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Supplementary Information for

A fully resolved backbone phylogeny reveals numerous dispersals and explosive diversifications throughout the history of Asteraceae

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Additional Methods

Taxon Sampling, Library Preparation, and Sequencing. For this study, we employed the Hyb-Seq method using Asteraceae-specific probes (baits) for target enrichment of approximately 1000 nuclear loci (1–3). We sampled a total of 256 species from 13 subfamilies, ~45 tribes, and 207 genera from across Asteraceae including one species from the sister family Calyceraceae and two from the closely related Goodeniaceae (Dataset S2). Sequence capture was performed on 238 samples using the CompCOS probes: myBaits COS Compositae/Asteraceae 1Kv1 (Arbor Biosciences). Data for 18 of the 256 species were provided by the 1000 Plant Transcriptomes (1KP; onekp.org) initiative (4–7). At the tribal level, we are missing only two small tribes consisting of 4 species total, Feddeeae (1 species) and Polymnieae (3 species). Samples were provided by the 1KP project (onekp.org), the Compositae Genome Project, Eric Carpenter, Mark Chase, Michael Deyholos, Benoît Loeuille, Jim Leebens-Mack, Rachel Jabaily, Norbert Kilian, Marinda Koekemoer, Rowan Sage, Ed Schilling, Douglas Soltis, C. Neal Stewart Jr., and Gane Ka-Shu Wong.

For 238 species, tissues samples were either freshly collected (dried in silica gel) or obtained from herbarium material, and for some samples previously extracted DNA was provided by colleagues. DNA extraction methods followed either the CTAB protocol (8), the Qiagen DNeasy plant mini kit, or the SP Omega Biotek Plant Kit. DNA quality was assessed using a Nanodrop 2000 spectrophotometer and quantified using the Qubit 2.0 or 3.0 Fluorometer. DNA samples with 260/280 ratios below 1.5 (measured on the Nanodrop) were cleaned with Omega Biotek E.Z.N.A. Cycle Pure Kit and DNA samples that were too dilute for library preparation were concentrated by vacuum centrifugation.

Up to 1 μg of genomic DNA in 65 μL water was sonicated using either the QSonica Q800R2 or Covaris instruments, targeting a fragment size of 400-500 bp. Individually-indexed sequencing libraries were constructed using the NEBNext Ultra (original or II) DNA Library Prep Kit and their quantity was assessed using the Qubit. Libraries were pooled (four per pool, ~500 ng total). Sequence capture was performed using the CompCOS probes: myBaits COS Compositae/Asteraceae 1Kv1 (Arbor Biosciences) as

described in (1), following the manufacturer protocols. The resulting captured, pooled libraries were checked for quality using an Agilent 2100 Bioanalyzer and quantified using the Qubit. Paired-end Illumina sequencing was carried out on either the Illumina MiSeq or HiSeq 2000.

Data Processing and Alignment. Data were processed following the bioinformatic workflow and methods of (1, 2) with minor modifications detailed below (scripts and associated files available at github.com/Smithsonian/Compositae-COS-workflow. Transcriptomes were assembled *de novo* using Trinity v2.5.1 (9), with the default normalization. The resulting contig file was incorporated into the PHYLUCE pipeline with the remaining files. Reads from the Illumina sequencing were cleaned and trimmed using Trimmomatic 0.36 (10) with a sliding window of 20 bp, retained only if they had a quality score of Q20 or greater, and assembled into contigs *de novo* using the SPAdes assembler (v. 3; 11). Contigs of each taxon were analyzed in the PHYLUCE pipeline (v. 1.5.0; 12, 13), which generates orthology predictions across loci and taxa in a conservative manner, specifically, when two or more contigs from a single taxon match a targeted locus, that locus is removed for that taxon. Nucleotide alignments on individual loci were carried out in MAFFT (v. 7.029b; 14).

Phylogenomic Analyses. We generated phylogenetic trees based on a concatenated data matrix of all loci using a maximum likelihood (ML) approach with RAxML (v. 8.2.7; 15) and Bayesian estimation with ExaBayes (16). For the ML analysis, we used PartitionFinder2 (17) with the rcluster search option and AICc criterion to identify the best nucleotide substitution model for our individual loci. For the majority of loci, GTR+I+G was the best model, and we therefore applied this model to the entire concatenated matrix. These RAxML analyses included 1000 rapid bootstrap replicates using the best tree search. Bayesian estimation was carried out using ExaBayes (4 chains with 10 million generations each, GTR model, discarding 25% of the sampled trees as burnin) to create a consensus tree. In addition to the concatenated approaches, we analyzed our data using a pseudo-coalescence method as employed in the software program ASTRAL-II (hereafter ASTRAL, v4.10.2, 18) to compute a consensus “species” tree based on individual gene trees. To

prepare the data for ASTRAL, gene trees were generated based on the individual loci recovered from PHYLUCE using best models from PartitionFinder2 in RAxML with 1000 bootstrap replicates each, which were then input into ASTRAL using the default parameters.

Divergence Time Analyses. We generated a time-calibrated ML phylogeny using the program RelTime which is suitable for large datasets (19–21). Local clocks were used for each lineage and the GTR model was employed with a gamma distributed model and five discrete gamma categories. The "Use all sites" option was employed for the analyses. For calibration points (*SI Appendix*, Table S1) to constrain nodes in the ML phylogeny, we utilized either seven or eight fossils by either excluding or including a putative (and controversial) fossil pollen sample from Antarctica, as variously included in other studies (22–24). We tested different calibration scenarios for the minimum and maximum ages of the root of the family, different age constraints of a key macrofossil, and the inclusion/exclusion of some taxa on particularly long branches at the base of the tree to assess the effect of different combinations (*SI Appendix*, Table S1). The presented chronogram (also used for biogeographic and diversification rate analyses) is based upon setting a maximum age for the root of the family to 91.5 MYA, which represents the Apiales/Asterales split that was used in previous studies (22, 23). Goodeniaceae was removed as an outgroup following Kumar et al. (25) and Mello et al. (26); *Chuquiraga* and *Fulcadea* (Barnadesioideae: Asteraceae) also were excluded because their inclusion during preliminary runs resulted in unreasonably old age estimates (*SI Appendix*, Table S1).

Historical Biogeography. Ancestral ranges were estimated using ML implemented in BioGeoBEARS (27, 28) on a dated phylogeny pruned to include only one species per genus. Six models were explored including dispersal–extinction–cladogenesis (DEC), the likelihood version of DIVA (DIVALIKE), and the BayArea likelihood version of the range evolution model (BAYAREALIKE), each run with and without the *j* parameter which incorporates founder-events into the model and allows for one of the descendants to jump to a new range outside the ancestral range without requiring anagenetic dispersal (*SI Appendix*, Table S2). All terminals were coded as present or absent in 10 broad geographic

areas based on present day distributions of each genus following (29) including: 1) southern South America and the southern Andes region, 2) north and central Andes region, 3) Brazil including Guiana Shield, 4) southern and central Africa, 5) northern Africa-Mediterranean, 6) Europe-Eurasia, 7) Asia, 8), southeast Asia to New Guinea and Australia, 9) North America (including Hawaii and Mexico), and 10) MesoAmerica-Caribbean (*SI Appendix*, Table S5). We also carried out biogeographical stochastic mapping (BSM) to estimate the number of dispersal events between each of the defined geographic regions based on ancestral-area estimation in BioGeoBEARS (30). This resulted in the mean and standard deviations for anagenetic dispersal or range expansions (A --> A+B, i.e., from geographic area A expanding to geographic areas A and B), extinctions (A+B --> A), cladogenetic (speciation) range expansions involving sympatry (A --> A, A) or jump-dispersal events (founder-events) (A --> A, B) from 50 stochastic maps following (31).

Diversification Analyses. Diversification rates were estimated with the software MEDUSA: Modeling Evolutionary Diversification Using Stepwise Akaike Information Criterion (AIC) (32) using the dated ultrametric tree described above and pruned to the level of tribe. Species richness data detailing the number of species per tribe were taken from Funk et al. (33) (*SI Appendix*, Table S6). The mixed model of either birth-death or Yule and the corrected AIC criteria were used in the analyses.

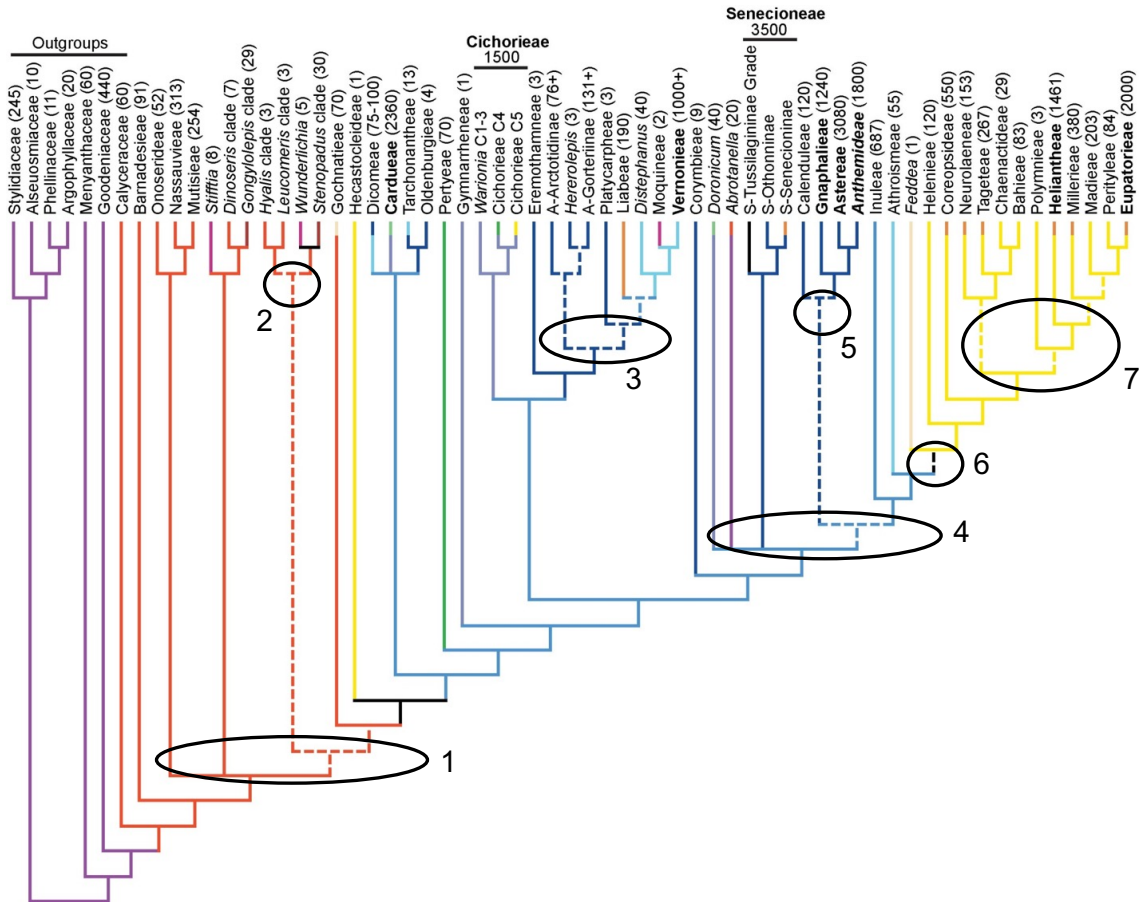

Fig. S1. Redrawn plastid supertree (metatree) of Funk et al. 2009 with unresolved nodes indicated as dashed lines; red circles indicate seven unresolved nodes discussed in Funk et al. 2009.

Fig. S2. Maximum likelihood tree of Asteraceae with all sampled species displayed.

Fig. S3 Bayesian tree of Asteraceae with all sampled species displayed.

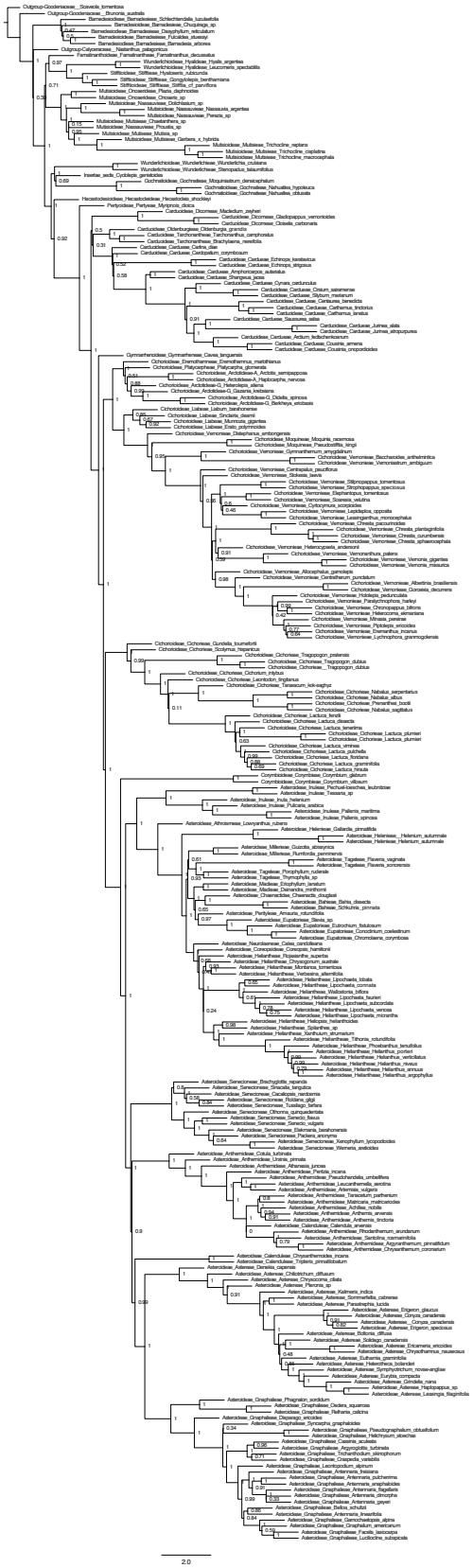

Fig. S4 ASTRAL tree of Asteraceae with all sampled species displayed.

Fig. S5 Chronogram of Asteraceae with all sampled species displayed.

Fig. S6 Chronogram with confidence intervals of Asteraceae with all sampled species displayed.

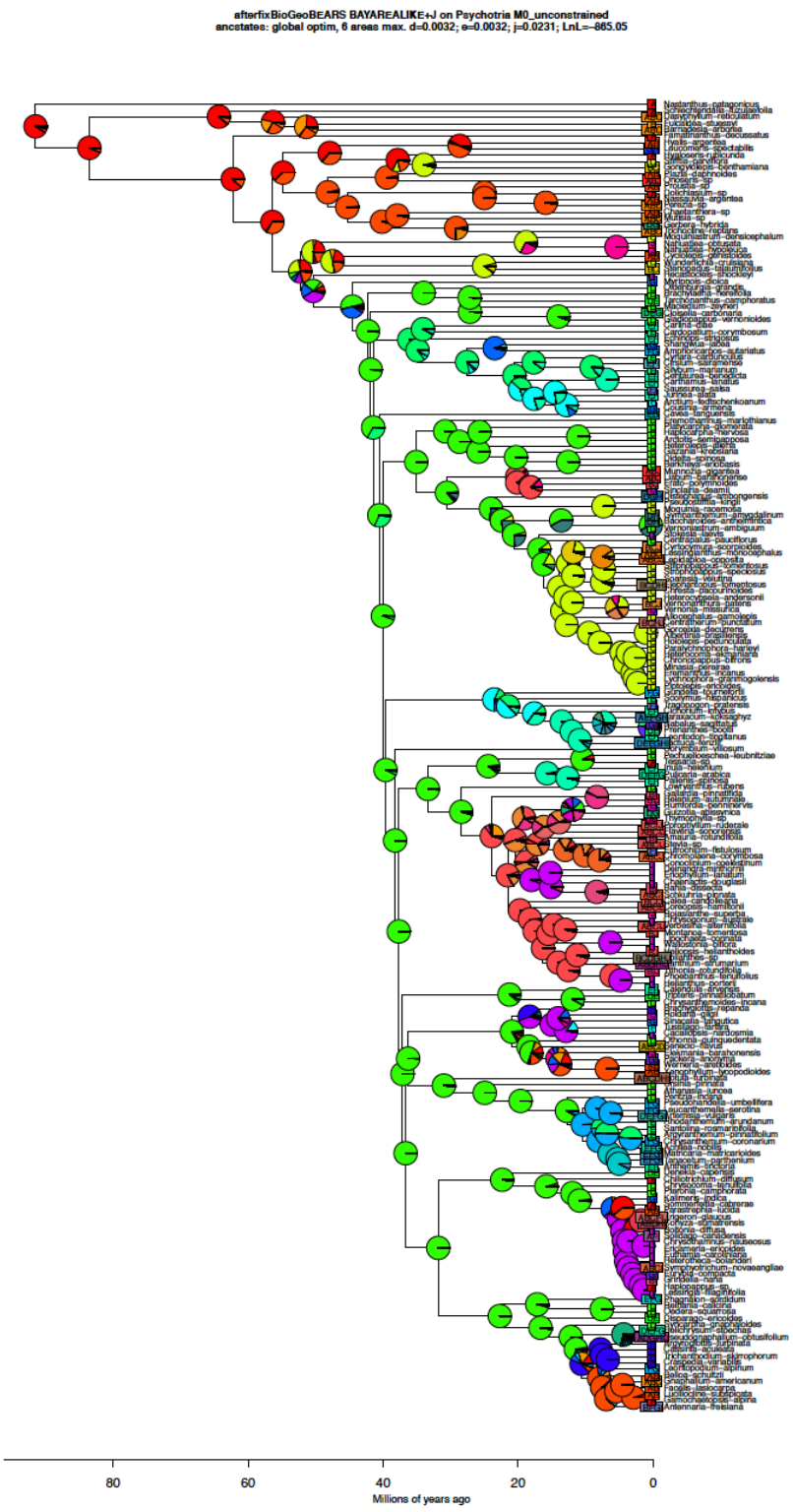

Fig. S7 Most likely ancestral range distributions of Asteraceae estimated using BAYAREA+J (raw plot from BioGeoBears).

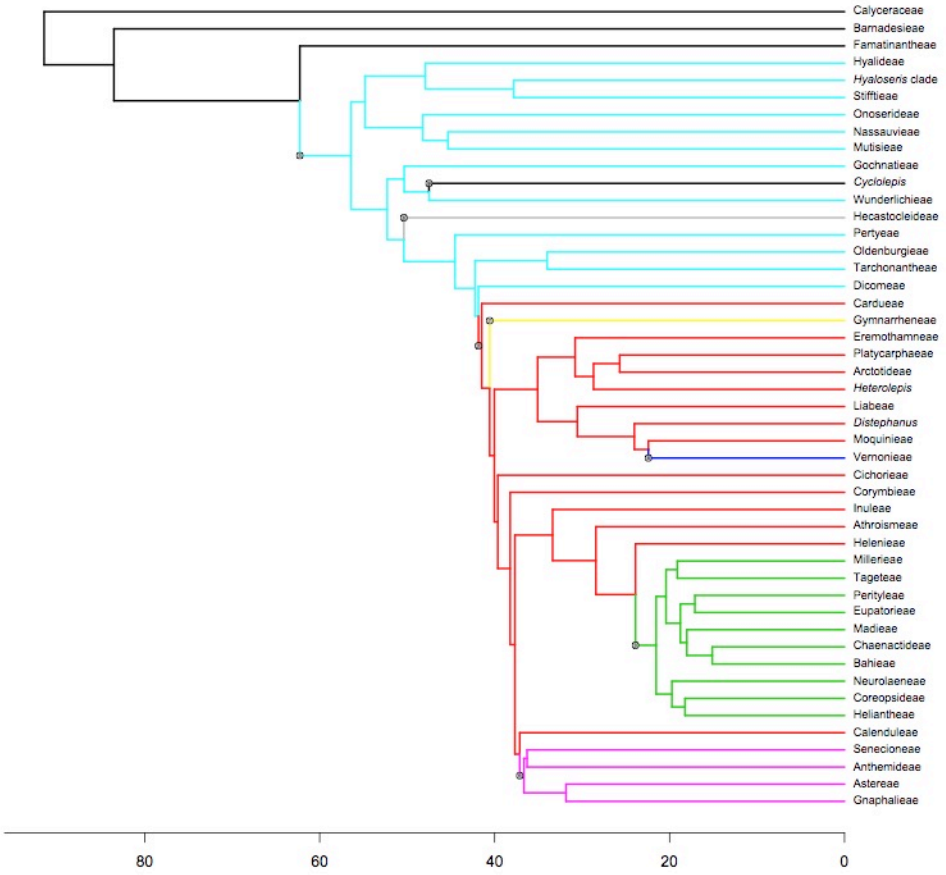

Fig. S8 Tribe-level phylogeny with diversification rate shifts as identified by MEDUSA.

Table S1. Fossil and calibration point information used for RelTime dating analyses.

Fossil name	**Clade**	**Type**	**Date**	**Reference**			
Raiguenrayun cura + Mutisiapollis tellleriae	Asteroideae-Mutisiodeae clade	inflorescences/attac	47.5	34, 24, 35			
Artemisia	*Artemisia-Chrysanthemum* node	pollen	31	36, 37			
Huanopollis crisci	Nassauvieae *Calopappus- Nasssauvia-Triptilion*	pollen	25.5	38, 39			
Quilembaypollis gamerroi	Barnadesioideae	pollen	23	40, 41			
Cichorium intybus type	core-Cichorieae	pollen	22	42-44			
Psilatricoporites protrudens	Calyceraceae *Gamacarpha-Nastanthus* node	pollen	22	40, 41			
Sonchus oleraceus type	stem *Sonchus*	pollen	5.4	43, 44			
Centauria type	Carduoideae	pollen	4.6	45			
Tubulifloridites lillei Type A	Calyceraceae-Asteraceae	pollen	72.1	24			
Different calibration scenarios							
	Scenario 1	**Scenario 2**	**Scenario 3**	**Scenario 4**	**Scenario 5**		
Max Age	100	100	91.5	91.5	91.5		
Include Tubulifloridites lillei Type A?	no	yes	no	no	yes		
Constrain Mutiseae node, 47-60?	no	yes	no	yes	yes		
Include *Chuquiraga* ?	no	no	no	no	no		
Ages of different calibration scenarios							
	Scenario 1	**Scenario 2**	**Scenario 3**	**Scenario 4***	**Scenario 5**		
Split or Node		Age Estimates				Averages	SD
Barnadesioideae - rest of family	91.7	90.5	84.3	83.5	85.3	87.1	3.77
Mutiseae - rest of family	67.5	58.6	63.4	56.4	57	60.6	4.74
Cardueae - rest of family	46.7	42.9	44.9	41.4	41.7	43.5	2.25
Corymbium - rest of family	41.5	38.9	40.2	38.2	38.4	39.4	1.39
Comparison to other studies	**Barreda et al. (24)**	**Huang et al. (23)**	**Panero and Crozier (22)**	**This study**			
Split or Node		Age Estimates					
Barnadesioideae - rest of family	85.9	72	65	83.5			
Mutiseae - rest of family	53	62	55	56.4			
Cardueae - rest of family	48	54	49.5	41.4			
Corymbium - rest of family	-	-	44	38.2			

Table S2. Biogeographic models tested in this study with estimated parameters and values and range probabilities for all nodes from BioGeoBears analyses.

Biogeographical models tested in this study with estimated parameters and AIC values.																
alt	**null**	**LnLalt**	**LnLnull**	**DFalt**	**DFnull**	**DF**	**Dstatistic**	**pval**	**test**	**tail**	**AIC1**	**AIC2**	**AICwt1**	**AICwt2**	**AICweight_r**	**AICweight_ratio_model2**
DEC+J	DEC	-909	-921.6	3	2	1	25.1	5.40E-07	chi-squared	one-tailed	1824	1847	1	9.60E-06	103661	9.60E-06
DIVALIKE+J	DIVALIKE	-918.7	-929.8	3	2	1	22.17	2.50E-06	chi-squared	one-tailed	1843	1864	1	4.20E-05	23957	4.20E-05
BAYAREALIKE+J	BAYAREALIK	-866.4	-901.4	3	2	1	70.07	5.70E-17	chi-squared	one-tailed	1739	1807	1	1.70E-15	6.05E+14	1.70E-15
Model	**LnL**	**numparams**	**d**	**e**	**j**	**AICc**	**AICc_wt**									
DEC	-921.6	2	0.0052	0.001	0	1847	3.00E-24									
DEC+J	-909	3	0.0048	1.00E-12	0.012	1824	3.00E-19									
DIVALIKE	-929.8	2	0.0058	0.001	0	1864	8.40E-28									
DIVALIKE+J	-918.7	3	0.0053	1.00E-12	0.0096	1843	1.90E-23									
BAYAREALIKE	-901.4	2	0.0035	0.035	0	1807	1.70E-15									
BAYAREALIKE+J	-866.4	3	0.0031	0.0034	0.023	1739	1									
Model	**AICc**	**numparams**	**ntips**	**deltaAICc**	**rel_likes**											
DEC	1847	2	12	108	3.5326E-24											
DEC+J	1824	3	12	85	3.4873E-19											
DIVALIKE	1864	2	12	125	7.1878E-28											
DIVALIKE+J	1843	3	12	104	2.6103E-23											
BAYAREALIKE	1807	2	12	68	1.7139E-15											
BAYAREALIKE+J	1739	3	12	0	1											

Table S3. Stochastic mapping statistics and data from BioGeoBears results.

Total disperal means (from column A to row 3)

	A	B	C	D	E	F	G	H	I	J	Sums
A	.	6.62	6.1	1.56	0.18	0.98	2.02	1.3	3.58	2.34	**24.68**
B	7.02	.	7.32	1.48	0.16	0.96	2.1	1.98	8.12	3.86	**33**
C	2.86	5.64	.	1.2	0.08	0.26	0.44	1.4	3.1	3.1	**18.08**
D	3.98	2.78	2.92	.	8.16	3.84	6.46	4.6	3.02	1.6	**37.36**
E	0.48	0.02	0.04	1.64	.	6.26	3.94	0.74	2.46	0.1	**15.68**
F	0.84	0.4	0.18	1.88	6.02	.	4.52	0.98	4.52	0.22	**19.56**
G	1	0.68	0.26	2.52	3.36	3.9	.	1.68	3.3	0.46	**17.16**
H	0.6	0.92	0.72	0.72	0.1	0.1	1.46	.	1.06	0.44	**6.12**
I	4.58	4.24	2.64	1.32	0.36	3.28	3.8	1.46	.	2.94	**24.62**
J	3	2.14	2.6	0.68	0.16	0.36	1.2	1.04	7.7	.	**18.88**
Sums	**24.36**	**23.44**	**22.78**	**13**	**18.58**	**19.94**	**25.94**	**15.18**	**36.86**	**15.06**	

A = Southern South America
B = North & Central -Andes
C = Brazil Guiana Shield
D = South & Central -Africa
E = North Africa-Mediterranean
F = Europe-Eurasia
G = Asia
H = South East Asia to Australia
I = North America
J = Meso-Carib

Anagenetic dispersal means 0

	A	B	C	D	E	F	G	H	I	J	Sums
A	.	5.98	4.5	0.66	0.16	0.58	0.52	0.8	2.12	1.74	**17.06**
B	6.68	.	6.96	1	0.14	0.54	0.86	1.58	4.62	3.48	**25.86**
C	2.48	5.24	.	0.66	0.06	0.14	0.38	1.28	1.9	2.24	**14.38**
D	1.2	1.1	1.14	.	5.44	1.32	4.24	3.64	1.3	0.38	**19.76**
E	0.46	0.02	0.04	1	.	5.14	2.42	0.74	2.18	0.08	**12.08**
F	0.68	0.32	0.16	1.66	4.14	.	3.42	0.78	3.94	0.2	**15.3**
G	0.62	0.3	0.2	1.88	2.2	3.68	.	1.48	2.82	0.26	**13.44**
H	0.54	0.64	0.52	0.64	0.08	0.04	1.24	.	0.62	0.4	**4.72**
I	3.1	4.08	2.34	0.8	0.34	2.24	2.68	1.08	.	2.64	**19.3**
J	2.74	1.98	2.3	0.46	0.12	0.22	0.8	0.98	4.66	.	**14.26**
Sums	**18.5**	**19.66**	**18.16**	**8.76**	**12.68**	**13.9**	**16.56**	**12.36**	**24.16**	**11.42**	

Founder dispersal means

	A	B	C	D	E	F	G	H	I	J	Sums
A	.	0.64	1.6	0.9	0.02	0.4	1.5	0.5	1.46	0.6	**7.62**
B	0.34	.	0.36	0.48	0.02	0.42	1.24	0.4	3.5	0.38	**7.14**
C	0.38	0.4	.	0.54	0.02	0.12	0.06	0.12	1.2	0.86	**3.7**
D	2.78	1.68	1.78	.	2.72	2.52	2.22	0.96	1.72	1.22	**17.6**
E	0.02	.	.	0.64	.	1.12	1.52	.	0.28	0.02	**3.6**
F	0.16	0.08	0.02	0.22	1.88	.	1.1	0.2	0.58	0.02	**4.26**
G	0.38	0.38	0.06	0.64	1.16	0.22	.	0.2	0.48	0.2	**3.72**
H	0.06	0.28	0.2	0.08	0.02	0.06	0.22	.	0.44	0.04	**1.4**
I	1.48	0.16	0.3	0.52	0.02	1.04	1.12	0.38	.	0.3	**5.32**
J	0.26	0.16	0.3	0.22	0.04	0.14	0.4	0.06	3.04	.	**4.62**
Sums	**5.86**	**3.78**	**4.62**	**4.24**	**5.9**	**6.04**	**9.38**	**2.82**	**12.7**	**3.64**	

	founder	a	d	e	subset	vicariance	sympatry	ALL_disp	ana_disp	all_ana	all_clado	total_events
means	58.98	0	156.2	0	0	0	147	215.1	156.2	156.2	206	362.2
stdevs	2.84	0	4.81	0	0	0	2.84	4.72	4.81	4.81	0	4.81
sums	2949	0	7808	0	0	0	7351	10757	7808	7808	10300	18108

Table S4. Results of MEDUSA diversification analyses.

	Model.ID	Shift.Node	Cut.At	Model	Ln.Lik.part	r	epsilon	r.low	r.high
1	1	48	node	yule	-21.1013	0.0464486	NA	0.0350422	0.0634364
2	2	57	stem	yule	-123.1464	0.171198	NA	0.1555977	0.1900465
3	3	70	stem	yule	-87.52522	0.358459	NA	0.3261214	0.398265
4	4	21	stem	yule	-8.312887	0.326149	NA	0.2600769	0.4538123
5	5	51	stem	yule	-100.8984	0.102519	NA	0.0902122	0.1174788
6	6	64	stem	yule	-41.15462	0.231712	NA	0.2062134	0.2671626
7	7	29	stem	yule	-1.386294	0.017087	NA	0	0.0805475
8	8	35	stem	yule	0	0	NA	0	0.0381142
9	9	37	stem	yule	0	0	NA	0	0.0404179

Table S5. Biogeographic areas assigned for BioGeoBears analyses.

Tribe	Genus	Southern	North & C	Brazil - Gu	South & C	Northern /	Europe-Eu	Asia	Southeast	North Ame	Mesoamer	Reference	Notes
Anthemideae	Argyranthemum	0	0	0	0	1	0	0	0	0	0	29	Macaronesia
Anthemideae	Achillea	0	0	0	0	1	1	1	0	0	0	26	Europe, Asia, northern Africa.
Anthemideae	Anthemis	0	0	0	0	1	1	1	0	0	0	26	Europe, south-western Asia, northern and eastern Africa
Anthemideae	Artemisia	0	0	0	0	1	1	1	1	0	1	26	Northern Hemisphere, South America, southern Africa, Pacific Islands
Anthemideae	Athanasia	0	0	0	1	0	0	0	0	0	0	26	South Africa, Namibia
Anthemideae	Chrysanthemum	0	0	0	0	1	1	0	0	0	0	26	Asia (Mon- golia, Russia, China, Japan, Korea), eastern Europe.
Anthemideae	Cotula	1	1	1	1	0	0	0	1	1	0	26	southern and eastern Africa, Australia, South America, Mexico, southern oceanic islands.
Anthemideae	Leucanthemella	0	0	0	0	0	1	1	0	0	0	26	western Europe (Slovakia, Ukraine, Bulgaria, Romania, Yugoslavia, Hungary), Far East (Mongolia, China, Korea, Japan).
Anthemideae	Matricaria	0	0	0	0	1	1	1	1	0	1	26	Europe, northern Africa, Macaronesia, western, south-western and central Asia, western North America.
Anthemideae	Pentzia	0	0	0	1	0	0	0	0	0	0	26	Namibia, South Africa, Botswana
Anthemideae	Pseudobrandelia	0	0	0	0	0	1	1	0	0	0	26	Iran, Afghanistan, central Asia, China.
Anthemideae	Rhodanthemum	0	0	0	0	1	0	0	0	0	0	26	South-western Europe, north-western Africa.
Anthemideae	Santolina	0	0	0	0	1	0	0	0	0	0	26	southern Europe, northern Africa.
Anthemideae	Tanacetum	0	0	0	0	1	1	1	0	1	0	26	Europe, Asia, northern Africa, North America
Anthemideae	Ursinia	0	0	0	1	0	0	0	0	0	0	26	South Africa, Namibia, Botswana, Ethiopia.
Arctotideae	Arctotis	0	0	0	1	0	0	0	0	0	0	26	South Africa, Namibia, Angola.
Arctotideae	Berkheya	0	0	0	1	0	0	0	0	0	0	26	southern and trop- ical Africa north to Nigeria and Ethiopia.
Arctotideae	Didelta	0	0	0	1	0	0	0	0	0	0	26	South Africa, Namibia.
Arctotideae	Gazania	0	0	0	1	0	0	0	0	0	0	26	South Africa, Namibia, one species extending into Tanzania and another into Mozambique.
Arctotideae	Haplocarpha	0	0	0	1	0	0	0	0	0	0	26	southern and eastern Africa north to Ethiopia
Arctotideae	Heterolepis	0	0	0	1	0	0	0	0	0	0	26	South Africa.
Asteraceae	Baltonia	0	0	0	0	0	0	0	0	1	0	26	western North America.
Asteraceae	Chiliotrichium	1	0	0	0	0	0	0	0	0	0	26	Argentina, Chile.
Asteraceae	Chrysocoma	0	0	0	1	0	0	0	0	0	0	26	southern Africa.
Asteraceae	Chrysothamnus	0	0	0	0	0	0	0	0	1	0	26	south-western Canada, western USA, north-central Mexico.
Asteraceae	Conyza	1	1	0	1	0	0	0	1	1	0	26	primarily tropical and subtropical
Asteraceae	Dimeka	0	0	0	1	1	0	0	0	0	0	26	Africa
Asteraceae	Ericameria	0	0	0	0	0	0	0	0	1	0	26	western USA, north-western Mexico.
Asteraceae	Erigeron	1	1	1	0	0	1	0	0	1	1	26	North to South America, West Indies, Galapagos, Eurasia.
Asteraceae	Eurybia	0	0	0	0	0	0	0	0	1	0	26	USA, Canada to Alaska, and north-eastern Asia.
Asteraceae	Euthamia	0	0	0	0	0	0	0	0	1	0	26	central and south-eastern USA, one south-western Canada to Baja California Norte.
Asteraceae	Grindelia	0	1	0	0	0	0	0	0	1	0	26	USA, Mexico, southern Andes.
Asteraceae	Haplopappus	1	0	0	0	0	0	0	0	0	0	26	southern South America.
Asteraceae	Heterotheca	0	0	0	0	0	0	0	0	1	0	26	USA, Canada, Mexico.
Asteraceae	Kalimeris	0	0	0	0	0	0	1	0	0	0	26	western Asia,
Asteraceae	Lessingia	0	0	0	0	0	0	0	0	1	0	26	south-western USA
Asteraceae	Perezia	1	1	0	0	0	0	0	0	0	0	26	Argentina, Chile, Bolivia and Peru.
Asteraceae	Pteronia	0	0	0	1	0	0	0	0	0	0	26	southern and south-western Africa to Zambia.
Asteraceae	Solidago	1	0	0	0	0	1	0	0	1	0	26	mostly North America, eight Mexico, one South America, 10–20 Eurasia.
Asteraceae	Sommerfeltia	1	0	0	0	0	0	0	0	0	0	26	southern Brazil, Uruguay, Argentina.
Asteraceae	Symphyotrichum	1	1	1	0	0	0	0	0	1	0	26	North America, some Mexico and South America
Athroismeae	Lowryanthus	0	0	0	0	1	0	0	0	0	0	46	Madagascar, more than half of the tribe Athroismeae is African, but one genus Centipeda (not sampled here) is found more widespread in Southern Hemisphere
Barnadesieae	Bahia	0	1	0	0	0	0	0	0	1	0	26	western USA, Mexico, Chile.
Barnadesieae	Schkuhria	1	1	1	0	0	0	0	0	1	0	26	North and South America,
Barnadesieae	Barnadesia	1	1	1	0	0	0	0	0	0	0	26	eastern Andes in Colombia southwards into north-western Argentina and south-eastern Brazil.
Barnadesieae	Dasyphyllum	1	1	1	0	0	0	0	0	0	0	26	Venezuela south to Chile and Argentina and eastwards to Brazil.
Barnadesieae	Fulcaldea	0	1	0	0	0	0	0	0	0	0	26	southern Ecuador and north-western Peru.
Barnadesieae	Schlechtendalia	1	0	0	0	0	0	0	0	0	0	26	Brazil, Uruguay and Argentina.
Calenduleae	Calendula	0	0	0	0	1	1	0	0	0	0	26	Macaronesia, northern Africa, Mediterranean region, southern and central Europe, Anatolia, Yemen, Iraq to Iran.
Calenduleae	Chrysanthemoides	0	0	0	1	0	0	0	0	0	0	26	southern and eastern tropical Africa, i
Calenduleae	Tripteris	0	0	0	1	1	0	0	0	0	0	26	southern and tropical Africa north to Egypt, Arabia and Jordan.
Calycoreaceae	Nastanthus	1	0	0	0	0	0	0	0	0	0	26	
Cardueae	Amphoricarpos	0	0	0	0	0	1	1	0	0	0	26	Balkan Peninsula, Turkey and Caucasus.
Cardueae	Arctium	0	0	0	0	0	1	0	0	0	0	26	temperate Eurasia
Cardueae	Cardopatium	0	0	0	0	1	0	0	0	0	0	26	western Mediterranean region, from the Caucasus to
Cardueae	Carlina	0	0	0	0	1	1	0	0	0	0	26	central Europe, Mediterranean region
Cardueae	Carthamus	0	0	0	0	1	1	0	0	0	0	26	Iran, Caucasus, eastern Mediterranean region to central Asia.
Cardueae	Centaurea	0	0	0	0	1	1	0	0	0	0	26	Eurasia, especially Irano-Turanian and Mediterranean region.
Cardueae	Cirsium	0	0	0	0	1	1	0	0	1	0	26	Eurasia, North America, northern and eastern Africa,
Cardueae	Cousinia	0	0	0	0	0	1	0	0	0	0	26	central and western Asia
Cardueae	Cynara	0	0	0	0	1	0	0	0	0	0	26	Mediterranean region
Cardueae	Echinops	0	0	0	0	1	1	0	0	0	0	26	Eurasia, northern and central Africa;
Cardueae	Jurinea	0	0	0	0	1	1	0	0	0	0	26	western and central Asia, Europe, northern Africa.
Cardueae	Saussurea	0	0	0	0	0	1	0	0	1	0	26	temperate Eurasia, North America, doubtfully native in Australia.
Cardueae	Shangwua	0	0	0	0	0	0	1	0	0	0	26	original publication Wang 2013
Cardueae	Silybum	0	0	0	0	1	0	0	0	0	0	26	Mediterranean region,
Chaenactideae	Chaenactis	0	0	0	0	1	0	0	0	1	0	26	western USA, north-western Mexico.
Cichorieae	Cicerbita	0	0	0	0	1	1	0	0	0	0	26	Eurasia,
Cichorieae	Cichorium	0	0	0	0	1	1	0	0	0	0	26	Europe, Mediterranean area, Near East.
Cichorieae	Gundelia	0	0	0	0	1	1	0	0	0	0	26	Middle East and Turkey to central Asia.
Cichorieae	Lactuca	0	0	0	0	1	1	1	1	1	0	26	Northern hemisphere, in Asia to New Guinea, in North America to Mexico, in tropical Africa to South Africa
Cichorieae	Leontodon	0	0	0	0	1	1	0	0	0	0	26	Europe, Mediterranean region to Iran.
Cichorieae	Notobasis	0	0	0	0	1	0	0	0	1	0	26	Eastern Asia, North America,
Cichorieae	Prenanthes	0	0	0	0	1	0	0	0	1	0	26	Eurasia, south to tropical Africa.
Cichorieae	Scolymus	0	0	0	0	1	0	0	0	0	0	26	Macaronesia, Mediterranean area.
Cichorieae	Taraxacum	1	0	0	0	1	1	1	1	0	0	26	northern hemisphere, a single section in southern South America, Australia and New Zealand.
Cichorieae	Tragopogon	0	0	0	0	1	1	0	0	1	0	26	Eurasia, introduced into other parts of the world
Corespsideae	Corespsis	1	1	1	0	0	0	0	0	1	1	26	America.
Corymbieae	Corymbium	0	0	0	1	0	0	0	0	0	0	26	Cape region of South Africa.
Dicomeae	Cloiselia	0	0	0	1	1	0	0	0	0	0	26	South Africa and tropical Africa, Madagascar, north-eastern Africa, Asia.
Dicomeae	Gladiopappus	0	0	0	1	0	0	0	0	0	0	26	endemic to Madagascar.
Dicomeae	Macledium	0	0	0	1	0	0	0	0	0	0	47	
Eremothamneae	Eremothamnus	0	0	0	1	0	0	0	0	0	0	26	Namibia.
Eupatorieae	Chromolaena	1	1	1	0	0	0	0	0	0	1	26	New World tropics and subtropics, one species a pantropical weed.
Eupatorieae	Conoclinium	0	0	0	0	0	0	0	0	1	0	26	Mexico, USA (south-western and eastern Texas).
Eupatorieae	Eutrochium	0	0	0	0	0	0	0	0	1	0	26	North America.
Eupatorieae	Stevia	1	1	1	0	0	0	0	0	1	1	26	
Famatinantheae	Famatinanthus	1	0	0	0	0	0	0	0	0	0	48	
Gnaphalieae	Anteinnaria	0	1	0	0	0	1	1	0	1	0	26	Asia, Europe, North and South America.
Gnaphalieae	Argyrogiottis	0	0	0	0	0	0	1	0	0	0	26	Australia
Gnaphalieae	Belloa	1	1	0	0	0	0	0	0	0	0	49	South America.
Gnaphalieae	Cassinia	0	0	0	0	0	0	1	0	0	0	26	Australia.
Gnaphalieae	Craspedia	0	0	0	0	0	0	0	1	0	0	26	Australia, New Zealand.
Gnaphalieae	Disparago	0	0	0	0	1	0	0	0	0	0	26	Africa.
Gnaphalieae	Facelis	1	1	0	0	0	0	0	0	0	0	26	
Gnaphalieae	Gnaphalium	1	1	1	0	0	0	0	0	1	1	26	South America.
Gnaphalieae	Gamochaetopis	1	0	0	0	0	0	0	0	0	0	49	
Gnaphalieae	Helichrysum	0	0	0	1	1	1	0	0	0	0	26	Africa, Madagascar, Europe and Asia.
Gnaphalieae	Leontopodium	0	0	0	0	0	1	1	0	0	0	26	Asia and Europ
Gnaphalieae	Luciliocline	1	1	0	0	0	0	0	0	0	0	49	
Gnaphalieae	Oedera	0	0	0	1	0	0	0	0	0	0	26	southern Africa.
Gnaphalieae	Phagnalon	0	0	0	0	1	1	1	0	0	0	26	western Asia, Europe and northern Africa.
Gnaphalieae	Pseudognaphalium	1	0	0	0	1	0	1	1	1	1	26	Africa, Asia, Central, North and South America, New Zealand.
Gnaphalieae	Relhania	0	0	0	1	0	0	0	0	0	0	26	southern Africa.
Gnaphalieae	Syncarpha	0	0	0	1	0	0	0	0	0	0	26	southern Africa.
Gnaphalieae	Trichanthodium	0	0	0	0	0	0	0	0	1	0	26	Australia.
Gochnatieae	Moquiniastrum	0	0	0	1	0	0	0	0	0	0	26	Brazil
Gochnatieae	Nahuatlea	0	0	0	0	0	0	0	0	1	0	26	Mexico
Gymnarrheneae	Cavea	0	0	0	0	1	0	1	0	0	0	26	north-eastern India, south-western China.
Heliantheae	Helianthella	0	0	0	0	0	0	0	0	1	0	26	USA
Heliantheae	Gaillardia	0	1	0	0	0	0	0	0	1	0	26	South- eastern Canada, northern Mexico, south-western USA, temperate eastern South America.
Heliantheae	Helenium	0	1	0	0	0	0	0	0	1	1	26	North and South America, most species in northern Mexico and southern USA.
Heliantheae	Chrysogonum	0	0	0	0	0	0	0	0	1	0	26	south-eastern USA.
Heliantheae	Helianthus	0	0	0	0	0	0	0	0	1	0	26	North America.
Heliantheae	Heliopsis	0	1	0	0	0	0	0	0	1	0	26	Central and northern South America.
Heliantheae	Lipochaeta	0	0	0	0	0	0	0	0	1	0	26	Hawaii.
Heliantheae	Melanthera	0	0	0	0	0	0	0	0	1	0	26	pantropical
Heliantheae	Montanoa	0	1	0	0	0	0	0	0	0	1	26	Mexico, Central America, northern South America south to northern Peru.
Heliantheae	Phoebanthus	0	0	0	0	0	0	0	0	1	0	26	Florida, USA.
Heliantheae	Rojasianthe	0	0	0	0	0	0	0	0	0	1	26	Mexico, Guatemala.
Heliantheae	Spilanthes	0	1	1	1	0	0	0	1	1	1	26	pantropical
Heliantheae	Tithonia	0	1	0	0	0	0	0	0	1	1	26	south-western USA to northern South America,
Heliantheae	Verbesina	1	1	1	0	0	0	0	0	1	1	26	America, highest number of species in Mexico and tropical Andes.
Heliantheae	Xanthium	1	1	1	0	0	0	0	1	1	1	26	disturbed habitats, warm and temperate regions of the world.
Hyaliideae	Hyalis	1	1	0	0	0	0	0	0	0	0	26	Bolivia, Paraguay, Argentina.
Hyaliideae	Leucomeris	0	0	0	0	0	0	1	0	0	0	26	Burma, China, India, Nepal, Pakistan, Thailand, Vietnam.
Inuleae-Iseadis	Cyclospis	1	1	0	0	0	0	0	0	0	0	26	Argentina, Peru, Chile(?), Paraguay
Inuleae	Inula	0	0	0	0	0	1	1	0	0	0	26	Old World.
Inuleae	Pallenis	0	0	0	0	0	1	1	0	0	0	26	Mediterranean region, Middle East,
Inuleae	Pechuel-loeschea	0	0	0	0	1	0	0	0	0	0	26	Namibia
Inuleae	Pulicaria	0	0	0	0	0	1	1	0	0	0	26	Europe, Africa, Arabia, Asia.
Inuleae	Tessaria	1	0	0	0	0	0	0	0	0	0	26	southern South America.
Liabeae	Eirata	0	0	1	0	0	0	0	0	0	1	26	Costa Rica to Peru.
Liabeae	Liabum	1	1	0	0	0	0	0	0	0	1	26	Mexico, Central America, Greater Antilles, and Andes of South America.
Liabeae	Munnozia	1	1	0	0	0	0	0	0	0	1	26	mostly from the Andes, few in Costa Rica, Panama.
Liabeae	Sinclairia	0	0	0	0	0	0	0	0	1	1	26	Mexico, Central America, one to western Colombia.
Madieae	Deinandra	0	0	0	0	0	0	0	0	1	0	26	western USA (mostly California), Mexico (Baja California).
Madieae	Eriophyllum	0	0	0	0	0	0	0	0	1	0	26	western USA.
Millerieae	Guizotia	0	0	0	0	1	0	0	1	0	0	26	mostly eastern Africa, one species in tropical western Africa and the Indian subcontinent.
Millerieae	Rumfordia	0	0	0	0	0	0	0	0	1	1	26	Mexico, Guatemala.
Mutisieae	Moquinia	0	0	1	0	0	0	0	0	0	0	26	Brazil
Mutisieae	Pseudostifftia	0	0	1	0	0	0	0	0	0	0	26	Brazil
Mutisieae	Chaetanthera	1	1	0	0	0	0	0	0	0	0	26	Argentina, Bolivia, Chile, Peru.
Mutisieae	Gerbera	0	0	0	1	0	0	0	1	0	0	26	China, Kenya, Malawi, Madagascar, Mozambique, South Africa, Tanzania, Uganda, Yemen, Zimbabwe
Mutisieae	Mutisia	1	1	1	0	0	0	0	0	0	0	26	Argentina, Brazil, Bolivia, Chile, Colombia, Ecuador, Paraguay, Peru, Uruguay.
Mutisieae	Trichocline	1	1	1	0	0	0	0	0	0	0	26	Argentina, Bolivia, Brazil, Chile, Colombia, Paraguay, Peru, Uruguay.
Nassauvieae	Dolichlasium	1	0	0	0	0	0	0	0	0	0	26	Argentina (Patagonia),
Nassauvieae	Nassauvia	1	1	0	0	0	0	0	0	0	0	26	Argentina, Bolivia, Chile, Falkland Islands.
Nassauvieae	Perezia	1	1	1	0	0	0	0	0	0	0	26	South America (Argentina, Bolivia, Brazil, Chile, Paraguay, Peru, Uruguay).
Nassauvieae	Proustia	1	1	0	0	0	0	0	0	0	0	26	Peru, Bolivia, Chile, Argentina.
Neurolaeneae	Calea	0	1	1	0	0	0	0	0	1	1	26	neotropical
Oldenburgieae	Oldenburgia	0	0	0	1	0	0	0	0	0	0	26	South Africa.
Onoserideae	Onoseris	1	1	0	0	0	0	0	0	0	1	26	Central and South America (Argentina, Bolivia, Colombia, Costa Rica, Ecuador, Guatemala, Mexico, Peru).
Onoserideae	Plazia	1	1	0	0	0	0	0	0	0	0	26	Peru, Bolivia, Argentina, Chile.
Perityleae	Amauria	0	1	0	0	0	0	0	0	1	0	26	Baja California, Mexico.
Pertyaea	Myripnois	0	0	0	0	0	0	0	0	1	0	26	Mongolia and China.
Platycarpheae	Platycarpha	0	0	0	1	0	0	0	0	0	0	26	South Africa.
Senecioneae	Brachyglottis	0	0	0	0	0	0	0	0	1	0	26	New Zealand.
Senecioneae	Cacalliopsis	0	0	0	0	0	0	0	0	1	0	26	western North America.
Senecioneae	Elekmania	0	0	0	0	0	0	0	0	0	1	26	Hispaniola.
Senecioneae	Othonna	0	0	0	1	0	0	0	0	0	0	26	southern Africa north to Angola and Zimbabwe.
Senecioneae	Packera	0	0	0	0	0	0	1	0	1	0	26	North America, Mexico, Siberia.
Senecioneae	Robbaea	0	0	0	0	0	0	0	0	1	1	26	south-western USA (Arizona), Mexico to Panama.
Senecioneae	Senecio	1	1	1	1	0	0	0	0	0	0	26	cosmopolitan, many in South America and southern Africa (*coded by main areas)
Senecioneae	Sinacalia	0	0	0	0	0	0	1	0	0	0	26	China.
Senecioneae	Tiaalagia	0	0	0	0	0	1	0	0	0	0	26	Eurasia.
Senecioneae	Werneria	1	1	0	0	0	0	0	0	0	0	26	high Andes of South America.
Senecioneae	Xenophyllum	1	1	0	0	0	0	0	0	0	0	26	high Andes from Argentina and Chile to Colombia.
Stifftieae	Gongylolepis	0	1	1	0	0	0	0	0	0	0	26	Brazil, Colombia, Guyana (Guyana Highlands) Venezuela (Venezuelan Guyana).
Stifftieae	Hyaloseris	1	0	0	0	0	0	0	0	0	0	26	western Andes in Colombia southwards into north-western Argentina and south-eastern Brazil.
Stifftieae	Stifftia	0	0	1	0	0	0	0	0	0	0	26	Brazil, French Guyana
Tageteae	Flaveria	1	1	1	0	0	0	0	0	1	1	26	America, one species in Australia;
Tageteae	Porophyllum	0	1	1	0	0	0	0	0	1	1	26	tropical and subtropical America.
Tageteae	Thymophylla	1	0	0	0	0	0	0	0	1	0	26	south-western USA, Mex- ico and north-western Argentina.
Tarchonantheae	Brachylaena	0	0	0	1	0	0	0	0	0	0	26	Angola, Botswana, Kenya, Madagascar, Mozambique, South Africa, Swaziland, Tanzania, Uganda, Zimbabwe.
Tarchonantheae	Tarchonanthus	0	0	0	1	1	0	0	0	0	0	26	Angola, Botswana, Ethiopia, Kenya, Lesotho, Mozambique, Namibia, Saudi Arabia, Somalia, South Africa, Swaziland, Tanzania, Uganda, Yemen, Zambia.
Vernonieae	Albertinia	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Allocephalus	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Baccharoides	0	0	1	0	0	0	0	1	0	0	50	Tropical Africa, southern Asia
Vernonieae	Centrapalus	0	0	0	1	0	0	0	0	0	0	50	Africa
Vernonieae	Centratherum	0	1	1	0	0	0	0	1	0	1	50	Tropical America, Philippines, Australia
Vernonieae	Chresta	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Chrononeppus	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Cyrtocymura	0	1	1	0	0	0	0	0	0	1	50	Mexico, Central America, West Indies, eastern South America
Vernonieae	Elephantopus	0	1	1	1	0	0	0	1	1	0	50	pantropical
Vernonieae	Eremanthus	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Gorceixia	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Gymnanthemum	0	0	0	1	0	0	0	1	0	0	50	Africa, southern and southeastern Asia
Vernonieae	Heterocoma	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Heterocoryphe	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Hoblidyia	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Lepidaploa	1	1	1	0	0	0	0	0	0	1	26	tropical America.
Vernonieae	Lessingianthus	1	1	1	0	0	0	0	0	0	0	50	Brazil, Argentina, Colombia, Venezuela
Vernonieae	Lychnophora	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Minasia	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Paralychnophora	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Piptolepis	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Soaresia	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Stilpnopappus	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Stokesia	0	0	0	0	1	0	0	0	1	0	50	western usa
Vernonieae	Strophopappus	0	0	1	0	0	0	0	0	0	0	50	Brazil
Vernonieae	Vernonanthura	0	1	1	0	0	0	0	0	0	1	50	tropical america
Vernonieae	Vernonia	0	0	0	0	0	0	0	0	1	1	50	Eastern North America, Mexico, Bahamas, South America
Vernonieae	Vernoniastrum	0	0	0	1	0	0	0	0	0	0	50	Tropical Africa
Vernonieae-O	Didelphanus	0	0	0	0	1	0	0	1	1	0	50	Africa, India, south and southeast Asia
Wunderlichieae	Stenopadus	0	1	1	0	0	0	0	0	0	0	26	Brazil, Colombia, Ecuador, Venezuela (Guyana Highlands).
Wunderlichieae	Wunderlichia	0	0	1	0	0	0	0	0	0	0	26	Brazil

Table S6. Species Richness data for MEDUSA diversification analyses.

Richness data for MEDUSA		
Tribe	taxon	n.taxa
Eremothamneae	Eremothamnus-marlothianus	3
Chaenactidae	Chaenactis-douglasii	29
Platycarpheae	Platycarpha-glomerata	3
Calenduleae	Calendula-arvensis	120
Calyceraceae-Outgroup	Nastanthus-patagonicus	50
Gymnarrheneae	Cavea-tanguensis	2
Vernonieae	Gymnanthemum-amygdalinum	1500
Wunderlichieae	Wunderlichia-crulsiana	35
Tarchonantheae	Tarchonanthus-camphoratus	13
Oldenburgieae	Oldenburgia-grandis	4
Cardueae	Carlina-diae	2500
Perityleae	Amauria-rotundifolia	84
Moquineae	Moquinia-racemosa	2
Neurolaeneae	Calea-candolleana	153
Hyaloseris clade	Hyaloseris-rubicunda	7
Astereae	Denekia-capensis	3080
Onoserideae	Onoseris-sp	52
incertae sedis	Cyclolepis-genistoides	1
Bahieae	Bahia-dissecta	83
Senecioneae	Brachyglottis-repanda	3500
Famatinantheae	Famatinanthus-decussatus	1
Dicomeae	Macledium-zeyheri	100
Mutisieae	Mutisia-sp	254
Gnaphalieae	Phagnalon-sordidum	1240
Hecastocleideae	Hecastocleis-shockleyi	1
Inuleae	Tessaria-sp	687
Athroismeae	Lowryanthus-rubens	55
Pertyeae	Myripnois-dioica	70
Madieae	Deinandra-minthornii	203
Coreopsideae	Coreopsis-hamiltonii	550
Stifftieae	Gongylolepis-benthamania	37
Millerieae	Guizotia-abyssinica	380
Heliantheae	Rojasianthe-superba	1461
Helenieae	Helenium-autumnale	120
Eupatorieae	Eutrochium-fistulosum	2200
Cichorieae	Gundelia-tournefortii	1100
Heterolepis	Heterolepis-aliena	131
Nassauvieae	Proustia-sp	313
Arctotideae	Arctotis-semipapposa	76
Hyalideae	Leucomeris-spectabilis	6
Gochnatieae	Moquiniastrum-densicephalus	70
Anthemideae	Cotula-turbinata	1800
Tageteae	Thymophylla-sp	267
Barnadesieae	Schlechtendalia-luzulaefolia	91
Vernonieae-Distephanus	Distephanus-ambongensis	40
Liabeae	Liabum-barahonense	174
Corymbieae	Corymbium-villosum	9

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