

Appendix 1. Data-set characteristics and model-selection information for all 250 phylogenetic data sets obtained from TreeBASE. Poor alignment regions and redundant haplotypes were removed before calculating the number of taxa, sequence length, and uncorrected p-distances for each data set. Consequently, these values may not always agree with the primary literature. Model selection was based on the hierarchical likelihood-ratio test (hLRT), corrected Akaike information criterion (AIC_c), Bayesian information criterion (BIC), and decision theory (DT) extension of the BIC. Bold face type indicates the least parameter-rich model(s) selected for each data set. The difference in number of model parameters (Δk) was free to vary between 0 and 10. References for each data set are given at the end of the model selection information.

Data Set	1	2	3
TreeBASE ID	S1266/M2209	S685/M1075	S388/M542
Haplotypes	5	9	64
Characters	638	1389	2252
P-distance	0.2 – 14.7%	1.5 – 10.2%	0 – 11.3%
hLRT	HKY+Γ	TrN+Γ	GTR+I+ Γ
AIC _c	GTR+ Γ	GTR+I+ Γ	GTR+I+ Γ
BIC	TVM	GTR+ Γ	GTR+I+ Γ
DT	TVM+I	GTR+ Γ	SYM+Γ
Models	4	3	2
Δk	4	4	4

Data Set	4	5	6
TreeBASE ID	S904/M1486	S631/M977	S1067/M1819
Haplotypes	52	36	11
Characters	1962	1056	812
P-distance	1.2 – 22.1%	0.1 – 18.4%	0 – 7.5%
hLRT	GTR+I+Γ	TrNef+I+Γ	TrN+ Γ

AIC _c	GTR+I+Γ	TrN+I+Γ	GTR+I
BIC	GTR+I+Γ	TrNef+I+Γ	TrN+I
DT	GTR+I+Γ	TrNef+I+Γ	TrN
Models	1	2	4
Δ k	0	3	4
Data Set	7	8	9

TreeBASE ID	S769/M1216	S1038/M1767	S320/M391
Haplotypes	61	15	17
Characters	677	654	2550
P-distance	0 – 30.3%	0 – 21.1%	3.0 – 16.9%
hLRT	TrN+I+Γ	K2P+Γ	GTR+I+Γ
AIC _c	TVM+I+Γ	K2P+I+Γ	GTR+I+Γ
BIC	HKY+Γ	K2P+Γ	GTR+I+Γ
DT	HKY+Γ	K2P+Γ	GTR+I+Γ
Models	3	2	1
Δ k	4	1	0

Data Set	10	11	12
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TreeBASE ID	S430/M630	S981/M1631	S869/M1410
Haplotypes	13	94	17
Characters	805	1499	491
P-distance	0 – 41.5%	0.1 – 17.5%	0 – 16.5%
hLRT	HKY+Γ	K3Puf+Γ	K3Puf+Γ
AIC _c	TrN+Γ	TIM+Γ	K3Puf+Γ
BIC	HKY+Γ	K3P+Γ	K3Puf+Γ
DT	HKY+Γ	K3P+Γ	K3Puf+Γ

Models	2	3	1
Δk	1	4	0

Data Set	13	14	15
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TreeBASE ID	S927/M1533	S1120/M1917	S1123/M1924
Haplotypes	28	23	30
Characters	1698	3025	7593
P-distance	0.2 – 10.7%	1.4 – 19.5%	1.6 – 16.4%
hLRT	TrN+I+Γ	TrN+Γ	TVM+I+Γ
AIC _c	GTR+I+ Γ	GTR+ Γ	GTR+I+ Γ
BIC	TrN+I+Γ	GTR+ Γ	TVM+I+Γ
DT	TrN+I+Γ	GTR+ Γ	TVM+I+Γ
Models	2	2	2
Δk	3	3	1

Data Set	16	17	18
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TreeBASE ID	S662/M1038	S736/M1168	S756/M1194
Haplotypes	295	22	39
Characters	2021	1106	677
P-distance	0 – 18.9%	0.2 – 23.3%	0 – 27.3%
hLRT	TrN+I+Γ	TIM+I+ Γ	TrN+Γ
AIC _c	GTR+I+ Γ	TIM+I+ Γ	TIM+ Γ
BIC	GTR+I+ Γ	TrN+Γ	TrN+Γ
DT	GTR+I+ Γ	TIM+ Γ	TrN+Γ
Models	2	3	2
Δk	3	2	1

Data Set	19	20	21
TreeBASE ID	S644/M1001	S1213/M2099	S1078/M1849
Haplotypes	93	38	30
Characters	3664	837	1892
P-distance	0.6 – 20.0%	0.1 – 7.0%	0.2 – 8.9%
hLRT	GTR+I+Γ	GTR+I+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
BIC	GTR+I+Γ	TIM+I+Γ	TrN+I+Γ
DT	GTR+I+Γ	TIM+I+Γ	TrN+I+Γ
Models	1	2	2
Δ k	0	2	3

Data Set	22	23	24
TreeBASE ID	S3x27x98c12c26c10/ M186c3x27x33c47	S1234/M2146	S1112/M1902
Haplotypes	55	15	206
Characters	1934	2270	931
P-distance	0.6 – 37.5%	1.1 – 17.3%	0 – 18.6%
hLRT	TrN+I+Γ	SYM+I+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
BIC	GTR+I+Γ	SYM+I+Γ	GTR+I+Γ
DT	GTR+I+Γ	SYM+I+Γ	GTR+I+Γ
Models	2	2	2
Δ k	3	3	3

Data Set	25	26	27
TreeBASE ID	S1316/M2309	S426/M620	S808/M1278

Haplotypes	32	24	86
Characters	2220	1477	698
P-distance	0 – 13.8%	1.2 – 27.4%	0.4 – 15.3%
hLRT	TrN+I+ Γ	GTR+I+Γ	K3Puf+I+Γ
AIC _c	TrN+I+ Γ	GTR+I+Γ	K3Puf+I+Γ
BIC	HKY+I+Γ	GTR+I+Γ	K3Puf+I+Γ
DT	TrN+I+ Γ	GTR+I+Γ	K3Puf+I+Γ
Models	2	1	1
Δk	1	0	0

Data Set	28	29	30
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TreeBASE ID	S1088/M1862	S498/M725	S1096/M1874
Haplotypes	19	38	34
Characters	988	350	1140
P-distance	0 – 3.8%	10.3 – 41.7%	1.2 – 20.3%
hLRT	HKY	TrN+I+Γ	TrN+I+ Γ
AIC _c	TVM+ Γ	GTR+I+ Γ	GTR+I+ Γ
BIC	F81	TrN+I+Γ	HKY+I+Γ
DT	HKY	TrN+I+Γ	HKY+I+Γ
Models	3	2	3
Δk	5	3	4

Data Set	31	32	33
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TreeBASE ID	S1315/M2308	S725/M1156	S259/M299
Haplotypes	26	35	42
Characters	2424	1166	1070
P-distance	1.1 – 16.1%	0 – 7.4%	0 – 11.5%

hLRT	TrN+I+Γ	HKY+I+Γ	TrN+I+Γ
AIC _c	TIM+I+Γ	HKY+I+Γ	GTR+I+Γ
BIC	TrN+I+Γ	K2P+I+Γ	TrNef+I+Γ
DT	TrN+I+Γ	K2P+I+Γ	TrNef+I+Γ
Models	2	2	3
Δ k	1	3	6

Data Set	34	35	36
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TreeBASE ID	S1069/M1823	S1095/M1873	S771/M1220
Haplotypes	46	38	15
Characters	618	3840	1018
P-distance	0 – 18.0%	0.2 – 19.4%	0 – 11.9%
hLRT	TrN+Γ	GTR+I+Γ	K3Puf+Γ
AIC _c	GTR+I	GTR+I+Γ	TVM+Γ
BIC	TrNef+Γ	GTR+I+Γ	K3Puf+Γ
DT	TrNef+Γ	GTR+I+Γ	K3Puf+Γ
Models	3	1	2
Δ k	6	0	2

Data Set	37	38	39
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TreeBASE ID	S428/M626	S553/M824	S1178/M2038
Haplotypes	10	48	40
Characters	1020	1866	1865
P-distance	0 – 16.1%	0.1 – 18.3%	0 – 28.7%
hLRT	HKY+Γ	TrNef+I+Γ	TrN+I+Γ
AIC _c	TVM+I	GTR+I+Γ	GTR+I+Γ
BIC	HKY+I	TrNef+I+Γ	TrN+Γ

DT	HKY+I	TrNef+I+Γ	TrN+Γ
Models	3	2	3
Δ k	3	6	4

Data Set	40	41	42
TreeBASE ID	S911/M1509	S570/M863	S724/M1155
Haplotypes	65	111	18
Characters	676	345	1350
P-distance	0 – 31.7%	0.3 – 32.8%	0 – 5.1%
hLRT	TrN+Γ	GTR+I+Γ	HKY
AIC _c	SYM+I+Γ	K3Puf+I+Γ	TrN
BIC	TrNef+Γ	K3P+I+Γ	K2P
DT	TIMef+Γ	K3P+I+Γ	K2P
Models	4	3	3
Δ k	4	6	4

Data Set	43	44	45
TreeBASE ID	S890/M1452	S390/M545	S693/M1102
Haplotypes	30	15	13
Characters	2428	645	435
P-distance	0 – 3.9%	0.2 – 25.0%	0.3 – 29.3%
hLRT	TIM+I+Γ	TVM+I+Γ	TrNef+Γ
AIC _c	TIM+I+Γ	TIM+I+Γ	SYM+Γ
BIC	TIM+I+Γ	HKY+I+Γ	TrNef+Γ
DT	TIM+I+Γ	HKY+I+Γ	TrNef+Γ
Models	1	3	2
Δ k	0	3	3

Data Set	46	47	48
TreeBASE ID	S1243/M2167	S425/M619	S1304/M2284
Haplotypes	47	35	39
Characters	1258	614	1633
P-distance	0 – 12.7%	0.2 – 14.7%	0 – 9.0%
hLRT	TrN+I+Γ	GTR+Γ	HKY+Γ
AIC _c	TrN+I+Γ	GTR+Γ	TVM+Γ
BIC	TrN+I+Γ	GTR+Γ	HKY+Γ
DT	TrN+I+Γ	GTR+Γ	HKY+I
Models	1	1	3
Δ k	0	0	3

Data Set	49	50	51
TreeBASE ID	S3x10x98c09c42c47/ M184c3x2x98c11c12c31	S333/M435	S1262/M2204
Haplotypes	30	27	33
Characters	3264	407	2034
P-distance	3.8 – 45.3%	0 – 18.5%	0 – 2.4%
hLRT	TrN+I+Γ	TVM+I+Γ	HKY+Γ
AIC _c	GTR+I+Γ	HKY+I+Γ	GTR+I
BIC	GTR+I+Γ	HKY+I+Γ	HKY+I
DT	GTR+I+Γ	HKY+I+Γ	HKY+I
Models	2	2	3
Δ k	3	3	4

Data Set	52	53	54
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TreeBASE ID	S2x14x97c16c11c45/ M165c2x14xM165c2x14x	S659/M1034	S711/M1134
Haplotypes	34	67	57
Characters	728	1871	1701
P-distance	1.8 – 27.5%	0 – 9.1%	0.5 – 27.5%
hLRT	TrN+Γ	TrNef+I+Γ	GTR+I+Γ
AIC _c	GTR+I+Γ	TrN+I+Γ	GTR+I+Γ
BIC	GTR+Γ	TrNef+I+Γ	GTR+I+Γ
DT	GTR+Γ	TrNef+I+Γ	GTR+I+Γ
Models	3	2	1
Δ k	4	3	0

Data Set	55	56	57
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TreeBASE ID	S1302/M2281	S679/M1064	S712/M1135
Haplotypes	41	40	46
Characters	1818	9237	1866
P-distance	1.8 – 40.8%	0.4 – 9.0%	0.5 – 12.9%
hLRT	TrN+I+Γ	GTR+I+Γ	TrN+I+Γ
AIC _c	TrN+I+Γ	GTR+I+Γ	TrN+I+Γ
BIC	TrN+I+Γ	GTR+I+Γ	TrN+I+Γ
DT	TrN+I+Γ	GTR+I+Γ	TrN+I+Γ
Models	1	1	1
Δ k	0	0	0

Data Set	58	59	60
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TreeBASE ID	S367/M502	S322/M401	S1046/M1782
Haplotypes	18	19	36
Characters	416	488	3486

P-distance	2.0 – 19.5%	3.1 – 31.4%	0.5 – 9.0%
hLRT	F81+Γ	TrN+Γ	TVM+I+Γ
AIC _c	TVM+Γ	TVM+Γ	GTR+I+Γ
BIC	F81+Γ	TVMef+Γ	TVM+I+Γ
DT	F81+Γ	TVMef+Γ	TVM+I+Γ
Models	2	3	2
Δ k	4	3	1

Data Set	61	62	63
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TreeBASE ID	S529/M777	S1217/M2104	S400/M568
Haplotypes	16	37	47
Characters	1521	3669	1017
P-distance	0.1 – 4.9%	1.1 – 23.5%	0.1 – 13.8%
hLRT	GTR+I+Γ	TrN+I+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	TIM+I+Γ
BIC	TIM+Γ	GTR+I+Γ	TIMef+I+Γ
DT	TIM+Γ	GTR+I+Γ	TIMef+I+Γ
Models	2	2	3
Δ k	3	3	3

Data Set	64	65	66
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TreeBASE ID	S958/M1589	S964/M1596	S522/M760
Haplotypes	51	20	20
Characters	1659	624	635
P-distance	0.2 – 15.0%	0.2 – 30.2%	2.2 – 50.0%
hLRT	TrN+I+Γ	HKY+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	TVM+I+Γ	GTR+I+Γ

BIC	GTR+I+Γ	K3Puf+Γ	TrNef+I+Γ
DT	GTR+I+Γ	K3Puf+Γ	TrNef+I+Γ
Models	2	3	3
Δ k	3	4	6

Data Set	67	68	69
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TreeBASE ID	S967/M1604	S608/M935	S385/M537
Haplotypes	21	43	18
Characters	1466	1177	702
P-distance	0 – 3.7%	0.1 – 17.8%	0.1 – 17.2%
hLRT	HKY+I+Γ	TVM+I+Γ	TrN+I+Γ
AIC _c	K3Puf+I+Γ	TIM+I+Γ	TrN+I+Γ
BIC	HKY+I	K3Puf+Γ	HKY+Γ
DT	HKY+I	K3Puf+Γ	HKY+Γ
Models	3	3	2
Δ k	2	3	2

Data Set	70	71	72
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TreeBASE ID	S6x22x97c14c38c41/ M170c6x22x97c14c48c20	S1000/M1688	S1227/M2133
Haplotypes	9	32	79
Characters	722	1566	3454
P-distance	2 – 13.0%	0.2 – 18.5%	0.1 – 36.6%
hLRT	TIM+I+Γ	TVM+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	TVM+Γ	GTR+I+Γ
BIC	TIM+I+Γ	TVM+Γ	GTR+I+Γ
DT	TIM+I+Γ	TVM+Γ	GTR+I+Γ
Models	2	1	2

Δk	2	0	3
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Data Set	73	74	75
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TreeBASE ID	S440/M647	S1212/M2098	S463/M676
Haplotypes	32	35	9
Characters	516	2977	902
P-distance	0.2 – 16.8%	0.8 – 15.4%	3.9 – 13.8%
hLRT	TrNef+I+Γ	TVM+I+Γ	TrN+I+Γ
AIC _c	TrNef+I+Γ	TVM+I+Γ	GTR+I+ Γ
BIC	TrNef+I+Γ	TVM+I+Γ	TrN+I+Γ
DT	TrNef+I+Γ	TVM+I+Γ	TrN+I+Γ
Models	1	1	2
Δk	0	0	3

Data Set	76	77	78
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TreeBASE ID	S990/M1650	S1013/M1709	S560/M847
Haplotypes	15	129	22
Characters	727	552	1047
P-distance	0 – 24.2%	0 – 15.3%	0.4 – 24.2%
hLRT	TrN+Γ	TVM+I+Γ	GTR+I+ Γ
AIC _c	TrN+I+ Γ	TVM+I+Γ	GTR+I+ Γ
BIC	TrN+Γ	TVM+I+Γ	TrN+I+Γ
DT	TrN+Γ	TVM+I+Γ	TrN+I+Γ
Models	2	1	2
Δk	1	0	3

Data Set	79	80	81
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TreeBASE ID	S1053/M1794	S980/M1630	S548/M808
Haplotypes	29	169	178
Characters	3427	1140	3251
P-distance	0.2 – 9.3%	0 – 27.5%	0.1 – 37.7%
hLRT	TrN+I+Γ	GTR+I+Γ	GTR+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
BIC	TVM+I+Γ	GTR+I+Γ	GTR+I+Γ
DT	TVM+I+Γ	GTR+I+Γ	GTR+I+Γ
Models	3	1	1
Δ k	3	0	0

Data Set	82	83	84
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TreeBASE ID	S1186/M2053	S605/M929	S1099/M1881
Haplotypes	64	66	77
Characters	1976	1335	611
P-distance	0.1 – 18.7%	0.2 – 16.1%	0 – 24.7%
hLRT	GTR+I+Γ	TIMEf+I+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
BIC	GTR+I+Γ	TIMEf+I+Γ	SYM+I+Γ
DT	GTR+I+Γ	GTR+I+Γ	SYM+I+Γ
Models	1	2	3
Δ k	0	5	3

Data Set	85	86	87
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TreeBASE ID	S945/M1568	S436/M641	S489/M714
Haplotypes	95	16	11

Characters	2967	841	738
P-distance	0 – 17.6%	0.1 – 10.7%	0 – 8.4%
hLRT	TVM+I+ Γ	TrN+I+ Γ	HKY+Γ
AIC _c	TVM+I+ Γ	TrN+I+ Γ	TVM+I
BIC	TVM+I+ Γ	TrN+Γ	TVM+I
DT	K3Puf+I+Γ	TrN+I	TVM+ Γ
Models	2	2	3
Δk	2	1	3

Data Set	88	89	90
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TreeBASE ID	S413/M603	S1192/M2059	S1313/M2305
Haplotypes	7	56	24
Characters	2308	4794	2371
P-distance	3.6 – 12.9%	0.2 – 76.4%	0 – 9.0%
hLRT	TIM+I+ Γ	TrN+I+Γ	TrN+I+ Γ
AIC _c	GTR+I+ Γ	GTR+I+ Γ	TIM+I+ Γ
BIC	TIM+Γ	GTR+I+ Γ	TrNef+I+Γ
DT	TIM+Γ	GTR+I+ Γ	TrNef+I+Γ
Models	3	2	3
Δk	3	3	4

Data Set	91	92	93
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TreeBASE ID	S472/M688	S1030/M1749	S1036/M1760
Haplotypes	34	74	43
Characters	1799	2253	568
P-distance	0.3 – 12.7%	0.2 – 32.1%	0.2 – 14.8%
hLRT	TrNef+I+Γ	TrN+I+ Γ	TVM+I+ Γ

AIC _c	TrN+I+Γ	K3Puf+I+Γ	GTR+I+Γ
BIC	TrNef+I+Γ	HKY+I+Γ	K3Puf+I+Γ
DT	TrN+I+Γ	HKY+I+Γ	K3Puf+I+Γ
Models	2	3	3
Δ k	3	1	3

Data Set	94	95	96
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TreeBASE ID	S432/M636	S578/M872	S804/M1270
Haplotypes	55	317	29
Characters	1456	530	1631
P-distance	3.9 – 32.2%	0 – 31.2%	0.1 – 9.2%
hLRT	TrN+I+Γ	GTR+Γ	TrNef+I+Γ
AIC _c	GTR+I+Γ	GTR+Γ	TrN+I+Γ
BIC	GTR+I+Γ	GTR+Γ	TrNef+I+Γ
DT	GTR+I+Γ	GTR+Γ	TrNef+I+Γ
Models	2	1	2
Δ k	3	0	3

Data Set	97	98	99
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TreeBASE ID	S821/M1318	S568/M861	S1051/M1792
Haplotypes	52	24	14
Characters	1303	1141	1756
P-distance	0.2 – 14.1%	0 – 17.3%	1.1 – 19.0%
hLRT	TIMef+I+Γ	GTR+Γ	GTR+I+Γ
AIC _c	GTR+I+Γ	TIM+I+Γ	GTR+I+Γ
BIC	TIMef+I+Γ	HKY+Γ	GTR+I+Γ
DT	TrN+I+Γ	HKY+Γ	GTR+I+Γ

Models	3	3	1
Δk	5	4	0

Data Set	100	101	102
TreeBASE ID	S11x6x95c10c11c33/ M58c11x6x95c10c13c27	S1094/M1869	S777/M1232
Haplotypes	13	14	41
Characters	718	7652	558
P-distance	0 – 19.5%	2.4 – 25.3%	0.2 – 14.0%
hLRT	TrNef+Γ	TrN+I+Γ	TrNef+I+Γ
AIC _c	SYM+ Γ	GTR+I+ Γ	TVM+I+ Γ
BIC	SYM+ Γ	GTR+I+ Γ	TVMef+I+ Γ
DT	SYM+ Γ	GTR+I+ Γ	TVMef+I+ Γ
Models	2	2	3
Δk	3	3	5

Data Set	103	104	105
TreeBASE ID	S421/M615	S916/M1516	S664/M1042
Haplotypes	50	10	44
Characters	1754	1042	1864
P-distance	0.4 – 19.4%	0.1 – 7.3%	0.4 – 12.6%
hLRT	GTR+I+ Γ	HKY	TrN+I+Γ
AIC _c	GTR+I+ Γ	HKY	TIM+I+ Γ
BIC	TrN+I+Γ	HKY	TrN+I+Γ
DT	TrN+I+Γ	HKY	TrN+I+Γ
Models	2	1	2
Δk	3	0	1

Data Set	106	107	108
TreeBASE ID	S1140/M1958	S671/M1053	S584/M880
Haplotypes	35	25	22
Characters	1433	583	1312
P-distance	0 – 8.4%	0 – 17.4%	0.1 – 7.1%
hLRT	TrN+I+Γ	TrNef+Γ	K2P+I+Γ
AIC _c	TrN+I+Γ	TrNef+I+Γ	TIM+I+Γ
BIC	TrN+I+Γ	TrNef+Γ	K2P+I
DT	TrN+I+Γ	TrNef+Γ	K2P+I
Models	1	2	3
Δ k	0	1	6

Data Set	109	110	111
TreeBASE ID	S753/M1189	S533/M780	S375/M515
Haplotypes	49	28	28
Characters	1668	707	406
P-distance	0.7 – 18.4%	2.3 – 39.6%	0.2 – 19.2%
hLRT	HKY+I+Γ	TrN+Γ	TVM+Γ
AIC _c	TVM+I+Γ	TIM+Γ	TrN+I+Γ
BIC	HKY+I+Γ	TrN+Γ	HKY+Γ
DT	HKY+I+Γ	TrN+Γ	HKY+Γ
Models	2	2	3
Δ k	3	1	3

Data Set	112	113	114
TreeBASE ID	S1197/M2066	S884/M1435	S1322/M2318

Haplotypes	11	25	134
Characters	1246	889	3688
P-distance	0.1 – 6.1%	0.2 – 14.5%	0 – 8.2%
hLRT	TVM+ Γ	HKY+Γ	GTR+I+Γ
AIC _c	TVM+I	TVM+ Γ	GTR+I+Γ
BIC	K3Puf+I	HKY+Γ	GTR+I+Γ
DT	K3Puf+I	HKY+Γ	GTR+I+Γ
Models	3	2	1
Δk	2	3	0

Data Set	115	116	117
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TreeBASE ID	S941/M1560	S6x23x97c17c57c34/ M171c6x23x97c18c01c10	S557/M837
Haplotypes	93	41	27
Characters	1204	1315	600
P-distance	0 – 8.7%	0.5 – 21.4%	5.7 – 17.1%
hLRT	F81+Γ	GTR+I+Γ	TVM+I+Γ
AIC _c	GTR+I+ Γ	GTR+I+Γ	GTR+I+ Γ
BIC	TVM+ Γ	GTR+I+Γ	GTR+I+ Γ
DT	TVM+ Γ	GTR+I+Γ	GTR+I+ Γ
Models	3	1	2
Δk	6	0	1

Data Set	118	119	120
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TreeBASE ID	S703/M1124	S1089/M1864	S1020/M1727
Haplotypes	104	122	112
Characters	2371	3304	2608
P-distance	0 – 7.3%	0 – 7.3%	0.1 – 31.3%

hLRT	TVM+ Γ	TVM+I+ Γ	GTR+I+ Γ
AIC _c	TVM+ Γ	TVM+I+ Γ	TVM+I+Γ
BIC	K3Puf+Γ	TVM+Γ	TVM+I+Γ
DT	K3Puf+Γ	TVM+Γ	TVM+I+Γ
Models	2	2	2
Δk	2	1	1

Data Set	121	122	123
TreeBASE ID	S1278/M2234	S1097/M1877	S619/M955
Haplotypes	44	33	18
Characters	1953	649	1420
P-distance	0.1 – 16.9%	0 -7.4%	1.5 – 9.7%
hLRT	TVM+I+ Γ	HKY+I+ Γ	GTR+I+ Γ
AIC _c	TVM+I+ Γ	HKY+I+ Γ	GTR+I+ Γ
BIC	K3Puf+I+Γ	K2P+I+Γ	SYM+I+Γ
DT	K3Puf+I+Γ	K2P+I+Γ	SYM+I+Γ
Models	2	2	2
Δk	2	3	3

Data Set	124	125	126
TreeBASE ID	S902/M1482	S824/M1323	S667/M1048
Haplotypes	28	18	30
Characters	950	936	3358
P-distance	0 – 17.8%	0.4 – 9.9%	0.3 – 27.2%
hLRT	TrN+I+ Γ	TrNef+I+Γ	TrN+I+Γ
AIC _c	TrN+I+ Γ	TrN+I+ Γ	GTR+I+ Γ
BIC	HKY+I+Γ	TrN+I+ Γ	TrN+I+Γ

DT	HKY+I+Γ	TrN+I+Γ	TrN+I+Γ
Models	2	2	2
Δ k	1	3	3

Data Set	127	128	129
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TreeBASE ID	S700/M1118	S1061/M1811	S731/M1163
Haplotypes	16	29	51
Characters	5113	598	535
P-distance	0.4 – 12.4%	0 – 13.1%	0.2 – 19.0%
hLRT	TrN+I+Γ	TrN+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	TrN+Γ	GTR+I+Γ
BIC	GTR+I+Γ	TrNef+Γ	TrN+I+Γ
DT	GTR+I+Γ	TrNef+Γ	TrN+I+Γ
Models	2	2	2
Δ k	3	3	3

Data Set	130	131	132
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TreeBASE ID	S1307/M2290	S470/M685	S681/M1066
Haplotypes	11	47	117
Characters	458	684	2233
P-distance	0.2 – 7.6%	0.1 – 14.8%	0 – 12.1%
hLRT	K3Puf+Γ	GTR+I+Γ	TVM+I+Γ
AIC _c	TVM+I	GTR+I+Γ	GTR+I+Γ
BIC	K3Puf+I	GTR+I+Γ	TVM+I+Γ
DT	K3Puf+Γ	GTR+I+Γ	TVM+I+Γ
Models	3	1	2
Δ k	2	0	1

Data Set	133	134	135
TreeBASE ID	S1052/M1793	S284/M322	S1071/M1827
Haplotypes	84	20	26
Characters	3434	345	1870
P-distance	0.1 – 22.5%	7.0 – 40.3%	2.0 – 18.4%
hLRT	TrN+I+Γ	SYM+I+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	TIM+I+Γ	TIM+I+Γ
BIC	GTR+I+Γ	TMef+I+Γ	TrN+I+Γ
DT	GTR+I+Γ	TMef+I+Γ	TrN+I+Γ
Models	2	3	2
Δ k	3	3	1

Data Set	136	137	138
TreeBASE ID	S554/M825	S1037/M1765	S816/M1305
Haplotypes	16	18	40
Characters	432	1276	725
P-distance	0 – 27.1%	0.4 – 4.8%	1.0 – 10.2%
hLRT	TVM+Γ	F81+Γ	TrNef+I+Γ
AIC _c	TVM+I+Γ	K3Puf+Γ	TrN+I+Γ
BIC	TVM+Γ	F81+Γ	TrNef+I+Γ
DT	TVM+Γ	F81+Γ	TrNef+I+Γ
Models	2	2	2
Δ k	1	2	3

Data Set	139	140	141
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TreeBASE ID	S643/M1000	S669/M1051	S1230/M2141
Haplotypes	8	13	101
Characters	835	2279	3259
P-distance	0.1 – 9.0%	7.9 – 19.8%	0 – 6.6%
hLRT	HKY	GTR+I+Γ	GTR+I+Γ
AIC _c	TrN+Γ	GTR+I+Γ	GTR+I+Γ
BIC	HKY	GTR+I+Γ	K3Puf+I+Γ
DT	TrN	GTR+I+Γ	K3Puf+I+Γ
Models	3	1	2
Δ k	2	0	3

Data Set	142	143	144
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TreeBASE ID	S647/M1013	S1296/M2273	S397/M565
Haplotypes	60	88	14
Characters	2804	837	7788
P-distance	0.1 – 11.9%	0 – 8.8%	1.5 – 60.7%
hLRT	GTR+I+Γ	TrN+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	TrNef+Γ	GTR+I+Γ
BIC	GTR+I+Γ	TrNef+Γ	GTR+I+Γ
DT	GTR+I+Γ	TrNef+Γ	GTR+I+Γ
Models	1	2	2
Δ k	0	3	3

Data Set	145	146	147
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TreeBASE ID	S404/M584	S997/M1673	S422/M616
Haplotypes	14	13	23
Characters	2145	1043	332

P-distance	1.5 – 8.4%	0 – 4.7%	3.4 – 19.6%
hLRT	TrNef+I+Γ	F81+Γ	TVM+I+Γ
AIC _c	GTR+I+Γ	TVM+Γ	TIM+I+Γ
BIC	TrNef+I+Γ	K3Puf+Γ	TrN+I+Γ
DT	TrNef+I+Γ	K3Puf+Γ	TrN+I+Γ
Models	2	3	3
Δ k	6	3	2

Data Set	148	149	150
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TreeBASE ID	S818/M1310	S357/M489	S1177/M2035
Haplotypes	25	21	106
Characters	1026	2513	2177
P-distance	0 – 6.4%	0.2 – 8.1%	0 – 25.1%
hLRT	TrNef+Γ	TrN+I+Γ	K3Puf+Γ
AIC _c	TIMef+I	TVM+I+Γ	GTR+Γ
BIC	TrNef+I	TVM+I+Γ	TIM+Γ
DT	TrNef+Γ	TVM+I+Γ	TIM+Γ
Models	3	2	3
Δ k	1	2	3

Data Set	151	152	153
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TreeBASE ID	S726/M1157	S351/M468	S971/M1612
Haplotypes	18	89	14
Characters	638	1143	2694
P-distance	0 – 19.6%	0.1 – 17.7%	0 – 1.3%
hLRT	HKY+Γ	GTR+I+Γ	F81
AIC _c	TVM+Γ	TVM+I+Γ	F81

BIC	TVM+ Γ	HKY+I+Γ	F81
DT	TVM+ Γ	HKY+I+Γ	F81
Models	2	3	1
Δk	3	4	0

Data Set	154	155	156
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TreeBASE ID	S1006/M1698	S1057/M1802	S658/M1032
Haplotypes	41	20	8
Characters	1689	2396	317
P-distance	0 – 11.4%	0 -12.0%	0.4 – 13.7%
hLRT	TrNef+I+Γ	GTR+I+Γ	F81
AIC _c	TIM+I+ Γ	GTR+I+Γ	K3Puf+I
BIC	TrNef+I+Γ	GTR+I+Γ	F81
DT	TrNef+I+Γ	GTR+I+Γ	F81
Models	2	1	2
Δk	4	0	3

Data Set	157	158	159
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TreeBASE ID	S657/M1031	S1180/M2041	S1090/M1865
Haplotypes	12	40	9
Characters	3628	2016	2088
P-distance	0.6 – 5.9%	0.1 – 9.3%	0 – 5.0%
hLRT	TrN+I+Γ	GTR+I+ Γ	K2P+I
AIC _c	GTR+I+ Γ	GTR+I+ Γ	TrN+I
BIC	GTR+I	TIM+I+Γ	K2P+I
DT	GTR+I	TIM+I+Γ	K2P+I
Models	3	2	2

Δk	3	2	4
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Data Set	160	161	162
TreeBASE ID	S466/M680	S799/M1265	S757/M1197
Haplotypes	12	41	121
Characters	532	461	539
P-distance	5.5 – 15.4%	0 – 17.9%	0 – 21.0%
hLRT	GTR+ Γ	TrN+ Γ	TVM+Γ
AIC _c	GTR+ Γ	TVM+I+ Γ	GTR+I+ Γ
BIC	TIM+Γ	TVMef+Γ	TVM+Γ
DT	TIM+Γ	TVMef+Γ	GTR+ Γ
Models	2	3	3
Δk	2	4	2

Data Set	163	164	165
TreeBASE ID	S928/M1538	S1023/M1734	S1229/M2139
Haplotypes	72	83	29
Characters	745	961	336
P-distance	0 – 26.0%	0 – 26.7%	0 – 2.1%
hLRT	TrN+I+ Γ	GTR+I+ Γ	HKY
AIC _c	GTR+I+ Γ	GTR+I+ Γ	HKY+I
BIC	TrNef+I+Γ	TVM+I+Γ	HKY
DT	TrNef+I+Γ	TVM+I+Γ	HKY+ Γ
Models	3	2	3
Δk	6	1	1

Data Set	166	167	168
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TreeBASE ID	S305/M347	S1161/M1998	S414/M604
Haplotypes	38	34	5
Characters	1171	873	256
P-distance	0.1 – 16.3%	0 – 35.5%	0.8 – 7.8%
hLRT	TrN+I+Γ	TrN+Γ	HKY
AIC _c	GTR+I+Γ	TIM+Γ	HKY
BIC	GTR+I+Γ	HKY+Γ	HKY
DT	GTR+I+Γ	HKY+Γ	HKY
Models	2	3	1
Δ k	3	2	0

Data Set	169	170	171
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TreeBASE ID	S1059/M1806	S969/M1606	S1125/M1928
Haplotypes	32	78	23
Characters	1832	613	1099
P-distance	0.1 – 15.3%	0 – 13.6%	0 – 26.9%
hLRT	TrNef+I+Γ	TVM+Γ	TrNef+Γ
AIC _c	GTR+I+Γ	GTR+Γ	TrN+Γ
BIC	TrNef+I+Γ	TVM+Γ	TrNef+Γ
DT	TrNef+I+Γ	TVM+Γ	TrNef+Γ
Models	2	2	2
Δ k	6	1	3

Data Set	172	173	174
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TreeBASE ID	S1301/M2279	S543/M801	S1041/M1775
Haplotypes	60	35	102

Characters	3487	4499	591
P-distance	1.1 – 31.6%	2.0 – 19.1%	0 – 26.7%
hLRT	HKY+I+Γ	TrN+I+Γ	HKY+Γ
AIC _c	TVM+I+Γ	GTR+I+Γ	HKY+Γ
BIC	K3Puf+I+Γ	GTR+I+Γ	HKY+Γ
DT	K3Puf+I+Γ	GTR+I+Γ	HKY+Γ
Models	3	2	1
Δ k	3	3	0

Data Set	175	176	177
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TreeBASE ID	S701/M1119	S887/M1438	S1199/M2068
Haplotypes	11	31	50
Characters	1178	433	1327
P-distance	0.1 – 12.4%	0.2 – 7.6%	0.2 – 13.4%
hLRT	TVM+Γ	HKY+I+Γ	HKY+Γ
AIC _c	TVM+I	TVM+I+Γ	TVM+Γ
BIC	K3Puf+I	HKY+I+Γ	TVM+Γ
DT	K3Puf+I	HKY+I+Γ	TVM+Γ
Models	3	2	2
Δ k	2	3	3

Data Set	178	179	180
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TreeBASE ID	S655/M1029	S709/M1131	S1028/M1746
Haplotypes	78	119	16
Characters	2555	5923	1337
P-distance	2.8 – 36.0%	0 – 29.8%	0.2 – 20.0%
hLRT	TrN+I+Γ	TrN+I+Γ	HKY+Γ

AIC _c	GTR+I+Γ	GTR+I+Γ	TVM+Γ
BIC	GTR+I+Γ	GTR+I+Γ	HKY+Γ
DT	GTR+I+Γ	GTR+I+Γ	HKY+Γ
Models	2	2	2
Δ k	3	3	3

Data Set	181	182	183
TreeBASE ID	S833/M1334	S672/M1054	S331/M433
Haplotypes	29	20	5
Characters	1633	513	617
P-distance	0.1 – 10.2%	0 – 29.3%	0.5 – 7.8%
hLRT	HKY+Γ	F81+Γ	HKY+Γ
AIC _c	HKY+Γ	TrN+Γ	HKY+I
BIC	HKY+Γ	TrN+Γ	K2P+I
DT	HKY+Γ	TrN+Γ	HKY+Γ
Models	1	2	3
Δ k	0	2	3

Data Set	184	185	186
TreeBASE ID	S903/M1483	S1162/M1999	S1001/M1692
Haplotypes	92	20	77
Characters	647	1718	701
P-distance	0 – 29.9%	0.1 – 18.5%	0 – 33.3%
hLRT	TrN+I+Γ	TVM+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	TVM+I+Γ	TIM+I+Γ
BIC	SYM+I+Γ	HKY+Γ	TrNef+I+Γ
DT	SYM+I+Γ	HKY+Γ	TrNef+I+Γ

Models	3	3	3
Δk	3	4	4

Data Set	187	188	189
TreeBASE ID	S892/M1465	S1195/M2064	S798/M1263
Haplotypes	26	136	36
Characters	887	5176	1010
P-distance	0 – 35.4%	0 – 4.1%	0.1 – 24.5%
hLRT	HKY+Γ	HKY+I+Γ	GTR+I+Γ
AIC _c	TVM+I+ Γ	GTR+I+ Γ	GTR+I+Γ
BIC	HKY+Γ	HKY+I+Γ	GTR+I+Γ
DT	HKY+Γ	HKY+I+Γ	GTR+I+Γ
Models	2	2	1
Δk	4	4	0

Data Set	190	191	192
TreeBASE ID	S1018/M1725	S1155/M1984	S979/M1629
Haplotypes	23	18	46
Characters	2708	585	3341
P-distance	1.5 – 23.7%	0 – 6.8%	0.1 – 14.6%
hLRT	TrN+I+Γ	HKY	TrN+I+Γ
AIC _c	GTR+I+ Γ	TrN+ Γ	GTR+I+ Γ
BIC	GTR+I+ Γ	HKY	GTR+I+ Γ
DT	GTR+I+ Γ	HKY	GTR+I+ Γ
Models	2	2	2
Δk	3	2	3

Data Set	193	194	195
TreeBASE ID	S532/M779	S935/M1550	S1101/M1883
Haplotypes	84	20	19
Characters	982	822	1016
P-distance	0.2 – 22.4%	0 – 30.7%	0 – 27.3%
hLRT	TrN+I+Γ	TrNef+Γ	TrN+Γ
AIC _c	GTR+I+Γ	GTR+I	GTR+I+Γ
BIC	GTR+I+Γ	TrNef+Γ	TIMEf+Γ
DT	GTR+I+Γ	TrNef+I+Γ	TIMEf+Γ
Models	2	3	3
Δ k	3	6	6

Data Set	196	197	198
TreeBASE ID	S1008/M1704	S1050/M1790	S621/M959
Haplotypes	16	28	15
Characters	1324	2504	532
P-distance	0 – 11.4%	0 – 3.2%	0 – 10.3%
hLRT	HKY+Γ	TVM+Γ	TIMEf+Γ
AIC _c	K3Puf+I+Γ	TVM+I	TIMEf+Γ
BIC	HKY+Γ	TVM+I	TIMEf+Γ
DT	HKY+Γ	TVM+I+Γ	TIMEf+I
Models	2	3	2
Δ k	2	1	0

Data Set	199	200	201
TreeBASE ID	S1092/M1867	S914/M1512	S1312/M2300

Haplotypes	13	43	21
Characters	810	1027	1870
P-distance	0 – 12.9%	0.1 – 16.9%	0.6 – 22.5%
hLRT	K3Puf+Γ	GTR+I+Γ	TrN+I+Γ
AIC _c	K3Puf+I	GTR+I+Γ	GTR+I+Γ
BIC	K3Puf+I	GTR+I+Γ	TrN+I+Γ
DT	K3Puf+I	GTR+I+Γ	TrN+I+Γ
Models	2	1	2
Δ k	0	0	3

Data Set	202	203	204
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TreeBASE ID	S1320/M2316	S838/M1354	S1044/M1780
Haplotypes	75	86	64
Characters	1154	1519	6399
P-distance	0.1 – 20.5%	0 – 16.8%	0 – 25.5%
hLRT	GTR+I+Γ	TVM+Γ	GTR+I+Γ
AIC _c	GTR+I+Γ	TVM+Γ	GTR+I+Γ
BIC	GTR+I+Γ	TVM+Γ	GTR+I+Γ
DT	GTR+I+Γ	TVM+Γ	GTR+I+Γ
Models	1	1	1
Δ k	0	0	0

Data Set	205	206	207
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TreeBASE ID	S1295/M2266	S920/M1521	S1298/M2276
Haplotypes	51	46	109
Characters	5638	4483	1611
P-distance	1.6 – 19.3%	0.2 – 41.9%	0.1 – 13.4%

hLRT	GTR+I+Γ	GTR+I+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
BIC	GTR+I+Γ	TVMef+I+Γ	TrN+I+Γ
DT	GTR+I+Γ	TrN+I+Γ	TrN+I+Γ
Models	1	3	2
Δ k	0	4	3

Data Set	208	209	210
TreeBASE ID	S1253/M2191	S338/M441	S565/M856
Haplotypes	18	19	44
Characters	510	664	1134
P-distance	0 – 17.0%	0.2 – 11.1%	0.1 – 22.6%
hLRT	HKY+Γ	HKY+Γ	K2P+Γ
AIC _c	HKY+Γ	TVM+Γ	GTR+I+Γ
BIC	K2P+Γ	HKY+Γ	HKY+Γ
DT	K2P+Γ	HKY+Γ	HKY+Γ
Models	2	2	3
Δ k	3	3	8

Data Set	211	212	213
TreeBASE ID	S1010/M1706	S384/M536	S1303/M2283
Haplotypes	143	33	28
Characters	458	2418	1705
P-distance	0 – 12.1%	1.1 – 25.1%	0.1 – 10.9%
hLRT	TrN+Γ	TrN+I+Γ	K2P+I+Γ
AIC _c	SYM+Γ	GTR+I+Γ	K2P+I+Γ
BIC	SYM+Γ	GTR+I+Γ	K2P+I+Γ

DT	SYM+Γ	GTR+I+ Γ	K2P+I+Γ
Models	2	2	1
Δk	0	3	0

Data Set	214	215	216
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TreeBASE ID	S524/M765	S837/M1353	S392/M548
Haplotypes	24	60	59
Characters	1012	2896	1429
P-distance	8.5 – 25.6%	0.4 – 36.6%	0.1 – 21.1%
hLRT	TVM+I+Γ	GTR+I+Γ	TrN+I+Γ
AIC _c	GTR+I+ Γ	GTR+I+Γ	GTR+I+ Γ
BIC	GTR+I+ Γ	GTR+I+Γ	TrN+I+Γ
DT	GTR+I+ Γ	GTR+I+Γ	TrN+I+Γ
Models	2	1	2
Δk	1	0	3

Data Set	217	218	219
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TreeBASE ID	S1072/M1828	S496/M722	S1122/M1919
Haplotypes	29	13	27
Characters	3505	633	567
P-distance	0 – 13.8%	0.2 – 26.4%	0.2 – 21.7%
hLRT	GTR+I+Γ	K2P+Γ	GTR+ Γ
AIC _c	GTR+I+Γ	SYM+I	SYM+I+ Γ
BIC	GTR+I+Γ	K2P+I	SYM+Γ
DT	GTR+I+Γ	K2P+I	SYM+Γ
Models	1	3	3
Δk	0	4	3

Data Set	220	221	222
TreeBASE ID	S1200/M2069	S983/M1636	S773/M1224
Haplotypes	53	6	26
Characters	651	953	430
P-distance	3.2 – 23.0%	0.3 – 14.4%	0 – 26.8%
hLRT	TVM+I+Γ	TrN+Γ	TVM+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	TIM+I+Γ
BIC	GTR+I+Γ	K2P+I	TrN+I+Γ
DT	GTR+I+Γ	K2P+Γ	TrN+I+Γ
Models	2	4	3
Δ k	1	8	2

Data Set	223	224	225
TreeBASE ID	S1310/M2295	S1126/M1930	S836/M1352
Haplotypes	44	18	27
Characters	3341	1081	2365
P-distance	0 – 19.3%	0 – 3.7%	1.2 – 9.3%
hLRT	GTR+I+Γ	TrN+I+Γ	GTR+I+Γ
AIC _c	GTR+I+Γ	TrN+I	GTR+I+Γ
BIC	K3Puf+I+Γ	TrNef+I	TVM+I+Γ
DT	K3Puf+I+Γ	TrNef+I	TVM+I+Γ
Models	2	3	2
Δ k	3	4	1

Data Set	226	227	228
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TreeBASE ID	S1102/M1884	S396/M564	S382/M529
Haplotypes	79	37	6
Characters	693	1377	2152
P-distance	0 – 13.5%	0.1 – 17.7%	0.5 – 10.3%
hLRT	TrN+I+Γ	TrN+I+Γ	TrNef+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	TrN+I
BIC	TrN+I+Γ	TrN+I+Γ	K2P+I
DT	TrN+I+Γ	TrN+I+Γ	TrNef+I
Models	2	2	4
Δ k	3	3	4

Data Set	229	230	231
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TreeBASE ID	S1305/M2286	S962/M1594	S1007/M1700
Haplotypes	36	28	18
Characters	2002	1603	842
P-distance	0.6 – 16.1%	0.1 – 19.2%	0 – 2.4%
hLRT	TrN+I+Γ	HKY+Γ	K3Puf
AIC _c	TrN+I+Γ	TVM+Γ	K3Puf
BIC	TrN+I+Γ	TVM+Γ	K3Puf
DT	TrN+I+Γ	TVM+Γ	K3Puf
Models	1	2	1
Δ k	0	3	0

Data Set	232	233	234
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TreeBASE ID	S1014/M1717	S737/M1169	S1289/M2256
Haplotypes	25	23	160
Characters	2889	1545	2273

P-distance	0 – 17.7%	3.6 – 24.5%	0 – 14.6%
hLRT	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
BIC	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
DT	GTR+I+Γ	GTR+I+Γ	GTR+I+Γ
Models	1	1	1
Δ k	0	0	0

Data Set	235	236	237
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TreeBASE ID	S792/M1215	S1270/M2218	S1231/M2143
Haplotypes	39	80	27
Characters	2066	764	416
P-distance	1.2 – 26.0%	0.1 – 13.9%	1.3 – 22.8%
hLRT	GTR+I+Γ	TrN+I+Γ	TVM+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	TVM+I+Γ
BIC	GTR+I+Γ	GTR+I+Γ	K3Puf+I+Γ
DT	GTR+I+Γ	GTR+I+Γ	K3Puf+I+Γ
Models	1	2	2
Δ k	0	3	2

Data Set	238	239	240
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TreeBASE ID	S1075/M1832	S1070/M1826	S403/M581
Haplotypes	81	49	11
Characters	1826	1693	1259
P-distance	0 – 21.1%	0.4 – 8.1%	0.4 – 30.2%
hLRT	TrN+I+Γ	HKY+Γ	K2P+Γ
AIC _c	TrN+I+Γ	TrN+Γ	HKY+I

BIC	TrN+I+Γ	HKY+Γ	K2P+I
DT	TrN+I+Γ	HKY+Γ	K2P+I
Models	1	2	3
Δ k	0	1	3

Data Set	241	242	243
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TreeBASE ID	S1127/M1933	S1163/M2000	S537/M787
Haplotypes	39	33	138
Characters	915	672	686
P-distance	0 – 13.0%	0 – 21.0%	0 – 17.2%
hLRT	HKY+Γ	K2P+Γ	TrN+I+Γ
AIC _c	TVM+Γ	GTR+Γ	SYM+I+Γ
BIC	K2P+Γ	K2P+Γ	TrNef+I+Γ
DT	K2P+Γ	K2P+Γ	TrNef+I+Γ
Models	3	2	3
Δ k	6	7	3

Data Set	244	245	246
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TreeBASE ID	S1235/M2149	S1216/M2102	S1039/M1769
Haplotypes	14	23	8
Characters	1669	896	1590
P-distance	0.9 – 10.7%	0 – 11.7%	0.1 – 12.5%
hLRT	TrN+I+Γ	TrNef+I+Γ	TrN+I+Γ
AIC _c	GTR+I+Γ	GTR+I+Γ	TrN+I+Γ
BIC	TrNef+I+Γ	TrN+I+Γ	HKY+Γ
DT	K2P+I+Γ	TrN+I+Γ	HKY+I
Models	4	3	3

Δk	7	6	2
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Data Set	247	248	249
TreeBASE ID	S1060/M1809	S368/M503	S389/M543
Haplotypes	57	25	54
Characters	1824	321	1018
P-distance	0.1 – 31.2%	0.4 – 31.5%	0 – 16.4%
hLRT	GTR+I+ Γ	GTR+ Γ	TrN+I+Γ
AIC _c	GTR+I+ Γ	GTR+ Γ	GTR+I+ Γ
BIC	TVM+I+Γ	TIM+Γ	TrN+I+Γ
DT	TVM+I+Γ	TIM+Γ	TrN+I+Γ
Models	2	2	2
Δk	1	2	3

Data Set	250
TreeBASE ID	S939/M1556
Haplotypes	57
Characters	684
P-distance	0 – 33.7%
hLRT	TrN+Γ
AIC _c	SYM+Γ
BIC	SYM+Γ
DT	SYM+Γ
Models	2
Δk	0

REFERENCES

1. Aedo, C., O. Fiz, M. L. Alarcón, C. Navarro, and J. J. Aldasoro. 2005. Taxonomic revision of *Geranium* sect. *Dissecta* (Geraniaceae). *Syst. Bot.* 30:533-558.
2. Agretious Thomas, K., U. Peintner, M. M. Moser, and P. Manimohan. 2002. *Anamika*, a new mycorrhizal genus of Cortinariaceae from India and its phylogenetic position based on ITS and LSU sequences. *Mycol. Res.* 106:245-251.
3. Alverson, W. S., B. A. Whitlock, R. Nyffeler, C. Bayer, and D. A. Baum. 1999. Phylogeny of the core Malvales: Evidence from *ndhF* sequence data. *Am. J. Bot.* 86:1474-1486.
4. Anderson, F. E., A. J. Córdoba, and M. Thollesson. 2004. Bilaterian phylogeny based on analyses of a region of the sodium-potassium ATPase α -subunit gene. *J. Mol. Evol.* 58:252-268.
5. Anderson, J. L., W. Chen, and C. A. Shearer. 2001. Phylogeny of *Halosarpheia* based on 18S rDNA. *Mycologia* 93:897-906.
6. Anikster, Y., L. J. Szabo, T. Eilam, J. Manisterski, S. T. Koike, and W. R. Bushnell. 2004. Morphology, life cycle biology, and DNA sequence analysis of rust fungi on garlic and chives from California. *Phytopathology* 94:569-577.
7. Austin, J. W., A. L. Szalanski, P. Uva, and A. Kence. 2002. A comparative genetic analysis of the subterranean termite genus *Reticulitermes* (Isoptera: Rhinotermitidae). *Ann. Entomol. Soc. Am.* 95:753-760.
8. Avis, P. G., D. J. McLaughlin, B. C. Dentinger, and P. B. Reich. 2003. Long-term increase in nitrogen supply alters above- and below-ground ectomycorrhizal communities and increases the dominance of *Russula* spp. in a temperate oak savanna. *New Phytol.* 160:239-253.
9. Baker, R. H., and R. DeSalle. 1997. Multiple sources of character information and the phylogeny of Hawaiian drosophilids. *Syst. Biol.* 46:654-673.
10. Bakkeren, G., J. W. Kronstad, and C. A. Levesque. 2000. Comparison of AFLP fingerprints and ITS sequences as phylogenetic markers in Ustilaginomycetes. *Mycologia* 92:510-521.
11. Barkman, T. J., S.-H. Lim, K. M. Salleh, and J. Nais. 2004. Mitochondrial DNA sequences reveal the photosynthetic relatives of *Rafflesia*, the world's largest flower. *P. Natl. Acad. Sci. USA* 101:787-792.
12. Barnes, I., J. Roux, B. D. Wingfield, M. J. Dudzinski, K. M. Old, and M. J. Wingfield. 2003. *Ceratocystis pirilliformis*, a new species from *Eucalyptus nitens* in Australia. *Mycologia* 95:865-871.
13. Behnke, A., T. Friedl, V. A. Chepurnov, and D. G. Mann. 2004. Reproductive compatibility and rDNA sequence analyses in the *Sellaphora pupula* species complex (Bacillariophyta). *J.*

Phycol. 40:193-208.

14. Bell, C. D., and M. J. Donoghue. 2003. Phylogeny and biogeography of Morinaceae (Dipsacales) based on nuclear and chloroplast DNA sequences. *Org. Divers. Evol.* 3:227-237.
15. Bell, C. D., E. J. Edwards, S-T. Kim, and M. J. Donoghue. 2001. Dipsacales phylogeny based on chloroplast DNA sequences. *Har. Pap. Bot.* 6:481-499.
16. Berbee, M. L. 2001. The phylogeny of plant and animal pathogens in the Ascomycota. *Physiol. Mol. Plant P.* 59:165-187.
17. Bergerow, D., R. Bauer, and F. Oberwinkler. 2001. *Muribasidiospora: Microstromatales or Exobasidiales?* *Mycol. Res.* 105:798-810.
18. Beyra-Matos, A., and M. Lavin. 1999. A monograph of Pictetia (Papilionoideae; Leguminosae) and a review of the tribe Aeschynomeneae. *Syst. Bot. Monographs* 56:1-93.
19. Binder, M., and D. S. Hibbett. 2002. Higher-level phylogenetic relationships of homobasidiomycetes (mushroom-forming fungi) inferred from four rDNA regions. *Mol. Phylogenet. Evol.* 22:76-90.
20. Bischoff, J. F., R. F. Sullivan, K. M. Kjer, and J. F. White, Jr. 2004. Phylogenetic placement of the anamorphic tribe Ustilaginoideae (Hypocreales, Ascomycota). *Mycologia* 96:1088-1094.
21. Blanco, O., A. Crespo, P. K. Divakar, J. A. Elix, and H. T. Lumbsch. 2005. Molecular phylogeny of parmotreoid lichens (Ascomycota, Parmeliaceae). *Mycologia* 97:150-159.
22. Blaxter M. L., P. De Ley, J. R. Garey, L. X. Liu, P. Scheldeman, A. Vierstraete, J. R. Vanfleteren, L. Y. Mackey, M. Dorris, L. M. Frisse, J. T. Vida, and W. K. Thomas. 1998. A molecular evolutionary framework for the phylum Nematoda. *Nature* 392:71-75.
23. Bleidorn, C., L. Vogt, and T. Bartolomaeus. 2005. Molecular phylogeny of lugworms (Annelida, Arenicolidae) inferred from three genes. *Mol. Phylogenet. Evol.* 34:673-679.
24. Bodensteiner, P., M. Binder, J.-M. Moncalvo, R. Agerer, and D. S. Hibbett. 2004. Phylogenetic relationships of cyphelloid homobasidiomycetes. *Mol. Phylogenet. Evol.* 33:501-515.
25. Brandli, L., L.-J. Lawson Handley, P. Vogel, and N. Perrin. 2005. Evolutionary history of the greater white-toothed shrew (*Crocidura russula*) inferred from analysis of mtDNA, Y and X chromosome markers. *Mol. Phylogenet. Evol.* 37:832-844.
26. Brower, A. V. Z., and R. DeSalle. 1998. Patterns of mitochondrial versus nuclear DNA sequence divergence among nymphalid butterflies: The utility of wingless as a source of

characters for phylogenetic inference. *Insect Mol. Biol.* 7:73-82.

27. Buck, W. R., B. Goffinet, and A. J. Shaw. 2000. Testing morphological concepts of orders of pleurocarpous mosses (Bryophyta) using phylogenetic reconstructions based on trnL-trnF and rps4 sequences. *Mol. Phylogenet. Evol.* 16:180-198.
28. Bunsawat, J., N. E. Elliott, K. L. Hertweck, E. Sproles, and L. A. Alice. 2004. Phylogenetics of *Mentha* (Lamiaceae): Evidence from chloroplast DNA sequences. *Syst. Bot.* 29:959-964.
29. Campbell, D. L., A. V. Z. Brower, and N. E. Pierce. 2000. Molecular evolution of the wingless gene and its implications for the phylogenetic placement of the butterfly family Riodinidae (Lepidoptera: Papilionoidea). *Mol. Biol. Evol.* 17:684-696.
30. Castillo A. H., M. N. Cortinas, and E. P. Lessa. 2005. Rapid diversification of South American tuco-tucos (*Ctenomys*; Rodentia, Ctenomyidae): Contrasting mitochondrial and nuclear intron sequences. *J. Mammal.* 86:170-179.
31. Chaverri P., J. F. Bischoff, H. C. Evans, and K. T. Hodge. 2005. *Regiocrella*, a new entomopathogenic genus with a pycnidial anamorph and its phylogenetic placement in the Clavicipitaceae. *Mycologia* 97:1225-1237.
32. Chaverri, P., L. A. Castlebury, G. J. Samuels, and D. M. Geiser. 2003. Multilocus phylogenetic structure within the *Trichoderma harzianum*/*Hypocrea lixii* complex. *Mol. Phylogenet. Evol.* 27:302-313.
33. Chen, W., C. A. Shearer, and J. L. Crane. 1999. Phylogeny of *Ophioceras* spp. based on morphological and molecular data. *Mycologia* 91:84-94.
34. Chen, Z. D., and J. Li. 2004. Phylogenetics and biogeography of *Alnus* (Betulaceae) inferred from sequences of nuclear ribosomal DNA ITS region. *Int. J. Plant Sci.* 165:325-335.
35. Cho, G. Y., S. H. Lee, and S. M. Boo. 2004. A new brown algal order, Ishigeales (Phaeophyceae), established on the basis of plastid protein-coding rbcL, psaA, and psbA region comparisons. *J. Phycol.* 40:921-936.
36. Coetzee, M. P. A, B. D. Wingfield, P. Bloomer, G. S. Ridley and M. J. Wingfield. 2003. Molecular identification and phylogeny of *Armillaria* isolates from South America and Indo-Malaysia. *Mycologia* 95:285-293.
37. Cohen, B. L., A. J. Baker, K. Blechschmidt, D. L. Dittmann, R. W. Furness, J. A. Gerwin, A. J. Helbig, J. De Korte, H. D. Marshall, R. L. Palma, H. U. Peter, R. Ramli, I. Siebold, M. S. Willcox, R. H. Wilson, and R. M. Zink. 1997. Enigmatic phylogeny of skuas (Aves: Stercorariidae). *P. Roy. Soc. Lond. B Bio.* 264:181-190.

38. Cohen, B. L., A. Gawthrop, and T. Cavalier-Smith. 1998. Molecular phylogeny of brachiopods and phoronids based on nuclear-encoded small subunit ribosomal RNA gene sequences. *Philos. T. Roy. Soc. B.* 353:2039-2061.
39. Crous, P. W., J. Z. Groenewald, K. Pongpanich, W. Himaman, M. Arzanlou, and M. J. Wingfield. 2004. Cryptic speciation and host specificity among *Mycosphaerella* spp. occurring on Australian *Acacia* species grown as exotics in the tropics. *Stud. Mycol.* 50:457-469.
40. Crous, P. W., J. Z. Groenewald, M. J. Wingfield, and A. Aptroot. 2003. The value of ascospore septation in separating *Mycosphaerella* from *Sphaerulina* in the Dothideales: A Saccardoan myth? *Sydowia* 55:136-152.
41. Cruickshank, R. H., K. P. Johnson, V. S. Smith, R. J. Adams, D. H. Clayton and R. D. M. Page. 2001. Phylogenetic analysis of partial sequences of elongation factor 1 α identifies major groups of lice (Insecta: Phthiraptera). *Mol. Phylogenet. Evol.* 19:202-215.
42. Cruse, M., R. Telerant, T. Gallagher, T. Lee, and J. Taylor. 2002. Cryptic species in *Stachybotrys chartarum*. *Mycologia* 94:814-822.
43. Datwyler, S. L., and A. D. Wolfe. 2004. Phylogenetic relationships and morphological evolution in *Penstemon* subg. *Dasanthera* (Veronicaceae). *Syst. Bot.* 29:165-176.
44. Davis, G. M., T. Wilke, C. Spolsky, C.-P. Qiu, D.-C. Qui, M.-Y. Xia, Y. Zhang and G. Rosenberg. 1998. Cytochrome oxidase I-based phylogenetic relationships among the Pomatiopsidae, Hydrobiidae, Rissoidae and Truncatellidae (Gastropoda: Caenogastropoda: Rissoacea). *Malacologia* 40:251-266.
45. Deckert, R. J., T. Hsiang, and R. L. Peterson. 2002. Genetic relationships of endophytic *Lophodermium nitens* isolates from needles of *Pinus strobus*. *Mycol. Res.* 106:305-313.
46. De Clerck, O., B. Gavio, I. Barbara, S. Fredericq, and E. Coppejans. 2005. Systematics of *Grateloupia filicina* (Halymeniaceae, Rhodophyta), based on *rbcl* sequence analyses and morphological evidence, including the reinstatement of *G. minima* and the description of *G. capensis* sp. nov. *J. Phycol.* 41:391-410.
47. DePamphilis, C. W., N. D. Young, and A. D. Wolfe. 1997. Evolution of plastid gene *rps2* in a lineage of hemiparasitic and holoparasitic plants: Many losses of photosynthesis and complex patterns of rate variation. *Proc. Natl. Acad. Sci. USA* 94:7367-7372.
48. Devos, N., S.-H. Oh, O. Raspe, A.-L. Jacquemart, and P. S. Manos. 2005. Nuclear ribosomal DNA sequence variation and evolution of spotted marsh-orchids (*Dactylorhiza maculata* group). *Mol. Phylogenet. Evol.* 36:568-580.
49. Donoghue, M. J., and S. Mathews. 1998. Duplicate genes and the root of the angiosperms, with an example using phytochrome sequences. *Mol. Phylogenet. Evol.* 9:489-500.

50. Douris V., R. A. D. Cameron, G. C. Rodakis, and R. Lecanidou. 1998. Mitochondrial phylogeography of the land snail *Albinaria* in Crete: Long-term geological and short-term vicariance effects. *Evolution* 52:116-125.
51. Edwards, C. E., D. E. Soltis, and P. S. Soltis. 2006. Molecular phylogeny of *Conradina* and other scrub mints (Lamiaceae) from the southeastern USA: Evidence for hybridization in Pleistocene refugia? *Syst. Bot.* 31:193-207.
52. Eriksson, T., M. J. Donoghue, and M. Hibbs. 1998. Phylogenetic analysis of *Potentilla* using DNA sequences of nuclear ribosomal internal transcribed spacers (ITS), and implications for the classification of Rosoideae (Rosaceae). *Plant Syst. Evol.* 211:155-179.
53. Erseus, C., M. Kallersjo, M. Ekman, and R. Hovmoller. 2002. 18S rDNA phylogeny of the Tubificidae (Clitellata) and its constituent taxa: Dismissal of the Naididae. *Mol. Phylogenet. Evol.* 22:414-422.
54. Fewer, D., T. Friedl, and B. Budel. 2002. *Chroococcidiopsis* and heterocyst-differentiating cyanobacteria are each other's closest living relatives. *Mol. Phylogenet. Evol.* 23:82-90.
55. Fischer, W. M., and J. D. Palmer. 2005. Evidence from small-subunit ribosomal RNA sequences for a fungal origin of Microsporidia. *Mol. Phylogenet. Evol.* 36:606-622.
56. Fishbein, M., C. Hibsche-Jetter, D. E. Soltis, and L. Hufford. 2001. Phylogeny of Saxifragales (Angiosperms, Eudicots): Analysis of a rapid, ancient radiation. *Syst. Biol.* 50:817-847.
57. Friedl, T. and C. J. O'Kelly. 2002. Phylogenetic relationships of green algae assigned to the genus *Planophila* (Chlorophyta): Evidence from 18S rDNA sequence data and ultrastructure. *Eur. J. Phycol.* 37:373-384.
58. Friedlander, T. P., J. C. Regier, C. Mitter, and D. L. Wagner. 1996. A nuclear gene for higher level phylogenetics: Phosphoenolpyruvate carboxykinase tracks Mesozoic-age levels within Lepidoptera (Insecta). *Mol. Biol. Evol.* 13:594-604.
59. Friedrich, M., and D. Tautz. 1997. Evolution and phylogeny of the Diptera: A molecular phylogenetic analysis using 28S rDNA sequences. *Syst. Biol.* 46:674-698.
60. Fritsch, P. W., F. Almeda, S. S. Renner, A. B. Martins, and B. C. Cruz. 2004. Phylogeny and circumscription of the near-endemic Brazilian tribe Microlicieae (Melastomataceae). *Am. J. Bot.* 91:1105-1114.
61. Fukatsu, T., H. Shibao, N. Nikoh, and S. Aoki. 2001. Genetically distinct populations in an Asian soldier-producing aphid, *Pseudoregma bambucicola* (Homoptera: Aphididae), identified by DNA fingerprinting and molecular phylogenetic analysis. *Mol. Phylogenet. Evol.* 18:423-433.

62. Galewski, T., J.-F. Mauffrey, Y. L. R. Leite, J. L. Patton, and E. J. P. Douzery. 2005. Ecomorphological diversification among South American spiny rats (Rodentia; Echimyidae): A phylogenetic and chronological approach. *Mol. Phylogenet. Evol.* 34:601-615.
63. Gernandt, D. S., and J. K. Stone. 1999. Phylogenetic analysis of nuclear ribosomal DNA places the nematode parasite, *Drechmeria coniospora*, in Clavicipitaceae. *Mycologia* 91:993-1000.
64. Goker, M., H. Voglmayr, A. Riethmuller, M. Weiss, F. Oberwinkler. 2003. Taxonomic aspects of Peronosporaceae inferred from Bayesian molecular phylogenetics. *Can. J. Botany* 81:672-683.
65. Guillon, J.-M. 2004. Phylogeny of horsetails (*Equisetum*) based on the chloroplast rps4 gene and adjacent noncoding sequences. *Syst. Bot.* 29:251-259.
66. Guo, L. D., K. D. Hyde, and E. C. Y. Liew. 2001. Detection and taxonomic placement of endophytic fungi within frond tissues of *Livistona chinensis* based on rDNA sequences. *Mol. Phylogenet. Evol.* 20:1-13.
67. Gurgel, C. F. D., S. Fredericq, and J. N. Norris. 2004. Phylogeography of *Gracilaria tikvahiae* (Gracilariaceae, Rhodophyta): A study of genetic discontinuity in a continuously distributed species based on molecular evidence. *J. Phycol.* 40:748-758.
68. Hagen, K. B., and J. W. Kadereit. 2001. The phylogeny of *Gentianella* (Gentianaceae) and its colonization of the southern hemisphere as revealed by nuclear and chloroplast DNA sequence variation. *Org. Divers. Evol.* 1:61-79.
69. Halanych, K. M., J. R. Demboski, B. J. van Vuuren, D. R. Klein, and J. A. Cook. 1999. Cytochrome b phylogeny of North American hares and jackrabbits (*Lepus*, Lagomorpha) and the effects of saturation in outgroup taxa. *Mol. Phylogenet. Evol.* 11:213-221.
70. Halanych, K. M., and Robinson, T. J. 1997. Phylogenetic relationships of cottontails (*Sylvilagus*, Lagomorpha): Congruence of 12S rDNA and cytogenetic data. *Mol. Phylogenet. Evol.* 7:294-302.
71. Hall, J. C., H. H. Iltis, and K. J. Sytsma. 2004. Molecular phylogenetics of core Brassicales, placement of orphan genera *Emblingia*, *Forchhammeria*, *Tirania*, and character evolution. *Syst. Bot.* 29:654-669.
72. Hansen, K., K. F. LoBuglio, and D. H. Pfister. 2005. Evolutionary relationships of the cup-fungus genus *Peziza* and Pezizaceae inferred from multiple nuclear genes: RPB2, β -tubulin, and LSU rDNA. *Mol. Phylogenet. Evol.* 36:1-23.
73. Harasewych, M. G., S. L. Adamkewicz, J. A. Blake, D. Saudek, T. Spriggs, and C. J. Bult.

1997. Phylogeny and relationships of pleurotomariid gastropods (Mollusca: Gastropoda): An assessment based on partial 18S rDNA and cytochrome c oxidase I sequences. *Mol. Mar. Biol. Biotech.* 6:1-20.
74. Harrington, M. G., K. J. Edwards, S. A. Johnson, M. W. Chase, and P. A. Gadek. 2005. Phylogenetic inference in Sapindaceae sensu lato using plastid matK and rbcL DNA sequences. *Syst. Bot.* 30:366-382.
75. Hausdorf, B. 1999. Molecular phylogeny of araneomorph spiders. *J. Evol. Biol.* 12:980-985.
76. Haywood, A. J., K. A. Steidinger, E. W. Truby, P. R. Bergquist, P. L. Bergquist, J. Adamson, and L. MacKenzie. 2004. Comparative morphology and molecular phylogenetic analysis of three new species of the genus *Karenia* (Dinophyceae) from New Zealand. *J. Phycol.* 40:165-179.
77. Hedderson, T. A., D. J. Murray, C. J. Cox and T. L. Nowell. 2004. Phylogenetic relationships of haplolepideous mosses (Dicranidae) inferred from rps4 gene sequences. *Syst. Bot.* 29:29-41.
78. Hedin, M. C. 2001. Molecular insights into species phylogeny, biogeography, and morphological stasis in the ancient spider genus *Hypochilus* (Araneae: Hypochilidae). *Mol. Phylogenet. Evol.* 18:238-251.
79. Helfgott, D. M., and R. J. Mason-Gamer. 2004. The evolution of North American *Elymus* (Triticeae, Poaceae) allotetraploids: Evidence from phosphoenolpyruvate carboxylase gene sequences. *Syst. Bot.* 29:850-861.
80. Herron, M. D., T. A. Castoe, and C. L. Parkinson. 2004. Sciurid phylogeny and the paraphyly of Holarctic ground squirrels (*Spermophilus*). *Mol. Phylogenet. Evol.* 31:1015-1030.
81. Hibbett, D. S., L.-B. Gilbert, and M. J. Donoghue. 2000. Evolutionary instability of ectomycorrhizal symbioses in basidiomycetes. *Nature* 407:506-508.
82. Hillis, D. M., and T. P. Wilcox. 2005. Phylogeny of the New World true frogs (*Rana*). *Mol. Phylogenet. Evol.* 34:299-314.
83. Hopple, J. S. Jr., and R. Vilgalys. 1999. Phylogenetic relationships in the mushroom genus *Coprinus* and dark-spored allies based on sequence data from the nuclear gene coding for the large ribosomal subunit RNA: Divergent domains, outgroups, and monophyly. *Mol. Phylogenet. Evol.* 13:1-19.
84. Hufford, L., and M. McMahon. 2004. Morphological evolution and systematics of *Synthyris* and *Besseyia* (Veronicaceae): A phylogenetic analysis. *Syst. Bot.* 29:716-736.

85. Hughes, C. E., G. P. Lewis, A. Daza Yomona, and C. Reynel. 2004. *Maraniona*. A new dalbergioid legume genus (Leguminosae, Papilionoideae) from Peru. *Syst. Bot.* 29:366-374.
86. Hughes, K.W., L. L. McGhee, A. S. Methven, J. E. Johnson and R. H. Petersen. 1999. Patterns of geographic speciation in the genus *Flammulina* based on sequences of the ribosomal ITS1-5.8S-ITS2 area. *Mycologia* 91:978-986
87. Hughes, K. W., R. H. Petersen, J. E. Johnson, J.-M. Moncalvo, R. Vilgalys, S. A. Redhead, T. Thomas, and L. L. McGhee. 2001. Infragenic phylogeny of *Collybia s. str.* based on sequences of ribosomal ITS and LSU regions. *Mycol. Res.* 105:164-172.
88. Hughey, B. D., G. C. Adams, T. D. Bruns, and D. S. Hibbett. 2000. Phylogeny of *Calostoma*, the gelatinous-stalked puffball, based on the nuclear and mitochondrial ribosomal DNA sequences. *Mycologia* 92:94-104.
89. Hyvönen, J., S. Koskinen, G. L. Smith Merrill, T. A. Hedderson, and S. Stenroos. 2004. Phylogeny of the Polytrichales (Bryophyta) based on simultaneous analysis of molecular and morphological data. *Mol. Phylogenet. Evol.* 31:915-928.
90. Inderbitzin, P., J. Harkness, B. G. Turgeon, and M. L. Berbee. 2005. Lateral transfer of mating system in *Stemphylium*. *Proc. Natl. Acad. Sci.* 102:11390-11395.
91. Inderbitzin, P., S. Landvik, M. A. Abdel-Wahab, and M. L. Berbee. 2001. Aliquandostipitaceae, a new family for two new tropical ascomycetes with unusually wide hyphae and dimorphic ascomata. *Am. J. Bot.* 88:52-61.
92. Ingram, A. L. and J. J. Doyle. 2004. Is *Eragrostis* (Poaceae) monophyletic? Insights from nuclear and plastid sequence data. *Syst. Bot.* 29:545-552.
93. Ivors, K. L., Hayden, K. J., Bonants, P. J. M., Rizzo, D. M., and Garbelotto, M. 2004. AFLP and phylogenetic analyses of North American and European populations of *Phytophthora ramorum*. *Mycol. Res.* 108:378-392.
94. Jackman, T. R., A. Larson, K. de Queiroz, and J. B. Losos. 1999. Phylogenetic relationships and tempo of early diversification in *Anolis* lizards. *Syst. Biol.* 48:254-285.
95. Kajita, T., H. Ohashi, Y. Tateishi, C. D. Bailey, J. J. Doyle. 2001. *rbcL* and legume phylogeny with special reference to Phaseoleae, Millettieae, and allies. *Syst. Bot.* 26:515-536.
96. Kasuga, T., T. J. White, and J. W. Taylor. 2002. Estimation of nucleotide substitution rates in Eurotiomycete fungi. *Mol. Biol. Evol.* 19:2318-2324.
97. Kelch, D. G, and B. G. Baldwin. 2003. Phylogeny and ecological radiation of New World thistles (*Cirsium*, Cardueae - Compositae) based on ITS and ETS rDNA sequence data. *Mol. Ecol.* 12:141-151.

98. Kennedy, M., R. D. Gray, and H. G. Spencer. 2000. The phylogenetic relationships of the shags and cormorants: Can sequence data resolve a disagreement between behaviour and morphology? *Mol. Phylogenet. Evol.* 17:345-359.
99. Kennedy, M., and H. G. Spencer. 2004. Phylogenies of the frigatebirds (Fregatidae) and tropicbirds (Phaethonidae), two divergent groups of the traditional order Pelecaniformes, inferred from mitochondrial DNA sequences. *Mol. Phylogenet. Evol.* 31:31-38.
100. Kim, K.-J., and R. K. Jansen. 1994. Comparisons of phylogenetic hypotheses among different data sets in dwarf dandelions (*Krigia*, Asteraceae): Additional information from internal transcribed spacer sequences of nuclear ribosomal DNA. *Plant Syst. Evol.* 190:157-185.
101. Kiontke, K., N. P. Gavin, Y. Raynes, C. Roehrig, F. Piano, and D. H. A. Fitch. 2004. *Caenorhabditis* phylogeny predicts convergence of hermaphroditism and extensive intron loss. *Proc. Natl. Acad. Sci. USA* 101:9003-9008.
102. Kiss, L., A. Bolay, S. Takamatsu, R. T. A. Cook, O. Szentivanyi, R. J. Boal, and P. Jeffries. 2002. Spread of the North American snowberry powdery mildew fungus, *Erysiphe symphoricarpi* (syn. *Microsphaera symphoricarpi*), to Europe. *Mycol. Res.* 106:1086-1092.
103. Kohlmeyer, J., J. W. Spatafora, and B. Volkmann-Kohlmeyer. 2000. Lulworthiales, a new order of marine Ascomycota. *Mycologia* 92:453-458.
104. Koster, B., J. Scott, B. Wong, D. Malloch and N. Straus. 2003. A geographically diverse set of isolates indicates two phylogenetic lineages within *Stachybotrys chartarum*. *Can. J. Bot.* 81:633-643.
105. Krienitz, L., I. Ustinova, T. Friedl, and V. A. R. Huss. 2001. Traditional generic concepts versus 18S rRNA gene phylogeny in the green algal family Selenastraceae (Chlorophyceae, Chlorophyta). *J. Phycol.* 37:852-865.
106. Kristiansen, K. A., M. Cilieborg, L. Drabkova, T. Jorgensen, G. Petersen, and O. Seberg. 2005. DNA Taxonomy - the Riddle of *Oxychloe* (Juncaceae). *Syst. Bot.* 30:284-289.
107. Koljalg, U., H. Tammi, S. Timonen, R. Agerer and R. Sen. 2002. ITS rDNA sequence-based phylogenetic analysis of *Tomentellopsis* species from boreal and temperate forests, and identification of the pink-type ectomycorrhizas. *Mycol. Prog.* 1:81-92.
108. Larsson E., and N. Hallenberg. 2001. Species delimitation in the *Gloeocystidiellum porosum-clavuligerum* complex inferred from compatibility studies and nuclear rDNA sequence data. *Mycologia* 93:907-914.
109. Lavin, M., E. Eshbaugh, J.-M. Hu, S. Mathews, and R. A. Sharrock. 1998. Monophyletic subgroups of the tribe Millettieae (Leguminosae) as revealed by phytochrome nucleotide

- sequence data. *Am. J. Bot.* 85:412-433.
110. Leander, C. A., and D. Porter. 2001. The Labyrinthulomycota is comprised of three distinct lineages. *Mycologia* 93:459-464.
 111. Lee, P. L. M., D. H. Clayton, R. Griffiths, and R. D. M. Page. 1996. Does behaviour reflect phylogeny in swiftlets (Aves: Apodidae)? A test using cytochrome b mitochondrial DNA sequences. *Proc. Natl. Acad. Sci. USA* 93:7091-7096.
 112. León-Règagnon, V., S. Guillén-Hernández, and M. A. Arizmendi-Espinosa. 2005. Intraspecific variation of *Haematoloechus floedae*. Harwood, 1932 (Digenea: Plagiorchiidae), from *Rana* spp. in North and Central America. *J. Parasitol.* 91:915-921.
 113. León-Règagnon, V. and D. R. Brooks. 2003. Molecular phylogeny of *Haematoloechus* Looss, 1899 (Digenea: Plagiorchiidae), with emphasis on North American species. *J. Parasitol.* 89:1206-1211.
 114. Levin, R. A., N. R. Myers, and L. Bohs. 2006. Evolutionary relationships among the "spiny solanums" (*Solanum* subgenus *Leptostemonum*, Solnaceae). *Am. J. Bot.* 93:157-169.
 115. Levin, R. A., W. L. Wagner, P. C. Hoch, W. J. Hahn, A. Rodriguez, D. A. Baum, L. Katinas, E. A. Zimmer, and K. J. Sytsma. 2004. Paraphyly in tribe Onagreae: Insights into phylogenetic relationships of Onagraceae based on nuclear and chloroplast sequence data. *Syst. Bot.* 29:147-164.
 116. Lewis, L. A., B. D. Mishler, and R. Vilgalys. 1997. Phylogenetic relationships of the liverworts (Hepaticae), a basal embryophyte lineage, inferred from nucleotide sequence data of the chloroplast gene *rbcL*. *Mol. Phylogenet. Evol.* 7:377-393.
 117. Leys, R., S. J. B. Cooper, and M. P. Schwarz. 2000. Molecular phylogeny of the large carpenter bees, genus *Xylocopa* (Hymenoptera: Apidae), based on mitochondrial DNA sequences. *Mol. Phylogenet. Evol.* 17:407-418.
 118. Liede, S. and Tauber, A. 2002. Circumscription of the genus *Cynanchum* (Apocynaceae – Asclepiadoideae). *Syst. Bot.* 27:789-800.
 119. Liede-Schumann, S., A. Rapini, D. J. Goyder and M. W. Chase. 2005. Phylogenetics of the New World subtribes of Asclepiadeae (Apocynaceae - Asclepiadoideae): Metastelmatinae, Oxypetalinae, and Gonolobinae. *Syst. Bot.* 30:184-195.
 120. Lin, C-P., B. N. Danforth, and T. K. Wood. 2004. Molecular phylogenetics and evolution of maternal care in membracine treehoppers. *Syst. Biol.* 53:400-421.
 121. Lindell, J., F. R. Méndez-de la Cruz, and R. W. Murphy. 2005. Deep genealogical history without population differentiation: Discordance between mtDNA and allozyme divergence in the zebra-tailed lizard (*Callisaurus draconoides*). *Mol. Phylogenet. Evol.* 36:682-694.

122. Lohwasser, U., A. Granda, and F. R. Blattner. 2004. Phylogenetic analysis of *Microseris* (Asteraceae), including a newly discovered Andean population from Peru. *Syst. Bot.* 29:774-780.
123. Lopez-Vaamonde, C., J. Yves Rasplus, G. D. Weiblen, and J. M. Cook. 2001. Molecular phylogenies of fig wasps: Partial cocladogenesis of pollinators and parasites. *Mol. Phylogenet. Evol.* 21:55-71.
124. Lu, B., I. S. Druzhinina, P. Fallah, P. Chaverri, C. Gradinger, C. P. Kubicek, and G. J. Samuels. 2004. *Hypocrea/Trichoderma* species with pachybasium-like conidiophores: Teleomorphs for *T. minutisporum* and *T. polysporum* and their newly discovered relatives. *Mycologia* 96:310-342.
125. Lumbsch, H. T., and I. Schmitt. 2001. Molecular data suggest that the lichen genus *Pertusaria* is not monophyletic. *Lichenologist* 33:161-170.
126. Lumbsch, H. T., N. Wirtz, R. Lindemuth, and I. Schmitt. 2002. Higher level phylogenetic relationships of Euascomycetes (Pezizomycotina) inferred from a combined analysis of nuclear and mitochondrial sequence data. *Mycological Progress* 1:57-70.
127. Lundrigan, B. L., S. A. Jansa, and P. K. Tucker. 2002. Phylogenetic relationships in the genus *Mus*, based on paternally, maternally, and biparentally inherited characters. *Syst. Biol.* 51:410-431.
128. Lutz, M., R. Bauer, D. Begerow, F. Oberwinkler. 2004. *Tuberculina* - *Helicobasidium*: Host specificity of the *Tuberculina*-stage reveals unexpected diversity within the group. *Mycologia* 96:1316-1329.
129. Maier, W., D. Begerow, M. Weiß, and F. Oberwinkler. 2003. Phylogeny of the rust fungi: An approach using nuclear large subunit ribosomal DNA sequences. *Can. J. Botany* 81:12-23.
130. Marek, P. E. and D. H. Kavanaugh. 2005. The evolutionary relationships of North American *Diplous* Motschulsky (Coleoptera: Carabidae: Patrobini) inferred from morphological and molecular evidence. *Invertebr. Syst.* 19:145-168.
131. Martin, F. N. 2000. Phylogenetic relationships among some *Pythium* species inferred from sequence analysis of the mitochondrially encoded cytochrome oxidase II gene. *Mycologia* 95:269-284.
132. Mast, A. R., S. Kelso, A. J. Richards, D. J. Lang, D. M. S. Feller, and E. Conti. 2001. Phylogenetic relationships in *Primula* L. and related genera (Primulaceae) based on noncoding chloroplast DNA. *Int. J. Plant Sci.* 162:1381-1400.
133. Matheny, P. B. 2005. Improving phylogenetic inference of mushrooms using RPB1 and

- RPB2 nucleotide sequences (*Inocybe*; Agaricales). *Mol. Phylogenet. Evol.* 35:1-20.
134. McHugh, D. 1997. Molecular evidence that echiurans and pogonophorans are derived annelids. *P. Natl. Acad. Sci. USA* 94:8006-8009.
 135. McLaughlin, D. J., R.W. Hanson Jr., E. M. Frieders, E. C, Swann, and L. J. Szabo. 2004. Mitosis in the yeast phase of the basidiomycetes *Bensingtonia yuccicola* and *Stilbum vulgare* and its phylogenetic implications. *Am. J. Bot.* 91:808-815.
 136. Medina, M., and P. J. Walsh. 2000. Molecular systematics of the order Anaspidea based on mitochondrial DNA sequence (12S, 16S, and COI). *Mol. Phylogenet. Evol.* 15:41-58.
 137. Meerow, A. W., and H. van der Werff. 2004. *Pucara* (Amaryllidaceae) reduced to synonymy with *Stenomesson* on the basis of nuclear and plastid DNA spacer sequences, and a new related species of *Stenomesson*. *Syst. Bot.* 29:511-517.
 138. Miller, S. L., T. M. McClean, J. F. Walker, and B. Buyck. 2001. A molecular phylogeny of the Russulales including agaricoid, gasteroid and pleurotoid taxa. *Mycologia* 93:344-354.
 139. Mirabolfathy, M., D. E. L. Cooke, J. M. Duncan, N. A. Williams, D. Ershad, H. Rahimian, and A. Alizadeh. 2001. *Phytophthora pistaciae* sp. nov. and *P. melonis*: The principal causes of pistachio gummosis in Iran. *Mycol. Res.* 105:1166-1175.
 140. Mitchell, A., F. A. H. Sperling, and D. A. Hickey. 2001. Higher level phylogeny of mosquitoes (Diptera: Culicidae): mtDNA data support a derived placement for *Toxorhynchites*. *Insect Syst. Evol.* 33:163-174.
 141. Mols, J. B., D. L. V. Co, B. Gravendeel, L. W. Chatrou, M. D. Pirie, R. W. J. M. van der Ham, E. J. van Marle, and P. J. A. Kessler. 2005. Morphological character evolution in the miliusoid clade (Annonaceae). *Int. J. Plant Sci.*, in press.
 142. Monteiro, A. and N. E. Pierce. 2001. Phylogeny of *Bicyclus* (Lepidoptera: Nymphalidae) inferred from COI, COII, and EF-1 α gene sequences. *Mol. Phylogenet. Evol.* 18:264-281.
 143. Moon, C. D., K. D. Craven, A. Leuchtmann, S. L. Clement, and C. L. Schardl. 2004. Prevalence of interspecific hybrids amongst asexual fungal endophytes of grasses. *Mol. Ecol.* 13:1455-1467.
 144. Moonan, F., J. Molina, and T. E. Mirkov. 2000. *Sugarcane yellow Leaf virus*: An emerging virus that has evolved by recombination between *Polerovirus* and *Luteovirus* ancestors. *Virology* 269:156-171.
 145. Mori, Y., Y. Sato, and S. Takamatsu. 2000. Evolutionary analysis of the powdery mildew fungi using nucleotide sequences of the nuclear ribosomal DNA. *Mycologia* 92:74-93.

146. Mort, M. E., D. J. Crawford, and K. N. Fairfield. 2004. Phylogeny and character evolution in California *Coreopsis* (Asteraceae): Insights from morphology and from sequences of the nuclear and plastid genomes. *Syst. Bot.* 29:781-789.
147. Murrell, A., N. J. H. Campbell, and S. C. Barker. 2000. Phylogenetic analyses of the Rhipicephaline ticks indicate that the genus *Rhipicephalinae* is paraphyletic. *Mol. Phylogenet. Evol.* 16:1-7.
148. Myllys, L., S. Stenroos, A. Thell, and T. Ahti. 2003. Phylogeny of bipolar *Cladonia arbuscula* and *Cladonia mitis* (Lecanorales, Euascomycetes). *Mol. Phylogenet. Evol.* 27:58-69.
149. Nadler, S. A., and D. S. S. Hudspeth. 1998. Ribosomal DNA and phylogeny of the Ascaridoidea (Nemata: Secernentea): Implications for morphological evolution and classification. *Mol. Phylogenet. Evol.* 10:221-236.
150. Nickrent, D. N., A. Blarer, Y.-L. Qiu, R. Vidal-Russell and F. E. Anderson. 2004. Phylogenetic inference in Rafflesiales: The influence of rate heterogeneity and horizontal gene transfer. *BMC Evol. Biol.* 4:40.
151. Nilsson, R. H., N. Hallenberg. 2003. Phylogeny of the *Hypochnicium punctulatum* complex as inferred from ITS sequence data. *Mycologia* 95:54-60.
152. Nunn, G. B., and Stanley, S. E. 1998. Body size effects and rates of cytochrome b evolution in tube-nosed seabirds. *Mol. Biol. Evol.* 15:1360-1371.
153. Oh, S-H., and D. Potter. 2003. Phylogenetic utility of the second intron of LEAFY in *Neillia* and *Stephanandra* (Rosaceae) and implications for the origin of *Stephanandra*. *Mol. Phylogenet. Evol.* 29:203-215.
154. O'Kelly, C. J., W. K. Bellows, and B. Wysor. 2004. Phylogenetic position of *Bolbocoleon piliferum* (Ulvophyceae, Chlorophyta): Evidence from reproduction, zoospore and gamete ultrastructure, and SSU ribosomal RNA gene sequences. *J. Phycol.* 40:209-222.
155. O'Kelly, C. J., B. Wysor, and W. K. Bellows. 2004. Gene sequence diversity and the phylogenetic position of algae assigned to the genera *Phaeophila* and *Ochlochaete* (Ulvophyceae, Chlorophyta). *J. Phycol.* 40:789-799.
156. Olson, M. E. 2001. Intergeneric relationships within the Caricaceae-Moringaceae clade (Brassicales), and potential morphological synapomorphies of the clade and its families. *Int. J. Plant Sci.* 163:51-65.
157. Omilian, A. R., and D. J. Taylor. 2001. Rate acceleration and long-branch attraction in a conserved gene of cryptic daphniid (Crustacea) species. *Mol. Biol. Evol.* 18:2201-2212.
158. O'Quinn, R. L., and L. Hufford. 2005. Molecular systematics of Montieae (Portulacaceae):

Implications for taxonomy, biogeography and ecology. Syst. Bot. 30:314-331.

159. Ott, S., M. Brinkmann, N. Wirtz, and H. T. Lumbsch. 2004. Mitochondrial and nuclear ribosomal DNA data do not support the separation of the Antarctic lichens *Umbilicaria kappenii* and *Umbilicaria antarctica* as distinct species. Lichenologist 36:227-234.
160. Pedersen, B. V. 1996. A phylogenetic analysis of cuckoo bumblebees (*Psithyrus*, Lepeletier) and bumblebees (*Bombus*, Latreille) inferred from sequences of the mitochondrial gene cytochrome oxidase I. Mol. Phylogenet. Evol. 5:289-297.
161. Peintner, U., M. M. Moser, K. Agretious Thomas, and P. Manimohan. 2003. First records of ectomycorrhizal *Cortinarius* species (Agaricales, Basidiomycetes) from tropical India and their phylogenetic position based on rDNA ITS sequences. Mycol. Res. 107:485-494.
162. Pennington, R. T., M. Lavin, H. Ireland, B. Klitgaard, J. Preston, and J.-M. Hu. 2001. Phylogenetic relationships of basal papilionoid legumes based upon sequences of the chloroplast trnL intron. Syst. Bot. 26:537-556.
163. Pennington, R. T., M. Lavin, D. E. Prado, C. A. Pendry, S. Pell, and C. A. Butterworth. 2004. Historical climate change and speciation: Neotropical seasonally dry forest plants show patterns of both Tertiary and Quaternary diversification. Philos. T. Roy. Soc. B. 359:515-537.
164. Percy, D. M. 2003. Radiation, diversity and host-plant interactions among island and continental legume-feeding psyllids. Evolution 57:2540-2556.
165. Peters, J. L., K. G. McCracken, Y. N. Zhuravlev, Y. Lu, R. E. Wilson, K. P. Johnson, and K. E. Omland. 2005. Phylogenetics of wigeons and allies (Anatidae: *Anas*): The importance of sampling multiple loci and multiple individuals. Mol. Phylogenet. Evol. 35:209-224.
166. Peterson, S., S. Corneli, T. J. Hjelle, M. A. Miller-Hjelle, D. M. Nowak, P. A. Bonneau. 1998. *Penicillium pimiteouiense*: A new species isolated from polycystic kidney cell cultures. Mycologia 91:269-277.
167. Phillips, A. J. L., A. Alves, A. Correia, and J. Luque. 2004. Two new species of *Botryosphaeria* with brown, 1-septate ascospores and *Dothiorella* anamorphs. Mycologia 97:513-529.
168. Piel, W. H., and K. J. Nutt. 2000. One species or several? Discordant patterns of geographic variation between allozymes and mtDNA sequences among spiders in the genus *Metetepeira* (Araneae: Araneidae). Mol. Phylogenet. Evol. 15:414-418.
169. Pinruan, U., J. Sakayaroj, E. B. G. Jones, and K. D. Hyde. 2004. Aquatic fungi from peat swamp palms: *Phruensis brunneispora* gen. et sp. nov. and its hyphomycete anamorph. Mycologia 96:1163-1170.

170. Plana, V. 2003. Phylogenetic relationships of the Afro-Malagasy members of the large genus *Begonia* inferred from trnL intron sequences. *Syst. Bot.* 28:693-704.
171. Pochon, X., T. C. LaJeunesse, and J. Pawlowski. 2004. Biogeographic partitioning and host specialization among foraminiferan dinoflagellate symbionts (*Symbiodinium*, Dinophyta). *Mar. Biol.* 146:17-27.
172. Poux, C, O. Madsen, E. Marquard, D. R. Vieites, W. W. de Jong and M. Vences. 2005. Asynchronous colonization of Madagascar by the four endemic clades of primates, tenrecs, carnivores and rodents as inferred from nuclear genes. *Syst. Biol.* 54:719-730.
173. Pryer, K. M., H. Schneider, A. R. Smith, R. Cranfill, P. G. Wolf, J. S. Hunt, S. D. Sipes. 2001. Horsetails and ferns are a monophyletic group and the closest living relatives to seed plants. *Nature* 409:618-622.
174. Razafimandimbison, S. G., E. A. Kellogg, and B. Bremer. 2004. Recent origin and phylogenetic utility of divergent ITS putative pseudogenes: A case study from Naucleaeae (Rubiaceae). *Syst. Biol.* 53:177-192.
175. Remigio, E. A., D. A. W. Lepitzki., J. S. Lee, and P. D. N. Hebert. 2001. Molecular systematic relationships and evidence for a recent origin of the thermal spring endemic snails *Physella johnsoni* and *Physella wrighti* (Pulmonata: Physidae). *Can. J. Zool.* 79:1941-1950.
176. Rokas, A., R. J. Atkinson, L. Webster, and G. N. Stone. 2003. Out of Anatolia: Longitudinal gradients in genetic diversity support an eastern origin for a circum-Mediterranean oak gallwasp *Andricus quercustozae*. *Mol. Ecol.* 12:2153-2174.
177. Roncal, J., J. Francisco -Ortega, C. B. Asmussen, and C. E. Lewis. 2005. Molecular phylogenetics of tribe Geonomeae (Arecaceae) using nuclear DNA sequences of phosphoribulokinase and RNA polymerase II. *Syst. Bot.* 30:275-283.
178. Ruiz-Trillo, I., M. Riutort, D. T. J. Littlewood, E. A. Herniou, and J. Bagun. 1999. Acoel flatworms: Earliest extant bilaterian metazoans, not members of the Platyhelminthes. *Science* 283:1919-1923.
179. Rydin, C., M. Kallersjo, and E. M. Friist. 2002. Seed plant relationships and the systematic position of Gnetales based on nuclear and chloroplast DNA: Conflicting data, rooting problems, and the monophyly of conifers. *Int. J. Plant Sci.* 163:197-214.
180. Sanchez, J. A., and S. D. Cairns. 2004. An unusual new gorgonian coral (Anthozoa: Octocorallia) from the Aleutian Islands, Alaska. *Zool. Med. Leiden* 78:265-274.
181. Sanchez J. A., C. S. McFadden, S. C. France, and H. R. Lasker. 2003. Molecular phylogenetic analyses of shallow-water Caribbean octocorals. *Mar. Biol.* 142:975-987.

182. Santos, S. R., D. J. Taylor, R. A. Kinzie III, M. Hidaka, K. Sakai, and M. A. Coffroth. 2002. Molecular phylogeny of symbiotic dinoflagellates inferred from partial chloroplast large subunit (23S)-rDNA. *Mol. Phylogenet. Evol.* 23:97-111.
183. Schilthuizen, M., E. Gittenberger, and A. P. Gultyaev. 1995. Phylogenetic relationships inferred from the sequence and secondary structure of ITS1 rRNA in *Albinaria* and putative *Isabellaria* species (Gastropoda, Pulmonata, Clausiliidae). *Mol. Phylogenet. Evol.* 4:457-462.
184. Schneeweiss, G. M., A. Colwell, J.-M. Park, C.-G. Jang, and T. F. Stuessy. 2004. Phylogeny of holoparasitic *Orobanche* (Orobanchaceae) inferred from nuclear ITS sequences. *Mol. Phylogenet. Evol.* 30:465-478.
185. Schulte II, J. A., J. R. Macey, and T. J. Papenfuss. 2006. A genetic perspective on the geographic association of taxa among arid North American lizards of the *Sceloporus magister* complex (Squamata: Iguanidae: Phrynosomatinae). *Mol. Phylogenet. Evol.* 39:873-880.
186. Schultheis, L. M., and M. J. Donoghue. 2004. Molecular phylogenetic and biogeographic analyses of *Ribes* (Grossulariaceae) with an emphasis on gooseberries (subg. *Grossularia*). *Syst. Bot.* 29:77-96.
187. Schurko, A. M., L. Mendoza, C. A. Levesque, N. L. Desaulniers, A. W. A. M. de Cock, and G. R. Klassen. 2003. A molecular phylogeny of *Pythium insidiosum*. *Mycol. Res.* 107:537-544.
188. Shaw, A. J., C. J. Cox, and S. B. Boles. 2005. Phylogeny, species delimitation, and sexual promiscuity in *Sphagnum* section *Acutifolia*. *Syst. Bot.* 30:16-33.
189. Sherwood, A. R., and R. G. Sheath. 2003. Systematics of the Hildenbrandiales (Rhodophyta): Gene sequence and morphometric analyses of global collections. *J. Phycol.* 39:409-422.
190. Shin, W., and R. E. Triemer. 2004. Phylogenetic analysis of the genus *Euglena* (Euglenophyceae) with particular reference to the type species *Euglena viridis*. *J. Phycol.* 40:759-771.
191. Sholberg, P. L., C. Harlton, P. Haag, C. A. Lévesque, D. T. O’Gorman, and K. Seifert. 2005. Benzimidazole and diphenylamine sensitivity and identity of *Penicillium* spp. that cause postharvest blue mold of apples using β -tubulin gene sequences. *Postharvest Biol. Tec.* 36:41-49.
192. Shoup, S. and L. A. Lewis. 2003. Polyphyletic origin of parallel basal bodies in swimming cells of chlorophycean green algae (Chlorophyta). *J. Phycol.* 39:789-796.
193. Simmons, M. P., V. Savolainen, C. C. Clevinger, R. H. Archer, and J. I. Davis. 2001.

- Phylogeny of the Celastraceae inferred from 26S nuclear ribosomal DNA, phytochrome B, rbcL, atpB, and morphology. *Mol. Phylogenet. Evol.* 19:353-366.
194. Simpson, B. B., A. Weeks, D. M. Helfgott, and L. L. Larkin. 2004. Species relationships in *Krameria* (Krameriaceae) based on ITS sequences and morphology: Implications for character utility and biogeography. *Syst. Bot.* 29:97-108.
195. Slippers, B., G. Fourie, P. W. Crous, T. A. Coutinho, B. D. Wingfield, and M. J. Wingfield. 2004. Multiple gene sequences delimit *Botryosphaeria australis* sp. nov. from *B. lutea*. *Mycologia* 96:1030-1041.
196. Slippers, B., G. I. Johnson, P. W. Crous, T. A. Coutinho, B. D. Wingfield, and M. J. Wingfield. 2005. Phylogenetic and morphological re-evaluation of the *Botryosphaeria* species causing diseases of *Mangifera indica*. *Mycologia* 97:99-110.
197. Small, R. L. 2004. Phylogeny of *Hibiscus* sect. *Muenchhusia* (Malvaceae) based on chloroplast rpl16 and ndhF, and nuclear ITS and GBSSI sequences. *Syst. Bot.* 29:385-392.
198. Smith, D. R., and G. R. Stanosz. 2001. Molecular and morphological differentiation of *Botryosphaeria dothidea* (anamorph *Fusicoccum aesculi*) from some other fungi with *Fusicoccum* anamorphs. *Mycologia* 93:505-515.
199. Smith, J. A., R. A. Blanchette, and G. Newcombe. 2004. Molecular and morphological characterization of the willow rust fungus, *Melampsora epitea*, from arctic and temperate hosts in North America. *Mycologia* 96:1330-1338.
200. Smith, J. J., M. Jaycox, M.R.B. Smith-Caldas, and G. L. Bush. 2003. Analysis of mitochondrial DNA and morphological characters in the subtribe Carpomyina (Diptera: Tephritidae). In: (A. Freidberg, Ed.) Proceedings of the First Tephritidologist Conference, Tel Aviv University, May 2000.
201. Stanley, W. T. and L. E. Olson. 2005. Phylogeny, phylogeography, and geographic variation of *Sylvisorex howelli* (Family Soricidae), an endemic shrew of the Eastern Arc Mountains, Tanzania. *J. Zool.* 266:341-354.
202. Starr, J. R., S. A. Harris, and D. A. Simpson. Phylogeny of the unispicate taxa in Cyperaceae tribe Cariceae II: the limits of Uncinia Pers. In *Sedges: Uses, diversity, and systematics of the Cyperaceae*, eds. R. F. C. Naczi and B. A. Ford. Monogr. Syst. Bot. Missouri Bot. Gard., in press.
203. Steane, D. A., K. L. Wilson, and R. S. Hill. 2003. Using *matK* sequence data to unravel the phylogeny of Casuarinaceae. *Mol. Phylogenet. Evol.* 28:47-59.
204. Steppan, S. J., R. M. Adkins, and J. Anderson. 2004. Phylogeny and divergence-date estimates of rapid radiations in muroid rodents based on multiple nuclear genes. *Syst. Biol.* 53:533-553.

205. Steppan, S. J., R. M. Adkins, P. Q. Spinks, and C. Hale. 2005. Multigene phylogeny of the Old World mice, Murinae, reveals distinct geographic lineages and the declining utility of mitochondrial genes compared to nuclear genes. *Mol. Phylogenet. Evol.* 37:370-388.
206. Steppan, S. J., B. L. Storz, and R. S. Hoffmann. 2004. Nuclear DNA phylogeny of the squirrels (Mammalia: Rodentia) and the evolution of arboreality using c-myc and RAG1. *Mol. Phylogenet. Evol.* 30:703-719.
207. Stoll, M., D. Begerow, and F. Oberwinkler. 2005. Molecular phylogeny of *Ustilago*, *Sporisorium*, and related taxa based on combined analyses of rDNA sequences. *Mycol. Res.* 109:342-56.
208. Stone, J. K. 2005. A reassessment of *Hemiphacidium*, *Rhabdocline*, and *Sarcotrochila* (Hemiphacidiaceae). *Mycotaxon* 91:115-126.
209. Sullivan, J., J. A. Markert, and C. W. Kilpatrick. 1997. Phylogeography and molecular systematics of the *Peromyscus aztecus* species group (Rodentia: Muridae) inferred using parsimony and likelihood. *Syst. Biol.* 46:426-440.
210. Sullivan, J. P., S. Lavoue, and C. D. Hopkins. 2000. Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs. *J. Exp. Biol.* 203:665-683.
211. Sun, F.-J., S. R. Downie, and R. L. Hartman. 2004. An ITS-based phylogenetic analysis of the perennial, endemic Apiaceae subfamily Apioideae of western North America. *Syst. Bot.* 29:419-431.
212. Tartar, A., D. G. Boucias, B. J. Adams, and J. J. Becnel. 2001. Phylogenetic analysis identifies the invertebrate pathogen *Helicosporidium* sp. as a green alga (Chlorophyta). *Int. J. Syst. Evol. Micr.* 52:273-279.
213. Taylor, D. J., H. L. Sprenger, and S. Ishida. 2005. Geographic and phylogenetic evidence for dispersed nuclear introgression in a daphniid with sexual propagules. *Mol. Ecol.* 14:525-537.
214. Thollessen, M. 2000. Increasing fidelity in parsimony analysis of dorid nudibranchs by differential weighting, or A tale of two genes. *Mol. Phylogenet. Evol.* 16:161-172.
215. Thollessen, M. and J. L. Norenburg. 2003. Ribbon worm relationships: A phylogeny of the phylum Nemertea. *P. Roy. Soc. Lond. B Bio.* 270:407-415.
216. Thorn, R. G., J.-M. Moncalvo, C. A. Reddy, and R. Vilgalys. 2000. Phylogenetic analyses and the distribution of nematophagy support a monophyletic Pleurotaceae within the polyphyletic pleurotoid-lentinoid fungi. *Mycologia* 92:241-252.

217. Thulin, M., M. Lavin, R. Pasquet, and A. Delgado-Salinas. 2004. Phylogeny and biogeography of *Wajira* (Leguminosae): A monophyletic segregate of *Vigna* centered in the horn of Africa region. *Syst. Bot.* 29:903-920.
218. Tooley, P. W., E. D. Goley, M. M. Carras, R. D. Frederick, E. L. Weber, and G. A. Kulda. 2001. Characterization of *Claviceps* species pathogenic on sorghum by sequence analysis of the β -tubulin gene intron 3 region and EF-1 α gene intron 4. *Mycologia* 93:541-551.
219. Tsuneda, A., S. Hambleton, and R. S. Currah. 2004. Morphology and phylogenetic placement of *Endoconidioma*, a new endoconidial genus from trembling aspen. *Mycologia* 96:1128-1135.
220. Uit de Weerd, D. R., W. H. Piel, and E. Gittenberger. 2004. Widespread polyphyly among Alopinae snail genera: When phylogeny mirrors biogeography more closely than morphology. *Mol. Phylogenet. Evol.* 33:533-548.
221. Usher, K. M., S. Toze, J. Fromont, J. Kuoand, and D.C. Sutton. 2004. A new species of cyanobacterial symbiont from the marine sponge *Chondrilla nucula*. *Symbiosis* 36:183-192.
222. Valdes, A. 2002. Preliminary molecular phylogeny of the radula-less dorids (Gastropoda: Opisthobranchia), based on 16S mtDNA sequence data. *J. Mollus. Stud.* 69:75-80.
223. Verboom, G. A. 2006. A phylogeny of the schoenoid sedges (Cyperaceae: Schoeneae) based on plastid DNA sequences, with special reference to the genera found in Africa. *Mol. Phylogenet. Evol.* 38:79-89.
224. Verkley, G. J. M., P. W. Crous, J. Z. Groenewald, U. Braun, and A. Aptroot. 2004. *Mycosphaerella punctiformis* revisited: Morphology, phylogeny, and epitypification of the type species of the genus *Mycosphaerella* (Dothideales, Ascomycota). *Mycol. Res.* 108:1271-1282.
225. Virtanen, V. 2003. Phylogeny of the Bartramiaceae (Bryopsida) based on morphology and on *rbcL*, *rps4*, and *trnL-trnF* sequence data. *Bryologist* 106: 280-296.
226. Voglmayr, H., A. Riethmuller, M. Goker, M. Weiss, and F. Oberwinkler. 2004. Phylogenetic relationships of *Plasmopara*, *Bremia* and other genera of downy mildew pathogens with pyriform haustoria based on Bayesian analysis of partial LSU rDNA sequence data. *Mycol. Res.* 108:1011-1024.
227. Voigt, K., E. Cigelnik, and K. O'Donnell. 1999. Phylogeny and PCR identification of clinically important zygomycetes based on nuclear ribosomal-DNA sequence data. *J. Clin. Microbiol.* 37:3957-3964.
228. Wagstaff, S. J., and M. I. Dawson. 2000. Classification, origin, and patterns of diversification of *Corynocarpus* (Corynocarpaceae) inferred from DNA sequences. *Syst. Bot.* 25:134-149.

229. Wang, Z., M. Binder, and D. S. Hibbett. 2005. Life history and systematics of the aquatic discomycete *Mitrula* (Helotiales, Ascomycota) based on cultural, morphological and molecular studies. *Am. J. Bot.* 92:1565-1574.
230. Waters, J. M., and M. S. Roy. 2004. Out of Africa: The slow train to Australasia. *Syst. Biol.* 53:18-24.
231. Weeks, A., and B. B. Simpson. 2004. Molecular genetic evidence for intraspecific hybridization among endemic Hispaniolan *Bursera* (Burseraceae). *Am. J. Bot.* 91:976-984.
232. Weimin Y., R. M. Giblin-Davis, H. Braasch, K. Morris and W. K. Thomas. Phylogenetic relationships among *Bursaphelenchus* species (Nematoda: Parasitaphelenchidae) inferred from nuclear ribosomal and mitochondrial DNA sequence. *Mol. Phylogenet. Evol.*, in press.
233. Wilcox, T. P., D. J. Zwickl, T. A. Heath, and D. M. Hillis. 2002. Phylogenetic relationships of the dwarf boas and a comparison of Bayesian and bootstrap measures of phylogenetic support. *Mol. Phylogenet. Evol.* 25:361-371.
234. Wilkie, P., A. Clark, R. T. Pennington, M. Cheek, C. Bayer, C. C. Wilcock. 2006. Phylogenetic relationships within the subfamily Sterculioideae (Malvaceae/Sterculiaceae-Sterculieae) using the chloroplast gene *ndhF*. *Syst. Bot.* 31:160-170.
235. Wilkinson, J. A., R. C. Drewes, and O. L. Tatum. 2002. A molecular phylogenetic analysis of the family Rhacophoridae with an emphasis on the Asian and African genera. *Mol. Phylogenet. Evol.* 24:265-273.
236. Wilson, A. W., and D. E. Desjardin. 2005. Phylogenetic relationships in the gymnopoid and marasmioid fungi (Basidiomycetes, euagarics clade). *Mycologia* 97:667-679.
237. Wilson, N. G. and M. S. Y. Lee. 2005. Molecular phylogeny of *Chromodoris* (Mollusca, Nudibranchia) and the identification of a planar spawning clade. *Mol. Phylogenet. Evol.* 36:722-727.
238. Wingfield, B. D., L. Ericson, T. Szaro, and J. J. Burdon. 2004. Phylogenetic patterns in the Uredinales. *Australas. Plant Path.* 33:327-335.
239. Winkworth, R. C., and M. J. Donoghue. 2004. *Viburnum* phylogeny: Evidence from the duplicated nuclear gene *GBSSI*. *Mol. Phylogenet. Evol.* 33:109-126.
240. Wipf, D., A. Fribourg, J.C. Munch, B. Botton, and F. Buscot. 1999. Diversity of the internal transcribed spacer of rDNA in morels. *Can. J. Microbiol.* 45:769-778.
241. Woerheide, G., S. A. Nichols, and J. Goldberg. 2004. Intragenomic variation of the rDNA internal transcribed spacers in sponges (Phylum Porifera): Implications for phylogenetic studies. *Mol. Phylogenet. Evol.* 33:816-830.

242. Woods, K., K. W. Hilu, T. Borsch, and J. H. Wiersema. 2005. Pattern of variation and systematics of *Nymphaea odorata*: II. Sequence information from ITS and trnL-trnF. Syst. Bot. 30:481-493.
243. Wojciechowski, M. F., M. J. Sanderson, and J-M. Hu. 1999. Evidence on the monophyly of Astragalus (Fabaceae) and its major subgroups based on nuclear ribosomal DNA ITS and chloroplast DNA trnL intron data. Syst. Bot. 24:409-437.
244. Worsaae, K. 2005. Phylogeny of Nerillidae (Polychaeta, Annelida) as inferred from combined 18S rDNA and morphological data. Cladistics 21:143-162.
245. Wu, S.-H., Z.-H. Yu, Y.-C. Dai, C.-T. Chen, C.-H. Su, L.-C. Chen, W.-C. Hsu, and G.-Y. Hwang. 2004. *Taiwanofungus*, a polypore new genus. Fung. Sci. 12:109-116.
246. Ye, W., C.-Y. Lee, R. H. Scheffrahn, J. M. Aleong, N.-Y. Su, G. W. Bennett, and M. E. Scharf. 2004. Phylogenetic relationships of nearctic *Reticulitermes* species (Isoptera: Rhinotermitidae) with particular reference to *Reticulitermes arenicola* Goellner. Mol. Phylogenet. Evol. 30:815-822.
247. Yoder, A. D., and Z. Yang. 2004. Divergence dates for Malagasy lemurs estimated from multiple gene loci: Geological and evolutionary context. Mol. Ecol. 13:757-773.
248. Zehethofer, K., and C. Sturmbauer. 1998. Phylogenetic relationships of central European wolf spiders (Araneae: Lycosidae) inferred from 12S ribosomal DNA sequences. Mol. Phylogenet. Evol. 10:391-398.
249. Zehnder, M., and J. Mariaux. 1999. Molecular systematic analysis of the order Proteocephalidea (Eucestoda) based on mitochondrial and nuclear rDNA sequences. Int. J. Parasitol. 29:1841-1852.
250. Zhang, L.-B., H. P. Comes and J. W. Kadereit. 2004. The temporal course of Quaternary diversification in the European high mountain endemic *Primula* sect. *Auricula* (Primulaceae). Int. J. Plant Sci. 165:191-207.