STRENGTHENING THE LINK BETWEEN INTERNATIONAL CONSERVATION POLICY AND PLANT CONSERVATION GENETICS TO ACHIEVE MORE EFFECTIVE PLANT CONSERVATION[1]

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ABSTRACT

Although both international conservation policymakers and conservation geneticists have the shared goal of halting the loss of biodiversity, currently these communities have very little interaction. Because the targets of international conservation policy focus very little on the conservation of genetic diversity in wild species, they have received little attention from the plant conservation genetics community. Conservation policymakers should more explicitly include the conservation of genetic diversity of wild species in future targets to ensure that this important aspect of biodiversity is not overlooked for the majority of species on earth and to attain more buy-in from the plant conservation genetics community; I highlight specific ways in which policymakers may more explicitly include genetic diversity in international policy targets. For their part, conservation geneticists need to conduct work that will advance the big-picture goals of conservation policy; here, I discuss specific actions that plant conservation geneticists can take, such as measuring the proportion of genetic diversity that is protected, designing experiments in such a way to measure genetic erosion, and developing protocols to increase the efficiency of ex situ collection efforts. By working together, plant conservation geneticists and conservation policymakers will more effectively accomplish the shared goal of halting the loss of plant biodiversity.

Key words: Aichi Biodiversity Targets, biodiversity indicators, genetic diversity, genetic erosion, Global Strategy for Plant Conservation, plant conservation genetics.

Worldwide, thousands of species are threatened with extinction as the result of stressors such as the destruction of natural ecosystems, degradation of habitats, unsustainable use, the spread of non-native invasive species, and climate change. In recognition of the fact that the biological diversity on the planet and the ecosystem services that it provides are essential for political, economic, and social stability, the United Nations Convention on Biological Diversity (CBD), a multilateral treaty, was developed to respond to this global extinction crisis. The main goal of the CBD is to halt the worldwide decline of biodiversity and ecosystem services. The specific goals of the CBD are: (1) the conservation of biological diversity, (2) the sustainable use of the components of biological diversity, and (3) the fair and equitable sharing of the benefits arising out of the utilization of genetic resources (<https://www.cbd.int/intro/default.shtml>).

In 2002, the CBD committed to the Strategic Plan for the Convention on Biological Diversity, which called for gathering information about the rate of change in biodiversity and "a more effective and coherent implementation of the three objectives of the Convention, to achieve by 2010 a significant reduction of the current rate of biodiversity loss at the global, regional and national level" (CBD, 2002). At the same time, in recognition that plants are essential to life on earth and are being driven to extinction at an alarming rate, an international framework to help protect plant species from extinction, the Global Strategy for Plant Conservation (GSPC), was developed in 2002 (Wyse Jackson & Kennedy, 2009). The GSPC was developed within the framework of the CBD, with targets that closely mirror those in the Strategic Plan for the Convention on Biological Diversity, but with the long-term objective of quantifying the rate of change in plant biodiversity

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Table 1. The main targets of the Strategic Plan for Biodiversity 2011–2020 and the Global Strategy for Plant Conservation that relate to the conservation of genetic diversity or may be achieved more effectively as a result of a contribution from the field of conservation genetics (CBD, 2010, 2012).

Theme	Aichi targets	GSPC targets
Conserve genetic diversity of species of agricultural or socioeconomic importance	Aichi T13: By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socioeconomically as well as culturally valuable species, is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity.	GSPC T9: 70% of the genetic diversity of crops including their wild relatives and other socioeconomically valuable plant species conserved, while respecting, preserving, and maintaining associated indigenous and local knowledge.
Prevent extinction of threatened species	Aichi T12: By 2020, the extinction of known threatened species has been prevented and their conservation status, particularly of those most in decline, has been improved and sustained.	GSPC T7: At least 75% of known threatened plant species conserved in situ. GSPC T8: At least 75% of threatened plant species in ex situ collections, preferably in the country of origin, and at least 20% available for recovery and restoration programs.
Protect and manage important lands for diversity	Aichi T11: By 2020, at least 17% of terrestrial and inland water areas, and 10% of coastal and marine areas, especially areas of particular importance for biodiversity and ecosystem services, are conserved through effectively and equitably managed, ecologically representative and well-connected systems of protected areas and other effective area-based conservation measures, and integrated into the wider landscapes and seascapes.	GSPC T5: At least 75% of the most important areas for plant diversity of each ecological region protected with effective management in place for conserving plants and their genetic diversity.

and halting the current and continuing loss of plant diversity (CBD, 2012).

Because the international conservation community was unable to accomplish the goals set by the Strategic Plan by 2010 (Walpole et al., 2009; SCBD, 2010: 93), the parties to the CBD introduced the Strategic Plan for Biodiversity 2011–2020, which is a renewed commitment to measure the rate of change in biodiversity and halt the loss of biodiversity by 2020 (CBD, 2010). The Aichi Biodiversity Targets were developed by the CBD to meet the goals of the Strategic Plan (available at <https://www.cbd.int/sp/targets/default.shtml>) and include objectives such as (1) integrating biodiversity awareness and protection into government and society, (2) reducing pressures on biodiversity, (3) protecting ecosystem, species, and genetic diversity, (4) protecting and ensuring access to essential ecosystem services, and (5) gathering resources, knowledge, and infrastructure to enable implementation of the strategy (CBD, 2010). Correspondingly, the targets of the GSPC were updated and closely match the updated Aichi Targets (see <http://www.plants2020.net/gspc-cbd>). This essay will focus primarily on Goal 3 (protecting

ecosystem, species and genetic diversity, Aichi Targets 11–13; Table 1) and the related goals in the GSPC (GSPC Targets 5, 7, 8, and 9; Table 1), and more specifically, on how the Aichi Targets and the GSPC relate to the conservation of genetic diversity in wild plant species.

The IUCN recognizes three fundamental levels of biodiversity that are worthy of conservation, namely ecosystem diversity, species diversity, and genetic diversity (McNeely et al., 1990). The field of conservation genetics is a major branch of conservation biology that uses genetic tools to measure the genetic diversity of wild species (most frequently those that are rare, threatened, or endangered) and develop strategies to ensure that genetic diversity is effectively conserved. Conservation of genetic diversity is important because it is related to performance at a variety of scales: greater genetic variation can result in increased individual-level fitness (Reed & Frankham, 2003; Leimu et al., 2006), greater potential for a species to adapt to environmental change (Sgro et al., 2011), and increased ecosystem stability, resilience, and function (Hughes & Stachowicz, 2004; Reusch et al., 2005; Hughes et al.,

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2008). Likewise, low genetic diversity in species of conservation concern has been associated with an increased risk of extinction (Spielman et al., 2004; Frankham, 2005). Data on the distribution of genetic diversity within and among populations can be used to reveal species and population status, life history attributes, and ecological and demographic processes (Karron, 1987; Milligan et al., 1994; Hamrick & Godt, 1996; Gitzendanner & Soltis, 2000; Nybom, 2004), and is frequently used to help guide conservation and management decisions to effectively conserve biological diversity in the face of limited resources (Petit et al., 1998; Fraser & Bernatchez, 2001; Caballero & Toro, 2002).

Although plant conservation geneticists and those working to advance international conservation policy have the shared goal of halting the loss of biodiversity, up until now these two communities have had very little connection or interaction. Notwithstanding the importance of genetic diversity for the persistence and stability of biological diversity at a variety of hierarchical levels, international conservation policy generally focuses on conserving ecosystem and species-level diversity, while the conservation of genetic diversity has received comparatively little attention (Laikre, 2010). Further, the little attention that genetic diversity does receive in the Aichi Targets and the GSPC is focused primarily on the conservation of genetic diversity of economically and agriculturally important species and their wild relatives. Correspondingly, plant conservation geneticists that focus on wild species generally have not participated in advancing the goals of the GSPC and the Aichi targets; for example, in November 2016, a Web of Science search using the keywords "Aichi Targets" and "plant conservation genetics" returned no matches. Despite the current lack of participation from the plant conservation genetics community, I argue that they are uniquely qualified to assist in conservation efforts and measure how well the conservation community is protecting genetic variation of plants. As such, they should play a more important role in helping to achieve the goals of the GSPC and the Strategic Plan for Biodiversity 2011–2020.

This essay will explore how international conservation policy targets relate to the conservation of genetic diversity of wild plant species and will discuss ways to strengthen the link between international conservation initiatives and the field of plant conservation genetics. Namely, policymakers should more strongly consider the conservation of genetic diversity in wild species. For their part, plant conservation geneticists need to conduct work that will help achieve goals set by

international conservation policymakers and evaluate how well the conservation community is achieving these goals. The accomplishment of several targets of international conservation policy may be furthered as the result of a contribution from conservation genetics. Since the goals in these documents are interrelated, they may be grouped into three subject areas that are united by a shared focus: (1) conserving genetic diversity of species of agricultural or socio-economic importance (Aichi Target 13, GSPC Target 9), (2) conserving threatened plant species (Aichi Target 12, GSPC Targets 7 and 8), and (3) protecting and managing important lands for biodiversity (Aichi Target 11, GSPC Target 5).

Conservation of Genetic Diversity of Species of Agricultural or Socio-economic Importance

Overall, the CBD and the GSPC focus very little on the conservation of genetic diversity in wild species (Laikre, 2010). Aichi Target 13, the target that most strongly focuses on genetic diversity, states, "By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species, [will be] maintained, and strategies [will] have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity" (CBD, 2010). Thus, to be considered under this framework, any wild species must fall into the category of "other socio-economically as well as culturally valuable species." Arguably, many wild plant species would not be considered as such. The corresponding target in the GSPC, Target 9, is even more strongly focused on crop species: "70 per cent of the genetic diversity of crops including their wild relatives and other socio-economically valuable plant species [will be] conserved, while respecting, preserving and maintaining associated indigenous and local knowledge" (CBD, 2012). In the case of the GSPC, all wild species that are unrelated to crop species would have to fall under the category of "other socio-economically valuable plant species" to be relevant for this target, which would not be applicable to many wild species.

Given that the Aichi Target 13 and the GSPC Target 9 largely focus on the conservation of genetic diversity only for species of agricultural importance and their relatives, they effectively overlook one of the three fundamental levels of biodiversity for the vast majority of wild plant species. Of particular note is the omission of any mention of the conservation of genetic diversity of threatened and endangered (T&E) plant species, in which genetic diversity is arguably most at risk. The omission of this large segment of

biodiversity is in contrast to widespread scientific consensus in the field of conservation biology, which recognizes the importance of genetic diversity for maintaining the ability of populations and species to adapt to a changing environment, long-term species viability, and the functioning and resilience of ecosystems (Frankham, 1995; Hughes et al., 2008; Sgro et al., 2011). To remedy the omission and to encourage more buy-in from the plant conservation genetics community, future international conservation policymakers should more explicitly consider and include targets that focus on the conservation of genetic diversity of wild species, which will likely lead to more effective conservation efforts.

Even though T&E wild plant species are not explicitly mentioned in Aichi Target 13 and the GSPC Target 9, because both extensive time and resources are needed to conserve them, many of them could arguably fall under the definition of a species of socio-economic and cultural importance. Furthermore, conservation efforts for T&E species would benefit from a consideration of whether they meet the internationally established standards for conservation. Given that the primary occupation of plant conservation geneticists is to conduct research on the status and trends in genetic diversity in T&E plant species, they are therefore best qualified to track progress toward the goals specified by Aichi Target 13, which are to "minimize genetic erosion" and "safeguard genetic diversity," and the goal of the GSPC Target 9, which is to conserve "70 per cent of the genetic diversity." However, most conservation genetics studies do not currently measure these parameters, such that it is impossible to measure how well the conservation community is achieving these goals.

One of the first major challenges preventing an assessment of how well the conservation community is meeting the goals of Aichi Target 13 and GSPC Target 9 for T&E plant species is the lack of accepted approaches to measure progress toward these targets. Indeed, in an interim evaluation of the progress made toward meeting the Aichi Targets, Tittensor et al. (2014) noted that it was impossible to measure progress toward achieving Target 13 because there were no accepted indicators that could be used to measure progress. The only currently accepted indicator to address Aichi Target 13 as recognized by the Biological Indicators Partnership (BIP) is the number and proportion of the world's breeds of terrestrial domesticated mammals reported to the Food and Agriculture Organization of the United Nations by risk status (Tyrrell, 2010). The BIP acknowledges that the indicator set is incomplete for this target (Tyrrell, 2010). With regard to wild species of "socio-economic importance," indicators and accepted protocols are needed to assess whether the conservation genetics community is "minimizing genetic erosion" and "safeguarding genetic diversity." Below, I discuss how each of these goals relates to current research on plant conservation genetics and how we can make improvements in our ability to meet these goals in the future.

SAFEGUARDING GENETIC DIVERSITY

Overall, safeguarding genetic diversity in wild plant species involves measuring how genetic diversity is structured across the landscape and then devising a strategy to conserve populations in such a way that will maximize the total amount of genetic diversity being protected (i.e., the principle of complementarity). Ideally, safeguarding genetic diversity involves in situ conservation of species in their natural habitat, which often requires populations to be publically acquired or put into conservation easements and managed. When populations cannot be conserved in situ because of practical considerations, genetic diversity of plants may also be safeguarded in ex situ collections, such as conservation seed banks or living collections in botanical gardens. The conservation genetics community has not reached a consensus on how much genetic diversity of a species should be protected, but in GSPC Target 9, international conservation policymakers have specified a goal of at least 70%.

The most common approach to understand the structuring of genetic variation across the landscape is using neutral genetic markers, which allow for inference of historical evolutionary divergences and demographic processes (Milligan et al., 1994). In plants, factors such as the mating system, pollination and seed dispersal mechanisms, and geographic distribution interact to affect how neutral genetic variation is partitioned within and among populations (Loveless & Hamrick, 1984; Nybom & Bartish, 2000), which can have consequences for devising strategies to conserve genetic diversity. For example, an outcrossing mating system and pollinators and seed dispersers that travel long distances frequently result in genetic variation being maintained primarily within a population (Loveless & Hamrick, 1984; Nybom & Bartish, 2000), such that relatively few populations are required to protect and maintain the genetic variation present in a species. In contrast, inbreeding, fragmentation, and pollinators/seed dispersers that travel very short distances act to distribute genetic variation mainly between populations (Loveless & Hamrick, 1984; Nybom & Bartish,

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2000), in which case a greater number of populations may be prioritized for protection.

Although most conservation genetics studies on plants utilize neutral genetic markers because of the relative low cost and ease of acquiring such data, there are many ways to measure the spatial structuring of genetic variation in order to identify lineages that demonstrate highly restricted gene flow from other lineages within a species. These different approaches frequently vary in their results, and conservation geneticists are still debating the relative merits of these different approaches (Merila & Crnokrak, 2001; McKay & Latta, 2002; Bonin et al., 2007; Leinonen et al., 2008; Kramer & Havens, 2009). For example, results of analyses that investigate the structuring of genetic variation using neutral genetic loci frequently differ from those using traits under selection, such as quantitative traits or loci that show signatures of selection (Bonin et al., 2007; DeFaveri et al., 2013; Rodriguez-Quilon et al., 2016). Results of analyses may also vary depending on the types of genetic markers (e.g., microsatellites vs. single nucleotide polymorphisms), the number of markers, the level of polymorphism in the markers used, and the way in which genetic structure is analyzed statistically (DeFaveri et al., 2013; Lozier, 2014; Bradbury et al., 2015; Puckett & Eggert, 2016; Yannic et al., 2016). Clearly, the optimal situation would be to measure the structuring of genetic variation at a large number of both neutral genetic markers and adaptive traits and use a variety of statistical approaches to obtain a holistic view of all of the evolutionary and demographic processes acting on a species to identify genetically distinct lineages (Fraser & Bernatchez, 2001).

There are also several different criteria used to prioritize populations for protection, which may be more or less relevant depending on the biology of the species and the funds available for conservation. However, in general, it is important to protect both evolutionary processes (such as adaptive divergence and historical isolation) and the ecological viability of populations, while protecting populations in a way that will maximize the protection of as much genetic diversity in a species as possible (i.e., complementarity) (Fraser & Bernatchez, 2001; Bonin et al., 2007). However, other practical considerations are often important determinants of which populations are protected, such as the funds available for conservation and the quality, size, availability, and cost of potential sites. It may not be feasible to protect some populations, in which case conservation seed banking or translocations may be necessary to ensure the protection of specific segments of genetic diversity.

The goal of this essay, however, is not to debate the relative merits of the ways to measure genetic variation or to prioritize populations for conservation, but rather to highlight how conservation geneticists can contribute to reaching Aichi Target 13 and GSPC Target 9. The relevant information needed from conservation geneticists is the proportion of genetic variation in each species that is safeguarded, both in wild populations and in ex situ collections. Currently, this is not something that is measured or standardly reported in the conservation genetics literature; however, this is something that could easily be calculated as long as several types of data are available. These estimates would require a comprehensive, range-wide genetic analysis to understand how genetic variation is structured across the landscape. It would also require a comprehensive assessment of the conservation status of each population, which could be collected at the same time as genetic sampling, including an estimation of population size and habitat condition and whether populations are publicly protected and appropriately managed. The estimate of conservation status should also include information about how many populations are conserved in ex situ collections. A simple proportion could be calculated that measures the total amount of genetic variation (i.e., allelic diversity) that is protected relative to the total amount of genetic diversity found in the species. An additional metric would be to conduct STRUCTURE analysis (Pritchard et al., 2000) and report the proportion of genetic clusters identified by STRUCTURE that are protected. These estimates could then be reported according to the approach used to measure genetic diversity and structure (i.e., using neutral loci, loci under selection, or quantitative genetic variation) and the way in which populations are protected (i.e., in situ vs. ex situ). The date of the assessment is also important; since the protection status, management, population size, and patterns of genetic diversity and structure may change over time, it is therefore important to periodically monitor populations to update this estimate. This explicit reporting of the proportion of genetic diversity that is safeguarded would likely be of great use for conservation officials tasked with coordinating recovery efforts for individual endangered species. Future research should also focus on an optimal format for compiling, summarizing, and reporting these estimates that would provide the most useful information for policymakers to evaluate progress toward achieving the targets of international conservation policy.

MEASURING GENETIC EROSION

The term "genetic erosion" generally refers to the loss of genetic diversity in a species, which may occur through the extirpation of populations containing a unique segment of genetic variation, or as a result of factors associated with small population size and fragmentation, such as genetic drift, inbreeding, or a genetic bottleneck. Detecting genetic erosion is important because the loss of genetic diversity may reduce the potential ability of a species to adapt to environmental changes and increase the probability of extinction (Frankham, 2005; Jump et al., 2009; Kramer & Havens, 2009). Conducting research on trends in the genetic diversity of a species is also important for highlighting where management and intervention are needed to halt the loss of genetic diversity. Detecting the erosion of genetic diversity requires either repeated genetic analysis of the same population over time (i.e., "genetic monitoring," Schwartz et al., 2007), which provides the highest resolution to detect genetic erosion, or through comparisons with closely related species, which provides less resolution but provides some informa- tion on genetic trends when no previous genetic sampling has been conducted.

In the last 10 years, the number of both theoretical and empirical studies that focus on temporal genetic monitoring have increased dramatically, based large- ly on the recognition that it is important to detect negative trends in the status of species and devise management activities that will halt such losses (Laikre et al., 2008; Aravanopoulos, 2011; Hoban et al., 2013; Bruford et al., 2017). Most of these studies have been conducted on species of economic importance, particularly in the fields of fisheries, forestry, and agriculture (Tessier & Bernatchez, 1999; Batchelor et al., 2002; Kuparinen & Merilä, 2007; Malysheva-Otto et al., 2007; Allendorf et al., 2008; Aravanopoulos, 2011; Graudal et al., 2014; Fussi et al., 2016). Theoretical studies have proposed a range of specific strategies and genetic metrics to detect changes in genetic diversity over time (Batchelor et al., 2002; Schwartz et al., 2007; Aravanopoulos, 2011; Hoban et al., 2014; Fussi et al., 2016). Of particular note is the simulation study of Hoban et al. (2014), which investigated the effectiveness of different genetic markers, temporal sampling strategies, and genetic metrics for detecting genetic erosion. Results of this study showed that the most effective metric for detecting genetic erosion through temporal sampling is allelic diversity, that genotyping as few as 20 microsatellite markers in a population showed good power to detect genetic erosion, and that power increased with the number of

genetic markers (Hoban et al., 2014). The authors of this study also suggested that a wide variety of temporal sampling schemes and genetic markers would be suitable for detecting genetic erosion (Hoban et al., 2014).

Although identifying the occurrence of genetic erosion in a T&E species is important for ensuring that it is effectively conserved, very few conservation genetics studies have used temporal sampling to measure changes in genetic diversity in T&E plant species (but see Morris et al., 2002; Ramp et al., 2006; Noel et al., 2010; Gordon et al., 2012; Sloop et al., 2012; Coates et al., 2013, 2015). One potential factor limiting the use of genetic monitoring in T&E plant species is the duration of grant funding, because many studies are funded for a maximum of three years and funding agencies may not be interested in reanalyzing a species that has already been analyzed genetically. Nonetheless, conservation geneticists need to begin making the case with funding agencies that it is important to conduct temporal sampling to ensure that any erosion of genetic diversity is detected and that appropriate management activities are initiated to halt the problem. Increased attention to temporal sampling in the conservation genetics literature may help it become standard protocol for the most at-risk plant species.

Although not as powerful as temporal sampling, detecting genetic erosion using comparisons between closely related species is the only way to detect genetic erosion without the benefit of a previous genetic study. Comparisons between closely related species that have similar morphological and life history characteristics allow any shared life history factors to be taken into account, such that differences in levels of genetic diversity may be attributed to the characteristics that differ between congeners (Godt & Hamrick, 1998; Gitzendanner & Soltis, 2000; Ouborg et al., 2006; Edwards et al., 2014). If one of the main factors that differs between congeners is geographic range size or population size, then low genetic diversity in a rare species may more confidently be attributed to factors associated with rarity or small population size, such as genetic drift, a genetic bottleneck, or inbreeding. Comparisons between closely related rare and widespread species can be conducted within the period of a single grant funding period and can still resolve whether genetic erosion is occurring in rare species, albeit with less resolution (Larsson et al., 2008). To make the results of genetic studies more applicable to the targets of international conservation policy, comparisons between closely related rare versus widespread species that share

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similar life history characteristics should be used in the absence of a previous genetic analysis to detect genetic erosion (Ouborg et al., 2006). Once baseline levels of genetic diversity have been established, conservation geneticists should also make the effort to periodically reanalyze the genetic diversity of populations to detect genetic erosion.

CONSERVING THREATENED PLANT SPECIES AND PROTECTING AND MANAGING IMPORTANT LANDS FOR BIODIVERSITY

Also relevant to plant conservation genetics are the targets that focus on protecting and managing lands for biodiversity and conserving threatened plant species. The targets that focus on land conservation are GSPC Target 5, stating that "at least 75 per cent of the most important areas for plant diversity of each ecological region [will be] protected with effective management in place for conserving plants and their genetic diversity" (CBD, 2012), and Aichi Target 11, stating that "by 2020, at least 17 per cent of terrestrial and inland water areas, and 10 per cent of coastal and marine areas, especially areas of particular importance for biodiversity and ecosystem services, [will be] conserved through effectively and equitably managed, ecologically representative and well connected systems of protected areas and other effective area-based conservation measures, and integrated into the wider landscapes and seascapes" (CBD, 2010). The targets that focus on the conservation of threatened species are Aichi Target 12, which states that "by 2020 the extinction of known threatened species [will have] been prevented and their conservation status, particularly of those most in decline, [will have] been improved and sustained" (CBD, 2010), and GSPC Target 7, which states that "at least 75 per cent of known threatened plant species [will be] conserved in situ" (CBD, 2012).

Overall, the primary motivation behind the field of conservation genetics is to facilitate efforts to prevent the extinction and ensure the proper management of T&E species, such that by definition, the work of conservation geneticists helps achieve the targets listed in the previous paragraph. There are many different ways in which genetic data are useful for both species and ecosystem conservation; for example, genetic data are used to identify areas that must be conserved to ensure that a species will remain viable and have sufficient genetic variation to maintain adaptive potential in the face of a changing climate (Petit et al., 1998; Fraser & Bernatchez, 2001; Diniz & Telles, 2002; Bonin et al., 2007), which contributes to efforts to protect species as well

as important areas for plant diversity. Conservation genetics can also contribute to ecosystem and species conservation by evaluating trends in the status of populations over time, identifying necessary management actions and evaluating the effects of management activities (Schwartz et al., 2007). Genetic data can also ensure the effectiveness of species conservation efforts by assessing the genetic distinctiveness of taxonomically questionable T&E species. By revealing whether a T&E species is genetically distinct from relatives or whether it is a subpopulation of a widespread species, conservation genetics can ensure that conservation efforts are devoted to unique species that truly deserve protection, while at the same time ensuring that time and resources are not wasted by working to conserve a population that is not distinct from widespread relatives (Edwards et al., 2008). Because a genetic perspective can increase the overall effectiveness of conservation efforts, I recommend that conservation managers incorporate conservation genetics into efforts to conserve T&E species whenever possible. For their part, conservation geneticists need to work closely with conservation managers and communicate clear, specific conservation recommendations to ensure that the genetic information is fully and effectively utilized to advance conservation efforts.

One additional target that focuses on preventing the extinction of threatened plant species is GSPC Target 8: "At least 75 per cent of threatened plant species in ex situ collections, preferably in the country of origin, and at least 20 per cent available for recovery and restoration programmes" (CBD, 2012). Ex situ collections may take the form of living plants or banked germplasm, which is material collected specifically for conservation purposes (Kramer et al., 2011). Seeds stored in conservation seed banks represent the vast majority of banked germplasm, but species whose seeds do not remain viable in seed banks may also be maintained by tissue culture or cryopreservation. In general, the main conservation value of banked germplasm is to safeguard against the loss of genetic diversity for threatened species and act as source material for reintroductions (Cohen et al., 1991; Falk & Holsinger, 1991; Guerrant & Havens, 2004; Kramer et al., 2011; Guerrant et al., 2014). Although GSPC Target 8 focuses on the number of taxa in ex situ collections, to be of conservation value, ex situ collections must represent the genetic diversity present in a species or population. To reflect the fact that the value of ex situ collections depend on their genetic diversity, conservation policymakers should specify genetic diversity in future targets involving ex

situ collections; for example, GSPC Target 8 could be revised to state, "At least 75% of threatened species in genetically representative ex situ collections. . ."

For their part, conservation geneticists need to conduct research that will streamline collection efforts for ex situ germplasm. Currently, a universal set of collection guidelines is used to ensure that germplasm collections capture as much genetic diversity as possible (Falk & Holsinger, 1991; Guerrant & Havens, 2004; Guerrant et al., 2014). However, the actual efficacy of these protocols for capturing genetic variation may vary depending on how genetic variation is partitioned within and among populations, which is strongly affected by life history characteristics, such as mating system, pollination mechanism, and seed dispersal strategy (Hoban & Strand, 2014). Similarly, since collecting from a large amount of populations of some species might not capture any additional genetic variation, utilizing universal protocols may not always be efficient. The ideal way to maximize the genetic variation found in collections with the least collection effort would be to use genetic data to develop ex situ collection strategies for each species; however, this is frequently not feasible because of the time and expense of genetic analysis. In lieu of genetic analysis, it may be possible to increase the efficiency of ex situ collection efforts by designing collection strategies tailored to the specific combination of life history characteristics of each species. Since this could potentially help capture the maximum genetic diversity in an ex situ collection with the lowest possible collection effort, this would enable collectors to collect more species; it would therefore be a great way for conservation geneticists to help make progress toward increasing the number of species represented in ex situ collections.

Conservation geneticists may also contribute to the improvement of ex situ collections by conducting genetic assessments of living collections (Namoff et al., 2010; Ensslin et al., 2011; Cibrian-Jaramillo et al., 2013; Christe et al., 2014; Griffith et al., 2015). Many institutions have poorly documented historical living collections of T&E plant species (Kramer et al., 2011; Kozlowski et al., 2012; Christe et al., 2014). Genetic analysis of these living collections and comparisons with natural populations can help clarify the species identification, collection location, levels of genetic diversity, and how well the ex situ collections represent the genetic diversity present in natural populations (Namoff et al., 2010; Cibrian-Jaramillo et al., 2013; Griffith et al., 2015). This type of analysis can also highlight necessary steps to improve the genetic diversity held in ex situ collections. Gaining additional information about ex situ collections can greatly increase their value for safeguarding against the loss of genetic diversity and for serving as a source of material for reintroductions.

Conclusions

Overall, the effectiveness of conservation efforts will increase if conservation policymakers more explicitly consider the conservation of genetic diversity in the targets of international conservation policy, and conservation geneticists focus on specifying and advancing the goals of international conservation policy. Coordinating efforts to work toward common goals will undoubtedly increase the rate of progress toward the crucial task of halting the loss of plant biodiversity.

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