Electronic Supplementary Materials

Materials and Methods

DNA extraction procedures were as described by Pellmyr et al. (2007). PCR reactions were performed in 30 µl reaction volumes, with 0.3 µL of 10 µM primers and 0.6 µL of 10 mM dNTP mixture, 3 µL of 10X reaction buffer, and 1.5 units of Fisher brand Taq polymerase. $MgCl_2$ and template volumes varied depending on the primers used for amplification (Table S1). PCR reactions were performed in an MJ Research PTC-100 thermal cycler. For all gene regions except the rps16 intron, sequences were amplified using standard PCR conditions (see Table S1 for primer-specific annealing temperatures). The rps16 intron was amplified using a touchdown procedure, with a starting annealing temperature of 56°C and a final annealing temperature of 42°C.

PCR reactions were analyzed by electrophoresis in 2% agarose gels stained with ethidium bromide and visualized using a UV light trans-illuminator. Successful PCR reactions were purified using QIAquick PCR Purification Kits (© 2002, Qiagen Corporation). Sequencing of purified PCR products followed Althoff et al (2006).

Raw sequence data were edited in Sequencher v. 4.1.2 (GeneCodes Corporation, Ann Arbor, MI). Multiple sequence alignment was completed in Clustal W using a gap opening penalty = 15 and a gap extension penalty = 6.66.

Phylogenetic analysis- Aligned sequences were concatenated in Mesquite v. 1.11 (Maddison & Maddison 2006). Indels were recoded by hand as presence/absence data according to the procedure described by Simmons and Ochoterena (2000). Tandem repeats were recoded as ordered, multi-state characters.

Data were analyzed using Bayesian inference. Analyses were executed in MrBayes v. 3.1.2 (Huelsenbeck & Ronquist 2001). All runs were implemented using two replicate runs, with 8 chains (7 heated, 1 unheated) and the temperature parameter set to 0.1. The program was set to terminate when the standard deviation of split frequencies between replicates reached $<$ 0.01. Post-burn-in trees were sampled every 1000 generations, and the Bayes consensus of these trees was calculated including all compatible subgroupings using SumT.

Analysis of AFLP data used a one-parameter, k-state model for standard data (Lewis 2001). Datasets that combined DNA sequences with AFLP or indel data used a partitioned model; the indel, tandem repeat, and AFLP data were analyzed under Lewis's model for standard data, and the DNA sequence data were analyzed under the K81+G model, selected by hierarchical likelihood ratio tests (HLRT) implemented in ModelTest v. 3.7 (Posada & Crandall 1998).

Support for the resultant topologies was assessed by calculating clade posterior probabilities, and by non-parametric bootstrapping under a maximum parsimony criterion. Non-parametric bootstrapping was conducted in PAUP* v. 4.0b10 (Swofford 2002) creating 1000 bootstrap replicates per dataset, using heuristic searches starting from random trees, with 100 addition sequence replicates, saving no more than 500 (153-taxa dataset) or 1000 (smaller datasets) trees per replicate.

***Assessing conflicts between data partitions* -** Inferring the age of clades using relaxed clock methods requires that the genes used to infer those ages accurately reflect the phylogenetic history of the organisms. Within Yuccas*,* it has been suggested that occasional introgression of chloroplast genomes between species may obscure true phylogenetic relationships (Hanson

1993). For this reason, we tested for chloroplast introgression between lineages within *Yucca* prior to estimating ages.

Because the AFLP data represent a snapshot of overall genetic similarity sampled from across the entire genome, we consider the AFLP topology to be the best available reconstruction of the true phylogenetic relationships. Unfortunately, high rates of homoplasy, and a lack of sufficient models to describe the evolution of AFLP markers make it problematic to infer molecular clock estimates from the AFLP data directly. However, by identifying areas of conflict between the AFLP and chloroplast sequence data, we can eliminate putatively introgressed taxa and then infer clock estimates from sequence data, using only samples where introgression could be definitively ruled out.

We used four methods to quantify differences between the AFLP and cpDNA data partitions. First, to examine overall disagreement between partitions in the 83-taxa (i.e., only those taxa with data from both partitions), we used an incongruence length difference (ILD) test using 100 random partitions. Second, to identify conflict localized in specific nodes, we computed the partitioned Bremer support indices (Baker & DeSalle 1997) for nodes found in a combined parsimony analysis of the two data partitions and for nodes in the Bayes consensus trees derived from the AFLP and cpDNA sequence data analyzed separately. Partitioned Bremer supports were calculated using TreeRot v2 (Sorenson 1999) and PAUP v4.0B10. Search strategies were the same for both the initial unconstrained search and the constrained searches used to evaluate support for each node in the respective trees. Because PAUP does not currently implement a maximum likelihood model for standard data (such as AFLPs), the partitioned Bremer supports were calculated under a parsimony criterion only.

Next, to evaluate the statistical evidence for conflict between data partitions in a Bayesian context, we filtered the post-burn-in trees produced from the separate MrBayes analyses of the cpDNA and AFLP datasets, retaining only trees compatible with the topologies inferred from the AFLP or cpDNA datasets, respectively. The proportion of the trees retained is approximately equal to the probability that gene tree and species (AFLP) tree are identical (Stevens 2004).

Finally, to identify areas of significant *agreement* between data partitions, we used the program ParaFit to evaluate topological congruence between the Bayes consenus trees inferred from the AFLP and cpDNA dataset analyzed separately. Although ParaFit was originally developed to compare host and parasite trees (Legendre et al. 2002), several phylogenetic systematists have pointed out that because many underlying processes in host-parasite interactions are directly analogous to processes in molecular evolution, methods developed for cospeciation studies also have utility for comparing gene trees with species trees (Charleston & Perkins 2006; Doyle 1997; Maddison 1997; Page & Charleston 1998; Ronquist 1997). ParaFit in particular is often used in place of other traditional methods for cospeciation analysis that can be extremely computationally intensive (Charleston & Perkins 2006; Legendre et al. 2002; Page & Charleston 1998), and has recently been applied to comparing gene trees and species trees (Penton & Crease 2004) to test for horizontal transfer of genetic elements between species.

We considered the two datasets to agree on the placement of a particular taxon if the match between the AFLP and cpDNA datasets for that taxon made a significant ($p<0.05$) contribution to the overall level of congruence between the topologies, under both the ParaFitLink1 and ParaFitLink2 statistics. Following Legendre et al. (2002) those taxa that did not show a significant match were removed. We treated the AFLP topology as the 'host' phylogeny, and the cpDNA topology as the 'parasite' phylogeny, but because we accepted only taxa for which both ParaFitLink statistics were significant, this distinction is inconsequential. The AFLP and cpDNA sequence data from the remaining taxa (see Table S3 and Fig. 4) were analyzed both together and separately in MrBayes and PAUP (above) to estimate a topology and compute clade posterior probabilities and non-parametric bootstrap supports. Age estimates for relationships within *Yucca* were inferred using r8s (see 'Divergence time and mutation rate estimates,' below) from the sequence data, using the Bayes consensus topology estimated from the combined, conflict-free dataset.

Divergence time and mutation rate estimates- Divergence times and mutation rates were estimated from the Bayes consensus trees for the Asparagales (153-taxa) dataset and the conflict-free (46-taxa) *Yucca* dataset. Because of the problems associated with inferring clock estimates from AFLP data, described above, branch lengths were calculated for the latter topology using the sequence data alone in PAUP. Because likelihood ratio tests strongly rejected the presence of a molecular clock for both datasets ($p < 0.001$), divergence times were estimated using penalized likelihood in r8s v. 1.71 (Sanderson 1997; Sanderson 2002). Divergence times within the Asparagales were calibrated by constraining the age of the monocotyledons to be between 105.5 (Magallón & Sanderson 2001) and 139 MY (Sanderson & Doyle 2001), and the age of the Asparagales to be between 37.5 MY (Magallón & Sanderson 2001) and 94 MY (Wikström et al. 2001). Divergence times within *Yucca* were calibrated by setting the age of the common ancestor of Sarcocarpa and Chaenocarpa to be between 6.06 and 6.81 MY, the age range inferred from the r8s analysis of the Asparagales (153-taxa) dataset. Optimal smoothing values were determined by cross-validation using 100 different parameter values, and the correctness of solutions was determined using “checkgradient”, with 10 different starting conditions. To account for uncertainty in phylogenetic inference, we profiled divergence time estimates for nodes of interest across 100 post-burn-in trees, sampled every 80,000 generations (153-taxa dataset) or every 18,000 generations (46-taxa dataset).

Mutation rates and standard errors were estimated in r8s, averaging across all branches, across 100 post-burn-in trees. Locus-specific substitution and insertion/deletion rates within *Yucca* were computed by re-estimating branch lengths for the post-burn-in trees using either parsimony (for indel data) or maximum likelihood (for DNA sequence data). Maximum-likelihood models used the mean parameter values estimated in the Bayesian analysis. To account for uncertainty in calibration for the age of *Yucca,* we calculated the range of possible mutation rates assuming that the age of the ingroup was either 6.41 MY (Bayes consensus) or 10.19 MY (mean age profiled across post-burn-in trees).

Comparisons of diversification rates- We used two approaches to compare rates of speciation in *Yucca* and *Agave.* First, because *Yucca* (*Yucca sensu stricto* + *Y. queretaroensis*) and *Agave sensu latissimus* (*Agave, Beschorneria, Furcraea, Manfreda, Polianthes,* and *Prochnyanthes*) were found to be sister-groups (see Results), relative species diversity can be compared directly. We assume that there are 240 species within *Agave s. latissimus* – (166 species of *Agave,* 7 of *Beschorneria,* 25 of *Furcraea,* 28 of *Manfreda,* 13 of *Polianthes,* and one of *Prochnyanthes)* (Good-Avila et al. 2006) and 34 species of *Yucca,* including *Yucca queretaroensis* (Pellmyr et al. 2007). Although Good-Avila et al (2006) compared speciation rates in *Yucca* with those in *Agave sensu lato* (*Agave* + *Polianthes* + *Prochnyanthes),* by using the *Agave s. latissimus* we could make a robust sister-group comparison.

Differences in the total numbers of species between these sister groups were compared using Slowinski & Guyer's (1989) method. The hypothesis that these groups differ in speciation rates was also tested using a likelihood ratio test, assuming a chi-squared distribution and one degree of freedom (Sanderson & Donoghue 1994) .

Both of the preceding tests consider only differences in total species numbers between clades (see discussion in Schluter (2000)), so in a second approach that incorporates information about phylogeny, we calculated rates of speciation under a Yule model as described by Baldwin & Sanderson (1998). We use the number of species of each group included in the trnL-trnF dataset (33 for *Agave s. latissimus* and 34 for *Yucca);* total tree length was calculated from the trnL-trnF Bayes consensus tree for *Agave s. latissimus,* and *Yucca.* Because including multiple individuals of any given species would inflate the total tree length, trees were pruned to include only one representative from each species: within the *Agave* lineage only one species was represented by multiple individuals; within *Yucca,* individuals were selected for pruning to maximize the congruence with the AFLP topology. The pruned topologies are shown in figure S2, below. Total tree lengths were calculated using TreeStat v. 1.1 (Rambaut & Drummond 2005)

Finally, changes in diversification rates were calculated using Pybus's gamma statistic (Pybus et al. 2002) for these same topologies. The gamma statistic is influenced both by diversification rates and by incomplete taxon sampling, so we estimated the expected distribution of the gamma statistics using data simulations. Simulations were completed in Phyl-O-Gen v. 1.1 (Rambaut 2002), under a pure birth model sampling 33 of 240 species for *Agave s. latissimus* and all 34 species for *Yucca*. One thousand trees were simulated for each genus, and gamma statistics were calculated using TreeStat v. 1.1 (Rambaut & Drummond 2005). Rates of diversification were visualized by drawing lineages-through-time plots for each of these groups.

Table S1: Primers used in this study and PCR conditions. Primer pairs are alternately shaded / unshaded to indicate primers used together.

Primer Name	Sequence	Target Region	Used In	Annealing Temperature	Volume MgCl2	Volume Genomic DNA
113105-for[1]	TCAACGTGTCGATTCCAATCCTATCT	clpP intron2	PCR	55	1uL	4uL
113720-rev[1]	AAAATCAAGTATCCAGGCTCCGTTC	clpP intron2	PCR	55	1uL	4uL
113290-for[1]	TTCGTCGAGATTCAAATCACG	clpP intron2	Sequencing	60	NA	NA
113523-rev[1]	GGGTGATCTCAAACTGCCATGC	clpP intron2	Sequencing	60	NA	NA
rps16-ex1-for[2]	CGTTTGAAACGATGTGGTAG	rps16 intron	PCR, Sequencing	Touchdown: 56-42	2uL	3uL
rps16-ex2-rev[3]	CGTATCGGATCGTAAAAACCTAC	rps16 intron	PCR, Sequencing	Touchdown: 56-42	2uL	3uL
rps16-for-alt[1]	CACCATTTTCTATAGGAATGAAGATGC	rps16 intron	PCR, Sequencing	Touchdown: 56-42	1uL	2uL
rps16-rev-alt[1]	CGATAGATCGCTCATTGGGATAGATGT	rps16 intron	PCR, Sequencing	Touchdown: 56-42	1uL	2uL
trnL-for[4]	CGAAATCGGTAGACGCTACG	trnL-trnF	PCR, sequencing	47-50	2uL	3uL
trnL-F-rev[4]	ATTTGAACTGGTGACACGAG	trnL-trnF	PCR, sequencing	47-50	2uL	3uL
trnT-L-internal-for-2[1]	TACATTATCATTATAGATAATATACG	trnT-trnL	PCR, sequencing	53	3.5	5uL
trnL-rev	GGGGATAGAGGGACTTGAAC	trnT-trnL	PCR, sequencing	53	3.5	5uL
trnS-T-for[5]	CGAGGGTTCGAATCCCCTCTC	trnT-trnL	PCR, sequencing	52	3.5	5uL
trnT-L-int-rev[1]	TACTTTTCTTAGAACCGATCCGC	trnT-trnL	PCR, sequencing	52	3.5	5uL
trnS-T-rev	AGAGCATCGCATTTCTAATG	trnT-trnL	Sequencing	60	NA	NA
trnT-for[3]	CGATGACCCTCGCATTAC	trnT-trnL	PCR, sequencing	53	2ul	3.5uL
trnL-ex1-rev[3]	AAGTCCGTAGCGTCTACC	trnT-trnL	PCR, sequencing	53	2ul	3.5uL

1 Designed by CIS
2 (Downie & Katz-Downie 1999)
3 Designed by JLM
4 (Taberlet et al. 1991)
5 (Demesure et al. 1995)

Table S2: Collections Data and GenBank Accessions. Locality information and botanical authorities are provided for data first published here.

***Species* Author** Collection Locality	**Locality Coordinates**	**GenBank Accession #'s**	**Reference**
Amborella trichopoda	-	NC 005086	(Goremykin et al. 2003)
Acorus calamus	-	NC_007407	(Goremykin et al. 2005)
Phalaenopsis aphrodite	-	NC_007499	(Chang et al. 2006)
Hosta ventricosa	-	AF508512.1	(Pires & Sytsma 2002)
Convallaria majalis	-	AF508515.1	(Pires & Sytsma 2002)
Agapanthus africanus	-	AF508516.1	(Pires & Sytsma 2002)
Nolina microcarpa	-	AJ441178.1	(Jang & Pfosser 2002)
Dasylirion acrotrichum	-	AJ441179.1	(Jang & Pfosser 2002)
Muscari parviflorum	-	AJ508003.1	(Pfosser et al. 2003)
Agave angustifolia	-	DQ500891.1 DQ500925.1	(Good-Avila et al. 2006)
A attenuata	-	DQ500898.1 DQ500932.1	(Good-Avila et al. 2006)
A celsii	-	AF508509.1	(Pires and Sytsma 2002)
A cerulata	-	DQ500895.1 DQ500929.1	(Good-Avila et al. 2006)
A deserti	-	DQ500894.1 DQ500928.1	(Good-Avila et al. 2006)
A karwinskii	-	DQ500893.1 DQ500927.1	(Good-Avila et al. 2006)
A kerchovei	-	DQ500888.1 DQ500922.1	(Good-Avila et al. 2006)
A macracantha	-	DQ500892.1 DQ500926.1	(Good-Avila et al. 2006)
A marmorata	-	DQ500889.1 DQ500923.1	(Good-Avila et al. 2006)
A parviflora	-	AF508510.1	(Pires and Sytsma 2002)
A petrophila	-	DQ500886.1 DQ500953.1	(Good-Avila et al. 2006)
A potatorum	-	DQ500890.1 DQ500924.1	(Good-Avila et al. 2006)
A schidigera	-	DQ500884.1 DQ500919.1	(Good-Avila et al. 2006)
A stricta	-	DQ500887.1 DQ500921.1	(Good-Avila et al. 2006)
A subsimplex	-	DQ500897.1 DQ500931.1	(Good-Avila et al. 2006)
A terraccianoi	-	DQ500918.1 DQ500883.1	(Good-Avila et al. 2006)
A victoriae reginae	-	DQ500896.1 DQ500930.1	(Good-Avila et al. 2006)
Agave victoriae reginae	-	AJ232447 AJ232570.1	(Pfosser and Speta 1999)
A vilmoriniana	-	DQ500920.1 DQ500885.1	(Good-Avila et al. 2006)
***A lecheguilla* Torr.** Dagger Flat, TX	29.5190 N 103.0466 W	EU092259 EU092354 EU092448 EU092542	-
Anthericum liliago	-	AF117005.1 AF117033.1	(Meerow et al. 1999)
A liliago	-	AF508513.1	(Pires and Sytsma 2002)

A liliago	-	AJ232444.1 AJ232567.1	(Pfosser and Speta 1999)
A ramosum	-	AJ232445.1 AJ232568.1	(Pfosser & Speta 1999)
Behnia reticulata	-	AF117007.1 AF117035.1	(Meerow et al. 1999)
Beschorneria calcicola	-	DQ500911.1 DQ500951.1	(Good-Avila et al. 2006)
B rigida	-	DQ500909.1 DQ500943.1	(Good-Avila et al. 2006)
B wrightii	-	DQ500910.1 DQ500944.1	(Good-Avila et al. 2006)
Camassia cusickii	-	AJ232450.1 AJ232573.1	(Pfosser and Speta 1999)
C leichtlinii	-	AJ232451.1 AJ232574.1	(Pfosser and Speta 1999)
C quamash	-	AF508511.1	(Pires and Sytsma 2002)
Chlorogalum palmatum	-	AJ232448.1 AJ232571.1	(Pfosser and Speta 1999)
C. pomeridianum	-	AJ232449.1 AJ232572.1	(Pfosser and Speta 1999)
Furcraea guatemalensis	-	DQ500907.1 DQ500941.1	(Good-Avila et al. 2006)
F longaeva,	-	DQ500906.1 DQ500940.1	(Good-Avila et al. 2006)
F macdougallii	-	DQ500908.1 DQ500942.1	(Good-Avila et al. 2006)
Hesperaloe funifera	-	DQ500913.1 DQ500946.1	(Good-Avila et al. 2006)
***H funifera*, (Koch) Trel.** Starr Nursery, Tucson, AZ	In cultivation	EU092260 EU092355 EU092449 EU092543	-
Hesperoyucca whipplei	-	DQ500912.1 DQ500945.1	(Good-Avila et al. 2006)
***H whipplei* (Torr.) Trel** Elliott Reserve, CA	32.8683 N 117.1425 W	EU092261 EU092356 EU092450 EU092544	-
H whipplei Tuweep, AZ	36.2111 N 113.05667 W	EU092262 EU092357 EU092451 EU092545	-
H whipplei Temecula, CA	33.4439 N 117.1767 W	EU092263 EU092358 EU092452 EU092546	-
Leucocrinum montanum	-	AF117003.1 AF117031.1	(Meerow et al. 1999)
Manfreda hauniensis	-	DQ500900.1 DQ500934.1	(Good-Avila et al. 2006)
M nanchititlensis	-	DQ500899.1 DQ500933.1	(Good-Avila et al. 2006)
M potosina	-	DQ500901.1 DQ500935.1	(Good-Avila et al. 2006)
Polianthes densiflora	-	DQ500905.1 DQ500939.1	(Good-Avila et al. 2006)
P geminiflora	-	DQ500903.1 DQ500937.1	(Good-Avila et al. 2006)
P longiflora	-	DQ500902.1 DQ500936.1	(Good-Avila et al. 2006)
P pringlei	-	DQ500904.1 DQ500938.1	(Good-Avila et al. 2006)
Prochnyanthes mexicana	-	DQ500917.1 DQ500952.1	(Good-Avila et al. 2006)
Simethis mattiazzii	-	AJ290275.1 AJ290309.1	(Chase et al. 2000)

Yucca aloifolia L. Ft. George Island FL	29.6922 N 84.7878 W	EU092264 EU092359 EU092453 EU092547	-
Y angustissima Engelm. ex Trel. Peach Springs, AZ	35.561 N 113.4226 W	EU092265 EU092360 EU092454 EU092548	-
Y arizonica McKelvey KM 182, Rte 89, SON	30.88058 N 110.0915 W	EU092266 EU092361 EU092455 EU092549	-
Y baccata Torr. Wickenburg, AZ	34.2267 N 113.0699 W	EU092267 EU092362 EU092456 EU092550	-
Y baccata Torr. Blanding, UT	37.7638 N 109.4028 W	EU092268 EU092363 EU092457 EU092551	-
Y baccata Torr. Zion NP, UT	37.4653 N 113.1875 W	EU092269 EU092364 EU092458 EU092552	-
Y baccata Torr. Walnut Canyon, AZ	35.1717 N 111.5097 W	EU092270 EU092365 EU092459 EU092553	-
Y baccata Torr. Peach Springs, AZ	35.5708 N 113.4283 W	EU092271 EU092366 EU092460 EU092554	-
Y baccata Torr. Las Cruces, NM	32.3077 N 106.7083 W	EU092272 EU092367 EU092461 EU092555	-
Y baileyi Wooton and Standley St Johns, AZ	34.6666 N 109.65 W	EU092273 EU092368 EU092462 EU092556	-
Y baileyi Wooton and Standley Winona, AZ	35.2291 N 111.425 W	EU092274 EU092369 EU092463 EU092557	-
Y brevifolia Engelm. Palmdale, CA	34.530 N 118.065 W	EU092275 EU092370 EU092464 EU092558	-
Y. brevifolia Engelm. Shivwits, UT	37.0536 N 113.8947 W	EU092276 EU092465 EU092559	-
Y brevifolia Engelm. Potosi Canyon NV	36.0238 N 115.5407 W	EU092277 EU092371 EU092466 EU092560	-
Y brevifolia Engelm. Kingston Mts, CA	35.77027 N 115.8355 W	EU092278 EU092372 EU092467 EU092559	-
Y campestris, McKelvey Wickett, TX	31.5451 N 103.0754 W	EU092279 EU092373 EU092468 EU092562	-
Y capensis Lenz San Antonio, BCS	23.8095 N 110.06827 W	EU092280 EU092374 EU092469 EU092563	-

Y capensis **Lenz** San Pedro de la Soledad, BCS	23.4597 N 109.97407 W	EU092281 EU092375 EU092470 EU092564	-
Y capensis **Lenz** Sierra de San Antonio, BCS	23.8095 N 110.0683 W	EU092282 EU092376 EU092471 EU092565	-
Y carnerosana **Trel.** San Luis Potosi, SLP	22.2259 N 100.8252 W	EU092283 EU092377 EU092472 EU092566	-
Y carnerosana **Trel.** Dagger Flat, TX	29.5190 N 103.0466 W	EU092284 EU092378 EU092473 EU092567	-
Y carnerosana **Trel.** Saltillo, COAH	25.2442 N 100.8927 W	EU092285 EU092379 EU092474 EU092568	-
Y cernua **Keith** Newton, TX	30.8625 N 93.8223 W	EU092286 EU092380 EU092475 EU092569	-
Y constricta **Buckley** Brady, TX	31.0353 N 99.4227 W	EU092287 EU092381 EU092476 EU092570	-
Y constricta **Buckley** Menard, TX	31.2475 N 97.1107 W	EU092288 EU092382 EU092477 EU092571	-
Y decipiens **Trel.** Durango, DUR	23.9865 N 104.747 W	EU092289 EU092383 EU092478 EU092572	-
Y decipiens **Trel.** Michilia DUR	23.5983 N 104.0026 W	EU092290 EU092384 EU092479 EU092573	-
Y elata, **Engelm.** Rodeo NM	31.9508 N 108.6379 W	EU092291 EU092385 EU092480 EU092574	-
Y elata **Engelm.** Roosevelt Dam, AZ	33.6986 N 111.1986 W	EU092292 EU092386 EU092481 EU092575	-
Y elata **Engelm.** Oak Creek, AZ	34.7185 N 111.7766 W	EU092293 EU092387 EU092482 EU092576	-
Y elata **Engelm.** Sierra Vista, AZ	31.5474 N 110.1417 W	EU092294 EU092388 EU092483 EU092577	-
Y elata **Engelm.** Hueco, TX	31.8279 N 105.9419 W	EU092295 EU092389 EU092484 EU092578	-
Y elata **Engelm.** Willcox Playa, AZ	32.2408 N 109.8181 W	EU092296 EU092390 EU092485 EU092579	-
Y elata **Engelm.** Big Bend Nat'l Park, TX	29.6542 N 103.1026 W	EU092297 EU092391 EU092486 EU092580	-

***Y elephantipes,* Regel** Brownsville TX	25.8484 N 97.4161 W	EU092298 EU092392 EU092487 EU092581	-
***Y elephantipes* Regel** Yahualica, HGO	20.9245 N 98.5614 W	EU092299 EU092393 EU092488 EU092582	-
***Y elephantipes* Regel** Rizo de Oro, CHIS	15.9667 N 92.4833 W	EU092300 EU092394 EU092489 EU092583	-
***Y filamentosa* L** Ocala, FL	29.1333 N 81.5166 W	EU092301 EU092395 EU092490 EU092584	-
***Y filamentosa* L** Archbold Biol. Stn., FL	27.1882 N 81.337 W	EU092302 EU092396 EU092491 EU092585	-
***Y filifera* Chab.** Poza de Santa Clara, SLP	23.2502 N 100.5474 W	EU092303 EU092397 EU092492 EU092586	-
***Y filifera* Chab.** San Vincente, HGO	19.9974 N 98.7005 W	EU09230 EU092398 EU092493 EU092587	-
***Y filifera* Chab.** San Jose, MICH	19.5549 N 101.3907 W	EU092305 EU092399 EU092494 EU092588	-
***Y filifera* Chab.** Bucareli, QUE	21.0517 N 99.6083 W	EU092306 EU092400 EU092495 EU092589	-
***Y filifera* Chab.** Morelia, MX	19.8916 N 101.1149 W	EU092307 EU092401 EU092590	-
***Y glauca,* Nuttall** Sarita TX	27.2166 N 97.7833 W	EU092308 EU092402 EU092499 EU092591	-
***Y glauca* Nuttall** Brownwood, TX	31.3804 N 99.1725 W	EU092309 EU092403 EU092496 EU092592	-
***Y glauca* Nuttall** Hershey, NE	41.1586 N 101.0026 W	EU092310 EU092404 EU092497 EU092593	-
***Y glauca* Nuttall** Cuervo, NM	35.03429 N 104.4003 W	EU092311 EU092405 EU092498 EU092594	-
***Y harrimaniae* Trelease** Wilson Arch, UT	38.2791 N 109.375 W	EU092312 EU092406 EU092500 EU092595	-
***Y harrimaniae* Trelease** I-70, UT	38.8166 N 111.1333 W	EU092313 EU092407 EU092501 EU092596	-
***Y baileyi intermedia* (McKelvey) Reveal** Cerillos, NM	35.51103 N 106.0619 W	EU092314 EU092408 EU092502 EU092597	-
***Y bailey intermedia* (McKelvey)Reveal**	34.955 N 107.1841 W	EU092315	-

Correo, NM		EU092409 EU092503 EU092598	
Y jaliscensis Trelease Apango, JAL	19.7833 N 103.7 W	EU092316 EU092410 EU092504 EU092599	-
Y jaliscensis Trelease *Mazamitla, JAL*	19.9188 N 103.0273 W	EU092317 EU092411 EU092505 EU092600	-
Y jaliscensis Trelease El Izote, JAL	19.6370 N 103.6488 W	EU092318 EU092412 EU092506 EU092601	-
Y angustissima kanabensis McKelvey Coral Sands, UT	37.17932 N 112.6352 W	EU092319 EU092413 EU092507 EU092602	-
Y lacandonica Pompa and Valdez Chiapa de Corzo, CHIS	16.7521 N 92.9597 W	EU092320 EU092414 EU092508 EU092603	-
Y lacandonica Pompa and Valdez Berriozabal, CHIS	16.9280 N 93.4515 W	EU092321 EU092415 EU092509 EU092604	-
Y linearifolia Clary Galeana, NL	24.9229 N 100.0678 W	EU092322 EU092416 EU092510 EU092605	-
Y linearifolia Clary Parras, COAH	25.4054 N 102.0500 W	EU092323 EU092511 EU092606	-
Y louisianensis Trelease Silsbee, TX	30.3893 N 94.2569 W	EU092324 EU092417 EU092607	-
Y louisianensis Trelease Mt Olive, MS	31.355 N 90.9352 W	EU092325 EU092418 EU092512 EU092608	-
Y periculosa Baker Acantepec, PUE	18.2092 N 97.6343 W	EU092326 EU092419 EU092609	-
Y periculosa Baker Rte 125, OAX	18.1200 N 97.6816 W	EU092327 EU092420 EU092610	-
Y pallida McKelvey Comanche, TX	31.8875 N 98.6458 W	EU092328 EU092421 EU092515 EU092611	-
Y pallida McKelvey Dublin, TX	32.0364 N 98.4005 W	EU092329 EU092422 EU092516 EU092612	-
Y periculosa Baker Zacatepec, PUE	19.3663 N 97.4345 W	EU092330 EU092423 EU092517 EU092613	-
Y periculosa Baker Azumbilla, PUE	18.683 N 97.3508 W	EU092331 EU092424 EU092518 EU092614	-
Y periculosa Baker Tehuacan, PUE	18.4073 N 97.4378 W	EU092332 EU092425 EU092519 EU092615	-

***Y queretaroensis* Piña Lujan** Bucareli, QUE	21.0517 N 99.6083 W	EU092333 EU092426 EU092520 EU092616	-
***Y reverchonii* Trelease** Sonora, TX	30.5980 N 100.6697 W	EU092334 EU092427 EU092521 EU092617	-
***Y rigida* (Engelm.) Trelease** Torreon, DGO	25.1799 N 103.7166 W	EU092335 EU092428 EU092522 EU092618	-
***Y rostrata,* Engelm. ex Trelease** Ft Stockton, TX	30.9578 N 102.5803 W	EU092336 EU092429 EU092523 EU092619	-
***Y rostrata* Engelm. ex Trelease** Black Gap, TX	29.55 N 102.1166 W	EU092337 EU092430 EU092524 EU092620	-
***Y rupicola* Scheele** Kyle, TX	29.9946 N 97.8869 W	EU092338 EU092431 EU092525 EU092621	-
***Y rupicola* Scheele** Brownwood, TX	30.25 N 98.5166 W	EU092526 EU092432 EU092622	-
***Y schidigera* Roezl ex Ortgies** Cataviña, BC	29.8650 N 114.8427 W	EU092339 EU092433 EU092527 EU092623	-
***Y. schidigera* Roezl ex Ortgies** Searchlight, NV	35.5063 N 115.1392 W	EU092340 EU092434 EU092528 EU092624	-
***Y. schidigera* Roezl ex Ortgies** Jacumba,CA	32.6666 N 116.2833 W	EU092341 EU092435 EU092529 EU092625	-
***Y schottii* Engelm.** Mt Lemmon, AZ	32.3583 N 110.7181 W	EU092342 EU092436 EU092530 EU092626	-
***Y schottii,* Engelm.** Chiricahua National Monument, AZ	32.0049 N 109.3665 W	EU092343 EU092437 EU092531 EU092627	-
***Y schottii* Engelm.** Florida Canyon, AZ	31.7634 N 110.8459 W	EU092344 EU092438 EU092532 EU092628	-
***Y schottii* Engelm.** Cochise Stronghold, AZ	31.8725 N 110.0183 W	EU092345 EU092439 EU092533 EU092629	
***Y treculeana* Carriere** Dagger Flat, TX	29.5190 N 103.0466 W	EU092346 EU092440 EU092534 EU092630	-
***Y treculeana* Carriere** Ft Stockton, TX	30.9578 N 102.5803 W	EU092347 EU092441 EU092535 EU092631	-
***Y treculeana* Carriere** Las Cruces, NM	32.3077 N 106.7083 W	EU092348 EU092442 EU092536 EU092632	-
***Y treculeana* Carriere** Cuencame, DUR	24.9645 N 103.7275 W	EU092349	-

		EU092443 EU092537 EU092633	
***Y treculeana* Carriere** Laguna Atascosa, TX	26.25 N 97.35 W	EU092350 EU092444 EU092538 EU092634	-
Yucca queretaroensis	-	DQ500915.1 DQ500948.1	(Good-Avila et al. 2006)
Yucca rigida	-	DQ500916.1 DQ500949.1	(Good-Avila et al. 2006)
***Y elata utahensis* (McKelvey)Reveal Snow Canyon, UT**	37.2166 N 113.6458 W	EU092351 EU092445 EU092539 EU092635	-
***Y valida* Brandegee Cd Constitucion, BCS**	24.4772 N 111.2537 W	EU092352 EU092446 EU092540 EU092636	-
***Y valida* Brandegee La Paz BC**	24.0555 N 110.5747 W	EU092353 EU092447 EU092541 EU092637	-

Table S3: ParaFit cospeciation analysis of congruence between cpDNA and AFLP datasets. Boldface entries show taxa that contributed significantly to the overall congruence between data sets, based on both the F1 and F2 tests.

Sample	F1	P1	F2	P2
Hesperoyucca whipplei **Elliott Reserve, CA**	**0.76453**	**0.01**	**0.03403**	**0.01**
H. whipplei **Temecula, CA**	**0.77248**	**0.01**	**0.03438**	**0.01**
Y. angustissima Peach Springs, AZ	0.11688	0.41	0.0052	0.27
Y. arizonica **KM 182, Sonora Rte 89, SON**	**0.19523**	**0.04**	**0.00869**	**0.02**
Y. baccata **Wickenburg, AZ**	**0.24056**	**0.02**	**0.01071**	**0.01**
Y. baccata Blanding, UT	0.08158	0.55	0.00363	0.32
Y. baccata **Zion NP, UT**	**0.26436**	**0.02**	**0.01177**	**0.01**
Y. baccata **Walnut Canyon, AZ**	**0.26707**	**0.02**	**0.01189**	**0.01**
Y. baccata **Peach Springs, AZ**	**0.23194**	**0.04**	**0.01032**	**0.03**
Y. baccata Las Cruces, NM	0.07954	0.5	0.00354	0.34
Y. baileyi St Johns, AZ	0.12305	0.36	0.00548	0.24
Y. baileyi Winona, AZ	0.12339	0.33	0.00549	0.18
Y. brevifolia Palmdale, CA	0.10778	0.07	0.0048	0.05
Y. brevifolia Potosi Canyon, NV	0.09681	0.14	0.00431	0.11
Y. brevifolia Kingston Mts, CA	0.12125	0.16	0.0054	0.09
Y. capensis San Antonio, BCS	-0.08636	0.99	-0.00384	0.99
Y. capensis **San Pedro de la Soledad, BCS**	**0.26944**	**0.03**	**0.01199**	**0.02**
Y. carnerosana San Luis Potosi, SLP	0.09271	0.19	0.00413	0.12
Y. carnerosana Dagger Flat, Big Bend NP, TX	0.06986	0.27	0.00311	0.15
Y. carnerosana Saltillo, COAH	0.10391	0.12	0.00463	0.07
Y. cernua **Newton, TX**	**0.18288**	**0.04**	**0.00814**	**0.01**
Y. constricta, **Brady, TX**	**0.31838**	**0.01**	**0.01417**	**0.01**
Y. constricta **Menard, TX**	**0.24706**	**0.01**	**0.011**	**0.01**
Y. decipiens Durango, DUR	0.07797	0.3	0.00347	0.14
Y. decipiens Michilia, DUR	0.07406	0.28	0.0033	0.15
Y. elata **Rodeo, NM**	**0.47556**	**0.03**	**0.02117**	**0.02**
Y. elata **Roosevelt Dam, AZ**	**0.43284**	**0.01**	**0.01927**	**0.01**
Y. elata **Oak Creek, AZ**	**0.4784**	**0.01**	**0.02129**	**0.01**
Y. elata **Sierra Vista, AZ**	**0.48444**	**0.02**	**0.02156**	**0.01**
Y. elata **Hueco, TX**	**0.7878**	**0.02**	**0.03506**	**0.01**
Y. elata **Willcox Playa, AZ**	**0.49356**	**0.01**	**0.02197**	**0.01**
Y. elephantipes, Brownsville TX	0.08677	0.23	0.00386	0.06
Y. elephantipes Yahualica, HGO	0.1003	0.18	0.00446	0.07
Y. elephantipes **Rizo de Oro, CHIS**	**0.26529**	**0.01**	**0.01181**	**0.01**
Y. filamentosa **Ocala, FL**	**0.41592**	**0.01**	**0.01851**	**0.01**
Y. filamentosa **Archbold Biol. Stn., FL**	**0.48507**	**0.01**	**0.02159**	**0.01**
Y. filifera **Poza de Santa Clara, SLP**	**0.37011**	**0.01**	**0.01647**	**0.01**
Y. filifera San Vincente, HGO	0.12012	0.12	0.00535	0.08
Y. filifera San Jose, MICH	0.12454	0.09	0.00554	0.04
Y. filifera Bucareli, QUE	0.10745	0.13	0.00478	0.06
Y. glauca **Brownwood, TX**	**0.3847**	**0.03**	**0.01712**	**0.02**

Sample	F1	P1	F2	P2
***Y. glauca* Hershey, NE**	**0.55127**	**0.01**	**0.02454**	**0.01**
***Y. glauca* Cuervo, NM**	**0.75818**	**0.01**	**0.03375**	**0.01**
***Y. glauca,* Sarita TX**	**0.32554**	**0.04**	**0.01449**	**0.01**
Y. harrimaniae Wilson Arch, UT	0.11286	0.45	0.00502	0.29
Y. harrimaniae I-70, UT	0.11936	0.45	0.00531	0.31
***Y. intermedia* Cerillos, NM**	**0.41326**	**0.03**	**0.01839**	**0.01**
***Y. intermedia* Correo, NM**	**0.44716**	**0.01**	**0.0199**	**0.01**
Y. jaliscensis Apango, JAL	0.07412	0.37	0.0033	0.21
***Y. jaliscensis* Mazamitla, JAL**	**0.37958**	**0.01**	**0.01689**	**0.01**
***Y. jaliscenis* El Izote, JAL**	**0.36919**	**0.01**	**0.01643**	**0.01**
Y. angustissima kanabensis Coral Sands, UT	0.11367	0.38	0.00506	0.27
***Y. lacandonica* Chiapa de Corzo, CHIS**	**0.43445**	**0.01**	**0.01934**	**0.01**
***Y. lacandonica* Berriozabal, CHIS**	**0.40928**	**0.01**	**0.01822**	**0.01**
Y. linearifolia Galeana, NL	0.10563	0.14	0.0047	0.09
Y. linearifolia Parras, COAH	0.10527	0.2	0.00469	0.06
***Y. louisianensis* Silsbee, TX**	**0.44866**	**0.01**	**0.01997**	**0.01**
***Y. louisianensis* Mt Olive, MS**	**0.33767**	**0.01**	**0.01503**	**0.01**
***Y. periculosa* Acantepec, PUE**	**0.14027**	**0.05**	**0.00624**	**0.02**
***Y. periculosa* Rte 125, OAX**	**0.21305**	**0.05**	**0.00948**	**0.02**
***Y. pallida* Comanche, TX**	**0.19252**	**0.05**	**0.00857**	**0.04**
***Y. pallida* Dublin, TX**	**0.20548**	**0.05**	**0.00915**	**0.03**
***Y. periculosa* Tehuacan, PUE**	**0.36977**	**0.01**	**0.01646**	**0.01**
Y. periculosa Zacatepec, PUE	0.0922	0.19	0.0041	0.11
Y. periculosa Azumbilla, PUE	0.14034	0.11	0.00625	0.04
***Y. reverchoni* Sonora, TX**	**0.1634**	**0.05**	**0.00727**	**0.02**
Y. rigida Torreon, DGO	0.07075	0.54	0.00315	0.23
Y. rostrata, Ft Stockton, TX	0.08271	0.34	0.00368	0.23
Y. rostrata Black Gap, TX	0.07809	0.36	0.00348	0.24
Y. rupicola Kyle, TX	0.21526	0.08	0.00958	0.06
Y. rupicola Brownwood, TX	0.20444	0.09	0.0091	0.05
***Y. schidigera* Cataviña, BC**	**0.23869**	**0.02**	**0.01062**	**0.01**
***Y. schottii* Mt Lemmon, AZ**	**0.33549**	**0.02**	**0.01493**	**0.01**
***Y. schottii,* Chiricahua NM, AZ**	**0.27752**	**0.02**	**0.01235**	**0.01**
***Y. schottii* Florida Canyon, AZ**	**0.23964**	**0.01**	**0.01067**	**0.01**
***Y. treculeana* Dagger Flat, TX**	**0.34371**	**0.01**	**0.0153**	**0.01**
***Y. treculeana,* Ft Stockton, TX**	**0.34931**	**0.01**	**0.01555**	**0.01**
Y. treculeana Las Cruces, NM	0.14369	0.14	0.0064	0.07
Y. treculeana Cuencame, DUR	0.08922	0.09	0.00397	0.06
Y. treculeana Laguna Atascosa, TX	0.0962	0.32	0.00428	0.16
Y. elata utahensis Snow Canyon, UT	0.14093	0.31	0.00627	0.16
Y. valida Cd Constitucion, BCS	0.18988	0.12	0.00845	0.05
***Y. valida* La Paz, BC**	**0.23497**	**0.04**	**0.01046**	**0.02**

Table S4: Node ages and support values. Node numbers refer to labeled nodes in Figure S1. Bootstrap supports refer to the support seen in the bootstrap consensus tree, including all compatible sub-grouping. Nodes labeled "NR" were not represented in the bootstrap consensus tree

Node	Bayes Posterior	Bootstrap	Node Age
1	NA	NA	105.50
2	100	100	94.00
3	100	100	62.50
4	99	88	43.52
5	48	NR	38.90
6	71	NR	34.74
7	100	100	5.48
8	98	88	2.54
9	100	94	20.66
10	99	88	17.69
11	100	95	11.95
12	100	91	6.89
13	100	66	4.18
14	100	68	2.66
15	100	68	14.48
16	45	22	12.96
17	36	26	11.29
18	100	93	6.85
19	100	99	1.13
20	100	68	5.22
21	100	70	3.59
22	54	NR	6.34
23	34	NR	5.32
24	49	NR	3.88
25	68	67	1.31
26	100	99	1.41
27	59	34	11.43
28	100	89	9.07
29	99	49	7.70
30	24	NR	7.03
31	26	19	5.81
32	99	83	5.34
33	77	37	7.82
34	100	58	6.15
35	77	NR	1.10
36	34	NR	5.59
37	95	NR	3.93
38	21	NR	2.96
39	22	NR	2.25
40	2	2	4.21
41	37	NR	2.91
42	6	NR	4.48
43	<1	NR	5.12
44	2	NR	4.48
45	22	NR	3.55
46	79	43	2.38
47	1	NR	5.14
48	<1	NR	5.12
49	<1	NR	3.00
50	3	NR	1.96
51	3	NR	1.98
52	<1	NR	4.72
53	4	NR	3.45
54	29	55	4.17
55	<1	NR	4.62
56	3	NR	3.85
57	8	NR	2.63
58	86	48	1.06
59	59	NR	9.52
60	87	66	6.41
61	32	NR	1.75
62	77	NR	5.84
63	7	NR	5.21
64	10	NR	4.65
65	1	NR	3.65
66	0	NR	2.20
67	2	NR	1.14
68	4	NR	0.89
69	<1	NR	1.79
70	4	NR	0.79
71	4	NR	0.78
72	3	NR	1.36
73	<1	NR	2.88
74	3	NR	2.28
75	99	60	1.22
76	23	36	0.77
77	21	NR	0.44
78	1	NR	3.31
79	22	5	2.44
80	79	61	1.38
81	12	NR	1.02
82	14	NR	0.55

Node	***Bayes Posterior***	***Bootstrap***	***Node Age***	***Node***	***Bayes Posterior***	***Bootstrap***	***Node Age***
83	14	NR	0.54	**117**	15	NR	0.74
84	62	44	2.73	**118**	15	NR	0.92
85	96	42	2.12	**119**	21	1	3.78
86	1	NR	1.58	**120**	7	NR	1.79
87	19	NR	1.12	**121**	11	NR	1.07
88	90	44	0.45	**122**	11	NR	0.78
89	5	NR	1.92	**123**	76	4	3.37
90	5	NR	0.56	**124**	16	2	3.06
91	<1	NR	1.08	**125**	24	NR	1.66
92	5	NR	0.58	**126**	51	7	0.86
93	<1	NR	1.57	**127**	24	NR	0.48
94	5	NR	0.60	**128**	14	2	2.77
95	<1	NR	1.16	**129**	35	NR	1.79
96	5	NR	0.76	**130**	55	3	1.17
97	33	34	3.49	**131**	27	NR	0.61
98	86	24	2.40	**132**	57	11	0.66
99	67	15	1.79	**133**	6	NR	2.47
100	99	59	0.62	**134**	6	8	2.08
101	58	31	1.15	**135**	91	47	0.98
102	54	31	2.19	**136**	3	7	1.71
103	9	NR	0.80	**137**	3	NR	0.80
104	6	NR	1.83	**138**	<1	NR	1.53
105	6	NR	1.83	**139**	<1	NR	1.10
106	2	NR	1.52	**140**	3	NR	0.72
107	9	NR	0.71	**141**	3	NR	0.59
108	9	NR	1.24	**142**	3	NR	0.77
109	99	66	0.79	**143**	<1	NR	1.18
110	20	NR	0.57	**144**	4	NR	0.60
111	20	NR	0.34	**145**	<1	NR	1.16
112	29	1	4.11	**146**	<1	NR	0.78
113	76	19	2.45	**145**	<1	NR	1.16
114	97	41	0.74	**146**	<1	NR	0.78
115	24	12	1.48	**147**	3	NR	0.44
116	97	41	0.74	**148**	3	NR	0.64

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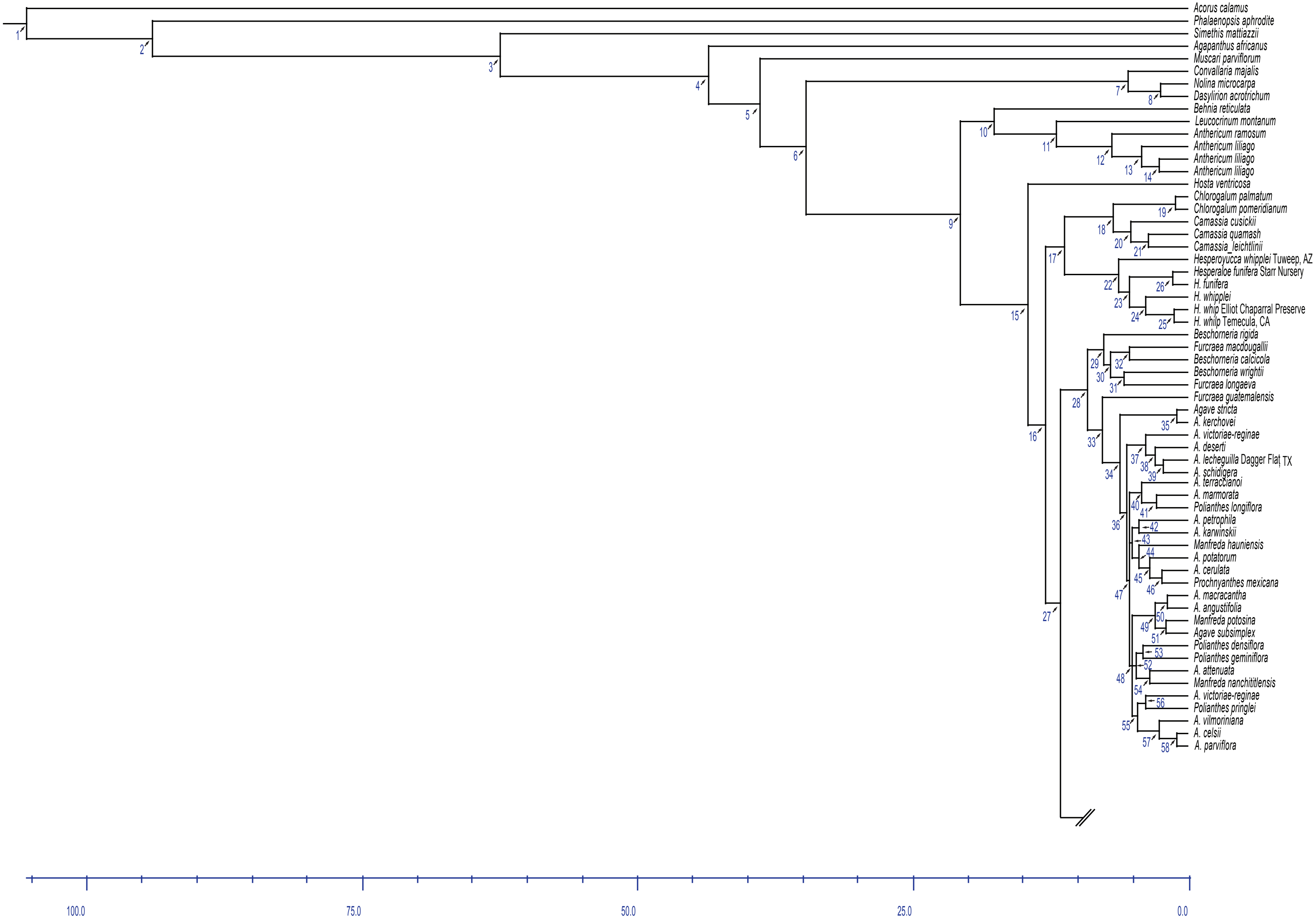
Supplemental Online Materials: Figure Legends:

Supplemental Figure S1: Complete chronogram of the Agavaceae based on Bayes consensus tree derived from 153 cpDNA sequences from the trnL gene and the the trnL – trnF intergenic spacer. *Amborella trichopoda* was used to root the topology and was pruned in the r8s analysis. Node numbers refer to labels and support indices in Supplemental Online Material Table S4.

Supplemental Figure S2: Chronograms of the pruned topologies used to calculate speciation rates in *Agave sensu latissimus* and *Yucca.* Underlying topology is based the Bayes consensus tree of the 153 taxa trnL-trnF cpDNA sequence dataset shown in figure S1. Taxa were pruned from the underlying topology so as to include only one individual per species and (in *Yucca)* to maximize agreement with the presumed species tree inferred from AFLP data.


Acorus calamus
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Simethis mattiazzii
Agapanthus africanus
Muscari parviflorum
Convallaria majalis
Nolina microcarpa
Dasylirion acrotrichum
Behnia reticulata
Leucocrinum montanum
Anthericum ramosum
Anthericum liliago
Anthericum liliago
Anthericum liliago
Hosta ventricosa
Chlorogalum palmatum
Chlorogalum pomeridianum
Camassia cusickii
Camassia quamash
Camassia_leichtlinii
Hesperoyucca whipplei Tuweep, AZ
Hesperaloe funifera Starr Nursery
H. funifera
H. whipplei
H. whip Elliot Chaparral Preserve
H. whilp Temecula, CA
Beschorneria rigida
Furcraea macdougallii
Beschorneria calcicola
Beschorneria wrightii
Furcraea longaeva
Furcraea guatemalensis
Agave stricta
A. kerchovei
A. victoriae-reginae
A. deserti
A. lecheguilla Dagger Flat, TX
A. schidigera
A. terracianoi
A. marmorata
Polianthes longiflora
A. petrophila
A. karwinskii
Manfreda hauniensis
A. potatorum
A. cerulata
Prochnyanthes mexicana
A. macracantha
A. angustifolia
Manfreda potosina
Agave subsimplex
Polianthes densiflora
Polianthes geminiflora
A. attenuata
Manfreda nanchititlensis
A. victoriae-reginae
Polianthes pringlei
A. vilmoriniana
A. celsii
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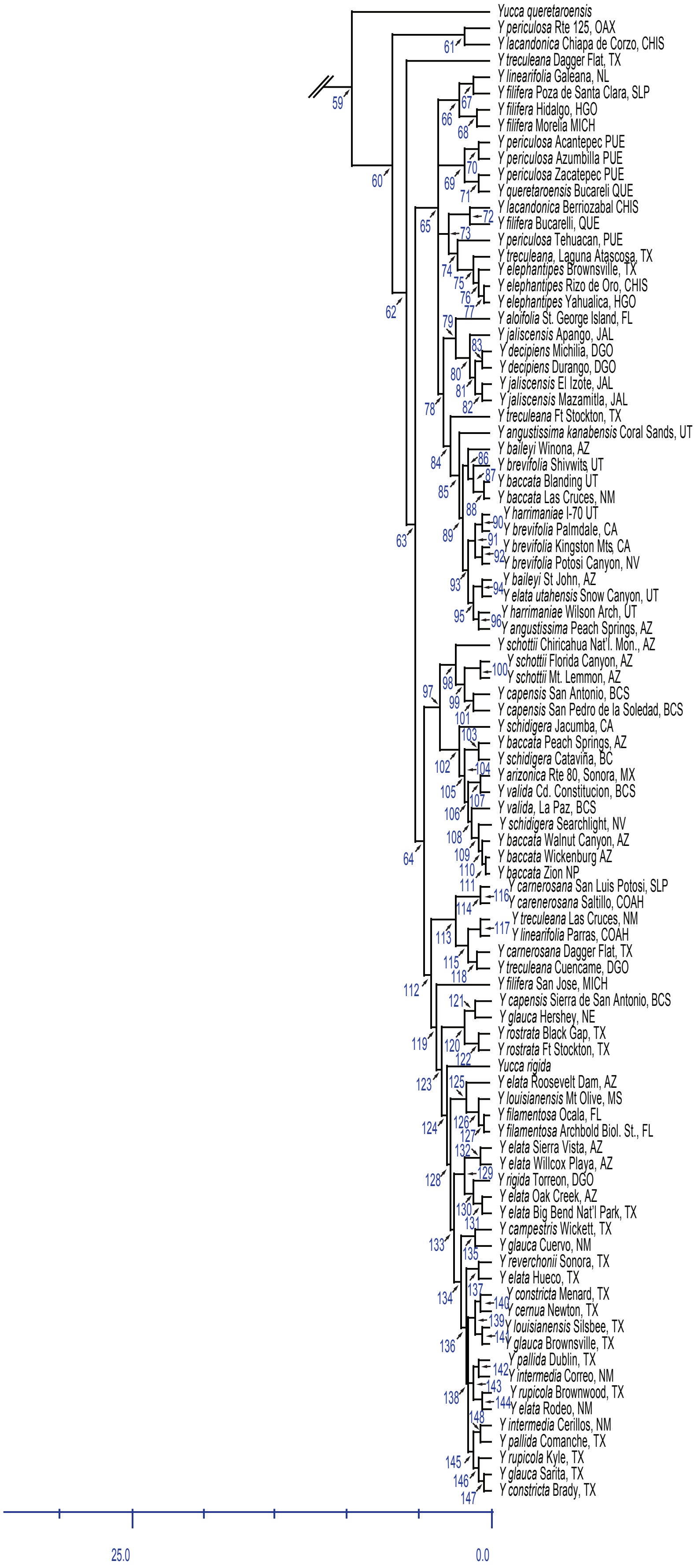
Yucca queretaroensis
Y *periculosa* Rte 125, OAX
Y *lacandonica* Chiapa de Corzo, CHIS
Y *treculeana* Dagger Flat, TX
Y *linearifolia* Galeana, NL
Y *filifera* Poza de Santa Clara, SLP
Y *filifera* Hidalgo, HGO
Y *filifera* Morelia MICH
Y *periculosa* Acantepec PUE
Y *periculosa* Azumbilla PUE
Y *periculosa* Zacatepec PUE
Y *queretaroensis* Bucareli QUE
Y *lacandonica* Berriozabal CHIS
Y *filifera* Bucarelli, QUE
Y *periculosa* Tehuacan, PUE
Y *treculeana*, Laguna Atascosa, TX
Y *elephantipes* Brownsville, TX
Y *elephantipes* Rizo de Oro, CHIS
Y *elephantipes* Yahualica, HGO
Y *aloifolia* St. George Island, FL
Y *jaliscensis* Apango, JAL
Y *decipiens* Michilia, DGO
Y *decipiens* Durango, DGO
Y *jaliscensis* El Izote, JAL
Y *jaliscensis* Mazamitla, JAL
Y *treculeana* Ft Stockton, TX
Y *angustissima kanabensis* Coral Sands, UT
Y *baileyi* Winona, AZ
Y *brevifolia* Shivwits, UT
Y *baccata* Blanding UT
Y *baccata* Las Cruces, NM
Y *harrimaniae* I-70 UT
Y *brevifolia* Palmdale, CA
Y *brevifolia* Kingston Mts, CA
Y *brevifolia* Potosi Canyon, NV
Y *baileyi* St John, AZ
Y *elata utahensis* Snow Canyon, UT
Y *harrimaniae* Wilson Arch, UT
Y *angustissima* Peach Springs, AZ
Y *schottii* Chiricahua Nat'l. Mon., AZ
Y *schottii* Florida Canyon, AZ
Y *schottii* Mt. Lemmon, AZ
Y *capensis* San Antonio, BCS
Y *capensis* San Pedro de la Soledad, BCS
Y *schidigera* Jacumba, CA
Y *baccata* Peach Springs, AZ
Y *schidigera* Cataviña, BC
Y *arizonica* Rte 80, Sonora, MX
Y *valida* Cd. Constitucion, BCS
Y *valida*, La Paz, BCS
Y *schidigera* Searchlight, NV
Y *baccata* Walnut Canyon, AZ
Y *baccata* Wickenburg AZ
Y *baccata* Zion NP
Y *carnerosana* San Luis Potosi, SLP
Y *carenerosana* Saltillo, COAH
Y *treculeana* Las Cruces, NM
Y *linearifolia* Parras, COAH
Y *carnerosana* Dagger Flat, TX
Y *treculeana* Cuencame, DGO
Y *filifera* San Jose, MICH
Y *capensis* Sierra de San Antonio, BCS
Y *glauca* Hershey, NE
Y *rostrata* Black Gap, TX
Y *rostrata* Ft Stockton, TX
Yucca rigida
Y *elata* Roosevelt Dam, AZ
Y *louisianensis* Mt Olive, MS
Y *filamentosa* Ocala, FL
Y *filamentosa* Archbold Biol. St., FL
Y *elata* Sierra Vista, AZ
Y *elata* Willcox Playa, AZ
Y *rigida* Torreon, DGO
Y *elata* Oak Creek, AZ
Y *elata* Big Bend Nat'l Park, TX
Y *campestris* Wickett, TX
Y *glauca* Cuervo, NM
Y *reverchonii* Sonora, TX
Y *elata* Hueco, TX
Y *constricta* Menard, TX
Y *cernua* Newton, TX
Y *louisianensis* Silsbee, TX
Y *glauca* Brownsville, TX
Y *pallida* Dublin, TX
Y *intermedia* Correo, NM
Y *rupicola* Brownwood, TX
Y *elata* Rodeo, NM
Y *intermedia* Cerillos, NM
Y *pallida* Comanche, TX
Y *rupicola* Kyle, TX
Y *glauca* Sarita, TX
Y *constricta* Brady, TX
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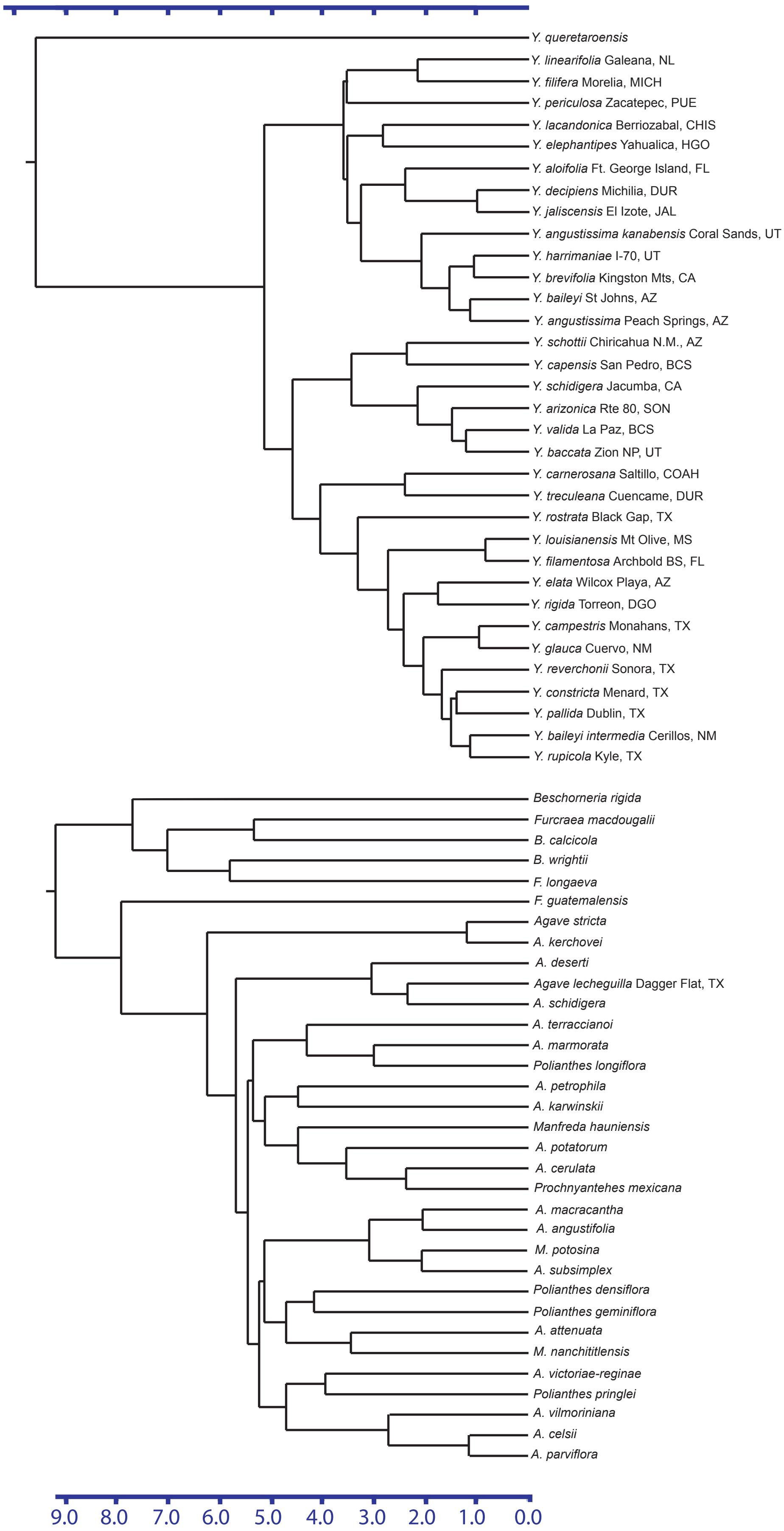
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Y. angustissima Peach Springs, AZ
Y. schottii Chiricahua N.M., AZ
Y. capensis San Pedro, BCS
Y. schidigera Jacumba, CA
Y. arizonica Rte 80, SON
Y. valida La Paz, BCS
Y. baccata Zion NP, UT
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Y. treculeana Cuencame, DUR
Y. rostrata Black Gap, TX
Y. louisianensis Mt Olive, MS
Y. filamentosa Archbold BS, FL
Y. elata Wilcox Playa, AZ
Y. rigida Torreon, DGO
Y. campestris Monahans, TX
Y. glauca Cuervo, NM
Y. reverchonii Sonora, TX
Y. constricta Menard, TX
Y. pallida Dublin, TX
Y. baileyi intermedia Cerillos, NM
Y. rupicola Kyle, TX
Beschorneria rigida
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B. calcicola
B. wrightii
F. longaeva
F. guatemalensis
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A. kerchovei
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Agave lecheguilla Dagger Flat, TX
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