

Supplementary material

Table S1. Stem and crown node divergence time estimates for animal and plant clades with information regarding calibration, the gene(s)/genetic region(s) used to construct the phylogeny and the dating method. Values in millions of years are rounded to a single decimal place. Empty cells indicate that no age estimate was available. All taxa from *Costus* downwards are plants.

Taxa	Calibration	Genome: gene/genetic region	Dating method	Stem min. age (Ma)	Stem max. age (Ma)	Crown min. age (Ma)	Crown max. age (Ma)	Reference
<i>Bufo</i> (Bufonidae)	Rate borrowed (other taxa)	mtDNA: ND3	Genetic distance conversion	2.7	2.7			1
<i>Physalaemus</i> (Leptodactylidae)	Geological event (Ecuadorean Andes)	mtDNA: COI	MULTIDIVTIME	4.1	13.3	1.7	9.3	2
<i>Cordylochernes</i> (Chernetidae)	Rate borrowed (arthropods)	mtDNA: COI	Genetic distance conversion	5.1	6.7	2.7	3.4	3
<i>Myioborus</i> (Parulinae)	Rate borrowed (birds)	mtDNA: cyt b, ND2, ND3	Genetic distance conversion			3.6	3.9	4
<i>Phaeothlypis</i> (Parulidae)	Rate borrowed (birds)	mtDNA: ND2, COI, COII ATP6, ATP8, cyt b	Genetic distance conversion	3.0	3.8	3.0	3.8	5
<i>Pionopsitta</i> (Psittacidae)	Rate borrowed (birds)	mtDNA: cyt b, ND2	Lintree	4.4	4.9	3.6	4.2	6
<i>Pionopsitta</i> (Psittacidae)	Rate borrowed (birds)	mtDNA: ATP6, ATP8, COI, cyt b	Genetic distance conversion	3.5	3.5	2.0	2.0	7
<i>Lepidothrix</i> (Pirridae)	Rate borrowed (birds)	mtDNA: cyt b, ND2, ND3	Genetic distance conversion	1.3	3.3	1.1	2.9	8
<i>Lepidothrix</i> (Pirridae)	Rate borrowed (birds)	mtDNA: cyt b, ND2, ND3	Genetic distance conversion	2.3	2.3			8
<i>Veniliornis</i> (Picidae)	Rate borrowed (other taxa)	mtDNA: cyt b, COI	Genetic distance conversion	5.1	5.1	3.3	3.3	9
<i>Anthus</i> (Motacilidae)	Rate borrowed (birds)	mtDNA: cyt b	Genetic distance conversion	4.0	4.8	4.4	5.5	10
<i>Trogon</i> (Trogonidae)	Rate borrowed (birds)	mtDNA: ND2	Penalised Likelihood	2.3	3.9			11
<i>Trogon</i> (Trogonidae)	Rate borrowed (birds)	mtDNA: ND2	Penalised Likelihood	2.2	2.6			11
<i>Trogon</i> (Trogonidae)	Rate borrowed (birds)	mtDNA: ND2	Penalised Likelihood	4.2	5.4			11
<i>Trogon</i> (Trogonidae)	Rate borrowed (birds)	mtDNA: ND2	Penalised Likelihood	1.3	2.2			11
<i>Trogon</i> (Trogonidae)	Rate borrowed (birds)	mtDNA: ND2	Penalised Likelihood	2.9	4.0			11
<i>Rhamdia</i> (Pimelodidae)	Rate borrowed (fish)	mtDNA: cyt b, ATP6, ATP8	Genetic distance Conversion	6.5	10.3	6.0	6.0	12

<i>Synbranchus</i> (Synbranchidae)	Rate borrowed (fish)	mtDNA: cyt b, ATP6, ATP8	Genetic distance conversion	7.7	12.4			13
<i>Stator</i> (Bruchidae)	Rate borrowed (arthropods)	mtDNA: COI	Genetic distance conversion	4.4	4.4			14
<i>Heliconius</i> (Nymphalidae)	Rate borrowed (arthropods)	mtDNA: cytochrome oxidase	Genetic distance conversion	1.5	1.5			15
<i>Alouatta</i> (Cebidae)	Rate borrowed (primates)	mtDNA: ATP6, ATP8 cyt b nrDNA: CAL, exon 3 & 4, RAG1	Lintree	6.6	6.8	3.0	3.0	16
<i>Ateles</i> (Cebidae)		mtDNA: HVI (CR), COI nrDNA: intron 5	Local molecular clock	2.0	2.0	1.3	1.3	17
<i>Balantiopteryx</i> (Emballonuridae)	Rate borrowed (other taxa)	mtDNA: ND3, ND4, ND4L	Genetic distance conversion	5.4	5.4			18
<i>Balantiopteryx</i> (Emballonuridae)	Rate borrowed (other taxa)	mtDNA: ND3, ND4, ND4L	Genetic distance conversion	10.6	10.6			18
<i>Myotis</i> (Vespertilionidae)	Rate borrowed (other taxa)	mtDNA: cyt b, ND1	Lintree	4.0	4.0	3.0	3.0	19
<i>Myotis</i> (Vespertilionidae)	Rate borrowed (other taxa)	mtDNA: cyt b, ND1	Lintree	4.0	4.0	2.8	3.0	19
<i>Saimiri</i> (Cebidae)	Fossils	mtDNA: cyt b, d-loop (CR) nrDNA: IRBP, ZFX	Lintree	3.0	4.7			20
Cervidae	Fossils	mtDNA: cyt b, CO2 nrDNA: intron 1 and 2	MULTIDIVTIME	4.2	5.7	3.4	4.9	21
<i>Leopardus</i> (Felidae)	Rate borrowed (felines)	mtDNA: 16S, ATP8, ND5	Genetic distance conversion	3.7	3.7	2.0	5.0	22
<i>Noctilio</i> (Noctilionidae)	Rate borrowed (other taxa)	mtDNA: cyt b, RAG2	Genetic distance conversion	0.3	0.7			23
Sigmodontinae (Cricetidae)	Fossils	mtDNA: cyt b	UPGMA Molecular clock	12.1	16.3	10.0	14.0	24
<i>Sciurus</i> (Sciuridae)	Fossils	mtDNA: 12S and 16S rDNA nrDNA: IRBP	Genetic distance conversion	3.1	3.4			25
<i>Crotalus</i> (Viperidae)	Fossils	mtDNA: cyt b, ND2, ND4	Penalised Likelihood	1.5	2.3	1.2	2.0	26
<i>Lachesis</i> (Viperidae)	Rate borrowed (reptiles)	mtDNA: cyt b, ND4	Genetic distance conversion	6.4	17.9	4	11	27
<i>Costus</i> (Costaceae)	Rate borrowed (herbaceous taxa)	nrDNA: ITS, ETS	Genetic distance conversion	1.5	7.1	1.1	5.4	28
<i>Costus</i> Costaceae	Rate borrowed (herbaceous taxa)	nrDNA: ITS, ETS	Genetic distance conversion	1.1	5.4			28
<i>Halenia</i> (Gentianaceae)	Rate borrowed (other taxa)	cpDNA: <i>ndhF</i> nrDNA: ITS	Genetic distance conversion	1.0	1.0			29
<i>Halenia</i> (Gentianaceae)	Rate borrowed (other taxa)	cpDNA: <i>ndhF</i> nrDNA: ITS	Genetic distance conversion	0.8	0.8			29
<i>Lupinus</i> (Leguminosae)	Fossils	nrDNA: ITS, CYCLOIDEA	Penalised Likelihood			1.5	1.9	30
Chamaedoreae (Areaceae)	Fossils	cpDNA: <i>trnL-F</i> , <i>matK</i> , <i>ndhF</i> , <i>trnD-T</i> , <i>rps16</i> intron nrDNA: PRK, RPB2	Penalised Likelihood	32.5	49.6	11.7	23.7	31

Arecaceae	Fossils	cpDNA: <i>trnL-F</i> , <i>matK</i> , <i>ndhE</i> , <i>trnD-T</i> , <i>rps16</i> intron nrDNA: PRK, RPB2	Penalised Likelihood	13.0	28.0	12.0	26.0	31
Protieae (Burseraceae)	Fossils	nrDNA: ETS	Penalised Likelihood	21.9	40.1			32
Valerianaceae	Fossils	cpDNA: <i>psbA-trnH</i> , <i>trnK-matK</i> , <i>trnL-F</i> nrDNA: ITS	Penalised Likelihood	22.4	26.4	21.1	26.4	33
<i>Ruprechtia</i> (Polygonaceae)	Fossils	nrDNA: ITS	Penalised Likelihood	3.6	4.6	1.0	1.4	34
<i>Nissolia</i> (Leguminosae)	Fossil	nrDNA: ITS	Penalised Likelihood	6.6	9.2	1.2	2.0	34
<i>Platymiscium</i> (Leguminosae)	Fossil	nrDNA: ITS cpDNA: <i>trnL-F</i> , <i>matK</i>	MULTIDIVTIME	7.1	7.1	5.9	5.9	35
<i>Platymiscium</i> (Leguminosae)	Fossils	nrDNA: ITS cpDNA: <i>trnL-F</i> , <i>matK</i>	MULTIDIVTIME	4.2	4.2	2.5	2.5	35
<i>Platymiscium</i> (Leguminosae)	Fossils	nrDNA: ITS cpDNA: <i>trnL-F</i> , <i>matK</i>	MULTIDIVTIME	6.9	6.9	3.9	3.9	35
<i>Symphonia</i> (Clusiaceae)	Fossils	nrDNA: ITS	Penalised Likelihood	15	15	5.0	5.0	36
<i>Guatteria</i> (Annonaceae)	Fossils	cpDNA: <i>matK</i> , <i>rbcL</i> , <i>trnL-F</i> , <i>psbA-trnH</i> , <i>trnT-L</i>	Penalised Likelihood	6.1	7.4	6.1	7.4	37
<i>Guatteria</i> (Annonaceae)	Fossils	cpDNA: <i>matK</i> , <i>rbcL</i> , <i>trnL-F</i> , <i>psbA-trnH</i> , <i>trnT-L</i>	Penalised Likelihood	1.0	2.2			37
<i>Guatteria</i> (Annonaceae)	Fossils	cpDNA: <i>matK</i> , <i>rbcL</i> , <i>trnL-F</i> , <i>psbA-trnH</i> , <i>trnT-L</i>	Penalised Likelihood	2.2	4.4			37
<i>Ocotea</i> (Lauraceae)	Fossils	nrDNA: ITS	Molecular clock	15.0	25.0	15.0	15.0	38
Melastomataceae	Fossils	cpDNA: <i>ndhF</i> , <i>rp116</i>	GTR+ Γ genetic distance	23.0	26.0	22.0	24.0	39
<i>Cynanchum</i> (Apocynaceae)	Fossils	cpDNA: <i>trnL-F</i>	NPRS	20.0	20.0	18.6	18.6	40
<i>Asclepias</i> (Apocynaceae)	Fossils	cpDNA: <i>trnL-F</i>	NPRS	7.5	7.5			40
<i>Ribes</i> (Grossulariaceae)	Fossils	nrDNA: ITS	NPRS	21.1	21.1	12.3	12.3	Hechenleitner unpubl.
<i>Picrasma</i> (Simaroubaceae)	Fossils	cpDNA: <i>rbcL</i> , <i>atpB</i> , <i>matK</i> , partial <i>trnK</i> intron, <i>phyC</i>	BEAST	23.0	23.0			Clayton unpubl.
<i>Cedrela</i> (Meliaceae)	Fossils	nrDNA: ITS1-5.8S- ITS2 cpDNA: <i>psbB</i> , <i>psbN</i> , <i>psbT</i> , <i>trnS-trnG</i>	BEAST	32.0	36.0	16.0	29.0	Muellner unpubl.
<i>Cedrela</i> (Meliaceae)	Fossils	nrDNA: ITS1-5.8S- ITS2 cpDNA: <i>psbB</i> , <i>psbN</i> , <i>psbT</i> , <i>trnS-trnG</i>	BEAST	6.0	22.0	1.0	7.0	Muellner unpubl.

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