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To cite this version:

Juliette Ducrettet, Sandrine Maurice, Eric Imbert. How much do we know and how much do we care about genetic diversity of threatened plants? A case study from the French flora. Botany Letters, In press, 170 (1), pp.110-118. 10.1080/23818107.2022.2125902 . hal-03786687

HAL Id: hal-03786687
https://hal.umontpellier.fr/hal-03786687v1

Submitted on 23 Sep 2022

How much do we know and how much do we care about genetic diversity of threatened plants? A case study from the French flora.

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Author contributions : SM and EI conceived the ideas. JD, JD, SM and EI designed the methodology; JD collected and analysed thedata and led the writing of the manuscript. All authors contributed critically to the drafts and gave final approval for publication.

Abstract

Small demographic size and reduced genetic diversity increase the extinction probability of a population. Genetic diversity within populations for neutral markers is an heuristic parameter, as it reflects past and ongoing processes acting on populations, and informs on possible futures. This study presents a synthesis of the knowledge on neutral genetic diversity for threatened plants in metropolitan France and the use of such data in management actions. Pairing threatened species with the closest non-threatened species for which we could find appropriate genetic data, we collected information on genetic diversity for 25 threatened species and non-threatened controls. We found that threatened species in France have on average a lower within-population genetic diversity than non-threatened controls and thus are exposed to risks linked to genetic erosion. Combining an analysis of recovery plans and a survey addressed to practitioners, we concluded that genetic diversity is rarely integrated in management actions. The integration of such information into applied conservation remains a challenge. We provide some guidelines to collect biological traits impacting within-population genetic diversity and some specific recommendations for a better incorporation of population genetics concepts into conservations actions.

Keywords: Genetic diversity, conservation, threatened plants, management, metropolitan France

Introduction

Anthropogenic activities such as intensive agricultural practices and urbanization lead to habitat destruction and fragmentation. For plant species, these environmental changes affect population dynamics by altering population size, population number and population isolation (Lande 1988; Camill 2010; Ralls et al. 2018). In particular, small populations are vulnerable to density-dependent effects (Allee effect) and demographic stochasticity (Lande 1988; Oostermeijer et al. 2003). The reduction in demographic size of a population is also accompanied by a reduction in effective population size, i.e an increase of genetic drift and thus a decrease in within-population genetic diversity (Ellstrand and Elam 1993). A positive correlation between neutral genetic diversity and population size is a common observation in natural populations (for a meta-analysis see Leimu et al. 2006). Furthermore, population fragmentation reduces gene flow among populations, which also contributes to decrease genetic diversity within populations (Ellstrand and Elam 1993). The level of both neutral genetic variation and quantitative genetic variation are expected to be reduced by drift and isolation (Allendorf and Luikart 2006) and neutral diversity is expected to covary with selected diversity (Kardos et al. 2021). In addition, in small populations, drift can lead to the fixation of deleterious alleles, thus increasing genetic load and inbreeding depression (Keller and Waller 2002), and a positive correlation between neutral genetic diversity and fitness is often observed (Reed and Frankham 2004; Leimu et al 2006). The general framework of evolutionary rescue has emphasized that population persistence relies partly on evolutionary potential (Gomulkiewicz and Holt 1995; Gonzalez et al. 2013; Carlson et al. 2014; Olivieri et al. 2016; Ralls et al. 2018; Thompson 2020), depending both on population size and standing genetic variation (Frankham et al. 2017).

Hence, risks linked to changes in population genetic diversity should also be included in threat detection (Allendorf and Luikart 2006; Olivieri et al. 2016) and the decision-making process that leads to management actions should integrate the concept of evolutionary potential, particularly in the context of global change (Ashley et al. 2003; Smith et al. 2014; Olivieri et al. 2016; Ralls et al. 2018; Thompson 2020). Evaluations of the integration of genetic issues into management have been carried out in several countries (Pierson et al. 2016; Taylor et al. 2017; Cook and Sgrò 2018). Using surveys addressed to people professionally involved in conservation actions, Taylor et al. (2017) and Cook and Sgrò (2018) showed a low level of integration of key evolutionary concepts in biodiversity management, in New Zealand and Australia, respectively. Pierson et al. (2016) used another approach by evaluating how genetic issues are incorporated into recovery plans. France was included in their analysis but only through the national action plans (PNA) which are clearly not representative of conservation actions in France.

Our study aims to assess within-population genetic diversity of threatened Angiosperm species in France and the use of such information in conservation actions. First, we evaluated the data available for neutral genetic diversity of plants species considered as threatened in France using the IUCN list and the legal protection status in

France. Although it would be best to make congeneric comparisons to control for confounding effects of phylogeny and life-history traits on genetic diversity (Gitzendanner and Soltis 2000; Spielman et al. 2004; Hamabata et al. 2019; Hamrick and Godt 1996; Leimu et al. 2006; Duminil et al. 2007), sometimes genetic data were not available for a non-threatened congener, in which case we instead compared the threatened species with its closest relative for which appropriate genetic data were available. Next, in order to assess the degree of consideration of genetic diversity in conservation actions in metropolitan France, we analysed available recovery plans and performed a survey addressed to managers.

Materials and Methods

Genetic diversity of threatened plant species in France

The IUCN Red List threatened categorization system (CR, EN, VU) was used to identify 452 threatened plant species and subspecies occurring in metropolitan France (https://uicn.fr/liste-rouge-flore/, November 2019). In addition, the list of the 387 legally protected Angiosperms species in France was extracted from the institutional website collecting data on biodiversity in France (https://inpn.mnhn.fr/, November 2019). The two lists were merged to define threatened Angiosperm species and subspecies in metropolitan France. We also added three species (*Arenaria grandiflora, Convolvulus lanuginosus, Pinguicula grandiflora*) with a local status of protection that are known to have been studied for genetic diversity in the area were there are protected. The final list included 749 plant taxa. We did not check for synonymy at this stage. It is important to note that genetic diversity is not considered neither in the IUCN criteria, nor for a legal protection status in France.

Using this list, automatic data mining was carried out on NCBI (https://www.ncbi.nlm.nih.gov/), on Google Scholar and on the French registry of Ph-D theses (http://theses.fr/) to find any study on these species. A search on the Web of Science database was also performed using the list of species (eg TITLE = “SPECIES1” *OR* “SPECIES2”…). We obtained 6779 results (20 April 2022), and we refined the results using the keyword *“genetic”*. Among the 625 results, we retained publication with at least one author from France (Countries/Regions = “France”). For two species (*Agropyron cristatum* and *Vitis vinifera)* related to largely cultivated plants, a dedicated search was done.

Among all the studies collected, only those with data on within-population genetic diversity were retained. We used genetic diversity at population scale since it is the pertinent scale to detect effects of drift, absence of migration and because selection needs within-population diversity to act. For each species, parameters estimating genetic diversity within populations were extracted from the studies. We also documented population size and sampling size, and several life-history traits known to influence genetic diversity such as mating system, longevity, vegetative reproduction, dispersion vector and pollination vector (see Appendix 1).

As our goal was to compare genetic diversity of threatened species to genetic diversity of non-threatened species, we searched for studies performed on related non-threatened species. The collection of data for non-threatened species was performed in several phases. Ideally, each pair of species should include a threatened and non-threatened congeneric species (see Lavergne et al. 2004) occurring in the same habitat and sharing common life-history traits. As we aimed to compare genetic diversity, we must also have genetic parameters estimated on the same type of genetic markers although the best comparison would use the same loci for those same markers. We made a first search on Web of Science using the name of the genus and the types of genetic markers (e.g. TOPIC= Anchusa *AND* TOPIC= AFLP). In absence of results, we relaxed the congeneric criteria and searched using the family name (e.g. TOPIC= Caryophyllaceae *AND* TOPIC= SSR). Species were not considered as a valid control if they were said to be “rare” or “threatened” by the authors of a study, if they were cultivated species, or if they were invasive species. When several non-threatened species were available, we selected the species the most similar to the threatened species within the pair for life-history traits. For 3 species (*Pinguicula rosea*, *Pinguicula grandiflora* and *Orobanche bartlingii*), we could not find any non-threatened species in the same family studied with the same markers (AFLP), so we used estimations of diversity in AFLP from the review on plants by Nybom (2004). For *Eryngium viviparum*, the comparison was made using the only French population and Iberic populations, since the species is not threatened in Spain (Rascle et al. 2019). One recent study on the threatened *Delphinium montanum* documents diversity using SNPs (Salvado et al. 2022), but we could not find any pertinent study for the non-threatened control. This species was not included in our comparison.

Data analyses

The raw data were the expected heterozygosity within populations, also named Nei’s gene diversity, extracted from published and unpublished papers (see Appendix 1). We computed the mean expected heterozygosity per population for each species. Expected heterozygosity was chosen to estimate genetic diversity because this measure is only slightly affected by sample size, in contrast to the number of alleles per locus. To test for the difference in expected heterozygosity between threatened and non-threatened controls, a non-parametric pairwise comparison test was performed. Because of the small sample size (see results), we adapted the classical Wilcoxon test for pairwise comparisons following Manly (1991). First, the V-value was computed using the *Wilcox.test* function in R (version 4.0.3). Next, the same statistic was computed for permuted dataset. Species status (threatened *vs* non threatened) was permuted 1,000 times within pairs, and the original V-value was compared to the distribution of the permuted values. Finally, the percentage difference in heterozygosity within pairs was estimated as the signed difference in expected heterozygosity between the threatened and the non-threatened members of the pair divided by the largest value of expected heterozygosity in the pair.

Considerations of genetic diversity in management actions

First, recovery plans (defined as in Pierson et al. 2016) implemented in France were downloaded from the website of each of the 10 National Botanic Conservatories acting in the metropolitan France (Alpin, Bailleul, Bassin Parisien, Brest, Corse, Franche-Comté, Massif Central, Midi-Pyrénées, Porquerolles, Sud-Atlantique) and from the website of the French Ministry in charge of biodiversity (https://www.ecologie.gouv.fr/). In each document, we searched for any mention of the term *genetic* (in French “génétique”), which led us to *population genetics* and *genetic data*. We also documented if any task was assigned to collect data on genetic diversity.

We searched for any mention of effective population size (in French “taille efficace”). We also searched for any reference to habitat and life-history traits such as mating system, longevity, vegetative reproduction, dispersion vector and pollination vector (Appendix 2). Finally, management actions directly impacting genetic diversity such as introduction, reintroduction, reinforcement (sensu Silcok et al. 2019) were also recorded (Appendix 2). Hereafter, the terms “manipulation of population size” will refer to these actions.

Additionally, as many management actions are not published or are reported in documents with a very narrow public access, a survey was also conducted using numerous professional mailing lists (*Conservatoires d’Espaces Naturels*, *Conservatoires Botaniques Nationaux*, *Parc Nationaux*, *Réseau d’acteurs pour la conservation de la flore méditerraneenne*) and using social networking (Tela Botanica, Ecodiff) to reach practitioners. The survey was developed using the *Limesurvey* interface and designed with the purpose of collecting the same types of information as we gathered from recovery plans (Appendix 3).

We thus used two sources of information to study the consideration of genetic diversity in management actions: the synthesis of management plans available on-line, hereafter “recovery plans”, and the answer of managers to the survey, hereafter “surveys”.

Results

Genetic diversity of threatened plant species in France

From the initial list containing more than 700 plant threatened species, within-population expected heterozygosity at neutral nuclear loci was gathered only for 25 threatened species (Appendix 1). Only 12 species are considered as threatened species under IUCN criteria on the French redlist, and two species (*Aster pyrenaeus* and *Biscutella neustriaca*) are considered as threatened at a global scale. All the 25 threatened species have a French legal protection status either at the national scale (17 species) or at the local scale (8 species). Twenty-two non-threatened species filled the require conditions to build the pairs, 13 in same genus and 9 in the same family than a threatened species. For the 3 other pairs, we used data from Nybom (2004, see Materials and Methods section, Appendix 1). AFLPs (N=20, He=0.20 SD 0.08) and microsatellites (N=16, He=0.43 SD 0.21) were the most frequently used marker types. ISSR (N=10, He= 0.14 SD 0.07) and allozymes (N=4, He=0.08 SD 0.05) are the least frequent and the least diverse markers.

All the threatened species in the dataset are perennials except *Ranunculus nodiflorus* and *R. lateriflorus* which are annuals (Appendix 1, Table S1). Threatened species are mainly polycarpic (76%) and their pollination is mostly entomophilous (76%). Agents of seed dispersal varied: anemochory (24%), barochory (28%), hydrochory (8%), and zoochory (8%) (missing data for 8 species). Mating system is generally considered as allogamous (36%) or mixed (20%). There are 44% of threatened species able to reproduce asexually. For most pairs, threatened species share the same life-history traits as their non threatened relatives (Appendix 1, Table S1). In contrast to life history-traits, demographic parameters of threatened species were highly variable. For threatened species, mean population sizes ranged from 56 (*Arenaria grandiflora*) to 50150 (*Narcissus triandrus* ssp. *capax*). Some species occur in a single locality (*Eryngium viviparum*) or few nearby localities (3 islets for *N. triandrus* ssp. *capax*, 6 populations for *Centaurea corymbosa*) while other species have a widespread distribution beyond the French territory (e.g. *Brassica insularis*, *Cyprepedium calceolus*).

Over all pairs, the average of the signed differences on within-population expected heterozygosity between threatened and non-threatened plants is -18.5%. For 6 pairs, the threatened species (*Anchusa crispa*, *Convolvulus lanuginosus*, *Cypripedium calceolus*, *Eryngium alpinum*, *Liparis loselii, Ranunculus lateriflorus*) showed a greater heterozygosity that the non-threatened species. Over the 19 pairs out of 25 showing a reduction of heterozygosity in the threatened species, the average difference is -33.2%. On the whole, threatened species had a lower expected heterozygosity than their non-threatened controls (Figure 1, P-value= 0.0065). When removing the three threatened species for which the within-population heterozygosity was compared to the average value from Nybom (2004), the result remains significant (p=0.0337 for N=22 pairs).

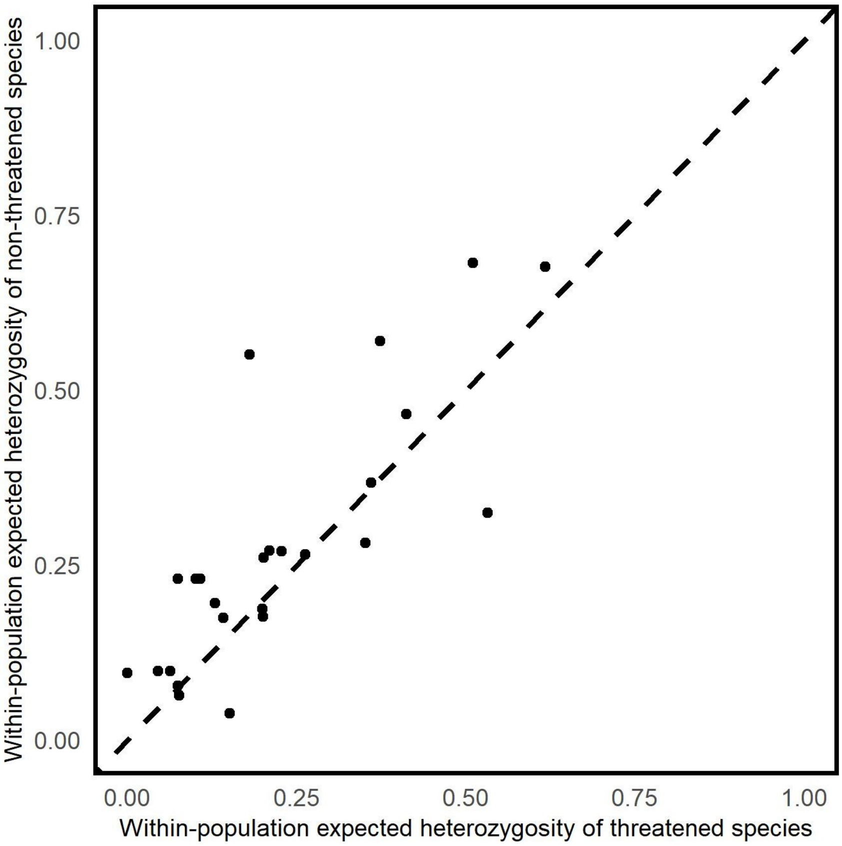

Figure 1: Within-population heterozygosity (He) of threatened plant species in France and non-threatened species. The dashed line represents the X=Y line, *i.e.* a point on this line would indicate that threatened and non-threatened species have the same level of heterozygosity.

Considerations of genetic diversity in management actions

Sixty-two recovery plans concerning 59 protected species were found on-line. Two species (*Centranthus trinervis* and *Liparis loeselii*) were studied in more than one plan. From the on-line survey, we collected data for 21 species, six species were mentioned both in recovery plans and in the survey. Overall, we collected information for 74 species. Among them, 20 are considered as threatened on the IUCN national list, 26 species are protected at the national level and the others are locally protected either at the department or regional level which justifies management actions. Habitat management, with 46 citations out of 74, is the most frequent action recommended for *in situ* management. Legal protection for habitat was recommended for 45 species. Manipulation of population size was recommended for 21 species with introduction for 11 species, reinforcement for 15 species, and reintroduction for 5 species. Among species in this dataset, six species (*Anchusa crispa*, *Aster pyrenaeus*, *Biscutella neustriaca*, *Eryngium viviparum*, *Liparis loeselii*, *Ranunculus nodiflorus*) were in the previous analysis on genetic diversity.

Life-history traits are unequally represented in recovery plans. While habitat and species longevity are well characterized (100%, 96.8% respectively Table 1), the ecology of dispersal and pollination are often not considered (29%, 22.6% respectively Table 1). Important information such as the mating system is even more rarely given in recovery plans (13 occurrences, Table 1), and tests for self-compatibility have also seldom been carried out (Table 1). When manipulations of population size are implemented, information on mating system and self-incompatibility are more often considered (Table 1). Population size is often known (92%) but no reference to *effective population size* could be found in any conservation plan. Mention of “genetic” occurred in more than 79% of plans (Table 1). Mention of “genetic” is often associated with the preservation of diversified *ex situ* material (80%) and rarely with threats such as genetic erosion (32%) or population persistence (14%). Only 10 recovery plans used already existing genetic data (Table 1) and 8 of these 10, plus 4 others called for the collections of genetic data (Table 1). Overall only 14 documents out of 62 refered in some way to the use of genetic data.

The 21 surveys collected also confirm that reproductive system is less reported than other life-history traits (Table 2). Habitats, longevity, seed dispersal and pollination vectors are known for all species addressed in the survey (Table 2). In contrast, mating system and self-incompatibility tests were reported by only 57% and 19% of respondents respectively (Table 2). In particular, self-incompatibility tests were carried out for only four species. Seven respondents (out of 21) indicated the use of genetic data. Twelve management actions including manipulation of population size were documented (Table 2) and nine of them used only a single population source. For two manipulations of population size, *Saxifraga hirculus* and *Acis nicaeensis*, two populations were used as seed source. For one of the manipulation of population size (*Orchis purpurea*), the number of populations source was not documented. Genetic data were available for five of the twelve species concerned by manipulation of population size (Table 2).

Table 1 : Information available in recovery plans about life-history traits of the species concerned and other topics related to genetics. In the second column, are given the number (percentage) of recovery plans in which the topics is fill in for the species considered. In the last column, are given the same informations for recovery plans including manipulation of population size. « Mention of genetic » means that the topic is discussed but not that genetic data is provided.

Topics	Overall (%)	Recovery plans including manipulation of population size (%)
Habitat	62 (100)	12 (100)
Longevity	60 (96.8)	11 (91.7)
Vegetative reproduction	14 (22.6)	6 (50.0)
Dispersion vector	18 (29.0)	10 (83.3)
Pollination vector	14 (22.6)	5 (41.7)
Mating system	13 (20.9)	5 (41.7)
Self-incompatibility test	7 (11.3)	3 (25.0)
Mention of genetic	49 (79.0)	10 (83.3)
Genetic data	10 (16.1)	4 (33.3)
Task to collect genetic data	12 (19.3)	4 (33.3)

Table 2 : Information available in surveys about life-history traits of the species concerned and other topics related to genetics. In the second column, are given the number (percentage) of surveys in which the topics is fill in for the species considered. In the last column, are given the same informations for actions including manipulation of population size.

Topics	Overall (%)	Actions including manipulation of population size (%)
Species habitat	21 (100)	12 (100)
Species longevity	20 (95.2)	12 (100)
Vegetative reproduction	20 (95.2)	12 (100)
Dispersion vector	21 (100)	12 (100)
Pollination vector	21 (100)	12 (100)
Mating system	12 (57.1)	8 (66.7)
Self-incompatibility test	4 (19.0)	4 (33.3)
Genetic data	7 (33.3)	5 (41.7)

Discussion

Our review of the studies performed on the French flora showed that genetic diversity is known for a low number of threatened species. When documented, within-population expected heterozygosity is usually lower in threatened species than in non-threatened controls. Threatened plants having lower genetic diversity is consistent with other studies of plants such as the one performed on 21 species considered to be threatened on the world IUCN redlist (Spielman et al. 2004). As the threatened species included in our study share common life-history traits (Table S1) with their widespread relatives, this low genetic diversity is likely to result from a reduced population size or geographic isolation. The relative contribution of these two factors need information on genetic structure to be quantified (Ellstrand and Elam 1993). For instance, the French population of *Eryngium viviparum* is highly isolated from the Iberian populations of the same species and showed much lower diversity than the Iberian populations indicating that the low genetic diversity is probably linked to geographical isolation (Rascle et al. 2019). Gitzendanner and Soltis (2000) have also found that overall rare species have lower genetic diversity than their common congeners, with some exceptions as we observed for 6 species. Some studies have reported that a narrow distribution or a threatened status does not necessarily result in low neutral genetic diversity (Jiménez-Mejías et al. 2015; Médail and Baumel 2018; Teixeira and Huber 2021), in particular because a lag is expected between population reduction and loss of genetic variation (Kardos et al. 2021).

A second major conclusion from our study is that population genetics was not considered in most recovery plans or by practitioners. Although some references to genetics can be found in recovery plans, collection of genetic data is only included or recommended in 14 plans out of 62 (23%). While Pierson et al. (2016) also found a low proportion of plans that included genetics, they noted that in France recovery plans propose the collection of genetic data at a relatively high rate (80%) in comparison to other European countries (e.g. Netherlands 35 %, UK 30 %). However, their study only included five *Plan National d'Actions (PNA),* which are the most complete but not the most common kind of conservation plans in France. In our study, we included other kinds of recovery plans and found 19.3% of them recommended the collection of genetic data. In Australia, the positive perception of genetics by practitioners is not always translated in an actual use of genetics (Cook and Sgrò 2018). In New Zealand, the actual use of genetic techniques varies according to conservation issues (Taylor et al. 2017). International and national policies usually insist on the importance of genetic diversity (Cook and Sgrò 2017; Hoban et al. 2021), in particular for long-term persistence. However practical recommendation fail to incorporate genetic factors into conservation plans (Cook and Sgrò 2017; Hoban et al. 2021), as we found here for France. Furthermore, specific concepts linked to genetic diversity, such as inbreeding depression, gene flow or mating system, are rarely mentioned in conservation plans, in contrast to the conservation scientific literature (Cook and Sgrò 2017). Hence, insufficient integration of genetic diversity and related concepts into conservation plans seems to be the rule in several countries including France. An international standard for species recovery plans explicitly including genetic aspects should be developed (Pierson et al. 2016).

Several recommendations can be made to improve the integration of population genetic diversity in conservation actions. A better spread of the concept of effective population size (Ne) would be one of the recommendations since it is directly related to genetic threats and population extinction (Allendorf and Luikart 2006; Hoban et al. 2022). Effective population size is often smaller than the demographic population size (eg. Allendorf and Luikart 2006; Hoban et al. 2020 but see Vitalis et al. 2004). So far, methods to estimate Ne are clearly too difficult to be applied in most natural populations because of the quality and quantity of genetic or demographic data necessary and because of the complexity of the statistical tools involved. However, collection of data on life-history traits particularly affecting genetic diversity and Ne can be recommended (Hoban et al. 2020), yet we have found that most conservation plans are conducted with only moderate knowledge on such ecological and biological traits. Acquisition of data about the mating system of the species is a minimum requirement since it directly affects Ne and the structure of genetic diversity (Duminil et al. 2007; Hoban et al. 2020). Nevertheless, there is much less information about mating systems than others traits in conservation plans in Australia (Cook and Sgrò 2018) and in France (this study). Life-history traits are also important for other aspects of management, for example, the longevity of a species decreases the probability to reach reproduction stage per seed, therefore, increases the number of seeds to use in an introduction (Machinsky and Haskin 2012). The absence of information about basic biological characteristics of plant species probably helps to explain some of the failures of reintroduction actions (Godefroid et al. 2011).

We also reported that the majority (nine out twelve) of manipulations of population size are performed with one source population and two others used only two populations as sources. Increasing population size reduces the demographic risk and future genetic erosion whatever the origin of the introduced individuals. However to address genetic issues linked to past genetic erosion, genetic mixing is required, thus individuals should originate from a different population, provided outbreeding and local adaptation issues are addressed before mixing populations (Hoffmann et al. 2021; Teixeira and Huber 2021). This would make conservation actions more effective, as would supplementing information on neutral genetic diversity with information on functional genetic diversity (Teixeira and Huber 2021). This highlights the importance of improving knowledge on evolutionary theory in the training of conservation management staff.

Several factors, including social, political and economic considerations, explain the absence of integration of evolutionary theory into conservation plans, but the training of practitioners is likely to be one of the most important causes (Taylor et al. 2017; Cook and Sgrò 2018; Sandstrom et al. 2019). Furthermore, despite the recommendation to use open-access research, results from research in conservation biology do not percolate to practitioners (Taylor et al. 2017). While scientific publications is an important source for general interpretations, several constraints were pointed out by practitioners, essentially the lack of time and language constraints for some non-native English speakers (Fabian et al. 2019). Another possible explanation to the conservation-genetic gap is that genetic is not directly considered in IUCN criteria to evaluate species status (Willi et al. 2022). Finally, because population genetic studies are costly and time-consuming, the lack of financial resources is also a problem (Taylor et al. 2017; Cook and Sgrò 2019). However, as we pointed out above, some biological traits, such as the mating system, can be collected in natural populations without technical requirements or costly technology. Another element to consider is that management strategies tend to focus on short-term responses and perceptible threats rather than imperceptible and dynamic processes (Mace and Purvis 2008). As a result, habitat management and the census of population size (i.e. number of flowering plants) are the most frequent actions.

A general recommendation concerns the importance of communication between researchers and practitioner (Taylor et al. 2017; Fabian et al 2019; Holderegger et al. 2019; Taft et al. 2020; Hohenlohe et al. 2021). Regular networking events between practitioners and conservation geneticists, such as Annual Meetings in Conservation Genetics (Holderegger et al. 2019), or conservation geneticist hub bringing together genetic researchers to provide one platform of expertise visible to managers (Taylor et al. 2017) should be more widespread. It also would beneficial to increase the number of collaborative partnerships between genetic researchers and conservation managers to support management strategies of specific wild populations (Taft et al. 2020; Hohenlohe et al. 2021).

Acknowledgements

We thank the practioners that participated in the on-line surveys, and the RESEDA-FLORE consortium. Khalid Belkihr contributed significantly to the scripts used for the data mining. We are also indebted to John Thompson for comment on a previous version of this paper. JD is funded by the OFB and Labex Cemeb RENPOP project.

Data availability statement

The data that support the findings of this study are available from supplementary materials.

Table S1: Description of 6 life-history traits within pairs of species according to the status of the species, Appendix 1: Dataset on genetic diversity of threatened plant species in France, Appendix 2: Information that has been searched in recovery plans, Appendix 3: Survey addressed to practitioners, Appendix 4: Dataset on considerations of genetic diversity in management actions

Literature cited

Allendorf F, Luikart G. 2006. Conservation and genetics of populations. Malden (MA). Blackwell Publ. ISBN-13: 978-1-4051-2145-3

Ashley MV, Willson MF, Pergams ORW, O'Dowd DJ, Gende SM, Brown JS. 2003. Evolutionary enlightened management. Biol Conserv. 111: 115–123. https://doi.org/10.1016/S0006-3207(02)00279-3

Camill, P. 2010. Global Change. Nature Education Knowledge 3: 49

Carlson SM, Cunningham CJ, Westley PAH. 2014. Evolutionary rescue in a changing world. Trends Ecol Evol. 29: 521–530. https://doi.org/10.1016/j.tree.2014.06.005

Cook CN, Sgrò CM. 2017. Aligning science and policy to achieve evolutionarily enlightened conservation. Conserv Biol. 31: 501–512. https://doi.org/10.1111/cobi.12863

Cook CN, Sgrò CM. 2018. Understanding managers' and scientists' perspectives on opportunities to achieve more evolutionarily enlightened management in conservation. Evol Appl. 11: 1371–1388. https://doi.org/10.1111/eva.12631

Cook CN, Sgrò CM. 2019. Conservation practitioners' understanding of how to manage evolutionary processes. Conserv Biol. 33: 993–1001. https://doi.org/10.1111/cobi.13306

Conservatoire botanique national alpin. 2020. [accessed Mar 2020]. http://www.cbn-alpin.fr/.

Conservatoire botanique national de Bailleul. 2020. [accessed Mar 2020]. https://www.cbnbl.org/.

Conservatoire botanique national du bassin parisien. 2020. [accessed Mar 2020]. https://cbnbp.mnhn.fr/cbnbp/.

Conservatoire botanique national de Brest. 2020. [accessed Mar 2020]. http://www.cbnbrest.fr/.

Conservatoire botanique national de Corse. 2020. [accessed Mar 2020]. http://cbnc.oec.fr/.

Conservatoire botanique national Franche-Comté. 2020. [accessed Mar2020]. http://cbnfc-ori.org/.

Conservatoire botanique national Massif Central. 2020. [accessed Mar 2020].https://www.cbnmc.fr/.

Conservatoire botanique national Midi-Pyrrénées. 2020. [accessed Mar 2020]. http://cbnpmp.blogspot.com/.

Conservatoire botanique national Méditerranéen de Porquerolles. 2020. [accessed Mar 2020]. http://www.cbnmed.fr/src/prez.php.

Conservatoire botanique national Sud Atlantique. 2020. [accessed Mar 2020]. http://www.cbnsa.fr/.

Duminil J, Fineschi S, Hampe A, Jordano P, Salvini D, Vendramin GG, Petit RJ. 2007. Can Population Genetic Structure Be Predicted from Life-History Traits?. Am. Nat. 169: 662–672.https://doi.org/10.1086/513490

Ellstrand NC, Elam DR. 1993. Population Genetic Consequences of Small Population Size: Implications for Plant Conservation. Annu Rev Ecol Syst. 24: 217–242. https://doi.org/10.1146/annurev.es.24.110193.001245

Fabian Y, Bollmann K, Brang P, Heiri C, Olschewski R, Rigling A, Stofer S, Holderegger R. 2019. How to close the science-practice gap in nature conservation? Information sources used by practitioners. Biol Conserv. 235: 93–101. https://doi.org/10.1016/j.biocon.2019.04.011

Frankham R, Ballou J, Ralls K, Eldridge M, Dudash M, Fenster C, Lacy R, Sunnucks P. 2017. Genetic Management of Fragmented Animal and Plant Populations. Oxford: Oxford University Press. https://doi.org/10.1093/oso/9780198783411.001.0001

Garner BA, Hoban S, Luikart G. 2020. IUCN Red List and the value of integrating genetics. Conserv Genet. 21: 795–801. https://doi.org/10.1007/s10592-020-01301-6

Gitzendanner MA, Soltis PS. 2000. Patterns of genetic variation in rare and widespread plant congeners. Am J Bot. 87: 783–792.

Godefroid S, Piazza C, Rossi G, Buord S, Stevens A-D, Aguraiuja R, Cowell C, Weekley CW, Vogg G, Iriondo JM, et al. 2011. How successful are plant species reintroductions? Biol Conserv. 144: 672–682. : https://doi.org/10.1016/j.biocon.2010.10.003

Gomulkiewicz R, Holt RD. 1995. When does evolution by natural selection prevent extinction? Evolution. 49: 201–207. https://doi.org/10.2307/2410305

Gonzalez A, Ronce O, Ferriere R, Hochberg ME. 2013. Evolutionary rescue: an emerging focus at the intersection between ecology and evolution. Philos Trans R Soc B Biol Sci. 368: 20120404. https://doi.org/10.1098/rstb.2012.0404

Hadjou Belaid A, Maurice S, Fréville H, Carbonell D, Imbert E. 2018. Predicting population viability of the narrow endemic Mediterranean plant Centaurea corymbosa under climate change. Biol Conserv. 223: 19–33. https://doi.org/10.1016/j.biocon.2018.04.019

Hamabata T, Kinoshita G, Kurita K, Cao P-L, Ito M, Murata J, Komaki Y, Isagi Y, Makino T. 2019. Endangered island endemic plants have vulnerable genomes. Commun Biol. 2: 1–10. https://doi.org/10.1038/s42003-019-0490-7

Hamrick JL, Blanton HM, Hamrick KJ. 1989. Genetic structure of geographically marginal populations of Ponderosa pine. Am J Bot. 76: 1559–1568. https://www.jstor.org/stable/pdf/2444394.pdf

Hardion L, Verlaque R, Rosato M, Rosselló JA, Vila B. 2015. Impact of polyploidy on fertility variation of Mediterranean Arundo L. (Poaceae). C R Biol. 338: 298–306. https://doi.org/10.1016/j.crvi.2015.03.013

Hoban S, Bruford M, D’Urban Jackson J, Lopes-Fernandes M, Heuertz M, Hohenlohe PA, Paz-Vinas I, Sjögren-Gulve P, Segelbacher G, Vernesi C, et al. 2020. Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. Biol Conserv. 248: e108654. https://doi.org/10.1016/j.biocon.2020.108654

Hoban S, Campbell CD, da Silva JM, Ekblom R, Funk WC, Garner BA, Godoy JA, Kershaw F, MacDonald AJ, Mergeay J, et al. 2021. Genetic diversity is considered important but interpreted narrowly in country reports to the Convention on Biological

Diversity: Current actions and indicators are insufficient. Biol Conserv. 261: 109233. https://doi.org/10.1016/j.biocon.2021.109233

Hoban S, Archer FI, Bertola LD, Bragg JG, Breed MF, Bruford MW, Coleman MA, Ekblom R, Funk WC, Grueber CE, Hand BK, Jaffé R, Jensen E, Johnson JS, Kershaw F, Liggins L, MacDonald AJ, Mergeay J, Miller JM, Muller-Karger F, O'Brien D, Paz-Vinas I, Potter KM, Razgour O, Vernesi C, Hunter M.E. 2022. Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. Biol Rev.e12852 https://doi-org.inee.bib.cnrs.fr/10.1111/brv.12852

Hoffmann AA, Miller AD, Weeks AR. 2021. Genetic mixing for population management: From genetic rescue to provenancing. Evol Appl. 14: 634–652. https://doi.org/10.1111/eva.13154

Holderegger R, Balkenhol N, Bolliger J, Engler JO, Gugerli F, Hochkirch A, Nowak C, Segelbacher G, Widmer A, Zachos FE. 2019. Conservation genetics: Linking science with practice. Mol Ecol. 28: 3848–3856. https://doi.org/10.1111/mec.15202

Hohenlohe PA, Funk WC, Rajora OP. 2021. Population genomics for wildlife conservation and management. Mol Ecol. 30: 62–82. https://doi.org/10.1111/mec.15720

Inventaire National du Patrimoine Naturel. 2019. [accessed Nov 2019]. https://inpn.mnhn.fr/accueil/index

IUCN/SSC. 2013. Guidelines for Reintroductions and Other Conservation Translocations. Gland, Switzerland: IUCN Species Survival Commission.Version 1.0.

Jiménez-Mejías P, Fernández-Mazuecos M, Amat ME, Vargas P. 2015. Narrow endemics in European mountains: high genetic diversity within the monospecific genus Pseudomisopates (Plantaginaceae) despite isolation since the late Pleistocene. J Biogeogr. 42: 1455–1468. https://doi.org/10.1111/jbi.12507

Kardos M, Armstrong EE, Fitzpatrick SW, Hauser S, Hedrick PW, Miller JM, Tallmon DA, Funk WC. 2021. The crucial role of genome-wide genetic variation in conservation. Proc Natl Acad Sci. 118: e2104642118. https://doi.org/10.1073/pnas.2104642118

Keller LF, Waller DM. 2002. Inbreeding effects in wild populations. Trends Ecol Evol. 17: 230–241. https://doi.org/10.1016/S0169-5347(02)02489-8

Lande R. 1988. Genetics and demography in biological conservation. Science. 241: 1455–1460. https://doi.org/10.1126/science.3420403

Lavergne S, Debussche M, Thompson JD. 2005. Limitations on reproductive success in endemic Aquilegia viscosa (Ranunculaceae) relative to its widespread congener Aquilegia vulgaris: the interplay of herbivory and pollination. Oecologia. 142: 212–220.https://doi.org/10.1007/s00442-004-1721-1

Lavergne S, Thompson JD, Garnier E, Debussche M. 2004. The biology and ecology of narrow endemic and widespread plants: a comparative study of trait variation in 20 congeneric pairs. Oikos. 107: 505–518. https://doi.org/10.1111/j.0030-1299.2004.13423.x

Leimu R, Mutikainen P, Koricheva J, Fischer M. 2006. How general are positive relationships between plant population size, fitness and genetic variation? J Ecol. 94: 942–952. https://doi.org/10.1111/j.1365-2745.2006.01150.x

Mace GM, Purvis A. 2008. Evolutionary biology and practical conservation: bridging a widening gap. Mol Ecol. 17: 9–19. https://doi.org/10.1111/j.1365-294X.2007.03455.x

Maschinski, J, Haskins K.E. 2012. Plant Reintroduction in a Changing Climate: Promises and Perils. Washington: Island Press. https://doi.org/10.5822/978-1-61091-183-2.

Manly BFJ. 1991. Randomization and Monte Carlo methods in biology. London: Chapman and Hall. ISBN 0-412-72130-9

Médail F, Baumel A. 2018. Using phylogeography to define conservation priorities: The case of narrow endemic plants in the Mediterranean Basin hotspot. Biol Conserv. 224: 258–266. https://doi.org/10.1016/j.biocon.2018.05.028

Ministère de la Transistion écologique. 2020. [accessed 2020 March]. https://www.ecologie.gouv.fr/.

National Center for Biotechnology Information. 2019. [accessed Nov 2019]. https://www.ncbi.nlm.nih.gov/

Nybom H. 2004. Comparison of different nuclear DNA markers for estimating intraspecific genetic diversity in plants: DNA-markers and plant genetic diversity. Mol Ecol. 13: 1143–1155. https://doi.org/10.1111/j.1365-294X.2004.02141.x

Olivieri I, Tonnabel J, Ronce O, Mignot A. 2016. Why evolution matters for species conservation: perspectives from three case studies of plant metapopulations. Evol Appl. 9: 196–211. https://doi.org/10.1111/eva.12336

Oostermeijer JGB, Luijten SH, den Nijs JCM. 2003. Integrating demographic and genetic approaches in plant conservation. Biol Conserv. 113: 389–398. https://doi.org/10.1016/S0006-3207(03)00127-7

Pierson JC, Coates DJ, Oostermeijer JGB, Beissinger SR, Bragg JG, Sunnucks P, Schumaker NH, Young AG. 2016. Genetic factors in threatened species recovery plans on three continents. Front Ecol Environ. 14: 433–440. https://doi.org/10.1002/fee.1323

Quilichini A, Debussche M, Thompson JD. 2004. Geographic differentiation of morphological traits and isozymes in the Mediterranean island endemic Anchusa crispa: implications for the conservation of a protected species. Biol Conserv. 118: 651–660. https://doi.org/10.1016/j.biocon.2003.10.014

Ralls K, Ballou JD, Dudash MR, Eldridge MDB, Fenster CB, Lacy RC, Sunnucks P, Frankham R. 2018. Call for a Paradigm Shift in the Genetic Management of Fragmented Populations. Conserv Lett. 11: e12412. https://doi.org/10.1111/conl.12412

Rascle P, Flaven E, Bioret F, Magnanon S, Glemarec E, Gallet S, Imbert E. 2019. Genetic consequences of long-term isolation for the last French population of Eryngium viviparum (Apiaceae). Bot J Linn Soc. 191: 285–298. https://doi.org/10.1093/botlinnean/boz035

Reed DH, Frankham R. 2003. Correlation between Fitness and Genetic Diversity. Conserv Biol. 17: 230–237. https://doi.org/10.1046/j.1523-1739.2003.01236.x

Rodger YS, Pavlova A, Sinclair S, Pickup M, Sunnucks P. 2021. Evolutionary history and genetic connectivity across highly fragmented populations of an endangered daisy. Heredity. 126: 846–858. https://doi.org/10.1038/s41437-021-00413-0

Salvado P, Aymerich Boixader P, Parera J, Vila Bonfill A, Martin M, Quélennec C, Lewin J-M, Delorme-Hinoux V, Bertrand JAM. 2022. Little hope for the polyploid endemic Pyrenean Larkspur (Delphinium montanum): Evidences from population genomics and Ecological Niche Modeling. Ecol Evol. 12: e8711. https://doi.org/10.1002/ece3.8711

Sandström A, Lundmark C, Andersson K, Johannesson K, Laikre L. 2019. Understanding and bridging the conservation-genetics gap in marine conservation. Conserv Biol. 33: 725–728. https://doi.org/10.1111/cobi.13272

Sarrazin F, Lecomte J. 2016. Evolution in the Anthropocene. Science. 351: 922–923. https://doi.org/10.1126/science.aad6756

Silcock JL, Simmons CL, Monks L, Dillon R, Reiter N, Jusaitis M, Vesk PA, Byrne M, Coates DJ 2019. Biological Conservation 236: 211-222.

Smith TB, Kinnison MT, Strauss SY, Fuller TL, Carroll SP. 2014. Prescriptive Evolution to Conserve and Manage Biodiversity. Annu Rev Ecol Evol Syst. 45: 1–22. https://doi.org/10.1146/annurev-ecolsys-120213-091747

Spielman D, Brook BW, Frankham R. 2004. Most species are not driven to extinction before genetic factors impact them. Proc Natl Acad Sci. 101: 15261–15264. https://doi.org/10.1073/pnas.0403809101

Taft HR, McCoskey DN, Miller JM, Pearson SK, Coleman MA, Fletcher NK, Mittan CS, Meek MH, Barbosa S. 2020. Research–management partnerships: An opportunity to integrate genetics in conservation actions. Conserv Sci Pract. 2: e218. https://doi.org/10.1111/csp2.218

Taylor RH, Dussex N, van Heezik Y. 2017. Bridging the conservation genetics gap by identifying barriers to implementation for conservation practitioners. Glob Ecol Conserv. 10: 231–242. https://doi.org/10.1016/j.gecco.2017.04.001

Teixeira JC, Huber CD. 2021. The inflated significance of neutral genetic diversity in conservation genetics. Proc Natl Acad Sci. 118: e2015096118. https://doi.org/10.1073/pnas.2015096118

Thompson JD. 2020. Plant Evolution in the Mediterranean: Insights for conservation. 2nd ed. Oxford: Oxford University Press. https://doi.org/10.1093/oso/9780198835141.001.0001

UICN comité français. 2019. [accessed Nov 2019]. https://uicn.fr/liste-rouge-flore/.

Vitalis R, Glémin S, Olivieri I. 2004. When Genes Go to Sleep: The Population Genetic Consequences of Seed Dormancy and Monocarpic Perenniality. Am Nat. 163: 295–311. https://doi.org/10.1086/381041

Weeks AR, Sgro CM, Young AG, Frankham R, Mitchell NJ, Miller KA, Byrne M, Coates DJ, Eldridge MDB, Sunnucks P, et al. 2011. Assessing the benefits and risks of translocations in changing environments: a genetic perspective. Evol Appl. 4: 709–725. https://doi.org/10.1111/j.1752-4571.2011.00192.x

Willi Y, Kristensen TN, Sgrò CM, Weeks AR, Ørsted M, Hoffmann AA. 2022. Conservation genetics as a management tool: The five best-supported paradigms to assist the management of threatened species. Proc Natl Acad Sci. 119: e2105076119. https://doi.org/10.1073/pnas.2105076119

Table S1. Description of 6 life-history traits within pairs of species according to the status of the species (threatened and not threathened NT, see text for details). Life-history traits are considered only for the 47 species in the dataset. Details are given in Appendix 1.

Longevity	Longevity of threatened species		
of NT species	Perennial	Annual	Total
Perennial	20	2	22
Missing data	3	0	3
Total	23	2	

Reproduction event	Reproduction event of threatened species		
of NT species	Monocarpic	Polycarpic	Total
Monocarpic	2	0	2
Polycarpic	3	17	20
Missing data	1	2	3
Total	6	19	

Vegetative reproduction	Vegetative reproduction of threatened species			
of NT species	Absent	Present	Missing data	Total
Absent	2	1	0	3
Present	2	6	3	11
Missing data	3	4	4	11
Total	7	11	7	

Pollination vector	Pollination vector of threatened species				
of NT species	Anemophily	Entomophily	Hydrophily	Missing data	Total
Anemophily	1	1	0	0	2
Entomophily	0	17	1	0	18
Hydrophily	0	0	0	0	0
Missing data	0	1	0	4	5
Total	1	19	1	4	

Dispersion vector	Dispersion vector of threatened species					
of NT species	Anemochory	Barochory	Hydrochory	Zoochory	Missing data	Total
Anemochory	3	2	0	0	0	5
Barochory	2	2	0	1	0	5

Hydrochory	0	1	2	0	1	4
Zoochory	0	1	0	1	0	2
Missing data	1	1	0	0	7	9
Total	6	7	2	2	8	

Table 1 (follow)

Mating system	Mating system of threatened species				
of NT species	Autogamy	Mixed	Allogamy	Missing data	Total
Autogamy	2	1	0	0	3
Mixed	0	2	1	1	4
Allogamy	1	1	7	1	10
Missing data	3	1	1	3	8
Total	6	5	9	5	