

GENETIC SCORECARD METHODOLOGY FOR WILD SPECIES IN SCOTLAND AND THE UK V2.0

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GENETIC SCORECARD METHODOLOGY FOR WILD SPECIES IN SCOTLAND AND THE UK V2.0

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EXECUTIVE SUMMARY

- The Genetic Scorecard method is designed for assessing risks to the genetic health of wild species including plants, animals and fungi in terrestrial, freshwater and marine ecosystems.
- The approach was developed for Scotland/UK, but is designed to be widely applicable.
- The Genetic Scorecard approach is not dependent on prior genetic knowledge. Direct genetic information is used where available but, where not, the approach uses structured expert opinion and demographic data.
- The core of the approach is assessments of genetic risk, viewed through three primary perspectives, namely whether:
 - Demographic declines are likely to have led to, or lead to, loss of genetic diversity (genetic erosion),
 - Hybridisation is likely to have led to, or lead to, undesirable replacement of genetic diversity (genetic swamping),
 - Restrictions to regeneration/turnover are likely to impede evolutionary change (genetic stasis).
- There follows an assessment of whether conservation actions for the species are sufficient to mitigate risks to genetic health.
- The approach was originally developed for the 2020 reporting on Aichi Biodiversity Target 13, which focused on conserving genetic diversity.
- The approach has since been refined, and updated here to align with indicators associated with the Kunming-Montreal Global Biodiversity Framework (GBF) Target 4: *Maintain and restore genetic diversity*, specifically, to accommodate:
 - Ne>500: An assessment of the proportion of populations measured with each species that have an effective population size of more than 500 individuals, as a proxy for the likelihood of genetic diversity being maintained *within* populations,
 - PM (Proportion of Populations Maintained): An assessment of the extent of population losses, as a proxy for the likelihood of genetic diversity being maintained *among* populations.
- This document describes the revised and updated methodology for implementing the Genetic Scorecard in Scotland for the 2025/2026 round of reporting to the GBF.

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Hollingsworth PM; O’Brien D; Ennos RA; Yahr R; Neaves L; Ahrends A; Ballingall KT; Brooker RW; Burke T; Cavers S; Dawson IK; Elston DA; Kerr J; Marshall DF; Pakeman RJ; Trivedi C; Wall E; Wright F; Ogden R (2020) Scotland’s Biodiversity Progress to 2020 Aichi Targets: Conserving Genetic Diversity – Development of a national approach for addressing Aichi Biodiversity Target 13 that includes wild species. Scottish Natural Heritage.

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Background

Defining Genetic Diversity

- Genetic diversity is a generic term for differences among individuals due to differences in their DNA sequence. It is useful to recognise that this generic definition encompasses two somewhat different components.
- *Genetic variability*: Genetic variability relates to the presence of different genetic types, with the focus being on the number and characteristics of different genetic types.
- *Genetic distinctiveness*: Genetic distinctiveness relates to the degree to which a given entity is different and distinct from other entities. This can include ‘evolutionary divergence’ (e.g., lineages that have been isolated for long periods of time and hence have become genetically distinct).

Why is Genetic Diversity Useful?

- Loss of genetic diversity can reduce fitness and elevate extinction risks of varieties, populations and species.
- Genetic diversity loss also reduces the genetic resources available to enhance species traits for human utilisation.
- Genetic diversity is involved in the adaptation of populations to the environmental conditions they occur in; different populations are often genetically adapted to those local conditions (e.g., wetter vs drier places, presence of endemic pathogens).
- Genetic diversity loss can impede future adaptive responses to environmental change (e.g., to climate change or new pest and pathogens).
- Loss of genetic diversity in key individual species can have impacts on diversity in other species and ecosystem processes (e.g., genetically determined differences in the chemistry of individual trees represents a form of habitat diversity for species associated with those trees).
- Genetically distinct lineages reflect an aspect of biodiversity that warrants conservation in its own right.

How Genetic Problems Can Arise

- Genetic diversity can be lost where there is a decline in the size of a given population: all things being equal, larger populations hold more genetic diversity than smaller populations (Frankham, 1996). This principle generally holds for populations in the wild (*in situ*) and populations held *ex situ* (e.g., in a botanic garden, seed bank, etc.).
- Genetic diversity can be lost when parts of a species’ range are lost (range contractions/loss of entire populations). As genetic diversity is typically geographically structured, the loss of a species from a given area can be associated with a loss of genetic diversity associated with that area (Frankham *et al.*, 2017).
- If hybridisation occurs between previously isolated lineages (or different species) there is the potential for a different type of genetic problem (Todesco *et al.*, 2016). This can occur due to a straightforward loss of purity or distinctiveness (the displacement of genetic diversity of one entity by another). It can also lead to a fitness reduction in offspring and an associated population decline if there are genetic incompatibilities between the taxa that hybridise. It is important to note, however, that hybridisation can sometimes be part of natural processes that confer adaptive traits and hence provide fitness benefits.

- Another important element for conservation of genetic diversity is the maintenance of adaptive potential and evolutionary processes. This is particularly relevant to long-lived organisms which may experience recruitment/regeneration limitations, which reduce opportunity for genetic change and adaptive evolution to new environmental conditions.

Traits of individual species can affect their sensitivity to genetic change. The ways in which traits interact with sensitivity to diversity loss are complex and generalisations are difficult. However, species which naturally inbreed (e.g., self-pollinating plant species) typically show low levels of genetic variability within individual populations (Aguilar *et al.*, 2006). This means that loss of individuals from populations of inbreeding species may have limited impacts on genetic diversity as most individuals may be genetically similar. This contrasts with the situation in outcrossing species, where reductions in the size of a given population can have marked impacts on maintenance of genetic diversity.

Approaches for Conserving Genetic Diversity

Genetic diversity can be conserved ‘in the wild’ (*in situ*), outside of species’ natural habitat, often in collections (*ex situ*), or in highly managed systems (*circa-situ* conservation).

In Situ

Conserving genetic diversity *in situ* has the intrinsic benefit of allowing natural evolution and genetic change as populations are exposed to new environmental conditions and pressures. A key aspect of *in-situ* management for genetic diversity is enabling these processes to take place, and of particular importance is turnover. This is relevant for long-lived organisms (e.g., forest trees) which can persist as individuals without regeneration if management conditions are sub-optimal, thus reducing opportunities for evolutionary change. An additional basic advantage of *in-situ* conservation is that in many cases there can be greater available land area and the ability to support more individuals (and hence more genetic diversity) than for other conservation approaches.

Ex Situ

Ex-situ collections (e.g. seed banks, farms, zoos, botanic gardens, plantations, arboretums, cryopreservation) provide an accessible genetic resource and a ‘safe house’ when continued survival *in situ* is uncertain. The approach is particularly well suited for propagules such as seeds which can be stored for long periods of time in a space-efficient fashion. The key challenges are assembly costs, storage costs (and space requirements where living individuals are the only practical *ex-situ* option). A general challenge for *ex-situ* collections is that removal from *in-situ* conditions typically precludes adaptation and evolution to changes in the *in-situ* environment. Furthermore, for *ex-situ* living collections (e.g., zoos, botanic gardens), generational turnover can lead to adaptation to *ex-situ* conditions which may be undesirable if reintroduction to the wild is an ultimate goal. There is also the potential for elevated levels of hybridisation and (sometimes cryptic) loss of genetic integrity in *ex-situ* collections if multiple species are kept in close proximity.

Circa Situ

Some species of agricultural importance are maintained *circa situ*, in highly managed systems within their native range. Examples include the management of stands of native forest trees as seed orchards, and more general management of species in an agricultural/agroforestry/urban landscape. These systems combine the benefits of the management control of *ex-situ* collections with some level of exposure to changes in ambient environmental conditions facilitating evolutionary change. Conversely, one limitation is that depending on the management practices applied, the species in question may be subject to atypical selection pressures leading to unwanted/unexpected evolutionary change.

How Genetic Diversity is Measured/Inferred

Table 1 summarises the different ways genetic diversity can be measured or inferred. There is no single measure of genetic diversity or methodology that is appropriate for all situations. As genetic diversity ultimately relates to differences in DNA sequence, an obvious starting assumption is that some measure of DNA sequence variation is the baseline unit of measurement. This, however, is not straightforward, and although DNA sequencing costs continue to fall, obtaining, managing and interpreting DNA sequence data for multiple species on a large scale is still expensive. Major biodiversity genomic sequencing projects such as the Darwin Tree of Life Project are addressing this (Darwin Tree of Life Project Consortium, 2022), but extensive work is still required before range-wide genome-wide sequence variation is available for *most* species.

Table 1. Approaches for measuring or inferring amounts and distribution of genetic diversity

Unit of measurement/surrogate	Description	Applicability
Total genetically determined phenotype	All aspects of an individual that are genetically determined (e.g., appearance, traits, adaptive characteristics).	Extremely useful, but practically intractable in most cases. Comprehensive direct measurement of genetically determined traits requires detailed experiments as much variation among individuals is environmentally induced.
Selected genetically determined trait/phenotype	Data on a selected subset of genetically determined traits or levels of fitness.	Direct measures of adaptation/fitness/traits of interest can directly inform strategies to conserve this type of diversity. This does not capture the full range of potentially important adaptive variation, and evaluation can be confounded by environmental effects unless in controlled conditions.
Completely sequenced genome	Comprehensive sequence and assembly of an individual’s genome providing a full representation of its genetic make-up.	Extremely useful and a direct focus of the Darwin Tree of Life project. Provides a way to directly compare levels of genetic variation and distinctiveness. However, producing a reference genome and subsequent whole genome sequencing of individuals from many different populations of many species remains expensive to deliver at scale.

Unit of measurement/ surrogate	Description	Applicability
Genetic marker data	DNA data from a subset of the genome gathered to assess levels of variability and distinctiveness.	Very useful measure of general amounts and distribution of genetic variation (and whether variation is higher or lower in some individuals/populations). Often uninformative about particular traits or degree of adaptation, although marker data can be targeted to candidate genes for adaptation.
Ecological, demographic and environmental information	Data on population sizes, isolation, distribution and environmental variation, indirect measure of underlying genetic and adaptive variation.	Basic distributional data represents a surrogate measure for the distribution of genetic diversity as (a) Population size and isolation shows some correlation with genetic diversity (small/isolated populations ≈ lower diversity); and (b) Geographic distribution shows some correlation with distribution of genetic diversity (more geographically distant ≈ more different). Populations inhabiting different environments may show adaptive differences (bigger environmental differences ≈ bigger adaptive differences). Involves making assumptions/extrapolation from other studies, rather than directly measuring genetic information from the species concerned. Distributional data are widely available, data on population sizes are less widely available.
Collection information	Data on number and richness of <i>ex-situ</i> collection events/accessions.	Classic metric for stored material (cryopreservation, seedbanks, zoos, botanic gardens). Can provide a surrogate measure of level of coverage against an ‘ideal’ as to the degree to which variation in the wild is conserved <i>ex situ</i> . It is usually based on the assumptions outlined for “Ecological, demographic and environmental information” rather than directly measuring any genetic information from the species concerned.

Summary

Conserving genetic diversity requires consideration of different aspects of genetic diversity (amounts/types of diversity and levels of distinctiveness); the factors which might cause genetic problems (diversity loss, unwanted genetic replacement, constraints on evolution); the relative importance of *in-situ*, *circa-situ*, and *ex-situ* conservation, and the practicalities of how genetic diversity can be measured and monitored.

THE GENETIC SCORECARD FOR WILD SPECIES V2.0

The Genetic Scorecard for Wild Species (hereafter, ‘the Scorecard’) is designed for assessing risks to the conservation of genetic diversity. It is based on a central working principle of a need to be flexible to allow use not only in Scotland/UK but also in other countries. Factors that vary among countries include:

- *The presence of endemic divergent genetic lineages:* Countries and regions which have not experienced major perturbations such as extinctions due to glacial cycles are more likely to have accumulated endemic divergent phylogenetic lineages, than countries with ‘young’ biotas which have been largely assembled over the last 10,000 years following ice-sheet retreat. A focus on divergent lineages is likely to be more appropriate in regions with long term historical climatic stability, compared to recent glaciated boreal countries like Scotland/UK.
- *Resource availability:* The capacity of a given country to report on genetic diversity in wild species will depend on the resources available, the level of knowledge of a given biota, and the diversity and scale of the country in question. Key requirements of an effective system for reporting on wild species genetic diversity are scalability and applicability in situations where resource availability is limited.
- *Geographical scales of data holdings:* Where spatial data are used for reporting, a practical issue relates to the scale at which data are held. Additional steps may be required to up-scale or down-scale reporting where different datasets are held and curated at different levels (e.g., state vs. national level). For example, this is a particular issue for the UK where considering priority species for Scotland requires either steps to extract Scotland-specific data from UK-wide compilations, or consideration of issues at a UK scale for Scottish priority species. In some cases, populations may extend over several countries and as a result, must be considered at this larger scale. This is often true of highly mobile species such as birds or marine mammals.

The Scorecard process involves the following stages (further details in Table 2) and populated examples can be found in Appendix 1:

- Summary of information on the target species, to articulate key issues and relevant species traits that may impact on susceptibility to genetic problems.
- A statement of the likely international importance of the national genetic diversity for the species, to contextualise the assessment.
- Evaluation of key genetic risks facing *in-situ* populations:
 - This section includes the formal quantitative Global Biodiversity Framework indicators which focus on the proportion of populations with an effective population size of >500 individuals (‘Ne500’), and the proportion of populations maintained (‘PM’).
 - Diversity loss – focusing on population declines (e.g., general diversity loss), the loss of functional diversity (e.g., important traits or adaptive differences), or loss of populations that are likely to hold unique evolutionary lineages.
 - Hybridisation – focusing on risks of elevated mixing of genetic diversity leading to negative consequences (e.g., genetic pollution, genetic swamping, outbreeding depression).
 - Low turnover – an approximation of the degree to which turnover is restricted. This is particularly important for long-lived species, such as forest trees, where lack of regeneration can impede evolutionary change.
- Production of an overall *in-situ* threat assessment based on expert opinion leading to a ‘negligible/moderate/serious’ genetic risk categorisation according to species attributes and the threats faced by the species.
- A statement of confidence on the overall *in-situ* threat assessment. This step aims to transparently capture the level of certainty among experts as to the risk categorisation.

- The level of representation in *ex-situ* collections. This step lends itself well to plant species that are suited for holding as *ex-situ* collections in seed banks, but may also be applied to other taxa in managed *ex-situ* conservation collections. An example of this approach for UK plant species would include:
 - The number of 10-km squares represented in seedbank collections, as a proportion of the 10-km squares in which the species is known to occur.
 - The extent of occurrence (EOO) of seed bank collections as a proportion of the EOO of *in-situ* populations (where EOO = the minimum convex polygon around all points).
 - The proportion of zones of provenance in which the species occurs in the UK that are represented in seedbank collections.
- A summary of existing management actions relevant to the species in the area of assessment.
- A final combined overall ‘traffic light score’ on the genetic health of the species. This is an expert opinion based on the species, its risks and current management responses.

Table 2. Structure of the Genetic Scorecard V2.0 approach

Header	Information required
Context - Background	Overview of what is known about the species, its distribution, key relevant biological traits (e.g., breeding system, mode of reproduction, any previous genetic studies).
Context - Current threats	Summary of threats facing the species (e.g., grazing, overharvesting, predation, persecution, climate change, etc.).
Context - Contribution of Scottish/UK population to total species diversity	Assessment of the relative contribution of the taxon in the area of assessment to total species diversity (e.g., whether Scotland/UK has internationally important range representation, endemic subspecies, population differentiation).
GBF Population definitions	How populations are defined when using the GBF indicators (Ne>500, and Proportion of Populations Maintained)
Ne500	The headline GBF indicator for genetic diversity – the proportion of populations with an effective population size of more than 500 individuals
PM	A complementary GBF indicator for genetic diversity – the Proportion of Populations Maintained (e.g., populations extant / extant+historical populations)
Genetic risks - Diversity loss: population declines	Narrative assessment of likelihood of diversity loss (e.g., small or reduced population sizes, range contraction or fragmentation). Incorporation of direct genetic evidence if available.
Genetic risks - Diversity loss: functional variation	Narrative assessment of likelihood of important functional diversity (e.g., particular threats to specific ecotypes or phenotypic trait classes). Incorporation of direct genetic evidence if available.

Genetic risks - Diversity loss: divergent lineages	Narrative assessment of likelihood of loss to divergent populations (e.g., known or suspected distinct lineages). This can be based on morphological, geographical or historical data, or if available direct genetic evidence of divergent lineages. In animals, but less commonly in plants, such lineages are often referred to as evolutionary significant units.
Genetic risks - Hybridisation/introgression	Narrative assessment of likelihood of loss of genetic integrity via inter-specific hybridisation or inappropriate mixing. This can be based on direct genetic data, morphological assessments of hybridity, or proximity and abundance of known threats.
Genetic risks - Low turnover/constraints on adaptive opportunities	Narrative assessment of reproduction and recruitment as an indicator of potential for evolvability. If there are limitations to recruitment, the narrative should indicate the proportion of populations that are affected.
Cumulative risk summary – <i>In-situ</i> genetic threat level	Expert opinion classifying <i>in-situ</i> genetic risk as serious, moderate, or negligible.
Confidence in <i>in-situ</i> threat level	Confidence based on evidence quality and agreement.
<i>Ex-situ</i> representation	Narrative and/or quantitative summary of representation in viable and accessible <i>ex-situ</i> conservation resource (e.g., number of zones of provenance represented in <i>ex-situ</i> collection, range representation of zones of provenance in <i>ex-situ</i> collection).
Current conservation actions	Narrative and ‘check-box’ summary of current approaches/ <i>in-situ</i> interventions to mitigate threat.
Overall genetic health status	Summary of genetic health status in the area of assessment, encompassing risk and efficacy of current mitigating actions.
Overall genetic health status explanation	Succinct explanation/justification of overall genetic health status.
Further research	Recommendations for future work to improve understanding of the species from the perspective of the Scorecard aims.
Assessor	Name of person or group who undertook the assessment.
Reviewer	Name of person or group who reviewed the assessment.

Methodological Details: Original Scorecard

Quantifying Genetic Risk

Compared to metrics focusing on demographic changes (e.g., IUCN Red Listing), there is no universally accepted standard for measuring genetic diversity, and by extension no universal standard for classifying loss of genetic diversity into different threat categories. Different genetic diversity metrics measure different properties (e.g., diversity of allelic variants within a population, diversity of allelic variants within individuals, overall differences between populations, the nature of the genetic differences between populations). Furthermore, different ways of measuring genetic diversity result in different sensitivities to genetic diversity loss (e.g., a population could

simultaneously lose half of its genetic variation for some regions of its genome and lose no variation for others).

A second difference between genetic change and demographic change relates to the reversibility of losses. Individuals and populations experience demographic decline due to mortality that can be replenished by local births or migration. Genetic variation can be replenished by migration, but not where unique genetic variants are lost – mutation rates operate on a temporal scale that is often measured in thousands of years. Thus, all things being equal, in perfect conditions for a species, a loss of 50% of its genetic diversity would have a much longer recovery time than loss of 50% of its individuals.

Collectively, these differences complicate direct adoption/translation of threat categories from standard IUCN Red-Listing to genetic variation. Instead, we have developed generalised statements to steer expert opinion to a relatively consistent classification of genetic problems. A deliberate aim is not to constrain definitions too tightly, in recognition that different data types and scenarios may frequently be experienced. Likewise, we avoid excessive numbers of categories to minimise ambiguity in assigning genetic risk/health status.

Our scorecard assesses contemporary genetic issues, and likely future issues, during a 25-year window from the point of assessment. Genetic risks are classed as:

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 which are likely to contain unique diversity or steep declines in these populations (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 and/or constraints in ability to adapt to environmental change.
- Marked and clearly observable loss of genetic integrity by hybridisation for 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 which are likely to contain unique diversity or steep declines in these populations (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 and/or constraints in ability to adapt to environmental change.
- Marked and clearly observable loss of genetic integrity by hybridisation at >25% of populations.

Currently low levels of genetic variation are often due to previous loss of genetic diversity. Where such losses are referred to in the narrative sections of the scorecard, we adopt the term ‘historical change/loss’ to refer to genetic diversity change/loss post-1750, and ‘past change/loss’ to refer to genetic diversity change/loss in the last 50 years (i.e., post-1975).

Quantifying Uncertainty

For quantification of certainty we use the approach adopted for the UK Biodiversity Climate Change Impacts Report Card (<https://www.ukri.org/wp-content/uploads/2021/12/101221-NERC-LWEC-BiodiversityClimateChangeImpacts-ReportCard2015-English.pdf>) (Figure 1). This combines the level of agreement among experts and the type of available evidence. The overall confidence level is governed by the lowest score for *either* expert agreement or evidence availability.

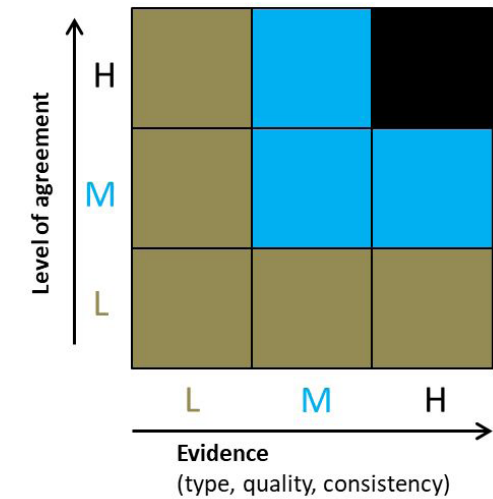


Figure 1. Summary of confidence levels used for genetic risk assessment (L = low, M= medium, H = high).

Methodological Details: GBF Indicators

The Ne>500 and PM Indicators

The Global Biodiversity Framework (GBF) Ne>500 and PM indicators are proxy measures for genetic diversity.

The headline indicator for genetic diversity within the GBF is the proportion of populations with an effective population size of more than 500 individuals.

The GEO BON indicator description states states: “The Ne>500 indicator measures *the proportion of populations within species which are of sufficient size to maintain genetic diversity and adaptive potential*. When a population is below a threshold of approximately Ne500, genetic diversity loss starts to occur, and at population sizes much smaller than this threshold, genetic diversity loss can be very rapid. The ideal state is a value of 1, indicating all populations are of sufficient size (that each population is above Ne500). The Ne>500 indicator can be calculated across many species to provide a country level estimate of whether species are maintaining genetic diversity within populations (www.geobon.org/genetic-diversity-indicator-proportion-of-populations-with-ne-500/)

A complementary indicator to Ne>500, is the Proportion of Populations Maintained (PM). This is simply estimated as the number of extant populations as a proportion of the total number of known populations, measured at a stated past timepoint. Adding the Ne>500 and Proportion of Populations Maintained to the scorecard was proposed in O’Brien *et al.*, (2022).

Defining Populations

A starting point for the Ne>500 indicator and the Proportion of Populations Maintained is to define what constitutes a population in the target species. This can be challenging. Our approach and considerations are outlined below.

Working Principles for Defining Populations

- Use best available evidence *collectively* (e.g., do not use a hierarchical decision tree, as much of the interpretation will be context dependent).
- Harmonise with existing monitoring classifications of populations (coming up with a population definition that does not match monitoring data will make implementation challenging).
- State clearly the method used.
- Where there is ambiguity, err on the side of ‘splitting’, recognising that subsequent aggregation is easier than disaggregation.

- Ranges of estimates can be provided using different groupings of ‘populations’. Sensitivity analyses can establish if different equally logical approaches to population definitions result in materially different outcomes.

Using Genetic Data to Define Populations

- Genetic marker data that show clear-cut discontinuities can provide clear evidence for a lack of gene flow between populations and thus help define population units. There are, however, some areas where caution is required:
 - Very large numbers of genetic markers can allow the discrimination of very genetically similar groups (e.g., there may be statistical significance, yet limited meaningful biological differences).
 - Clear genetic differences can be found between populations in organelle loci despite extensive gene flow in species with asymmetric sex dispersal. For instance, wind-pollinated tree species can show strong population structure for plastid DNA (which is predominantly transmitted by seed), despite high-levels of pollen mediated gene flow and low levels of differentiation for the nuclear genes. Thus, organelle markers can lead to overestimation of population differentiation in these circumstances.
 - Genetic marker data that show similarity among populations can be challenging to interpret in recently fragmented systems, as it can be difficult to distinguish similarity attributable to historical (pre-fragmentation) gene flow versus contemporary gene flow.

Defining Populations within Continuously Distributed Ranges

- Widespread continuously distributed populations may have high levels of gene flow, but still have uneven distribution of adaptive genetic variation across their range and thus be susceptible to genetic diversity loss if parts of this continuously distributed range are lost.
- Continuously distributed species can thus be treated as single populations or divided into:
 - Management units representing defined geographical areas within a given species range.
 - Pros – understood by stakeholders and likely to have data at this level of unit;
 - Cons – may overestimate number of populations, possibly with broad environmental heterogeneity within these units – e.g., lowland and montane environments within a single management unit.
 - Ecogeographic zones representing areas of environmental similarity within a given species range
 - Pros – logical proxy for adaptive variation;
 - Cons - monitoring data may not be structured and recorded in a way that corresponds to the boundaries between ecogeographic zones making recording/monitoring of population size and population persistence challenging.

Accommodating Non-Geographical Isolation when Defining Populations

- Isolation can occur at a single site where there are clearly different niches. This can include shallow versus deep water populations, or differentially adapted populations occurring on different substrates which are distributed in a mosaic fashion.
- Where there is good evidence for ecotypic differentiation, a given site may be split into multiple populations, with the most granular unit being the habitat-type within a site (e.g., Site XX deep water population; Site XX shallow water population).
- Isolation can occur at a single site where there are temporally isolated populations. This may occur due to non-synchronous migratory patterns (e.g., alternative year breeding populations), or it could occur due to phenological differences (e.g., spring versus autumn breeding populations).

- Where there is good evidence for temporal differentiation, a given site may be split into multiple populations, with the most granular unit being the temporally connected breeding group within a site (e.g., Site YY even year breeding population; Site YY odd year breeding population).

Population Typologies

Using the preceding considerations, we have adopted the following *default* positions for defining populations, recognising that on a case-by-case basis other definitions and data sources may be appropriate.

1. Species exists in small, isolated populations in the landscape and dispersal distances are likely to be limited:
 - Use geography to define the populations
2. Species is continually distributed and efficiently dispersed over wider geographic distances, treat as:
 - A single population, or
 - Management units (e.g., defined by geographical units - zones of provenance*)
3. Species is patchily but widely distributed and sites are possibly connected by high levels of gene flow and/or show metapopulation dynamics:
 - Treat connected (or most likely connected) clusters of occurrences as a single population
 - If major ambiguity exists, treat as a large single population, broken into Management Units
4. Species is highly mobile over wide geographical distances:
 - Count as a single population, and
 - If there are well established Management Units within this – undertake a sensitivity analysis by also considering the population as equivalent to the Management Unit
5. Species has a composite mix of clearly distinct populations and more continuously distributed populations:
 - Treat spatially discrete populations as per point 1
 - Treat continuous populations as per point 2
6. Species occurs as distinct spatial patches within a small geographical area (e.g., different plant patches on a single mountain):
 - Treat as a single population unless there is very good evidence to do otherwise
7. Migratory species have clearly different breeding grounds:
 - Treat the clearly distinct breeding grounds as separate populations
 - If movement or dispersal between breeding grounds is likely (particularly in juvenile life stages) treat as a single population (as per point 3)
8. Species shows clear local ecotypic variants associated with adaptation to different micro-habitats:
 - Treat the different ecotypes within a site as distinct populations
9. Species shows clear temporal breeding differences within a given geographic location:
 - Treat the different temporal breeding groups as distinct populations (e.g., even year versus odd year populations)

*For example, for widely distributed terrestrial species with continuous distributions in the UK, **our default approach for the 2025/26 reporting is subdivision of continuous ranges into the four zones of provenance for UK seeds zones, treating Northern Ireland as a 5th zone** (Herbert *et al.*, 1999). These zones of provenance are a pragmatic method of dividing widely distributed species into smaller geographically defined units.

Defining Individuals

Another practical challenge in implementing the Ne>500 indicator is how to define an individual. For obligately sexually reproducing organisms this is often straightforward, and there is no ambiguity where one individual starts and another finishes. For asexual or facultatively asexual individuals, it can be far from straightforward, and in organisms like clonal plant species, the number of genetically distinct individuals can be many orders of magnitude lower than the number of distinct stems/individual plants in a population. In cases like this, without genetic data to estimate the extent of individual clones, there will be considerable uncertainty in the estimates of population sizes.

Options are to (a) extrapolate from direct genetic studies of clone distributions where available, (b) use a coverage area where known, and use area as a proxy for number of individuals, (c) report that it is not meaningfully calculable.

Specific Challenges in Estimating Ne>500

Estimates of Ne can be obtained from direct genetic data but in many cases will be estimated from counts of individuals within populations. Where the concept of an individual cannot be meaningfully defined and major uncertainty remains, the estimation of Ne will not be meaningful, and should not be calculated, and be marked as such in the scorecard.

Where a census count/census estimate is possible, a ‘census size to effective-population-size ratio’ of 0.1 can be used (e.g., a population with more than 5000 individuals is considered to have an effective population size of Ne>500) (Mastretta-Yanes *et al.*, 2024). We have applied this 0.1 ratio as a default where there is no information to the contrary. This is a conservative approach to minimise over-estimating the number of populations with Ne>500.

While this is a widely applied rule of thumb and derived from the paper of Frankham *et al.* (1995) and subsequent studies, the ratio does vary across taxa, where for instance there is variation in reproductive success, breeding system and/or sex ratio (Waples, 2024). Furthermore, in some taxa, demographic survey data is recorded as the number of reproductive individuals, or breeding pairs (rather than all individuals) and in such cases a ratio closer to 1:1 would apply (Waples, 2024).

Thus while the 0.1 ratio is used as the default for converting census counts (N) to effective population size (Ne), where there is good evidence to support a more specific estimation of Ne, this should be used and reported in individual scorecards.

Another issue that needs handling in the scorecard is how to report Ne in recently extirpated populations. Including such populations will lower the overall Ne metric (adding zero scores to the numerator). Excluding them from the denominator, on the other hand, may lead to an artificial ‘improvement’ in the Ne metric. This could occur in a situation where there are some larger populations (Ne>500) which persist, and some smaller populations (Ne<500) which are lost. Erring on the side of being conservative, our approach has been to include populations extirpated since 2000 in our Ne metric, giving extirpated populations an effective population size value of Ne=0.

Specific Challenges in Calculating PM

Biological recording data can provide rich evidence of range contractions and species no longer being found in sites where they have been recorded in the past. Accommodating these recent historical population losses in the derivation of PM metrics, however, can represent a challenge as information on the spatial extent and nature of past populations may be patchy. The further back in time a population was lost, the more likely information will be lacking. One possible approach is to treat these past populations as ‘presence in a given geographical region’ – and take a broad-brush approach to population continuity (e.g., assess whether there is there still a population present in a given geographical region, even if individual sites have been lost). Another is to express PM as a proportion of current records/past records at a fixed geographical scale (e.g., number of 10-km x 10-km squares currently occupied/number of 10-km x 10-km squares ever occupied).

A second challenge with PM is that past continuously distributed populations may become fragmented into multiple smaller populations leading to the counter-intuitive position of (numerically)

more populations being present now than in the past, despite there being ‘losses’. A simplistic approach is just to consider whether or not the species still occurs in at least one location, within the original non-fragmented range, and in this case, the population is considered maintained. However, this approach could mask large scale demographic losses. The situation could be accommodated by a moving baseline approach; e.g.:

- Time point 1 – a widely distributed species has a baseline of a single population
- Time point 2 – the range is fragmented into multiple populations, but presence in the original geographical area persists, means that the original population is still maintained.
- Time point 3 takes the ‘time point 2’ fragments as the start point and assesses the proportion of these that are still extant.
- Time point 4 takes the ‘time point 3 fragments’ as the start point, etc.

The downside of this approach is that there can be multiple sequential fragmentation events not being registered in a cumulative fashion.

A third challenge is dealing with reintroduced/translocated populations. Where these are genuine conservation translocations these represent a demographic net gain, and an increase in genetic resilience (e.g., lower likelihood of future genetic losses), even though genetic diversity has often simply been moved from elsewhere. In this case, there is an argument for treating these translocated populations as a genuine gain for PM. Conversely, there are also many cases of occasional individuals being translocated not for conservation purposes, and these may be recorded as a new population/occurrence. In cases where there is little conservation value to the ‘new population’ it should not be included as a ‘gain’ in PM calculations.

Recognising these challenges, our default approach for calculating PM for the 2025/6 assessment was to use the year 2000 as a start point. Our approach asks whether a population that was present in 2000 is still present now (regardless of whether it is fragmented into smaller units).

Where there have been well-documented conservation translocations they are treated as gains (e.g. added to the numerator). There are thus some circumstances where PM (a proportion typically bound between 0-1) will exceed 1, where gains exceed losses. In such cases, the contribution of translocated populations is reported in the accompanying narrative to give context.

Use of the KOBO ToolBox for Managing Ne and PM Data

The Kobo ToolBox has been used as a data gathering tool for Ne and PM to support organisation and review of data complying with the **Code of Practice for Statistics** (<https://code.statisticsauthority.gov.uk/>). The Kobo ToolBox has been configured to allow structured upload of data on Ne and PM, with detailed guidance on use provided **here**.

Methodological Details: Species Choice

It is important to consider and define the method used to choose species for inclusion in the Genetic Scorecard, based on criteria relevant to biodiversity monitoring within the geographic area of assessment. In selecting species for the 2025/26 round of Genetic Scorecard analysis in Scotland/UK, we wanted to maintain continuity with the original species list but also expand our approach to include additional taxa. To achieve this, we adopted the species selection approach developed by the Programme Advisory Group to the Scottish Biodiversity Strategy/Natural Environment Bill and informed by the IUCN. This identified the following categories:

- Species that are threatened with extinction.
- Species that are indicators of habitat restoration success.
- Species that are indicators of responses to pressures/drivers of change.
- Species for which Scotland/UK has a globally important representation.
- Species which are common but declining.

We identified one additional category to add to this, namely:

- Species providing ecosystem services (encompassing cultural, provisioning and regulating services).

The above approach overlaps heavily with that used in the original 2020 scorecard – which included:

- Species prioritised for conservation value.
- Species identified as being culturally important.
- Species providing important ecosystem services.
- Game species (wild species of direct commercial value through hunting).
- Species collected for food or medicine (forage species).

In finalising the choice of species within these categories, on pragmatic grounds, we have favoured species that are already included in monitoring programmes, and hence likely to have suitable data available.

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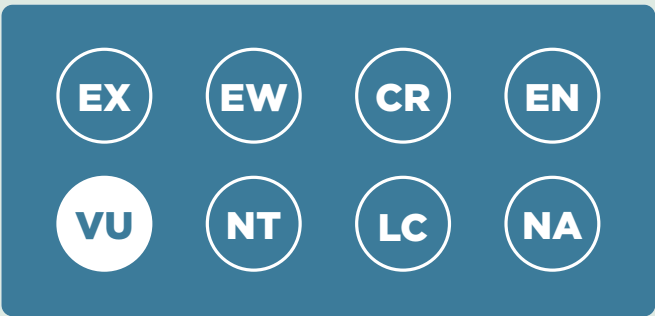
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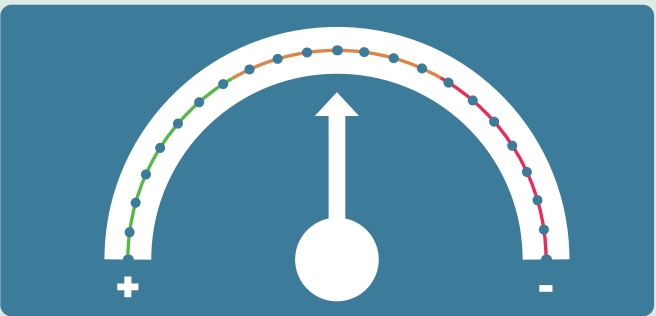
SCIENTIFIC NAME

Salix lanata



COMMON NAME

Woolly willow

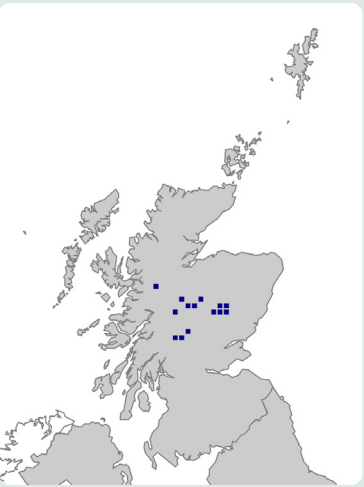


IUCN CATEGORY

Great Britain: Vulnerable (indicated above)
Europe: Least Concern
Global: Least Concern

GENETIC HEALTH STATUS

Scottish risk: Moderate (indicated above)
UK risk: Moderate
Scottish mitigation status: Mitigation Effective
UK mitigation status: Mitigation Effective



CONTEXT

Background

Salix lanata is a perennial dioecious long-lived shrub confined to wet and steep mountain crags with late snow-lie at 600–1000 m elevations. In Scotland, the species has traditionally been accepted from 13 native extant sites (Marriot *et al.*, 2016; Watts and Hutchinson, 2020). In 2007, only five of these sites had > 100 individuals, and three sites consisted of a single individual. There has since been extensive population augmentation and establishment of new populations with c 35K individuals being planted into the wild (Watts, 2025). S. lanata remains the rarest willow species in the highly threatened sub-arctic willow scrub habitat in Scotland. Elsewhere S. lanata is widespread with a circumboreal distribution. It is capable of local clonal spread, but a detailed study in one Scottish

population showed limited evidence for clonal growth with most individual bushes showing unique genotypes (Stamati *et al.*, 2007). The main relevant genetic data is the Stamati *et al.* (2007) assessment of clonal growth, a general SSR-based population genetic survey of Scottish populations (Scottish Montane Willow Research Group, 2005), and an AFLP based assessment of hybridisation (Forrest, 2006).

Current Threats

The primary threat is over-grazing, and the species is also increasingly threatened by reduced snow-lie which increases susceptibility to grazing.

Contribution of Scottish/UK Population to Total Species Diversity

S. lanata is common elsewhere in its range, and there is no evidence for divergent endemic genetic lineages in Scotland, although the populations may be adapted to the local environment. The Scottish populations are the sole natural locations within the British Isles.

Global Biodiversity Framework Indicators

Population Definitions for GBF Indicators

Populations are defined based on geographical discontinuities. Combining the population classification of Marriot *et al.* (2016), and Watts (2025), gives 16 sites (five of which have been supplemented, and four which are newly established by translocation).

Ne500: The proportion of populations that have an effective population size of more than 500.

- Proportion of populations with Ne > 500 (Scotland) = 3/16
- Proportion of populations with Ne > 500 (UK) = 3/16

Estimates based on count data of census size and applied the 0.1 rule of thumb for conversion to Ne

PM: Proportion of populations that existed in 2000 that still exist in 2025.

- Proportion of populations maintained (Scotland) = 16/13 Not Assessed
- Proportion of populations maintained (UK) = 16/13 Not Assessed

GENETIC RISKS

DIVERSITY LOSS

Population Declines

Populations are small, fragmented and isolated but genetic studies shows low differentiation between populations and little correlation between genetic diversity and population size, consistent with the longevity of individuals retarding genetic drift and ameliorating short-term risks of further loss of genetic diversity.

Functional Variation

No immediate risk to functional variation from population declines. Populations occupy relatively similar environmental conditions, minimising likelihood of loss of unique adaptive variants.

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 genetic swamping or risk of extinction-by-hybridisation (Forrest, 2006).

LOW TURNOVER/CONSTRAINTS ON ADAPTIVE OPPORTUNITIES

Regeneration is considered to be a limiting factor due to grazing limiting flower production, coupled with poor seedling establishment (Forrest, 2006). This may constrain adaptive change.

CUMULATIVE RISK SUMMARY

IN-SITU GENETIC THREAT LEVEL

- In-situ risk for Scotland: Moderate
- In-situ risk for UK: Moderate

Small, fragmented populations of a hybridising species presents genetic risks, mitigated by longevity of individual plants and extensive translocations.

CONFIDENCE IN IN-SITU THREAT LEVEL

- Confidence score for Scotland: High
- Confidence score for UK: High

Assessment based on good demographic data and direct genetic observation of some populations.

EX-SITU REPRESENTATION



Dark blue = species distribution, red = represented in ex situ collection.

Seed collections in the Millennium Seed Bank cover (a) one of 14 occupied 10-km squares (7%); (b) an EOO of <1 km² out of 4,550 km² occupied (0%); and (c) 1 out of 2 occupied Regions of Provenance (20%). Additional material is held in botanic garden and nursery collections in the UK.

CURRENT CONSERVATION ACTIONS

Restoration underway at native sites and new sites in Scotland. This includes *ex-situ* propagation and translocations to reinforce extant populations as well as the establishment of new sites. Deer management and the wider grazing controls plans as part of the 2024 Scottish Biodiversity Strategy should be beneficial to *S. lanata* and other scrub forming montane *Salix* species.

<i>Ex situ</i>	Translocation	Habitat management	Legal protection of habitat or species	Regulation of exploitation	Control of INNS/ pests/ pathogens
X	X	X	X	-	-

OVERALL GENETIC HEALTH STATUS

- Scotland
- Risk: Moderate
 - Mitigation: Effective
- Great Britain/UK
- Risk: Moderate
 - Mitigation: Effective

Overall Genetic Health Status Explanation

Despite fragmented distribution and small population sizes, conservation efforts such as *ex-situ* collections, *in-situ* reinforcement and new site establishment through translocations have led to an increase in the number of individuals and a positive trajectory. The overall risk level is expected to drop if translocated populations establish.

FURTHER RESEARCH

The genetic approaches used are now somewhat dated and a resurvey of populations with contemporary methods would be useful. The Darwin Tree of Life project is producing a reference genome for *S. lanata* which is facilitating ongoing genetic studies. Demographic surveys need repeating.

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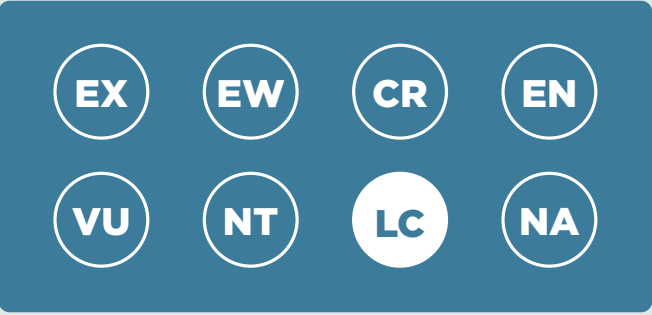
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Assessor:
Pete Hollingsworth, Royal Botanic Garden Edinburgh

Reviewer:
Rob Ogden, University of Edinburgh

SCIENTIFIC NAME

Pinus sylvestris

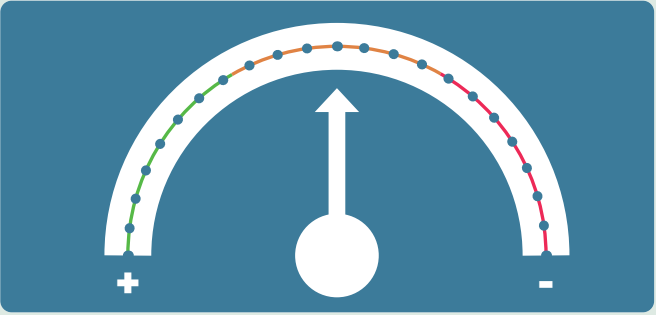


IUCN CATEGORY

Great Britain: Least Concern (indicated above)
Europe: Least Concern
Global: Least Concern

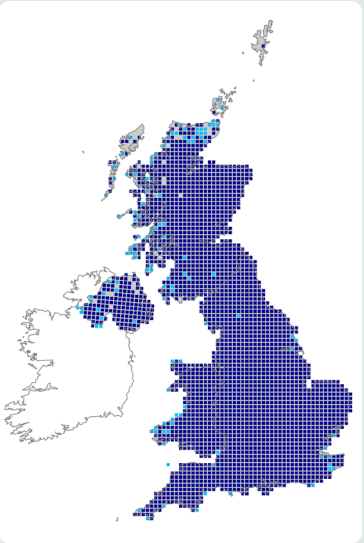
COMMON NAME

Scots pine



GENETIC HEALTH STATUS

Scottish risk: Moderate (indicated above)
UK risk: Moderate
Scottish mitigation status: Partially Effective
UK mitigation status: Partially Effective



CONTEXT

Background

Hermaphrodite, wind pollinated, widely distributed tree. Currently recognised as being present in 84 natural stands (Forestry Commission, 1994; Steven & Carlisle, 1959), which are often small and fragmented; work is underway to assess additional sites outside the current list (Rainey & Holmes, 2023; Manning *et al.*, 2010). Natural stands represent only ~10% of trees in Scotland and extensive plantations have been established across the UK, although usually from seed sources that originated in Scotland. At some sites in southern Scotland and England, questions persist regarding the native status of trees, and work is underway to assess their genetic composition (Manning *et al.*, 2010). Genetic marker studies show large amounts of neutral genetic diversity and very low genetic

structure (Wachowiak *et al.*, 2011, 2013), consistent with the species’ high seed and pollen dispersal capability, although a spatial cline in differentiation suggests weakly biased dispersal (Gonzalez-Diaz *et al.*, 2018). Common garden studies have shown genetic differences in multiple phenotypic traits among plants originating from different sites across Scotland, which suggests local adaptation (Salmela, 2011; Donnelly *et al.*, 2018; Perry *et al.*, 2016 a, b; Beaton *et al.*, 2022).

Current Threats

Plant pathogens represent a significant threat, with novel races of the needle blight pathogen *Dothistroma septosporum* apparently introduced with Corsican and lodgepole pine (an indigenous race of the pathogen appears also to be present, Piotrowska *et al.*, 2018) and there is concern regarding apparently growing occurrence of the rare fungus *Curreya pithyophila* (Forest Research, 2023). Caledonian pinewoods remain under-protected with frequently poor regeneration and extensive invasion by exotic tree species (Summers & Cavers, 2021). Evidence for declining growth in western populations suggests the impact of climate change is already being felt (Wilson, 2023).

Contribution of Scottish/UK Population to Total Species Diversity

Scots pine in the Caledonian pinewoods appears to have adapted to its distinct northwest Atlantic environment and represents a valuable and distinct component of global genetic diversity in the species (Ennos *et al.*, 1997; Perry *et al.*, 2016 a, b; Donnelly *et al.*, 2018; Beaton *et al.*, 2022). Some molecular evidence exists for a putative separate lineage in north-western Scotland (Ennos *et al.*, 1997), although nuclear markers indicate very low differentiation of Scottish populations, even from continental Europe (Wachowiak *et al.*, 2014, 2023).

Global Biodiversity Framework Indicators

Population Definitions for GBF Indicators

Populations are defined based on management units. This species is widely distributed across UK in large numbers. The set of naturally established populations known as the Caledonian pinewoods represent a distinctive occurrence of *in-situ* unique genetic diversity that should be evaluated in its own right with the highest conservation priority. The wider population, which is many times larger and includes commercial plantations, plantings of ‘native pinewood’, forest restoration and amenity plantings, is most likely overwhelmingly derived from genetic resources originating in or near the Caledonian pinewoods, some of which have undergone a cycle of improvement (Lee, 2002). This wider population therefore constitutes a substantial contribution to the maintenance of the UK’s genetic diversity in this species, including – via gene flow – the native pinewood fragments.

The four Great British Regions of Provenance (Herbert *et al.*, 1999) were selected here to represent the major population groupings/management units (treating Northern Ireland as an additional region) as they broadly reflect the environmental variation across which the species is distributed and are likely to capture major patterns of genetic structure.

Ne500: The proportion of populations that have an effective population size of more than 500.

- Proportion of populations with Ne > 500 (Scotland) = 2/2
- Proportion of populations with Ne > 500 (UK) = 5/5

An estimate of Ne is made below, using the rule of thumb 0.1 x census size. This should be considered highly uncertain: tree species generally maintain large population sizes with overlapping generations that stabilise the gene pool over time. However, a wide range of factors including variation in reproductive success among individuals, and demographic bottlenecks (e.g., in response to arrival of a novel disease) can affect population genetic diversity, and consequently estimates of Ne.

PM: Proportion of populations that existed in 2000 that still exist in 2025.

- Proportion of populations maintained (Scotland) = 2/2
- Proportion of populations maintained (UK) = 5/5

GENETIC RISKS

DIVERSITY LOSS

Population Declines

Multiple small populations with no regeneration coupled with an age-structure biased towards older trees compromises the sustainability of many populations. Invasion of pinewood populations by exotic species may compromise their regeneration further. 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) and highly effective gene dispersal mechanisms, although signs of slowing growth rates in western sites are concerning and may threaten locally adapted populations in future.

Functional Variation

The general persistence of the species across its range in Scotland is not threatened, which minimises the likely loss of adaptive variation, although efforts to ensure the demographic health of important indigenous populations are still insufficient. There are risks to loss of high elevation and western populations through climate change, and to other populations through disease, which may lead to some loss of adaptive variation although current disease threats are low impact.

Divergent Lineages

Limited divergence from European populations and a massive planted or naturalised *ex-situ* population largely derived from genetic resources originating in the native distribution precludes loss of major divergent lineages. The most genetically distinct populations are in the northwest of Scotland around Shieldaig and are not currently threatened.

HYBRIDISATION/INTROGRESSION

Buffer zones in which planting of non-local seed is prohibited around existing native stands limits risk to loss of integrity from exotic stands.

LOW TURNOVER/CONSTRAINTS ON ADAPTIVE OPPORTUNITIES

Deer and other herbivore grazing is a major limitation on turnover and regeneration, which can be mitigated by active management.

CUMULATIVE RISK SUMMARY

IN-SITU GENETIC THREAT LEVEL

- *In-situ* risk for Scotland: Moderate
- *In-situ* risk for UK: Moderate

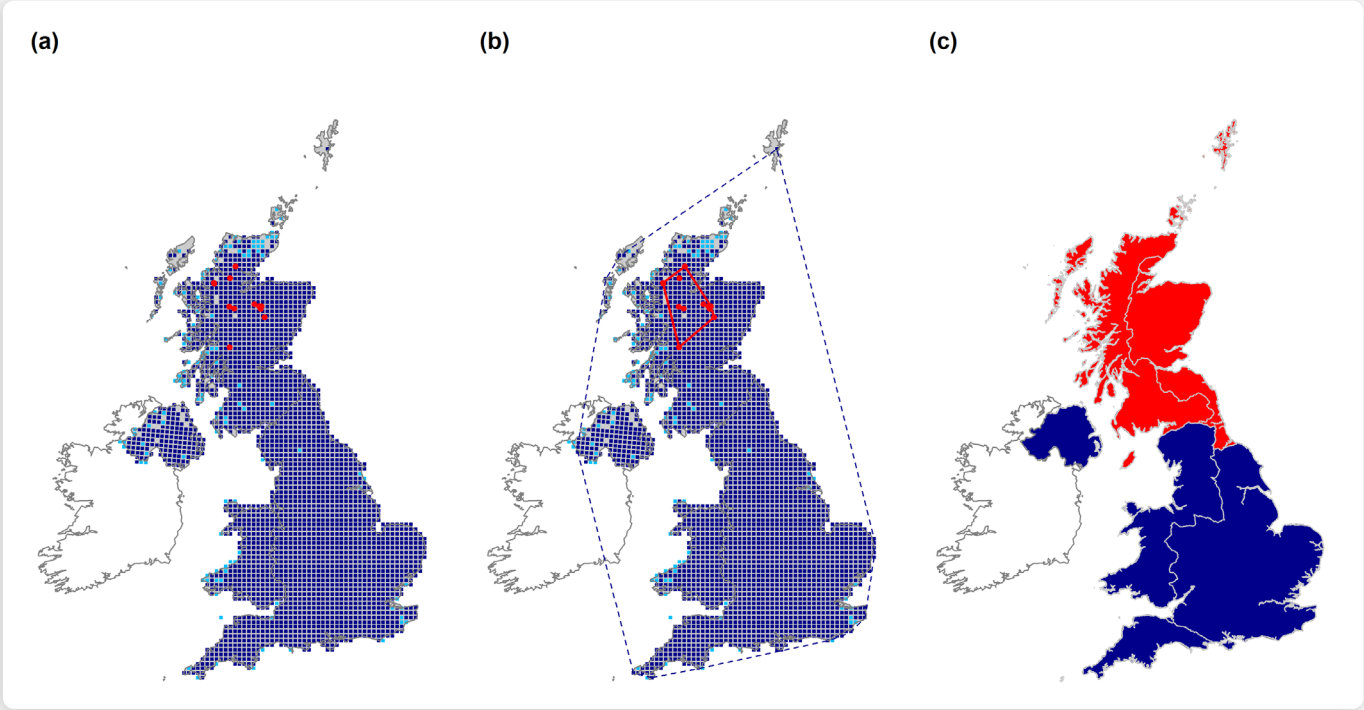
Scotland and the UK: in the face of emerging pathogen threats, major limitations to regeneration present a moderate risk of genetic variation loss and constraints to adaptation.

CONFIDENCE IN IN-SITU THREAT LEVEL

- Confidence score for Scotland: High
- Confidence score for UK: High

Assessment based on good demographic data and direct data on genetic variation, population differentiation and biology.

EX-SITU REPRESENTATION



Dark blue = species distribution, red = represented in *ex-situ* collection, light blue= pre 2000 records.

Seed collections in the Millennium Seed Bank cover: (a) 11 of 2540 occupied 10-km squares (0%); (b) an EOO of 10,408 km² out of 510,516 km² occupied (2%); (c) two out of five Regions of Provenance (40%). The seed collections are concentrated on, and cover, the recognised regions of native Caledonian pinewoods. Underlying distribution map from the BSBI Plant Atlas 2020 (Stroh et al. 2023).

CURRENT CONSERVATION ACTIONS

Key actions required are: 1) Improve the management of the recognised Caledonian pinewoods including: grazing control to promote natural regeneration within extant stands, removal of invasive non-native tree species, and expansion of extant stands through natural colonisation. 2) Secure consensus on the status of putative native pine sites in Scotland beyond those on the Caledonian pinewood inventory and in England. 3) Declaration of further Gene Conservation Units within the EUFORGEN system to add to the three existing ones (Beinn Eighe National Nature Reserve, Shieldaig and Glen Derry) - a minimum of 10 should be the target (Action 21.4, Scottish Biodiversity Strategy Delivery Plan). 4) Favour natural regeneration over planting of nursery-derived saplings wherever possible to minimise transfers of diseases. 5) Prevent planting of exotic pine species in proximity of Caledonian pinewoods to minimise pathogen transfer risk. See also the recommendations of Willoughby et al. (2026).

Ex situ	Translocation	Habitat management	Legal protection of habitat or species	Regulation of exploitation	Control of INNS/ pests/ pathogens
X	X	X	X	-	X

OVERALL GENETIC HEALTH STATUS

Scotland

- Risk: Moderate
- Mitigation: Partially Effective

Great Britain/UK

- Risk: Moderate
- Mitigation: Partially Effective

Overall Genetic Health Status Explanation

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 has likely captured a wide sample of genetic diversity.

FURTHER RESEARCH

Extensive data now exist on the genetic diversity in the Caledonian pinewoods, including genotypic data (Kastally et al., 2022) and quantitative genetic data on a suite of traits evaluated in common gardens (Beaton et al., 2022). Efforts to infuse genetic diversity from the pinewoods into the Scots pine breeding programme are underway and a new trial series to be planted across a much wider environmental range and including continental European provenances will be established in 2026. Priorities include evaluation of genetic diversity in UK populations relative to that in continental European populations (i.e., assessment of the new trial series), re-characterisation of the putative northwestern lineage identified in Ennos et al. (1997), and establishing monitoring to assess population changes in response to climatic shifts, disease and changes to grazing.

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