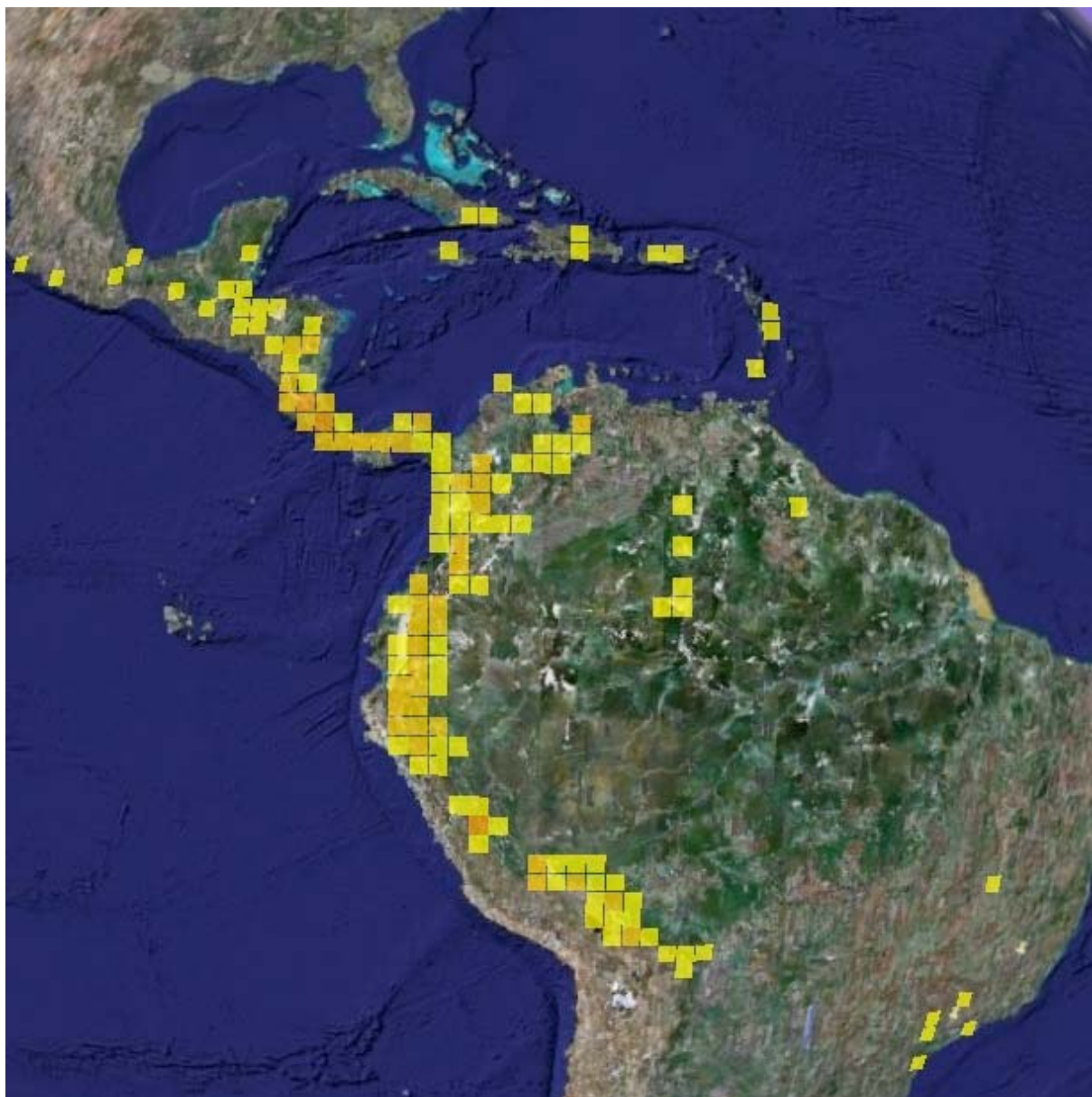


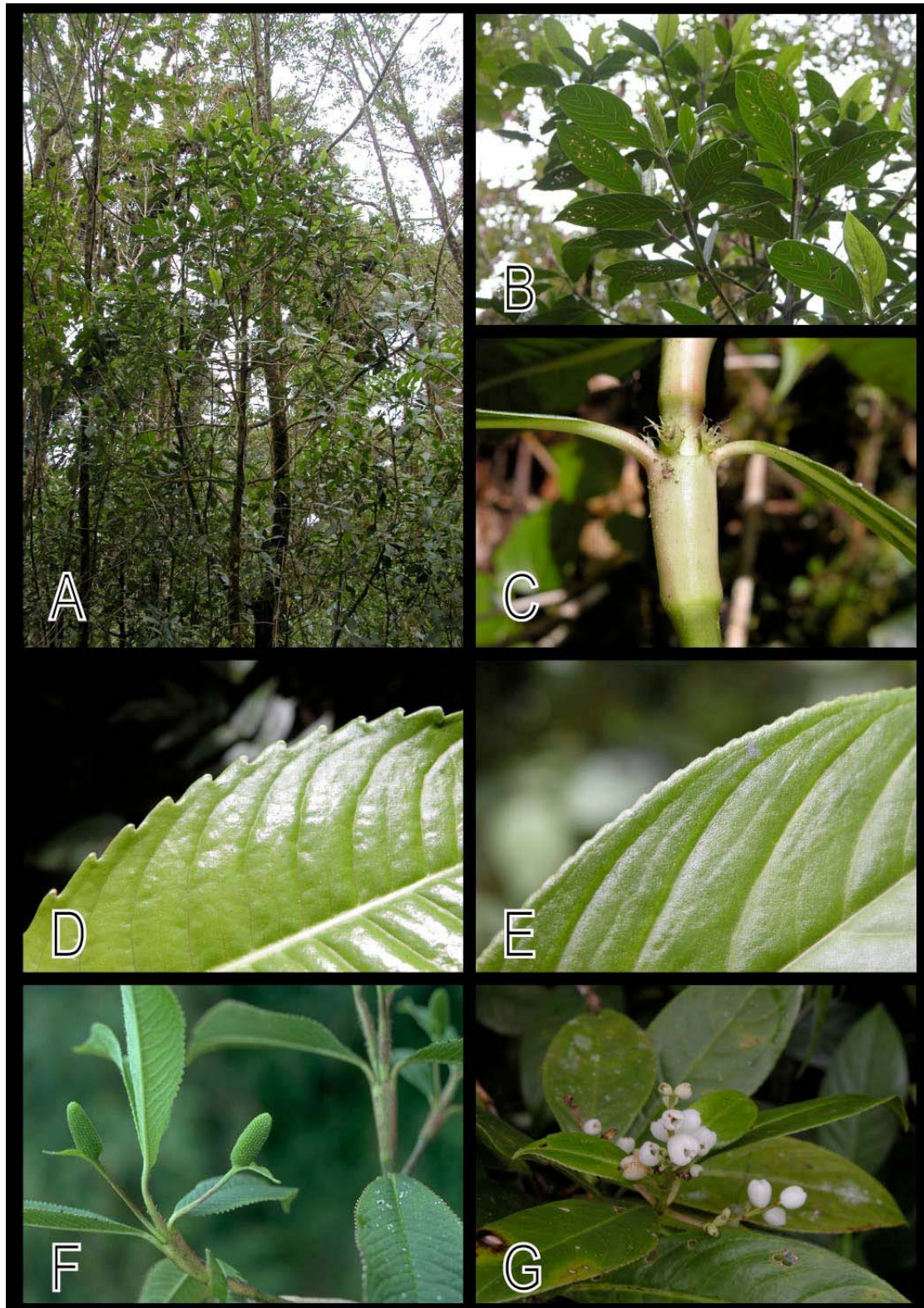
Supplemental Material

Mass Extinction, Gradual Cooling, or Rapid Radiation? Reconstructing the Spatiotemporal Evolution of the Ancient Angiosperm Genus *Hedyosmum* (Chloranthaceae) Using Empirical and Simulated Approaches

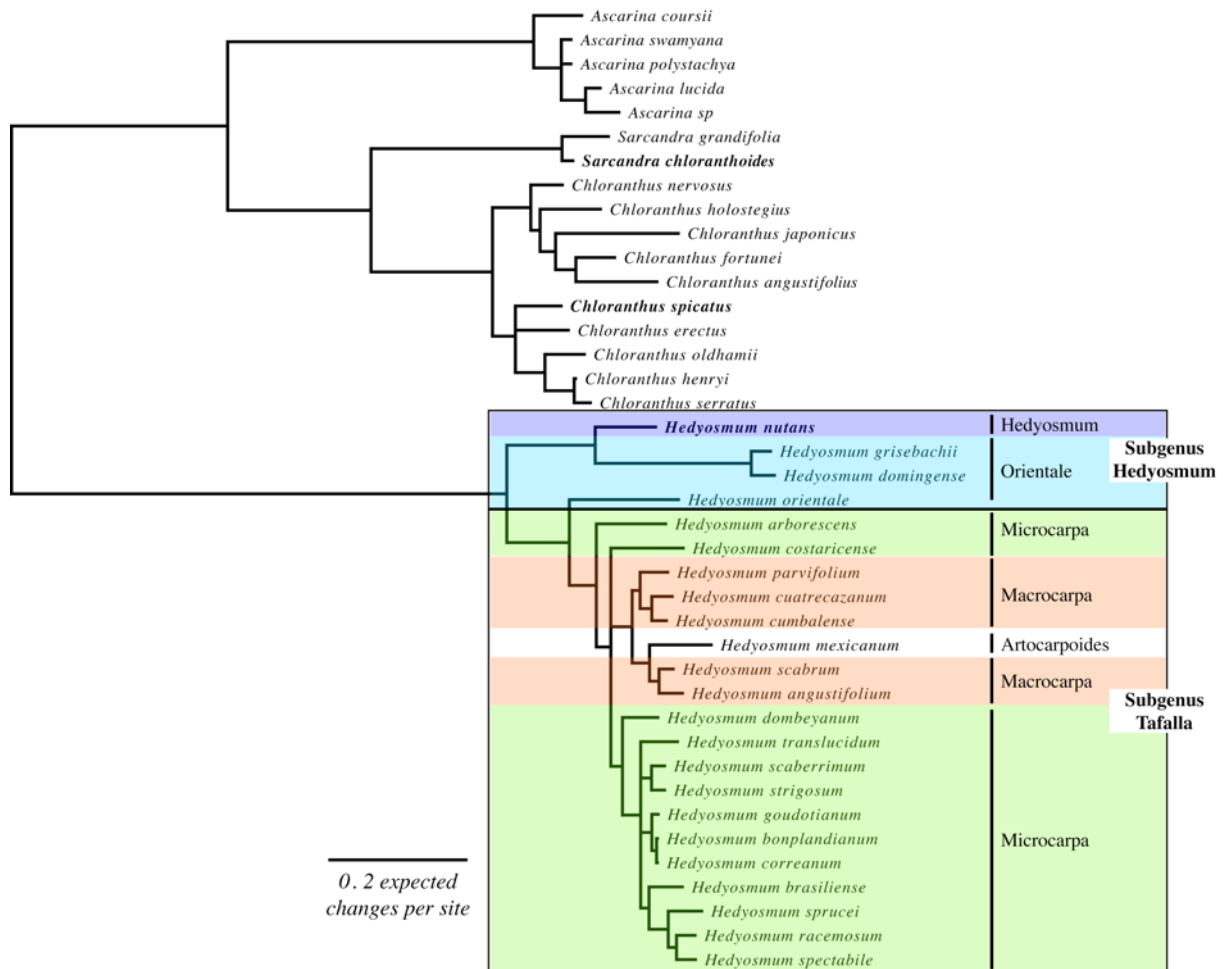
Alexandre Antonelli & Isabel Sanmartín



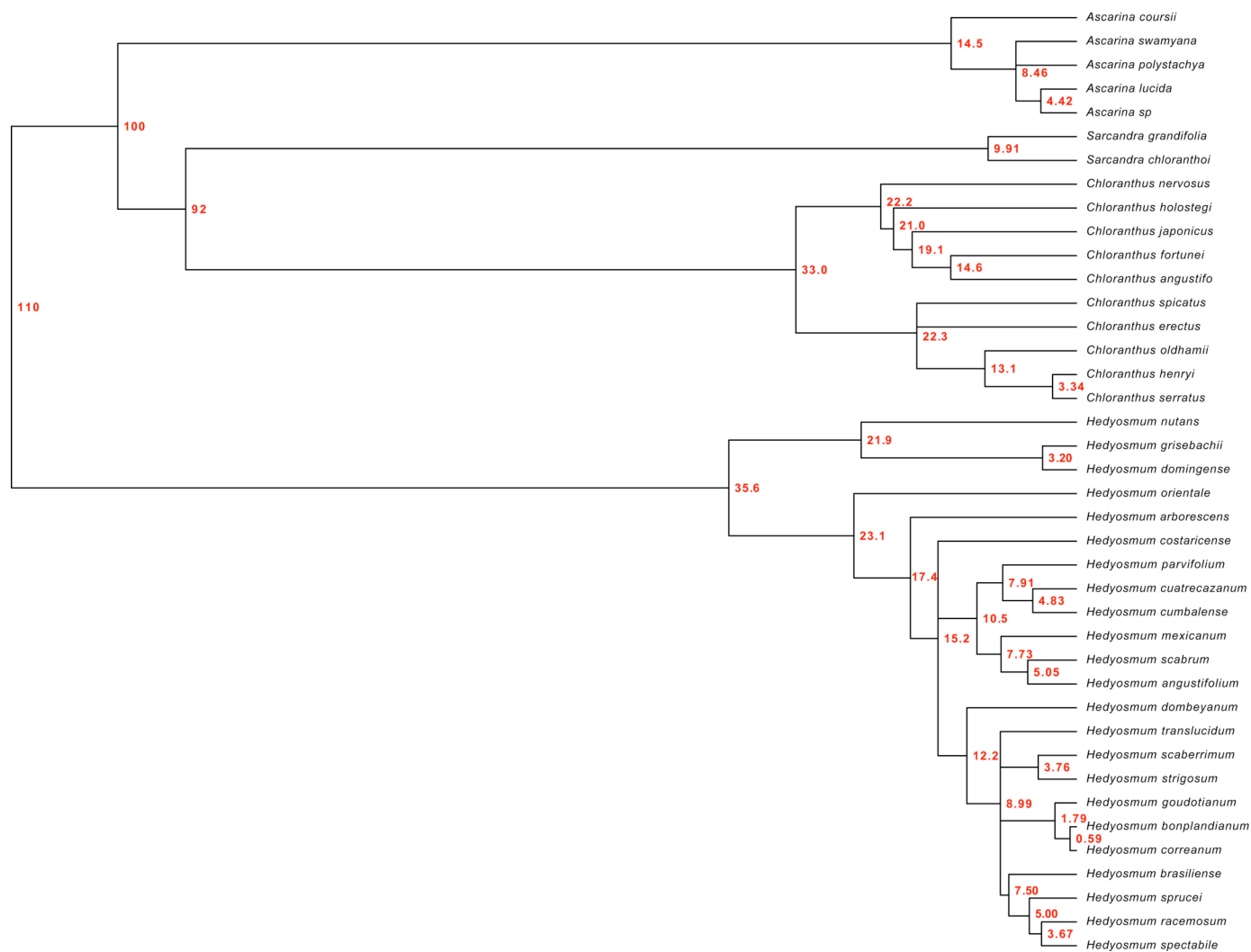
Appendix S1. Species density map of the genus *Hedyosmum* in the Neotropics Density based on 3,312 collection records from America (data from www.gbif.org plotted with permission from Google Maps™) and complemented with locations cited in Todzia (1988).



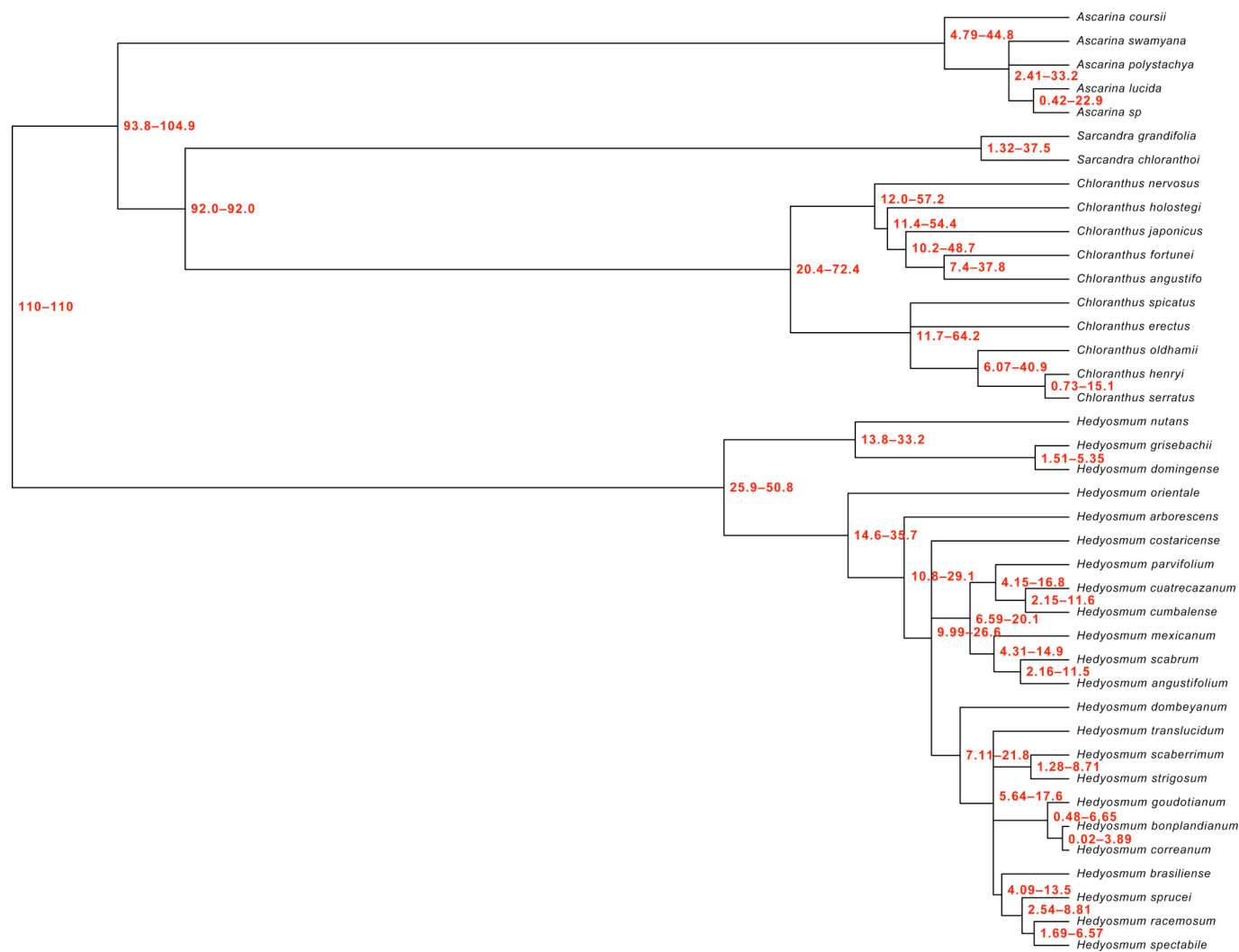
Appendix S2. Diagnostic features of *Hedyosmum*. A) Typical treelet habit; B) Detail of a branch, showing the opposite and entire leaves; C) Detail of the swollen petiole bases, showing stipular appendages; D-E) Dentate leaf margins exhibiting “chloranthoid” teeth; F) staminate inflorescence; G) pistillate inflorescence. (Photos by A.A.)



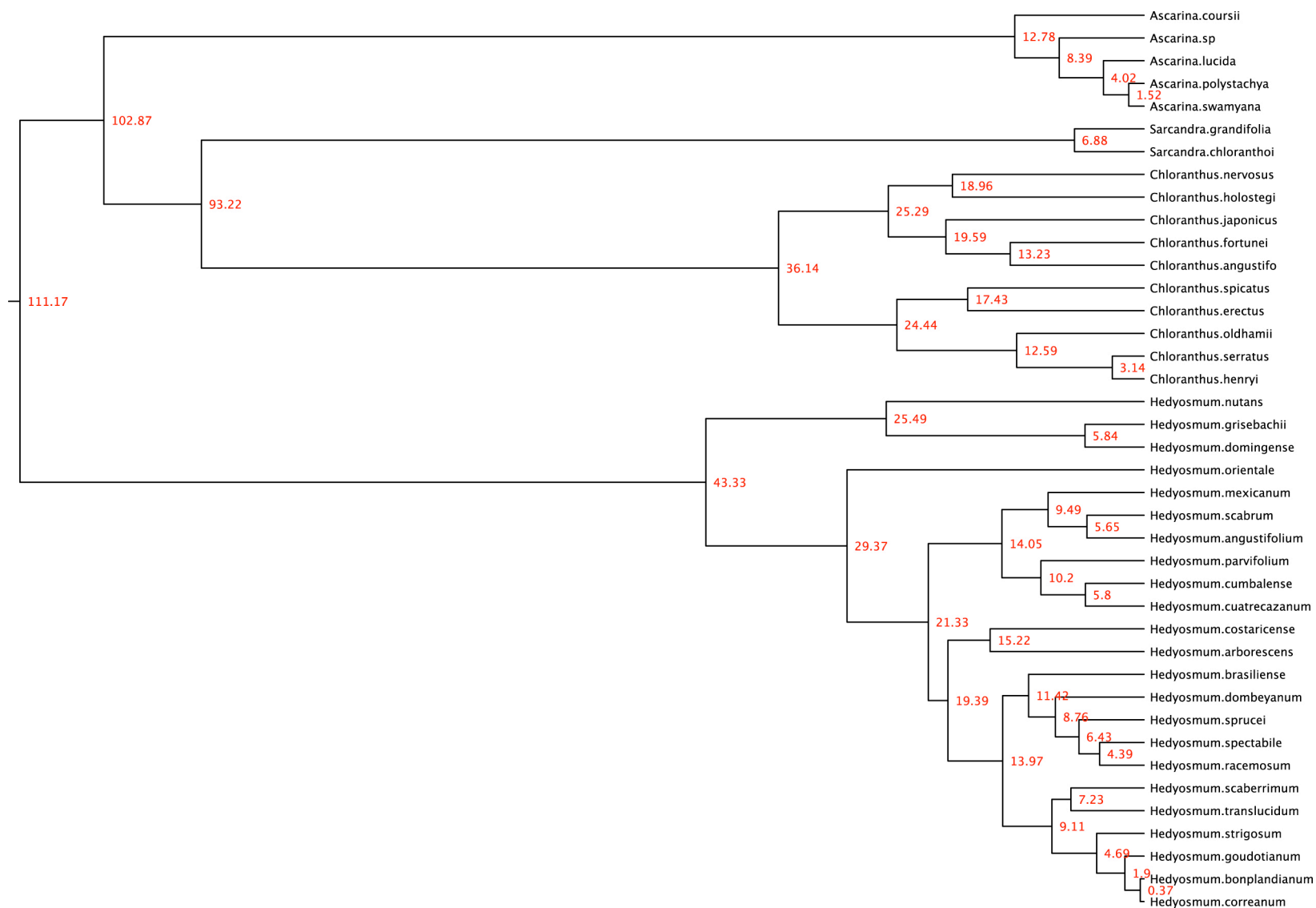
Appendix S3. Consensus phylogram from the MCMC Bayesian analysis. Mean branch lengths ($n=16000$) are shown on the topology of the most likely Bayesian tree. The scale bar indicates estimated number of changes per site.



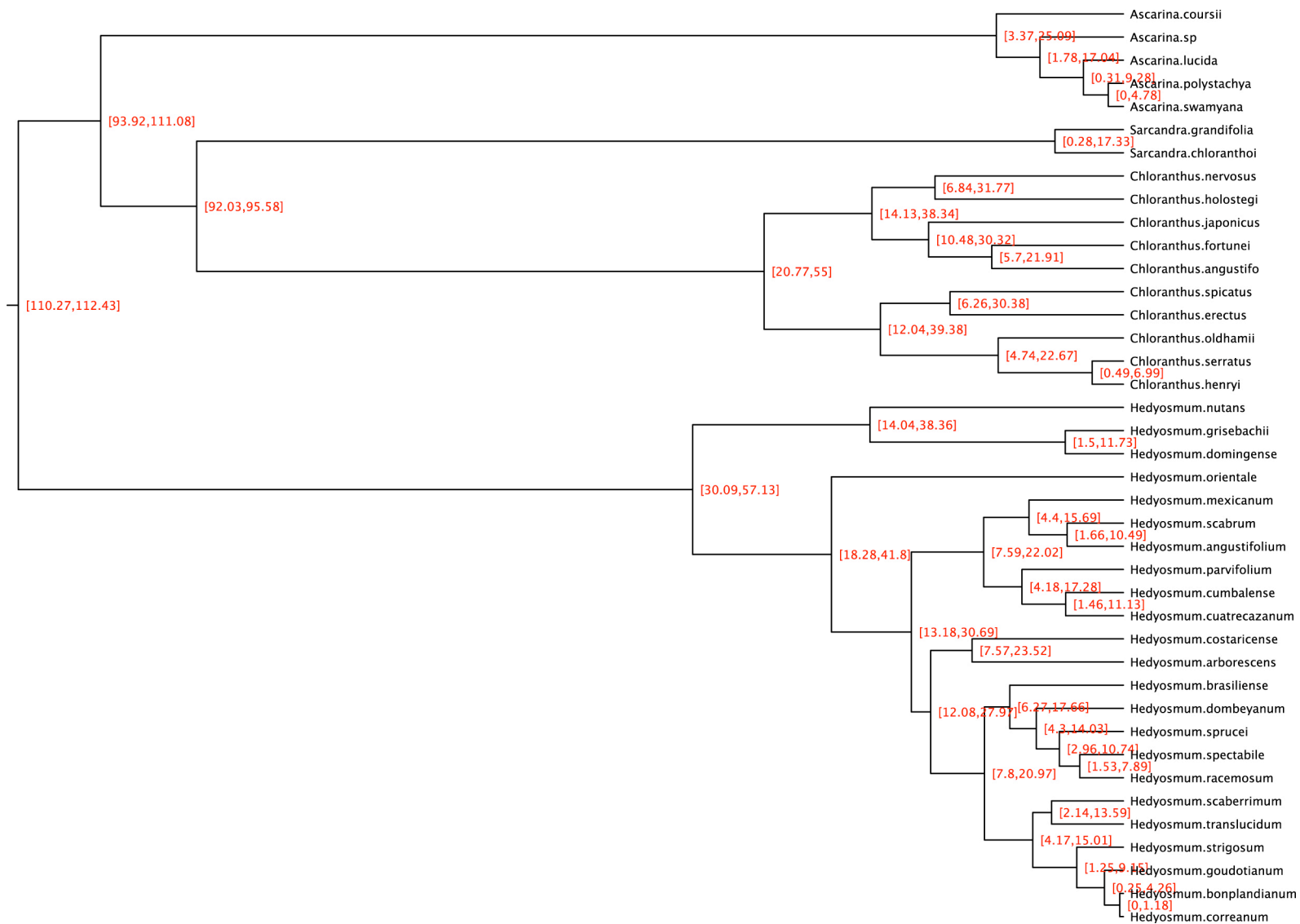
Appendix S4. Mean ages of nodes obtained with Penalized Likelihood. Statistics calculated by independently dating 1000 trees randomly sampled from the MCMC Bayesian stationary distribution. The tree topology is the same as in Fig. 1.



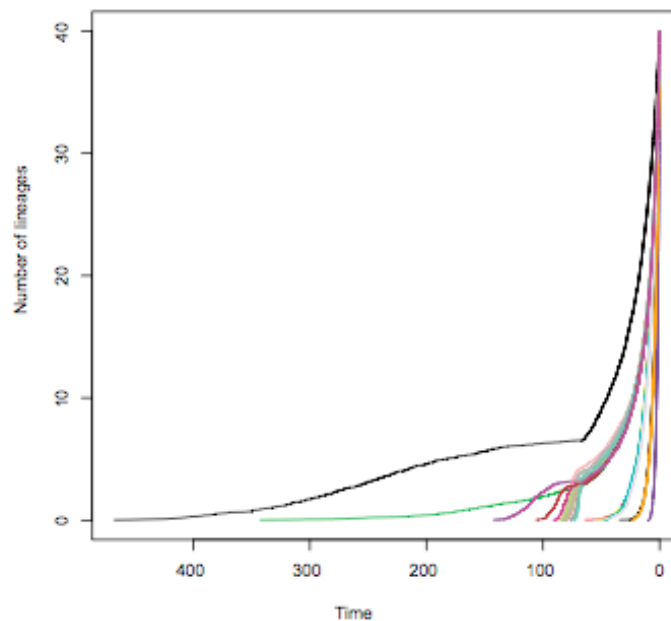
Appendix S5. 95% confidence intervals of node ages obtained with Penalized Likelihood. Statistics calculated by independently dating 1000 trees randomly sampled from the MCMC Bayesian stationary distribution. The tree topology is the same as in Fig. 1.



Appendix S6. Mean ages of nodes obtained with BEAST.

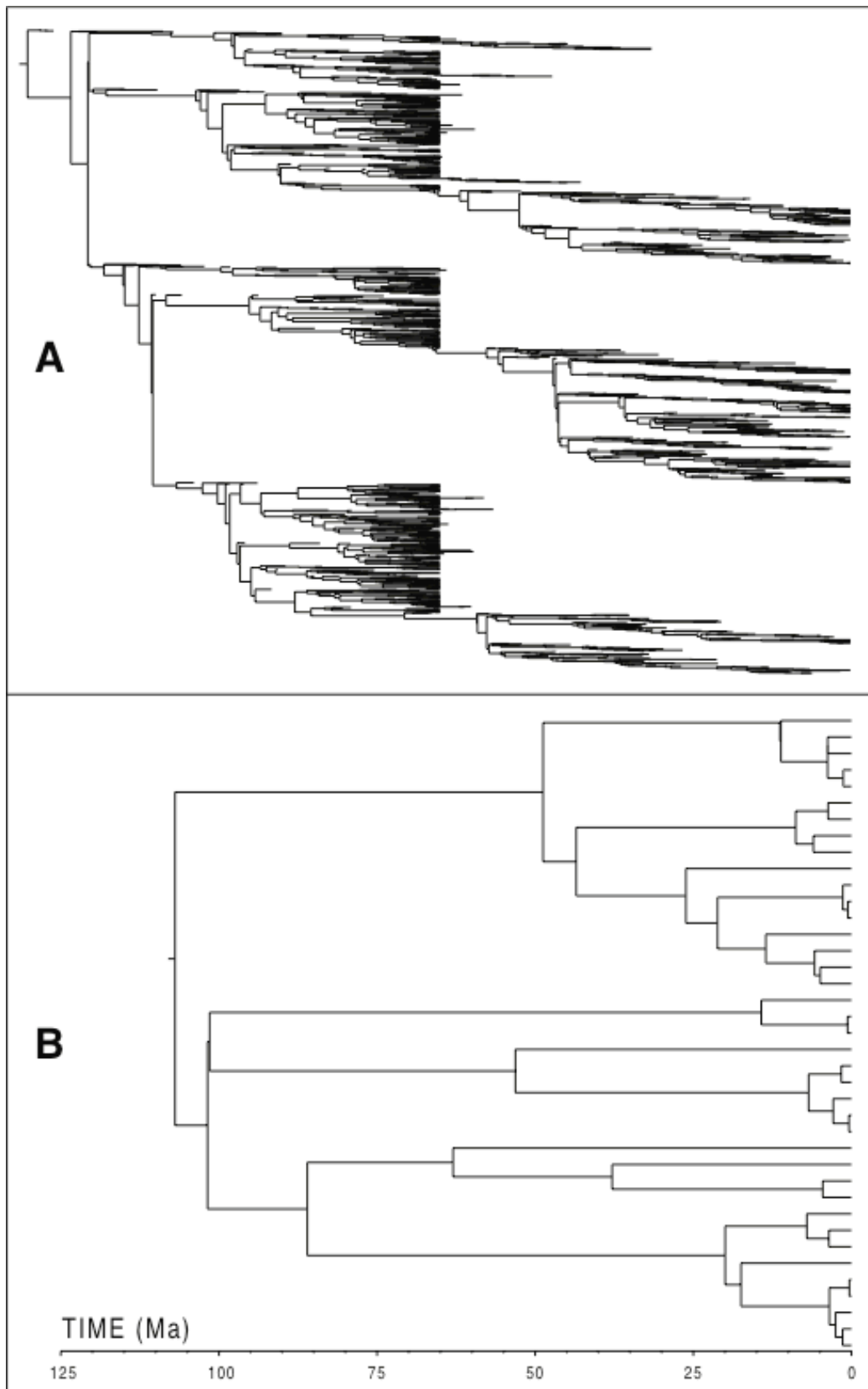


Appendix S7. 95% highest posterior densities of node ages obtained with BEAST.

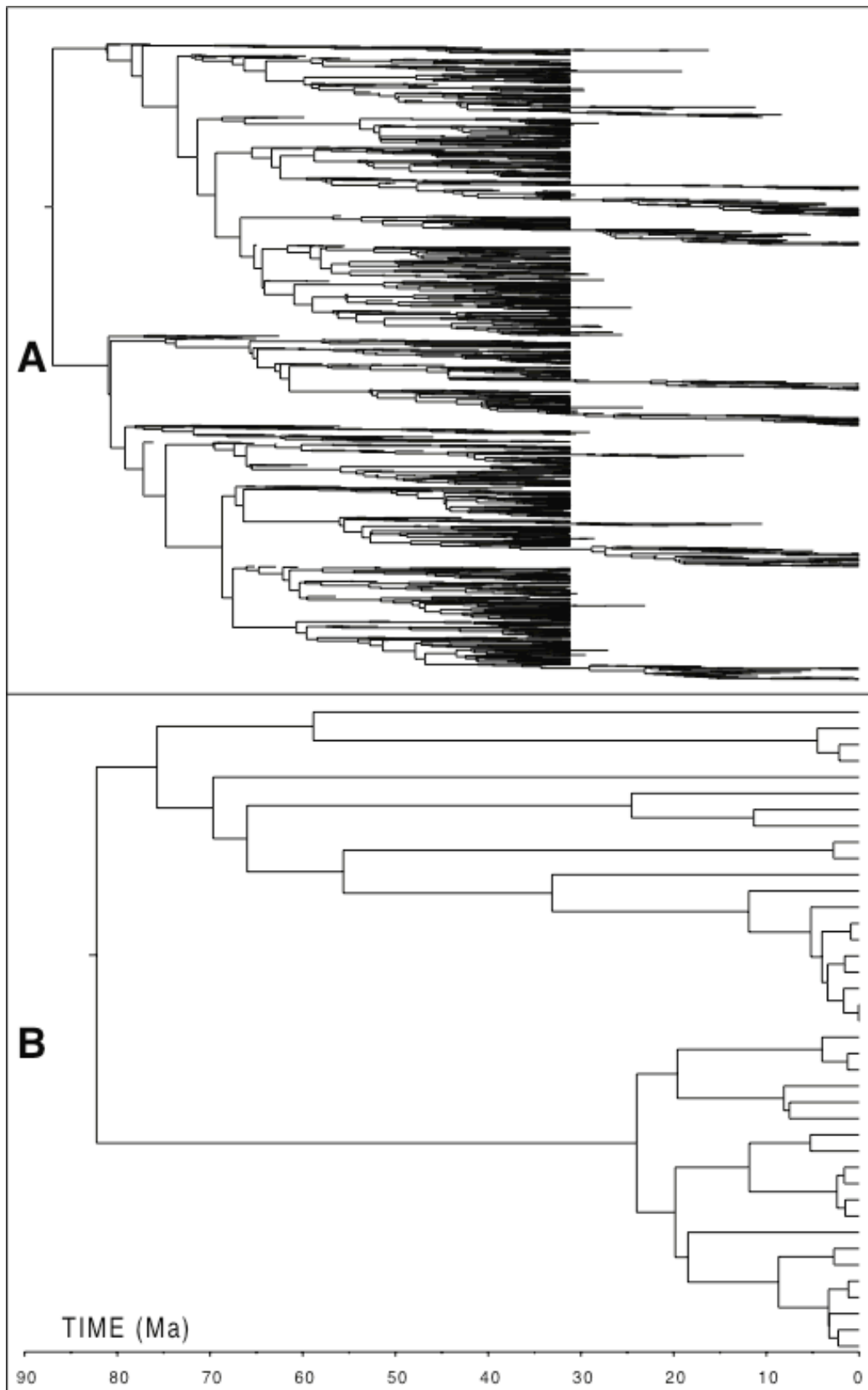


Appendix S8: Simulating a constant-rate birth-death model punctuated by a mass extinction event at 65 Ma. Average LTT plot of 100 phylogenies simulated under alternative mass extinction scenarios conditioning on 65 extant species of which 40 are sampled at the end of the last growth episode to mimic incomplete taxon sampling. Abbreviations: number of extant species sampled, n° simulations, (speciation rate birth-death episode after mass extinction), (speciation rate birth-death episode before mass extinction), (extinction rate before mass extinction, extinction rate after mass extinction), (fraction of species sampled at the end of last episode = incomplete taxon sampling, percentage of species surviving the mass extinction event), (0 = present time), time of mass extinction event = 65 Ma). Reconstructed phylogenies: only extant, sampled species are represented.

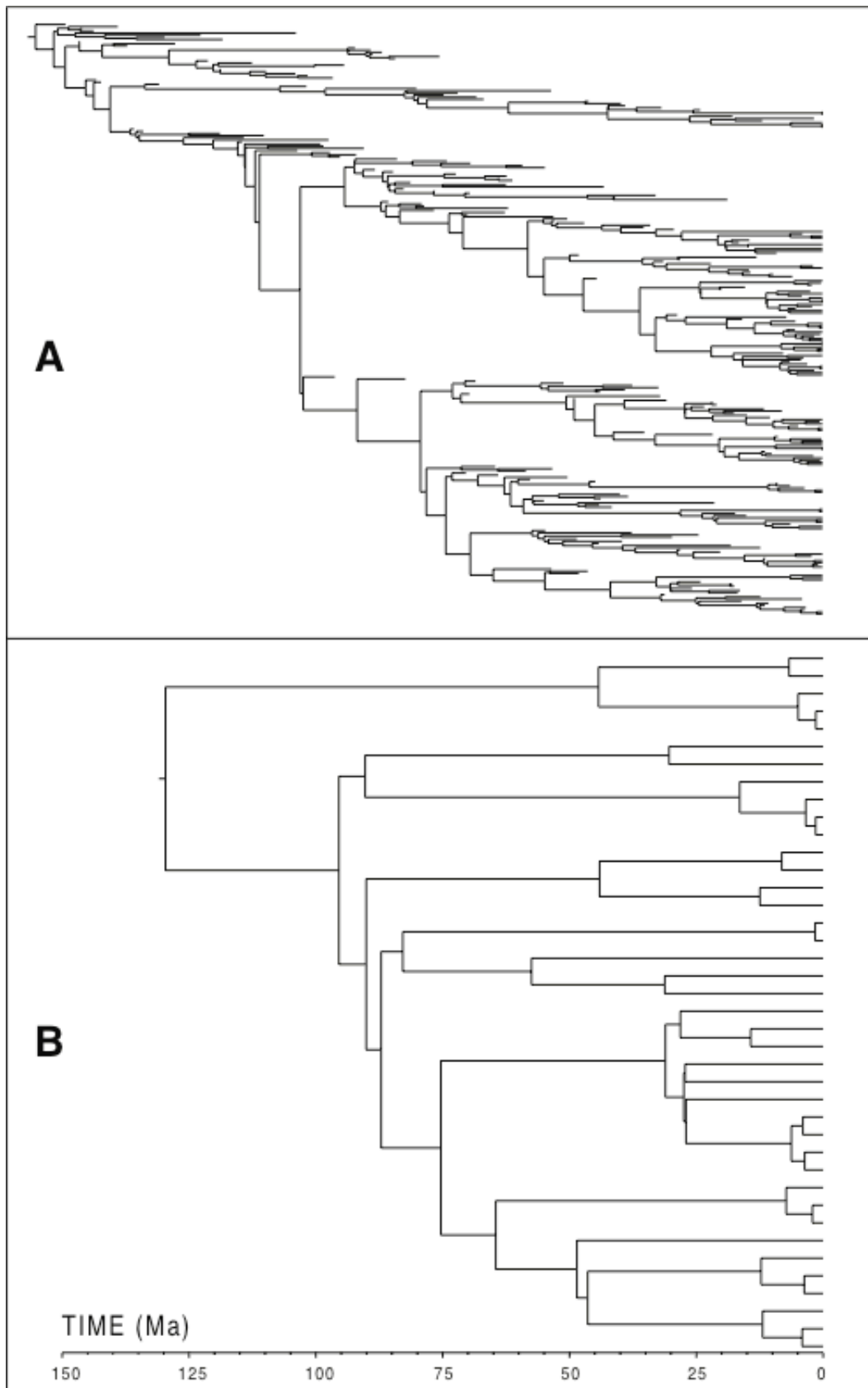
N1_40_100_[0.0822, 0.0822]_[0.0674, 0.0674]_[0.615, 0.05]_[0, 65].tre (black-longest line)
 N2_40_100_[0.2, 0.2]_[0.1, 0.1]_[0.615, 0.5]_[0, 65].tre (red)
 N3_40_100_[0.2, 0.2]_[0.19, 0.19]_[0.615, 0.5]_[0, 65].tre (green)
 N4_40_100_[0.4, 0.2]_[0.2, 0.19]_[0.615, 0.5]_[0, 65].tre" (black)
 N5_40_100_[0.2, 0.2]_[0.1, 0.1]_[0.615, 0.25]_[0, 65].tre (yellow)
 N6_40_100_[1, 0.2]_[0.5, 0.1]_[0.615, 0.25]_[0, 65].tre (purple)
 N8_40_100_[0.4, 0.2]_[0.2, 0.19]_[0.615, 0.25]_[0, 65].tre (orange)
 N9_40_100_[0.2, 0.4]_[0.2, 0.1]_[0.615, 0.25]_[0, 65].tre (pink)
 N10_40_100_[0.2, 0.5]_[0.2, 0.1]_[0.615, 0.25]_[0, 65].tre (grey)
 N11_40_100_[0.2, 0.5]_[0.1, 0.1]_[0.615, 0.25]_[0, 65].tre (turquoise)
 N12_40_100_[0.2, 0.5]_[0.19, 0.1]_[0.615, 0.25]_[0, 65].tre (tan)
 N13_40_100_[0.2, 1.0]_[0.19, 0.5]_[0.615, 0.25]_[0, 65].tre (darkgrey)
 N14_40_100_[0.2, 1.0]_[0.19, 0.2]_[0.615, 0.25]_[0, 65].tre (aquamarine)
 N15_40_100_[0.2, 0.5]_[0.19, 0.1]_[0.615, 0.05]_[0, 65].tre (darkolivegreen)
 N16_40_100_[0.2, 0.4]_[0.19, 0.1]_[0.615, 0.05]_[0, 65].tre (violetred)
 N17_40_100_[0.2, 0.3]_[0.19, 0.1]_[0.615, 0.05]_[0, 65].tre (brown)
 N18_40_100_[0.2, 0.3]_[0.1, 0.1]_[0.615, 0.05]_[0, 65].tre (lavender)
 N19_40_100_[0.2, 0.2]_[0.19, 0.1]_[0.615, 0.05]_[0.0, 65.0].tre (magenta)



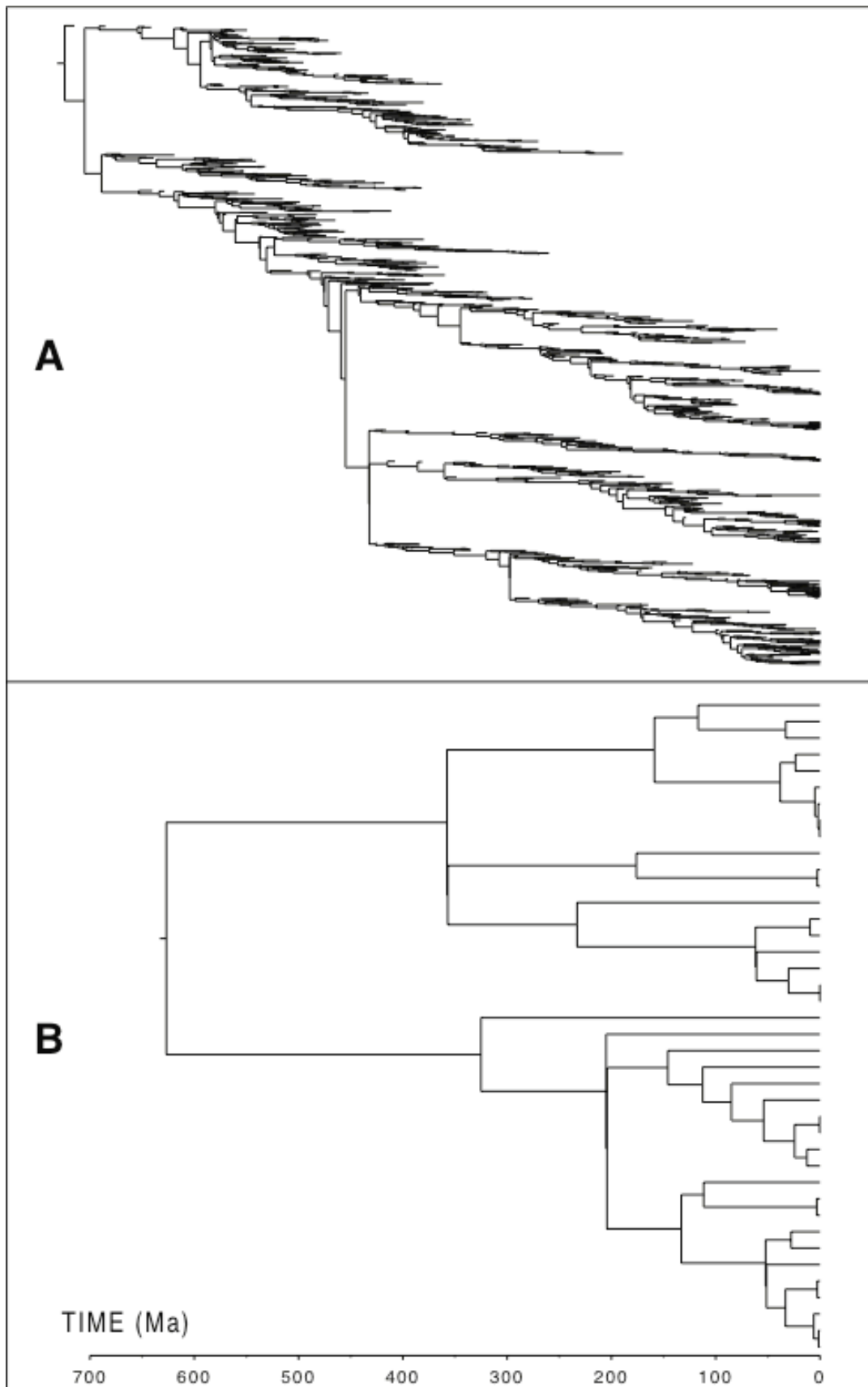
Appendix S9. **A)** Complete phylogeny including extinct and extant (sampled and non sampled) species and **B)** reconstructed phylogeny (including only extant and sampled species) simulated under a constant-rate birth-death model punctuated by a mass extinction event at 65 Ma that removes 95% of the lineages. Birth and death parameters before ($b = 0.2$, $d = 0.1$, $a=0.5$) and after ($b = 0.2$, $d = 0.19$, $a=0.95$) the mass extinction event.



Appendix S10. **A)** Complete phylogeny including extinct and extant (sampled and non sampled) species and **B)** reconstructed phylogeny (including only extant and sampled species) simulated under a constant-rate birth-death model punctuated by a mass extinction event at 35 Ma that removes 95% of the lineages. Birth and death parameters before ($b = 0.19$, $d = 0.1$, $a=0.5$) and after ($b = 0.2$, $d = 0.19$, $a=0.95$) the mass extinction event.



Appendix S11. : **A)** Complete phylogeny including extinct and extant (sampled and non sampled) species and **B)** reconstructed phylogeny (including only extant and sampled species) simulated using ML birth and death parameter values estimated in LASER ($b = 0.082$, $d = 0.067$, $a=0.78$).



Appendix S12. **A)** Complete phylogeny including extinct and extant (sampled and non sampled) species and **B)** reconstructed phylogeny (including only extant and sampled species) simulated using a high relative extinction rate ($a = 0.95$) with ML birth parameter value estimated in LASER under "purebirth" model ($b = 0.046$, $d = 0.044$, $a = 0.78$).

Online Table S1. Studied taxa, genbank accession numbers and voucher information. *Sequences produced in this study. Voucher and country information for species not sequenced here are listed when known.

TAXON	VOUCHER	COUNTRY	RBCL	ITS	RPS16
<u>Outgroup</u> <i>Ceratophyllum demersum</i> L			M77030	-	-
<u>Ingroup</u> <i>Ascarina</i> J. R. Forster & G. Forster					
<i>coursii</i> (Humbert & Capuron) J.-F. Leroy & Jérémie	D. Ravelonarivo 1139 (MO)	Madagascar	AY236844	-	-
<i>lucida</i> Hook. f.			AF238050	-	-
<i>polystachya</i> Foster	T. Feild s.n. (no voucher)	Tahiti	AY236842	-	-
Sp.	Qiu-M149		AF197592	-	-
<i>swamyana</i> A. C. Smith	T. Feild s.n. (no voucher)	Fiji	AY236843	-	-
<i>Chloranthus</i> Sw.					
<i>angustifolius</i> Oliver	KHZ 97701	China	AY236839	AF280416	-
<i>erectus</i> (Buch.-Ham.) Verdc.	KHZ 97602	China	AY236834	AF280410	-
<i>fortunei</i> (A. Gray) Solms-Laub.	KHZ 97403	China	AY236840	AF280419	-
<i>henryi</i> Hemsl.	KHZ 97124	China	AY236837	AF280415	-
<i>holostegius</i> (Hand.-Mazz.) P'ei & San			AF332097	AF280749	-
<i>japonicus</i> Sieb.	KHZ 96040	China	-	AF280418	-
<i>japonicus</i> Sieb.	Chase 204 (NCU)	Japan	L12640	-	-
<i>nervosus</i> Coll. et Hemsl.	KHZ 97603	China	AY236841	AF280417	-
<i>oldhamii</i> Solms.-Laub.	WJN 99001	China	AY236838	AF280414	-
<i>serratus</i> (Thunb.) Roem. et Schult.	KHZ 97402	China	AY236836	AF280412	-
<i>spicatus</i> (Thunb.) Makino	KHZ 97101	China	AY236835	AF280411	-

<i>Hedyosmum</i> Sw.						
<i>angustifolium</i> (Ruiz & Pavón) Solms-Laubach	Persson 715 (GB)	Peru	*EU302194	*EU302153	*EU302175	
<i>arborescens</i> Swartz	Chase 338 (NCU)	Puerto Rico	AY236750	*EU302146	*EU302168	
<i>bonplandianum</i> Humboldt	T. Feild 1025	Costa Rica	*EU302199	*EU302159	*EU302181	
<i>brasiliense</i> Miquel	Antonelli & Andersson 297 (GB)	Brazil	*EU302201	*EU302161	*EU302183	
<i>correanum</i> D'Arcy & Liesner	Hammel 3064 (AAU)	Panama	*EU302200	*EU302160	*EU302182	
<i>costaricense</i> Burger	T. Feild 1023	Costa Rica	*EU302188	*EU302147	*EU302169	
<i>cuatrecazanum</i> Occhioni	Gavilanes & Tivira 653-A (AAU)	Ecuador	*EU302190	*EU302149	*EU302171	
<i>cumbalense</i> Karsten	Harling 25488 (GB)	Ecuador	*EU302191	*EU302150	*EU302172	
<i>dombeyanum</i> Solms-Laubach	Steinbach 543 (S)	Bolivia	*EU302195	*EU302154	*EU302176	
<i>domingense</i> Urban	J. Richard Abbott 20902 (FLAS)	Dominican Republic	*EU302187	*EU302145	*EU302167	
<i>goudotianum</i> Solms-Laubach	McPherson 15898 (MO)	Panama	*EU302198	*EU302158	*EU302180	
<i>grisebachii</i> Solms-Laubach	J. Richard Abbott 19948 (FLAS)	Cuba	*EU314674	*EU302144	*EU302166	
<i>mexicanum</i> Cordemoy	Santamaría S-970 (GB)	Costa Rica	*EU302192	*EU302151	*EU302173	
<i>nutans</i> Swartz	Veloz et al. 2903 (JBSD)	Dominican Republic	*EU314673	*EU302143	-	
<i>orientale</i> Merril & Chun.	KHZ 97125 (PE)	China	-	*EU302142	*EU302165	
<i>orientale</i> Merril & Chun.	T. Feild & Li 23 (PE)	China	AY236848	-	-	
<i>parvifolium</i> Cordemoy	Todzia et al. 2432 (AAU)	Colombia	*EU302189	*EU302148	*EU302170	
<i>racemosum</i> (Ruiz & Pavón) G. Don	Asplund 13151 (S)	Peru		*EU302163		
<i>racemosum</i> (Ruiz & Pavón) G. Don	Andersson & Nilsson 2483 (GB)	Ecuador	*EU302203	-	*EU302185	
<i>scaberrimum</i> Standley	Santamaría S-1029 (GB)	Costa Rica	-	*EU302156	*EU302178	
<i>scabrum</i> (Ruiz & Pavón) Solms-Laubach	Andersson & Nilsson 2539 (GB)	Ecuador	*EU302193	*EU302152	*EU302174	
<i>spectabile</i> Todzia	Øllgaard & Madsen 90562 (GB)	Ecuador	*EU302204	*EU302164	*EU302186	
<i>sprucei</i> Solms-Laubach	Harling & Andersson 24138	Ecuador	*EU302202	*EU302162	*EU302184	

<i>strigosum</i> Todzia	(GB) Andersson & Nilsson 2412	Ecuador	*EU302197	*EU302157	*EU302179
<i>translucidum</i> Cuatrecasas	(GB) Harling & Andersson 21980	Ecuador	*EU302196	*EU302155	*EU302177
<i>Sarcandra</i> Gardn. <i>chloranthoides</i> Gardn.			AY236833	-	-
<i>grandifolia</i> (Miq.) Subramanyam & A.N.Henry			L12663	-	-

Online Table S2. List of primers used.

⁽¹⁾ Andersson and Antonelli (2005); ⁽²⁾ Antonelli (2008); ⁽³⁾ White *et al.* (1990)

Marker	Use (<u>A</u>mplification / <u>S</u>equencing)
<i>rbcL</i> ^{1,2}	A: <i>rbcL</i> 26f and <i>rbcL</i> t, or <i>rbcL</i> 26f and <i>rbcL</i> 1312r, or <i>rbcL</i> 30f and <i>rbcL</i> 1312r S: <i>rbcL</i> 26f, <i>rbcL</i> 358f, <i>rbcL</i> 361r, <i>rbcL</i> 667r, <i>rbcL</i> 799f, <i>rbcL</i> 1010r, <i>rbcL</i> 1117f, <i>rbcL</i> 1312r
<i>rps16</i> ¹	A: <i>rpsF</i> , <i>rpsR2</i> S: <i>rpsF</i> , <i>rpsR2</i>
ITS ^{1,3}	A: ITS 10, ITS 4 S: ITS 1, ITS 2, ITS 3, ITS 4 , ITS 5

Additional reference:

White, T. J., T. Bruns, S. Lee, and J. Taylor. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: a guide to methods and applications:315–322.