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Application of a biological trait-based framework for plant species conservation assessments in ecological restoration

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Author contributions:

JV, KW, CC, TC, EM conceived and designed the research; KW, EM, TC selected the species to assess; KW gathered the data; KW, FCD, JV conducted the species assessments; FCD, JV wrote and edited the manuscript; all authors contributed to its revisions; all authors read and approved the final version of the manuscript.

Abstract

The UK is one of the most nature depleted countries in the world, with only 50% of its native biodiversity remaining, leading to an overall decline in UK ecosystems and genetic diversity. Genetic diversity is essential for evolutionary processes, including genetic drift, gene flow, selection, and mutation, as it provides the raw material for populations to respond adaptively to changing environments. Although recognised as a form of biodiversity, genetic diversity is often overlooked in conservation programmes due to lack of genetic data and difficulties in generating it. We have devised a framework which utilizes life history data as an alternative to genetic data to infer population genetics parameters which are used to inform conservation recommendations. Our framework combines approaches incorporating risk assessments predicting species population genetics parameters based on a combination of specific biological trait values and provides management recommendations to ensure conservation of genetic diversity. Here we apply our framework to the assessment of 52 UK native or archaeophyte plant species of conservation and ecological restoration interest. We found that species assessed as least likely to require conservation management were in line with the IUCN's assessment of Least Concern species. While our framework aligns with IUCN's categories, it extends beyond threat classification by providing targeted management recommendations. In the absence of genetic

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data, this framework proved to be very informative for conservation practitioners. However, further species-specific genetic analysis is still needed to confirm the results of this study and provide robust conservation management recommendations.

Key words:

Genetic Essential Biodiversity Variables, life history traits, genetic diversity, genetic differentiation, inbreeding, management recommendations, risk assessments.

Implications for practice:

This framework can provide conservation and management recommendations based on estimates of genetic diversity patterns using available life-history traits and distribution range data for plants.

The 52 species-specific assessments provide management and conservation recommendations for stakeholders with emphasis on the risks on sampling, donor selection and negative outcomes of mixing populations based on estimates of genetic diversity and differentiation parameters.

Introduction

Loss of biodiversity is a current global threat that is being exacerbated by climate change (Habibullah et al. 2022). This is particularly concerning due to the consequences of species loss on ecosystem function (Duffy 2009). Since the early 19th century, the average abundance of native species in major terrestrial habitats has decreased by at least 20% and this is expected to accelerate due to anthropogenic factors (Watson et al. 2019). The UK is one of the most nature-depleted countries in the world, with only half of its native biodiversity remaining, compromising the health of ecosystems (Newbold et al. 2016, Natural History Museum 2021). Several UK government plans to conserve and restore species and habitats have been introduced as the long-term survival of many species, habitats and ecosystems is dependent on proactive conservation (Scottish Government, 2013; Welsh Government 2015; Defra, 2018; Chapman et al. 2019; Gann et al. 2019; Defra, 2023).

One of the most well-known and accessible conservation assessment methods is the IUCN Red List of Threatened Species which classifies species' conservation threat statuses (IUCN 2020). It comprises individual conservation assessments for many species which aim to guide conservation management decisions. Although genetic diversity has been recognized as a fundamental component of biodiversity by the IUCN (McNeely et al. 1990), it has never been explicitly or systematically incorporated into IUCN Red List assessments. This limitation has drawn substantial criticism, as these assessments primarily focus on species-level metrics, such as population size and extinction risk and do not consider genetic diversity (e.g., Rivers et al. 2014), while largely neglecting the genetic variation essential for species' adaptive potential and resilience to environmental change (Hoban et al. 2020; Laikre et al. 2020). Genetic diversity underpins key evolutionary mechanisms (genetic drift, gene flow, natural selection, and mutation) by supplying the variation necessary for populations to adapt and persist in changing environments (Booy et al. 2000; Hoffman & Srgò 2011; Chapman et al. 2019). Higher genetic diversity underpins long-term persistence of populations as it is linked to increased heterozygosity and decreased inbreeding which have both been associated with increased fitness (Reed and Frankham, 2003). Genetic diversity has significant ecological consequences and has substantial effects on productivity and population recovery (Hughes et al. 2008). In the face of the climate change and biodiversity crises, maintaining genetic diversity is essential to the long-term survival of populations and should therefore form a fundamental part of conservation management strategies.

Threatened species often have small, fragmented populations and are therefore more likely to suffer the negative effects associated with low genetic diversity. Long-term small population size can lead to inbreeding, resulting in the accumulation of deleterious mutations (Liu et al. 2021). Furthermore, small populations are vulnerable to high levels of genetic drift that can decrease genetic diversity and increase extinction risk (Reed & Frankham 2003; Keyghobadi et al. 2021). The implementation of risk management strategies

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and frameworks can help to drastically improve the outcomes of conservation management strategies and enable conservation practitioners to make more informed decisions (Byrne et al. 2011). Mixing populations is sometimes suggested as a management strategy to increase genetic diversity or introduce adaptive traits into a population (Weeks et al. 2011). However, if genetic diversity is not carefully considered, mixing genetic material from genetically different populations can have negative effects such as outbreeding depression and maladaptation (Broadhurst et al. 2008) which can reduce the viability of populations and the likelihood of the success of conservation management (Furlan et al., 2020). Outbreeding depression can cause decreased offspring fitness when crossing with genetically different lineages (Weeks et al. 2011). It can occur when translocating individuals or mixing populations belonging to different species, with chromosomal differences, not having exchanged gene flow in 500 years,) or when populations are adapted to different environments (Frankham et al 2011; Weeks et al 2011). Nevertheless, mixing populations can be a valuable tool to avoid negative impacts of inbreeding or bottlenecks if genetic differences and diversity are carefully considered (Broadhurst et al. 2008; Byrne et al. 2011).

The inclusion of genetic diversity in conservation management has been recommended to conservation practitioners previously and is often incorporated in programmes such as ex-situ seed banking (Booy et al. 2000; León-Lobos et al. 2012; Hoban et al. 2013; Chapman et al. 2019; Ray & Bordolui 2021). However, it is not always prioritised in conservation management decisions (Kahilainen et al. 2014). This is unsurprising, given that its inclusion requires specific scientific information resulting from complex genetic analysis which for some species can be impossible to gain for reasons such as the lack of funding and access to genetic material (Theissinger et al. 2023). Incorporating the conservation biology principles of redundancy, representation, and resilience can also support the protection of genetic diversity, even in the absence of direct genetic data. These principles are central to the Species Status Assessment (SSA) process, which evaluates species' viability by considering factors like distribution, population structure, and potential environmental changes. By focusing on broader ecological and population-level factors, the SSA can guide conservation decisions that protect genetic diversity through strategic conservation efforts, even when specific genetic data are difficult to obtain (Smith et al. 2018).

Frameworks that prioritise genetics often require expensive materials and time-consuming work to provide estimates of genetic diversity, population differentiation, gene flow, hybridisation and inbreeding to inform decisions (Hoffman et al. 2015; Ottewell et al. 2016). Several models have been proposed which operate without the need for, or in the absence of, genetic data. These have been developed in the context of seed sourcing based on environmental differences between populations (Breed et al. 2013) and life-history traits and genetic factors (Walker et al. 2004; Byrne et al. 2011; Ottewell et al. 2016). A more recent study also proposed a "reactive/proactive" approach based on the synthesis of the risks and benefits of using local seed in revegetation programmes (Török et al. 2024). However, these approaches are often difficult to apply in real-world situations and depend on the availability of applicable data, which is often difficult to obtain. Neaves (2019) proposed a risk assessment framework which, in contrast to the model proposed by Walker et al. (2004), utilises only life-history traits to estimate genetic diversity, genetic differentiation and inbreeding metrics. Neaves' (2019) framework then uses these metrics to evaluate the risks of sampling and donor selection for ecological restoration based on the estimated effects of mixing populations. This approach has previously been successfully applied to UK trees and shrubs to evaluate knowledge gaps related to UK native tree genetics and has since been used to develop policy recommendations and funding for native tree seed supply (Gargiulo 2019; Sustainable Seed Sourcing Project, 2023). For example, Gargiulo (2019) used Neave's framework in 44 species and The Tree Seed Species Strategies (2023) includes recommendations for 17 tree species, such as establishing clonal seed orchards for aspen (*Populus tremula* L.) or recommending sampling strategies to represent the distribution range (e.g., hazel (*Corylus avellana* L.), elder (*Sambucus nigra* L.)). Ottewell et al. (2016) proposed a framework which relies on genetic data to estimate levels of genetic differentiation, genetic diversity and inbreeding metrics. This framework is further utilised to deliver comprehensive management recommendations for conservation practitioners. Such an approach has been applied to threatened species like *Androsace cantabrica* (Losa & P. Monts.) Kress, where conservation units were defined based on genetic structure. Specific conservation strategies, including translocations to boost genetic diversity and habitat

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threat management, were recommended for each genetic group (Liang et al. 2024). Combining Neaves' approach, which infers genetic metrics without requiring genetic data, with Ottewell's framework, which uses genetic data to guide conservation actions for threatened species, could provide a flexible and cost-effective strategy. This integration would allow practitioners to make informed decisions in scenarios where genetic data is unavailable or impractical to obtain, while still enabling precise and targeted management when such data is accessible, ultimately enhancing the adaptability and impact of conservation and restoration efforts. Here, we propose a framework for species conservation assessments that prioritise population genetic parameters, but do not require genetic testing and analysis. Our framework builds on the approaches of Neaves (2019) and Ottewell et al. (2016) by combining the strengths of both methodologies. While Neaves' framework estimates genetic parameters from life history traits, it does not provide management strategies. Conversely, Ottewell's genetic assessment framework relies heavily on genetic data, which is often unavailable. Our combined framework uses life history traits to genetic essential biodiversity variables (EBVs; Hoban et al. 2022): genetic diversity, differentiation, and inbreeding potential (following Neaves) and integrates these estimates to provide actionable conservation management recommendations (adapted from Ottewell). The Group on Earth Observations Biodiversity Observation Network (GEO BON) developed EBVs as metrics to interpret biodiversity data from a range of sources (Pereira et al. 2013). Genetic EBVs, proposed by Hoban et al. (2022), have been suggested as a good measure to summarise and compare biodiversity among species, especially for conservation policy (Schmidt et al. 2023). It is also possible for some genetic EBVs to be estimated without molecular data (O'Brien et al. 2022). In our rationale, we estimated genetic EBV values based on life history traits, similarly to Neaves' (2019) estimations of genetic diversity and differentiation, and we also included the inbreeding EBV (Hoban et al. 2022). This allowed us to combine these trait values with the conservation management strategies outlined in Ottewell et al. (2016) which also uses similar metrics. These three approaches combined provide a comprehensive, applicable framework that provides conservation strategy recommendations as well as risks of sampling and donor selection as in Neaves (2019).

We use a selection of 52 native or archaeophyte UK plant species of conservation and ecological restoration interest to present this framework and its application for conservation practitioners.

Materials and Methods

Species selection

We established a list of 716 UK plant species of conservation and ecological restoration interest according to the IUCN UK Red List (JNCC 2023), Section 41 of the 2006 Natural Environment and Rural Communities (NERC) Act (Natural England 2013) and the European restoration species pool proposed by Ladouceur et al. (2018). We prioritised species present in all three sources and removed species for which IUCN listed only one location (JNCC 2023). Species that were not considered to have native or archaeophyte status and those with unresolved taxonomy were also removed, as assessments that estimate genetic parameters can only be applied once the taxonomy is clear (Stace, 2010). The remaining species were then ranked for priority based on the availability of data (see methods below). The most highly ranked species were selected resulting in a list of 52 species (Table 1).

Biological and species distribution data gathering

Data were gathered from a variety of sources for each of the selected 52 species (Table 2), and included categories such as threat status, taxonomy, distribution as well as biological and life history traits. Data were cross-referenced across multiple sources to create a database with information for all assessed species.

Species Conservation Assessment design:

Predicting the Effect of Life History Traits on the Organisation of Genetic Diversity and Differentiation and Negative Outcomes of Mixing Populations.

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We followed Neaves (2019) to create a table of life history traits (Table 3) to estimate their effect and impact on the organisation of genetic diversity, differentiation and negative outcomes of mixing (Table 4). In contrast to Neaves (2019), however, we did not include the column stating the level of agreement/evidence to reduce repeating the statements already included in the original publication. In each individual assessment (Supplement S1), this table is named "Life history traits".

Conservation Management Recommendations

The next stage of our assessment involved developing a table of conservation management recommendations named "Genetic Conservation Management" (Supplement S1). This table used a life history trait analysis to evaluate two major in ecological restoration practices: failing to capture genetic diversity during sampling and the potential issues associated with mixing populations (i.e., donor selection). Following the framework of Neaves (2019), we adopted their risk definitions and recommendations for ecological restoration while expanding on them by incorporating EBVs into our discussions. Sampling risks were assessed based on the genetic diversity and genetic differentiation EBVs: species with high genetic diversity and low differentiation were assigned a low risk of sampling limited diversity, species with moderate differentiation were considered at moderate risk, and species with low diversity and high differentiation species were classified as high risk. Donor selection risks were primarily informed by genetic differentiation EBVs and distribution data from the Botanical Society of the British Isles (2024b). Species with low differentiation and widespread and continuous UK distributions were considered low risk of mixing; those with high differentiation were assigned moderate risk; and species with high differentiation and/or narrow and fragmented UK distributions were deemed high risk of mixing.

We also included three further discussions of life history traits, one for each genetic EBV (genetic diversity, genetic differentiation and inbreeding potential) and assigned an EBV value to each (high or low). The life history traits used to infer these values are outlined in Table 5A-D. An overall value was determined by calculating the number of traits signifying either a high or low EBV value. If a species had more traits that suggested a lower value, a low EBV value was selected and vice versa. In ambiguous cases (for example if a species had an equal number of traits suggesting higher or lower differentiation or diversity), more weight was given to species distribution and evidence of connected gene flow. These three EBV values were then used to assign an overall conservation management recommendation from Ottewell et al. (2016) which are summarised in Table 5E.

Results

We completed assessments for 52 plant species of restoration and conservation interest in the UK; the full assessments can be found in Supplement S1. A summary of all the species assessed, and the associated conservation management recommendations can be found in Table 1.

Of the 52 assessed species, 27 were categorized as Least Concern (LC) by the IUCN, one Near Threatened (NT), five Vulnerable (VU), seven Endangered (EN) and 12 Critically Endangered (CR). We assessed the risk of sampling limited diversity for all species. In total, 14 species were assessed as low risk, 22 species as moderate risk and 16 species as high risk. In general, LC species were more likely to have low sampling risks while EN and CR species were more likely to have high sampling risks (Figure 1A). Additionally, the species that were assessed as high risk were often associated with life history traits such as being rare in the UK, with a scattered distribution or poor seed dispersal method. Species that were associated with low risk of sampling limited diversity were often widespread with no evidence of population fragmentation or had an effective dispersal method. These species were more likely to have connected gene flow.

We also assessed the vulnerability or risks of mixing populations for all species. In total, 10 species were assessed as low risk, 31 species with some risks, and 11 species as a high risk of mixing. Overall, LC species were more likely to have lower or some risks associated with mixing while NT, VU, EN and CR species all had at least some risks associated with mixing populations and most of the CR species were assessed as

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a high risk of negative outcomes due to mixing populations (Figure 1B). In general, species with genetic incompatibilities such as multiple ploidy levels or hybridising species were more likely to be assessed with high risk of mixing. In addition, obligatory sexual reproduction, low longevity and population fragmentation all increased the risk of mixing populations.

Conservation management strategies were assigned to each species based on genetic EBV values. Among the 52 species assessed, two were recommended for active conservation management to reduce inbreeding, and 23 were advised to undergo active conservation management to increase genetic diversity. The remaining 27 species required no conservation management; notably, 26 of these were classified as LC species. Generally, species not requiring management were common in the UK with well-connected populations. The 27th species that required no conservation management, *Euphrasia nemorosa* (Pers.) Wallr., categorised as NT, despite moderate sampling risk and high donor selection risk, is widespread throughout England; thus, no management was recommended at this time (see Supplement S1). Of the species for which management to increase genetic diversity was recommended, 12 were CR, seven were EN and four were VU. The majority of these species are rare in the UK, exhibiting scattered distributions and limited dispersal mechanisms, which likely result in unconnected gene flow, leading to populations with low genetic diversity and high genetic differentiation. Of the two species recommended for management to reduce inbreeding, one was of LC and the other was VU (Figure 1C). These two species identified due to their scattered distributions, and broad ecological amplitude, life history traits that suggest a high potential for inbreeding, possibly due to local adaptation to varied environments.

Examples of three species conservation assessments

To illustrate the general patterns observed in our assessments, we provide three examples of assessments (Tables 3 and 4) from those reported in Supplement 1. *Armeria maritima* subsp. *elongata* (Hoffm.) Bonnier was selected as examples to an assessment of a Critically Endangered species that was recommended management to increase genetic diversity. *Silene latifolia* Poir was selected to illustrate an assessment in which management to decrease inbreeding was recommended. *Achillea millefolium* L. was selected to show a Least Concern species where no management was recommended.

Armeria maritima subsp. *elongata* is a threatened species and has been included in the UK Biodiversity Action Plan (BAP 2007) as well as England's Biodiversity List (Natural England 2013). It is a diploid native herbaceous and perennial plant without available genetic data for its UK distribution, and usually grows in rough grasslands overlying river gravels or alluvium, formerly one site in limestone grassland, altitude 0-300 m. In Great Britain, it is Red Listed as Critically Endangered, A2a, with decline noted in its locations. In the UK, it is found in England only; and its range is declining, having been found in the 1950s in at least 12 localities of one county but now lost from all but one location due to ploughing, reseeding and agricultural improvement. Its conservation management recommendation is to increase genetic diversity as it is unlikely to have connected gene flow due to a scattered distribution and poor seed dispersal ability. It has a high risk of sampling limited diversity. The species also reproduces sexually so it is more likely to have higher differentiation and consequently has a high risk of mixing (Table 4). Given the high risk of genetic fragmentation and inbreeding in *Armeria maritima*, our framework recommends increasing genetic diversity through translocations. However, we emphasize that such interventions should be preceded by targeted genetic studies to confirm fragmentation levels and mitigate risks of outbreeding depression.

Silene latifolia is a Least Concern species in the UK with a probable decline in range, particularly in its western range (Leach 2019). It has been identified as a species of potential interest for ecological restoration for European grasslands and has five subspecies described and currently accepted (Ladoucer et al. 2018). *Silene latifolia* itself has little evidence for hybridisation, but one subspecies (*S. latifolia subsp. alba*) hybridises with *S. dioica* (L.) Clairv. creating the hybrid *S.* x *hampeana* Meusel & K.Werner (*S. dioica* x *S. latifolia* subsp. *alba* (Mill.) Greuter & Burdet). It is a diploid native herbaceous hemicryptophytic plant that grows on free draining mildly acidic to mildly alkaline soils, tolerant to drought and frost but intolerant to heavy metals. Connected gene flow is somewhat unlikely as despite its effective dispersal method, *S. latifolia* has a patchy distribution in Wales, Scotland and Ireland but is not rare throughout England. It is therefore

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likely to have a moderate risk of sampling limited diversity. There are also likely to be some risks associated with mixing as the species is outcrossing and occurs in divergent ecological conditions. The hybridisation of intraspecific taxa also increases this risk. This species is an example of a species with low-moderate differentiation, higher diversity and moderate-high risk of inbreeding. In this case, management to reduce inbreeding was recommended (Tables 3 and 4) while genetic information is gathered for this species.

Achillea millefolium is a Least Concern species with six subspecies described and currently accepted. Hexaploid cytotypes have been found in the UK ($2n = 54$), and outside of the UK diploids ($2n = 28$) and tetraploids ($2n = 36$) have been described. It is widespread; frequent and abundant where occurring. It has a soil seedbank longevity of 1-5 years; a stable range with no significant change since the 1962 Atlas Survey. It was identified as a species of potential interest for ecological restoration within European grasslands (Ladoucer et al. 2018). It grows in a range of grassland types; waysides and waste grounds; coastal sand dunes and stabilised shingle, in an altitude range of 0-1210 m (Botanical Society of the British Isles 2024b). It is likely to have connected gene flow as the species shows no evidence of fragmentation and it has an effective dispersal method. Despite reproducing sexually, the species is long-lived and common. It is therefore likely to have higher diversity and lower differentiation with a low risk of sampling limited diversity and a low risk of mixing. Based on this evidence, the species does not require management at this time (Tables 3 and 4); however, we recommend gathering genetic data to confirm these recommendations.

Discussion

By integrating life-history traits and distribution data into the frameworks developed by Neaves (2019) and Ottewell et al. (2016) and including Genetic EBVs (Hoban et al. 2022), we have given informed recommendations and risk evaluations for conservation management and ecological restoration activities for 52 UK plant species. LC species were the least likely category to be recommended for conservation management; while all threatened species (VU, EN or CR) were instead recommended conservation action aiming to increase genetic diversity at population level. Regarding recommendations for ecological restoration, all plant species classified as NT, VU, EN or CR were predicted to have risks associated with sampling limited genetic diversity and selecting donors for mixing populations. While some least concern species also had some risks associated with sampling and donor selection, none of this group was classed as being at high risk for sampling, and only *Daucus carota* L. was categorised as high risk for donor selection due to taxonomic uncertainties. It is important to recognize that some threatened species may primarily require habitat protection and establishment of new populations rather than interventions to increase genetic diversity. These scenarios should be assessed on a case-by-case basis.

Certain traits were more associated with high sampling or donor selection risks. Species with genetic incompatibilities such as hybridising species and species with multiple ploidy levels were more likely to be high risk for donor selection. Hybridizing species are generally considered high risk for ecological restoration due to concerns like outbreeding depression, which can disrupt locally adapted gene complexes and reduce fitness (Frankham et al. 2011). However, hybridization also offers significant benefits, such as increased genetic diversity and adaptive potential, which are essential for responding to environmental changes like climate shifts or disease outbreaks (Abbott et al. 2013). Recent studies have highlighted how hybridization can result in heterosis (hybrid vigor), enhancing growth, reproduction, or survival in hybrids compared to parental species, and how it facilitates the introgression of advantageous traits, enabling populations to adapt to novel environments (Rieseberg et al. 2007). These benefits are particularly relevant in rapidly changing ecosystems, where adaptive advantages may outweigh potential risks. Careful management, including robust genetic monitoring, is required to balance these risks and ensure hybridization supports restoration goals (Taylor et al. 2015). Management strategies should carefully weigh these risks and benefits. On the other hand, hybridisation has been associated with lower fitness through a variety of mechanisms such as rapid genomic changes and genetic pollution of species integrity (Baack & Rieseberg, 2007; Moran et al. 2021). For example, *Silene dioica* hybridises with *S. latifolia* subsp. *alba* to create the hybrid *Silene* × *hampeana*.

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If a population of *S. dioica* hybridising with *S. latifolia* subsp. *alba* was translocated to a population of *S. dioica* which does not usually overlap ranges with *S. latifolia* subsp. *alba*, alleles from another species may be introduced into a new population with unknown consequences. Furthermore, the risk is higher with threatened species because mixing hybridising populations could also decrease genetic diversity of a species by breaking down reproductive barriers and merging two previously distinct lineages (Todesco et al. 2016).

Species with multiple ploidy levels were also associated with higher risks of donor selection as it can contribute to outbreeding depression. Outbreeding depression has been linked to crossing populations with chromosomal differences (Frankham et al. 2011). For example, *Campanula rotundifolia* L., despite being classified as a species of least concern by the IUCN was assessed as having some risks of donor selection due to its multiple ploidy levels (Royal Botanic Gardens, Kew 2024a). Throughout the UK, populations of *Campanula rotundifolia* can be either diploid, tetraploid or hexaploid (Stevens et al. 2012), so mixing individuals from different populations could lead to non-viable or infertile offspring. Outbreeding depression can have an even larger effect on threatened species (Frankham et al. 2011). Threatened species often have lower genetic diversity and fragmented populations so introducing individuals from other populations can disrupt local adaptations leading to lower fitness (Liddell et al. 2021). Hence, all species that were classified as Vulnerable, Endangered or Critically Endangered by the IUCN were either high risk or had some risks associated with donor selection.

A key trait associated with a high risk of sampling limited genetic diversity is population fragmentation. Connected gene flow is the transfer of genetic material from one population to another and is important for maintaining genetic diversity (Gómez-Fernández et al. 2016). Fragmented populations are less likely to have connected gene flow, and can also increase genetic structure between populations and lead to higher inbreeding rates (Wang et al. 2011). As well as population fragmentation, a poor dispersal method also contributes to poor gene flow among populations (Vandewoestijne et al. 2008) and, therefore, species with both a poor dispersal method and evidence of population fragmentation or a scattered distribution were assessed as a higher risk of sampling limited diversity. Moreover, the interaction between fragmented distribution and broad ecological amplitude is crucial in understanding inbreeding risk. In species with a broad ecological amplitude, local adaptation to specific environmental conditions can reduce gene flow between populations, increasing the likelihood of genetic isolation. This isolation, while potentially enhancing local fitness through local adaptation, can also lead to inbreeding depression due to the accumulation of deleterious alleles in small, isolated populations (Lopez et al. 2009; Verhoeven et al. 2010). This link between fragmented distribution, ecological amplitude and inbreeding has been documented in several plant species (e.g., Zhao et al. 2006; Vanden-Broeck et al. 2011).

In conclusion, we conducted species conservation assessments for 52 UK native plant species and gave conservation management recommendations based on their predicted genetic diversity, differentiation, and vulnerability to mixing populations. In general, we found that certain life-history traits were more likely to come with risks for sampling and donor selection such as genetic incompatibilities and population fragmentation. Also, species that are classified by the IUCN as threatened were more likely to be recommended for conservation management. The likely cause for this is that threatened species are rare in the UK, are more likely to have fragmented distributions and therefore are less likely to have connected gene flow, leading to the need for management to increase genetic diversity. Our data reflect conclusions made by Rivers et al. (2014), that IUCN red list classifications seem to broadly represent the genetic diversity of a species. For example, species categorised as Endangered were more likely to have low genetic diversity. However, genetic data are still necessary for effective restoration programmes.

In the absence of genetic data, this framework is useful to recommend conservation management strategies; however, genetic data are needed to make more informed decisions and ensure the conclusions made by each assessment are more robust. We acknowledge that while our framework links life history traits to genetic diversity and differentiation, exceptions to these patterns are common in biology, which highlight the need for caution when implementing our recommendations. Recognizing these possibilities, we advocate for conservation management strategies that adopt our framework as a conservative approach. These strategies

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act as interim protective measures for plant species until genetic information can be gathered to confirm, refine and optimise conservation actions. Furthermore, the integration of our proposed framework with the approaches of Ottewell et al. and Neaves leverages the complementary strengths of both methodologies. While Neaves' life-history-based estimates provide a practical solution in data-limited scenarios, Ottewell's genetic assessments offer precise insights when genetic data are available. Our combined approach benefits from the estimates of EBV genetic variables from Neaves' approach to provide conservation recommendations for threatened species using Ottewell's decision-making framework, and enhances the applicability and adaptability of conservation recommendations, ensuring more robust outcomes in ecological restoration and biodiversity preservation.

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Table 1. Summary of conservation management recommendations for each of the 52 UK native plant species assessed in th

TAXON
Sp. name
Achillea millefolium L.
Agrostis stolonifera L.
Alchemilla monticola Opiz
Alisma gramineum Lej.
Anthoxanthum odoratum L.
Anthyllis vulneraria L.
Armeria maritima subsp. *elongate (Hoffm.) Bonnier*
Astragalus danicus Retz.
Bupleurum rotundifolium L.
Campanula patula L.
Campanula rotundifolia L.
Cardamine pratensis L.
Carex ericetorum Pollich
Carex flacca Schreb.
Centaurea nigra L.
Centaurea scabiosa L.
Cephalanthera rubra (L.) Rich.
Clinopodium acinos (L.) Kuntze
Crepis mollis (Jacq.) Asch.
Dactylorhiza incarnata subsp. *ochroleuca (Wüstnei ex Boll) P.F.Hunt & Summerh.*
Dactylorhiza viridis (L.) R.M.Bateman, Pridgeon & M.W.Chase
Daucus carota L.
Euphrasia nemorosa (Pers.) Wallr.
Festuca ovina L.
Galeopsis angustifolia Ehrh. ex Hoffm.
Galium pumilum Murray
Galium tricornutum Dandy
Gentianella campestris (L.) Börner
Jacobaea paludosa (L.) G.Gaertn., B.Mey. & Scherb.
Juniperus communis L.
Koeleria macrantha (Ledeb.) Schult.
Leucanthemum vulgare Lam.
Lolium temulentum L.
Lotus corniculatus L.
Lythrum salicaria L.
Neotinea ustulata (L.) R.M.Bateman, Pridgeon & M.W.Chase
Oxybasis urbica (L.) S.Fuentes, Uotila & Borsch
Plantago lanceolata L.
Polygala amarella Crantz
Prunella vulgaris L.
Ranunculus acris L.
Ranunculus arvensis L.
Ranunculus bulbosus L.
Rhinanthus minor L.
Rumex acetosa L.

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Table 1. Summary of conservation management recommendations for each of the 52 UK native plant species assessed in th

Rumex acetosella L.
Saxifraga hirculus L.
Scandix pecten-veneris L.
Scorzoneroides autumnalis (L.) Moench
Silene dioica (L.) Clairv.
Silene flos-cuculi (L.) Greuter & Burdet
Silene latifolia Poir.

Table 2. Data Sources accessed to inform species conservation assessments. MSB refers to the Millennium Seed Bank at W

Source
POWO
BiFlora (Main tab)
BiFlora (GS tabs)
BSBI Cytology
Plant DNA C-Values
PLANTATT
New Atlas of the Flora of the British Isles
MSB-BSBI
GB Red List (2018)
JNCC
EcoFlora
PlantAtlas

Table 3: Life history traits and how they affect a species organization of diversity and differentiation and vulnerability to ne

Armeria maritima subsp. *elongata*
Life History Traits?
Mode(s) of reproduction
Dispersal method(s) / Ability
Time to maturity / Longevity
Reproductive output
Recruitment / Turnover potential
UK distribution
Fragmentation, scattered distribution
Ecological amplitude
Demography
Silene latifolia
EBV
Mode(s) of Reproduction
Dispersal Method(s) / Ability
Time to Maturity / Longevity
Reproductive Output
Recruitment / Turnover Potential
UK Distribution (New Atlas, Preston et al. 2002); GB & IR 10-km^2 (PLANTATT, Hill et al., 2004)
Fragmentation, Scattered Distribution / Ecological Amplitude
Demography

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Table 3: Life history traits and how they affect a species organization of diversity and differentiation and vulnerability to ne

Achillea millefolium
EBV
Mode(s) of reproduction
Dispersal method(s) / Ability
Time to maturity / Longevity
Reproductive output
Recruitment / Turnover potential
UK distribution
Fragmentation, scattered distribution
Ecological amplitude
Demography

Table 4. Examples of Conservation management recommendations for three species to illustrate the patterns observed.

Genetic conservation management	
Armeria maritima subsp. *elongata*	
Risks and Essential Biodiversity Variables (EBVs)	Di
Sampling	Co
Donor selection	Sp
Genetic differentiation	Sp
Genetic diversity	Sp
Inbreeding potential	Ge
Silene latifolia	
Essential Biodiversity Variables (EBVs)	Di
Sampling	Co
Donor selection	De
Genetic differentiation	Th
Genetic diversity	
Inbreeding potential	Ge
Achillea millefolium	
Essential Biodiversity Variables (EBVs)	Di
Sampling	Co
Donor selection	Al
Genetic differentiation	Sp
Genetic diversity	
Inbreeding potential	Ge

Table 5. Life history trait values used for proving ecological restoration and conservation management recommendations fo

5a. Organisation of genetic diversity (Genetic Diversity EBV)
Attribute or trait
Mode of reproduction
Dispersal ability
Longevity
Distribution
Fragmentation or scattered distribution
Recruitment, turnover
Demography

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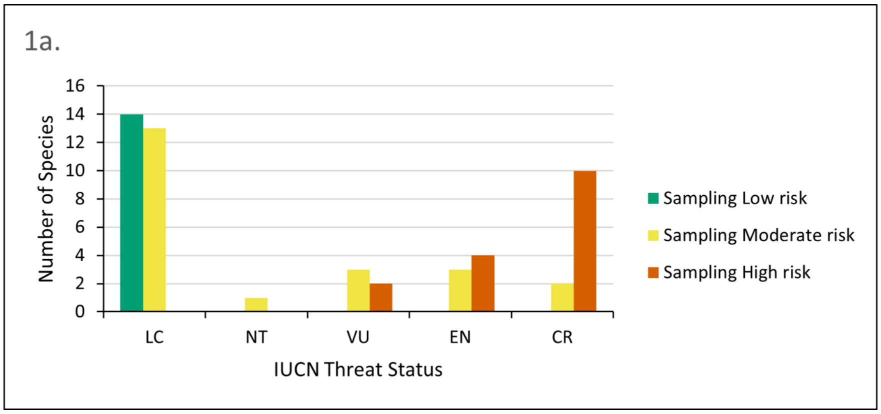
Table 5. Life history trait values used for proving ecological restoration and conservation management recommendations fo

5b. Organisation of genetic differentiation (Genetic Differentiation EBV)
Attribute or trait
Mode of reproduction
Dispersal ability
Longevity
Distribution
Fragmentation or scattered distribution
Ecological amplitude
5c. Inbreeding EBV
Attribute or Trait
Genetic diversity
Fragmentation or scattered distribution
Population Sizes
5d. Negative outcomes of mixing
Attribute or trait
Mode of reproduction
Longevity
Reproductive output
Fragmentation, scattered distribution or ecological amplitude
Known genetic incompatibilities
5e. Conservation management recommendations
Genetic differentiation / Genetic diversity / Inbreeding
Low / High / Low Populations have historically been connected maintaining high levels of gene flow and are genetically hea
Low / High / High Populations have historically been connected maintaining high levels of gene flow. Risk of population de
Low / Low / Low Populations have historically been connected. Mating patterns are maintained but diversity has eroded d
Low / Low / High Populations have historically been connected. Inbreeding is present and exacerbated by low genetic diver
High / High / Low Populations historically isolated, little, or no current gene flow. Healthy genetic diversity but population
High / High / High Populations historically isolated, little, or no current gene flow, thus genetically divergent. Populations
High / Low / Low Populations historically isolated. Mating patterns maintained but gene flow and genetic diversity are low
High / Low / High Populations historically isolated, little, or no current gene flow, thus genetically divergent. Genetic diver



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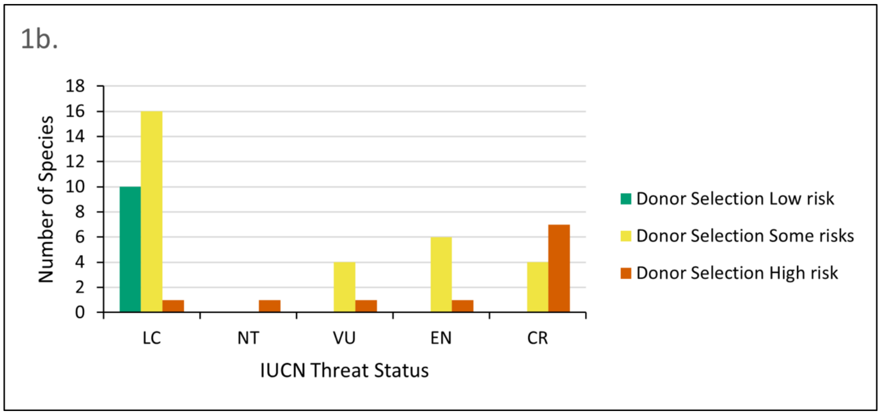

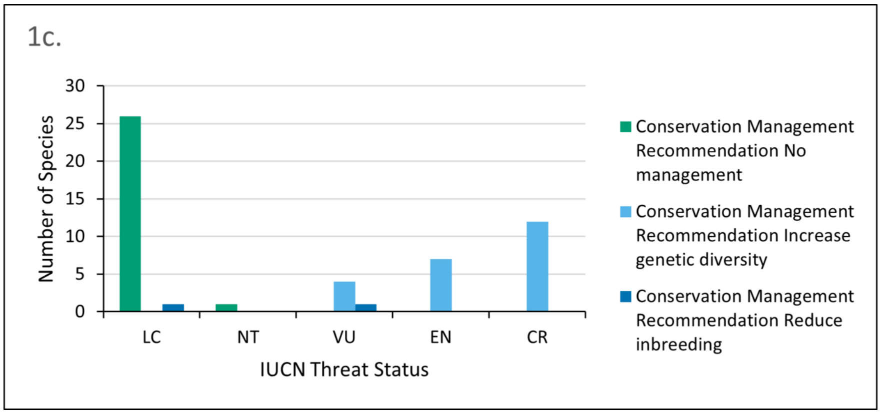

Figure 1. Summary of risks and management decisions for species dependent on IUCN threat status. LC refers to Least Concern species, NT refers to Near Threatened species, VU refers to Vulnerable species, EN refers to Endangered species and CR refers to Critically Endangered species. 1a. Summary of the number of species that were assigned low, moderate or high risk for sampling limited diversity. 1b. Summary of the number of species that were assigned low risk, some risks or high risk for vulnerability to mixing (donor selection). 1c. Summary of the conservation management recommendations that were assigned to all the assessed species.