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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12   **Abstract**

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

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

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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

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

82 **Materials and Methods**

83 *Genetic diversity of threatened plant species in France*

84 The IUCN Red List threatened categorization system (CR, EN, VU) was used to
85 identify 452 threatened plant species and subspecies occurring in metropolitan France
86 (https://uicn.fr/liste-rouge-flore/, November 2019). In addition, the list of the 387
87 legally protected Angiosperms species in France was extracted from the institutional
88 website collecting data on biodiversity in France (https://inpn.mnhn.fr/, November
89 2019). The two lists were merged to define threatened Angiosperm species and
90 subspecies in metropolitan France. We also added three species (*Arenaria grandiflora*,
91 *Convolvulus lanuginosus, Pinguicula grandiflora*) with a local status of protection that
92 are known to have been studied for genetic diversity in the area were there are
93 protected. The final list included 749 plant taxa. We did not check for synonymy at this
94 stage. It is important to note that genetic diversity is not considered neither in the IUCN
95 criteria, nor for a legal protection status in France.
96   Using this list, automatic data mining was carried out on NCBI
97 (https://www.ncbi.nlm.nih.gov/), on Google Scholar and on the French registry of Ph-D
98 theses (http://theses.fr/) to find any study on these species. A search on the Web of
99 Science database was also performed using the list of species (eg TITLE = "SPECIES1"
100 *OR* "SPECIES2"…). We obtained 6779 results (20 April 2022), and we refined the
101 results using the keyword *"genetic"*. Among the 625 results, we retained publication
102 with at least one author from France (Countries/Regions = "France"). For two species
103 (*Agropyron cristatum* and *Vitis vinifera)* related to largely cultivated plants, a dedicated
104 search was done.
105   Among all the studies collected, only those with data on within-population
106 genetic diversity were retained. We used genetic diversity at population scale since it is
107 the pertinent scale to detect effects of drift, absence of migration and because selection
108 needs within-population diversity to act. For each species, parameters estimating genetic
109 diversity within populations were extracted from the studies. We also documented
110 population size and sampling size, and several life-history traits known to influence
111 genetic diversity such as mating system, longevity, vegetative reproduction, dispersion
112 vector and pollination vector (see Appendix 1).
113   As our goal was to compare genetic diversity of threatened species to genetic
114 diversity of non-threatened species, we searched for studies performed on related non-
115 threatened species. The collection of data for non-threatened species was performed in
116 several phases. Ideally, each pair of species should include a threatened and non-
117 threatened congeneric species (see Lavergne et al. 2004) occurring in the same habitat
118 and sharing common life-history traits. As we aimed to compare genetic diversity, we
119 must also have genetic parameters estimated on the same type of genetic markers
120 although the best comparison would use the same loci for those same markers. We
121 made a first search on Web of Science using the name of the genus and the types of
122 genetic markers (e.g. TOPIC= Anchusa *AND* TOPIC= AFLP). In absence of results, we

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123   relaxed the congeneric criteria and searched using the family name (e.g. TOPIC=
124   Caryophyllaceae *AND* TOPIC= SSR). Species were not considered as a valid control if
125   they were said to be "rare" or "threatened" by the authors of a study, if they were
126   cultivated species, or if they were invasive species. When several non-threatened
127   species were available, we selected the species the most similar to the threatened species
128   within the pair for life-history traits. For 3 species (*Pinguicula rosea, Pinguicula*
129   *grandiflora* and *Orobanche bartlingii*), we could not find any non-threatened species in
130   the same family studied with the same markers (AFLP), so we used estimations of
131   diversity in AFLP from the review on plants by Nybom (2004). For *Eryngium*
132   *viviparum*, the comparison was made using the only French population and Iberic
133   populations, since the species is not threatened in Spain (Rascle et al. 2019). One recent
134   study on the threatened *Delphinium montanum* documents diversity using SNPs
135   (Salvado et al. 2022), but we could not find any pertinent study for the non-threatened
136   control. This species was not included in our comparison.

137   *Data analyses*

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

154   *Considerations of genetic diversity in management actions*

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

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

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

178   We thus used two sources of information to study the consideration of genetic
179 diversity in management actions: the synthesis of management plans available on-line,
180 hereafter "recovery plans", and the answer of managers to the survey, hereafter
181 "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).

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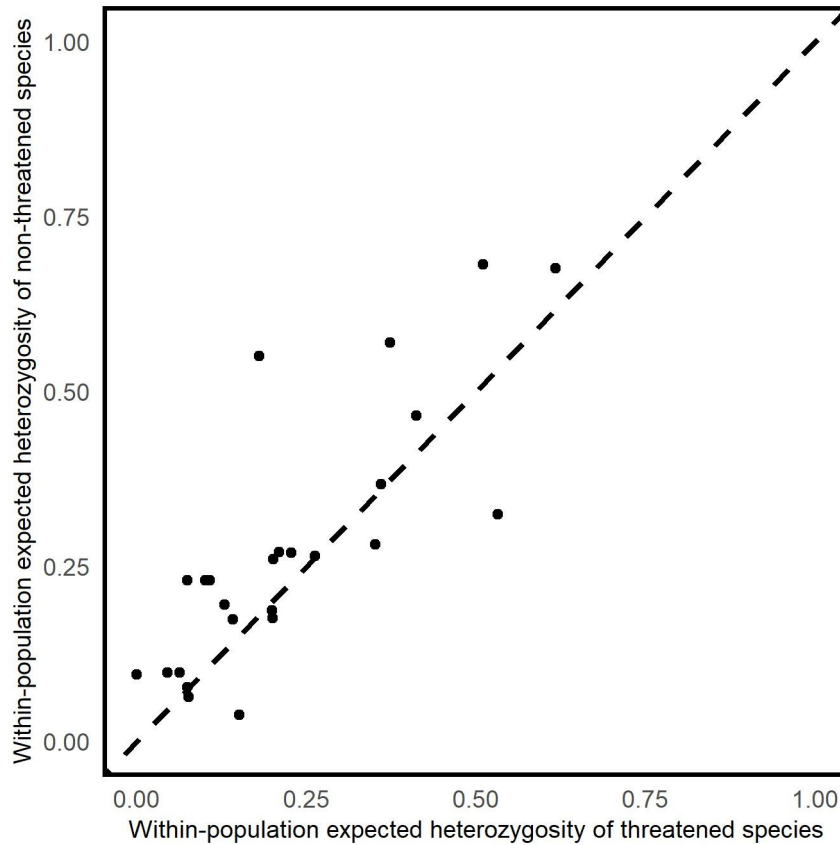
Figure 1: Within-population heterozygosity (He) of threatened plant species in France and non-threatened species. The dashed line represents the X=Y line, *i.e.* a point on this line would indicate that threatened and non-threatened species have the same level of heterozygosity.

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

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264   considered (Table 1). Population size is often known (92%) but no reference to *effective*
265   *population size* could be found in any conservation plan. Mention of "genetic" occurred
266   in more than 79% of plans (Table 1). Mention of "genetic" is often associated with the
267   preservation of diversified *ex situ* material (80%) and rarely with threats such as genetic
268   erosion (32%) or population persistence (14%). Only 10 recovery plans used already
269   existing genetic data (Table 1) and 8 of these 10, plus 4 others called for the collections
270   of genetic data (Table 1). Overall only 14 documents out of 62 refered in some way to
271   the use of genetic data.

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

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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.

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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)

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287 **Table 2** : Information available in surveys about life-history traits of the species
288 concerned and other topics related to genetics. In the second column, are given the
289 number (percentage) of surveys in which the topics is fill in for the species considered.
290 In the last column, are given the same informations for actions including manipulation
291 of population size.
292

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)

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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

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336 seems to be the rule in several countries including France. An international standard for
337 species recovery plans explicitly including genetic aspects should be developed (Pierson
338 et al. 2016).
339   Several recommendations can be made to improve the integration of population
340 genetic diversity in conservation actions. A better spread of the concept of effective
341 population size (Ne) would be one of the recommendations since it is directly related to
342 genetic threats and population extinction (Allendorf and Luikart 2006; Hoban et al.
343 2022). Effective population size is often smaller than the demographic population size
344 (eg. Allendorf and Luikart 2006; Hoban et al. 2020 but see Vitalis et al. 2004). So far,
345 methods to estimate Ne are clearly too difficult to be applied in most natural populations
346 because of the quality and quantity of genetic or demographic data necessary and
347 because of the complexity of the statistical tools involved. However, collection of data
348 on life-history traits particularly affecting genetic diversity and Ne can be recommended
349 (Hoban et al. 2020), yet we have found that most conservation plans are conducted with
350 only moderate knowledge on such ecological and biological traits. Acquisition of data
351 about the mating system of the species is a minimum requirement since it directly
352 affects Ne and the structure of genetic diversity (Duminil et al. 2007; Hoban et al.
353 2020). Nevertheless, there is much less information about mating systems than others
354 traits in conservation plans in Australia (Cook and Sgrò 2018) and in France (this
355 study). Life-history traits are also important for other aspects of management, for
356 example, the longevity of a species decreases the probability to reach reproduction stage
357 per seed, therefore, increases the number of seeds to use in an introduction (Machinsky
358 and Haskin 2012). The absence of information about basic biological characteristics of
359 plant species probably helps to explain some of the failures of reintroduction actions
360 (Godefroid et al. 2011).
361   We also reported that the majority (nine out twelve) of manipulations of
362 population size are performed with one source population and two others used only two
363 populations as sources. Increasing population size reduces the demographic risk and
364 future genetic erosion whatever the origin of the introduced individuals. However to
365 address genetic issues linked to past genetic erosion, genetic mixing is required, thus
366 individuals should originate from a different population, provided outbreeding and local
367 adaptation issues are addressed before mixing populations (Hoffmann et al. 2021;
368 Teixeira and Huber 2021). This would make conservation actions more effective, as
369 would supplementing information on neutral genetic diversity with information on
370 functional genetic diversity (Teixeira and Huber 2021). This highlights the importance
371 of improving knowledge on evolutionary theory in the training of conservation
372 management staff.
373   Several factors, including social, political and economic considerations, explain
374 the absence of integration of evolutionary theory into conservation plans, but the
375 training of practitioners is likely to be one of the most important causes (Taylor et al.
376 2017; Cook and Sgrò 2018; Sandstrom et al. 2019). Furthermore, despite the
377 recommendation to use open-access research, results from research in conservation
378 biology do not percolate to practitioners (Taylor et al. 2017). While scientific
379 publications is an important source for general interpretations, several constraints were

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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).

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

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

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

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

Pollination vector of NT species	Pollination vector of threatened species				Total
	Anemophily	Entomophily	Hydrophily	Missing data	
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 of NT species	Dispersion vector of threatened species					Total
	Anemochory	Barochory	Hydrochory	Zoochory	Missing data	
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 of NT species	Mating system of threatened species				Total
	Autogamy	Mixed	Allogamy	Missing data	
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	

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