

Review

# Plant Conservation Practitioners Can Benefit from Neutral Genetic Diversity

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**Abstract:** Several papers deal with a conservation genetics gap in which plant conservation and restoration managers or practitioners do not soundly integrate population genetics information into conservation management. Authors concerned about this issue point out that practitioners perceive genetic research results to be impractical or unnecessary in the short term due to time and financial constraints. In addition, researchers often fail to translate research findings into comprehensive, jargon-free recommendations effectively. If possible, conservation-related or conservation-oriented articles should be easily written to bridge the research–implementation gap. Finally, based on a previously published prioritization framework for conservation genetics scenarios, we introduce four simple genetic categories by exemplifying each case. We hope that conservation practitioners could employ these suggested guidelines for the prioritization of population- and species-level management.

**Keywords:** adaptive genetic variation; conservation; geneticists; implementation; neutral genetic variation; practitioners



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## 1. Introduction

Traditionally, neutral genetic variation (hereafter, NGV) surveys that use neutral (or nearly neutral) genetic markers (e.g., allozymes, RAPDs (random amplified polymorphic DNAs), AFLPs (amplified fragment length polymorphisms), ISSRs (inter simple sequence repeats), microsatellites or SSRs (simple sequence repeats) or STRs (short tandem repeats), and more recently, neutral single nucleotide polymorphisms (SNPs)) are cheaper and take much less time than adaptive genetic variation (hereafter, AGV). However, variation at any of the abovementioned genetic markers does not (usually) directly influence fitness. In other words, different alleles at a single locus would not provide higher or lower adaptability among the individuals of a given population. To date, the vast majority of studies on conservation genetics have been based on NGV. One of the reasons researchers use NGV is that a reservoir of genetic diversity in plant populations that is neutral now could become adaptive when the environmental conditions change in the future [1,2].

In plants, common garden and/or reciprocal transplant studies have traditionally been conducted to assess levels and degrees of AGV within and among populations, which require plenty of time and resources [3–9]. The most comprehensive studies in this regard are those conducted with commercially important timber-yielding tree species because their well-adapted genotypes are used to replant clear-cut areas [10–15]. Due to the advent of genomic tools by high throughput sequencing (HTS), researchers on population and

landscape genomics have primarily studied model species on the adaptation of local populations, climate change adaptation, and conservation (or restoration) biology (reviewed in [16–18]). Furthermore, recent advances in computational methods and reduced HTS-related costs for using genetic data (e.g., SNPs) to identify adaptive loci through association with phenotypic traits or environmental factors have increased the number of published papers [19,20]. Recently, some conservation geneticists have suggested that policy makers integrate genomics into decision making for laws protecting endangered species [9,21].

In very recent times, a debate about the assumption that NGV would be considered a proxy for AGV has arisen [2,20,22–24]. In particular, Teixeira and Huber [24] claim that NGV does not predict adaptive potential (AGV). However, García-Dorado and Caballero [22] stress that NGV is “a useful tool for conservation biology.” In the era of HTS, it is important to understand AGV. Still, conservation geneticists and practitioners should appreciate that demography and many ecological and evolutionary processes relevant to conservation can only be understood (estimated) through neutral markers (NGV). In this light, it is clear that the study of AGV and NGV are very complementary.

In this short review, we briefly recommend bridging the gap between conservation geneticists and conservation practitioners. We further encourage researchers and managers to collaborate to bring together knowledge and experience to develop appropriate management strategies for individual species/populations. Finally, to make conservation practitioners easily employ population genetics information in conservation practice, we propose a series of simplified and expected scenarios according to levels of neutral genetic parameters (which originally were proposed by Ottewell et al. [25]), providing examples in detail.

## **2. Bridging the Gap between Conservation Geneticists and Conservation Practitioners: Some Examples**

As of 2011, there were only 20 (8%) out of 249 plant species reintroductions worldwide with some knowledge on genetic diversity [26]; this ratio may be higher now, yet statistics are lacking. In addition, it may be challenging and crucial to know precisely how practitioners have used genetic information for conservation implementation because many data are either currently unpublished or included in technical reports with restricted access [26,27]. Taylor et al. [28] contended that these barriers to implementation or similar adverse situations for conservation practitioners exist internationally. Britt et al. [29], using a meta-analysis of published conservation studies that employed genetic and genomic data sets, found that only 38% of the studies could inform conservation or management through clearly stated recommendations for action or policy. Thus, conservation researchers should communicate better with practitioners to integrate genetic findings into conservation implementation [25,29–35].

Recently, there has been increasing interest in reducing the gap between conservation science and practice [27–29,33,34,36–38]. In New Zealand, Taylor et al. [28] interviewed 148 conservation practitioners from the Department of Conservation regarding their attitude to, knowledge of, and experiences employing population genetics for conservation. Several important results emerged from the survey. First, conservation practitioners want to use population genetics for conservation management, but they do not routinely do so. Second, funding and expertise are the main barriers to the use of genetics in conservation (practitioners want to work with geneticists at universities or other institutes but are unsure how to reach them and do not fully understand how genetics might benefit them). Recent advances in understanding the genomic basis of adaptation would have widened the gap in incorporating genomic knowledge into active management plans [21,39,40]. To bridge the conservation gap between researchers and managers/practitioners, Taylor et al. [28] proposed “a plan to address barriers to use of genetics by conservation practitioners”, aiming to improve understanding and the integration of population genetics into conservation management. Specifically, this plan had three main suggestions. First, the improvement of the communication between conservation geneticists and practitioners through “genetics surgery” (where researchers answer genetics-based queries), “speed dating” (practitioners

are introduced to multiple conservation geneticists to identify overlapping interests), and sabbaticals/exchanges (practitioners work closely with conservation geneticists and vice versa). Second, the increase of expertise among practitioners via one-day workshops, a YouTube channel, and online self-taught courses. Third, the creation of conservation genetics “hubs” through contact points and large-scale funding opportunities. Initiatives such as surveys may improve the researcher’s understanding of the problems and obstacles faced by practitioners, paving the way for enhanced communication and partnerships that enable more effective conservation strategies and activities. Recently, Cook et al. [40] proposed a “hypothetical sequential scenario” for an isolated but important population of a threatened and declining plant or animal species: first, understanding of management context; second, generation of relevant evidence (e.g., population genetics and fitness data); third, supporting the use of appropriate evidence; finally, collaboration between researchers and practitioners. Considering suggestions by Taylor et al. [28] and Cook et al. [40], we believe that the practitioners’ clear understanding of NGV and AGV presented in the previous section will help bridge the “research–implementation gap”.

It would be meaningful to introduce an example where conservation/restoration managers have directly applied genetic information. To develop a model of integrated (neutral) genetic and demographic conservation for threatened plants, Izumi Washitani and his colleagues [41] conducted a long-term project on restoring the threatened aquatic plant *Nymphoides peltata* in Lake Kasumigaura, Japan. As a result of restoration efforts, increases in the number of local populations and genetic diversity in the Lake Kasumigaura metapopulation led to population recovery. Unfortunately, although the population increased in the early stages of reintroduction, more recently, *N. peltata* populations are declining in almost all the sites in the lake, including the introduced site, and the genetic diversity (measured using neutral markers) is also declining (J. Nishihiro, pers. comm. in 2019). This result may not be surprising, given that the expected survival rate for reintroduced native species is low (on average, 52%, 19%, and 16% for survival, flowering, and fruiting, respectively, for reintroduced plants, based on 249 plant species reintroductions worldwide [26]). However, at present, it may be premature to determine whether the reintroduction of *N. peltata* in Lake Kasumigaura has been successful or not. Thus, there is no choice but to wait for their long-term monitoring. Despite the fact that restoration efforts will not always be entirely successful, conservation researchers, managers, and practitioners should keep in mind that knowledge of the NGV of target species, if the information of AGV is unavailable, is one of the most important traits that positively influence plant reintroduction outcomes [26]. The total absence of data on species’ genetic variation has often condemned the actions of restoration to failure, e.g., the failed reintroduction attempts of *Lysimachia minoricensis* on Minorca Island, Spain, probably occurred because the seeds that were used came from a single collection and thus lacked genetic variability [42]. This stresses the importance of assessing overall, genome-wide genetic diversity for rare and endangered plant species [43].

As noted above, to put population genetics information into the field, conservation practitioners may need a simplified prioritization framework for conservation strategies that are easily used [25], which helps to bridge the research–implementation gap. In the following two sections, we discuss this issue.

### 3. Expected Scenarios According to Levels of Neutral Genetic Parameters: A Simplified Proposal

Thanks to the large body of plant allozyme literature, researchers have demonstrated that a series of life history and ecological traits account for considerable variance in within- and among-population genetic diversity [44–46]. These traits include life forms, breeding systems, geographic ranges, and seed dispersal mechanisms, which can be used, therefore, to predict the levels and distribution of genetic diversity in seed plant species.

Focusing on life forms, forest trees, on average, have more allozyme genetic diversity within their populations than annuals or herbaceous perennials as measured by  $H_{eP-N}$  (0.144 versus 0.101 or 0.096; the subscript  $N$  refers to neutral),  $\%P_{P-N}$  (47.9 versus 29.4

or 27.5; Table 1), and  $A_{P-N}$  (1.74 versus 1.45 or 1.38; Table 1). A similar pattern was also found in overall species-level genetic diversity across life forms as measured by  $H_{eS-N}$  (0.170 versus 0.154 or 0.125; Table 1),  $\%P_{S-N}$  (62.7 versus 49.2 or 42.8; Table 1), and  $A_{S-N}$  (2.16 versus 2.02 or 1.75; Table 1). Furthermore, the degree of among-population allozyme genetic diversity in trees is substantially lower than in herbaceous perennials or annuals as measured by  $G_{ST-N}$  (0.089 versus 0.256 or 0.355; Table 1). A similar pattern is found for DNA-based markers (Table 1). Several factors are suggested to explain the higher within-population genetic diversity and the lower among-population genetic divergence in trees. These include a predominantly outcrossing mating system, higher levels of gene flow, longevity, tall statures, low population densities, occurrence in late successional communities, polycarpic nature, larger  $N_e$ , low linkage disequilibrium, presumably high levels of AGV, a higher basic number of chromosomes, more diversifying selection, or delayed maturity [45,47,48].

**Table 1.** Mean levels and distribution of allozyme, RAPD, and SSR diversity of plant species representing different life forms (for allozymes from [48] and for RAPDs and SSRs from [49])<sup>a</sup>.

Parameter	Annuals	Herbaceous Perennials	Woody Perennials
Allozyme			
$N_P, N_S$	226, 226	228, 215	213/214
$\%P_{P-N}$	29.4 <sup>b</sup>	27.5 <sup>b</sup>	47.9 <sup>a</sup>
$\%P_{S-N}$	49.2 <sup>b</sup>	42.8 <sup>b</sup>	62.7 <sup>a</sup>
$A_{P-N}$	1.45 <sup>b</sup>	1.38 <sup>b</sup>	1.74 <sup>a</sup>
$A_{S-N}$	2.02 <sup>ab</sup>	1.75 <sup>b</sup>	2.16 <sup>a</sup>
$H_{eP-N}$	0.101 <sup>b</sup>	0.096 <sup>b</sup>	0.144 <sup>a</sup>
$H_{eS-N}$	0.154 <sup>b</sup>	0.125 <sup>c</sup>	0.170 <sup>a</sup>
$G_{ST-N}$	0.355 <sup>a</sup>	0.256 <sup>b</sup>	0.089 <sup>c</sup>
Parameter	Annuals	Short-lived perennials	Long-lived perennials <sup>b</sup>
RAPD <sup>c</sup>			
$N$	6	17	37
$H_{pop}$	0.13 <sup>b</sup>	0.20 <sup>ab</sup>	0.25 <sup>a</sup>
$N$	10	45	60
$\Phi_{ST-N}$	0.62 <sup>a</sup>	0.41 <sup>b</sup>	0.25 <sup>c</sup>
$N$	2	18	24
$G_{ST-N}$	0.47 <sup>a</sup>	0.32 <sup>ab</sup>	0.19 <sup>b</sup>
SSR			
$N$	15	29	59
$H_{eP-N}$	0.46 <sup>b</sup>	0.55 <sup>b</sup>	0.68 <sup>a</sup>
$N$	4	12	17
$G_{ST-N}$	0.40 <sup>a</sup>	0.31 <sup>ab</sup>	0.19 <sup>b</sup>

<sup>a</sup>  $N_P, N_S$ , number of entries at population and species levels, respectively;  $N$ , number of entries; subscripts “p” and “s” indicate population and species levels, respectively, and subscript “N” indicates neutral.  $\%P$ , the percentage of polymorphic loci;  $A$ , mean number alleles per locus;  $H_e$ , gene diversity or Hardy–Weinberg expected heterozygosity both at monomorphic and polymorphic loci;  $G_{ST}$  (or  $F_{ST}$ ), among-population genetic differentiation;  $\Phi_{ST}$ , fixation index among populations relative to the total genetic variation among individuals. Values sharing the same letter in a column are not significantly different at  $p < 0.05$ . The table was modified from Tables 2 and 3 of Chung et al. [48]. <sup>b</sup> To facilitate the comparisons between allozymes and other molecular markers, we equate “long-lived perennials” to “woody perennials”. <sup>c</sup> Nybom [49] provides the only means of  $H_{pop}$  and  $\Phi_{ST-N}$  (or  $G_{ST-N}$ ) for RAPDs, but for practical reasons these thresholds are also applicable to AFLPs and ISSRs.

As Ottewell et al. [25] emphasized, the  $G_{ST-N}$  (or  $F_{ST-N}$ ) and  $H_{e-N}$  parameters are preferentially used to measure NGV because they could be, at least partly, proxies of ecological and evolutionary processes, such as random genetic drift, habitat fragmentation, founder effects, or gene flow. Four main scenarios can be delineated to provide a clear, general guide to implement genetic management (“LH” or low  $G_{ST-N}$  (L) and high  $H_e$  (H), “HL” or high  $G_{ST-N}$  and low  $H_e$ , “LL” or low  $G_{ST-N}$  and low  $H_e$ , and “HH” or high  $G_{ST-N}$  and high  $H_e$  [25]; Figure 1). As Ottewell et al. [25] proposed, if the parameter  $F_{IS}$  (inbreeding coefficient) is also considered, then eight combinations are produced; however, here, we

only deal with  $G_{ST-N}$  (or  $F_{ST-N}$ ) and  $H_{e-N}$  because estimates of  $F_{IS}$  are often sensitive to sampling strategies and the clonal structure of vegetatively reproducing plants.

Based on the mean values for allozymes reported in Table 1 (based on an extensive database of about 740 species), we proposed a classification of both the  $G_{ST-N}$  and  $H_{eP-N}$  values into two levels (high (H) or low (L); see [48] for more details). For trees,  $G_{ST-N}$  and  $H_{eP-N}$  values below 0.089 and 0.144, respectively, were considered as “L”, whereas values higher than these thresholds were regarded as “H”. For herbaceous perennials, using the same scheme,  $G_{ST-N} < 0.256$  as L and  $G_{ST-N} > 0.256$  as H, whereas  $H_{eP-N} < 0.096$  as L, and  $H_{eP-N} > 0.096$  as H. Compared with allozymes, mean values for SSRs and other DNA-based dominant markers were obtained from a much smaller body of studies [49]. Since Nybom [49] classified plants according to the life form category as annuals, short-lived perennials, and long-lived perennials, the categories “long-lived perennials” and “woody perennials” were considered as equivalent. As with allozymes, we took the means provided by Nybom [49] as threshold values (Table 1). For long-lived perennials, the threshold values of  $\Phi_{ST-N}$ ,  $G_{ST-N}$ , and  $H_{POP}$  for RAPDs were 0.25, 0.19, and 0.25, respectively, and  $G_{ST-N}$  and  $H_{eP-N}$  values for SSRs were 0.19 and 0.68, respectively. For short-lived perennials, the threshold values of  $\Phi_{ST-N}$ ,  $G_{ST-N}$ , and  $H_{POP}$  for RAPDs were 0.41, 0.32, and 0.20, respectively, and  $G_{ST-N}$  and  $H_{eP-N}$  values for SSRs were 0.31 and 0.55, respectively. Threshold values for annuals for each marker are also detailed in Table 1. As Nybom [49] only provides means of  $H_{POP}$  and  $\Phi_{ST-N}$  (or  $G_{ST-N}$ ) for RAPDs, for practical reasons we consider that these thresholds could also be applicable to other dominant markers such as AFLPs and ISSRs.

The first category (LH; low among-population differentiation ( $G_{ST-N}$  or  $F_{ST-N}$ ) and high within-population diversity ( $H_{eP-N}$ )) is expected to be found in many outcrossing and high dispersal species with regional or wide distributions. Populations of these species would have been historically connected, likely having kept large  $N_e$  (“healthy” populations [25]). In contrast, the HL (high differentiation and low diversity) type is often found for rare, endemic, or threatened tree and herbaceous species. This genetic pattern would result from populations with historically low  $N_e$  and disjunct distribution, traits that would have persisted for a long period of time. Compared to the LH and HL categories, the LL (low differentiation and low diversity) and the HH (high differentiation and high diversity) ones are less commonly found. The LL category is expected to be found fairly often in plant species with populations that have been historically connected but with low  $N_e$  and/or a signature of historical founder effects or bottlenecks. Species recovering from range contractions (e.g., post-glacial founder effects through post-glacial recolonizations) would show the LL pattern. The HH category would be expected in plant species with disjunct distribution but large  $N_e$  and little contemporary gene flow; examples may include species with special habitats or species contracted to refugial areas with historically large  $N_e$  [25].

#### 4. A Prioritization Framework for Conservation Strategies Based on Neutral Genetic Diversity Scenarios

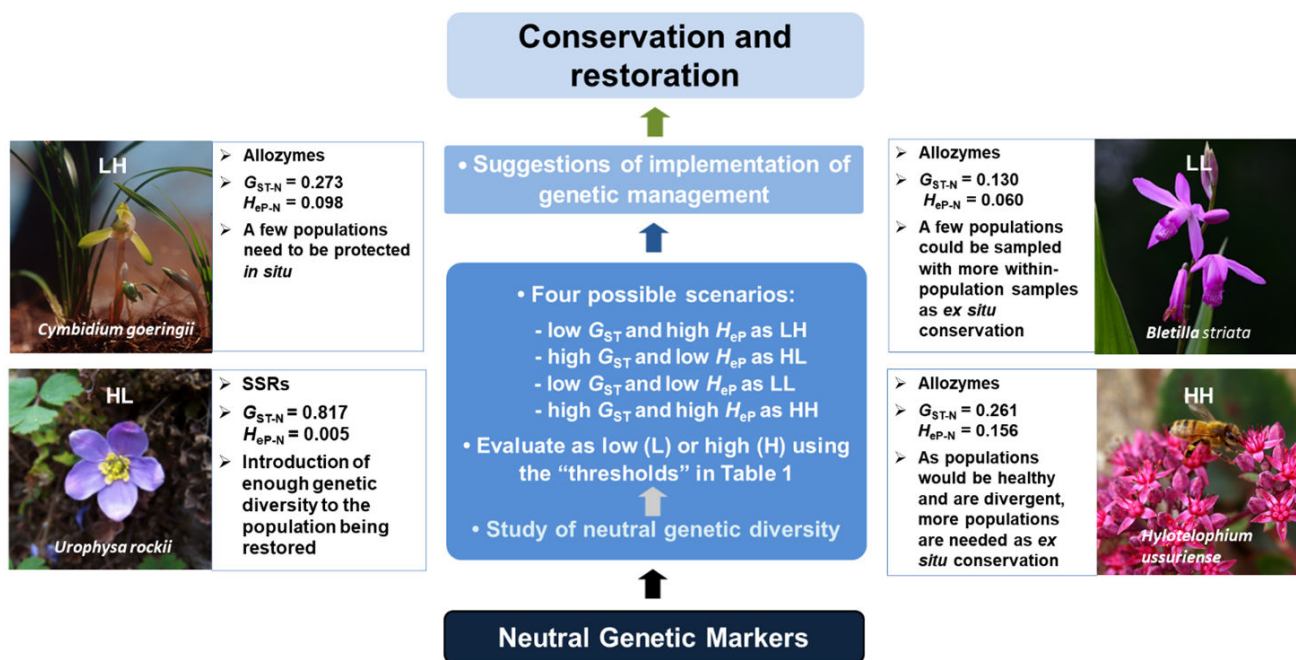
To be useful for conservation, however, the four genetic categories (LH, HL, LL, and HH) should be linked to specific recommendations and guidelines for the prioritization of population-level management [25,48]. As for the long-term management and conservation of those plant species under the LH scenario, Ottewell et al. [25] suggested that translocation between populations is a viable option to enhance  $N_e$ . Management of ecological and demographic threats at the species level is needed to maintain population size and gene flow. Facilitation of pollen and seed immigration would be necessary to minimize the effects of inbreeding and outbreeding depression. As for in situ restoration efforts (e.g., reinforcements), we suggest that seeds of these species could be sourced from a few populations with low pairwise  $G_{ST}$  values with the population to be restored. This strategy will improve the chances of successful restoration if adaptive traits are correlated with neutral marker loci. In addition, just a few populations would be needed to be protected in situ yet contrasting habitats should be taken into consideration. As for ex situ and in situ conservation efforts, populations with high  $H_{eP-N}$  (and  $AR$ ) should be targeted, as-

suming that these populations also harbor high genetic diversity (AGV) at phenotypically important traits.

Representative allozyme-based examples of the LH category are the trees *Pinus rigida* ( $G_{ST-N} = 0.023$  and  $H_{eP-N} = 0.146$  [50]) and *Fagus grandifolia* ( $G_{ST-N} = 0.056$  and  $H_{eP-N} = 0.165$  [51]) in the northeastern USA, and the herbaceous perennials *Liatris helleri* ( $G_{ST-N} = 0.159$  and  $H_{eP-N} = 0.219$  [52]) and *Asclepias exaltata* ( $G_{ST-N} = 0.093$  and  $H_{eP-N} = 0.182$  [53]) in the southeastern USA, and *Cymbidium goeringii* ( $G_{ST-N} = 0.098$  and  $H_{eP-N} = 0.240$  [54]; Figure 1) in the Korean Peninsula. Except for *C. goeringii*, all four species occur in the old-growth forests of the Appalachians in the southeastern USA, which are considered refugia at the Last Glacial Maximum (21,000–18,000 years ago). We must keep in mind that many published papers using NGV belong to the LH scenario.

Under the HL scenario, conservation managers and practitioners should consider that the management activities for HL plants (e.g., ongoing translocations) are more expensive in terms of management intensity and cost than those for LH ones. Notably, many rare and threatened species fall into this category [44]. Translocation between populations is a recommended measure, but it should be done with special caution to minimize potential outbreeding depression. Ottewell et al. [25] also indicate that a means for recovering in situ presumed total genetic diversity from seed banks would be necessary and, since the small population sizes of these species make them susceptible to the loss of total genetic diversity, in situ conservation efforts should emphasize habitat protection. We suggest that ex situ seed conservation in HL plant species should also be a priority, and germplasm resources should be established from seeds collected from as many populations as possible with high  $H_{eP-N}$  (and  $AR$ ), rather than only from a few populations. The introduction of enough total genetic diversity is necessary so that natural selection can respond to the population's environment being restored [55]. In addition, the planting of seedlings of these species in potential habitats that represent future climatic conditions could also be a successful conservation strategy [48].

The HL scenario is commonly found in rare herbaceous understory species. Examples include the herbaceous perennial *Helonias bullata* (allozymes,  $G_{ST-N} = 0.306$  and  $H_{eP-N} = 0.029$  [56]) in the old-growth forests of the Appalachians, the herb *Urophysa rockii* (SSRs,  $\Phi_{ST-N} = 0.669$  and  $H_{eP-N} = 0.341$  [57]; Figure 1) in southwestern China, the narrow endemic perennial herb *Clematis acerifolia* (allozymes,  $G_{ST-N} = 0.273$  and  $H_{eP-N} = 0.072$  [58]) in north-eastern China, and the rare small carnivorous plant *Drosera rotundifolia* in southern Korea (allozymes,  $G_{ST-N} = 0.817$  and  $H_{eP-N} = 0.005$  [59]). However, this pattern has also been observed in some trees. Despite their current wide distributions, some woody species with a history of small and disjunct populations, smaller founder populations, or populations that have experienced past bottlenecks might harbor low  $H_{eP-N}$ . This scenario has been observed for *Pinus resinosa* (SSRs,  $H_{eP-N} = 0.078$  [60]) in two populations in Virginia and West Virginia in the Southern Appalachians (eastern USA), and for *Picea asperata* (allozymes,  $G_{ST-N} = 0.311$  and  $H_{eP-N} = 0.096$  [61]) in southwestern China.



**Figure 1.** Flow chart on the applications of neutral genetic markers to conservation, restoration, and management strategies. We follow the four genetic scenarios according to levels and degree of neutral genetic diversity (i.e., LH or low  $G_{ST-N}$  (L) and high  $H_e$  (H), HL or high  $G_{ST-N}$  and low  $H_e$ , LL or low  $G_{ST-N}$  and low  $H_e$ , and HH or high  $G_{ST-N}$  and high  $H_e$ , where “L” and “H” stand for “low” and “high”, respectively; Ottewell et al. (2016)). For details of conservation management strategies for each genetic scenario, refer to the text. Reference for LH is from Chung et al. [54], HL from Xie et al. [57], LL from Chung et al. [62], and HH from Chung et al. [63]. Photo of *Urophysa rockii* was taken from Xie et al. [64], which is under license CC BY 4.0 (<https://creativecommons.org/licenses/by/4.0/> accessed on 21 September 2021)—no changes were made by us.

Under the LL scenario, a few populations could be sampled, but seeds should be taken from a high number of individuals within each selected population for *ex situ* conservation. As for *in situ* restoration, management to increase recruitment and facilitate pollen and seed immigration, and the active translocation of individuals (by sourcing recruits from genetically diverse populations elsewhere) to increase population size, especially when remnant populations are highly inbred, would be suitable measures [25]. At the same time, conservation managers should employ a means for recovering total genetic diversity *in situ* (e.g., facilitating recoveries from seed banks). Examples fitting the LL scenario include the two terrestrial orchids *Bletilla striata* (allozymes,  $G_{ST-N} = 0.130$  and  $H_{eP-N} = 0.060$  [62]; Figure 1) in southern Korea, a species of presumably post-glacial origin (immigrated from southern Japan), and *Dendrobium officinale* (AFLPs,  $\Phi_{ST-N} = 0.263$  and  $H_{pop} = 0.143$  [65]) from six populations in refugia in southwestern China. Other allozyme-based examples are the rhizomatous evergreen small shrub *Chimaphila japonica* ( $G_{ST-N} = 0.028$  and  $H_{eP-N} = 0.030$  [66]) and the perennial herb *Lycoris sanguinea* var. *koreana* ( $G_{ST-N} = 0.092$  and  $H_{eP-N} = 0.052$  [67]), both in southern Korea.

Finally, under the HH scenario, a large number of populations are needed, but with a small number of samples per population, for *ex situ* conservation because extant populations would be healthy but divergent, constituting individual management units [25]. Perhaps, ecological efforts, rather than genetic ones, have to be taken into account, e.g., by focusing on managing habitats and ecological threats to maintain as many populations as possible across the species range and to maintain large sizes for them. There are some allozyme-based examples of trees showing an HH pattern, including *Pinus pungens*, which occurs in several disjunct populations ranging from north Georgia to Pennsylvania in the eastern USA ( $G_{ST-N} = 0.135$  and  $H_{eP-N} = 0.242$  [68]), the tree *Manglietia patungensis* ( $G_{ST-N} = 0.165$  and  $H_{eP-N} = 0.192$  [69]) from southwestern China, and *Hylotelephium* (= *Sedium*) *ussuriense* ( $G_{ST-N} = 0.261$  and  $H_{eP-N} = 0.156$  [63]; Figure 1), found in only one loca-

tion in Juwangsang National Park in the southern Korean Peninsula region. This pattern has also been observed in the diploid populations of the perennial weed *Turnera ulmifolia* var. *intermedia* from Central and South America (allozymes,  $G_{ST-N} = 0.480$  and  $H_{eP-N} = 0.130$  [70]), and in *Trillium grandiflorum* (allozymes,  $G_{ST-N} = 0.530$  and  $H_{eP-N} = 0.170$  [71]) in the eastern USA, for which samples were included from both glaciated and non-glaciated regions.

## 5. Conclusions

What stands out in Ottewell et al. [25] is that they are proposing a prioritization framework that is, notably, very clearly defined and efficiently written, which makes the genetic management strategies for each scenario easy to be understood by non-experts. As an improvement of Ottewell et al.'s [25] treatment, we here provide representative examples for each of the four scenarios that are based on our proposal of genetic judgment as “H” or “L” using average values. We expect that such kinds of studies will help researchers and managers/practitioners to work in partnership to bring together knowledge, expertise, and experience, which is a mandatory step for developing appropriate synthetic management strategies for individual species. Indeed, the NGV information could still be useful for bridging the gap between researchers and practitioners developing and implementing appropriate conservation measures.

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