Implications of Commercial Wildflower Plantings for Wild Populations: A Multi-Criteria Framework for Species Risk Assessment

Elisabeth Cooke

Supervised by Dr Adrian Brennan

Department of Biosciences, Durham University

Laidlaw Leadership & Research Scholarship

Introduction

Because of human impact, species diversity has been reduced across many ecosystems (Bischoff et al. 2010). Intending to support wildlife and enhance local biodiversity, planting commercially sourced wildflowers has become popular with individuals and groups including local councils, farmers and land developers. However, there is a growing awareness that the planting of these wildflowers may disrupt the ecology and evolution of pre-established wildflower populations (Barry, Hodge, 2023).

With scarce intention to emulate the natural local plant composition or gene pool, seed mixes have been produced and distributed into ecologically unsuitable locations (Barry & Hodge, 2023). The cultivated origins of these species means that they may have undergone a degree of human selection, artificially manipulating the seeds' genetics, with producers intentionally or unintentionally preserving and producing seeds from plants with certain desirable traits such as earlier germination (Heiser, 1987). Further, often the provenance of the seed is disregarded, so non-local genotypes are introduced among local populations (Mijnsbrugge et al. 2010). Local provenance is considered central to ecological restoration, as plants with regionally adapted genotypes typically exhibit superior performance under the local environmental conditions that they are evolutionarily aligned with (Kiehl et al., 2014). The introduction of these cultivated and non-local populations has widely unexplored genetic implications for both the pre-established and introduced populations of the same species, with several potential evolutionary outcomes for both populations (Turner et al. 2017).

There is potential for the commercially sourced wildflower species to hybridise and homogenise with pre-established populations of the same species (Burton & Burton, 2002), making individuals more genetically similar and altering the gene pool. This has presented itself as low organisation and distribution of genetic variation and individuals within and between introduced and established populations (Turner et al. 2017). On top of reduced genetic diversity, as adaptation to a specific planting site is expected to decrease with the source of a plant being at increasing distance from it and the plant being genetically isolated (seeds are collected from a limited number of sources) (Bischoff et al. 2010), as is common with commercially produced wildflowers in seed mixes (Barry & Hodge, 2023), established populations at that site are put at risk from the inheritance of likely maladaptive genes, and therefore reduced fitness (Bischoff et al. 2010, Keller et al, 2001). All of these consequences have the potential to negatively impact wildflower populations' adaptation to changes in their environment.

The factors described below are highlighted to capture key ecological and genetic factors influencing hybridisation risk of individual species between commercial and natural populations. Species planted more frequently from commercial sources are more likely to co-occur with pre-established populations, increasing the potential for hybridisation. Rarity further amplifies vulnerability as rare species are more susceptible to acquiring maladaptive genes, as evidence suggests that widespread, well-connected species exhibit greater resilience to genetic introgression through enhanced gene flow and population buffering (Sampson & Byrne, 2008; Aavik et al., 2014; Richards et al., 1999).

Spatial proximity was also considered to determine whether a species naturally occurs near planting sites. Where substantial natural populations are located close to planting areas, the likelihood of hybridisation increases due to stronger spatial connectivity and overlap (Sampson & Byrne, 2008; Aavik et al., 2014; Richards et al., 1999). Intraspecific variation was included on the premise that species exhibiting high internal diversity are more likely to experience disruption to native patterns of variation through hybridisation/introgression, particularly where population differentiation is considerable (Des Roches et al., 2018).

Dispersal ability influences the potential for gene flow between commercial and natural populations, with highly dispersive species more likely to spread and mix across landscapes (Gamba & Muchhala, 2020). Similarly, a high outcrossing rate increases the likelihood of cross-pollination between populations as individuals are reliant on reproducing with other individuals other than themselves, while high pollinator specificity implies that successful pollination is more likely to occur between conspecifics as the species is visited by a limited range of pollinators (Neequaye et al., 2025).

This study aims to evaluate wild-commercial hybridisation risk across wildflower species identified as being used in recent ecological restoration and biodiversity management practices. A multi-criteria framework was used, with the objective of identifying the species most vulnerable to intraspecific introgression with commercially sourced populations under current restoration practices, integrating planting frequency, rarity, the presence of natural populations near planting sites, intraspecific variation, dispersal ability, outcrossing rate and pollinator specificity as the criteria. This study also aims to assess broader hybridisation risk, with a general evaluation incorporating supplier sourcing practices, provenance considerations, and the relationship between planting frequency and species rarity.

First, this study measured planting frequency and rarity data to create a subset of 30 wildflower species. Following this, the further traits were compiled from database and published scientific literature sources, as well as through cross-referenced map sources, and analysed using weighted sum aggregation to generate composite risk scores. Species were ranked accordingly, and seven species were identified for targeted conservation attention: *Daucus carota, Geranium pratense, Origanum vulgare, Rhinanthus minor, Anthyllis vulnearia, Centaurea scabiosa, and Silene flos-cuculi*. By highlighting the species deemed here most at risk, this framework informs more ecologically responsible decisions around seed sourcing, supply, and procurement.

Methodology

Seven decision criteria were selected based on published literature and expert discussion. These included:

1. Frequency of planting by local councils
2. Relative rarity of the species
3. Proximity of planting locations to protected areas where the species is naturally present
4. Known intraspecific variation
5. Dispersal ability
6. Outcrossing rate
7. Pollinator specificity

These criteria were chosen to reflect both ecological risk and current relevance, enabling a multi-dimensional assessment of species suitability.

Frequency/location collection

The study focused on wildflower species planted in public schemes managed by local authorities/councils across Britain. This approach was designed to capture a geographically diverse sample of planting sites (Figure 1), given that preliminary research found many local authorities choosing seed mixes and using curated seed mixes that reflect the already locally-present wildflower species, and to reflect the varied natural distributions of target species (BSBI distribution maps). Local authorities were selected for this study due to their extensive management of green spaces and the practical constraints of broader landowner investigation.

Figure 1. Map of Britain showing the approximate locations of the local authorities used in this study.
.

Figure 2. Map of Britain divided into the Forestry Commissions' provenance zones (ArcGIS Online, 2016)

To ensure ecological representativeness, the Forestry Commission's provenance zone map (ArcGIS Online, 2016., Figure 2), which also correlates with climatic and edaphic conditions that help capture the range of environments inhabited by different wildflower species (Herbert et al. 1999), was used to guide local authority selection. Within each provenance zone, up to three local authorities were included using ONS regional boundaries (ONS Geography, 2022). Keyword searches ('biodiversity', 'wildflower', 'planting') were conducted on council websites to identify planting schemes, biodiversity action plans, and relevant news items. Where species lists were unavailable, councils were contacted directly using a standardized email template explaining the research, which was the case for 23 of 39 authorities.

Native status list and rarity

From the initial list of 182 species, only native species were retained, excluding non-natives and archaeophytes (11 archaeophytes and 51 non-natives) based on BSBI Plant Atlas 2020 classifications. This ensured the focus remained on genotypes reflective of the natural gene pool.

Species rarity was quantified using image analysis in Fiji/ImageJ (Schindelin *et al.*, 2012), measuring the total pixel area of tetrad (2×2 km) squares from 2010 onwards in BSBI distribution maps. This resolution provided a consistent basis for comparing rarity across species. Scores for rarity and planting frequency were normalized and aggregated using a weighted sum method (Tofallis, 2014), with a weighting of 0.7 assigned to rarity to prioritize conservation-relevant species (Rejeb-Mzah *et al.*, 2025), including those planted by very few (mostly one to three) councils with considerable rarity that wouldn't have been highlighted without this weighting.

The 30 species with the highest planting-frequency-rarity aggregate scores from this ranking were selected for further analysis, focussing further investigation on the most relevant species.

To infer potential hybridisation risk and its consequences, a correlation analysis was conducted between planting frequency and species rarity, based on the premise that frequent planting of rare species may amplify hybridisation risk (Sampson & Byrne, 2008; Aavik et al., 2014; Richards et al., 1999).

Planting proximity

To assess the relevance of planting locations, the proximity of each site to natural populations of the same species was calculated, as a substantial natural population of a species located near a planting site elevates the potential for hybridisation due to enhanced spatial connectivity and close proximity (Sampson & Byrne, 2008; Aavik *et al.*, 2014; Richards *et al.*, 1999). Planting sites identified through council responses and online data were compared to Sites of Special Scientific Interest that overlapped with tetrads containing verified species observations (BSBI distribution maps). Distances were measured between centroids of planting locations and SSSIs and averaged per species.

SSSIs were chosen over general tetrad records due to regulatory requirements for planting consultation within these areas (Natural England, 2024), reducing the likelihood of including introduced populations. Two species (*Myosotis alpestris and Arabis alpina)* were excluded from the investigation due to their extremely low spatial proximity (an average of 314km vs 13.8km) to natural populations of the same species. In these cases, the geographic isolation significantly reduces the likelihood of interaction or gene flow with wild genotypes, making hybridisation with commercial plantings ecologically implausible due to the absence of nearby conspecifics, resulting in a final set of 28 species.

Further trait-based decision making

For the remaining characteristics investigated for these 28 species, qualitative descriptions of these for each species were acquired. The main source for these descriptions was the Ecoflora database (Fitter & Peat, 1994), as well as BSBI's Farmanagh accounts and BSBI Plant Atlas 2020, or published scientific literature for where these details were otherwise absent.

To turn these descriptions into quantitative values for aggregation and analysis, they were each assigned ordinal scores (Table 1) based on published scientific literature evidence and judgement.

Table 1. Table describing the remaining trait criteria used in this investigation.

Trait	Description	Score range
Intraspecific variation	The degree of genetic and phenotypic diversity observed among individuals within a single species, including	0-5

	recognised subspecies and ecotypes.	
Dispersal ability	The capacity of a plant to produce and effectively distribute seeds across the landscape.	0-3
Outcrossing rate	The proportion of reproduction that occurs through cross-pollination with other individuals of the same species, rather than through self-fertilisation.	0-6
Pollinator specificity	For insect-pollinated species, this refers to the diversity and identity of insect taxa known to facilitate pollination.	0-4

For variation, this was judged based on the number of known subspecies, ecotypes and known phenotypic plasticity. For dispersal ability, this was based mostly on number of seeds produced per flower/plant, seed size and the presence/absence of specialized dispersal agents. For outcrossing rate, this mainly was based on dicliny (floral sexuality) and dichogamy (timing of female and male reproductive elements at maturity) as well as the presence/absence of self-incompatibility systems. For pollinator specificity, this was mostly based on published observations of visiting insects and floral morphology.

Composite scoring and Sensitivity Testing

The weighted sum method (Tofallis, 2014), widely used in multi-criteria decision-making (e.g. Amabogha *et al.*, 2023; Rehman & Khan, 2017), was employed to aggregate trait scores. To address subjectivity in normalization and weighting, a sensitivity analysis was conducted using four normalization techniques (min-max, max, sum, vector) (Vafaei *et al.*, 2022) and two weighting schemes (equal and entropy weighting) (Zhu *et al.*, 2020). Final species ranks were calculated as the mean of ranks across all combinations of normalisation and weighting methods.

To support final species selection, a hierarchical cluster analysis was performed using these mean rank values. A dendogram was generated using Past 5.2.2 software to visualise species rank similarity and grouping (Penn State Statistics Online, 2025). The species within the highest-ranking cluster (the final 7 species) were identified for the final literature review.

All rank calculations were performed in Microsoft Excel, and exploratory analysis was conducted using Past 5.2.2 software.

Literature review of the final shortlist

A literature review was conducted for the final seven species using Google Scholar. Searches combined Latin binomials with keywords including ‘introgression’, ‘population genetics’, ‘gene flow’, ‘local adaptation’, and ‘environmental correlations’. This review informed species-specific assessments of genetic risk and other restoration considerations.

Results

From consultations with 39 local authorities across Britain, 181 species of wildflower were identified as having been planted, 120 of which are defined as native in Britain (BSBI Plant Atlas 2020). The final shortlist are highlighted in Table 2, among the 28 species prioritized for further study based on the composite scores of the planting frequency and species rarity analysis.

Table 2. Shortlisted 28 species trait and composite scores.

species	Planting frequency	Relative rarity	Proximity to wild populations	Intraspecific variance	Dispersal ability	Outcrossing frequency	Pollinator specificity	Mean weighted sum rank (2dp)
Echium Vulgare L.	18	0.955813	0.44646	2	1	4	3	8.375
Galium Verum L.	30	0.735348	0.78008	1	1	2	3	10
Silene nutans L.	1	0.998977	0.534252	0	1	4	3	22.25
Leontodon hispidus L.	14	0.867	0.58151	0	2	4	2	13
Knautia Arvensis L.	20	0.882136	0.58113	1	0	3	2	19.875
Geranium sanguineum L.	1	0.983504	0.5196	0	0	3	1	27.125
Daucus carota	26	0.919044	0.47682	5	1	4	1	3.75
Primula Veris	28	0.82383	0.58686	1	0	5	3	9.625
Anthyllis vulneraria	10	0.940358	0.62038	4	2	2	4	4.75
Campanula glomerata	7	0.989875	0.22558	2	2	2	1	18.75
Ligusticum scoticum	2	0.991096	0.39157	0	1	2	2	26
Geranium pratense	21	0.874887	0.44721	3	1	5	2	6.25
Origanum vulgare	11	0.91754	0.66154	5	2	5	2	1
Silene flos-cuculi	11	0.843725	0.66776	1	3	4	3	5.75
Malva moschata	18	0.880163	0.686831	2	0	3	2	15.5
Rhinanthus minor	20	0.782555	0.69997	4	2	2	3	2.875
Betonica officinalis	14	0.89317	0.785865	1	0	1	3	21.625
Silaum silaus	3	0.981513	0.40545	1	0	1	1	27.875
Sanguisorba minor	15	0.953485	0.45587	2	1	0	0	24.125
Silene vulgaris	9	0.93202	0.51358	3	1	3	3	11.5
Centaurea scabiosa	9	0.932159	0.60663	1	3	6	2	3.875

Scabiosa columbaria	8	0.965709	0.45527	1	2	1	3	17.25
Salvia verbenaca	5	0.987673	0.4147	2	2	1	2	17.75
Sanguisorba officinalis	3	0.949827	0.348	1	2	2	2	22
Onobrychis viciifolia	4	0.978024	0.41334	2	0	5	2	20.375
Serratula tinctoria	2	0.982337	0.43421	3	2	4	1	10.875
Geranium sylvaticum	3	0.960836	0.3376	3	1	5	2	12.875
Verbascum nigrum	2	0.986097	0.42383	0	1	6	2	20.375

The final average ranks converged on a single branch of the dendogram, forming a cluster of the highest ranking species according to the multi-criteria aggregation framework (Figure 3).

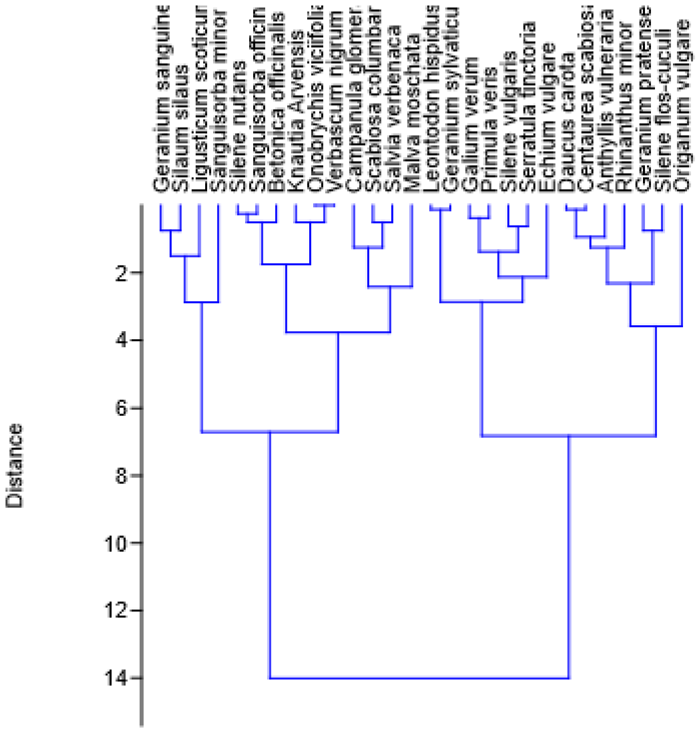

Figure 2. Cluster Analysis results showing a cluster of the final 7 species shortlist.

Seed Provenance and Supplier Practices

The use of genetically diverse, locally sourced seed in ecological restoration is widely recognized as best practice, with numerous studies highlighting its importance for maintaining adaptive potential and genetic integrity (Kiehl *et al.*, 2014; Basey *et al.*, 2015). Despite this, only 2 out of the 39 councils investigated in this study reported using directly sourced local-provenance seed in their planting schemes, with one council only sourcing seed locally for one species which it planted.

This predominant use of commercially sourced wildflower seed is of particular concern due to the current lack of regulation surrounding wildflower seed production and use in the UK (Lyall, 2024). Suppliers are under no formal obligation to consider provenance or genetic diversity, leaving buyers reliant on supplier claims. Nevertheless, 44% (Table 3) of councils with known suppliers sourced seed from companies that explicitly promote the use of wild and locally sourced material, notably Emorsgate Seeds and Scotia Seeds. Emorsgate Seeds claim to offer “completely wild” seed with guaranteed genetic variation (Emorsgate Seeds, 2024), while Scotia Seeds provide provenance-traceable wild seed (Scotia Seeds, 2025). One council, Denbighshire, went further by producing a bespoke local seed mix directly from regional flora.

Table 3. Table showing the number of councils that sourced wildflower seeds/turf from the identified suppliers/sources.

Supplier/source	Number of councils that used the supplier/source
John Chambers	2
Kew Garden	1
Scouse Flower House	1
Naturescape	3
Boston Seeds	3
Wildflower Turf	2
Pictorial meadows	2
Emorsgate Seeds	5
Origin Amenity	2
TurfOnline	1
MeadowMania	1
Landlife	1
Scotia Seeds	10
Rigby Taylor	2
Locally Sourced	2
Unknown	5

In contrast, other suppliers demonstrate minimal concern for provenance. Pictorial Meadows, for example, prioritizes aesthetic appeal and includes many non-native species in mixes with extended flowering seasons. Naturescape makes no mention of provenance or genetic considerations, and Boston Seeds offers only limited information too, although its species are primarily of native origin.

A negative correlation ($p < 0.01$) was observed between species rarity and planting frequency, suggesting that more commonly planted species tend to be less rare. This may reduce immediate concern over genetic risks for frequently used species, though it also highlights the underrepresentation of rarer species in public planting schemes.

Sensitivity Testing and Scoring Robustness

Sensitivity testing was conducted to evaluate the stability of species rankings across different normalization and weighting methods. Strong positive correlations ($p < 0.01$, Table 4 & 5) were found between all normalization techniques (min-max, max, sum, vector) and both weighting schemes (equal and entropy, t=0.92278, p<0.01), indicating methodological consistency.

Table 4. Correlations between the normalisation method rankings for all 28 shortlisted species Spearman's rank correlation statistics (entropy weighting)

Normalisation method	Min-max	Max	Sum	Vector
Min-max		0.87302	0.92649	0.97314
Max	0.87302		0.96208	0.94505
Sum	0.92649	0.96208		0.98824
Vector	0.97314	0.94505	0.98824	

Table 5. Correlations between the normalisation method rankings for all 28 shortlisted species Spearman's rank correlation statistics (equal weighting)

Normalisation method	Min-max	Max	Sum	Vector
Min-max		0.97865	0.96442	0.97318
Max	0.97865		0.97318	0.9896
Sum	0.96442	0.97318		0.99124
Vector	0.97318	0.9896	0.99124	

Species rankings within the final 7 species shortlist were generally robust. Across all normalization and weighting combinations, the maximum variation in rank was four positions. While most other species' rankings remained stable, though with some variation, across normalisation and weighting methods, *Origanum vulgare* consistently held the top rank under every scenario.

One exception was *Geranium pratense*, which ranked higher under equal weighting but fell outside the top seven when entropy weighting was applied.

Final shortlist and literature review

1. *Origanum vulgare* (Wild Marjoram/Oregano), Mean Rank: 1

Origanum vulgare is a perennial herb with highly colourful (mostly pink-purple) small flowers arranged in a whorl inflorescence (Forbes, 2012a., Fitter & Peat, 1994). Its extreme variability in floral colour and morphology has led to its classification as a polymorphic species (Forbes, 2012a), thus scoring highly on variability. Its reproductive traits, including protandry and self-sterility, contribute to a high outcrossing rate (Fitter & Peat, 1994; Forbes, 2012a). In Britain and Ireland, four subspecies are recognised: subsp. *vulgare, hirtum, virens* and *viride* (Forbes, 2012a). O. vulgare subsp. *glandulosum* has also been discussed below where studies have been conducted the environmental variation of its populations.

Genetic studies support this variability. Microsatellite analysis comparing pre-established and introduced populations found increased inbreeding coefficients in the latter (Alekseeva et al., 2020; Helsen et al., 2013). Provenance differentiation is well documented in *O. vulgare* subsp. *glandulosum*, with significant genetic structuring between populations (Mechergui et al., 2016). Looy et al. (2009) reported high within-population diversity and strong differentiation between fragmented populations, while Azizi et al. (2012) confirmed high genetic and chemical variability among individuals. Tascioglu (2022) demonstrated effective use of molecular markers to track gene flow.

Introgression has been observed between *O. onites* and *O. vulgare* subsp. *hirtum* (Bariotakis et al., 2016), further supporting its hybridisation risk. Environmental variability is also well documented as Gavalas (2011) identified distinct ecotypes of *O. vulgare* subsp. *hirtum*, and Mechergui et al. (2017) showed that populations of *O. vulgare* subsp. *glandulosum* can be discriminated morphologically and molecularly. Chemical variation has been linked to geography (Goyal et al., 2021) and altitude (Giuliani et al., 2013). Non-local provenance has been negatively correlated with viability (Myagkikh et al., 2021; Kokkini et al., 1994).

2. *Rhinanthus minor* (Yellow Rattle), Mean Rank: 2.875

Rhinanthus minor is an annual hemiparasite widely used in restoration due to its parasitic function (Houston & Wolff, 2012). It is highly variable, with numerous ecotypes and variants (Forbes, 2012b).

Introgression has been observed with *R. angustifolius* (Wesselingh & Natalis, 2012; Ducarme & Wesselingh, 2005, 2012; Ducarme et al., 2010), *R. major* (Wesselingh et al., 2019; Mirzaei & Wesselingh, 2021), and *R. serotinus* (Kwak, 1980). Genetic comparisons between UK and European populations showed minor differences, but no clear structuring by subspecies or habitat (Houston & Wolff, 2012). Sullivan et al. (2019) emphasized the need to maintain large populations to preserve genetic diversity, especially in fragmented landscapes.

Microsatellite markers have been developed for population studies (Houston & Wolff, 2009). *R. minor* was found to have the second-lowest genetic variation among *Rhinanthus* species (Talve et al., 2013), but displays ecotypic variation (Westbury, 2004). Restricted genetic variation has been shown to constrain elevational range expansion (Ensing, 2019). Seed quality has been linked to restoration success and plant fitness (Marin et al., 2018).

3. *Daucus carota* (Wild carrot), Mean Rank: 3.75

Daucus carota, is an umbellifer that may behave as an annual or persist for several years before fruiting (Forbes, 2012c). It is widely planted and described as highly variable, both environmentally and genetically, with polymorphic traits across populations (Forbes, 2012c). Its cultivated relative (*D. carota* subsp. *sativus*) has made it a model species for studying wild-cultivated introgression.

Numerous studies document gene flow between wild and cultivated carrots. Introgression has been observed at both molecular and phenotypic levels, with hybrids persisting in natural habitats and cultivar alleles remaining detectable over time (Hauser & Shim, 2007; Mandel et al., 2016; Umehara et al., 2005). Long-distance pollen dispersal and high outcrossing rates contribute to this gene flow, raising concerns about the genetic integrity of wild populations (Rong et al., 2010). Hybridisation has also been shown to influence life history traits, including flowering time and survival, with potential fitness consequences (Van Dijk et al., 2016).

Studies comparing wild and introduced populations reveal significant differences in phenotypic traits (Reiker et al., 2020), while others report negligible genetic differentiation and no clear signs of local adaptation, suggesting non-local provenance may not always compromise restoration outcomes (Reiker et al., 2020). However, the persistence of cultivar alleles and the ecological plasticity of *D. carota* underscore the need for greater care with restoration strategies.

4. *Centaurea scabiosa* (Greater knapweed), Mean Rank: 3.875

Centaurea scabiosa is a perennial wildflower with high dispersal ability, producing 1,000–10,000 seeds per plant with pappus extensions (Fitter & Peat, 1994). It is obligately outcrossing and self-incompatible, scoring highly on reproductive isolation (Fitter & Peat, 1994).

Genetically, it exhibits low variation between populations, suggesting high gene flow (Ehlers, 2008). However, within-genus hybridization has been documented (Vonica & Cantor, 2011), indicating potential for introgression under certain conditions.

5. *Anthyllis vulneraria* (Kidney vetch), Mean Rank: 4.75

Anthyllis vulneraria is a usually perennial, highly polymorphic wildflower with up to 24 subspecies. Its wind-dispersed seeds and reliance on large bees for pollination contribute to high scores in dispersal, variability, and pollinator specialization (Forbes, 2012d).

Genetic studies reveal strong geographic structuring. Lukaszweska et al. (1978) identified three genetically distinct groups, while Helsen et al. (2015) observed spatial genetic structure and inbreeding in introduced populations. Subarctic populations show both diversity and differentiation (Daco et al., 2022), with adaptive differentiation along elevational and latitudinal gradients (Daco, 2023). Environmental variation is a key driver of local adaptation (Kesselring et al., 2019), supported by studies on demographic variation (Sterk, 1975) and individual responses to environmental factors (Daco et al., 2021).

Introduced populations show lower genetic diversity but low differentiation, suggesting high gene flow (Helsen et al., 2016). Habitat heterogeneity also influences local adaptation (Kesselring & Schweiz, 2017).

6. *Silene flos-cuculi* (Syn. *Lychnis flos-cuculi,* Ragged Robin), Mean Rank: 5.75

Silene flos-cuculi is a perennial wildflower with small terminal flowers and tubercled seeds (Fitter & Peat, 1994) (with small cell protrusions or bumps on the seed surface which may help seeds adhere to animal coats (Rodriguez-Lorenzo *et al.*, 2023)), contributing to high dispersal ability and proximity to planting sites.

Hybrid success and introgression within the genus have been documented (Jiang, 2011; Jiang et al., 2014; Kruckeberg, 1962).

Comparative studies between wild and introduced populations show genetic distinctiveness and elevated inbreeding in the latter (Aavik et al., 2012). Conrady et al. (2023) found rapid trait evolution in cultivated lineages. Fragmentation studies consistently report negative impacts, including inbreeding depression and reduced local adaptation (Vergnerie, 2006; Galeuchet et al., 2005; Rossum, 2009; Aavik et al., 2013; Dulya & Mikryukov, 2015). Aavik et al. (2013) emphasized the importance of spatially coherent population networks for maintaining genetic diversity.

However, Hauser & Loeschcke (1994) found no clear fitness relationship with population size or isolation. Other studies explored environmental correlations (Hoehn, 2006), outbreeding effects (Leimu & Fischer, 2010), and linear fitness decline with increased inbreeding (Hauser & Loeschcke, 1995). Regional adaptation and restoration failure of non-local populations were reported by Bucharova et al. (2016), while seed quality varied significantly by origin (Biere et al., 1989).

Phenological and fitness differences between sown and natural populations support the use of local seed (Aavik et al., 2013; Biere, 1991), echoed by Bowman et al. (2008). Gene flow between natural and sown populations was low, likely due to landscape connectivity (Aavik et al., 2013). Physiological differences among genotypes were also observed (Biere, 1991; Biere, 1996). Genetic studies identified polymorphic loci useful for population tracking (Galeuchet et al., 2002). Geographic correlations in germination were noted (Thompson, 1970).

7.*Geranium pratense* (Meadow cranesbill), Mean Rank: 6.25

Geranium pratense is a perennial wildflower scoring highly in outcrossing rate and planting frequency due to its gynodioecious and protandrous reproductive system (Fitter & Peat, 1994). Its large, vibrant flowers enhance pollinator attraction and restoration appeal (Conrady et al., 2023).

Interspecific hybridisation within the genus has been demonstrated, with embryo rescue and AFLP markers confirming successful crosses and hybrid viability (Akbarzadeh et al., 2024). Genetic distance between parental species has been shown to predict hybrid success, with a threshold value (Jaccard < 0.8) facilitating viable offspring (Akbarzadeh et al., 2021).

Despite its high outcrossing rate, *G. pratense* exhibits limited gene flow and strong spatial genetic structure, with significant differentiation among populations and evidence of adaptive divergence (Michalski & Durka, 2012). These findings support the use of locally adapted seed sources and caution against broad provenance mixing in restoration contexts.

Discussion

This study reveals a critical issue in current restoration practice: while a substantial proportion of councils source wildflower seed from suppliers that claim to prioritize local provenance and genetic diversity, the species being planted often exhibit traits that heighten their vulnerability to intraspecific hybridisation. Among the 28 species examined (Table 1), many are relatively rare or geographically scattered, and several display high outcrossing rates, documented polymorphism, or histories of introgression, all of which increase the likelihood of genetic mixing when planted near wild populations.

These findings carry important biological implications. Restoration schemes that overlook species-level genetic risk may inadvertently facilitate the erosion of local genotypes, disrupt adaptive trajectories, or introduce maladaptive alleles into wild populations (Bischoff et al. 2010, Keller et al, 2001). The presence of traits that elevate hybridisation risk and significance in commonly planted species underscores the need for restoration decisions to be informed not only by aesthetic or ecological function, but by evolutionary and genetic considerations.

While considerable effort was made to ground trait scoring in published scientific literature and ecological reasoning, some limitations remain. The conversion of qualitative trait descriptions into quantitative scores required subjective judgment, and these scores should be interpreted as relative indicators rather than absolute measures of risk. Additionally, the weighted sum aggregation method used to rank species is one of several available in multi-criteria decision analysis, and no universal consensus exists on the optimal approach. However, given its simplicity and transparency, the method was deemed appropriate for this exploratory study.

Beyond local authorities, many seed suppliers also sell to private individuals and corporate clients who may unknowingly distribute wildflowers with inappropriate genetic profiles. Although these plantings occur at smaller scales, their cumulative impact, particularly in fragmented landscapes or near sensitive populations, warrants further investigation. Future research should assess the genetic consequences of non-regulated planting across sectors, including commercial landscaping and community-led greening initiatives.

The absence of regulatory standards for wildflower seed provenance and genetic quality represents a significant gap in UK biodiversity policy. Without clearer guidance or enforcement mechanisms, restoration efforts risk becoming ecologically damaging, and genetically disruptive. To safeguard the integrity of wild plant populations, restoration must become a scientifically grounded practice that respects the genetic and ecological complexity of the species it seeks to conserve.

Conclusion

This study developed and applied a multi-criteria scoring framework to assess hybridisation risk between wild and commercial wildflower populations across 28 wildflower species. By including seven criteria: planting frequency by local councils, species rarity, proximity to protected areas, intraspecific variation, dispersal ability, outcrossing rate, and pollinator specificity, the framework enabled species prioritization grounded in both published literature and original data collection. Beyond species-specific rankings, the study also considered generalised hybridisation risk across the full cohort, revealing broader hybridisation vulnerability and ecological concerns.

Seven species: *Daucus carota*, *Geranium pratense*, *Origanum vulgare*, *Centaurea scabiosa*, *Anthyllis vulneraria*, *Silene flos-cuculi*, and *Rhinanthus minor*, emerged as particularly significant. Each exhibited complex trait profiles, each with a unique set of distinguishing criteria. Their elevated composite scores reflect not only species-level risk but also broader themes identified in the scientific literature, such as the importance of genetic diversity, the risks of population fragmentation as well as close population proximity, and the ecological consequences of provenance mismatch.

Bibliography

Aavik T, Bosshard D, Edwards JP, Holderegger R, Billeter R. 2013. Fitness in Naturally Occuring and Restored Populations of a Grassland Plant Lychnis flos-cuculi in a swiss Agricultural Landscape. Restoration Ecology 22(1): 98-106.

Aavik T, Edwards JP, Holderegge R, Graf R, Billeter R. 2012. Genetic consequences of using seed mixtures in restoration: a case study of a wetland plant Lychnis flos-cuculi. Biological Conservation 145(1): 195-204.

Aavik T, Holderegger R, Bolliger J. 2013. The structural and functional connectivity of the grassland plant Lychnis flos-cuculi. Heredity 112: 471-478

Aavik T, Holderegger R, Edwards JP, Billeter R. 2013. Patterns of contemporary gene flow suggest low functional connectivity of grasslands in a fragmented agricultural landscape. Journal of Applied Ecology 50(2): 395-403

Akbarzadeh M, Van Laere K, De Keyser E, Van Huylenbroeck J, Werbouck OPS, Dhooge E. 2024. Interspecific hardy geranium progenies: morphological characterization and genetic evaluation. *Horticulturae* 10(7):723.

Akbarzadeh M, Van Laere K, Leus L, De Riek J, Van Huylenbroeck J, Werbrouck OPS, Dhooge E. 2021. Can knowledge of genetic distances, genome sizes and chromosome numbers support breeding programs in hardy geraniums? *Genes* 12(5):730.

Alekseeva M, Zagorcheva Tz, Atanassov I, Rusanov K. 2020. Origanum vulgare L. - a review on genetic diversity, cultivation, biological activities and perspectives for molecular breeding. Bulgarian Journal of Agricultural Science 26: 1183-1197.

Amabogha NO, Garelick H, Jones H, Purchase D. 2023. Combining phytoremediation with bioenergy production: developing a multi-criteria decision matrix for plant species selection. Environmental Science and Pollution Research 30: 40698-40711.

ArcGIS Online. 2016. Forest Reproductive Materials Regions Of Provenance. URL https://data-forestry.opendata.arcgis.com/datasets/8abdd8b5963140ba85309164ced05460_0/explore. [accessed 2 July 2025]

Azizi A, Hadian J, Gholami M, Friedt W, Honermeier B. 2012. Correlations between Genetic, Morphological, and Chemical Diversities in a Germplasm Collection of the Medicinal Plant Origanum vulgae L. Chemistry & Biodiversity 9(12): 2784-2801.

Bariotakis M, Koutroumpa K, Karousou R, Pirintsos AS. 2016. Environmental (in)dependence of a hybrid zone: Insights from molecular markers and ecological niche modeling in a hybrid zone of Origanum (Laiaceae) on the island of Crete. Ecology and Evolution 6(24): 8727-8739.

Barry, C. and Hodge, S. (2023) You Reap What You Sow: A Botanical and Economic Assessment of Wildflower Seed Mixes Available in Ireland. Conservation, 3(1), pp. 73-86.

Basey CA, Fant BJ, Kramer TA. 2015. Producing native plant materials for restoration: 10 rules to collect and maintain genetic diversity. Native Plants Journal 16(1): 37-52

Biere A. 1991. Parental effects in Lychnis flos-cuculi. I: Seed size, gemination and seedling peformance in a controlled environment. Journal of Evolutionary Biology 4(3): 447-465.

Biere A. 1996. Intra-specific variation in relative growth rate: impact on competitive ability and performance of Lychnis flos-cuculi in habitats differing in soil fertility. Plant and soil 182: 313-327.

Biere A. 1991. Phenotypic variation in Lychnis flos-cuculi: An ecological genetic analysis. PhD Thesis. University of Groningen, Groningen, Netherlands.

Biere A, Cappers R, Andel VJ. 1989. Quantitative and qualitative aspects of fecundity in Lychnis flos-cuculi. Acta Botanica Neerlandica 38(2): 203-218

Bischoff, A., Steinger, T. and Muller-Scharer, H. (2010) The Importance if Plant Provenance and Genotypic Diversity of Seed Material Used for Ecological Restoration. Restoration Ecology, 18(3), pp. 338-348.

Bowman G, Perret C, Hoehn S, Galeuchet JD, Fischer M. 2008. Habitat fragmentation and adaptation: a reciprocal replant-transplant experiment among 15 populations of Lychnis flos-cuculi. Journal of Ecology 96(5): 1056-1064.

BSBI. 2025. BSBI maps. Available at: https://database.bsbi.org/maps/. [accessed 12 July 2025]

Bucharova A, Michalski S, Hermann J, Heveling K, Durka W, Holzel N, Kollmann J, Bossdorf O. 2016. Genetic differentiation and regional adaptation among seed origins used for grassland restoration: lessons from a multispecies transplant experiment. Journal of Applied Ecology 54(1): 127-136.

Burton, J.P. and Burton, C.M. (2002) Promoting Genetic Diversity in the Production of Large Quantities of Native Plant Seed. Ecological Restoration., 20(2), p. 117.

Conrady M, Lampei C, Bossdorf O, Bucharova A. 2023. Plants cultivated for ecosystem restoration can evolve toward a domestication syndrome. Proceedings of the National Academy of Sciences 120(20): e2219664120

Conrady M, et al. 2023. Trait evolution in cultivated lineages of *Geranium pratense*. *Journal of Ecology 111(12): 2750-2780*.

Daco L, Colling G, Matthies D. 2021. Altitude and latitude have different effects on population characteristics of the widespreas plant Anthyllis vulneraria. Oecologia 197: 537-549.

Daco L, Matthies D, Hermant S, Colling G. 2022. Genetic diversity and differentiation of populations of Anthyllis vulneraria along elevational and latitudinal gradients. Ecology and Evolution 12(8): e9167

Daco L. 2023. Plasticity and genetic variation along elevational and latitudinal gradients: Insights from the widespread plant Anthyllis vulneraria. PhD Thesis. Philipps-Universitat Marburg, Marburg, Germany.

Des Roches S, Post MD, Turley EN, Bailey KJ, Hendry PA, Kinnison TM, Schwaitzer AJ, Palkovacs PE. 2017. The ecological importance of intraspecific variation. Nature Ecology & Evolution 2: 57-64.

Ducarme V, Wesselingh AR. 2012. Outcrossing rates in two self-compatible, hybridising Rhinanthus species: implications for hybrid formation. Plant Biology 15(3): 541-547.

Ducarme V, Wesselingh AR. 2005. Detecting hybridisation in mixed populations of Rhinanthus angustifolius. Folia Geobotanica 40: 151-161.

Ducarme V, Vranken J, Wesselingh AR. 2010. Hybridisation in Annual Plants:Patterns and Dynamics During a Four-Year Study in Mixed Rhinanthus Populations. Folia Geobotanica 45: 387-405.

Dulya VO, Mikryukov SV. 2015. Genetic variation and selfing rate in Lychnis flos0cuculi along an industrial pollution gradient. New Phytologist 209(3): 1083-1095.

Dulya OV, Mikryukov VS, Hlystov IA. 2015. Interspecific differences in determinants of plant distribution in industrial polluted areas: Endogenous spatial autocorrelation vs. environmental parameters. Plant and Soil 394: 329-342.

Ehlers KB. 2008. Variation in fruit set within and among natural populations of the self-incompatible herb Centaurea scabiosa (Asteraceae). Nordic Journal of Botany 19(6): 653-663.

Emorsgate Seeds. 2024. Wild Flower Seeds and Seed Mixtures. URL https://wildseed.co.uk/. [accessed 26 July 2025]

Ensing JD. 2019. Evolutionary Constraints: Phenology and Elevational Range Limits in an Annual Plant. PhD Thesis. Queen's University, Kingston, Ontario, Canada.

Fitter AH, and Peat HJ. 1994. The Ecological Flora Database. J. Ecol 82: 415-425. Also available from: http://www.ecoflora.co.uk [accessed 29 July 2025]

Forbes R. 2012a. Farmanagh Species Accounts: Origanum vulgare L., Wild Marjoram. Botanical Society of Britain and Ireland. Available from: https://fermanagh.bsbi.org/origanum-vulgare-l?q=wild%20marjoram [accessed 1 August 2025]

Forbes R. 2012b. Farmanagh Species Accounts: Rhinanthus minor L., Yellow-Rattle. Botanical Society of Britain and Ireland. Available from: https://fermanagh.bsbi.org/rhinanthus-minor-l?q=yellow%20rattle [accessed 1 August 2025]

Forbes R. 2012c. Farmanagh Species Accounts:Daucus carota subsp. carota L., Wild Carrot. Botanical Society of Britain and Ireland. Available from: https://fermanagh.bsbi.org/daucus-carota-subsp-carota-l?q=wild%20carot [accessed 1 August 2025]

Forbes R. 2012d. Farmanagh Species Accounts: Anthyllis vulnearia L., Kidney Vetch. Botanical Society of Britain and Ireland. Available from: https://fermanagh.bsbi.org/anthyllis-vulneraria-l#:~:text=A.%20vulneraria%20is%20a%20more%20important%20member%20of,south-facing%20screes%20to%20the%20W%20of%20Lough%20Erne. [accessed 1 August 2025]

Galeuchet DJ, Husi R, Perret C, Fischer M, Gautschi B. 2002. Characterisation of microsatellite loci in Lychnis flos-cuculi (Caryophyllaceae). Molecular Ecology Notes 2(4): 491-492.

Galeuchet DJ, Perret C, Fischer M. 2005. Microsatellite variation and structure of 28 populations of the common wetland plant, Lychnis flos-cuculi L., in a fragmented landscape. Molecular Ecology 14(4): 991-1000

Galeuchet DJ, Perret C, Fischer M. 2005. Performance of Lychnis Flos-cuculi from Fragmented Populations Under Experimental Biotic Interations. Ecology 86(4): 1002-1011.

Gamba D, Muchhala N. 2020. Global patterns of population genetic differentiation in seed plants. Molecular Ecology 29: 3413-3428

Gavalas PN, Kalburtji LK, Kokkini S, Mamolos PA, Veresoglou SD. 2011. Ecotypic variation in plant characteristics for Origanum vulgare subsp. Hirtum populations. Biochemical Systematics and Ecology 39(4-6): 562-569.

Giuliani C, Maggi F, Papa F, Bini ML. 2013. Congruence of Phytochemical and Morphological Profiles along an Altitudinal Gradient in Origanum vulgare ssp. Vulgare from Venetican Region (NE Italy). Chemistry & Biodiversity 10(4): 569-583.

Goyal S, Tewari G, Pandey HK, Kumari A. 2021. Exploration of Prodictivity, Chemical Composition, and Antioxidant Potential of Origanum vulgare L. Grown at Different Geographical Locations of Western Himalaya, India. Journal of Chemistry 2021(1): 6683300.

Grebenstein C, Kos PS, de Jong JT, Tamis MLW, de Snoo RG. Morphological markers for the detection of introgression from cultivated into wild carrot (Daucus carota L.) reveal dominant domestication traits. 2012. *Plant Biology* 15(3):531-540.

Hauser PT, Loeschcke V. 1994. Inbreeding depression and mating-distance dependent offspring fitness in large and small populations of Lychnis flos-cuculi (Caryophyllaceae). Journal of Evolutionary Biology 7(5): 609-622

Hauser PT, Loeschcke V. 1995. Inbreeding depression in Lychnis flos-cuculi (Caryophyllaceae): effects of different levels of inbreeding. Journal of Evolutionary Biology 8(5): 589-600.

Hauser TP, Shim SI. 2007. Survival and flowering of hybrids between cultivated and wild carrots (*Daucus carota*) in Danish grasslands. *Environmental Biosafety Research* 6(4):237–247.

Helsen K, Jacquemyn H, Hermy M, Vandepitte K, Honnay O. 2013. Rapid Buildup of Genetic Diversity in Founder Populations of the Gynodioecious Plant Species Origanum vulgare after Semi-Natural Grassland Restoration. PLoS ONE 8(6): e67255.

Helsen K, Honnay O, Hermy M. 2016. The genetic consequences of species colonisation following calcerous grassland restoration. Consev Genet 17:105-117.

Herbert R, Samuel S, Gordon Patterson. 1999. Using Local Stock for Planting Native Trees and Shrubs. Forestry Comission, Edinburgh.

Hoehn S. 2006. Multi-year Demography and Ecological Genetics of the Common Plant Lychnis flos-cuculi in a Fragmented Landscape. PhD Thesis. Universitat Zurich, Zurich, Switzerland.

Houston K, Wolff K. 2012. Rhinanthus minor population genetic structure and subspecies: Potential seed sources of a keystone species in grassland restoration projects. Perspectives in Plant Ecology, Evolution and Systematics 14(6): 423-433.

Houston K, Wolff K. 2009. Eight polymorphic microsatellite markers for Rhinanthus minor. Molecular Ecology Resources 9(1): 174-176.

Jefferson GR, Wagner M, Sullivan E, Tatarenko I, Westbury BD, Ashton P, Hulmes L. 2023. Biological Flora of Britain and Ireland: Geranium pratense. Journal of Ecology 111(12): 2750-2780.

Jiang L. 2011. Hybridization, Genetic Manipulation, and Asexual Propogation of Lychnis Species. Maters Thesis. Oklahoma State University, Stillwater, Oklahoma, USA.

Jiang L, Wang Y, Dunn LB. 2014. Cross-compatibility in Intraspecific and Interspecific Hybridisation within Lychnis and Integeneric Hybridisation between Lychnis and Silene. HortScience 49(9): 1136-1141.

Keller M, Kollmann J, Edwards JP. 2001. Genetic intogression from distant provenances reduces fitness in local weed populations. Journal of Applied Ecology 37(4): 647-659

Kesselring H, Hamann E, Armbruster JFG, Stocklin J, Scheepens JF. 2019. Local adaptation is stronger between than within regions in alpine populations of Anthyllis vulneraria. Evolutionary Ecology 33: 737-750.

Kesselring H, Schweiz B. 2017. Local Adaptation and Phenotypic Plasticity in Alpine Plants. PhD Thesis. Universitat Basel, Basel, Switzerland.

Kiehl K, Kirmer A, Shaw N, Tischew S. 2014. Guidelines for Native Seed Production and Grassland Restoration. Newcastle, UK: Cambridge Scholars Publishing.

Kokkini S, Karousou R, Vokou D. 1994. Pattern of geographic variations of Origanum vulgare trichomes and essential oil content in Greece. Biochemical Systematics and Ecology 22(5): 517-528.

Kruckeberg AR. 1962. Integeneric Hybrids in the Lychnideae (Caryophyllaceae). Brittonia 14(4): 311-321.

Kwak MM. 1980. Artificial and natural hybridisation and introgression in Rhinanthus (Scrophulariaceae) in relation to bumblebee pollination. TAXON 29(5-6): 613-628.

Leimu R, Fischer M. 2010. Between-Population Outbreeding Affects Plant Defence. PLoS ONE 5(9): e12614.

Looy VK, Jacquemyn H, Breyne P, Honnay O. 2009. Effects of flood events on the genetic structure of riparian populations of the grassland plant origanum vulgare. Biological conservation 142(4): 870-878.

Lukaszweska K, Sweykowska J, Kaczmarek Z. 1978. Analysis of the variability of nine natural Anthyllis vulneraria s. l. populations. Part II. Biometry of flowers. Acta Societatis Botanicorum Poloniae 47(4): 325-342.

Lyall A. 2024. Genetic integrity needed for Biodiversity Net Gain to flower. Earlham Institute. Available at: https://www.earlham.ac.uk/articles/genetic-integrity-needed-biodiversity-net-gain-flower [accessed 27 July 2025]

Mandel JR, Ramsey AJ, Iorizzo M, Simon PW. 2016. Patterns of gene flow between crop and wild carrot (*Daucus carota*) in the United States. *PLoS ONE* 11(9):e0161971.

Marin M, Laverack G, Matthews S, Powell AA. 2018. Germination characteristics of Rhinanthus minor influence field emergence, competitiveness and potential use in restoration projects. Plant Biology 21(3): 470-479.

Mechergui K, Jaouadi W, Bekele WA, Larbi M, Friedt K, Friedt W. 2016. genetic structure and differentiation among oregani[origanum vulgare subsp. Glandulosum (Desf. Letswaart] provenances from North Africa: bioinformatic approaches cause systematic bias. Genetic Resource Crop Evolutions 64: 717-732.

Mechergui K, Khaldi S, Jaouadi W, Friedt W, Chalh A. 2017. Morphological and Molecular Evolution of Genetic Diversity of Wild Tunisian Oregano, Origanum vulgare L. subsp. Glandulosum Desf. Letswaart. Asian Journal of Biology 3(2): 1-15

Mendez, M., Vogeli, M., Tella, L.J. and Godoy, A.J. (2014) Joint effects of population size and isolation on genetic erosion in fragmented populations: finding fragmentation thresholds for management. Evol Appl., 7(4), pp. 506-518.

Michalski SG, Durka W. 2012. Assessment of provenance delineation by genetic differentiation patterns and estimates of gene flow in *Geranium pratense*. *Conservation Genetics* 13:581–592.

Mijnsbrugge V.K., Bischoff A., Smith B. 2010. A question of origin: Where and how to collect seed fo ecological restoration. Basic and Applied Ecology vol 11 300-311

Mirzaei K, Wesselingh AR. 2021. Development of a large set of diagnostic SNP markers using ddRAD-seq to study hybridisation in Rhinanthus major and R.minor (Orobanchaceae). Conservation Genetics Resources 13: 31-33.

Myagkikh E, Babanina S, Mishnev A, Radchenko L, Pashtetskiy V, Nevkrytaya N, Loretts O. 2021. Ecological Adaptability of Some Cultivars and Breeding Samples of Origanum vulgare L. Agronomy 12(1): 16.

Natalis CL, Wesselingh AR. 2012. Post-pollination barriers and their role in asymmetric hybridisation in Rhinanthus (Orobanchaceae). American Journal of Botany 99(11): 1847-1856.

Natural England. 2024. SSSI Regulation. [WWW document] [accessed 15 July 2025]

Neequaye M, Kellenberger TR, Collier R, Paajanen P, Antoniou-Kourounioti R, Wenzell EK, Hill L, Schluter MP, Byers JRPK. 2025. John Innes Centre. Pollinator-relevant floral traits underlie bidirectional hybridisation in the orchid genus Gymnadenia. [WWW document] URL https://www.jic.ac.uk/research-impact/publications/pollinator-relevant-floral-traits-underlie-bidirectional-hybridisation-in-the-orchid-genus-gymnadenia/ [accessed 15 July 2025]

ONS Geography. 2022. UK: Local authority districts, counties and unitary authorities, 2022. URL https://geoportal.statistics.gov.uk/documents/23169ce9c3c94fd38d93fd9882c1e471/explore. [Accessed 2 July 2025]

Penn State Statistics Online. (2025). Lesson 14: Cluster Analysis. Available at: https://online.stat.psu.edu/stat505/book/export/html/742 [accessed 1 August 2025]

Rehman S, Khan AS. 2017. Multi-Criteria Wind Turbine Selection using Weighted Sum Approach. International Journal of Advanced Computer Science and Applications 8(6):128-132

Rejeb-Mzah BI, Jaubert N, Vincent A, Ajerame Z. 2025. Quantifying Biodiversity Loss Risk. [WWW document] URL https://betterinsurancenetwork.com/wp-content/uploads/2025/02/BNP_Quantifying-biodiversity-loss-risk.pdf. [accessed 20 July 2025]

Reiker J, Rühl AT, Wissemann V, Gemeinhüzer B. 2020. Intraspecific phenotypic variability of *Daucus carota* used for restoration purposes. *Acta Botanica Hungarica* 62(1–2):137–150.

Reiker J, Schulz B, Wissemann V, Gemeinholzer B. 2015. Does origin always matter? Evaluating the influence of nonlocal seed provenances for ecological restoration purposes in a widespread and outcrossing plant species. Ecology and Evolution 5(23): 5642-5651.

Richards MC, Church S, McCauley ED. 1999. The Influence of Population Size and Isolation on Gene Flow by Pollen in Silene alba. Evolution 53(1): 63-73.

Rodriguez-Lorenzo LJ, Martin-Gomez JJ, Juan A, Tocino A, Cervantes E. 2023. Quantitative Analysis of Seed Surface Tubercles in *Silene* Species. Plants 2023, 12(19), 3444.

Rong J, Janson S, Umehara M, Ono M, Vrieling K. 2010. Historical and contemporary gene dispersal in wild carrot (Daucus carota ssp. Carota) populations. Annals of Botany 106(2): 285-296.

Rossum VF. 2009. Conservation of Wet Meadow Species in an Urban Context: Lychnis flos-cuculi as Study Case. Belgian Journal of Botany 142(2): 98-110.

Sampson FJ, Byrne M. 2008. Outcrossing between an agroforestry plantation and remnant native populations of Eucalyptus loxophleba. Mulecular Ecology 17: 2769-2781

Sapir, Y., Brunet, J., Byers, L.D., Imbert, E., Schonenberger,J. and Staedler, Y. (2019) Floral evolution: Breeding systems, pollinators, and beyond. International Journal of Plant Sciences., 180(9), pp. 929-933.

Schindelin, J., Arganda-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T., … Cardona, A. (2012). Fiji: an open-source platform for biological-image analysis. *Nature Methods*, *9*(7), 676–682

Scotia Seeds. 2025. About Us. URL https://www.scotiaseeds.co.uk/about-us/. [accessed 26 July 2025]

Smith S, Rausher MD. 2011. Gene loss and parallel evolution contribute to species difference in flower color. Molecular Biology and Evolution 28: 2799–2810.

Sterk AA. 1975. Demographic studies of Anthyllis vulneraria L. in the Netherlands. Acta botanica neerlandica 24(3/4): 315-337.

Sullivan RE, Barker C, Powell I, Ashton AP. 2019. Genetic diversity and connectivity in fragmented populations of Rhinanthus minor in two regions with contrasting land-use. Biodiversity and Conservation 28: 3159-3181.

Talve T, McGlaughlin EM, Helenurm K, Wallace LE, Oja T. 2013. Population genetic diversity and species relationships in the genus Rhinanthus L. based on microsatellite markers. Plant Biology 16(2): 495-502.

Tascioglu T. 2022. Molecular Genetic Analyses in Origanum (Lamiaceae) Taxa in Turkiye. PhD thesis, Izmir Institute of Technology, Izmir, Turkiye.

Thompson PA. 1970. Germination of Species of Caryophyllaceae in Relation to their Geographic Distribution in Europe. Annals of Botany 34(2): 427-449.

Tofallis C. 2014. Add or Multiply? A Tutorial on Ranking and Choosing with Multiple Criteria. INFORMS Transactions on Education 14(3):109-119.

Turner, G.K., Huang, I.D., Cronk, B.C.Q. and Rieseberg, H.L. (2017) Homogenization of Populations in the Wildflower, Texas Bluebonnet (Lupinus texensis).Journal of Heredity, 109(2), pp. 152-161.

Umehara M, Eguchi I, Kaneko D, Ono M, Kamada H. 2005. Evaluation of gene flow and its environmental effects in the field. *Plant Biotechnology* 22(5):497–504.

Vafaei N, Ribeiro AR, Camarinha-Matos ML. 2022. Assessing Normalisation Techniques for Simple Additive Weighting Method. Procedia Computer Science 199: 1229-1236.

Van Dijk H, et al. 2016. Demography and life history of *Daucus carota* populations in the Netherlands. *Plant Ecology* 217(6):729–744

Vergnerie G. 2006. Experimental Ecological Genetics of Fragmented Populations of the Common Plant Lychnis flos-cuculi L. PhD Thesis. Universitat Zurich, Zurich, Switzerland.

Vonica G, Cantor M. 2011. Problems and conflicts in the identification of Centaurea species. Brukenthal. Acta Musei 3: 61-68.

Wesselingh AR, Horcicova S, Mirzaei K. 2019. Fitness of reciprocal F1 hybrids between Rhinanthus minor and Rhinanthus major under controlled conditions and in the field. Journal of Evolutionary Biology 32(9): 931-942.

Wesselingh AR, Natalis CL. 2012. Shared pollinators and pollen transfer dynamics in two hybridising species, Rhinanthus minor and R. angustifolius. Oecologia 170: 709-721.

Westbury BD. 2004. Rhinanthus Minor L. Journal of Ecology 92(5): 906-927.

Zhu Y, Tian D, Yan F. 2020. Effectiveness of Entropy Weight Method in Decision-Making. Mathematical Problems in Engineeing vol 2020: 1-5.