

Supplementary data - Phylogenetic and evolutionary reconstruction of the rainforest lineage *Fontainea* Heckel (Euphorbiaceae) based on chloroplast DNA sequences and reduced-representation SNP markers.

Table S1. Accession details of seven *Fontainea* taxa with indication of markers assignments and sampling locations (accession numbers in brackets represent DArTseq labels of *F. oraria*).

Accession number	Species	cpDNA	DArT seq	Location Name	GPS Location*
FA002	<i>F. australis</i>	x	x	Tyalgum, NSW, Australia	-28.3196, 153.1582
FA007, FA018, FA023,	<i>F. australis</i>	x	x	Crystal Creek, NSW, Australia	-28.2735, 153.2584
FA033, FA041, FA049, FA066	<i>F. australis</i>	x	x	Curumbin Valley, QLD, Australia	-28.2401, 153.3594
FA069	<i>F. australis</i>	x	x	Mooball, NSW, Australia	-28.4360, 153.4943
FO001 (418), FO002 (420), FO003 (421), FO004 (422), FO005 (325), FO006 (401), FO007 (402), FO008 (403), , FO009 (404)	<i>F. oraria</i>	x	x	Lennox Heads, NSW, Australia	-28.8076, 153.6047
FF011, FF018, FF023, FF035, FF037, FF042	<i>F. fugax</i>	x	x	Gurgeena SF, QLD, Australia	-25.4817, 151.411
FR013	<i>F. rostrata</i>		x	Goomboorian NP, QLD, Australia	-26.1453, 152.7993
FR045	<i>F. rostrata</i>	x		Ormes Rd, QLD, Australia	-26.1167, 152.8148
FR050	<i>F. rostrata</i>	x		Laurel Rd, QLD, Australia	-26.1333, 152.7000
FR068, FR071	<i>F. rostrata</i>	x	x	Gympie NP, QLD, Australia	-26.0908, 152.7200
FR075	<i>F. rostrata</i>	x	x	Ormes Rd, QLD, Australia	-26.1167, 152.8148
FR080	<i>F. rostrata</i>		x	Ormes Rd, QLD, Australia	-26.1167, 152.8148
FR140	<i>F. rostrata</i>	x		Rossmount, QLD, Australia	-26.100, 152.7333
FR149	<i>F. rostrata</i>		x	Pullers, QLD Australia	-25.7896, 152.6869
FR153	<i>F. rostrata</i>	x	x	Pullers, QLD, Australia	-25.7896, 152.6869
FR160	<i>F. rostrata</i>	x	x	Tahiti Rd, QLD, Australia	-25.7114, 152.6567
FR170	<i>F. rostrata</i>	x	x	Pullers, QLD, Australia	-25.7896, 152.6869
FPiA03	<i>F. picrosperma</i>	x		Evelyn Highlands, Atherton Tablelands, Qld	-17.4989, 145.4731
FPiC02	<i>F. picrosperma</i>	x		East Barron, Atherton Tablelands, Qld	-17.1667, 145.6167
FPiD03	<i>F. picrosperma</i>	x		Malanda, Atherton Tablelands, Qld	-17.3575, 145.5878
FPiD023	<i>F. picrosperma</i>		x	Malanda, Atherton Tablelands, Qld	-17.3575, 145.5878
FPiE04	<i>F. picrosperma</i>	x		Topaz, Atherton Tablelands, Qld	-17.4697, 145.7226
FPiF10	<i>F. picrosperma</i>	x		Gadgarra, Atherton Tablelands, Qld	-17.2833, 145.7000
FPiG124	<i>F. picrosperma</i>	x		Boonjie, Atherton Tablelands, Qld	-17.3333, 145.6667

FPIJ010	<i>F. picrosperma</i>		x	Evelyn Highlands, Atherton Tablelands, Qld	-17.4989, 145.4731
FPIJ091	<i>F. picrosperma</i>	x	x	Evelyn Highlands, Atherton Tablelands, Qld	-17.4989, 145.4731
FPIJ096	<i>F. picrosperma</i>		x	Evelyn Highlands, Atherton Tablelands, Qld	-17.4989, 145.4731
FPIJ401	<i>F. picrosperma</i>		x	Evelyn Highlands, Atherton Tablelands, Qld	-17.4989, 145.4731
FPILO24	<i>F. picrosperma</i>	x	x	Evelyn Highlands, Atherton Tablelands, Qld	-17.4989, 145.4731
FPIPO79	<i>F. picrosperma</i>	x		Evelyn Highlands, Atherton Tablelands, Qld	-17.4989, 145.4731
FPIE025	<i>F. picrosperma</i>		x	Topaz, Atherton Tablelands, Qld	-17.4697, 145.7226
FPIB014	<i>F. picrosperma</i>		x	Boonjie, Atherton Tablelands, Qld	-17.3333, 145.6667
FPIA314	<i>F. picrosperma</i>		x	Evelyn Highlands, Atherton Tablelands, Qld	-17.4989, 145.4731
FV015, FV017, FV019, FV037, FV039	<i>F. venosa</i>	x	x	Marys Creek SF, QLD, Australia	-26.2498, 152.5583
FV043, FV045,	<i>F. venosa</i>	x	x	Brooyar SF, QLD, Australia	-26.1567, 152.5094
FV086, FV094, FV126	<i>F. venosa</i>	x	x	Boyne Valley, QLD, Australia	-24.4320, 151.2175
FPa004, FPa006, FPa008, FPa010, FPa013, FPa014	<i>F. pancheri</i>	x	x	Grand Terre, New Caledonia	-21.3333, 164.9667

* Accuracy of some GPS data points has been intentionally inflated for privacy of landholders and sensitive nature of rare, threatened populations.

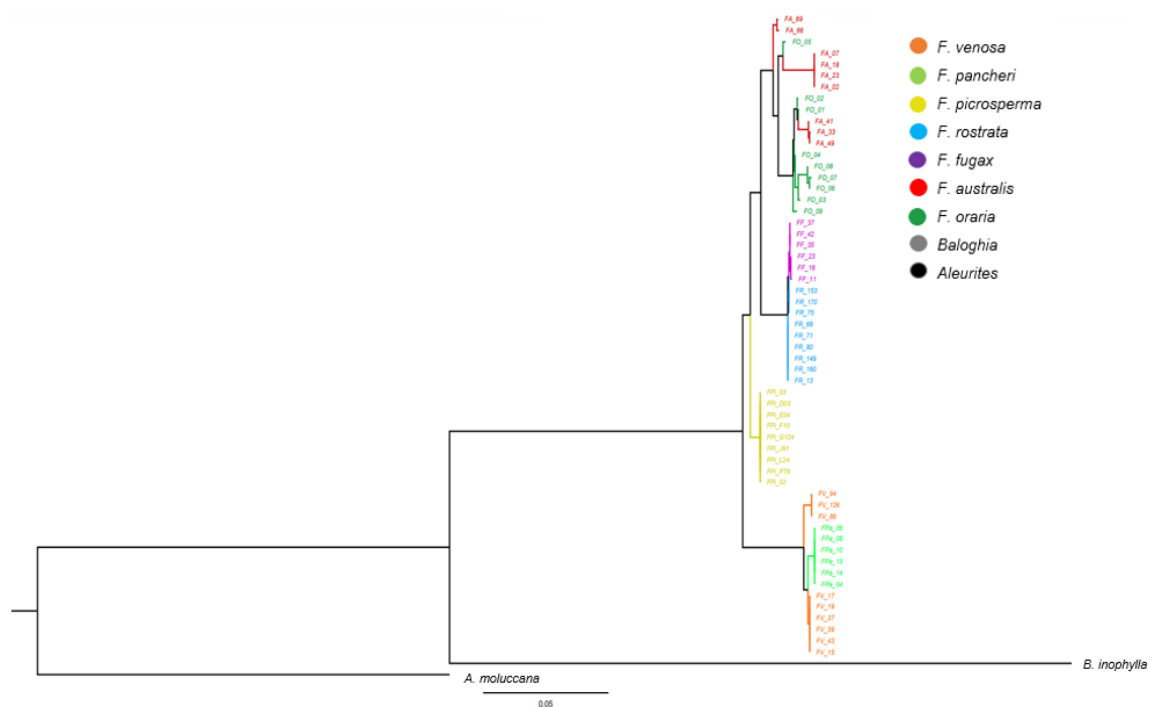


Figure S1. Maximum-Likelihood phylogenetic tree of the Austral-Pacific *Fontainea* complex constructed from individually aligned and concatenated cpDNA sequence markers based on the best-fit GTR + G + I model.

Baloghia inophylla and *Aleurites moluccana* were used as outgroup representatives to root the tree. The scale bar represents substitutions per site and tip labels are coloured by species; see inset legend.

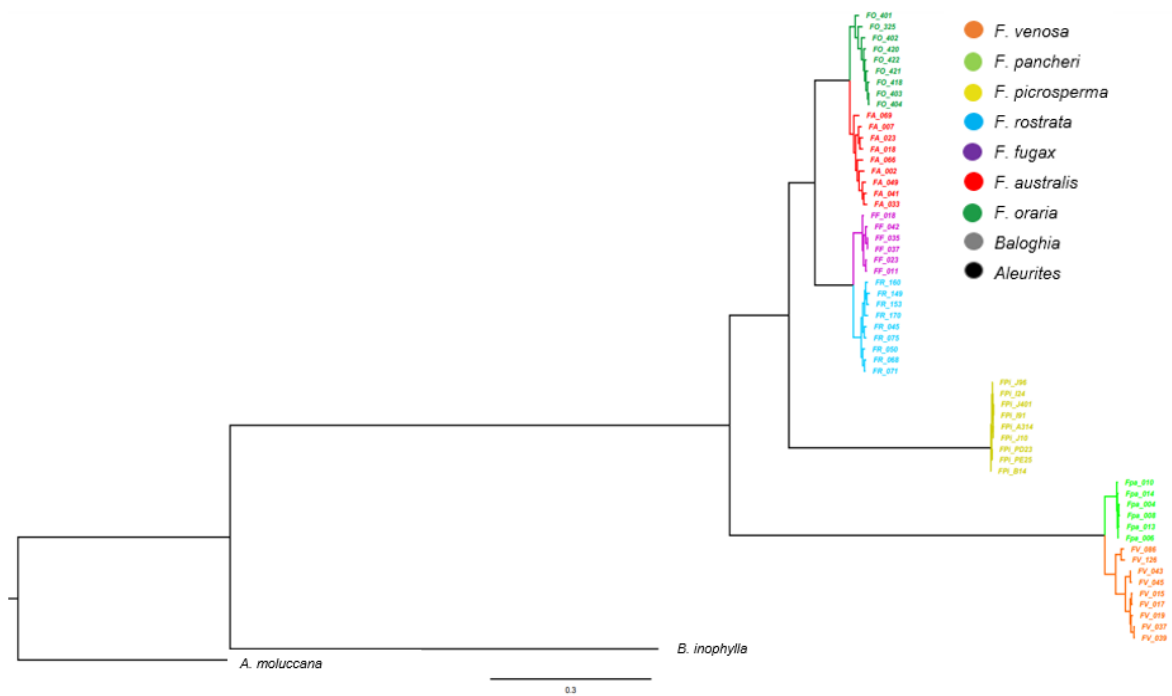


Figure S2. Maximum-Likelihood phylogenetic tree of the Austral-Pacific *Fontainea* complex constructed from the individually aligned and concatenated sequences of reduced-representation SNP markers (5,608 loci) based on the best-fit GTR model. *Baloghia inophylla* and *Aleurites moluccana* were used as outgroup representatives to root the tree. The scale bar represents substitutions per site and tip labels are coloured by species; see inset legend.

Table S2. Values for nucleotide substitution models used to select best-fit model of *Fontainea* phylogenetic tree construction from concatenation of three cpDNA markers.

Model	df	logLik	AIC	AICw	AICc	AICcw	BIC
JC	115	-117947	236125	0	236126.6	0	237012.4
JC+I	115	-117947	236124.8	0	236126.4	0	237012.2
JC+G	116	-117952	236136.9	0	236138.6	0	237032.1
JC+G+I	116	-117952	236136.9	0	236138.6	0	237032.1
F81	118	-117844	235923.2	0	235924.9	0	236833.8
F81+I	118	-117844	235923.1	0	235924.8	0	236833.6
F81+G	119	-117849	235935.5	0	235937.2	0	236853.8
F81+G+I	119	-117849	235935.5	0	235937.2	0	236853.8
K80	116	-115704	231639.6	5.73E-70	231641.3	6.35E-70	232534.8
K80+I	116	-115704	231639.6	5.86E-70	231641.2	6.49E-70	232534.7
K80+G	117	-115709	231651	1.90E-72	231652.7	2.07E-72	232553.9
K80+G+I	117	-115709	231651	1.90E-72	231652.7	2.07E-72	232553.9
HKY	119	-115597	231431.5	9.03E-25	231433.2	9.59E-25	232349.8

HKY+I	119	-115597	231431.4	9.26E-25	231433.1	9.82E-25	232349.7
HKY+G	120	-115601	231442.9	3.02E-27	231444.6	3.16E-27	232368.9
HKY+G+I	120	-115601	231442.9	3.02E-27	231444.6	3.16E-27	232368.9
SYM	120	-115607	231453.2	1.72E-29	231455	1.80E-29	232379.2
SYM+I	120	-115607	231453.2	1.75E-29	231454.9	1.83E-29	232379.2
SYM+G	121	-115611	231464.7	5.49E-32	231466.5	5.66E-32	232398.4
SYM+G+I	121	-115611	231464.7	5.49E-32	231466.5	5.66E-32	232398.4
GTR	123	-115538	231322.2	0.49246	231324	0.492483	232271.3
GTR+I	123	-115538	231322.1	0.504487	231324	0.504511	232271.3
GTR+G	124	-115543	231333.7	0.001526	231335.6	0.001503	232290.6
GTR+G+I	124	-115543	231333.7	0.001526	231335.6	0.001503	232290.6

Table S3. Values for nucleotide substitution models used to select best-fit model of Fontainea phylogenetic tree construction from concatenation of DArTseq SNPs (33170 nucleotides).

Model	df	logLik	AIC	AICw	AICc	AICcw	BIC
JC	115	-111114	222457.4	0	222459	0	223344.7
JC+I	115	-111114	222457.4	0	222459	0	223344.7
JC+G(4)	116	-111116	222464.6	0	222466.3	0	223359.7
JC+G(4)+I	116	-111116	222464.6	0	222466.3	0	223359.7
F81	118	-111081	222398.4	0	222400.1	0	223308.9
F81+I	118	-111081	222398.4	0	222400.1	0	223308.9
F81+G(4)	119	-111084	222405.6	0	222407.4	0	223323.9
F81+G(4)+I	119	-111084	222405.6	0	222407.4	0	223323.9
K80	116	-108869	217970.9	7.15E-47	217972.5	7.88E-47	218866
K80+I	116	-108869	217970.9	7.16E-47	217972.5	7.89E-47	218866
K80+G(4)	117	-108872	217977.7	2.35E-48	217979.4	2.55E-48	218880.5
K80+G(4)+I	117	-108872	217977.7	2.35E-48	217979.4	2.55E-48	218880.5
HKY	119	-108838	217913.8	1.77E-34	217915.5	1.87E-34	218832
HKY+I	119	-108838	217913.8	1.78E-34	217915.5	1.87E-34	218832
HKY+G(4)	120	-108840	217920.6	5.82E-36	217922.4	6.05E-36	218846.6
HKY+G(4)+I	120	-108840	217920.6	5.82E-36	217922.4	6.05E-36	218846.6
TrNe	117	-108868	217969.6	1.34E-46	217971.3	1.46E-46	218872.4
TrNe+I	117	-108868	217969.6	1.35E-46	217971.3	1.46E-46	218872.4
TrNe+G(4)	118	-108870	217976.5	4.40E-48	217978.2	4.71E-48	218887
TrNe+G(4)+I	118	-108870	217976.5	4.40E-48	217978.2	4.71E-48	218887
TrN	120	-108837	217913.2	2.39E-34	217915	2.49E-34	218839.2
TrN+I	120	-108837	217913.2	2.39E-34	217915	2.49E-34	218839.2
TrN+G(4)	121	-108839	217920	7.83E-36	217921.8	8.02E-36	218853.7
TrN+G(4)+I	121	-108839	217920	7.84E-36	217921.8	8.03E-36	218853.7
TPM1	117	-108868	217970.9	6.92E-47	217972.6	7.52E-47	218873.8
TPM1+I	117	-108868	217970.9	6.93E-47	217972.6	7.52E-47	218873.8
TPM1+G(4)	118	-108871	217977.8	2.27E-48	217979.5	2.43E-48	218888.3
TPM1+G(4)+I	118	-108871	217977.8	2.27E-48	217979.5	2.43E-48	218888.3
K81	117	-108868	217970.9	6.92E-47	217972.6	7.52E-47	218873.8
K81+I	117	-108868	217970.9	6.93E-47	217972.6	7.52E-47	218873.8

K81+G(4)	118	-108871	217977.8	2.27E-48	217979.5	2.43E-48	218888.3
K81+G(4)+I	118	-108871	217977.8	2.27E-48	217979.5	2.43E-48	218888.3
TPM1u	120	-108837	217914.2	1.45E-34	217916	1.51E-34	218840.2
TPM1u+I	120	-108837	217914.2	1.45E-34	217916	1.51E-34	218840.2
TPM1u+G(4)	121	-108840	217921	4.76E-36	217922.8	4.88E-36	218854.7
TPM1u+G(4)+I	121	-108840	217921	4.76E-36	217922.8	4.88E-36	218854.7
TPM2	117	-108815	217863.4	1.54E-23	217865.1	1.68E-23	218766.2
TPM2+I	117	-108815	217863.4	1.55E-23	217865.1	1.68E-23	218766.2
TPM2+G(4)	118	-108817	217870.2	5.13E-25	217871.9	5.49E-25	218780.8
TPM2+G(4)+I	118	-108817	217870.2	5.13E-25	217871.9	5.49E-25	218780.8
TPM2u	120	-108797	217833.4	5.20E-17	217835.1	5.41E-17	218759.3
TPM2u+I	120	-108797	217833.4	5.20E-17	217835.1	5.41E-17	218759.3
TPM2u+G(4)	121	-108799	217840.2	1.71E-18	217842	1.75E-18	218773.9
TPM2u+G(4)+I	121	-108799	217840.2	1.71E-18	217842	1.75E-18	218773.9
TPM3	117	-108828	217890.1	2.42E-29	217891.8	2.63E-29	218793
TPM3+I	117	-108828	217890.1	2.43E-29	217891.8	2.63E-29	218793
TPM3+G(4)	118	-108830	217897	7.97E-31	217898.7	8.53E-31	218807.5
TPM3+G(4)+I	118	-108830	217897	7.97E-31	217898.7	8.53E-31	218807.5
TPM3u	120	-108803	217846	9.50E-20	217847.7	9.87E-20	218771.9
TPM3u+I	120	-108803	217846	9.50E-20	217847.7	9.88E-20	218771.9
TPM3u+G(4)	121	-108805	217852.8	3.11E-21	217854.6	3.19E-21	218786.5
TPM3u+G(4)+I	121	-108805	217852.8	3.11E-21	217854.6	3.19E-21	218786.5
TIM1e	118	-108867	217969.7	1.30E-46	217971.4	1.39E-46	218880.2
TIM1e+I	118	-108867	217969.7	1.30E-46	217971.4	1.39E-46	218880.2
TIM1e+G(4)	119	-108869	217976.5	4.26E-48	217978.3	4.49E-48	218894.8
TIM1e+G(4)+I	119	-108869	217976.5	4.26E-48	217978.3	4.49E-48	218894.8
TIM1	121	-108836	217913.6	1.96E-34	217915.4	2.01E-34	218847.3
TIM1+I	121	-108836	217913.6	1.96E-34	217915.4	2.01E-34	218847.3
TIM1+G(4)	122	-108838	217920.4	6.42E-36	217922.3	6.48E-36	218861.8
TIM1+G(4)+I	122	-108838	217920.4	6.42E-36	217922.3	6.48E-36	218861.8
TIM2e	118	-108813	217862.2	2.83E-23	217863.9	3.03E-23	218772.7
TIM2e+I	118	-108813	217862.2	2.83E-23	217863.9	3.03E-23	218772.7
TIM2e+G(4)	119	-108816	217869	9.38E-25	217870.8	9.90E-25	218787.3
TIM2e+G(4)+I	119	-108816	217869	9.38E-25	217870.8	9.90E-25	218787.3
TIM2	121	-108795	217833	6.36E-17	217834.8	6.51E-17	218766.6
TIM2+I	121	-108795	217833	6.36E-17	217834.7	6.51E-17	218766.6
TIM2+G(4)	122	-108798	217839.8	2.09E-18	217841.6	2.11E-18	218781.2
TIM2+G(4)+I	122	-108798	217839.8	2.09E-18	217841.6	2.11E-18	218781.2
TIM3e	118	-108826	217888.8	4.65E-29	217890.6	4.97E-29	218799.4
TIM3e+I	118	-108826	217888.8	4.65E-29	217890.5	4.98E-29	218799.4
TIM3e+G(4)	119	-108829	217895.7	1.53E-30	217897.4	1.61E-30	218813.9
TIM3e+G(4)+I	119	-108829	217895.7	1.53E-30	217897.4	1.61E-30	218813.9
TIM3	121	-108802	217845.1	1.44E-19	217846.9	1.48E-19	218778.8
TIM3+I	121	-108802	217845.1	1.44E-19	217846.9	1.48E-19	218778.8
TIM3+G(4)	122	-108804	217852	4.73E-21	217853.8	4.77E-21	218793.4
TIM3+G(4)+I	122	-108804	217852	4.73E-21	217853.8	4.77E-21	218793.4

TVMe	119	-108770	217778.6	3.94E-05	217780.4	4.16E-05	218696.9
TVMe+I	119	-108770	217778.6	3.95E-05	217780.4	4.16E-05	218696.9
TVMe+G(4)	120	-108773	217785.5	1.31E-06	217787.2	1.36E-06	218711.4
TVMe+G(4)+I	120	-108773	217785.5	1.31E-06	217787.2	1.36E-06	218711.4
TVM	122	-108759	217761.5	0.20394	217763.4	0.205808	218702.9
TVM+I	122	-108759	217761.5	0.203995	217763.4	0.205863	218702.9
TVM+G(4)	123	-108761	217768.4	0.006714	217770.2	0.006675	218717.5
TVM+G(4)+I	123	-108761	217768.4	0.006714	217770.2	0.006675	218717.5
SYM	120	-108769	217777.4	7.39E-05	217779.2	7.68E-05	218703.4
SYM+I	120	-108769	217777.4	7.39E-05	217779.2	7.68E-05	218703.4
SYM+G(4)	121	-108771	217784.2	2.46E-06	217786	2.52E-06	218717.9
SYM+G(4)+I	121	-108771	217784.2	2.46E-06	217786	2.52E-06	218717.9
GTR	123	-108757	217760.9	0.279944	217762.8	0.278302	218710
GTR+I	123	-108757	217760.9	0.280013	217762.8	0.27837	218710
GTR+G(4)	124	-108760	217767.7	0.009223	217769.6	0.009031	218724.6
GTR+G(4)+I	124	-108760	217767.7	0.009223	217769.6	0.009031	218724.6