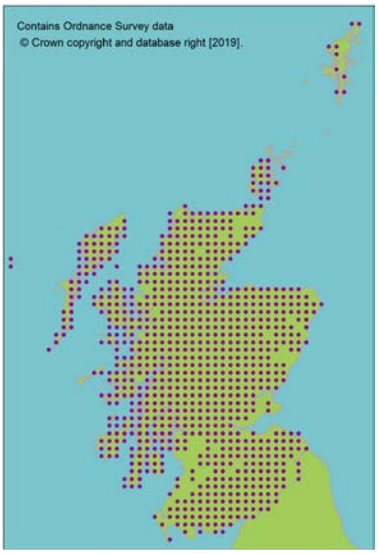
Context	**Background**	Perennial, hermaphrodite low shrub, widespread with a cool-temperate Eurasian oceanic distribution and wide ecological amplitude, dominant in oceanic heaths (Gimingham, 1960). Insect pollinated; spreads by outcrossed seed (Rendell & Ennos, 2002).
	Current threats	Evidence for declines across UK and Europe due to habitat loss (afforestation, agricultural expansion and changes in pastoral management; Stevenson & Birks, 1995) and nitrogen deposition: direct effects of ammonia toxicity. Marked decreases in *Calluna* from increases in competitive grasses, especially in lowland heath (Bobbink *et al*., 2010). Upland *Calluna* at risk from winter damage; dwarf shrub heath at risk from heather beetle (APIS, 2019b). Grazing and burning regimes can also result in declines (Marrs *et al*., 2004).
	Contribution of Scottish population to total species diversity	Scottish and Belgian populations closely related and separate from other European populations (Mahy *et al*., 1999a), with Scotland probably harbouring core populations. Ecotypic variation known for some flower forms and populations on toxic soil (Gimingham, 1960).
Genetic risks	**Diversity loss: population declines**	Habitat losses due to conversion and eutrophication over centuries, have resulted in long, slow declines in heathland (Norton *et al*., 2009) and *Calluna* distribution (Braithwaite *et al*., 2006). Long-lived individuals and persistent seed banks (150 years) help ensure standing diversity. High levels of temporal and spatial gene flow minimize risks to genetic variation (Rendell & Ennos, 2002).
	Diversity loss: functional variation	Negligible imminent risk of loss of adaptive / functional variation, as despite demographic changes, *Calluna* remains abundant and widespread in Scotland.
	Diversity loss: divergent lineages	Negligible risk as no divergent lineages have been detected in genetic studies.

<table>
<tr><td rowspan="2"></td><td>Hybridisation/ introgression</td><td colspan="5">None known.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Heavy grazing can lead to loss of stands and reduction of seedling establishment (Stevenson & Birks, 1995), but seed banks have similar levels of genetic diversity as above ground plants (Mahy <i>et al</i>., 1999b). Overall, negligible risk from limits on turnover.</td></tr>
<tr><td rowspan="9">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (significant population declines UK-wide, but the plant covers 16% of Scotland; no evidence of unique variation).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (based on good distribution data and by direct data on most aspects of species’ biology including population level variation).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Accessions from two 10 km squares held at Millennium Seed Bank but no coverage of Scottish distribution. Five wild collected accessions in RBGE living collection.</td></tr>
<tr><td colspan="6">Representation in seed bank collection
 </td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Upland and lowland heaths are UK Biodiversity Action Plan Habitats, leading to restoration (Mitchell <i>et al</i>., 2008), though outcomes vary with starting conditions (Marrs <i>et al</i>., 2004). Attempts to curb nitrogen deposition have had some effect, but many sites exceed critical loads, and ammonia is still on the rise (Plantlife, 2017).</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td>X</td><td>X</td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation not required</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Nitrogen critical loads are still widely exceeded, but populations in Scotland are large and represent the species’ demographic stronghold.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Rebecca Yahr, Royal Botanic Garden Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Richard Ennos, University of Edinburgh</td></tr>
</table>

Scientific name	*Vaccinium myrtillus*	**Common Name**	Blaeberry
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation not required



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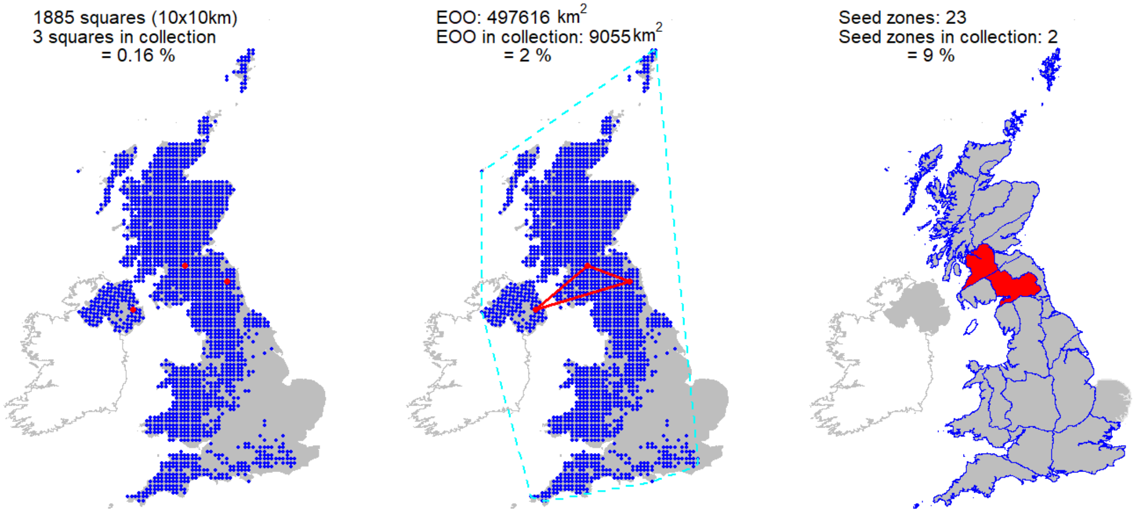
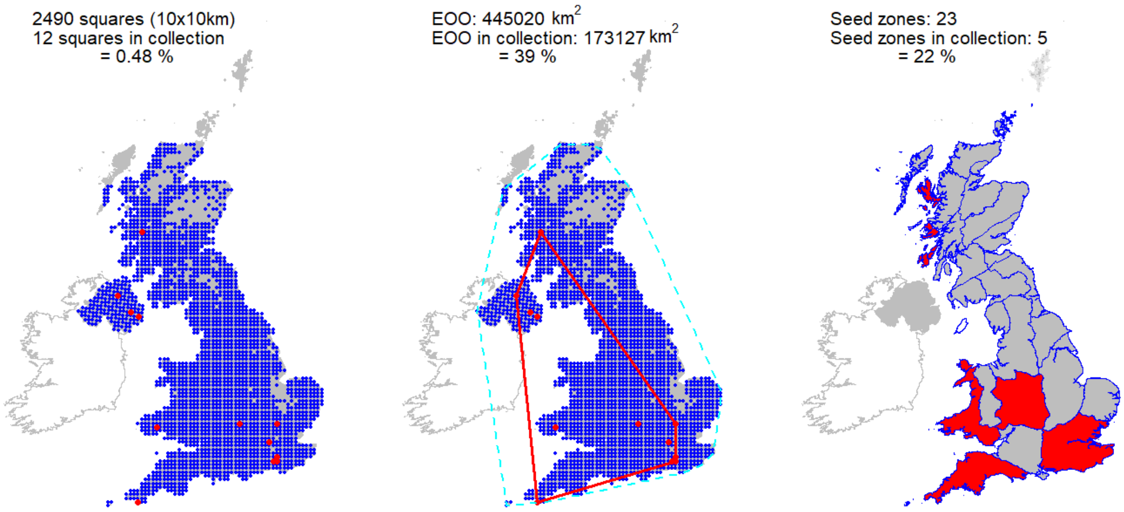
Context	**Background**	Perennial, rhizomatous hermaphrodite shrub, common and locally dominant across boreal Europe and Asia, in heaths, bogs, and woodland. Pollination by insects, spreads by rhizomes; animal-dispersed outcrossed seeds rarely result in seedlings in Scotland (Ritchie, 1956). Economically important wild berry.
	Current threats	Continued gradual habitat loss of heath in lowlands and potential changes to upland vegetation from increased nitrogen deposition (APIS, 2019b; Braithwaite *et al*., 2006; Norton *et al*., 2009). Declines reported by BSBI (Braithwaite *et al*. 2006) and Countryside Survey (Norton *et al*., 2009) up to mid-2000s, probably representing population losses at range edges and loss of habitat. The species is highly susceptible to the *Phytophthora* pathogens *P. ramorum* and *P. kernoviae*. 22 cases have been reported in England (Fera, 2012) and two cases affecting *V. myrtillus* have been found in Scotland (Scottish Government Status Report, 2015)
	Contribution of Scottish population to total species diversity	Several close relatives and subspecies are found in Europe and North America (Ritchie, 1956), all with similar life-history and regionally-distinct gene pools (Bjedov *et al*., 2015), but no data from UK/Scotland. Geographic and ecotypic variation in morphology and in common garden experiments (Ritchie, 1956) suggest locally adapted gene pools may be present.
Genetic risks	**Diversity loss: population declines**	Low risk, as population declines are still small compared with the overall abundance of the species, suggesting any imminent losses of genetic diversity will be negligible.
	Diversity loss: functional variation	Range edge losses often correlate with losses of genetically differentiated populations (Eckert *et al*., 2008), but no evidence of losses in functional variation, and high-elevation populations are within stable core of distribution.
	Diversity loss: divergent lineages	Negligible risk. No evidence of divergent lineages being under threat.

<table>
<tr><td rowspan="2"></td><td>Hybridisation/ introgression</td><td colspan="5"><i>Vaccinium x intermedium</i> is a hybrid with <i>V. vitis-ideae</i>, found uncommonly in UK and elsewhere, but probably limited by staggered flowering times (Ritchie, 1956; Stace <i>et al.</i>, 2015).</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Regeneration from seed appears limited; muirburn promotes clonal re-sprouting from rootstocks (Welch <i>et al.</i>, 1994).</td></tr>
<tr><td rowspan="9">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (losses are currently restricted to lowlands, with Scottish populations largely intact and no evidence of unique variation here).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">Medium (assessment based on good distribution data supported by BSBI and CEH repeat surveys; no UK direct genetic evidence).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Three UK accessions, from three 10 km squares held at the Millennium Seed Bank. Minimal coverage of the Scottish distribution. Representation in Royal Botanic Garden Edinburgh living collection of three wild collected UK accessions.</td></tr>
<tr><td colspan="6">Representation in seed bank collection

</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Widespread and well-characterized threats to heath from nitrogen deposition mean that actions to limit nitrogen are ongoing.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation not required</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Core populations in Scotland are stable. Should demographic situation change (e.g. major <i>Phytophthora</i> outbreak), risk should be revisited.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Rebecca Yahr, Royal Botanic Garden Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Jim McIntosh, Botanical Society of Britain & Ireland
Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Hyacinthoides non-scripta*	**Common Name**	British bluebell
GB IUCN Category	LC	**T13 Status**	Moderate risk Mitigation effective

Context	**Background**	The British bluebell is a diploid herbaceous predominantly outcrossing perennial, able to reproduce sexually via seed and asexually via bulbs. It is widespread and abundant in the UK, with strongholds in woodlands and more open habitats towards the west-coast (Kohn *et al.* 2009).
	Current threats	Introduced non-natives or “Spanish bluebells” (likely originally to have been horticultural introductions of *Hyacinthoides hispanica* from the Iberian peninsula and later of commercial varieties of uncertain provenance, often sold as *H. hispanica* but now widely ascribed to the hybrid, *H. x massartiana*, between *H. non-scripta* and *H. hispanica*) have been considered to be a major threat to the British bluebell either via competitive displacement or extinction by hybridisation (summarised in Kohn *et al.* 2019). Non-natives occur frequently throughout the range of *H. non-scripta*, particularly near urban areas, roadsides, and other sites of human disturbance.
	Contribution of Scottish population to total species diversity	The British Isles are the global stronghold for the British bluebell and the species is abundant in Scotland, with many populations far from urban centres and hence likely to have more limited co-occurrence (and thus hybridisation potential) with non-natives (Kohn 2009). The Scottish population is thus globally important from a demographic perspective and may contain unique locally adapted variants.
Genetic risks	**Diversity loss: population declines**	No clear evidence for demographic declines. The species is widespread and abundant across the UK. There is the possibility of loss via competition with the non-native bluebell in the UK, but the current evidence of high bulb densities suggests physical encroachment is likely to have limited effects.
	Diversity loss: functional variation	No evidence for loss of adaptive variants. The species remains common and abundant across the UK.

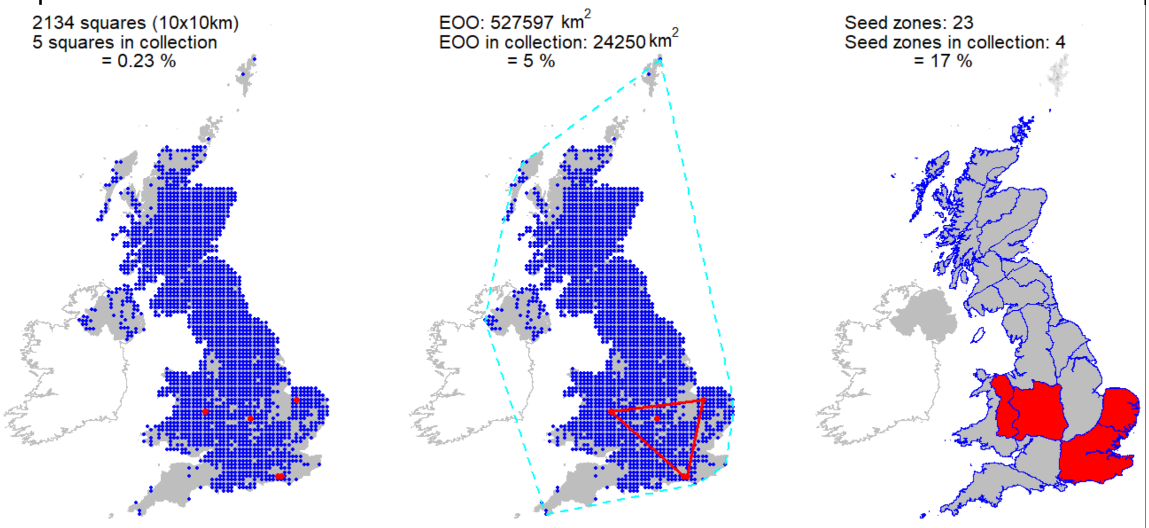
	Diversity loss: divergent lineages	As the British Isles are the global stronghold of the species, any decline in the UK runs the risk of loss of unique diversity. However, at present, there is no evidence for catastrophic loss across its range in the UK.
	Hybridisation/ introgression	Hybridisation has been considered a major concern. There is very high co-occurrence with non-native bluebell, and the concern is particularly acute for important large natural populations in ancient woodlands close to urban areas. However, recent genetic data shows that the native bluebell has a fertility advantage compared to non-natives, and considerably greater numbers of individuals (Kohn *et al.* 2009, 2019). Thus, although persistent, naturalised non-natives are widespread and continued crossing at low levels can be expected, it is unlikely to lead to systematic and widespread genetic diversity loss in the *H. non-scripta.*
	Low turnover/ constraints on adaptive opportunities	No evidence of limitation to recruitment. Populations appear to reproduce via a mixture of sexual and asexual reproduction (Blackman & Rutter 1954; Wilson 1959).
Cumulative risk summary	***In situ* genetic threat level**	Moderate (high co-occurrence with non-native bluebells with hybridisation and competition a clear threat at individual sites; however, the reduced fertility of non-natives, perennation and reproduction by bulbs, and the numerical supremacy of the native bluebell substantially limits any threat of overall catastrophic losses).
	Confidence in *in situ* threat level	High (assessment based on extensive genetic data and quantitative demographic surveys).
	***Ex situ* representation**	Collections from 12 10 km squares are represented in the Millennium Seed Bank, but only minimal coverage in Scotland. Two wild collected accessions represented in the living collection of the Royal Botanic Garden Edinburgh.
		
	Current conservation actions	Increased awareness of the concern associated with non-native “Spanish bluebells” has led to management interventions around important sites, and discouragement of sales and planting of non-native bluebell varieties. The British bluebell is protected under Schedule 8 of the Wildlife and Countryside Act.

		Ex situ	Translocation	Habitat management	Legal protection of habitat or species	Control of INNS/pests/ pathogens
		X		X	X	X
	Overall T13 status	Moderate risk; Mitigation effective				
	Overall T13 status explanation	There is a clear threat from non-native bluebells; however, the sheer numbers of the native bluebell, the longevity of individual plants via bulb production, and its greater fertility mean that in the immediate future there is limited threat to the overall genetic diversity of the British bluebell. Growing awareness of the problems from non-native bluebells should help				
	Assessor	Pete Hollingsworth, Royal Botanic Garden Edinburgh				
	Reviewer	Deborah Kohn, Royal Botanic Garden Edinburgh				

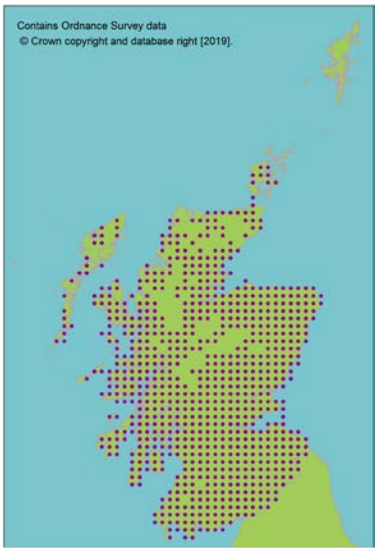
Scientific name	*Campanula rotundifolia*	**Common Name**	Harebell or Scottish bluebell
GB IUCN Category	LC	**T13 Status**	Moderate risk Mitigation not in place

Context	**Background**	Perennial, hermaphrodite herb, widespread with a circumpolar distribution and wide ecological amplitude. Pollination by insects, self-incompatible, spreads by seed and rhizomes. UK populations represent two subspecies, corresponding to polyploid races (tetraploid *ssp. rotundifolia* and hexaploid *ssp. montana*) (Stevens *et al*., 2012).
	Current threats	Declines in abundance and range due to intensification of agriculture and regeneration of woodlands and scrub; nitrogen deposition associated with population declines (Stevens *et al*., 2012). Potential for introgression from non-native genotypes planted for habitat restoration (Walker *et al.*, 2004a,b). Seedlings are poor competitors and require disturbed open ground. Seed banks mostly persist for short intervals (<5 yrs).
	Contribution of Scottish population to total species diversity	Hexaploid plants and susbp. m*ontana* have their strongholds in Scotland (Stevens *et al*., 2012).
Genetic risks	**Diversity loss: population declines**	Moderate risk of genetic diversity loss. Diploid race 2n=34 apparently lost from Britain (Stevens *et al*., 2012). Population declines reported, especially at range edges (Braithwaite *et al*., 2006) and 39% in Countryside Survey (as cited in Stevens *et al*., 2012). These population declines may lead to further genetic diversity loss.
	Diversity loss: functional variation	Population declines have been reported in the north of Scotland (Stevens *et al*., 2012) and this may disproportionately affect the hexaploid cytotype / subsp. *Montana*.
	Diversity loss: divergent lineages	Strong local structuring is apparent in distribution of tetraploids vs hexaploids: declines in north Scotland mostly impact the hexaploid populations (Stevens *et al*., 2012).

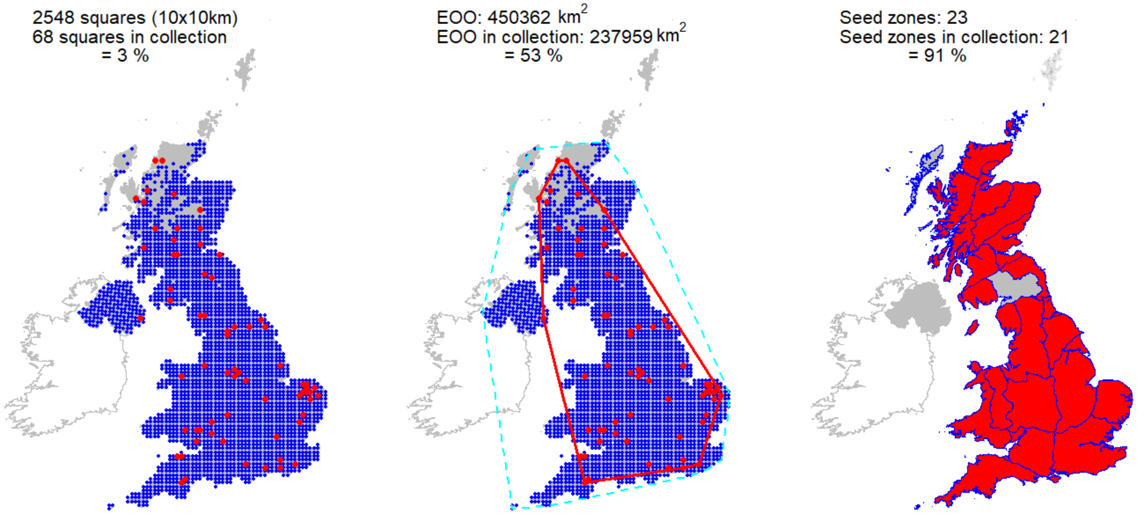
<table>
<tr><td rowspan="2"></td><td>**Hybridisation/ introgression**</td><td colspan="5">Tetraploids and hexaploids are usually geographically separate, but rare hybrids occur in range overlap with occasional aneuploids. Potential for genetic problems via hybridisation with non-native genotypes in seed mixes used for habitat restoration.</td></tr>
<tr><td>**Low turnover/ constraints on adaptive opportunities**</td><td colspan="5">Late summer mowing in road verges can prevent regeneration and spread from seed.</td></tr>
<tr><td rowspan="9">**Cumulative risk summary**</td><td>***In situ* genetic threat level**</td><td colspan="5">Moderate (loss of diploids from UK, losses in hexaploid *ssp. montana* range, continuing threat from land use change, agricultural intensification and nitrogen pollution).</td></tr>
<tr><td>**Confidence in *in situ* threat level**</td><td colspan="5">Medium (assessment based on good distribution data supported by direct data on most aspects of species' biology including cytotypes, but lacking a comprehensive genetic diversity study).</td></tr>
<tr><td>***Ex situ* representation**</td><td colspan="5">Five UK accessions, covering five 10 km squares held at the Millennium Seed Bank, but no collections from Scotland. Three wild collected accessions represented in the Royal Botanic Garden Edinburgh living collection.</td></tr>
<tr><td colspan="6">Representation in seed bank collection

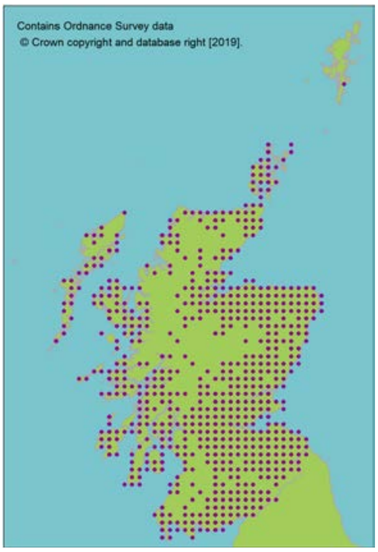

</td></tr>
<tr><td rowspan="3">**Current conservation actions**</td><td colspan="5">Nitrogen deposition control beginning to show results with declines in NOx over the last decade, but approximately 40% of nitrogen-sensitive habitats in Scotland exceed critical loads, and ammonia still rising. Restoration projects need awareness of local provenance.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>**Overall T13 status**</td><td colspan="5">Moderate risk; Mitigation not in place</td></tr>
<tr><td>**Overall T13 status explanation**</td><td colspan="5">A lag time between emissions controls and slowing nitrogen deposition rates is in evidence and critical loads are still being widely exceeded. Extirpation of diploid populations and declines in *ssp. montana* evidence loss of genetically distinctive lineages.</td></tr>
</table>

	Assessor	Rebecca Yahr, Royal Botanic Garden Edinburgh
	Reviewer	Aline Finger, Royal Botanic Garden Edinburgh Pete Hollingsworth, Royal Botanic Garden Edinburgh

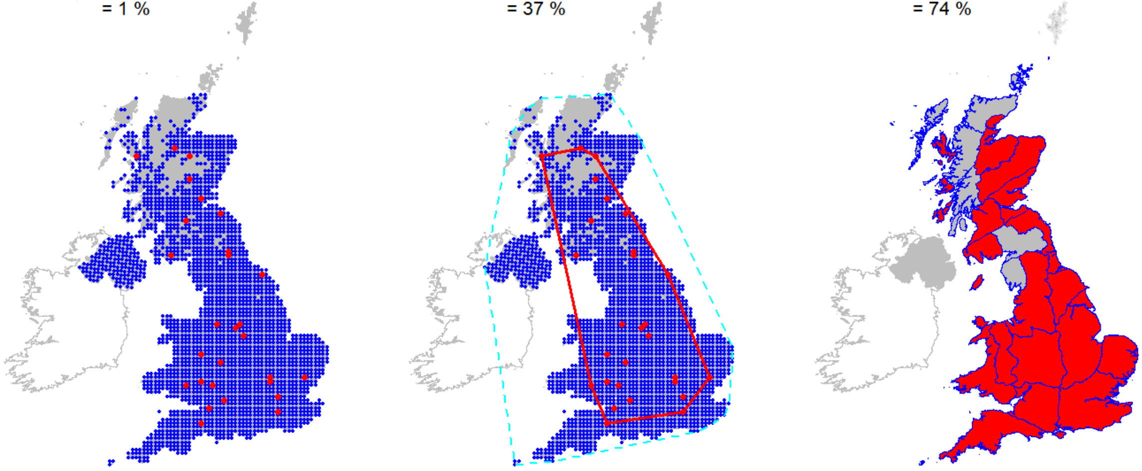
Scientific name	*Fraxinus excelsior*	**Common Name**	European ash
GB IUCN Category	NT (global status; assessed 2017)	**T13 Status**	Serious risk Mitigation not effective
			
Context	**Background**	Subdieocious, wind-pollinated, wind-dispersed, widely distributed woodland and wayside tree. Predominantly European distribution extending into southwestern Asia. In the UK abundant locally, especially as younger trees due to recent woodland expansion (Maskell *et al*., 2013) and currently the second most common broadleaf tree. Soil feedbacks from high-nutrient litterfall make this a keystone species where it dominates stands. Prolific reproduction via seed and with ability to coppice, but severe risk from introduced fungal and potentially insect pests, with losses as high as 95% predicted (Thomas, 2016). Over 1000 other species are associated - with 44 restricted to ash alone in the UK – suggesting that losses of ash will result in knock-on effects for ecosystems (Mitchell *et al*., 2014).	
	Current threats	Severely threatened throughout the UK by the introduced ash dieback plant pathogen *Hymenoscyphus pseudoalbidus* (first reported in the UK in 2012). Another potential threat is from the emerald ash borer *Agrilus planipennis,* currently causing damage on European ash in Russia where the American green ash *F. pennsylvanica* has been introduced. Both of these risks can be aggravated by other environmental stressors (moisture, drought) or opportunistic pathogens (e.g. *Armillaria*).	
	Contribution of Scottish population to total species diversity	Scotland and the UK are part of a western European genetic lineage that colonised from an Iberian refugium. Scottish populations show local adaptation in terms of morphology and phenology, and retain high levels of genetic variation as a consequence of high pollen and seed flow, even when fragmented (Heuertz *et al*., 2004; Bacles *et al*., 2005, 2006; Whittet *et al*., 2019).	

Genetic risks	**Diversity loss: population declines**	High likelihood of diversity loss. The general persistence of the species across its range in Scotland is threatened by huge predicted population losses from areas where ash dieback has been long established, with mortality ranging from ~70-85% depending on stand-type (DEFRA, 2019). Highest population losses from ash dieback are predicted for young trees, those in very moist soils and those which are ash-dominated. Presence and impacts are correlated with time since first arrival, and currently Scotland has a relatively low incidence of ash dieback.
	Diversity loss: functional variation	High likelihood of loss of functional variation, as locally adapted populations may encounter catastrophic losses. In all studied stands, only 1-5% of trees are suggested to be tolerant to ash dieback, but with a measurable genetic component, suggesting the potential for increasing tolerance by breeding and through natural selection *in situ* (Cavers & Cottrell, 2015; DEFRA, 2019). Maintaining old, healthy trees ensures production of seed and promotes continued natural selection.
	Diversity loss: divergent lineages	Limited divergence from European populations precludes loss of major divergent lineages, but there is potential for loss of locally adapted populations.
	Hybridisation/ introgression	No major hybridisation issue threatening genetic diversity. In some parts of Europe where ranges overlap, *F. excelsior* can hybridize with *F. angustifolia* and other species of *Fraxinus*.
	Low turnover/ constraints on adaptive opportunities	High mortality and severe pressures are predicted to limit regeneration and adaptive change. Risks due to combined stresses from soil conditions, pest and pathogen pressures, and competition from faster-growing species all result in higher susceptibility to tree- and stand-scale losses, which limit healthy population turnover and adaptive evolution.
	***In situ* genetic threat level**	Serious (in the face of emerging pathogen threats, major population losses and limitations to regeneration present a high risk of genetic variation loss).
	Confidence in *in situ* threat level	High (assessment based on good demographic data from Europe, where the effects of slow-to-manifest ash dieback can be assessed; direct data on genetic variation, population differentiation and biology).
	***Ex situ* representation**	Collections from 68 10km squares held at the Millennium Seed Bank, with comprehensive coverage of Scotland. It is estimated these collections capture >90% of genetic diversity (Hoban *et al*., 2018). They encompass 2.3 million seeds from 59 sites in 22 seed zones, representing 659 trees sampled as a case study of genetic protection (Hoban *et al*., 2018). One wild collected accession is held at Royal Botanic Garden Edinburgh living collection, plus two other European wild collected and four cultivated accessions. Two UK wild collected accessions are also held in Royal Botanic Garden Kew.

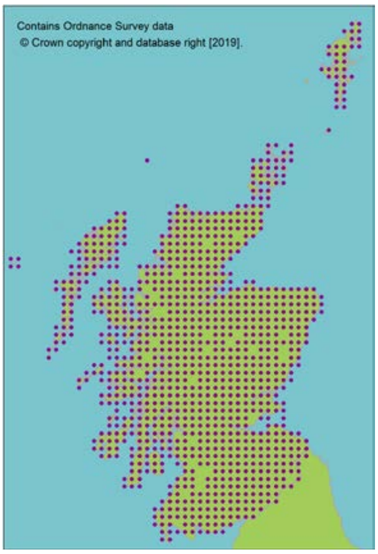
<table>
<tr><td rowspan="6">Cumulative risk summary</td><td colspan="6">Representation in seed bank collection
 </td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Active projects to understand and map stresses on ash stands, understand the genetic basis for tolerance (including resistance, avoidance, the role of microbiota) and to plan breeding programmes to promote tolerance. Control of movement of nursery stocks and timber to prevent emerald ash borer.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td>X</td><td>X</td><td>X</td><td>X</td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Serious risk; Mitigation not effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Despite widespread distribution and abundance, population losses are predicted to catastrophic. Intensive management strategies, such as resistance breeding, require huge investment and benefits to wild populations and will only be realised with persistent and long-term intervention. <i>Ex situ</i> collections are very strong, with good representation of contemporary diversity, but do not secure a long-term future for ash genetic diversity and presence of viable and evolving ash populations. Managing populations to promote natural regeneration is the most effective way of promoting long-term adaptation to ash dieback through natural selection.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Rebecca Yahr, Royal Botanic Garden Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Richard Ennos, University of Edinburgh
Peter Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Sambucus nigra*	**Common Name**	Elderberry
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation not required
		 Contains Ordnance Survey data © Crown copyright and database right [2019].	

Context	**Background**	Perennial, hermaphrodite, deciduous shrub, common and widely distributed in eutrophic woodlands, hedges and disturbed sites in the UK and continental Europe. Pollination by generalist beetles, flies and bees. Fertilisation mostly from the same individual, though both outcrossing and fruit set without pollination have been observed. Seeds are bird dispersed (Atkinson & Atkinson, 2002).
	Current threats	None known. This species probably benefits from periodic human disturbance and an agricultural landscape. Some sensitivity to acidification of soils for seed germination and risks to vegetative parts from late frosts and drought (Atkinson & Atkinson, 2002).
	Contribution of Scottish population to total species diversity	The species is common elsewhere in its range and there is no expectation of divergent endemic genetic lineages in Scotland, although the populations may be adapted to the local environment.
Genetic risks	**Diversity loss: population declines**	No evidence for genetic diversity loss and individual plant longevity ameliorates short-term risks.
	Diversity loss: functional variation	Populations are large and widespread and without evidence for significant decline (Braithwaite *et al.*, 2006). No immediate risk of loss to functional variation.
	Diversity loss: divergent lineages	Limited risk as no evidence for phylogenetically divergent lineages present in Scotland.
	Hybridisation/ introgression	Hybrids are not reported from Britain and very rare elsewhere.

<table>
<tr><td></td><td>**Low turnover/ constraints on adaptive opportunities**</td><td colspan="5">No constraints apparent.</td></tr>
<tr><td rowspan="9">**Cumulative risk summary**</td><td>***In situ* genetic threat level**</td><td colspan="5">Negligible (large, widespread populations and no evident threats).</td></tr>
<tr><td>**Confidence in *in situ* threat level**</td><td colspan="5">Medium (assessment based on good demographic data supported by direct data on most aspects of species’ biology and no obvious threats; no direct genetic data available).</td></tr>
<tr><td>***Ex situ* representation**</td><td colspan="5">Clonally propagated collections held in 15 International Phenological Gardens in addition to accessions, covering 28 10km squares held at the Millennium Seed Bank. Comprehensive coverage of Scottish seed zones. Representation in the Royal Botanic Garden Edinburgh living collection of one wild collected accession.</td></tr>
<tr><td colspan="6">Representation in seed bank collection

</td></tr>
<tr><td rowspan="3">**Current conservation actions**</td><td colspan="5">None required.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td></td><td></td><td></td></tr>
<tr><td>**Overall T13 status**</td><td colspan="5">Negligible risk; Mitigation not required</td></tr>
<tr><td>**Overall T13 status explanation**</td><td colspan="5">With large populations, wide distribution and populations generally promoted by current landscape structure, no risks to genetic variation require attention.</td></tr>
<tr><td></td><td>**Assessor**</td><td colspan="5">Rebecca Yahr, Royal Botanic Garden Edinburgh</td></tr>
<tr><td></td><td>**Reviewer**</td><td colspan="5">Iain Macdonald, Scottish Natural Heritage
Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Holcus lanatus*	**Common Name**	Yorkshire fog
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation not required



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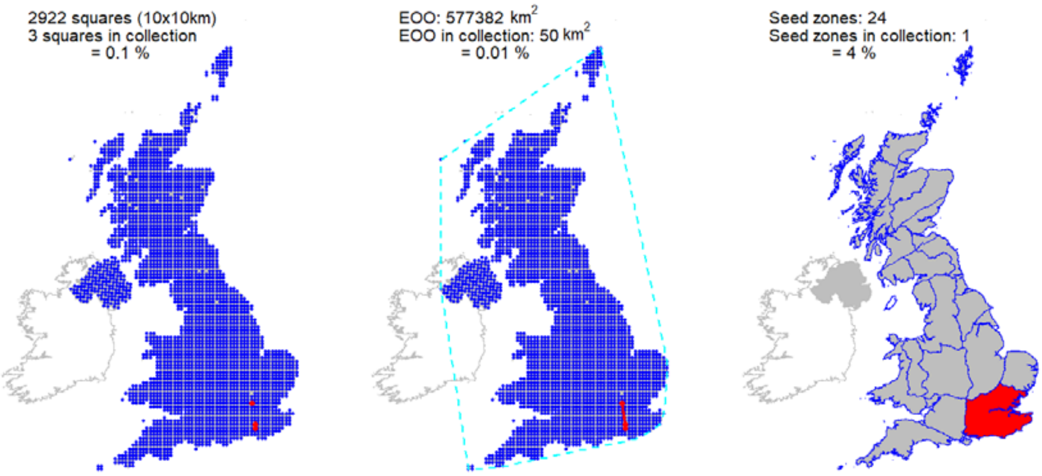
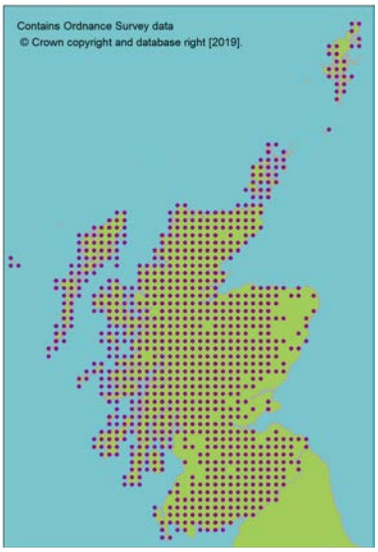
Context	**Background**	Perennial tufted grass, mostly outcrossing with limited potential for vegetative spread (Bischoff *et al*., 2006) and persistent seed banks (Beddows, 1961). One of the commonest plants in the UK (Braithwaite *et al*., 2006). Used in seed mixtures for restoration and revegetation and for improving grazing in native swards (Beddows, 1961; Bischoff *et al*., 2006). *Holcus lanatus* comprises two varieties, both found throughout their ranges (Rich & Jermy, 1998).
	Current threats	Genetic swamping from introduction of non-native or non-local seed sources in restoration projects (Walker *et al*., 2004a).
	Contribution of Scottish population to total species diversity	Scottish populations are likely to be among the most oceanic and may contain locally adapted genotypes.
Genetic risks	**Diversity loss: population declines**	No evidence of declines (Braithwaite *et al*., 2006), but rather of human-mediated propagation for restoration.
	Diversity loss: functional variation	Functional variation is well characterized, but not apparently under threat: Evidence of local adaptation in seed collected from chalk vs mesotrophic grasslands (Bischoff *et al*., 2006); used as a model system for genetics of metal tolerance (e.g. Meharg *et al*., 1993).
	Diversity loss: divergent lineages	No direct evidence of losses; widespread evidence of local adaptation to extreme conditions, e.g. metalliferous soil and climate (Macel *et al*., 2007).
	Hybridisation/ introgression	*Holcus mollis* is the tetraploid counterpart to diploid *H. lanatus* (Rich & Jermy, 1998). Some hybrids are known in the wild and can be produced by crossing (Beddows, 1961). Primary concern is hybridisation with non-local seed from restoration projects, but the species' abundance limits the overall potential for negative impacts.

<table>
<tr><td></td><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Large populations, reproduction mostly by outcrossed seed and ability to re-establish on disturbed sites (e.g. Lowday <i>et al</i>., 1992) suggests no limits to adaptive opportunities. Studies suggest a loss of biomass production due to drought (Beierkuhnlein <i>et al</i>., 2011).</td></tr>
<tr><td rowspan="9">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (widespread and large populations reduce impacts of any existing pressures).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">Medium (assessment based on good demographic data supported by direct data on most aspects of species’ biology, cytotype distribution, and no obvious threats; however, no direct genetic data available).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Four UK accessions, covering three 10 km squares held at the Millennium Seed Bank, but no coverage in Scotland. Representation in the Royal Botanic Garden Edinburgh living collection of one wild collected accession.</td></tr>
<tr><td colspan="6">Representation in seed bank collection

 </td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Recent consideration of policy shifts towards using local seed in restoration should help mitigate any potential risks from genetic swamping (De Vitis <i>et al</i>., 2017; Abbandonato <i>et al</i>., 2018)</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td></td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Though some potential risk from genetic swamping could be pinpointed in restoration projects using commercial seed, this species is able to colonize easily without seed additions (e.g. Lowday <i>et al</i>., 1992).</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Rebecca Yahr, Royal Botanic Garden Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Aline Finger, Royal Botanic Garden Edinburgh
Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Molinia caerulea*	**Common Name**	Purple moor-grass
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation not required



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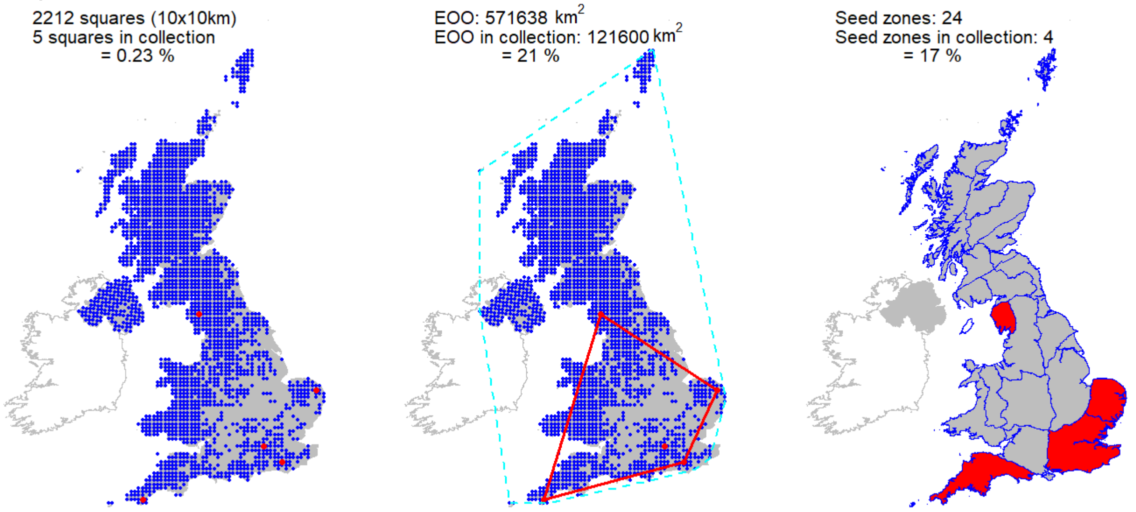
Context	**Background**	Perennial grass forming tussocks or extensive swards, capable of spreading clonally and dominating stands. A peat-forming member of acid-grasslands, wet heath, and bog; losses in the former are contrasted with a need for controlling populations in the latter habitats. Two subspecies (tetraploid ssp. *caerulea* and diploid and decaploid ssp. *arundinacea*) are known in Britain (Taylor *et al*., 2001). Ecotypic variation within subspecies can be due to both genetic and ecological factors. Common and locally abundant in north and west Britain and widespread in Europe and Asia. Can form a persistent seed bank (Taylor *et al*., 2001).
	Current threats	Not considered to be under threat.
	Contribution of Scottish population to total species diversity	Locally adapted gene pools may be present, but the contribution to global species diversity is not considered particularly high.
Genetic risks	**Diversity loss: population declines**	The distribution is broadly stable with local increases in abundance potentially due to increased nitrogen deposition, reduced grazing and / or muirburn.
	Diversity loss: functional variation	Ecotypic variation is likely to be preserved by large populations across a wide distribution.
	Diversity loss: divergent lineages	No evidence for divergence from European populations, precluding loss of major divergent lineages.
	Hybridisation/ introgression	No threats known.

<table>
<tr><td></td><td>Low turnover/ constraints on adaptive opportunities</td><td>None known. Seed viability is low, but bare ground is readily colonized.</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td>Negligible (this species is stable or locally increasing).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td>Medium (assessment based on good distribution data supported by experimental evidence on competitive abilities and quantitative changes in cover in wet heath and blanket bog habitats; no direct genetic data available for populations in Scotland).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td>Four UK accessions from three 10 km squares held at the Millennium Seed Bank, but no coverage in Scotland.</td></tr>
<tr><td colspan="2">Representation in seed bank collection

</td></tr>
<tr><td>Current conservation actions</td><td>Burning, grazing and nitrogen regimes largely control the shifts between wet <i>Calluna</i>-dominated heath and <i>Molinia</i>-dominated heath over short and long time spans (APIS, 2019b). Recent shifts are mostly toward <i>Molinia</i>, especially in continental lowland heath, and attributed to increases in nitrogen. Most management interventions aim to reduce <i>Monilia</i> in favour of promoting <i>Calluna</i>.
<table>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td></td><td></td><td></td></tr>
</table></td></tr>
<tr><td>Overall T13 status</td><td>Negligible risk; Mitigation not required</td></tr>
<tr><td>Overall T13 status explanation</td><td>Losses to genetic variation in lowlands are possible, but overall population size is very large and increasing across its range.</td></tr>
</table>

<table>
<tr><td></td><td>Assessor</td><td>Rebecca Yahr, Royal Botanic Garden Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td>Iain Macdonald, Scottish Natural Heritage
Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Hypocreopsis rhododendri*	**Common Name**	Hazel gloves
GB IUCN Category	Not formally assessed	**T13 Status**	Negligible risk Mitigation effective

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Context	**Background**	Hazel gloves is an ascomycete fungus parasitic on the wood-decay 'glue fungus' *Pseudochaete corrugata* (Grundy *et al*., 2012). Within Europe it is restricted to Atlantic hazel woodland (Dahlberg *et al*., 2010), and in North America to understory shrubs in the Appalachian woodlands (Grundy, 2014). It is a flagship species for Atlantic woodland (Coppins & Coppins, 2010).
	Current threats	The main threats it faces in Scotland and elsewhere are fragmentation and loss of habitat; for example as a result of scrub clearance (Dahlberg *et al*., 2010). These issues have been exacerbated by the negative impacts of grazing and a lack of resources to ameliorate poor management, and the incursion of invasive species such as *Rhododendron ponticum*.
	Contribution of Scottish population to total species diversity	Scottish and European populations show evidence of a recent population bottleneck, with source populations and higher genetic diversity in North America (Grundy, 2014).
Genetic risks	**Diversity loss: population declines**	Heavy grazing, concentrated grazing, coppicing and historic scrub clearance and invasive species has led to a reduction in the old-growth hazel habitat suitable for this species (Genney *et al*., 2016). However, the species is considered to be well dispersed which should retard loss of genetic diversity due to habitat fragmentation. In addition, European populations overall show very low levels of genetic variation compared to North American populations – essentially meaning that there is limited genetic variation in the first place to be lost in Scotland.
	Diversity loss: functional variation	Considered negligible risk as the habitat for this species is relatively homogenous, and there are no identified concerns about populations in atypical habitat that would be candidates for housing important adaptive genetic variation.

<table>
<tr><td rowspan="3"></td><td>Diversity loss: divergent lineages</td><td colspan="5">Considered negligible risk as the existing data suggest that Scottish populations contain a subset of genetic variation found elsewhere.</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">No evidence of risk of hybridisation/introgression (Grundy, 2014).</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">There is relatively high population turnover, with reproductive stromata living only for about two years. These rely on abundant populations of their host fungus (Grundy, 2014).</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (relatively uncommon but well-dispersed species benefiting from favourable management which should limit future declines).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (assessment based on recent genetic and ecological research).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Attempts to establish the species <i>ex situ</i> have been unsuccessful.</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Interventions to favour the species as part of the Species Action Plan (2007-2012) led to increased awareness of the species and appropriate management of its habitat (Genney <i>et al</i>., 2016). Since 2017, the Atlantic Woodland Alliance has developed an action plan to meet the needs of this and other species including control of invasive species.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td>X</td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation effective.</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">The overall low levels of genetic diversity in the species may constrain evolutionary potential, but there is no explicit evidence of genetic problems for the species to-date.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">David Genney, Scottish Natural Heritage</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Cantharellus cibarius*	**Common Name**	Chanterelle
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation not required

Context	**Background**	A locally common and widely distributed native ectomycorrhizal basidiomycete. Associated with woodland containing *Betula*, *Fagus* and *Quercus* species, occasionally reported in conifer plantations. Dispersal occurs via spores and vegetative growth. It is one of eight European species of *Cantharellus* recorded in Scotland, and it is currently considered genetically distinct from similar species in North America. It is highly prized as an edible mushroom.
	Current threats	Not currently considered threatened (LC) although negatively impacted by loss of habitat and nitrogen deposition in parts of Europe (Pilz *et al*., 2003). There is a perceived localised threat from trampling resulting in soil compaction and over-picking; however, the impact is not substantiated and would not be significant at a Scottish scale.
	Contribution of Scottish population to total species diversity	Research over the past decade has demonstrated that this is a European species distinct from North American species that were previously classified as *C. cibarius* (Buyck *et al*., 2016), and sequence diversity in public databases suggests divergent lineages even within Europe. However, there is no evidence that Scottish populations are distinct from those elsewhere in Europe.
Genetic risks	**Diversity loss: population declines**	No evidence for recent declines, and losses are likely to have been offset to some extent due to the species' ability to colonise the roots of non-native species to Scotland such as beech and, possibly, commercial conifers.
	Diversity loss: functional variation	There is no information on functional diversity within Scotland but because *C. cibarius* is widely distributed across Scotland, with a large population, loss of functional diversity is unlikely at present.
	Diversity loss: divergent lineages	No clear information available, but no evidence for divergent lineages being present.

<table>
<tr><td rowspan="2"></td><td>Hybridisation/ introgression</td><td colspan="5">There is no evidence of hybridisation or introgression.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Turnover is a difficult concept to define for a species with an indeterminate subterranean growth form, and there is little further evidence to inform this assessment. Sexual reproduction appears to occur on a regular basis with the faithful annual production of basidiomes/fruitbodies at well-known locations. It has been suggested that intensive harvesting of the fruitbodies may cause localised suppression of long-distance dispersal, but this is not substantiated by evidence.</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (the wide distribution of the fungus across a number of woodland habitats with no perceived evidence of ongoing decline leads to this assessment).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">Medium (the lack of understanding of trend data in Scotland is likely to be outweighed by its wide distribution and likely trajectory given native woodland expansion targets).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">The fungus can be cultured, with difficulty, on agar. It is likely that isolates are maintained in a number of mycology labs around the world but we have no evidence to substantiate this. Re-synthesis of mycorrhizal plants is fraught with difficulty and is not currently practical for reintroduction into the wild.</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Scottish targets to increase woodland extent are likely to benefit this species.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation not required.</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">This fungus is widespread, with large populations in Scotland. No evidence for genetic distinctiveness and no evidence of population declines.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">David Genney, Scottish Natural Heritage</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Rebecca Yahr, Royal Botanic Garden Edinburgh
Pete Hollingsworth, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Margaritifera margaritifera*	**Common Name**	Freshwater pearl mussel
GB IUCN Category	CR	**T13 Status**	Serious risk Mitigation not effective

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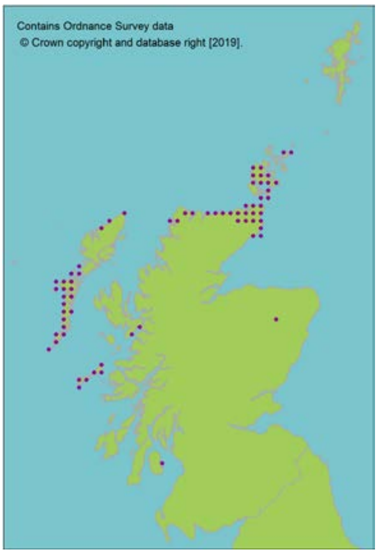
Context	**Background**	The freshwater pearl mussel is an endangered long-lived, bivalve mollusc present in at least 116 watercourses in Scotland, with evidence of recruitment in 74 (Cosgrove *et al*., 2016; Jones, unpublished data). It is one of the longest-living invertebrates, with individuals able to live for more than a century in Scotland. Historically widespread in the UK but the majority of current UK populations are restricted to the Highlands (Watt *et al*., 2015). The species has a long and complex lifecycle, requiring a fish host, and the juvenile stage is extremely vulnerable to habitat disturbance and damage.
	Current threats	Pollution and siltation from surrounding land use, and the physical alteration of rivers pose the most significant threats. Illegal harvesting, the status of their host fish populations (pearl mussels reproduce parasitically on salmonid fish gills), flow modification and climate change all represent other threats (Watt *et al*., 2015).
	Contribution of Scottish population to total species diversity	Scotland holds all but one of the remaining breeding populations in the UK. It also holds several of the largest remaining recruiting populations in the world. Scottish populations appear to retain a higher level of genetic diversity than populations elsewhere in Great Britain (Cauwelier *et al*., 2009).
Genetic risks	**Diversity loss: population declines**	High risk of loss of genetic diversity due to the consistent and significant population declines recorded globally, with populations in many European countries close to extinction (Lopes-Lima *et al*., 2017). In Scotland, freshwater pearl mussels appear to have become extinct in 73 rivers, 11 of these since 1998 (Watt *et al*., 2015). Some small Scottish populations show signs of population bottlenecks likely resulting in loss of genetic diversity.

<table>
<tr><td rowspan="4"></td><td>Diversity loss: functional variation</td><td colspan="5">Limited risk, as no functional differences have been identified between populations within the UK. However, there is evidence of genetic differences between rivers, which may reflect local adaptations (Cauwelier <i>et al</i>., 2009) that may be lost if declines and local extirpation continues. In addition, there is some risk from changes to fish stocks as some Scottish populations prefer salmon or trout host species (Baum, 2018), which may reflect local adaptation and is associated with genetically structured populations elsewhere in Europe (Karlsson <i>et al</i>., 2014).</td></tr>
<tr><td>Diversity loss: divergent lineages</td><td colspan="5">Some risk as freshwater pearl mussels in Scotland (and Northern England) belong to a single lineage, which is distinct from southern populations.</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">No risk of hybridisation/introgression with other species. Potential risk from translocations between genetically divergent/differently adapted populations within species.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Long generation times of at least 10-15 years and complex lifecycle coupled with low juvenile recruitment in many populations mean that adaptive constraints are a concern in many small populations.</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Serious (populations continue to be lost, with poor understanding of genetic structuring between remaining populations).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">Medium (good data on population demography based on structured surveys but limited genetic data).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Captive breeding populations have been established for Irish populations, but not yet for Scottish populations.</td></tr>
<tr><td rowspan="3">Current conservation management interventions</td><td colspan="5">Conservation measures underway, particularly focussed on populations with statutory designations.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td>X</td><td>X</td><td>X</td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Serious risk; Mitigation not effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Populations continue to be lost, despite concerted efforts. Significant declines in some populations are still predicted and, with limited understanding of local genetic variation/ adaptation, additional genetic problems may arise. Reduced juvenile recruitment is also widespread, despite significant conservation measures in many catchments.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Sam Jones & Jenny O’Dell, University of the Highlands and Islands</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Iain Sime, Scottish Natural Heritage
Pete Hollingsworth, Royal Botanic Garden Edinburgh
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Bombus distinguendus*	**Common Name**	Great yellow bumblebee
GB IUCN Category	EN	**T13 Status**	Serious risk Mitigation not effective



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Context	**Background**	Widely distributed but uncommon bumblebee species, with colonies presence across Europe, Asia, and North America (Alaska). In Europe, this species has an estimated overall decline of over 30% between 2004 and 2014 (Hatfield *et al*., 2016) and a catastrophic range contraction in the UK (Tonhasca & Macdonald, 2016). In the UK, this species is now only found on islands off the north and west of Scotland (Inner Hebrides, Outer Hebrides, Orkney islands) and some localities in the northern Scottish mainland (Goulson, 2003). Population genetic studies showed significant genetic differentiation at large geographical scale (i.e. between the islands of South Uist, Coll, Tiree, and Orkney) but not at smaller scales (Charman *et al*., 2010).
	Current threats	The main threat is land-use change resulting in loss of suitable foraging habitat to maintain the colony cycle (Jun – Sep) and sites for nesting, mating and hibernation (Charman *et al*., 2009). As a species with late phenology and narrow climatic niches, the increase in heat waves associated with climate change is another factor that might lead to population decline (Williams *et al*., 2007).
	Contribution of Scottish population to total species diversity	Data regarding species diversity across its distribution is not available. Based on losses elsewhere in the UK, the Scottish populations will hold the last remnants of genetic diversity of the entire GB population. Distribution models predict that under climate change suitable climatic conditions in Europe will only remain in restricted areas of the Alps, Scotland and Scandinavia (Rasmont *et al*., 2015). Thus, Scottish populations may represent an important genetic diversity refugia in the NW of Europe.
	Diversity loss: population declines	Substantial diversity loss has already likely occurred due to widespread declines, with lower levels of genetic diversity reported for this species in Scotland, compared to other scarce or declining bumblebees (Charman *et al*., 2010). Further loss is predicted if population declines/loss continue.

<table>
<tr><td rowspan="4">Genetic risks</td><td>Diversity loss: functional variation</td><td colspan="5">No data available on functional diversity but it is likely that adaptive variation has been lost during recent range contractions in UK given the narrowing of its extant climatic range (Rasmont <i>et al</i>., 2015).</td></tr>
<tr><td>Diversity loss: divergent lineages</td><td colspan="5">No data on divergent genetic lineages within Scotland are available.</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">Low concern. No reports of hybridization or introgression for this species.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Low concern. Short lived species with high natural turnover.</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Serious (low genetic diversity, evidence of recent major catastrophic population declines).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">Low (demographic and genetic data give strong indication that diversity has been lost, but uncertainty as to ongoing picture).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">No known <i>ex-situ</i> representation of this species.</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Saving the Great Yellow Bumblebee conservation project has commenced, initially focusing on better understanding the species distribution, with a longer-term plan for improved habitat management. This follows on from a Species Action Framework conservation plan for this species (Tonhasca & Macdonald, 2016).</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Serious risk; Mitigation not effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Major declines and now confined to a small portion of former range. Some small-scale conservation actions in place, but no certainty that the decline has been arrested, resulting in concern of ongoing loss of the remaining genetic diversity.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Sílvia Pérez-Espona, University of Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Linda Neaves, Royal Botanic Garden Edinburgh
Richard Comont, Bumblebee Conservation Trust</td></tr>
</table>

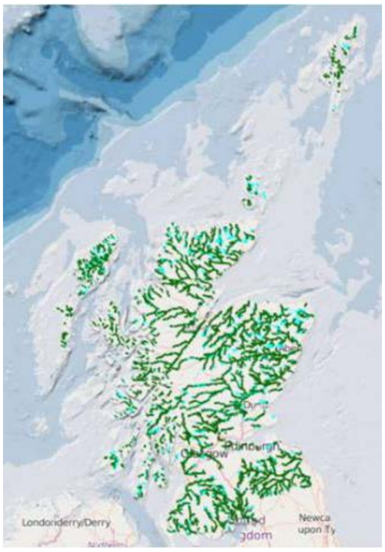
Scientific name	*Salmo trutta*	**Common Name**	Sea trout/brown trout
GB IUCN Category	LC (Europe – no GB freshwater fish Red Data Book)	**T13 Status**	Moderate risk Mitigation not in place
	 NBN Data – Trout presence 10km² grids		

Context	**Background**	Native to Europe but now widely introduced across the globe (Sanz, 2018) and an important element of the Scottish angling industry. Brown trout is a polytypic species that can adopt multiple life history strategies (Klemetsen *et al*., 2003), which can be divided into non-anadromous (freshwater resident) and anadromous (sea-run migratory) forms. The postglacial colonization of Scotland by this species involved one or more of six lineages (see Bernatchez, 2001). Introgression may have occurred between some, but not all, lineages (Verspoor *et al*., 2019). Anadromous (sea) trout play a key role in maintaining gene flow between trout populations in adjacent catchments (Ferguson, 2006). Both environmental and genetic factors drive expression and maintenance of these life histories (Ferguson *et al*. 2019).
	Current threats	Infections from pathogens or parasites may have contributed to local population declines of sea trout in Scotland (Urquhart *et al*., 2010). Higher parasitic sea louse (*Leophtheirus salmonis*) burdens (Moore *et al*., 2018) may also contribute to declines in areas near salmon farms (e.g. Thorstad *et al*., 2014). Hybridisation with non-native farmed stock (see Ferguson, 2007) poses a risk and has led to a restriction on the introduction of diploid fish for recreational angling, but fish farm escapes may also occur in some locations. Natural hybridisation with Atlantic salmon also occurs, although the extent and threat level are unknown (Adams *et al*., 2014). Environmental threats include climate change impacts, such as increased frequency of flood events or droughts, and increased river temperature (Jackson *et al*., 2018), while acidification, pollution and habitat fragmentation (Prodöhl *et al*., 2019) have had significant impacts in the past. Improvements to air and water quality, and stream connectivity may reduce the scale of these threats in future.

<table>
<tr><td></td><td>Contribution of Scottish population to total species diversity</td><td colspan="5">Scottish, and particularly small, isolated populations, may have lower genetic variation than other populations in NW Europe (Vøllestad, 2018). Scotland may contain unique, potentially locally adapted genetic and phenotypic variation (Bernatchez, 2001; Duguid <i>et al</i>., 2006).</td></tr>
<tr><td rowspan="5">Genetic risks</td><td>Diversity loss: population declines</td><td colspan="5">Moderate risk of loss due to declines over the last decade and isolation of some brown trout populations (Palm <i>et al</i>., 2003). The loss of sea trout, which facilitate gene flow between adjacent catchment and support resident coastal brown trout populations, may increase the risk.</td></tr>
<tr><td>Diversity loss: functional variation</td><td colspan="5">No data on functional diversity within Scotland, although some adaptation to local conditions may exist in isolated loch populations (Duguid <i>et al</i>., 2006). Irish populations show reduced Major Histocompatibility Complex diversity, possibly due to selection caused by exposure to diseases from farmed Atlantic salmon (Coughlan <i>et al</i>., 2006).</td></tr>
<tr><td>Diversity loss: divergent lineages</td><td colspan="5">Limited risk as Scottish brown trout populations are part of the Atlantic lineage, which is widespread in Europe (Bernatchez, 2001). However, Scottish populations contain the highest levels of diversity within this lineage present in the UK, including some unique variants (Bernatchez, 2001; McKeown <i>et al</i>., 2010; Duguid <i>et al</i>., 2006).</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">Hybridisation between native and non-native brown trout (or Atlantic salmon) is known to have occurred in Scotland but levels of introgression, and the impact of this, have not been assessed.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Data on turnover of wild brown trout populations are not available.</td></tr>
<tr><td rowspan="7">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Moderate (relatively widespread species but multiple threats create possibility of repeated local declines/local genetic diversity loss).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">Low (multiple threats with limited data, available genetic data is variable meaning detailed direct data required understand risks).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Brown trout are maintained in captive populations as part of commercial farming and stocking for angling.</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Stocking of diploid hatchery reared fish to support recreational fisheries is being phased out (2016-2020) to avoid the potential negative impact on the genetic composition of wild populations. Where stocking is allowed, this will only be carried out using triploid stock. No conservation-focused interventions.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Moderate risk; Mitigation not in place</td></tr>
</table>

	Overall T13 status explanation	There are multiple potential threats to local populations, and thus genetic diversity in Scotland, but relatively little baseline / monitoring data available at a national level. Conservation strategies of brown (and sea) trout populations in Scotland would benefit from large scale genetic diversity and population structure assessments, and a greater understanding of current and future risks of diversity loss.
	Assessor	Sílvia Pérez-Espona, University of Edinburgh
	Reviewer	Colin Bean, Scottish Natural Heritage Linda Neaves, Royal Botanic Garden Edinburgh

Scientific name	*Salmo salar*	**Common Name**	Atlantic salmon
GB IUCN Category	VU (Europe – no GB freshwater fish Red Data Book)	**T13 Status**	Moderate risk Mitigation not effective



Context	**Background**	Globally significant species, found in the temperate and arctic regions of the northern hemisphere, and supporting commercial fishing industry and recreational angling. Present in ~389 Scottish river systems, comprising 74% of the UK stock. An anadromous species where adults return as 'grilse' (1-sea winter) or 'salmon' (multi-sea-winter) fish. Growing concerns over the decline in the numbers of grilse returning throughout Scotland and the long-term decline in the 'Spring' stock component due to habitat loss and other threats.
	Current threats	Over 95% mortality in the marine environment. Climate change and by-catch of post-smolts by marine fisheries are key factors, alongside the impact of epizootic outbreaks of pathogens from aquaculture along smolt migratory routes. In freshwater, climate change, water quality and quantity, barriers to migration and invasive non-native species are also key issues. Predation also an issue. Exploitation may threaten individual populations. Stocking, to compensate for declining returns, and introgression from aquaculture escapees, may result in the loss of locally adapted traits and reduce fitness in some populations.
	Contribution of Scottish population to total species diversity	Scottish Atlantic salmon populations make up a significant proportion of the European stock and therefore represent much of its overall genetic diversity. Analyses confirm genome-wide patterns of geographical divergence across its global (Bourret *et al.*, 2013) and national (Gilbey *et al.*, 2016) range.
	Diversity loss: population declines	High risk of loss, with catch statistics indicating a reduction in adult population size of 55% over the past 50 years. Large east coast populations appear more resilient than those in small west coast rivers and less affected by salmon farming and sea lice. Nationally, the genetically distinct 'Spring' MSW stock component is undergoing long-term decline.

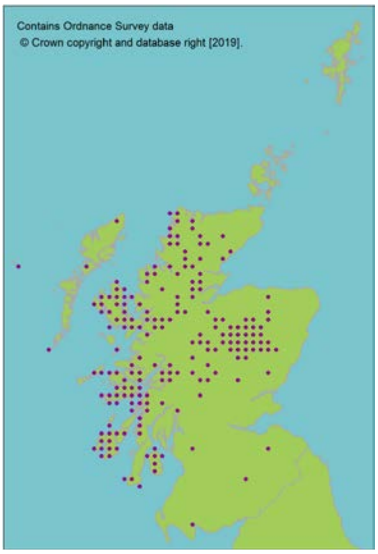
<table>
<tr><td rowspan="4">Genetic risks</td><td>Diversity loss: functional variation</td><td colspan="5">Moderate risk. Loss of genetically distinct ‘Spring’ stock present in some rivers, likely represents the loss of adaptive variation. Similarly, the occurrence of genetic differentiation across Scotland at adaptive makers, reflecting environmental variation (Cauwelier <i>et al.,</i> 2018), suggests that populations losses may result in loss of adaptive variation.</td></tr>
<tr><td>Diversity loss: divergent lineages</td><td colspan="5">Limited risk as Scottish populations are part of the widespread Atlantic lineage (Bourret <i>et al.</i>, 2013), but evidence of genetic differentiation both within and between natal rivers (Cauwelier <i>et al.,</i> 2018; Gilbey <i>et al.</i>, 2016).</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">Significant risk of introgression with aquaculture escapees and stocked fish, leading to loss of adaptive traits and reduced fitness in wild salmon (Gilbey <i>et al.</i> 2018).</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Low adult survival and return to spawning affecting all populations linked primarily to climate change and incidental by-catch may constrain adaptive opportunities.</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Moderate (relatively widespread species but multiple potential threats create the potential for genetic diversity loss).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (good demographic data and direct genetic data).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Farmed fish are plentiful, but do not represent wild genetic diversity; the majority having a Norwegian broodstock origin. Very limited <i>ex situ</i> representation of wild stocks.</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Exploitation managed through The Conservation of Salmon (Scotland) Regulations 2016 (amended in 2019). Habitat improvements delivered through Water Framework Directive. Greater regulation of the aquaculture industry.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td>X</td><td>X</td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Moderate risk; Mitigation not effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Scottish Atlantic salmon are heavily monitored and managed but threats to genetic diversity, due to poor marine survival, sea lice, aquaculture escapees and stocking remain. Long-term future of some genetically based stock components is uncertain.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Colin Bean, University of Glasgow</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Martin Llewellyn, University of Glasgow
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Rana temporaria*	**Common Name**	Common frog
GB IUCN Category	LC (Europe – no GB amphibian Red Data Book)	**T13 Status**	Negligible risk Mitigation not required

Context	**Background**	The common frog is a widespread species of northern and central Europe and north-western Asia. Its abundance and adaptability make it an important part of food webs both as a predator and as prey. It is found naturally throughout the Scottish mainland, including urban areas, and has been introduced to several Scottish islands (Minting, 2016).
	Current threats	The common frog has declined across much of its European range due to loss of habitat (drainage and urban expansion), pesticide use and pollution, and novel pathogens. Although currently uncommon in Scotland, ranaviruses are predicted to spread northwards under likely climate change scenarios and may pose the greatest threat (Price *et al*., 2019).
	Contribution of Scottish population to total species diversity	Mitochondrial DNA sequences from Scottish samples were identical to, or clustered with, the common haplotype previously identified from Western Europe (Muir *et al*., 2013).
Genetic risks	**Diversity loss: population declines**	Negligible risk. Although local declines have been observed, re-colonisation can be rapid in urban (O'Brien, 2015) and rural areas (McKinnell *et al*., 2016). Frogs using urban Green Infrastructure have similar levels of genetic diversity to those in rural areas (O'Brien *et al*., 2017).
	Diversity loss: functional variation	Negligible risk of loss despite adaptations to local conditions (Muir *et al*., 2014), because there is high gene flow between high and low altitude populations (Muir *et al*., 2013) and, in urban settings, via green infrastructure (O'Brien *et al*., 2017).
	Diversity loss: divergent lineages	Risk appears low as there is no evidence of structuring within Scottish populations, which themselves are little different from those of wider western European.

<table>
<tr><td rowspan="2"></td><td>Hybridisation/ introgression</td><td colspan="5">There are no species in Scotland, native or introduced, known to produce fertile hybrids with common frog, although introductions of conspecifics from elsewhere in its range have occurred.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Common frogs in Scotland typically produce up to 2000 eggs per breeding pair and can use a wide range of water bodies to breed and reproduce readily (Minting, 2016).</td></tr>
<tr><td rowspan="7">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (genetically diverse, with evidence of gene flow between populations despite natural and artificial barriers).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (assessment based on good demographic data, direct data on genetic variation, population differentiation and biology).</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">The common frog benefits from the creation of generalist wildlife ponds in urban and rural areas. The Green Infrastructure Strategic Intervention is creating new habitats for urban amphibians.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation not required</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Despite post-war declines in both rural and urban areas, the high fecundity, population connectivity and colonisation ability of the species suggest low risk of genetic loss. However, that very connectivity leaves it at risk of novel pathogens and must inform future management.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">David O’Brien, Scottish Natural Heritage</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Robert Jehle, University of Salford
Pete Hollingsworth, Royal Botanic Garden Edinburgh
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Aquila chrysaetos*	**Common Name**	Golden eagle
GB IUCN Category	NT	**T13 Status**	Negligible risk Mitigation effective



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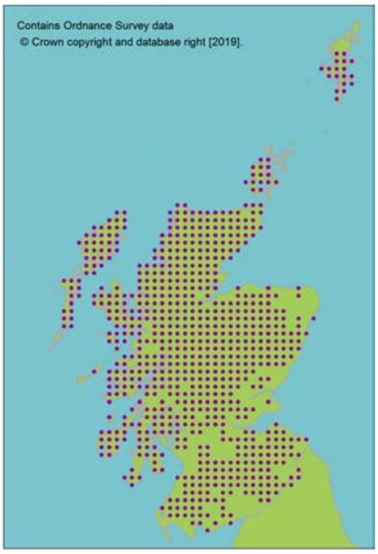
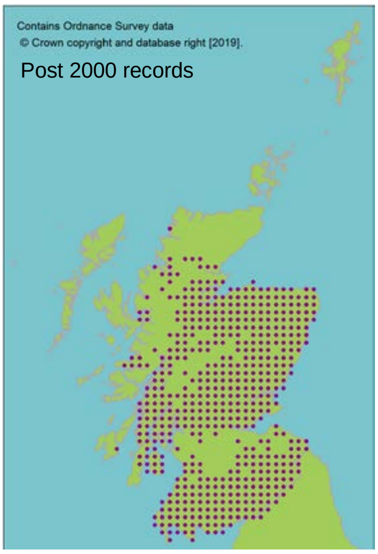
Context	**Background**	Iconic raptor that has suffered historic reductions in range and population size across the UK. Population currently limited to Scotland but are considered stable/recovering (Watson, 2010; Hayhow *et al.,* 2017).
	Current threats	Ongoing persecution, particularly in East Scotland threatens maintenance/growth of eagle populations in the region. Reproduction rates in certain other areas are considered below expectation, with unknown causes but shortage of live prey is likely a key factor and subject of current research.
	Contribution of Scottish population to total species diversity	Scotland is the only GB region with golden eagles, however, the contribution to global species diversity is not considered particularly high. Part of a circumglobal species distribution.
Genetic risks	**Diversity loss: population declines**	Negligible risk as the population is considered stable and the Scottish golden eagle population is not heavily structured (Ogden *et al.,* 2015), meaning the loss of genetic diversity through individual population declines is limited. However, low population numbers elevate sensitivity to diversity loss through random genetic drift, especially outwith the Scottish Highlands and Islands core range.
	Diversity loss: functional variation	Population unlikely to have strong local adaptive diversity within Scotland, minimising risk of loss to functional variation at a national scale. Functional differentiation of Scottish birds within the species unknown but subject of ongoing research.
	Diversity loss: divergent lineages	Risk of loss considered low. One DNA lineage observed in Scotland not seen elsewhere to date, however, Scotland shares many other lineages with populations across Eurasia (Nebel *et al.,* 2015).
	Hybridisation/ introgression	No risk of hybridisation/introgression.

<table>
<tr><td></td><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Very low population numbers/recruitment in certain regions (e.g., southern Scotland) and Northern Ireland may limit range of adaptive responses.</td></tr>
<tr><td rowspan="7">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (stable and sustainable population of a vagile species with no imminent threat of diversity loss).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (high-quality genetic and demographic data).</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Close annual monitoring of breeding success through national surveys (Hayhow <i>et al.,</i> 2017) and ringing studies. Ongoing south Scotland translocation project to reinforce population across southern counties.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td>X</td><td></td><td>X</td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">The overall population is currently stable/increasing. Measures are in place to increase small isolated sub-populations. Lack of observed genetic structure within Scotland and sharing of evolutionary lineages beyond Scotland minimises risk of losing genetic diversity.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Rob Ogden, University of Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Des Thompson, Scottish Natural Heritage
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Lagopus lagopus scotica*	**Common Name**	Red grouse
GB IUCN Category	LC	**T13 Status**	Moderate risk Mitigation effective
			 Contains Ordnance Survey data © Crown copyright and database right [2019].
Context	**Background**	Iconic upland species widely distributed in heather (*Calluna vulgaris*) dominated moorland areas. Culturally and economically important in rural Scotland as game species, with most revenue obtained through sport hunting (Storch, 2007). Long-term declines of this species in range and abundance have been reported (Eaton *et al*., 2009). Declines are associated with the loss or deterioration of heather moorland habitats, as a result of land use change from management of the habitat for hunting to an increase in sheep grazing and forestry plantations (Robertson *et al*., 2001, 2017; Ludwig *et al*., 2018). There is no evidence of lower than expected levels of genetic diversity across either functionally important or neutral markers given the population size (Piertney *et al*., 1998; 2000; Quintela *et al*., 2010; Meyer-Lucht et al. 2016).	
	Current threats	The main threat to red grouse is the disappearance of heather moorland, an upland habitat with internationally recognised conservation importance (Robertson *et al*., 2017). Other threats include infections by the nematode *Trichostrongylus tenuis* and the louping ill virus, and predation by avian and mammalian species (Martínez-Padilla *et al*., 2014).	
	Contribution of Scottish population to total species diversity	Red grouse is considered a subspecies of willow grouse (*Lagopus lagopus*) and has been shown to be genetically distinct using both neutral and adaptive genetic markers (Kozma *et al*., 2019). Scottish grouse have also been shown to be genetically distinct from the Irish subspecies *L. l. hibernicus*. As an endemic subspecies of northern and western Britain, Scottish populations contribute significantly to overall species diversity.	
	Diversity loss: population declines	Population genetic studies have found no evidence of reduced genetic diversity in red grouse, though the spatial pattern of genetic variation is affected by landscape features, social structure and levels of population isolation. Continuing habitat loss and population fragmentation could lead to diversity loss.	

<table>
<tr><td rowspan="4">Genetic risks</td><td>Diversity loss: functional variation</td><td colspan="5">There are no genome-wide studies of variation in genetic diversity across populations from Scotland. Genetic variation at several adaptive genetic markers (Wenzel <i>et al</i>., 2015 a,b,c) and patterns of epigenetic methylation (Wenzel & Piertney, 2014) have been shown to be affected by parasite burden of the gastrointestinal nematode <i>T. tenuis</i>.</td></tr>
<tr><td>Diversity loss: divergent lineages</td><td colspan="5">Red grouse is a distinct genetic lineage from willow ptarmigan (<i>L. lagopus</i>) and the Irish subspecies (<i>L. l. hibernicus</i>) (Quintela <i>et al</i>., 2010; Höglund <i>et al</i>., 2013; Meyer-Lucht <i>et al</i>., 2016).</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">Limited risk. Hybridisation between red grouse and willow ptarmigan can occur in captivity (Sharp & Moss, 1981), although the geographic isolation between these forms means in the wild means hybridisation does not occur in natural populations. There is some evidence of occasional introgression between red grouse and ptarmigan (<i>L. muta</i>) where their distributions overlap.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Relatively short generation time and no observed loss of reproductive fitness.</td></tr>
<tr><td rowspan="7">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Moderate (widely distributed species but immediate threats due to land use change and disappearance of heather moorlands)</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (detailed data on land use change in Scotland and population declines associated with disappearance of heather moorland, direct genetic data).</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">The fate of this species is tightly linked to its management as a game species, i.e. maintenance of heather moorland and control of parasites and predators; Robertson <i>et al</i>. (2017).</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td>X</td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Moderate risk; Mitigation effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Disappearance of habitat threatens population sustainability, although commercial management interventions in game regions is likely to support red grouse numbers in the immediate future.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Sílvia Pérez-Espona, University of Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Stuart Piertney, University of Aberdeen
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Sciurus vulgaris*	**Common Name**	Red squirrel
GB IUCN Category	EN NT (Scotland)	**T13 Status**	Moderate risk Mitigation effective



Context	**Background**	Iconic UK mammal species found in woodland habitats with a wide Eurasian distribution. Within the UK, there have been many translocations of red squirrels. It is a flagship species for many nature reserves.
	Current threats	Habitat competition and displacement by invasive grey squirrel, *Sciurus carolinensis* (Kenward *et al*., 1998). Loss of reproductive fitness and risk of death due to diseases, including squirrelpox virus, adenovirus and potentially leprosy (McInnes *et al*., 2006; Avanzi *et al*., 2016).
	Contribution of Scottish population to total species diversity	No unique lineages currently recognised in the UK (Barratt *et al*., 1999), despite a historical description of a UK subspecies. The Scottish populations represent the last remaining UK stronghold. Contribution to total diversity across the species range is not high but may harbour unique genotypes and adaptations due to its edge of range distribution.
Genetic risks	**Diversity loss: population declines**	Risk of ongoing diversity loss through population declines in southern Scotland. Lack of knowledge of population structure or distribution of genetic diversity hampers risk assessment of local extirpation on genetic diversity in Scotland.
	Diversity loss: functional variation	Reduced immunogenetic diversity relative to European populations observed (Ballingall *et al*., 2016) but potential rate of loss unknown. Scottish population is edge-of-range and may contain locally-adapted genetic variants.
	Diversity loss: divergent lineages	Risk considered negligible, as evolutionary lineages were derived from continental Europe relatively recently. Phylogeographic studies show no distinct monophyletic lineages in England and Wales; Scotland poorly studied.
	Hybridisation/ introgression	No risk of hybridisation/introgression with other species. Unmanaged translocations risk undesirable introgression between divergent populations.

<table>
<tr><td></td><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Species reproduces annually with sufficient fecundity for rapid mammalian population growth.</td></tr>
<tr><td rowspan="7">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Moderate (clear threats from competition/disease set against extensive conservation management for red squirrel and its habitat).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">Medium (red squirrels have been subject to detailed studies in Scotland resulting in its conservation status being well understood and the species has been subject to many genetic studies elsewhere).</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Active conservation management of red squirrel populations in the Scottish borders, maintenance of a grey squirrel boundary line across the country, south of the Highlands. Forest and Land Scotland currently considers promotion of red squirrel habitat within strategic planning. Some ad-hoc translocation programmes underway to populate the western Highlands from central and eastern areas.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td>X</td><td>X</td><td>X</td><td>X</td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Moderate risk; Mitigation effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Populations considered stable in most of Scotland. The replacement of red squirrels by greys seen throughout England and Wales has been retarded in southern Scotland, and grey squirrel encroachment into the Highlands has currently been prevented. A lack of molecular genetic data across Scotland prevents identification of possible population genetic structure or genetic diversity in Scotland.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Rob Ogden, University of Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Peter Lurz, University of Edinburgh
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Felis silvestris*	**Common Name**	Scottish wildcat
GB IUCN Category	CR	**T13 Status**	Serious risk Mitigation not effective

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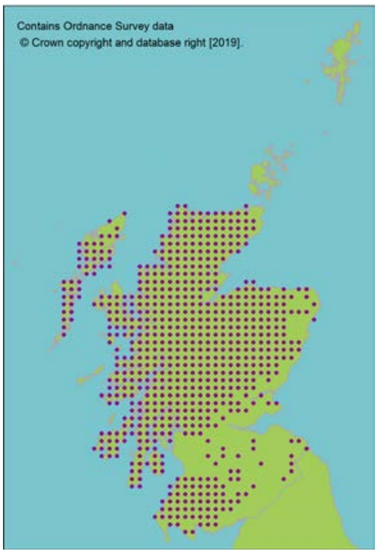
Context	**Background**	A Scottish icon and the only remaining native British cat. Scottish wildcats are a subpopulation of the European wildcat (Kitchener *et al.* 2017), although previously described as a subspecies. Although once found throughout the UK, they are now restricted to Scotland due to declines resulting from persecution and possibly other drivers, such as habitat change. The range contracted to the far north west before recovering to areas north of the Highland boundary fault (Langley & Yalden, 1977). Further contractions occurred in 21st C, due to illegal or accidental persecution and/or declines in prey (rabbit) populations, with no recent records from the north west of Scotland (Sainsbury *et al*., 2019). Genetic analysis has shown existence of a hybrid swarm, with all wildcats showing some hybridisation and most showing significant introgression (Senn *et al*., 2018). Hybridisation risks misidentification and consequently wildcats being killed during legal predator control by land managers.
	Current threats	Primary threats are genetic introgression with domestic cat, *Felis catus* and persecution.
	Contribution of Scottish population to total species diversity	The species is common elsewhere in its range and there is no evidence of divergent genetic lineages in Scotland, although the populations may be adapted to the local environment.
	Diversity loss: population declines	There is a high risk of diversity loss associated with recent range-contractions and most remaining populations being small, fragmented and isolated. Low population numbers elevate sensitivity to diversity loss through random genetic drift and inbreeding, although no data is available on genetic relatedness within the remaining populations. (Introgression is the primary threat in all populations; see below).
	Diversity loss: functional variation	No data available. Functional variation may be retained within hybridised individuals, but populations lost from the far north and west may have had unique adaptations to those environments.

<table>
<tr><td rowspan="3">Genetic risks</td><td>Diversity loss: divergent lineages</td><td colspan="5">Limited risk as no evidence for phylogenetically divergent lineages in Scotland. Kitchener <i>et al</i>. (2017) concluded there was insufficient evidence to recognise the wildcats in Scotland as a separate subspecies from <i>F. s. silvestris</i> in central and western Europe.</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">Serious risk. Wildcats in Scotland have very high rates of introgressive hybridisation with domestic cats. Since 2014, all wild-living cats sampled have shown domestic cat ancestry (Senn <i>et al.</i>, 2018). Typically, phenotypic wildcats exhibit 60-80% wildcat genetic heritage.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">Excessive influx of domestic cats into the wild-living population could limit adaptive opportunities but insufficient data is available to confidently state this. Hybrids may be better adapted to a human-influenced landscape than wildcats, but not enough research has been conducted to be confident of this.</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Serious (small fragmented populations of hybridising species present genetic risks).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (assessment based on public records across the range and intensive camera trap surveys repeated in Wildcat Priority Areas, supported by direct data on genetic introgression).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Genetic tests on individuals held in captivity show around 80 cats with low or very low (near zero) introgression with domestic cat. However, initial genetic analysis and studbook records suggest the captive population is inbred and new genetic variation is needed. Two wildcats taken from the wild have been included in this breeding programme but it is likely that individuals will need to be obtained from other parts of the European wildcat range.</td></tr>
<tr><td rowspan="3">Current conservation actions</td><td colspan="5">Thresholds based on appearance (a pelage score) and, when available, genetic tests have been set to ensure wildcats are not accidentally neutered or killed, and that highly introgressed individuals are neutered. Conservation focused in five Wildcat Priority Areas and includes the neutering (and vaccinating) of feral cats and campaigns for neutering and vaccination of pets. Local education on the risk to wildcats from pet cats and land management activities such as predator control.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td>X</td><td></td><td>X</td><td>X</td><td>X</td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Serious risk; Mitigation not effective</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Current conservation efforts will not halt cryptic extinction. As a minimum, supplementing existing populations with wildcats from captivity or from elsewhere in the wildcat's range in Europe is needed. This has not yet begun.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Roo Campbell, Scottish Natural Heritage</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Rob Ogden, University of Edinburgh
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

<table>
<tr><td>**Scientific name**</td><td>*Cervus elaphus*</td><td>**Common Name**</td><td>Red deer</td></tr>
<tr><td>**GB IUCN Category**</td><td>LC</td><td>**T13 Status**</td><td>Negligible risk
Mitigation not required</td></tr>
<tr><td colspan="3"></td><td>Contains Ordnance Survey data
© Crown copyright and database right [2019].</td></tr>
<tr><td rowspan="3">**Context**</td><td>**Background**</td><td colspan="2">Ecologically important species for the maintenance of upland diversity and an important element of the Scottish rural economy through revenue from stalking, venison and tourism, as well as a valued Scottish cultural icon (Pérez-Espona *et al*., 2009b). The current Scottish population is c. 445,000 – 505,000, with populations widely-distributed across the mainland and most of the islands (SNH, 2016). Overall genetic diversity measured at multiple markers is considered high (Pérez-Espona *et al*., 2009a; 2019).</td></tr>
<tr><td>**Current threats**</td><td colspan="2">The main threat is hybridization with sika deer (see Hybridisation section). The risk and manifestation of disease in European wild deer is not as high as that reported in North America but has increased in the past years, e.g., detection of Chronic Wasting Disease in Norway, introduction and spread of bluetongue virus (BTV), re-emergence of bovine tuberculosis (bTB), and prevalence of paratuberculosis in red deer (Ferroglio *et al*., 2011).</td></tr>
<tr><td>**Contribution of Scottish population to total species diversity**</td><td colspan="2">Scotland holds the largest red deer population in Europe (Burbaite & Csányi, 2010; Pérez-Espona *et al*., 2009b). Genetic diversity has been found to be similar or higher to other European populations (Pérez-Espona *et al*., 2008; 2009a), with high genetic diversity at the Major Histocompatibility Complex DRB exon 2 loci (Pérez-Espona *et al*., 2019).</td></tr>
<tr><td rowspan="2"></td><td>**Diversity loss: population declines**</td><td colspan="2">The current large populations of red deer in Scotland suggest there is no threat of diversity loss due to population declines.</td></tr>
<tr><td>**Diversity loss: functional variation**</td><td colspan="2">No evidence of risks to loss of functional variation.</td></tr>
</table>

<table>
<tr><td rowspan="3">Genetic risks</td><td>**Diversity loss: divergent lineages**</td><td colspan="5">Scottish populations are part of the Western European red deer lineage (Pérez-Espona *et al*., 2009a; Skog *et al*. 2009). Scottish population may harbour unique diversity but risks are negligible given the current population sizes.</td></tr>
<tr><td>**Hybridisation/ introgression**</td><td colspan="5">Hybridisation between red deer and sika deer *Cervus nippon* is one of the main threats to the maintenance of genetic distinctiveness in Scottish red deer populations. Hybrid individuals are mainly found on the Kintyre Peninsula (Senn & Pemberton, 2009; Smith *et al*., 2018), with smaller numbers in the North Highlands. No hybrids have been detected in the Central Highlands or the Hebrides (Smith *et al*., 2018) but this is likely underestimated due to limitations of detection.</td></tr>
<tr><td>**Low turnover/ constraints on adaptive opportunities**</td><td colspan="5">No indication of limited recruitment that would constrain adaptive opportunities.</td></tr>
<tr><td rowspan="9">Cumulative risk summary</td><td>***In situ* genetic threat level**</td><td colspan="5">Negligible (large populations with high genetic diversity in mainland Scotland; limited hybridisation with sika deer; CWD not reported in Scotland).</td></tr>
<tr><td>**Confidence in *in situ* threat level**</td><td colspan="5">High (direct estimates of genetic diversity and levels of hybridisation).</td></tr>
<tr><td>***Ex situ* representation**</td><td colspan="5">Red deer individuals with Scottish origin can be found in deer parks and in New Zealand wild populations, although it is likely that some *ex situ* populations are introgressed after crossing with other red deer populations and North American wapiti (*Cervus canadensis)*.</td></tr>
<tr><td rowspan="3">**Current conservation actions**</td><td colspan="5">Deer populations managed for production and to control densities in certain habitats; not directly managed for species conservation.</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>**Overall T13 status**</td><td colspan="5">Negligible risk; Mitigation not required</td></tr>
<tr><td>**Overall T13 status explanation**</td><td colspan="5">Population size in Scotland is large and stable. Good information on genetic diversity across Scotland, although further areas need to be studied for a complete overview. In particular, genetic studies need to be conducted in Dumfries and Galloway (southwest Scotland); areas were sika deer have expanded.</td></tr>
<tr><td></td><td>**Assessor**</td><td colspan="5">Sílvia Pérez-Espona, University of Edinburgh</td></tr>
<tr><td></td><td>**Reviewer**</td><td colspan="5">Josephine Pemberton, University of Edinburgh
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

Scientific name	*Capreolus capreolus*	**Common Name**	Roe deer
GB IUCN Category	LC	**T13 Status**	Negligible risk Mitigation not required
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Context	**Background**	Iconic forest-dwelling species. Economically important game species, due to the revenue gained through deer stalking, venison production, and tourism. Although associated with woodland, it is increasingly found in urban areas due to its ecological plasticity and adaptability. Numbers were drastically reduced by overhunting and deforestation but remnant populations are thought to have remained in some areas in Scotland (Whitehead, 1964). Marked expansion reported since 1972 with roe deer now found across most of the Scottish mainland and some islands (Ward, 2005). Total current estimated population size of 200,000 – 350,000, with the highest densities found in lowland areas (Edwards & Kenyon, 2013).
	Current threats	The main threat to populations in Scotland is introgression from non-native stock (see Hybridisation section). Other potential threats to populations may arise as the result of emergence and re-emergence of disease, or due to transmission of disease from livestock. Disease manifestation and risk in European wild ungulates is not as high as that reported in North America, but has increased in the past years, e.g. detection of Chronic Wasting Disease in Norway, introduction and spread of BTV, re-emergence of bTB, and prevalence of paratuberculosis (Ferroglio *et al*., 2011).
	Contribution of Scottish population to total species diversity	Despite an increase in harvest of 735% over the last twenty years, the UK holds one of the largest populations in Europe, with the largest continuous population being found in Scotland (Burbaité & Csányi, 2009). There is a lack of studies assessing genetic diversity of roe deer across Scotland, relative to the species range.
	Diversity loss: population declines	Considering the sizeable range expansion and large populations in Scotland, there are no apparent current threats that would lead to population declines and genetic diversity loss.

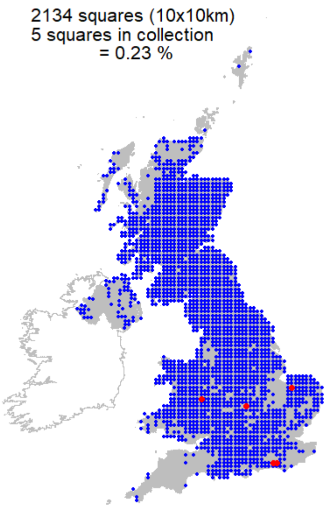
<table>
<tr><td rowspan="4">Genetic risks</td><td>Diversity loss: functional variation</td><td colspan="5">There are no studies regarding functional variation in Scottish populations.</td></tr>
<tr><td>Diversity loss: divergent lineages</td><td colspan="5">No evidence for divergent lineages but Scottish populations contain unique diversity not found elsewhere in the UK (Baker & Hoelzel, 2013). Risk of loss is negligible given current population trends.</td></tr>
<tr><td>Hybridisation/ introgression</td><td colspan="5">Hybridisation with other species is unlikely, as no introductions of Siberian roe deer have been reported. Introductions of a small number of non-native roe deer stock in Strathclyde and Dumfries during the 18th and 19th centuries have been documented (Baker & Hoelzel, 2013) but detailed genetic studies in these areas are not available.</td></tr>
<tr><td>Low turnover/ constraints on adaptive opportunities</td><td colspan="5">No indication of limited recruitment that would constrain adaptive opportunities. Roe deer is the most widely distributed species of deer in Scotland, occupying most of the mainland. Densities vary in forested areas but are particularly high in lowland areas. The species' rapid increase reported from the 1970s onward suggests recruitment is not limiting.</td></tr>
<tr><td rowspan="8">Cumulative risk summary</td><td><i>In situ</i> genetic threat level</td><td colspan="5">Negligible (large expanding populations in Scotland presenting adaptability to a range of habitats; introduction of non-native stock not a current management practice; no imminent threats identified).</td></tr>
<tr><td>Confidence in <i>in situ</i> threat level</td><td colspan="5">High (good demographic data on range expansion; some direct genetic data).</td></tr>
<tr><td><i>Ex situ</i> representation</td><td colspan="5">Scottish roe deer genetic diversity is likely to be represented in English roe deer populations as a result of re-introductions (Whitehead, 1964). Roe deer from Scottish populations may be represented in deer parks.</td></tr>
<tr><td rowspan="3">Current conservations actions</td><td colspan="5">None</td></tr>
<tr><td>Ex situ</td><td>Translocation</td><td>Habitat management</td><td>Legal protection of habitat or species</td><td>Control of INNS/pests/ pathogens</td></tr>
<tr><td></td><td></td><td>X</td><td></td><td></td></tr>
<tr><td>Overall T13 status</td><td colspan="5">Negligible risk; Mitigation not required</td></tr>
<tr><td>Overall T13 status explanation</td><td colspan="5">Population size in Scotland is large and stable. No hybridisation risk. Some existing data on genetic diversity relative to UK and continental European populations. Further studies on the impact of past reintroductions in the genetic make-up of Scottish populations would be particularly useful.</td></tr>
<tr><td></td><td>Assessor</td><td colspan="5">Sílvia Pérez-Espona, University of Edinburgh</td></tr>
<tr><td></td><td>Reviewer</td><td colspan="5">Josephine Pemberton, University of Edinburgh
Linda Neaves, Royal Botanic Garden Edinburgh</td></tr>
</table>

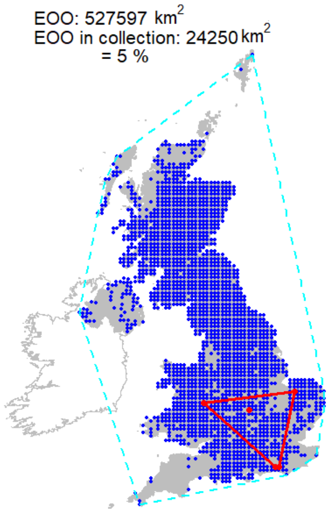
Technical note on interpretation of maps of ex situ representation in seed banks

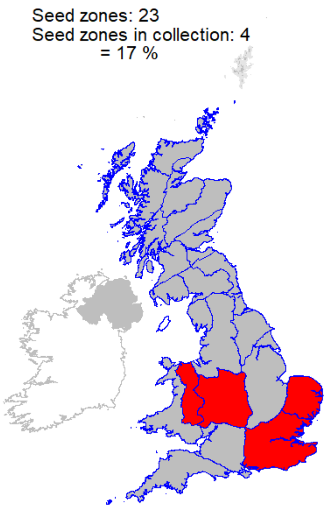
For seed plants (angiosperms and conifers), where major structured seed banking programmes are underway, we present maps at the 10 km scale summarising the degree to which the seed collections represent the species distribution. The baseline data for these maps are from the Botanical Society of the British Isles.

The maps are structured as follows:

- The left side map shows the distribution of the species in 10 km squares in the UK, with blue squares indicating presence and red squares showing where the species occurs *and* which are represented in the Millennium Seed Bank (MSB).
- The middle map shows the Extent-of Occurrence (EOO) of the species in the UK (pale blue convex polygon around all 10 km square records), and the EOO of the sampled squares represented in *ex situ* collections in the MSB (in red). For situations where three or more 10 km squares are represented in the MSB, the proportion of the range that is represented by the *ex situ* collection is summarised. When only two squares are represented, area calculations are not relevant and we report the linear distance between these 10 km squares as a proportion of the maximum linear distance between occupied 10 km squares. Where only a single square is represented in the MSB, this metric is undefined.
- The right side map shows the number of seed zones in Great Britain where the species occurs, with the red shading indicating the number of seed zones that are represented in the MSB.







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