Supplement 1.1–1.5

Phylogenetic biogeography of Hamamelidaceae s. l. based on molecular data.

Alexey V. Bobrov, Maxim S. Roslov, Mikhail S. Romanov

Supplement 1.1 Species and GenBank accession numbers (Source: GenBank, 2019).

Species	*ITS–5.8S rRNA*	*matK*	*rbcL*	*trnL–trnF*	*psaA–ycf3*	*psbA–trnH*
Itea chinensis Hook. & Arn.	KP092690.1	KC737245.1	KC737397.1	MH191391.1	MH191391.1	KP095319.1
Paeonia brownii Douglas ex Hook.	U27674.1	AF033588.1	AF274592.1	MH191385.1	MH191385.1	MH191385.1
Paeonia lactiflora Pall.	U27682.1	AF033597.1	KT944713.1	MG897127.1	MG897127.1	KU525672.1
Cercidiphyllum japonicum Siebold & Zucc. ex J.J.Hoffm. & J.H.Schult.bis	HQ652479.1	KC737246.1	JN541237.1	AM397171.1	AF377996.1	AB445234.1
Daphniphyllum oldhamii (Hemsl.) K.Rosenthal	KP093233.1	KC737244.1	KC737396.1	MH191390.1	MH191390.1	KP095969.1
Altingia chinensis (Champ.) Oliv. ex Hance	AF133232.1	AF133225.1	DQ352376.1	DQ352202.1	AF304542.1	KP095964.1
Altingia excelsa Noronha	AF304525.1	AF304520.1	DQ352374.1	DQ352225.1	AF304533.1	EU595859.1
Altingia gracilipes Hemsl.	AF133233.1	AF133223.1	DQ352379.1	DQ352205.1	AF304535.1	–
Altingia obovata Merr. & Chun	AF133234.1	AF133224.1	DQ352377.1	DQ352204.1	AF304540.1	EU595862.1

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Species	*ITS–5.8S rRNA*	*matK*	*rbcL*	*trnL–trnF*	*psaA–ycf3*	*psbA–trnH*
Altingia yunnanensis Rehder & E.H.Wilson	GU576644.1	GU576679.1	DQ352378.1	DQ352211.1	DQ352242.1	GU576748.1
Liquidambar acalycina H.T.Chang	AF133231.1	AF015649.1	DQ352380.1	DQ352215.1	DQ352246.1	GU576771.1
Liquidambar formosana Hance	AF133230.1	AF015650.1	DQ352384.1	DQ352220.1	AF304539.1	KP095966.1
Liquidambar macrophylla Oerst.	–	–	DQ352382.1	DQ352218.1	DQ352249.1	–
Liquidambar orientalis Mill.	AF133229.1	AF015651.1	DQ352383.1	DQ352222.1	DQ352253.1	EF138729.1
Liquidambar styraciflua L.	AF133227.1	AF015652.1	AF119181.1	DQ352217.1	AF304531.1	GU576773.1
Semiliquidambar cathayensis H.T.Chang	AF133235.1	AF133226.1	KX527048.1	DQ352199.1	AF304536.1	–
Chunia bucklandioides H.T.Chang	AF162211.1	AF108466.1	MG644608.1	EF456729.1	MG644608.1	MG644608.1
Corylopsis coreana Uyeki	AY726625.1	MG835449.1	MG835449.1	MG835449.1	MG835449.1	MG835449.1
Corylopsis glabrescens Franch. & Sav.	AF127516.1	AB236993.1	AB237027.1	GU576816.1	GU576715.1	GU576749.1
Corylopsis pauciflora Siebold & Zucc.	AB299314.1	AB236994.1	AB237030.1	AF147465.1	DQ352363.1	AB237077.1
Dicoryphe stipulacea J.St.-Hil.	GU576646.1	AF013040.1	–	AF147466.1	–	GU576750.1
Disanthus cercidifolius Maxim.	AF127507.1	AF128826.1	AF081069.1	AF147467.1	GU576716.1	GU576751.1
Distyliopsis dunnii (Hemsl.) P.K.Endress	KP093236.1	KP093939.1	–	–	–	KP095976.1
Distyliopsis tutcheri (Hemsl.) P.K.Endress	AH005557.2	AF013042.1	–	AF147470.1	–	–
Distylium myricoides Hemsl.	AF074249.1	GU576683.1	AM183408.1	AF147468.1	GU576717.1	–
Distylium racemosum Siebold & Zucc.	GU576648.1	AF013041.1	AF061998.1	AF147469.1	–	KP095971.1

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Species	*ITS–5.8S rRNA*	*matK*	*rbcL*	*trnL–trnF*	*psaA–ycf3*	*psbA–trnH*
Eustigma balansae Oliv.	KP093235.1	HQ415379.1	–	–	–	KP095972.1
Eustigma oblongifolium Gardner & Champ.	AF127518.1	AF013043.1	–	AF147471.1	–	KJ686840.1
Exbucklandia populnea (R.Br. ex Griff.) R.W.Br.	GU576649.1	AF128831.1	AF081071.1	AF147472.1	GU576718.1	GU576752.1
Exbucklandia tonkinensis (Lecomte) H.T.Chang	GU576650.1	AF128832.1	DQ352372.1	DQ352198.1	GU576719.1	GU576753.1
Fortunearia sinensis Rehder & E.H.Wilson	AF127515.1	AF013044.1	AF081068.1	AF147473.1	MK533616.1	MK533616.1
Fothergilla gardenii Murray	GU576651.1	KT438384.1	–	KT438462.1	GU576720.1	GU576754.1
Fothergilla major G.Lodd.	AF074250.2	AF013045.1	AM183407.1	AF147474.1	–	–
Hamamelis japonica Siebold & Zucc.	GU576652.1	AF248617.1	AY263940.1	GU576826.1	AF304543.1	GU576758.1
Hamamelis mexicana Standl.	GU576656.1	AF248618.1	–	GU576827.1	GU576725.1	GU576759.1
Hamamelis mollis Oliv. ex F.B.Forbes & Hemsl.	GU576657.1	KC737241.1	KC737393.1	DQ352357.1	DQ352362.1	GU576762.1
Hamamelis ovalis S.W.Leonard	GU576660.1	GU576695.1	–	GU576831.1	GU576729.1	GU576763.1
Hamamelis vernalis Sarg.	GU576661.1	AF013047.1	–	GU576832.1	GU576734.1	GU576768.1
Hamamelis virginiana L.	GU576666.1	AF013046.1	DQ352368.1	DQ352196.1	DQ352227.1	GU576770.1
Loropetalum chinense (R. Br.) Oliv.	GU576672.1	AF013059.1	DQ352370.1	AF147476.1	DQ352364.1	KP095974.1

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Species	*ITS–5.8S rRNA*	*matK*	*rbcL*	*trnL–trnF*	*psaA–ycf3*	*psbA–trnH*
Loropetalum subcordatum (Benth.) Oliv.	AF022242.1	MG457805.1	DQ352371.1	AF147489.1	DQ352365.1	HM369154.1
Maingaya malayana Oliv.	AF022241.1	AF025393.1	AM183403.1	AF147477.1	–	–
Matudaea trinervia Lundell	AF015437.1	AF013048.1	AM183409.1	AF147478.1	–	KJ002052.1
Molinadendron guatemalense (Radlk. ex Harms) P.K.Endress	AF015438.1	AF013049.1	–	AF147479.1	–	–
Mytilaria laosensis Lecomte	AF127501.1	AF128828.1	AF081070.1	EF456731.1	AF304544.1	–
Neostrearia fleckeri L.S.Sm.	AF015439.1	AF013050.1	–	AF147480.1	–	–
Noahdendron nicholasii P.K.Endress, B.Hyland & Tracey	AF015440.1	AF013051.1	–	AF147481.1	–	–
Ostrearia australiana Baill.	AF015441.1	AF013052.1	AM183404.1	AF147482.1	–	–
Parrotia persica (DC.) C.A.Mey.	AF015443.1	AF013053.1	AM183411.1	AF147483.1	–	MF348740.1
Parrotia subaequalis (Hung T.Chang) R.M.Hao & H.T.Wei	GU576674.1	AF013055.1	MG252374.1	AF147486.1	GU576743.1	GU576776.1
Parrotiopsis jacquemontiana (Decne.) Rehder	AF015442.1	AF013054.1	–	AF147484.1	–	–
Rhodoleia championii Hook. f.	GU576675.1	AF128833.1	AF062002.1	AF147485.1	GU576744.1	GU576777.1
Rhodoleia henryi K.Y.Tong	GU576676.1	GU576711.1	AF081072.1	GU576847.1	GU576745.1	GU576778.1
Sinowilsonia henryi Hemsl.	AF127512.1	AF013056.1	AM183406.1	AF147487.1	MF687003.1	NC036069.1

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Species	*ITS–5.8S rRNA*	*matK*	*rbcL*	*trnL–trnF*	*psaA–ycf3*	*psbA–trnH*
Sycopsis sinensis Oliv.	AF127517.1	AF013057.1	–	AF147488.1	GU576746.1	GU576779.1
Trichocladus crinitus Pers.	AF147755.1	AF013058.1	AF060711.1	AF147490.1	GU576747.1	GU576780.1

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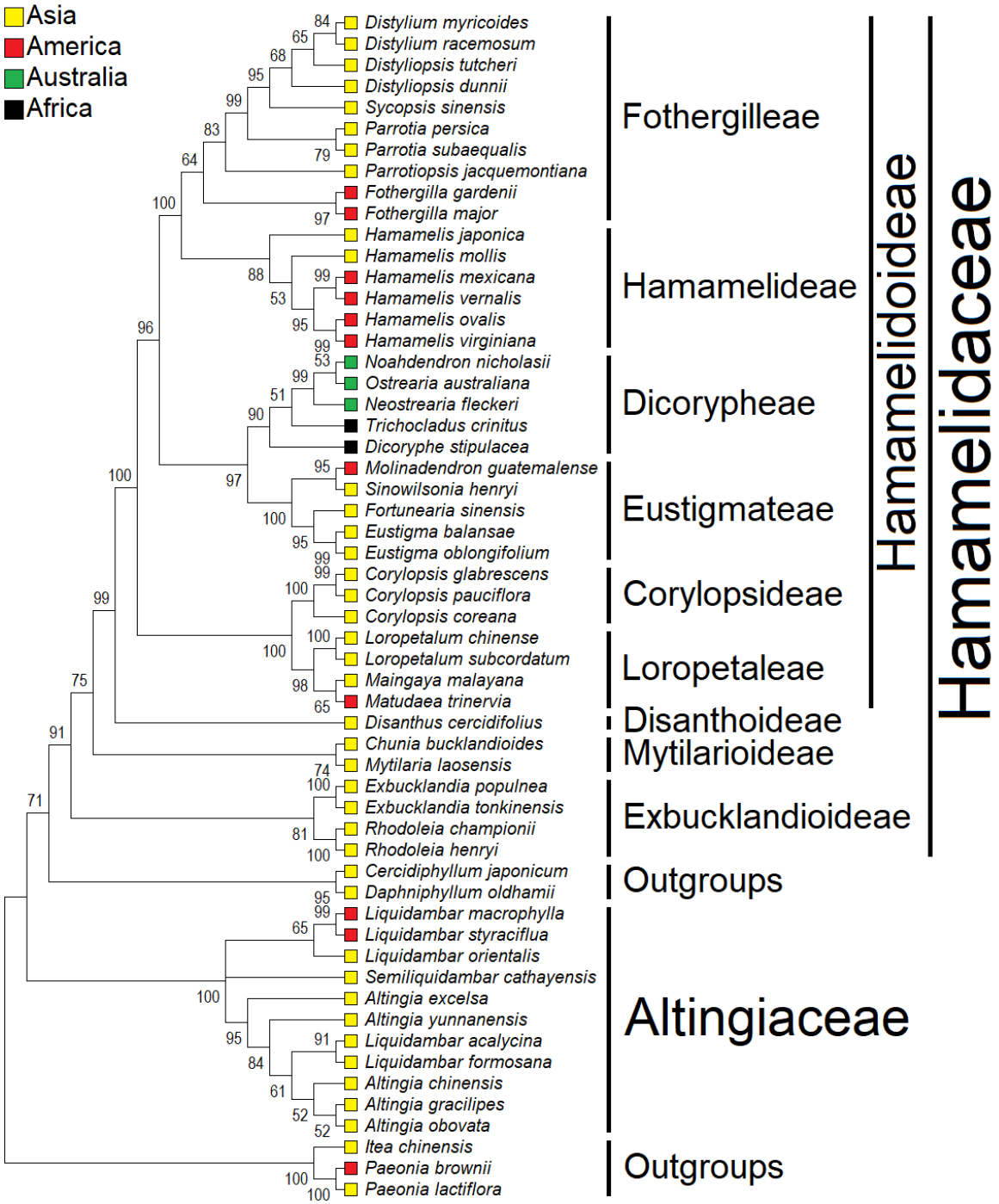
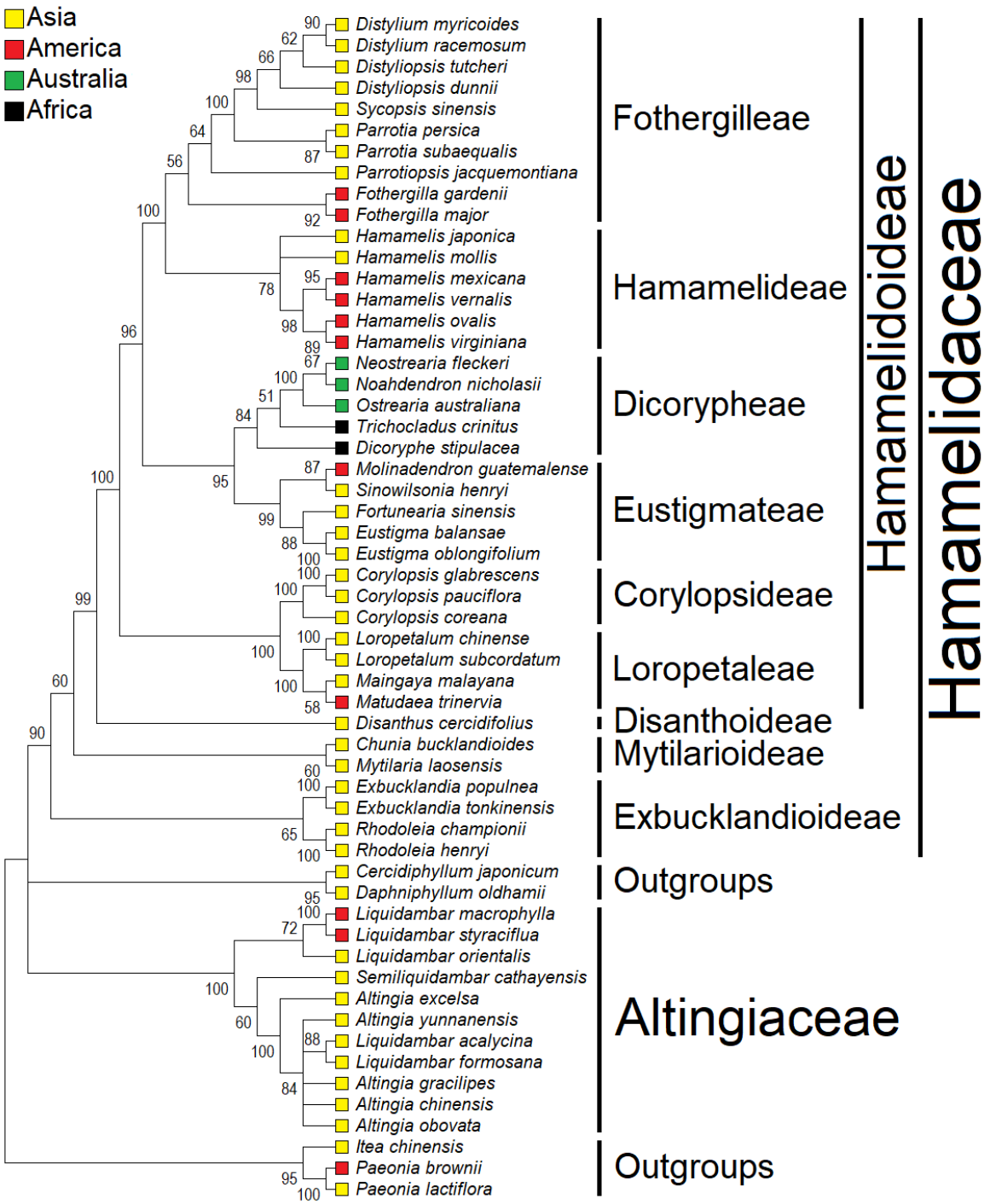
Supplement 1.2 Phylogeny of Hamamelidaceae s. l. based on maximum parsimony analysis in MEGA X software. Numbers at nodes are the maximum parsimony bootstraps. Branches corresponding to partitions reproduced in less than 50 % bootstrap replicates are collapsed. Average bootstrap is 85,8 %.



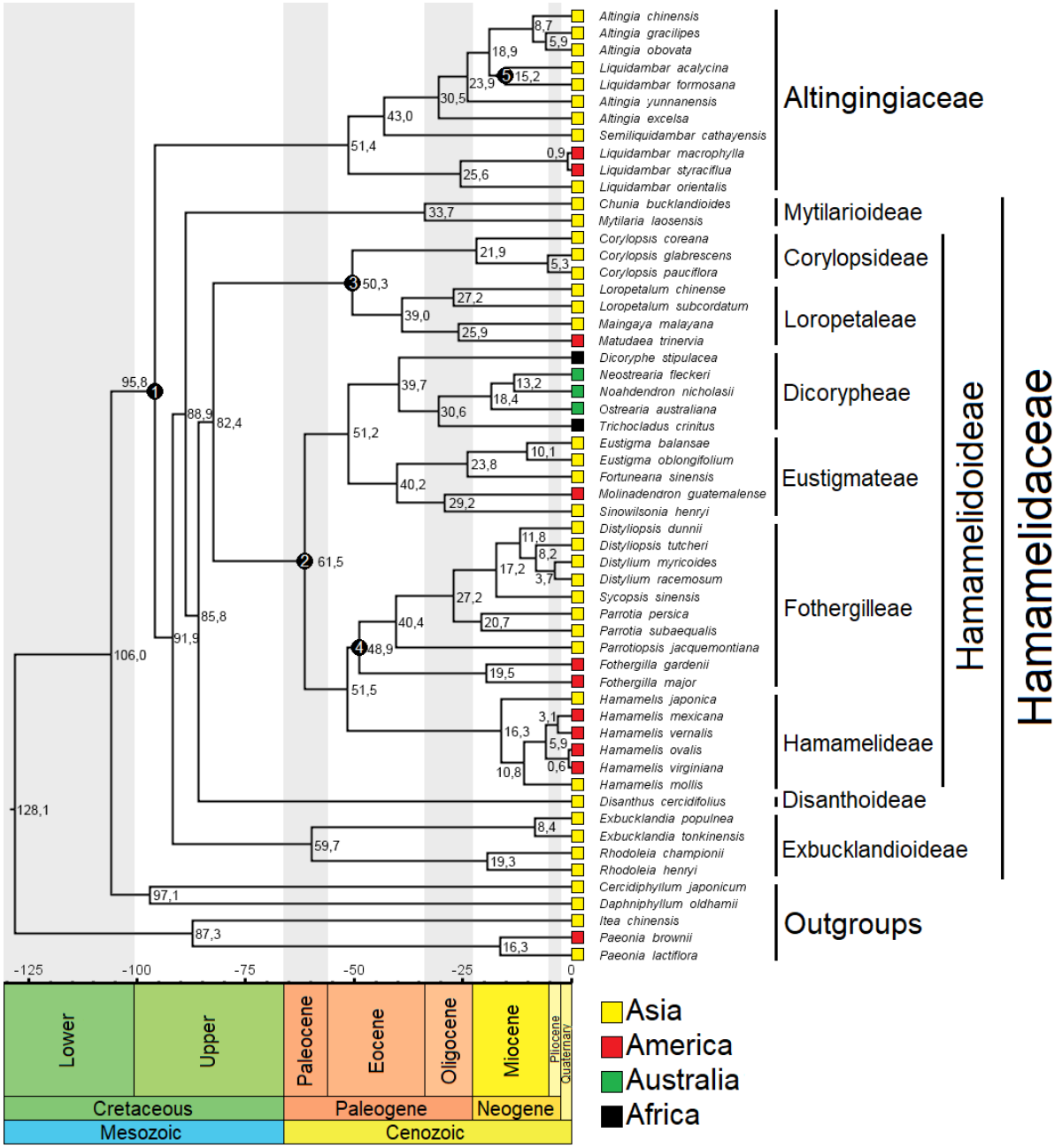
https://doi.org/10.21638/spbu07.2020.201

Supplement 1.3. Phylogeny of Hamamelidaceae s. l. based on maximum likelihood analysis in MEGA X software. Numbers at nodes are the maximum likelihood bootstraps. Branches corresponding to partitions reproduced in less than 50 % bootstrap replicates are collapsed. Average bootstrap is 83,1 %.



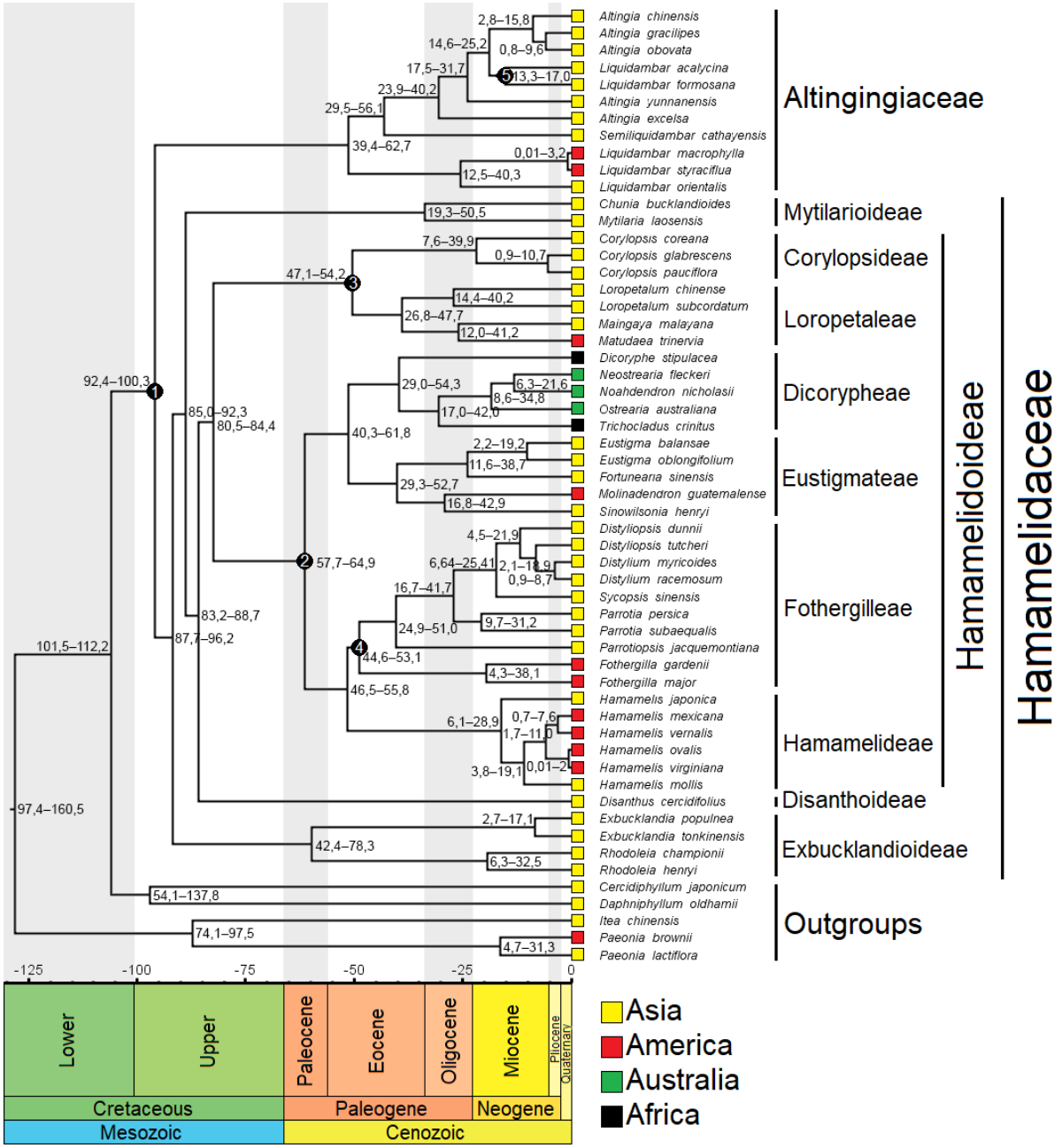
https://doi.org/10.21638/spbu07.2020.201

Supplement 1.4 Chronogram of Hamamelidaceae s. l. based on bayesian probability in BEAST v2.5.2 software. Numbers at nodes are average divergence times. Average posterior probability is 0,986. Numbers in black circles indicate calibration points used in the estimation of divergence times.



https://doi.org/10.21638/spbu07.2020.201

Supplement 1.5 Chronogram of Hamamelidaceae s. l. based on bayesian probability in BEAST v2.5.2 software. Numbers at nodes indicate 95% highest probability density credibility intervals. Average posterior probability is 0,986. Numbers in black circles indicate calibration points used in the estimation of divergence times.



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