

Table S1. Genes analyzed in *Schiedea* species

Gene	Proportion of gene length, %	Species analysed	Sequence length		Substitutions			Divergence, %		
			exon	intron	N*	S*	Nc*	N*	S*	Nc*
Dymeclin	14	27	285	574	4	1	33	0.13	0.12	0.79
DUF1191 superfamily protein	30	23	288	252	5	5	10	0.54	1.58	0.58
Glyceraldehyde-3-P dehydrogenase	21	26	219	425	4	9	39	0.4	2.43	2.13
40S ribosomal protein S4	51	27	405	521	3	10	63	0.19	3.12	2.73
LuxR transcriptional regulator	35	27	279	486	2	6	58	0.07	1.79	1.8
EXS family protein	33	25	399	312	5	7	27	0.39	1.22	1.31
Lhcb1	64	27	516	45	7	20	8	0.29	3.45	3.13
NAC domain protein	28	27	354	377	20	9	54	1.17	3.27	2.5
1-aminocyclopropane oxidase	13	22	123	92	1	5	18	0.09	5.56	5.04
Tubulin beta	17	27	222	81	7	9	9	0.46	3.23	1.74
Fructose-biphosphate aldolase	34	27	369	0	2	9	NA	0.05	1.45	NA
NHL repeat-containing protein	11	23	249	234	10	7	31	0.78	2.55	2.61
Cell division protein	10	27	420	54	43	18	4	1.89	2.42	1.36
Integral membrane family protein	48	23	243	546	6	11	91	0.6	3.39	3.46
Adenosylmethionine decarboxylase	23	27	246	0	3	1	NA	0.12	0.13	NA
Enolase	25	20	327	541	1	9	53	0.08	2.08	1.88
Metallothionein	68	27	162	110	2	7	21	0.4	1.61	2.85
Proteophosphoglycan	32	22	570	593	4	14	33	0.22	2.68	1.05
Sucrose synthase	15	20	354	613	3	8	42	0.28	1.53	1.02
Malate dehydrogenase	34	27	339	431	6	9	51	0.26	2.06	1.83
CBP5	44	27	348	0	5	14	NA	0.49	2.48	NA

Table S1 (continued). Genes analyzed in *Schiedea* species

Gene	Proportion of gene length, %	Species analysed	Sequence length		Substitutions			Divergence, %		
			exon	intron	N*	S*	Nc*	N*	S*	Nc*
Ornithine carbamoyltransferase	35	27	393	436	10	12	47	0.48	2.14	1.76
Glycosyl hydrolase	11	20	246	587	9	8	41	0.85	1.81	1.97
Monodehydroascorbate reductase	17	22	249	333	5	1	33	0.72	0.46	2.14
Thioredoxin H-type	95	24	450	1061	22	18	100	1.5	6.39	2.11
Ran-binding protein	9	27	285	484	10	6	59	0.58	1.26	1.88
Adenosyl-homocysteine hydrolase	10	27	150	252	1	5	29	0.07	1.82	1.88
Auxin-responsive protein IAA1	47	20	282	170	12	7	24	0.95	1.56	2.57
Mannitol dehydrogenase	22	20	234	159	9	5	15	1.05	3.25	2.3
Ubiquitin activating enzyme	11	27	363	0	10	11	NA	0.62	2.53	NA
G-protein beta (wd40 protein)	40	23	429	336	8	7	20	0.37	1.52	1.03
Aldehyde dehydrogenase	29	20	471	695	17	24	66	1.4	8.71	4.02
Endomembrane protein 70	21	25	411	112	3	7	19	0.08	1.69	2.59
Glycerol 3-phosphate permease	12	25	432	109	11	15	22	0.51	2.19	4.16
Delta tonoplast integral protein	47	22	348	345	4	10	39	0.14	1.37	2.03
Oxidoreductase	15	20	255	0	5	9	NA	0.39	4.22	NA

* N, S and Nc stand for Nonsynonymous, Synonymous and Non-coding

Table S2. Taxonomy, distribution and ecological characteristics of 27 analyzed*Schiedea* species [after Wagner et al. 2005]

Section	Island ¹	Species	Ecotype ²	
Former genus <i>Schiedea</i> s.s.				
<i>Alphaschiedea</i>	Kaua`i	<i>helleri</i> Sherff	HW	
		<i>membranacea</i> H.St.John	HM	
<i>Anestioschiedea</i>	Kaua`i	<i>apokremnos</i> H.St.John	SD	
<i>Mononeura</i>	Kaua`i	<i>kauaiensis</i> H.St.John	SM	
		<i>perlmanii</i> W.L.Wagner & Weller	HM	
		<i>stellarioides</i> H.Mann	SM	
	O`ahu	<i>kaalae</i> Wawra	HM	
		<i>nuttallii</i> Hook.	SM	
			<i>pentandra</i> W.L.Wagner & E.M.Harris	HM
	Maui Nui		<i>jacobii</i> W.L.Wagner, Weller & Medeiros	HW
		<i>loui</i> W.L.Wagner & Weller	SW	
<i>Schiedea</i>	Kaua`i	<i>spergulina</i> A.Gray	SD	
	O`ahu	<i>adamantis</i> H.St.John	SD	
		<i>globosa</i> H.Mann	SD	
		<i>hookeri</i> A.Gray	SM	
		<i>kealiae</i> Caum & Hosaka	SD	
		<i>ligustrina</i> Cham. & Schltdl.	SD	
		<i>mannii</i> H.St.John	SD	
	Maui Nui	<i>haleakalensis</i> Deg. & Sherff	SD	
		<i>lydgatei</i> Hillebr.	SD	
		<i>menziesii</i> Hook.	SD	

		<i>Salicaria</i> Hillebr.	SD
		<i>sarmentosa</i> Deg. & Sherff	SD
Former genus <i>Alsinidendron</i>			
<i>Alsinidendron</i>	O`ahu	<i>obovata</i> (Sherff) W.L.Wagner & Weller	SM
		<i>trinervis</i> (H.Mann) Pax & K.Hoffm.	SW
<i>Nothoschiedea</i>	Kaua`i	<i>viscosa</i> H.Mann	HM
<i>Polyneura</i>	Nihoa	<i>verticillata</i> F.Brown	HD

¹We consider Moloka`i, Lana`i and Maui as a single island (Maui Nui), because they were interconnected for more than 75% of their existence.

²The first letter is for habit (S = shrub or subshrub; H = perennial herb or vine), the second letter is for habitat (W = wet; M = mesic; D = dry).

Table S3. Molecular functions of analyzed genes (after <http://www.brenda-enzymes.org/> and <http://www.geneontology.org/> databases)

Gene	EC number	molecular function	biological process
1-aminocyclopropane-1-carboxylate oxidase	1.14.17.4	aminocyclopropanecarboxylate oxidase activity	biosynthesis of plant hormones, methionine metabolism
40S ribosomal protein S4		RNA binding	translation
Aldehyde dehydrogenase	1.2.1.3	benzaldehyde dehydrogenase (NAD ⁺) activity	oxidation reduction developmental responses in plants (cell division, differentiation of embryo responses, body patterns)
Auxin-responsive protein IAA1		identical protein binding	development
Cell division protein			cell division
CBP5		chlorophyll binding water channel, methylammonium transmembrane transporter and	photosynthesis
Delta tonoplast integral protein		ammonia transporter activity	transport
Dymeclin			regulation of smoothened signaling pathway

DUF1191 superfamily protein		unknown function	
Endomembrane protein 70		transporter activity	transport
Enolase (2-phosphoglycerate dehydratase)	4.2.1.11	phosphopyruvate hydratase activity	glycolysis / gluconeogenesis
EXS family protein		unknown function	
			carbon fixation, fructose and mannose metabolism,
		fructose-biphosphate aldolase	glycolysis / gluconeogenesis, inositol metabolism, pentose
Fructose-biphosphate aldolase	4.1.2.13	activity	phosphate pathway
G-protein beta (wd40 protein)		unknown function	
		glyceraldehyde-3-phosphate	gluconeogenesis, glycolysis, response to heat, response to
Glyceraldehyde-3-phosphate dehydrogenase, C subunit	1.2.1.12	dehydrogenase (phosphorylating) activity	oxidative stress, response to stress, response to sucrose stimulus
Glycerol 3-phosphate permease	3.6.3.20	transporter activity	transport
Glycosyl hydrolases family 17 protein		hydrolase activity	may be involved in defense of plants against pathogens
Integral membrane family protein		membrane channel	transport
Lhcb1		Light harvesting	photosynthesis

LuxR family transcriptional regulator		transcription factor activity	regulation of transcription carbon fixation, citrate cycle (TCA cycle), glyoxylate and dicarboxylate metabolism, pyruvate metabolism, reductive
Malate dehydrogenase	1.1.1.37	malate dehydrogenase activity	carboxylate cycle (CO2 fixation), response to cold
Mannitol dehydrogenase (cinnamyl alcohol dehydrogenase)	1.1.1.195	aryl-alcohol dehydrogenase and oxidoreductase activity, protein and zinc ion binding	phenylpropanoid biosynthesis
Metallothionein		metal ion binding	cellular copper ion homeostasis
Monodehydroascorbate reductase	1.6.5.4	monodehydroascorbate reductase (NADH) activity	ascorbate and aldarate metabolism
NAC domain protein		unknown function	
NHL repeat-containing protein		unknown function	
Ornithine carbamoyltransferase	2.1.3.3	amino acid binding / carboxyl- and carbamoyltransferase	arginine and proline metabolism
Oxidoreductase	1.8.1.8	protein-disulfide reductase activity	oxidative stress

Proteophosphoglycan		DNA binding	regulation of transcription, DNA-dependent
Ran-binding protein		unknown function	
S-Adenosyl-L-homocysteine			methionine metabolism, selenoamino acid metabolism,
hydrolase (adenosylhomocysteinase)	3.3.1.1	adenosylhomocysteinase activity	one-carbon compound metabolic process
		adenosylmethionine	
S-Adenosylmethionine		decarboxylase and electron	methionine metabolism, spermidine biosynthetic process,
decarboxylase 2	4.1.1.50	carrier activity	spermine biosynthetic process
			starch and sucrose metabolism, response to osmotic stress,
Sucrose synthase	2.4.1.13	sucrose synthase activity	response to flooding, response to cold
			protection against oxidative stress and carbon/nitrogen
Thioredoxin H-type			metabolism regulation
Tubulin beta		structural molecule activity	constituent parts of eukaryotic cell structures
		ubiquitin activating enzyme	response to other organism, ubiquitin-dependent protein
Ubiquitin activating enzyme		activity	catabolic process

Table S4. Primers used in the study

Gene	Forward primer	Reverse primer
1-aminocyclopropane-1-carboxylate oxidase	CAACTGCTGGACTTGCTCTG	CAGTGCTTTCCATTGCCTTC
40S ribosomal protein S4	TTTAAGGACTCTATGGTAACCAGAG	CAAAGGGTAGATTCAGGTTGC
Aldehyde dehydrogenase, mitochondrial	TGAAAGACGCTCAGTCGGAG	AATCACGCCACATAATCGTC
Auxin-responsive protein IAA1	ATGGCCACCAATAAGATCAT	TTCACGTTTATTAATCTGCC
Cell division protein	GACATCATAACAGAGACGCTCC	CCCAGAGACCCTGATTCTCTG
CBP5	AATCGAATTCAACATCAAAGGC	TTTGCCAAGAACCGTGAACT
Delta tonoplast integral protein	CAAATAAGGCAGAAACAACATCTT	CGGTTCTTTCCTTCTTAAGGCT
Dymeclin	TTTTCATTTCTGCATTGGGTC	GCATCCATACGACTATTGAAGAA
DUF1191 superfamily protein	TATCAGTCAACCATCGACAGTGG	ATTGCTCCTTCTCCATCCCC
Endomembrane protein 70	AATAAAATACCTAGGCAAATCCCG	GCTGAACAAGCATCCTAAGGAT
Enolase	AAGAAAAAGGTCACCACACATCT	TGTTGGTGATGACCTCTTGGT
EXS family protein	AAACTACAAAATGGTTGTTTCAGTCG	CACTCAAATATCACGTGTTCCCT
Fructose-biphosphate aldolase	TGCTGAGGTTTCCGAGCGAG	TGTACTTTCCGAGGGTTGCC
G-protein beta (wd40 protein)	GTGCCTTGCTGTGGACTTTG	AATTGGCAGGAGTGGTGCAG
Glyceraldehyde-3P dehydrogenase	ACTCCTTTACAGACTGCAAACCTCAG	TTTCGGTTGTTGATCTTACTGTCAG

Glycerol 3-phosphate permease	CCGTTGCTACTTTTACAATATCAA	TTCGGATAAACTAGATGCCAGA
Glycosyl hydrolase	TTACTCAATTACTACTTGGACGAGG	GCTAGTTGTTCTTGGTGGAAAGTTA
Integral membrane family protein	CCATTACTTTCTTTTCCTCCATG	GTCCCTTTTTTTCACATTTAGAAT
Lhcb1	CATTCGCCAAGAACCGTGAG	GCATTGTTAGCCACTGGGTCTG
LuxR family transcriptional regulator	GAGGGCAATTTCAAAGGCTC	GAAGAACGTGGCTTAGAAAGGT
Malate dehydrogenase	AACCAGCTCAAATAGTCTCGTCA	TCAACCATGCAACCGTATGC
Mannitol dehydrogenase	TTTTCAGTGAAAAGCATCTC	CGTTGCTGTCAAGTTTGCTA
Metallothionein	CGGAGGGTGCAAGATGTTTG	CAAACCCTAACAAAGACGAGTCAC
Monodehydroascorbate reductase	TTTTTGCTATTGGAGATGTTGC	AATGCTTTGTGGACAATTTCC
NAC domain protein	GCCGATTCTAGAATTTAGATGACG	AGCAAGCGATGAAGATGACA
NHL repeat-containing protein	TCACGCTAATTGCTAACTTAACTC	CACCATCATAGGAAGTCAAAGTCT
Ornithine carbamoyltransferase	CTGCCTAAAACATCAAACACAC	GAGATGGAAACAATATCGTGCA
Oxidoreductase	TGACATTCTCGAAAAGAAGAGCTGG	AGGTGCAATAAGCTGTCTTTTCG
Proteophosphoglycan	GGTTTCTCTATGGACGCTCC	CGTTCCGATCACTGGTAATG
Ran-binding protein	TTGCAAAAACCTTTCCCTGTTC	CAATTGATCACCTGGCAACTT
S-Adenosyl-L-homocysteine hydrolase	TGCTCTTGCCTTAAAGGCTG	TTGGGCAATAACTTGGTTGG
S-Adenosylmethionine decarboxylase	GCTCTCTGATGAACGCCATT	CATGGGAGGGCTAACAGTACTAG

Sucrose synthase	AAACGCTGCTCATCTTATTTCA	TGTGGTTGAAGCTATGACTTGTG
Thioredoxin H-type	TTGAGGGTTCTCATATTTTC	CCACATCATAACATACACAA
Tubulin beta	GTTGAGTGGATCCCGAACAA	CAAACCAGTATGACTAACATGTCCT
Ubiquitin activating enzyme	TTTACTGTATTTTATATCCGCAGCG	ATACGTTTGCGAATCTGGCA

Table S6. PAML results for *Schiedea* and mainland groups

Schiedea

Gene	N species	M0		M8/M8a LRT	
		tree length	dN/dS	p-value	FDR
Dymeclin	27	0.05	1.12	0.500	1.000
DUF1191 superfamily protein	23	0.11	0.43	0.171	1.000
Glyceraldehyde-3-P dehydrogenase	26	0.21	0.23	0.042	1.000
40S ribosomal protein S4	27	0.13	0.04	0.500	1.000
LuxR transcriptional regulator	27	0.14	0.05	0.103	1.000
EXS family protein	25	0.11	0.25	0.137	1.000
Lhcb1	27	0.24	0.11	0.500	1.000
NAC domain protein	27	0.37	0.71	0.003	0.096
1-aminocyclopropane oxidase	22	0.29	0.03	0.500	1.000
Tubulin beta	27	0.27	0.26	0.219	1.000
Fructose-biphosphate aldolase	27	0.09	0.07	0.500	1.000
NHL repeat-containing protein	23	0.35	0.55	0.000	0.000
Cell division protein	27	0.57	1.44	0.000	0.000
Integral membrane family protein	23	0.25	0.18	0.500	1.000
Adenosylmethionine decarboxylase	27	0.05	1.00	0.500	1.000
Enolase	20	0.14	0.03	0.500	1.000
Metallothionein	27	0.22	0.09	0.065	1.000
Proteophosphoglycan	22	0.12	0.07	0.500	1.000
Sucrose synthase	20	0.10	0.13	0.500	1.000
Malate dehydrogenase	27	0.17	0.21	0.376	1.000
CBP5	27	0.28	0.50	0.000	0.000
Ornithine carbamoyltransferase	27	0.22	0.32	0.021	0.609
Glycosyl hydrolase	20	0.14	0.96	0.001	0.034
Monodehydroascorbate reductase	22	0.12	1.18	0.006	0.186
Thioredoxin H-type	24	0.42	0.82	0.007	0.210
Ran-binding protein	27	0.23	0.52	0.219	1.000
Adenosyl-homocysteine hydrolase	27	0.17	0.05	0.500	1.000
Auxin-responsive protein IAA1	20	0.25	0.58	0.090	1.000
Mannitol dehydrogenase	20	0.29	0.36	0.147	1.000
Ubiquitin activating enzyme	27	0.31	0.26	0.001	0.034
G-protein beta (wd40 protein)	23	0.14	0.21	0.500	1.000
Aldehyde dehydrogenase	20	0.23	0.18	0.500	1.000
Endomembrane protein 70	25	0.08	0.08	0.500	1.000
Glycerol 3-phosphate permease	25	0.24	0.31	0.103	1.000
Delta tonoplast integral protein	22	0.14	0.16	0.500	1.000
Oxidoreductase	20	0.28	0.14	0.500	1.000
Average		0.21	0.38		

Table S6. PAML results for *Schiedea* and mainland groups (continued)

Poaceae					
Gene	N species	M0		M8/M8a LRT	
		tree length	dN/dS	p-value	FDR
Glyceraldehyde-3-P dehydrogenase	26	3.46	0.06	0.810	1.000
40S ribosomal protein S4	20	2.08	0.02	0.889	1.000
Lhcb1	19	2.96	0.00	0.949	1.000
1-aminocyclopropane oxidase	15	1.42	0.01	0.909	1.000
Tubulin beta	21	3.34	0.02	0.877	1.000
Fructose-biphosphate aldolase	24	2.98	0.07	0.793	0.903
Enolase	24	3.38	0.03	0.858	1.000
Sucrose synthase	15	2.78	0.05	0.824	1.000
Malate dehydrogenase	24	2.70	0.07	0.784	1.000
CBP5	20	3.17	0.01	0.903	1.000
Ornithine carbamoyltransferase	15	1.68	0.09	0.766	1.000
Glycosyl hydrolase	14	1.50	0.02	0.887	1.000
Monodehydroascorbate reductase	14	1.88	0.08	0.774	1.000
Adenosyl-homocysteine hydrolase	24	3.38	0.06	0.808	1.000
Auxin-responsive protein IAA1	17	2.43	0.08	0.778	1.000
Mannitol dehydrogenase	14	2.54	0.06	0.810	1.000
Aldehyde dehydrogenase	21	3.33	0.02	0.890	1.000
Endomembrane protein 70	16	1.15	0.01	0.924	1.000
Glycerol 3-phosphate permease	12	2.23	0.06	0.807	1.000
Delta tonoplast integral protein	12	1.76	0.02	0.889	1.000
Average		2.51	0.04		

Table S6. PAML results for *Schiedea* and mainland groups (continued)

Asteraceae

Gene	N species	M0		M8/M8a LRT	
		tree length	dN/dS	p-value	FDR
Glyceraldehyde-3-P dehydrogenase	17	2.38	0.05	0.947	1.000
40S ribosomal protein S4	19	4.47	0.02	1.000	1.000
Lhcb1	14	1.90	0.01	1.000	1.000
1-aminocyclopropane oxidase	20	2.27	0.03	0.750	1.000
Tubulin beta	14	3.53	0.01	0.779	1.000
Fructose-biphosphate aldolase	13	3.59	0.04	1.000	1.000
NHL repeat-containing protein	18	1.80	0.06	0.305	0.996
Cell division protein	16	3.16	0.05	1.000	1.000
Integral membrane family protein	16	1.18	0.03	0.996	1.000
Adenosylmethionine decarboxylase	17	3.28	0.06	1.000	1.000
Enolase	18	1.80	0.06	0.305	0.996
Sucrose synthase	16	3.16	0.05	1.000	1.000
Malate dehydrogenase	16	1.18	0.03	0.996	1.000
CBP5	17	3.28	0.06	1.000	1.000
Glycosyl hydrolase	19	2.42	0.05	1.000	1.000
Adenosyl-homocysteine hydrolase	19	3.32	0.06	1.000	1.000
Auxin-responsive protein IAA1	15	1.75	0.18	1.000	1.000
Delta tonoplast integral protein	19	2.85	0.07	1.000	1.000
Average		2.63	0.05		

Table S6. PAML results for *Schiedea* and mainland groups (continued)

Fabaceae

Gene	N species	M0		M8/M8a LRT	
		tree length	dN/dS	p-value	FDR
Glyceraldehyde-3-P dehydrogenase	18	4.20	0.07	0.049	0.508
40S ribosomal protein S4	15	3.38	0.05	0.658	1.000
Lhcb1	16	3.58	0.02	0.310	0.995
Enolase	19	1.92	0.08	1.000	1.000
Metallothionein	19	4.70	0.32	0.414	1.000
Sucrose synthase	16	2.63	0.07	0.167	0.922
Malate dehydrogenase	15	1.82	0.09	0.059	0.573
CBP5	13	1.65	0.05	1.000	1.000
Ornithine carbamoyltransferase	11	1.38	0.20	0.205	0.960
Glycosyl hydrolase	11	1.31	0.04	1.000	1.000
Adenosyl-homocysteine hydrolase	16	2.50	0.08	0.690	1.000
Auxin-responsive protein IAA1	12	3.40	0.11	1.000	1.000
Ubiquitin activating enzyme	11	2.27	0.10	1.000	1.000
Average		2.67	0.10		

Table S6. PAML results for *Schiedea* and mainland groups (continued)

Helianthus

Gene	M0			M8/M8a LRT	
	N species	tree length	dN/dS	p-value	FDR
Glyceraldehyde-3-P dehydrogenase	6	0.83	0.07	0.500	1.000
40S ribosomal protein S4	7	0.33	0.03	0.500	1.000
Lhcb1	7	1.49	0.01	0.500	1.000
1-aminocyclopropane oxidase	7	0.15	0.61	0.001	0.019
Tubulin beta	7	3.73	0.00	0.500	1.000
Fructose-biphosphate aldolase	7	1.79	0.05	0.142	1.000
Enolase	6	0.13	0.12	0.500	1.000
Sucrose synthase	5	0.50	0.03	0.500	1.000
CBP5	6	3.72	0.05	0.120	1.000
Ornithine carbamoyltransferase	4	0.23	0.20	0.034	0.578
Glycosyl hydrolase	7	0.20	0.23	0.216	1.000
Monodehydroascorbate reductase	5	0.10	0.14	0.500	1.000
Adenosyl-homocysteine hydrolase	7	1.30	0.04	0.500	1.000
Auxin-responsive protein IAA1	7	3.38	0.06	0.500	1.000
Mannitol dehydrogenase	6	4.02	0.25	0.500	1.000
Ubiquitin activating enzyme	4	8.29	0.01	0.500	1.000
Endomembrane protein 70	6	1.36	0.03	0.500	1.000
Delta tonoplast integral protein	7	0.30	0.30	0.005	0.090
Average		1.77	0.12		

Table S6. PAML results for *Schiedea* and mainland groups (continued)

Populus

Gene	N species	M0		M8/M8a LRT	
		tree length	dN/dS	p-value	FDR
Glyceraldehyde-3-P dehydrogenase	6	2.86	0.06	0.084	1.000
40S ribosomal protein S4	6	0.75	0.07	0.485	1.000
Lhcb1	6	0.25	0.02	0.500	1.000
Tubulin beta	6	4.33514	0.0182	0.500	1.000
Fructose-biphosphate aldolase	6	0.85986	0.1605	0.500	1.000
Enolase	4	5.37	0.01	0.303	1.000
Sucrose synthase	6	0.86	0.14	0.500	1.000
CBP5	6	0.15	0.37	0.500	1.000
Adenosyl-homocysteine hydrolase	6	0.08	1.52	0.018	0.252
Auxin-responsive protein IAA1	4	0.69	0.11	0.500	1.000
Mannitol dehydrogenase	5	0.29	0.23	0.261	1.000
Ubiquitin activating enzyme	4	0.57	0.12	0.500	1.000
Aldehyde dehydrogenase	5	2.80	0.05	0.500	1.000
Delta tonoplast integral protein	6	0.24	0.28	0.135	1.000
Average		1.44	0.23		

Table S6. PAML results for *Schiedea* and mainland groups (continued)

Cichorieae

Gene	N species	M0		M8/M8a LRT	
		tree length	dN/dS	p-value	FDR
Glyceraldehyde-3-P dehydrogenase	7	0.49	0.02	0.500	1.000
40S ribosomal protein S4	7	1.37	0.02	0.485	1.000
Lhcb1	6	0.48	0.01	0.500	1.000
Tubulin beta	5	0.27	0.04	0.500	1.000
Fructose-biphosphate aldolase	6	0.61	0.04	0.087	1.000
Enolase	6	0.63	0.05	0.394	1.000
Sucrose synthase	6	0.85	0.05	0.477	1.000
CBP5	7	0.75	0.03	0.500	1.000
Glycosyl hydrolase	8	1.26	0.09	0.123	1.000
Adenosyl-homocysteine hydrolase	7	0.90	0.08	0.500	1.000
Auxin-responsive protein IAA1	7	0.56	0.15	0.350	1.000
Ubiquitin activating enzyme	4	0.83	0.01	0.500	1.000
Delta tonoplast integral protein	7	0.77	0.07	0.500	1.000
Average		0.75	0.05		

Table S6. PAML results for *Schiedea* and mainland groups (continued)

Citrus

Gene	N species	M0		M8/M8a LRT	
		tree length	dN/dS	p-value	FDR
Glyceraldehyde-3-P dehydrogenase	7	1.48	0.03	0.014	0.154
40S ribosomal protein S4	6	0.03	0.00	0.500	1.000
Lhcb1	7	0.10	0.03	0.009	0.108
Tubulin beta	5	0.06	0.41	0.500	1.000
Fructose-biphosphate aldolase	7	0.10	0.14	0.500	1.000
Sucrose synthase	7	0.08	0.04	0.500	1.000
CBP5	7	0.04	0.00	0.499	1.000
Adenosyl-homocysteine hydrolase	7	0.13	0.00	0.499	1.000
Auxin-responsive protein IAA1	4	0.02	0.24	0.500	1.000
Mannitol dehydrogenase	7	0.11	0.29	0.064	0.640
Delta tonoplast integral protein	5	0.09	0.04	0.500	1.000
Average		0.20	0.11		

Table S6. PAML results for *Schiedea* and mainland groups (continued)

Solanum

Gene	N species	M0		M8/M8a LRT	
		tree length	dN/dS	p-value	FDR
Glyceraldehyde-3-P dehydrogenase	5	0.28	0.17	1.000	1.000
40S ribosomal protein S4	7	0.53	0.12	1.000	1.000
Lhcb1	5	0.80	0.01	1.000	1.000
Fructose-biphosphate aldolase	5	0.76	0.07	1.000	1.000
Enolase	7	0.21	0.00	1.000	1.000
Malate dehydrogenase	6	0.24	0.09	1.000	1.000
Adenosyl-homocysteine hydrolase	6	0.43	0.02	1.000	1.000
Mannitol dehydrogenase	5	1.70	0.08	1.000	1.000
Ubiquitin activating enzyme	5	0.30	0.12	1.000	1.000
Delta tonoplast integral protein	5	0.47	0.06	1.000	1.000
Average		0.57	0.07		