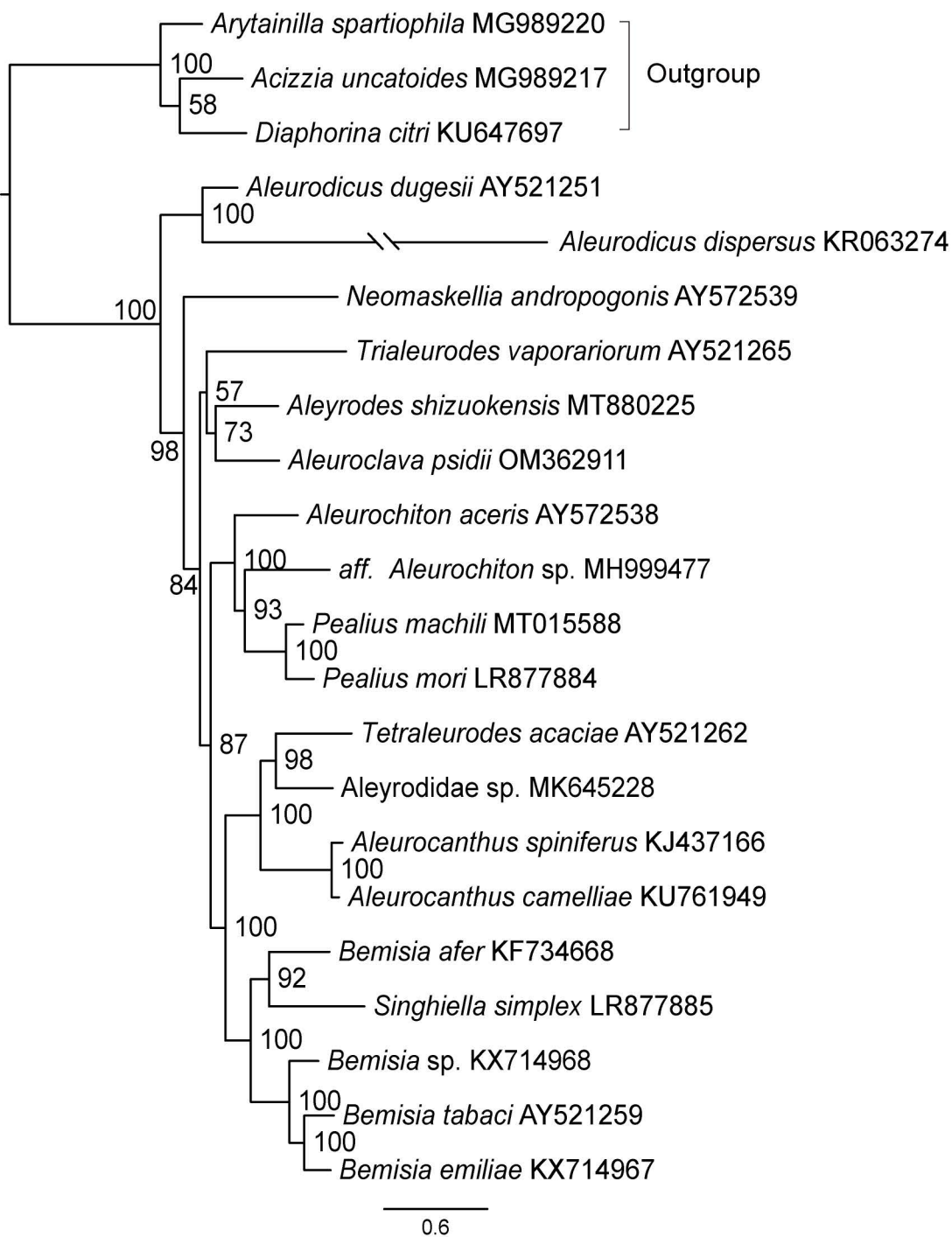
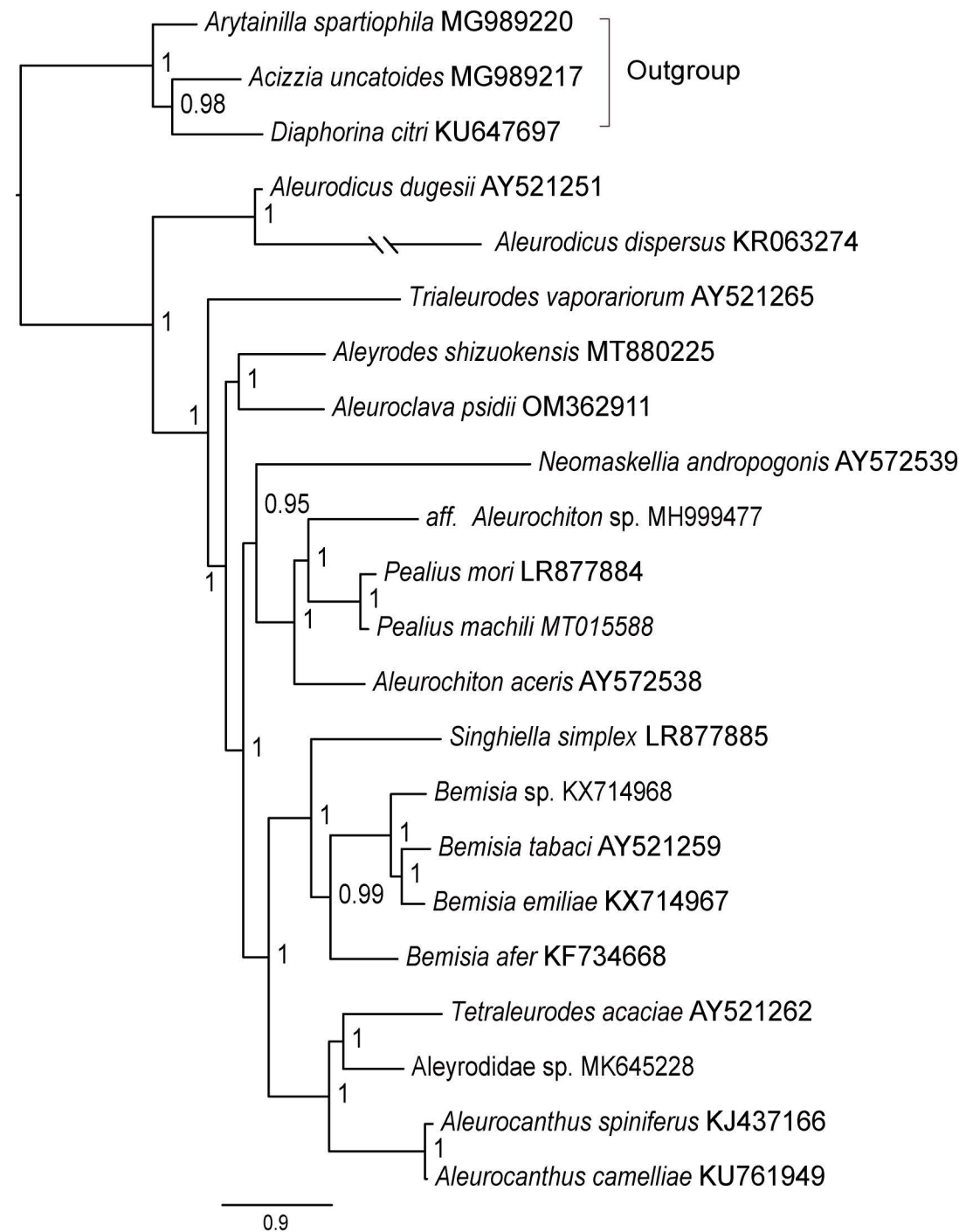


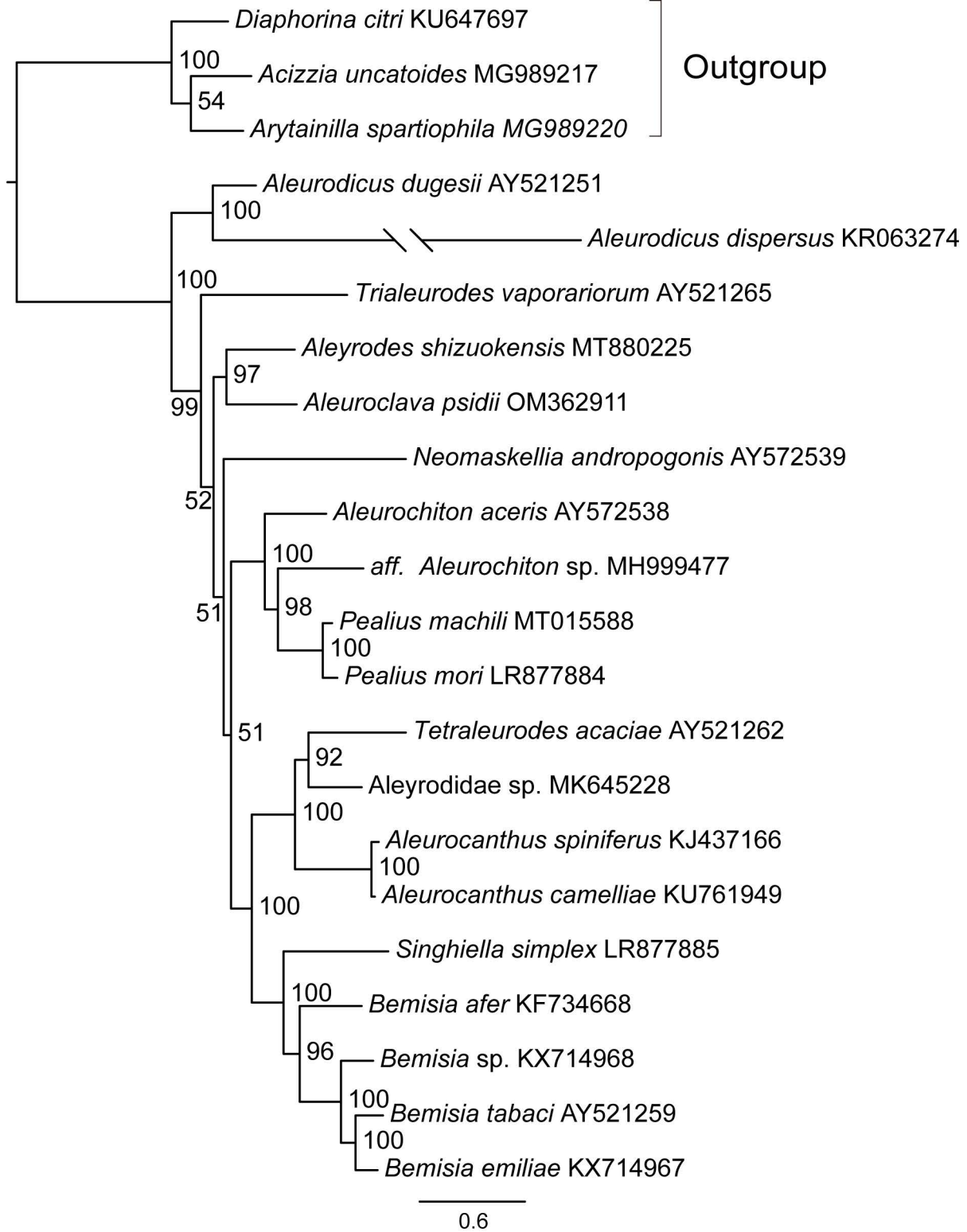
(A)



(B)

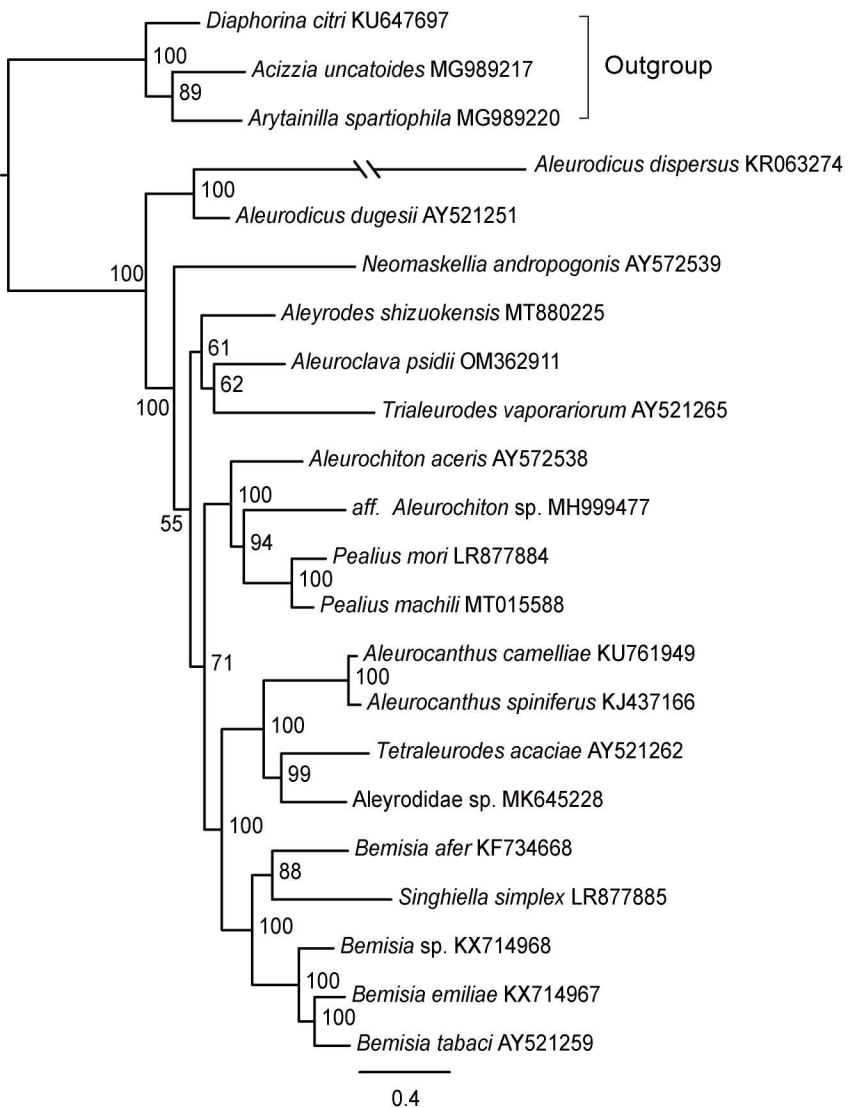


Supplementary Fig. 1 The phylogenetic trees inferred from the dataset PCG_nt. (A) ML analysis of the nucleotide dataset. The branch of *Aleurodicus dispersus* is depicted as half of its original branch length. Node numbers show the bootstrap support values. The scale bar represents substitutions/site. (B) Bayesian inference of the nucleotide dataset. The branch of *Aleurodicus dispersus* is depicted as half its original branch length. Node numbers show the posterior probability values. The scale bar represents substitutions/site.

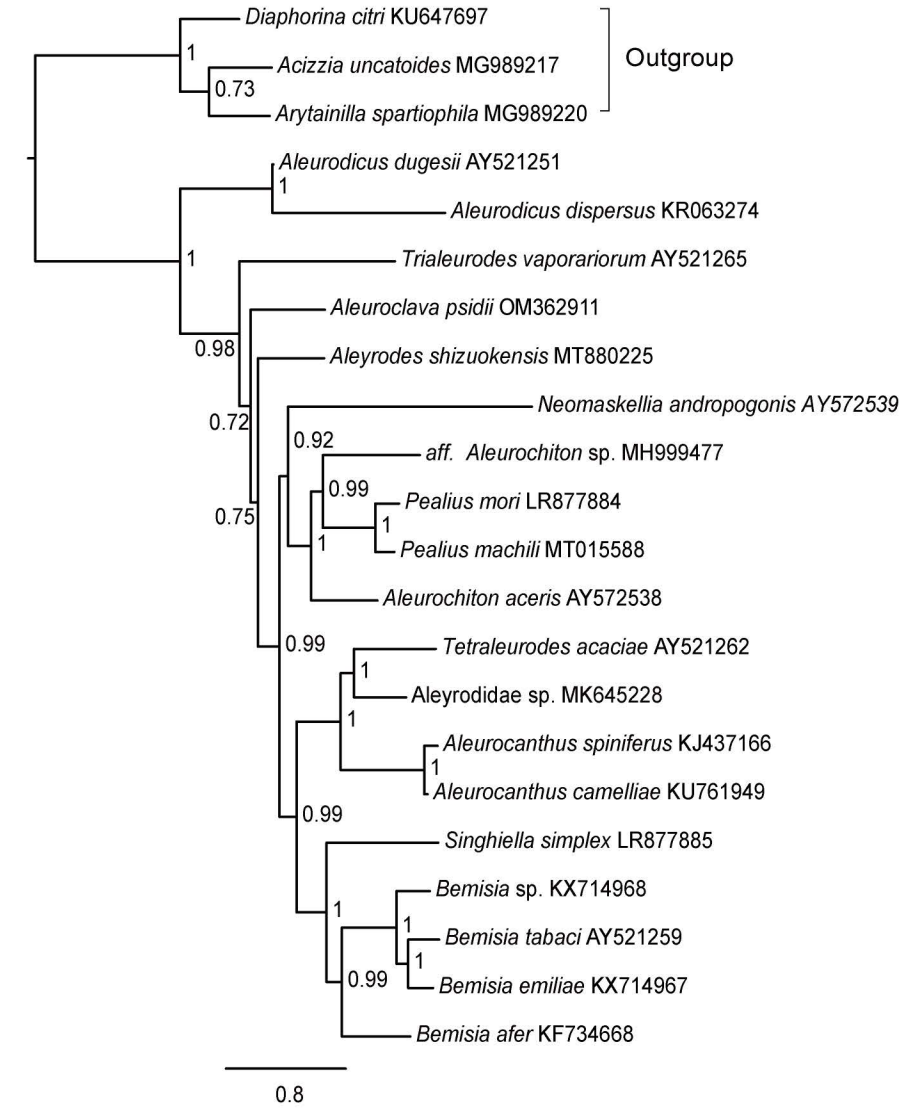


Supplementary Fig. 2 The phylogenetic tree inferred from the dataset PCG_aa under the ML analysis. The branch of *Aleurodicus dispersus* is depicted as half of its original branch length. Node numbers show the bootstrap support values. The scale bar represents substitutions/site.

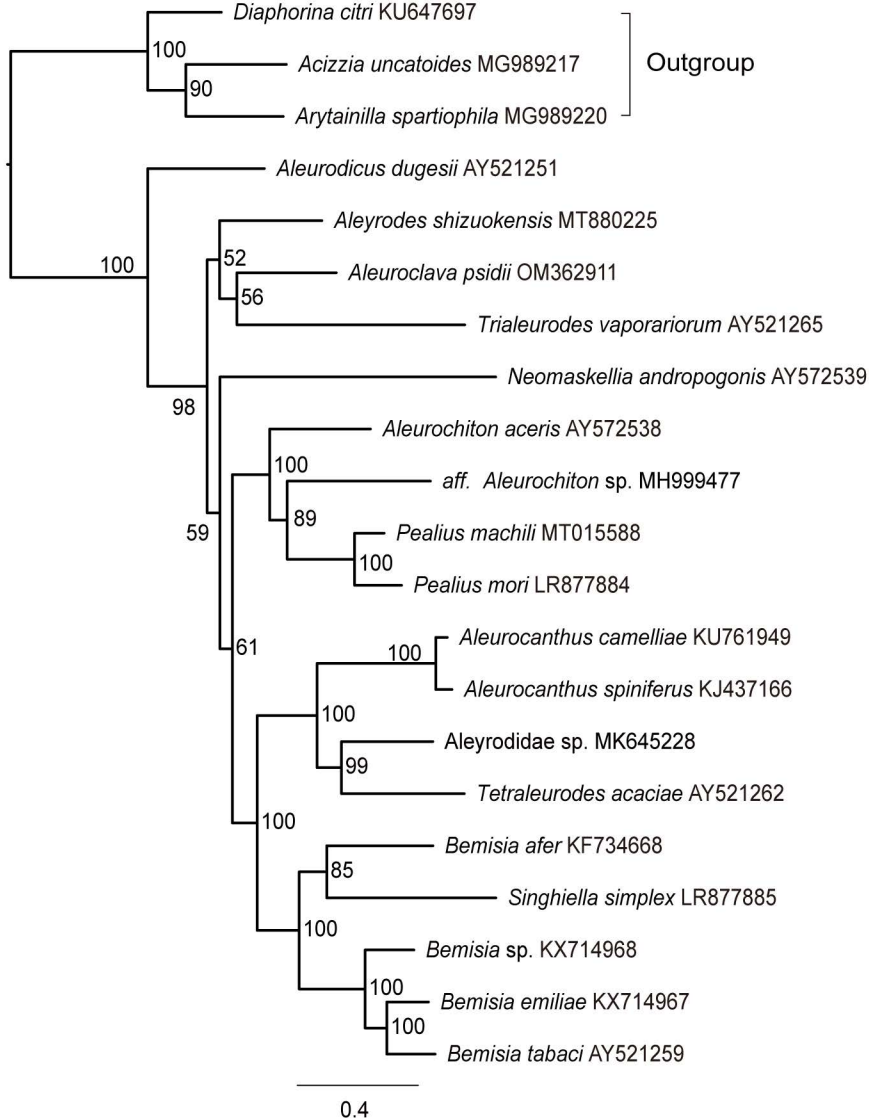
(A)



(B)



Supplementary Fig. 3 The phylogenetic trees inferred from the dataset PCGRNA. (A) ML analysis of the dataset. The branch of *Aleurodicus dispersus* is depicted as half its original branch length. Node numbers show the bootstrap support values. The scale bar represents substitutions/site. (B) Bayesian inference of the dataset. Node numbers show the posterior probability values. The scale bar represents substitutions/site.



Supplementary Fig. 4 Phylogenetic tree based on Maximum likelihood analysis of the dataset PCGRNA, with the long-branched *Aleurodicus disperses* removed. Node numbers show the bootstrap support values. The scale bar represents substitutions/site.

Supplementary Table 1 A. The partitioning schemes and best-fitting modes selected by ModelFinder for the dataset PCG_nt.

Best Model	Partition names
GTR+F+I+G4	atp6_pos1, atp8_pos1, atp8_pos2, atp8_pos3, cob_pos1, cox1_pos1, cox2_pos1, cox3_pos1, nad2_pos1, nad3_pos1, nad6_nt_pos1
TVM+F+I+G4	atp6_pos2, cob_pos2, cox1_pos2, cox2_pos2, cox3_pos2, nad2_pos2, nad3_pos2, nad6_nt_pos2
HKY+F+I+G4	atp6_pos3, cob_pos3, cox1_pos3, cox2_pos3, nad2_pos3, nad6_nt_pos3
HKY+F+G4	cox3_pos3, nad1_pos3, nad3_pos3, nad4_pos3, nad4l_pos3, nad5_nt_pos3
GTR+F+G4	nad1_pos1, nad4_pos1, nad4l_pos1, nad5_nt_pos1
TVM+F+G4	nad1_pos2, nad4_pos2, nad4l_pos2, nad5_nt_pos2

Note: pos1, first codon positions; pos2, second codon positions; pos3, third codon positions.

Supplementary Table 1 B. The partitioning schemes and best-fitting modes selected by ModelFinder for the dataset PCG_aa.

Best Model	Partition names
mtInv+G4	atp6, cob, cox2, cox3, nad3
mtInv+G4	atp8, nad2, nad6
mtZOA+I+G4	cox1
mtZOA+F+G4	nad1, nad4, nad4l, nad5

Supplementary Table 1 C. The partitioning schemes and best-fitting modes selected by ModelFinder for the dataset PCGRNA.

Best Model	Partition names
GTR+F+I+G4	atp6_pos1, atp8_pos1, atp8_pos2, atp8_pos3, cob_pos1, cox1_pos1, cox2_pos1, cox3_pos1, nad2_pos1, nad3_pos1, nad6_pos1
GTR+F+I+G4	atp6_pos2, cob_pos2, cox1_pos2, cox2_pos2, cox3_pos2, nad2_pos2, nad3_pos2, nad6_pos2
HKY+F+I+G4	atp6_pos3, cob_pos3, cox1_pos3, cox2_pos3, nad2_pos3, nad6_pos3
HKY+F+G4	cox3_pos3, nad1_pos3, nad3_pos3, nad4_pos3, nad4l_pos3, nad5_pos3
GTR+F+G4	nad1_pos1, nad4_pos1, nad4l_pos1, nad5_pos1
TVM+F+G4	nad1_pos2, nad4_pos2, nad4l_pos2, nad5_pos2
TIM3+F+I+G4	rrnL
TN+F+G4	rrnS, trn

Note: pos1, first codon positions; pos2, second codon positions; pos3, third codon positions.

Supplementary Table 2. Estimation of the evolutionary rates for each protein-coding gene by PAML.

Species	<i>atp6</i>		<i>atp8</i>		<i>cob</i>		<i>cox1</i>		<i>cox2</i>		<i>cox3</i>		<i>nad1</i>	
	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>
<i>aff. Aleurochiton</i> sp.	0.3747	2.5283	-	-	0.2401	2.9094	0.1487	3.9540	0.2627	3.4680	0.4830	2.6660	0.4119	3.0571
<i>Aleurocanthus camelliae</i>	0.3236	2.2666	1.1270	1.0236	0.2418	3.2193	0.1563	3.8236	0.2174	3.3329	0.4557	2.4357	0.3603	3.1601
<i>Aleurocanthus spiniferus</i>	0.3422	2.8009	0.9469	1.0316	0.2455	3.0017	0.1596	3.6392	0.2179	3.3675	0.5209	2.7840	0.3623	3.3150
<i>Aleurochiton aceris</i>	0.3275	2.9695	0.9725	0.7196	0.2225	2.8871	0.1454	3.5258	0.2307	3.1526	0.3906	2.3935	0.3531	3.0607
<i>Aleuroclava psidi</i>	0.3587	2.3416	1.0297	0.4918	0.2137	1.5257	0.1430	3.6749	0.2171	3.3076	0.4115	2.7239	0.3529	3.1932
<i>Aleurodicus dispersus</i>	0.3080	2.1909	1.0912	0.5135	0.5961	3.4582	0.1562	3.7848	0.2448	2.9736	0.4335	2.1810	0.8723	3.1712
<i>Aleurodicus dugesii</i>	0.3064	1.0495	0.9547	0.5521	0.2303	0.9679	0.1555	2.6396	0.2386	2.8279	0.3984	2.6261	0.3778	2.7576
<i>Aleyrodes shizuokensis</i>	0.3293	2.6934	0.8993	0.8649	0.2290	2.0202	0.1492	3.6984	0.2287	3.3490	0.4295	2.7171	0.3607	2.8917
<i>Aleyrodidae</i> sp.	0.3067	2.6488	0.7943	0.8228	0.2366	1.7197	0.1487	3.9739	0.2436	3.2962	0.4302	2.3309	0.4155	2.7480
<i>Bemisia afer</i>	0.3308	3.3207	1.7780	0.6478	0.2417	3.5372	0.1470	4.3573	0.2583	2.9166	0.4606	2.3260	0.4022	2.8583
<i>Bemisia emiliae</i>	0.3263	3.3308	1.2670	0.8814	0.2153	3.2611	0.1457	3.9557	0.2280	3.3055	0.4047	2.3017	0.3696	3.1615
<i>Bemisia</i> sp.	-	-	1.3211	0.9824	0.2343	3.2213	0.1442	3.9206	0.2290	3.3946	0.3773	2.5970	0.3519	3.0805
<i>Bemisia tabaci</i>	0.3408	3.3579	1.1883	0.9896	0.2225	2.5782	0.1418	3.9251	0.2392	3.1762	0.4133	2.5764	0.3480	3.1559
<i>Neomaskellia andropogonis</i>	0.4441	2.1977	1.0474	1.0619	0.2863	1.8095	0.1890	0.9445	0.3026	3.3642	0.5077	2.6272	0.4179	3.3235
<i>Pealius machili</i>	0.3335	3.3209	1.0246	0.5709	0.2299	3.0839	0.1360	3.7106	0.2133	3.0726	0.4048	2.4974	0.3535	2.8511
<i>Pealius mori</i>	0.3192	2.4880	1.1318	0.4252	0.2298	2.7410	0.1427	3.6386	0.2288	3.1878	0.4127	2.5355	0.3673	3.1905
<i>Singhiella simplex</i>	0.3702	3.3360	1.9986	0.8574	0.2510	3.6712	0.1545	3.8863	0.2406	3.5408	0.4744	2.4223	0.4480	3.0513
<i>Tetraleurodes acaciae</i>	0.3317	2.7305	1.2984	1.0296	0.2524	3.3070	0.1535	3.9577	0.2322	3.3340	0.4248	2.6313	0.4478	2.8110
<i>Trialeurodes vaporariorum</i>	0.3946	2.9324	1.6586	0.6071	0.2337	2.5973	0.1703	3.3894	0.2615	3.3890	0.5998	2.3217	0.4178	3.3238

Note: *dN*, non-synonymous substitution rates; *dS*, synonymous substitution rates.

Supplementary Table 2 (continued).

Species	<i>nad2</i>		<i>nad3</i>		<i>nad4</i>		<i>nad4l</i>		<i>nad5</i>		<i>nad6</i>	
	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>	<i>dN</i>	<i>dS</i>
<i>aff. Aleurochiton</i> sp.	0.4119	3.0571	0.5478	2.1900	0.4918	2.3867	0.5963	1.7523	0.4158	3.4563	0.5341	2.2526
<i>Aleurocanthus camelliae</i>	0.3603	3.1601	0.4823	2.0577	0.4596	2.2608	0.5772	1.5400	0.4102	3.1585	0.5888	2.0869
<i>Aleurocanthus spiniferus</i>	0.3623	3.3150	0.4918	1.9059	0.4635	2.1415	0.5990	1.3369	0.4100	3.3215	0.5749	1.8289
<i>Aleurochiton aceris</i>	0.3531	3.0607	0.4733	2.2022	0.4449	2.5249	0.5573	1.6785	0.4041	3.1956	0.4837	2.7102
<i>Aleuroclava psidi</i>	0.3529	3.1932	0.4436	2.8590	0.4344	2.2232	0.5340	1.9759	0.3905	3.3447	0.4519	2.1184
<i>Aleurodicus dispersus</i>	0.8723	3.1712	0.4936	2.2636	1.0853	1.9475	1.2368	1.4782	1.0219	2.4312	1.0413	1.9842
<i>Aleurodicus dugesii</i>	0.3778	2.7576	0.5014	2.1187	0.4738	3.0120	0.6343	0.9392	0.4169	3.1472	0.5698	2.2335
<i>Aleyrodes shizuokensis</i>	0.3607	2.8917	0.4487	2.5449	0.4301	2.2646	0.5079	1.6746	0.4001	2.8689	0.4906	2.0851
<i>Aleyrodidae</i> sp.	0.4155	2.7480	0.4457	2.6502	0.4682	1.9278	0.6698	1.6365	0.4353	2.9624	0.5644	2.0965
<i>Bemisia afer</i>	0.4022	2.8583	0.5431	1.9346	0.5039	1.7989	0.6123	1.5870	0.4768	2.2735	0.5700	2.1063
<i>Bemisia emiliae</i>	0.3696	3.1615	0.4993	2.0732	0.4310	1.9856	0.5586	1.5364	0.4216	2.7330	0.4956	2.3922
<i>Bemisia</i> sp.	0.3519	3.0805	-	-	0.4105	2.0656	0.5747	1.1874	0.4147	3.0048	0.5035	1.9622
<i>Bemisia tabaci</i>	0.3480	3.1559	0.5039	1.7212	0.4309	2.0712	0.5393	1.7109	0.4142	3.1304	0.5020	2.1734
<i>Neomaskellia andropogonis</i>	0.4179	3.3235	0.5144	2.1243	0.5312	2.3748	0.6036	1.7198	0.4571	3.6664	0.5638	2.1406
<i>Pealius machili</i>	0.3535	2.8511	0.4622	2.0472	0.4444	2.6348	0.5447	1.6646	0.4058	3.1924	0.5648	1.8624
<i>Pealius mori</i>	0.3673	3.1905	0.4813	2.1510	0.4563	1.9428	0.5487	1.6161	0.4070	2.9810	0.5226	2.0196
<i>Singhiella simplex</i>	0.4480	3.0513	0.5548	1.7941	0.5045	2.1352	0.7511	1.2560	0.4758	1.9755	0.6448	2.5136
<i>Tetraleurodes acaciae</i>	0.4478	2.8110	0.4593	2.0257	0.4831	2.0929	0.6549	1.7351	0.4512	2.3886	0.5055	2.4588
<i>Trialeurodes vaporariorum</i>	0.4178	3.3238	0.5520	2.3631	0.5264	2.0307	0.6479	1.4921	0.5203	2.3842	0.7555	2.4517

Note: *dN*, non-synonymous substitution rates; *dS*, synonymous substitution rates.