

What is the Conservation Value of a Plant in a Botanic Garden? Using Indicators to Improve Management of Ex Situ Collections

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Abstract Living botanic garden plant collections are a fundamental and underutilized worldwide resource for plant conservation. A common goal in managing a botanical living collection is to maintain the greatest biodiversity at the greatest economic and logistic efficiency. However to date there is no unified strategy for managing living plants within and among botanic gardens. We propose a strategy that combines three indicators of the management priority of a collection: information on species imperilment, genetic representation, and the operational costs associated to maintaining genetic representation. In combination or alone, these indicators can be used to assay effectiveness and efficiency of living collections, and to assign a numeric conservation value to an accession. We illustrate this approach using endangered palms that have been studied to varying degrees. Management decisions can be readily extended to other species based on our indicators. Thus, the conservation value of a species can be shared through existing databases with other botanic gardens and provide a list of recommendations toward a combined management strategy for living collections. Our approach is easily implemented and well suited for decision-making by gardens and organizations interested in plant conservation.

Resumen Las colecciones vivas en jardines botánicos son una parte fundamental y poco utilizada en la conservación de plantas a nivel mundial. Un objetivo común en el manejo de las colecciones botánicas vivas es mantener la mayor biodiversidad al menor costo económico y logístico. Sin embargo hasta ahora no existe una estrategia

unificada para el manejo de plantas vivas dentro y entre jardines botánicos. Aquí proponemos una estrategia que combina tres indicadores para establecer prioridades de manejo de una colección: información acerca del riesgo en estado silvestre de la especie, representación genética, y los costos operativos asociados a mantener la representación genética. En combinación o solos, estos indicadores pueden ser utilizados para evaluar la efectividad y eficiencia de las colecciones vivas, y para asignar un valor numérico de conservación a un espécimen. Demostramos esta estrategia con palmas que tienen diversos tipos de estudios e información disponible. Decisiones de manejo basadas en nuestros indicadores se pueden extender y aplicar fácilmente a otras especies de manera similar a como lo demostramos aquí. Además, el valor de conservación de un especie puede ser compartido con otros jardines botánicos utilizando bases de datos pre-existentes y así proveer una serie de recomendaciones hacia el manejo integrado de las colecciones vivas. Nuestra estrategia se puede implementar fácilmente y es apropiada para la toma de decisiones en jardines y organizaciones interesadas en la conservación de recursos en plantas.

Keywords Botanic gardens · C-value · *Chamaedorea ernesti-augustii* · *Leucothrinax morrisii* · Conservation genetics · Ex situ conservation, living collections

Introduction

Despite progress in plant species conservation efforts, the increasing loss of plant species worldwide demands rethinking and invigorating unexploited conservation strategies that are both effective and resource-efficient for plant conservation. One such strategy is to characterize and make use of the vast number of plant species maintained at botanic gardens. Botanic gardens are central to an integrated in situ and ex situ conservation strategy (Maunder et al., 2001; Kramer et al., 2011). The Global Strategy for Plant Conservation highlights that need by requiring a minimum of 75 % of threatened plant species within ex situ collections, with at least 20 % available for recovery and restoration (Wyse Jackson & Kennedy, 2009).

Living collections are already an important element of robust conservation programs (Havens et al., 2004c; Griffith & Husby, 2010; Namoff et al., 2010; Oldfield, 2010). Botanic gardens are increasing in number and intensifying their focus on living conservation collections (Dosmann, 2006; Crane et al., 2009; Oldfield, 2009). There are over 3,000 botanic gardens and arboreta internationally (BGCI, 2011). Five hundred of them are registered in the US as members of the American Public Gardens Association, an increase from 360 within the past 20 years (Watson et al., 1993). Increased focus on living plant collections can be seen in the growth of the North American Plant Collections Consortium, which currently lists 51 nationally recognized collections, and rising at a rate of around six new collections per year. Gardens have various strategies to handle collections, which include long-term storage methods like seed-banking (Martyn et al., 2009), tissue culture (Yam et al., 2010), and cryopreservation (Volk, 2010). The fundamental conservation contribution of botanic gardens remains in cultivating living plant collections of imperiled species (Griffith et al., 2011).

Despite this progress, most living collections in botanic gardens are an underutilized source of plant genetic and species diversity in conservation and management.

There is no unified management strategy for conserving threatened plants among living collections (Wyse Jackson & Sutherland, 2000; CBD, 2002; Havens et al., 2004a, b, 2006; Farnsworth et al., 2006; Seaton et al., 2010). Furthermore, it can be difficult to assess the conservation value of an ex situ collection (Schaal & Leverich, 2004; Namoff et al., 2010) and as a result evaluation of conservation value is not often performed. Perhaps a strictly unified strategy will not best serve the diversity of plant life histories but a unified concept can be broadly adaptable by many gardens.

Here, we suggest that management and use of living collections can be better aligned with threatened species conservation goals. We propose using species threat rank, and genetic tools and their association to the operational costs of maintaining a living collection. We exemplify this approach with current practices at the Arnold Arboretum at Harvard University and the Montgomery Botanical Center (MBC). We propose a strategy for an efficient and sustainable use of living collections towards threatened species conservation via an integrated Conservation Value assigned to a species within a collection. This approach can be implemented in many gardens worldwide, shared through existing databases, and used in decision-making by other interested organizations.

Indicator 1: Species Rarity and Imperilment Assessment - Arnold Arboretum

Since its founding in 1872, the Arnold Arboretum of Harvard University has been a leader in living collections management and the study and preservation of woody plant species. Recent efforts have focused on collections management to support threatened species conservation within the Arboretum's living collection (Hird, 2010). With the goal to establish and maintain an ex situ collection of living plants that has direct, on-the-ground conservation value for natural populations (Havens et al., 2004b), we began by a better understanding of the Arboretum's current living collections in light of plant conservation, and then strategically utilize and build upon that foundation during a two-year process.

The first task was to determine which species in the Arboretum's living collection were threatened in the wild. Plant records database were a tool for dynamic collections information and analysis. Typically, existing functional conservation status fields contained minimal contemporary data that could be used to recognize or categorize threatened species. A survey of American Public Garden Association (APGA) member gardens revealed that most gardens maintain plant records databases, and also maintain threatened species (Hird & Dosmann, unpublished data). A majority of those gardens did not track threat ranks and could not provide basic statistics such as the total number of threatened species maintained in their collections. Similar to the Arnold Arboretum's plant records at that time, we found a nationwide deficiency in threatened species information actually integrated into living plant collections.

An obstacle was discovered when we sought out basic threatened species information such as threat rank (Yatskievych & Spellenberg, 1993). We found numerous and varied threatened species lists and ranking schemes at various geographic levels all relevant to the Arboretum's living collections, such as the International Union for Conservation of Nature (IUCN) Red List of globally threatened species, the NatureServe global (G), national (N), and subnational (S) ranks for North American species, and the Massachusetts Endangered

Species Act (MESA). The wide variety of threat lists and ranks confounded efforts to assign meaningful and consistent conservation information to each taxon and specimen in the living collection. To compare threat level among threatened species lists, as well as evaluate taxa with multiple, sometimes conflicting threat ranks, an Arnold Arboretum Conservation Value was developed using a threatened species “Rosetta Stone” (Table 1, Indicator 1). Threat ranks and descriptions were compared and harmonized into the “Rosetta Stone”, which served to unify threatened species information and help us, for the first time, assess and prioritize the Arnold Arboretum living collections according to a single, meaningful Conservation Value scale (C-value).

Once relevant threatened species lists were identified and threat ranks harmonized, an additional obstacle arose in incorporating threatened species information into the plant records database for the nearly 4,000 total taxa in the Arnold Arboretum living collections. To avoid a manual, taxon-by-taxon comparison with each threatened species list, the BGCI Plant Upload was utilized to assign threat ranks to the entire living collection and connect our collections to a global botanical community (BGCI, 2011). The Plant Upload cross-referenced IUCN Red List (IUCN, 2001), CITES, and NatureServe G-rank (NatureServe, 2009) data with the Arboretum’s taxa list, and threat ranks were entered into the plant records database. We found this to be a fairly efficient approach for assigning relevant threatened species data at the global and North American levels. The “Rosetta Stone” was then used to assign an Arnold Arboretum Conservation Value to each threatened species in the living collections, and entered in the database.

Table 1 Conservation Value assessment. This “Rosetta Stone” provides a common assessment utility from various species imperilment lists. A Conservation Value (C-value) can be estimated from adding genetic tools and costs of producing and managing genetic studies in botanic gardens

Indicator 1 global threatened species lists			Indicator 2 genetics		Indicator 3 cost % genetic capture divided by the cost of that collection	C-value
IUCN red list ¹	CITES ²	NatureServe G-Rank ³	Allelic capture (%)	Reintroduction potential (% assignments)		
EX		GX	90	90	Low Y value	1
EW	I	GH	80	80		2
CR	II	G1	70	70	Intermediate Y value	3
EN	III	G2	60	60		4
VU		G3	50	50	High Y value	5
NT		G4	–	–		6
LC		G5	–	–		–

¹ IUCN, 2001. IUCN Red List Categories. Prepared by the IUCN Species Survival Commission. IUCN, Gland, Switzerland

² CITES 2009. Appendices I, II, and III: Convention on International Trade in Endangered Species of Wild Fauna and Flora. Geneva, Switz

³ NatureServe, 2009. NatureServe Explorer: An online encyclopedia of life [www.natureserve.org/explorer]. Version 7.1. Arlington, Virginia

Once threatened species information was incorporated into the plant records database in a meaningful way, further analyses could be done on threatened taxa in the living collections. The Arnold Arboretum Conservation Value allowed us to filter taxa according to greatest threat, and then include other collections parameters such as provenance and current health condition to identify greatest conservation, curatorial, educational, horticultural, and research needs and uses. Gaps and strengths found in the living collections provided focal points for increasing genetic diversity via future acquisitions; distribution of backup germplasm to other institutions; appropriate management and documentation of living specimens; and interpretation and research opportunities. This was the first time we were able to assess the value of the Arnold Arboretum living collections in light of threatened species conservation, and make informed collections management decisions for the future.

Indicator 2. Genetic Tools to Evaluate the Conservation Value of Living Collections – Montgomery Botanical Center

Living plant collections strive to represent natural variation and serve as a reservoir for potential reintroductions. It is thus critical to include knowledge of the genetic representation of the collections. In particular, a structured collecting method is essential to maintain genetically diverse living collections in ex situ collection management decisions. A broader sample maintained can enable studies on minimum viable populations and breeding strategies, such as those that currently take place in zoos and aquaria (DeSalle & Amato, 2004).

At many botanic gardens, progress has been made towards maximizing the genetic diversity in plant collections through cultivation of multiple individuals from several populations (Valois, 1994; Vaxevanidou et al., 2006).

A main concern in this effort is to avoid genetic drift in botanic garden collections, which could lead to the fixation of detrimental variation common in small populations. Very substantial drift was found for *Cochlearia polonica* E. Fröhl (Rucińska & Puchalski, 2011), a biennial mustard in protective cultivation for over 30 years. For *Cynoglossum* L. (Boraginaceae), genetic drift in garden collections appeared to increase with the duration of cultivation and in particular in plants with short generation times such as annuals, biennials, or short-lived monocarpic perennials, compared to long-lived pleonanthic perennials, such as most tree species (Enßlin et al., 2011). Other species depend entirely on living collections for their survival and reintroduction to the wild, such as the Talipot Rendah, *Corypha taliera* Roxb. (Arecaceae). This taxon is known from perhaps fewer than 20 living individuals and is extinct in the wild (Dhar, 1996). Its century-long, monocarpic life history adds further complexity to its management. Likewise, the Wollemi Pine, *Wollemia nobilis* W. G. Jones, K. D. Hill & J. M. Allen (Araucariaceae), has no resolvable genetic variation in the wild (Peakall et al., 2003), so any single-specimen garden collection could be considered a complete genetic collection for this Critically Endangered species.

At MBC we have sought to integrate and apply population genetic information into a generalized decision-making framework that can be adapted at other botanic gardens to establish conservation value of species within their collections. This framework consists of three measures of genetic variation that can be applied to answer questions related to

collection management and future field planning: (1) Allelic Capture, (2) Baseline Genetic Variation, and (3) Reintroduction Potential (Fig. 1).

We previously proposed Allelic Capture as an indicator of the degree of genetic variation found through a population-based collection protocol in botanic gardens, and as a measure of optimal sampling for ex situ conservation (Namoff et al., 2010). We used the living collection of *Leucothrinax morrisii* (H. Wendl.) C. Lewis & Zona (Arecaceae) derived from a single collecting event (Namoff et al., 2010) to test this as a proof-of-principle. We estimated mean genetic diversity (H_E), genetic distance, and percentage of polymorphic loci of Intersimple Sequence Repeat (ISSRs) markers using the freely available software GenAIEx v6.4 (Peakall & Smouse, 2006). Genetic capture was studied by comparing 58 specimens from an ex situ collection with 100 individuals from the parent population. Same sample sizes with different numbers of accessions—a common scenario in living collections—were compared regarding change in allele capture, as measured by the percent of private alleles. A 3-parameter logistic model (Meyer et al., 1999) was fitted by least squares using Loglet Lab 3.0 (Rockefeller University) to evaluate the value of increasing accessions. Allelic capture was greater than 94 % in the living collection of *L. morrisii*, while resampled collections of different sizes captured from 48 % to 94 % of alleles. This study supported that: (1) larger collections conserve greater genetic diversity; (2) as collection size increases, genetic capture increases at a diminishing rate, and (3) there is a point at which increased investment in a collection (as reflected by more plants maintained) does not appreciably increase the conservation value of the collection (Namoff et al., 2010).

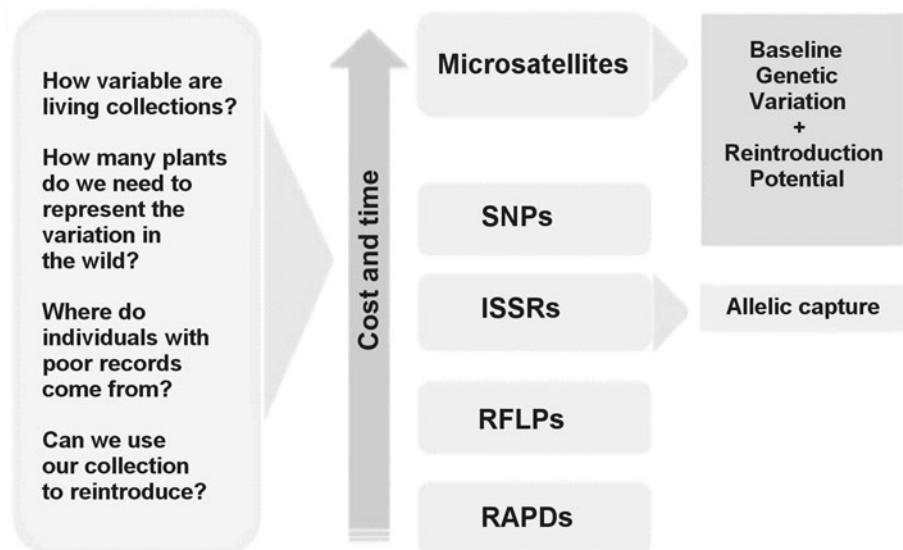


Fig. 1 Framework to evaluate the conservation value of living collections from a genetic standpoint. Three measures of genetic variation can be applied to answer questions related to collection management and future field planning: Allelic Capture, Baseline Genetic Variation and Reintroduction Potential. Allelic Capture is a measure of optimal sampling for ex situ conservation based on mean genetic diversity (H_E), genetic distance, and percentage of polymorphic loci. Baseline Genetic Variation is based on measures of allelic richness and heterozygosity, and Reintroduction Potential is based on the likelihood of a sample being assigned to its population of origin

Here we detail two new genetic estimates of a species' conservation value in botanical collections: Baseline Genetic Variation and Reintroduction Potential. Both estimates are indicators of how representative a living collection is compared to the population from which it was collected, or compared to a population of known genetic background. Both estimates can be easily obtained via free software (Genalex v6.4; Peakall & Smouse, 2006).

Baseline Genetic Variation is based on measures of allelic richness and heterozygosity. Allelic richness is critical to long-term evolutionary processes, while heterozygosity is an indicator of the extent of inbreeding in a population (Petit et al., 1998). Both are important evolutionary factors in small populations. Allelic richness is measured as the number of alleles per locus and population (N_a), and the number of private alleles (N_p). Heterozygosity as the unbiased expected heterozygosity (H_E), and observed heterozygosity (H_O) corrected for sample size (Nei, 1978).

To measure Reintroduction Potential we used the likelihood of a sample being assigned to its population of origin. If one assumes that the best-case scenario for reintroductions is to maintain the original patterns of genetic variation, then one can infer an accession's reintroduction potential based on how well the accession represents the population of interest. Accessions that are most likely assigned to the original population or population of interest are presumed to be the best sources for reintroduction of seeds or whole plants (i.e. minimize outbreeding depression) unless the goal of managing collections is not to maximize variation. We used a frequency-based assignment test which calculated a log likelihood value for each sample to estimate if that sample is more likely assigned to itself (Population 1) or to another population (Population 2) (Paetkau et al., 2004).

As a proof-of-principle of this approach we estimated the Baseline Genetic Variation and Reintroduction Potential of 23 individuals of the tropical understory palm *Chamaedorea ernesti-augustii* H. Wendl. from the MBC living collections. These samples were originally collected from Mexico ($n=8$) and Belize ($n=15$). *Chamaedorea ernesti-augustii* is a small, dioecious, perennial and long-lived palm (Hodel, 1992). *Chamaedorea* Willd. species are prominent ecological components of the understory in Neotropical evergreen forests, constituting up to 50 % of the number of understory species in these habitats (Oyama et al., 1992). They are among the most traded ornamental palms worldwide with more than 17 million seeds and cut leaves sold annually, 99 % extracted from Mexico's natural populations (Sosa-Martinez, 1996; Ramírez, 2001; CEC, 2002; Hodel, 2002; Eccardi, 2003). This genus provides a good example of the conservation value of living collections as several *Chamaedorea* species have gone locally extinct due to overharvesting and habitat loss (Escalera-Más, 1993; Radachowsky et al., 2004), including *C. ernesti-augustii* in some parts of Guatemala (Reyes-Rodas et al., 2006) and Mexico (Ramírez, 2001; De los Santos et al., 2003). *Chamaedorea* is also biologically interesting as wild populations are characterized by varying gradients of population abundance over short geographic distances (Zarco, 1999; Garwood et al., 2006) that often represent unique genetic groups at a local scale (Cibrián-Jaramillo, 2007). These patterns of human use and biological distribution have direct implications on ex situ collection management of representative samples of wild populations.

We compared estimates for the 23 ex situ individuals to assays of wild populations from Mexico and Belize. In Mexico we sampled 158 individuals from five sites within

the tropical evergreen broadleaf forests of Los Tuxtlas, Veracruz; while in Belize we used information from 138 individuals from eight sites (Fig. 2) (Cibrián-Jaramillo et al., 2009; Cibrián-Jaramillo, *In press*).

The 23 MBC accessions from Mexico and Belize fall within the Baseline Genetic Variation found in wild populations, with an average number of alleles $N_a=6.3$ and 6.2; number of private alleles $N_p=1.3$ and 1.5; and expected heterozygosity $H_E=10.0$ and 8.3; and observed heterozygosity $H_O=8.0$ and 5.2, respectively (Fig. 3). Wild populations of this species have generally high allelic richness and high inbreeding compared to other palms (Cibrián-Jaramillo, 2007). These results suggest that MBC sampling and management have been adequate to maintain the genetic variation found in some natural populations in this species.

Figure 4 shows the proportion of assigned MBC accessions to wild populations of *C. ernesti-augustii* based on the calculated Reintroduction Potential. About half of the MBC accessions from Belize were assigned to wild populations of Belize, while most of Mexico's MBC collections were not assigned to the majority of Mexico's wild populations, possibly due to the smaller sample size ($n=8$) of the living collections. Samples from the Cerro Borrego wild populations were similarly distant from the general variation in Mexico. Other population genetic parameters of interest are discussed elsewhere (Cibrián-Jaramillo et al., 2009; Cibrián-Jaramillo, *In press*).

These two measures show that MBC's collections from Mexico and Belize have similar genetic variation compared to wild populations. However, only the Belize MBC accessions would be recommended as a source of seeds for reintroduction in



Fig. 2 Distribution of *Chamaedorea ernesti-augustii* plants from wild populations in evergreen broadleaf forests in Mexico and Belize. In Mexico we sampled 158 individuals from five sites from Los Tuxtlas, Veracruz. In Belize 138 individuals were gathered from eight sites throughout the country

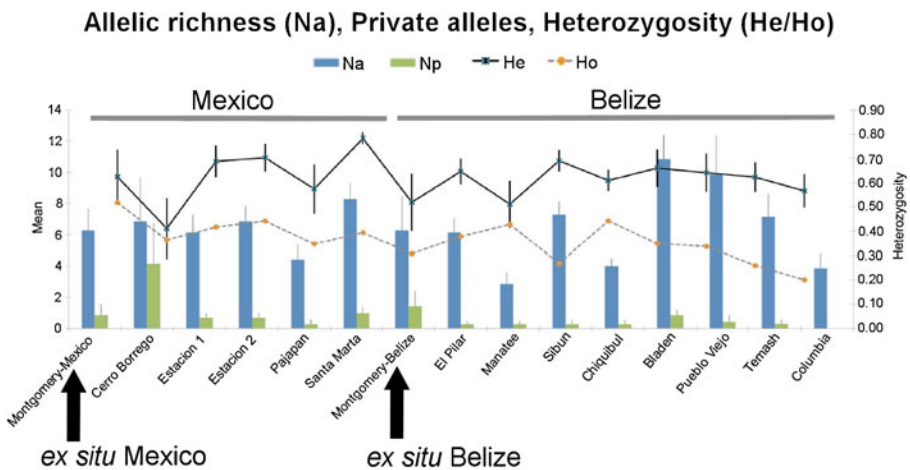


Fig. 3 Baseline Genetic Variation found in wild populations and living collections (arrow) of *Chamaedorea ernesti-augustii* in Mexico and Belize. There is an average number of alleles $N_a=6.3$ and 6.2 ; number of private alleles $N_p=1.3$ and 1.5 ; and expected heterozygosity $H_E=10.0$ and 8.3 ; and observed heterozygosity $H_O=8.0$ and 5.2 , respectively

Belize wild populations. If maintaining a high level of genetic variation in the living collection is the primary goal, further targeted collecting of *C. ernesti-augustii* material from specific sites from both countries will be needed (Table 2). Assay for percent allelic capture via the garden collection (Namoff et al., 2010) shows that capture of allelic variation for each population ranges from 15 % to 43 % when the MBC plants are treated as a single group (Table 2). Compared to the previous *Leucothrinax* C. Lewis & Zona study (Namoff et al., 2010), this is a low percent allelic capture. This low percentage can likely be explained by this assay’s design as a post hoc assessment, without strictly congruent geographic sampling between the ex situ collection and the populations of interest.

Indicator 3: Integrating Genetic Tools and Management Operations

A desired goal in managing an ex situ living plant collection is to conserve greatest diversity at the greatest economic efficiency. Inclusion of new molecular tools with robust accounting of expenses is an innovative way to assay effectiveness and efficiency of ex situ conservation collections. To accomplish this we compared direct measure of genetic capture by living collections to operations costs. Specifically, data was collected on three parameters. First, using molecular tools, genetic diversity in wild populations is measured as described in the previous section. Then population diversity is compared to living collections genetic diversity via the same assay. Concurrently, the total monetary cost of building and maintaining the living collection is closely evaluated. These metrics can be synthesized to produce an efficiency model.

A preliminary model has been proposed for exploring the relationships among living collections conservation, cost, and efficient application of resources (Griffith & Husby,

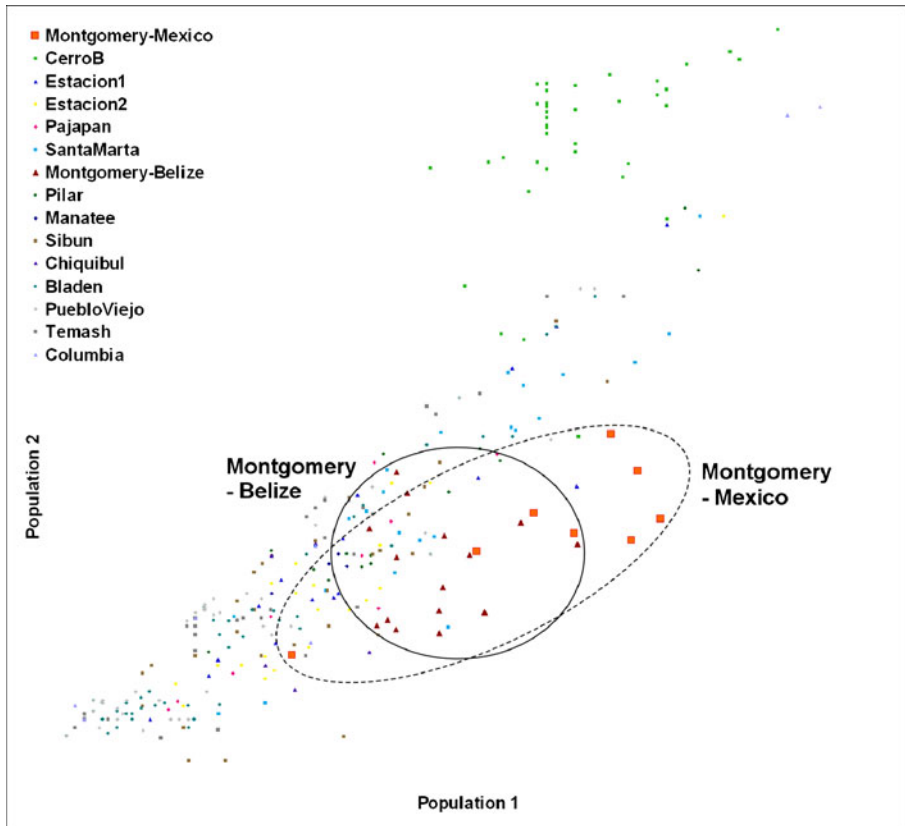


Fig. 4 Proportion of assigned MBC accessions to wild populations of *Chamaedorea ernesti-augustii*. Population 1 refers to the population of origin, and Population 2 to a population other than the one of origin. A portion of MBC accessions from Belize were assigned to wild populations of Belize, while most of Mexico's MBC collections were not assigned to the Mexican wild populations. Samples from the wild populations of Cerro Borrego were similarly distant from the general variation in Mexico

2010). As described in the previous section, we explored the population genetics of an extensive living collection of *Leucothrinax morrisii* derived from a single collecting event (Namoff et al., 2010). From an economic standpoint, this study supported that: (1) larger collections conserve greater genetic diversity; (2) as collection size increases, genetic capture increases at a diminishing rate, and (3) there is a point at which increased investment in a collection (as reflected by more plants maintained) does not appreciably increase the in situ conservation value of the collection (Namoff et al., 2010). Exploring the relationship between monetary investment over the life of the collection (obtaining, documenting, germinating, and caring for the plants) and the efficacy of conservation was performed by integrating these two metrics. The interrelationship of these results for the case study can be represented as an easily interpreted model (Fig. 5). The interaction of these three variables – number of plants in collection, genetic capture, and investment – has implications for living conservation collections management. Evaluating the MBC sampling and management protocol through this case study, it was found that the existing ex situ conservation target of 15 individuals per population (Walters & Decker-Walters,

Table 2 Percent allelic capture by the living collections at MBC, for each population of *Chamaedorea augusti-ernestii* (Fig. 2)

Population	% Allele capture	<i>n</i>
Chiquibul, Belize	42.86 %	5
Pajapan, Mexico	32.26 %	10
Estacion 1, Mexico	27.91 %	16
El Pilar, Belize	27.91 %	18
Santa Marta, Mexico	27.59 %	24
Sibun, Belize	27.45 %	29
Bladen, Belize	25.00 %	58
Cerro Borrego, Mexico	22.92 %	41
Temash, Belize	22.00 %	31
Pueblo Viejo, Belize	21.74 %	62
Estacion 2, Mexico	20.83 %	22
Manatee, Belize	15.00 %	5
Columbia, Belize	14.81 %	7

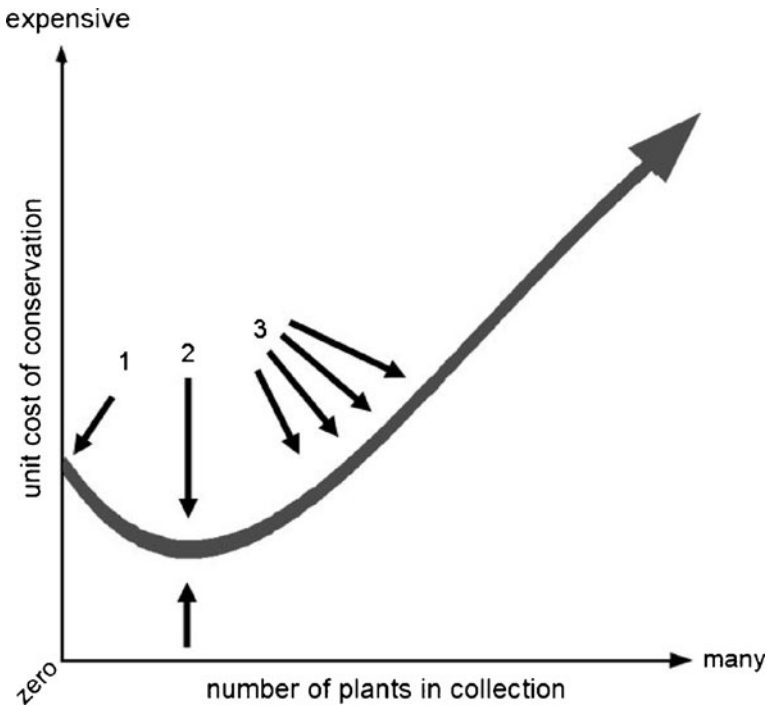


Fig. 5 Relationship between conservation collections investment and outcomes (Adapted from Griffith & Husby, 2010). “Unit cost of conservation” is % genetic capture divided by the cost of that collection. The rate of increase in genetic capture diminishes while the cost of maintaining the collection increases steadily, as the collection size increases. Position of the Y-intercept (arrow 1) is equal to the fixed cost of bringing plants to the garden, and is never equal to zero. There are an optimum number of plants to reach an efficient “unit cost of conservation,” at the lowest Y-value (arrow 2). Greater numbers of plants will result in a steadily increased unit cost of conservation (arrow 3)

1991) can provide for a healthy level of genetic capture, consistent with institutional goals. Highest efficiency in conservation value versus resource investment occurs at around five individuals, although planned redundancy may call for a larger number (cf. Li & Pritchard, 2009, for seed bank work).

In generalized terms, this approach recommends maximizing genetic capture represented in living collections (which motivates larger collections), balanced with careful allocation of resources (which motivates smaller collections). Finding the most efficient point (Fig. 5) helps balance these two parameters.

Finally, how feasible is it to characterize collections genetically? Genetic characterization of plant germplasm collections offers valuable information (Meerow, 2005), but efficacy and economics – time and resources – of the genetics work must also be considered. Table 3 compares three commonly used assay methods: Random Amplified Polymorphic DNA (RAPDs; Williams et al., 1990), Amplified Fragment Ligase Polymorphism (AFLP; Vos et al., 1995), and Simple Sequence Repeat (SSR; Powell et al., 1996), based on experiences at the USDA-ARS Subtropical Horticulture Research Station (i.e. Chapman Field). Development and assay using RAPDs is easiest and least expensive, and requires only modest lab equipment. Issues with reproducibility (McGregor et al., 2000) can limit application of RAPD data for comparative purposes. AFLP analysis offers a more reliable approach (Meerow et al., 2004), but the costs are greater. SSR data offers a more reliable and finer-scale assay approach (Meerow et al., 2002, 2007), but development, assay, and equipment costs for this work are the most expensive of the three. Microsatellite discovery assays using increasingly cheaper next-generation sequencing technology (Castoe et al., 2009; Santana et al., 2009; Csencsics et al., 2010) offers a cost effective alternative approach to laborious isolation procedures (e.g., Edwards et al., 1996), and can yield significantly more informative loci.

For many botanic gardens (e.g., MBC), DNA lab infrastructure and equipment may not be a priority. Thus, a collaborative, project-based approach involving botanic garden plants and university or research collaborators can provide the expertise and lab facilities needed for collections characterization (Griffith et al., 2011). Reciprocally, botanic gardens can benefit by cultivating collections used in genetics research, such as the genotyped *Cocos nucifera* L. ‘Niu Leka’ (‘Fiji Dwarf’) collections currently kept at MBC (Meerow et al., 2002).

Table 3 Comparison of function and feasibility among three common genetic assays

Feature	RAPD	AFLP	SSR
Transferability	Within species	Within species	Within genus or species
Reproducibility	Low to medium	Med. to high	Med. to high
Development	Easy	Moderate	Difficult
Assay	Easy to mod.	Mod. to difficult	Easy to mod.
Development cost	Inexpensive	Mod.	Expensive
Assay cost	Inexpensive	Mod. to exp.	Mod.
Equipment cost	Mod.	Mod. to exp.	Mod. to exp.

Information Sharing Across Gardens

An important aspect of successful ex situ plant conservation is to connect gardens and researchers to plants and information available in living plant collections. Facilitating the use of living collections to support research, and literally connecting individual collections to the rest of the world, is crucial as the conservation community wrestles with large-scale issues such as climate change, species and habitat loss, invasive species, and pollution. Collaboration with the broader public garden and plant conservation communities can increase the value and use of an individual collection, and support broader conservation efforts. A single garden may hold extremely rare specimens, or valuable local germplasm, and the synergy that can exist among collections has been identified as a very powerful tool for plant conservation and collection-building efforts (Kramer et al., 2011).

Sharing plant material can serve as an insurance policy against loss of that germplasm at a single institution. Institutions can also share their unique expertise and facilities to support efforts such as specialized propagation and horticultural protocols (e.g. Kay et al., 2011, for *Microcycas*). Furthermore, each time exchange takes place, an auditing process occurs to verify the identity and accuracy of the material and associated data, which can lead to data corrections or improvements and even new botanical discoveries.

Online facilities such as BGCI's PlantSearch database (BGCI, 2011) are emerging as effective tools for connecting researchers directly to plants in living collections. PlantSearch is the only global database of gardens and the plants they cultivate. Gardens can upload a taxon list for free via the BGCI Plant Upload (BGCI, 2011). The benefits of the Upload are three-fold. First, the upload process completes a basic names audit via the International Plant Names Index, through which misspellings and similar database errors can be identified and later corrected. Additionally, the Plant Upload cross-checks all valid plant names with the global threatened plant lists: the IUCN Red List of Threatened Species (IUCN, 1994, 2001; Walter & Gillette, 1998), Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES), and NatureServe G-ranks (NatureServe, 2009). Finally, all valid names uploaded to BGCI are included in PlantSearch queries; and blind email requests for plant material and information connect online users (i.e., researchers, other garden staff, etc.) to collection managers at gardens maintaining species of interest.

For the individual garden, BGCI's Plant Upload supplies relevant information to a living collection that can aid in strategically building ex situ collections, as demonstrated with the Arnold Arboretum Conservation Value (Hird & Dosmann, unpublished data). As living collections become more accessible to a broader community via BGCI's PlantSearch database and others, exciting possibilities arise. One possibility is to include the quantitative C-value estimated from our indicators (Table 1) into global databases. The North American Collections Assessment demonstrates how PlantSearch data can be used to guide broader plant conservation efforts (Kramer et al., 2011). This assessment utilized the framework of PlantSearch, combined with a broad call for data sharing, to assess gaps between imperiled plant species and botanic garden living collections. This approach outlines a clear path forward for continued collections development.

Integrating Indicators into a Conservation Value - Conclusions and Recommendations

The current world situation includes limited resources and imperiled plants, and this is expected to continue going forward. Allocating botanic garden resources for maximum conservation value within their living collections is therefore important for future efforts in plant conservation. Additionally, strategic efforts in the short term will allow for more effective long term planning.

We proposed that botanic gardens are an important and currently underutilized resource for threatened species management and conservation. The first step to make better use of these collections is to determine their value. We have discussed here three main areas to consider when assessing the value of living collections for plant conservation: their conservation status in situ via a species rarity and imperilment assessment; how well they represent wild populations genetically; and the cost of management operations in maintaining a specimen.

We suggest that these three measures of a living botanical collection can be used to decide the species' Conservation Value (Fig. 6). We have summarized this idea in an expanded version of the Conservation Value "Rosetta Stone" discussed previously (Table 1). A botanic garden manager can characterize a species based on these three metrics using the approach and tools highlighted in this paper. We add here a list of specific recommendations to facilitate the integration of our approach into the utilization of plant resources in botanic gardens to support ex situ plant conservation:

- (1) **Single individuals and multiple plants help capture genetic diversity.** A single individual can help capture significant genetic diversity – one individual of an imperiled plant is better than none at all. However, multiple individuals tend to capture greater genetic diversity and have direct conservation applications. Larger collection sizes ensure adequate genetic representation. Coordination of management methods and plant records among multiple collections can increase the effective ex situ collection size and genetic capture for a species.
- (2) **Increasing sample size will eventually yield diminishing returns on genetic capture.** Balancing allocation of limited resources against these diminishing returns requires careful consideration of specific circumstances. As an example, growing excessive acres of a single imperiled species may tie up resources that may be better utilized maintaining multiple species.
- (3) **Genetic data on conservation collections offers direct insight.** Investing resources to assay diversity of cultivated plants can help advance understanding of the behavior of conservation genetics within botanic garden living collections. This is a strategic investment of resources that will benefit ex situ conservation in the long term. We encourage conservation genetic experts to run samples of living collections parallel to the other samples in their investigations. In most cases, this additional sampling should not increase the resources or workload for modern population genetic studies by a significant amount, given the relative sizes of cultivated collections and wild populations. This will, however provide useful information for collection holders and the collective efforts to preserve a given species.
- (4) **Including garden plant collection genetic assay costs in grants can improve management.** Researchers can factor in the cost of processing a subset of their

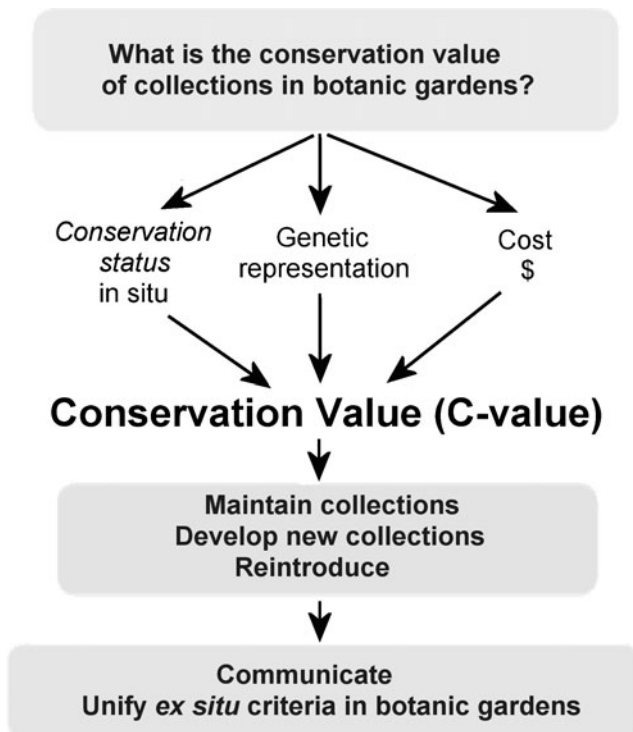


Fig. 6 Strategy towards evaluating the conservation value of living collections in botanical gardens. At least one of three main factors should be taken into account to evaluate a collection: the status of a species in the wild (species risk assessments), the genetic representation of the collection in the context of wild variation or among the collection itself, and the operational cost of maintaining collections. A conservation value (C-value) of a species can be shared via online databases (e.g. BGCI's PlantSearch database), leading towards a unified effort of ex situ conservation in Botanic Gardens

wild collections for the genetic profile we propose here into their grants. Even a few individuals processed for genetic data would be a valuable contribution to botanic gardens where corresponding living collections are kept.

- (5) **Conservation journals can encourage ex situ investigation.** Much like requirements for deposit of type specimens (Mottram & Gorelick, 2008), enabling open-access of findings and data (Lawrence, 2001), and ensuring lack of conflict of interest, conservation journal editors can encourage parallel study of garden living collections for inclusion in basic research.
- (6) **Conservation journals can encourage expert recommendations for botanic gardens.** Conservation genetic study or review can include clear interpretation of results for botanic garden curators and managers. Such interpretation may be as simple as a bullet point list or a priority of management units for developing ex situ collections.
- (7) **Gardens can incorporate threatened species data into living collections.** Gardens can build their living collections around plant conservation objectives more effectively by incorporating threatened species ranks into their plant records databases. This will allow for strategic collections management and prioritization that more effectively supports threatened species conservation.

- (8) **Gardens must connect their collections.** Gardens should share their collections data with broader databasing efforts, such as BGCI's PlantSearch database. By completing the BGCI Plant Upload, gardens gain valuable threatened species data about their collection, and connect and integrate their collections with the botanical research and conservation communities.

The need for effective ex situ plant conservation, and the role living collections can play, is only going to grow in the future. The obstacles and solutions presented above are examples of how to take the first steps toward effective ex situ collections management of living plant collections. Simply put, ex situ plant conservation cannot be an effective component of living collections management if threatened species are not easily recognized, documented, assayed and monitored within a collection. Further, effective collections management will ultimately allow ex situ collections of threatened species to be accessible and useful for conservation, education, horticulture and research applications.

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