

***Attalea crassispata* Species Management Plan**

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Introduction: *Attalea crassispata* is a species of palm tree native to the southwest region of Haiti. A recent survey found only 25 individuals in the wild, which places this taxon in the IUCN Redlist category of Critically Endangered. Palms of this species are monoecious, self compatible, but predominantly outcrossing. Palms grow up to 20 meters (66 ft) tall, and hold up to 20 pinnately compound leaves. The species is confined to the Southern Peninsula of Haiti, and it is the only species of *Attalea* found on the Caribbean islands, as the rest of the genus is found in Mexico, Central, and South America. Widespread deforestation and lightning strikes in Haiti have also led to a decrease in the population. The genotyped population consists of 74 ex situ individuals which are housed at six different institutions. To our knowledge, the ex situ individuals included here are all known living ex situ palms of this species. All but two individuals are included in the empirical (i.e., genotyped) population and all individuals are included in the pedigree population. We consider the managed population to include all those individuals in the empirical population.

Analytical Assumptions and Exclusions: For the pedigree population, the maternal sources of each wild collected individual was based on accession information and parentage analysis (Diaz-Martin et al. 2023). If individuals came from the same maternal plant, they were given the same wild maternal source ID (e.g., WILD1). If the maternal source was unknown, the wild born individual was given a unique maternal source ID. In addition, paternal sources were all WILD. These two latter assumptions will overestimate the number of founders. However, as a result, 100% of the pedigree is known and certain.

For the empirical population, we estimated relatedness using the Trio ML measure from the program CoAncestry (see Diaz-Martin et al. 2023 for details). Two ex situ individuals (FTG-26, FTG-35) were excluded from the empirical population because they failed to sequence. In total, we estimated relatedness between 2,080 pairs of individuals ex situ. The average relatedness was 0.11 ± 0.18 . 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. We summarize what is known here for the 67 ex situ plants:

(1) The oldest three plants are of unknown origin and age, but were established prior to 1958.

(2) The vast majority of ex situ individuals (57 plants) are founder plants derived from two seed collections from the wild just over 30 years ago. 15 plants were collected in 1989, 39 were collected in 1991, and the remaining 3 were collected in 2000.

(3) All of the remaining ex situ plants (7 captive born individuals) derived from open pollination in 2011 and 2013. Two of these, germinated in 2011, derive from a single known mother plant of unknown origin. Two of these, also germinated in 2013, derive from a single known mother plant that was collected from the wild. Three of these, also germinated in 2013, derive from wild collected founders, but parentage is unknown.

(4) It is unknown how many ex situ individuals are reproductively active, but as the species is inconsistently dioecious, reproductive individuals may not set seed in any given year. In addition, because the species is long-lived, no individuals in cultivation have yet died. The lack of demographic analyses prohibits the inclusion of demographically oriented goals.

Genetics: Analysis of the pedigree population indicates that the population is descended from 43 founders. Analysis of the empirical population shows that the gene diversity is 93.57%, which is equivalent to the gene diversity found in 7 - 8 individuals (FGE = 7.78). The current mean kinship of the empirical population is 0.0643 meaning that, on average, individuals have similar kinship coefficients as do half-cousins (0.0625) or first cousins once removed (0.0625). See glossary below for definitions of terms in Table 1.

Table 1. Genetic status of empirical population

Genetics Summary - 2023	
Founders	43
Potential (additional)	0
Living Individuals	
N Individuals	65
Living Descendants	65
% Pedigree Known	100.00%
% Ancestry Certain	100.00%
Gene Diversity	
Based on Kinship Matrix	0.9357
Based on Gene Drop	0.9683
Potential	0.9820
Gene Value	0.9351
Population Mean Kinship	0.0643
Founder Genome Equivalents	

Based on Kinship Matrix	7.78
Based on Gene Drop	15.75
Potential	27.77
Founder Genomes Surviving	27.77
Mean Inbreeding	0.0000
Mean Ne	10.37
Over Generations:	1.11
Current Ne	3.00
Ne/N	0.0462

Recommended breeding plan: We recommend that future management plans prioritize the breeding pairs outlined 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. Individuals were not considered for breeding if they were < 25 years in age. 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. Important future plans should incorporate the individuals that have low mean kinship rankings (Table 3), meaning they are genetically valuable, but are not yet reproductively active. 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 (ID1), the location of that parent (Location1), the Unique ID for the second recommended parent (ID2), and the location of that parent (Location2), 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

ID1	Location1	ID2	Location2	F (offspring)	Gene Diversity (+)
TREC-15	TREC	MBCA-09	MBCA	0.0000	0.0009
MBCA-03	MBCA	TREC-05	TREC	0.0000	0.0007
TREC-13	TREC	FTG-01	FTG	0.0000	0.0006
TREC-13	TREC	TREC-03	TREC	0.0000	0.0008

TREC-11	TREC	MBCA-10	MBCA	0.0094	0.0009
MBCA-09	MBCA	TREC-08	TREC	0.0000	0.0006
FTG-04	FTG	TREC-15	TREC	0.0000	0.0008
MBCA-01	MBCA	TREC-05	TREC	0.0000	0.0006
TREC-10	TREC	TREC-11	TREC	0.0000	0.0006
TREC-03	TREC	FTG-01	FTG	0.0000	0.0004
TREC-08	TREC	FTG-34	FTG	0.0000	0.0003
FTG-34	FTG	MBCA-10	MBCA	0.0093	0.0005
FTG-04	FTG	TREC-12	TREC	0.0000	0.0003
TREC-09	TREC	TREC-10	TREC	0.0000	0.0003
MBCA-01	MBCA	MBCC-03	MBCC	0.0000	0.0003
MBCA-10	MBCA	MBCA-01	MBCA	0.0105	0.0005

Mean kinship ranking: Below we include the mean kinship for the empirical population and their rankings. Included is the Unique ID of each individual, its current location, the LocalID or accession number, the Age in years, the empirical mean kinship (MK), and the rank of each individual based on empirical mean kinship (MKRank).

Table 3. Empirical mean kinship rankings

UniqueID	Location	LocalID	Age	MK	MK Rank
SBG-02	Singapore Botanic Gardens	20002092*D	19	0.0219	1
SBG-01	Singapore Botanic Gardens	20002092*B	19	0.0223	2
TREC-05	Tropical Research and Education Center		29	0.0267	3
TREC-13	Tropical Research and Education Center		29	0.0281	4
TREC-15	Tropical Research and Education Center		29	0.0284	5
TREC-11	Tropical Research and Education Center		29	0.0307	6
MBCA-09	Montgomery Botanical Center	91441*A	28	0.0323	7
MBCA-10	Montgomery Botanical Center	91441*B	28	0.033	8
FTG-04	Fairchild Tropical Botanic Garden	91198*A	28	0.0418	9
MBCC-03	Montgomery Botanical Center	20130722*C	4	0.0461	10
FTG-01	Fairchild Tropical Botanic Garden	2000845*A	19	0.0474	11
MBCA-03	Montgomery Botanical Center	91327*J	28	0.0489	12

TREC-03	Tropical Research and Education Center		29	0.049	13
TREC-10	Tropical Research and Education Center		29	0.0496	14
TREC-08	Tropical Research and Education Center		29	0.0498	15
TREC-02	Tropical Research and Education Center		29	0.05	16
MBCC-02	Montgomery Botanical Center	20130722*B	4	0.0527	17
MBCB-01	Naples Botanical Garden	20130520	5	0.0531	18
MBCA-01	Montgomery Botanical Center	91327*G	28	0.0533	19
FTG-05	Fairchild Tropical Botanic Garden	91327*A	28	0.0535	20
TREC-07	Tropical Research and Education Center		29	0.0537	21
TREC-09	Tropical Research and Education Center		29	0.0541	22
FTG-34	Fairchild Tropical Botanic Garden	P1338*E	60	0.0544	23
TREC-04	Tropical Research and Education Center		29	0.0548	24
MBCC-01	Montgomery Botanical Center	20130722*A	4	0.0553	25
TREC-01	Tropical Research and Education Center		29	0.0553	26
FTG-08	Fairchild Tropical Botanic Garden	91327*S	28	0.0557	27
MBCB-02	Montgomery Botanical Center	20130520*A	5	0.0568	28
TREC-06	Tropical Research and Education Center		29	0.0571	29
FTG-02	Fairchild Tropical Botanic Garden	2011-0403*B	8	0.0578	30
FTG-11	Fairchild Tropical Botanic Garden	91327*D	28	0.0582	31
FTG-33	Fairchild Tropical Botanic Garden	P1338*A	60	0.0582	32
TREC-14	Tropical Research and Education Center		29	0.0585	33
FTG-09	Fairchild Tropical Botanic Garden	91327*T	28	0.0588	34
FTG-06	Fairchild Tropical Botanic Garden	91327*B	28	0.0604	35
TREC-12	Tropical Research and Education Center	20130722	29	0.0617	36
FTG-10	Fairchild Tropical Botanic Garden	91327*U	28	0.0623	37
FTG-25	Fairchild Tropical Botanic Garden	91411*G	28	0.0636	38
FTG-03	Fairchild Tropical Botanic Garden	2011-0403*C	8	0.0648	39
MBCA-02	Montgomery Botanical Center	91327*H	28	0.0667	40

MBCA-05	Montgomery Botanical Center	91409*B	28	0.0764	41
FTG-07	Fairchild Tropical Botanic Garden	91327*C	28	0.081	42
MBCA-04	Montgomery Botanical Center	91409*A	28	0.0815	43
FTG-17	Fairchild Tropical Botanic Garden	91409*K	28	0.082	44
FTG-18	Fairchild Tropical Botanic Garden	91409*L	28	0.0821	45
FTG-22	Fairchild Tropical Botanic Garden	91411*C	28	0.0838	46
FTG-21	Fairchild Tropical Botanic Garden	91411*B	28	0.0845	47
FTG-20	Fairchild Tropical Botanic Garden	91411*A	28	0.0849	48
MBCA-07	Montgomery Botanical Center	91440*B	28	0.0852	49
FTG-31	Fairchild Tropical Botanic Garden	91440*H	28	0.0854	50
FTG-27	Fairchild Tropical Botanic Garden	91411*K	28	0.0864	51
FTG-19	Fairchild Tropical Botanic Garden	91409*N	28	0.0867	52
FTG-16	Fairchild Tropical Botanic Garden	91409*J	28	0.0868	53
FTG-32	Fairchild Tropical Botanic Garden	91440*J	28	0.0881	54
FTG-13	Fairchild Tropical Botanic Garden	91409*F	28	0.089	55
MBCA-06	Montgomery Botanical Center	91409*C	28	0.0893	56
FTG-15	Fairchild Tropical Botanic Garden	91409*H	28	0.0902	57
FTG-24	Fairchild Tropical Botanic Garden	91411*F	28	0.0908	58
FTG-30	Fairchild Tropical Botanic Garden	91440*F	28	0.0908	59
MBCA-08	Montgomery Botanical Center	91440*C	28	0.0914	60
FTG-23	Fairchild Tropical Botanic Garden	91411*D	28	0.0924	61
FTG-29	Fairchild Tropical Botanic Garden	91440*E	28	0.0927	62
FTG-14	Fairchild Tropical Botanic Garden	91409*G	28	0.0953	63
FTG-12	Fairchild Tropical Botanic Garden	91409*D	28	0.0964	64
FTG-28	Fairchild Tropical Botanic Garden	91440*A	28	0.0969	65

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 ($= 1 - \text{inbreeding}$) 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 $1 - m_k$, where 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 $1 - (1/2\text{FGE}_{\text{potential}})$, where $\text{FGE}_{\text{potential}}$ 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.