

***Phyllostegia electra* Species Management Plan**

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Introduction: *Phyllostegia electra* is a mint plant native to Hawai'i, specifically the island of Kaua'i between 671-1563 meters elevation. Data as recent as 2015 has shown that there are only 52 mature individuals of the species *in situ*, placing the species in the IUCN Red List of Threatened Species category of Critically Endangered (Clark, 2015). Flowers are perfect, white and the fruit is a drupe-like nutlet, ranging from dark green to black in color. Similar to the other 63 taxa of mint endemic to Hawai'i, *P. electra* is scentless. The species is mesophytic and is rarely seen outside of the mesic and wet forests of Kaua'i, leading to its strict geographic confinement in these areas of the island. The population of *P. electra* has decreased due to the threat of non-native feral animals, such as pigs and goats. The genotyped population consists of seven *ex situ* individuals which are housed at the National Tropical Botanical Garden (NTBG).

Analytical Assumptions and Exclusions: For the pedigree population, all individuals were grown from wild collected material. Five originated from wild collected seed, three of which were from the same maternal individual (PHY ELE KA MOH A 0002) and two were from untagged, wild maternal plants which may or may not be from the same three individuals (seeds representing each separate accession were collected on different dates but from the same general area as each other and the three other seed collections from the tagged individual). One of the individuals part of the pedigree population resulted from a cutting collected from a wild individual (PHY ELE KA IOL A 0001) and one was grown up in the nursery from a wild collected seedling from a different area (wild unique ID PHY ELE KA KOI A 0002). All paternal sources are unknown. The two individuals that were collected as seed from the wild with an undocumented maternal founder were given a unique maternal source ID. In addition, we can assume that all paternal sources were WILD although we do not know whether collected seeds or plants from which cuttings were collected were the result of a self pollination or an outcrossing event. These two latter assumptions will overestimate the number of founders.

For the empirical population, we estimated relatedness using the Dyad ML measure from the program CoAncestry. In total, we estimated relatedness between 15 pairs of individuals. The average relatedness was 0.59 ± 0.24 . Relatedness estimates were then formatted into a pairwise matrix and uploaded into PMx as relatedness coefficients.

Demography: Demographic analyses were beyond the scope of the analyses based on the limited amount of demographic information documented for the species.

Genetics: Analysis of the pedigree population indicates that the population is descended from 6 founders. Analysis of the empirical population shows that the gene diversity is 67.06%, which is equivalent to the gene diversity found in 1 - 2 individuals (FGE = 1.52). The current mean kinship of the empirical population is 0.3294 meaning that, on average, individuals are more related to one another than are parents and offspring (kinship coefficient for parents and offspring is 0.25). See glossary below for definitions of terms in Table 1.

Table 1. Genetic status of empirical *ex situ* population

Genetics Summary - 2023	
Founders	6
Potential (additional)	0
Living Individuals	
N Individuals	6
Living Descendants	4
% Analytic known	100.0%
% Pedigree Known	66.7%
% Ancestry Certain	66.7%
Gene Diversity	
Based on Kinship Matrix	0.6706
Based on Gene Drop	0.8276
Potential	0.8517
Gene Value	—
Population Mean Kinship	0.3294
Founder Genome Equivalents	
Based on Kinship Matrix	1.52
Based on Gene Drop	2.9
Potential	3.37
Founder Genomes Surviving	3.37
Mean Inbreeding	0.0000
Mean Ne	1.86
Over Generations:	1.00
Current Ne	0.000
Ne/N	0.000

Recommended breeding plan: We recommend that future management plans prioritize increasing the *ex situ* population by bringing in more wild collected seed and/or cuttings from a

variety of maternal sources. Currently the *ex situ* population is small with little genetic diversity and high amount of mean kinship. We also recommend pollen storage of as many *ex situ* and *in situ* individuals as possible.

If managers decide to breed current *ex situ* individuals, we have outlined recommended breeding pairs below (Table 2). Breeding decisions should seek to increase the genetic representation of genetically unique individuals (or founder genomes) that are currently under-represented *ex situ*. In ensuring equal representation of individuals, managers can reduce the amount of genetic diversity lost over time. Ideally, breeding would include few offspring per breeding event. To be included in a breeding pair, individuals must (1) be ranked as a genetically valuable individual (see MKRank below, Table 3), (2) be in a pair that results in offspring with little inbreeding (F), and (3) be in a pair that results in a positive or no change in gene diversity. In the pairs below, it is possible to increase gene diversity of the *ex situ* population by identifying individuals that are genetically under-represented in the population

Table 2 includes the Unique ID for the first recommended parent (Unique ID1), the location of that parent (Local ID 1), the Unique ID for the second recommended parent (Unique ID2), and the location of that parent (Local ID 2), the inbreeding coefficient of the offspring of the recommended pairing (F), and the change in gene diversity of the population that results from the recommended pairing (Gene Diversity).

Table 2. Recommended breeding pairs - not ordered by change in gene diversity

Unique ID1	Local ID 1	MKRank ID1	Unique ID2	Local ID2	MKRank ID2	F	Gene Diversity (+)
NTBG-01	Greenhouse 20170254	1	MF-02	SKW755	2	0.1846	0.0040

Mean kinship ranking: Table 3 includes the mean kinship for the empirical *ex situ* population and their rankings. Included is the Unique ID of each individual, the Local ID or accession number, the empirical mean kinship (MK), and the rank of each individual based on empirical mean kinship (MKRank).

Table 3. Empirical mean kinship rankings

Unique ID	Local ID	MK	MKRank
NTBG-01	Greenhouse 20170254	0.2650	1
MF-01	SKW754	0.3007	2
MF-02	SKW755	0.3177	3
NTBG-02	NTBG Greenhouse 20170292	0.3575	4
M-14	SKW69 20150470 013	0.3678	5

M-12	SKW69 20150470 001	0.3679	6
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Glossary:

PMx definition of a founder - PMx considers a founder to be an individual with Wild/Wild parentage that has living descendants in the selected population

Potential Founder - living individuals that have no living relatives in the population but have the potential to reproduce and contribute to the population

Living Descendants - The number of living individuals descended from founders. This may be a fractional number because PMx normally excludes all individuals with unknown parents from genetic analyses, and includes only those parts of individuals that can be traced back to known founders. For example, an individual with a known dam but an unknown sire will be tallied as half an individual in genetic analyses

N Individuals - Number of living individuals in the currently selected population for genetic analysis

% Ancestry Certain - The percentage of the living individuals' pedigree that can be completely identified (exact identity of both parents is known) and traceable back to known founders. Individuals that are 100% Certain do not have any MULTs or UNKs in their pedigree. Certainty represents a higher degree of knowledge than Known and therefore is always less than or equal to Known.

Gene Diversity - Proportional gene diversity (as a proportion of the source population) is the probability that two alleles from the same locus sampled at random from the population are not identical by descent from a common ancestor. Gene diversity is the heterozygosity of founder alleles (= 1 – inbreeding) expected in progeny produced by random mating

Gene Value - Gene value is the gene diversity of the living individuals weighted for the reproductive value of individuals. Gene value is the heterozygosity of founder alleles expected in progeny produced by random mating and if each individual were to produce the number of offspring expected from its age-based reproductive value

Gene Diversity (Based on Kinship Matrix) - Gene diversity calculated from the kinship matrix as $1 - \bar{m}_k$, where \bar{m}_k is the average mean kinship in the population

Gene Diversity (Based on Gene Drop) - Gene diversity (GD) calculated from gene drop simulations. Each founder is assigned two unique alleles that pass stochastically through the pedigree. Final GD is calculated from the final distribution of alleles and is based on the number of alleles and the evenness of allele frequencies

Potential Gene Diversity - Potential GD of the population if optimal reproduction of potential founders were to be achieved (calculated as $1 - (1/2FGE_{\text{potential}})$, where $FGE_{\text{potential}}$ is the population's potential founder genome equivalent).

Gene Value - Gene value of the current living population and is the gene diversity of the population weighted for the reproductive value of individuals

Population Mean Kinship - Average mean kinship value of individuals in the current living population

Founder Genome Equivalent - The number of unrelated individuals (founders) that would represent the same amount of gene diversity as does the population of currently living individuals. A population's FGE becomes smaller than the actual number of population founders over time, as founder representations vary and gene diversity is lost from the population

Founder Genome Equivalent (Potential) - Maximum FGE that can be attained (if all founder allele retentions are set to their potential retention). Provides an upper limit to what might be achieved through perfect genetic management but is not usually realistically achievable

Founder Genomes Surviving - The sum of allelic retentions of the individual founders (i.e., the product of the mean Genomes allelic retention and the number of founders)

Mean Ne - Average effective population size of the selected population over the analysis time span. Given in relation to the number of Generations over which Ne is calculated

Current Ne - Effective population size of the selected living population, based on the number of living males and females that have produced offspring

Ne/N - Ratio of the effective population size to census size of living, captive-born individuals

Mean Inbreeding - The average of the inbreeding coefficients among the living individuals, weighted by the % known for each individual. The mean inbreeding coefficient of a population will be the proportional decrease in observed heterozygosity relative to the expected heterozygosity of the founder population.