

SUPPLEMENTARY INFORMATION

Supplementary Tables

Table 1. Summary of the Generalized Linear Model testing the factors affecting the degree of specialization across clades (N= 116 systems). The degree of specialization (generalist *versus* specialist) was fitted to a binomial distribution. Taxonomic resolution of host use was included as a covariate only to control for its potential effect on the observed relationship.

Source	DF	L-R ChiSquare	P value
Interaction Sign	1	0.612	0.4340
Intimacy	1	1.075	0.2998
Domain	2	12.305	0.0021
N spp/genus	1	2.091	0.1482
N spp/ network	1	6.454	0.0111
Prop Species included in networks	1	0.023	0.8796
Taxonomic resolution of host use	7	15.301	0.0323

Virus mean host range= 1.30 ± 0.29 host/species, N = 21 clades; Eukaryote mean host range= 2.55 ± 0.25 ; N = 76 clades; Prokaryote mean host range= 1.87 ± 0.30 , N = 19 clades.

Table 2: Outcomes of the statistical analysis to test the significance of the modularity (M) for each system. We first calculated the value of the modularity in a random graph with the same degree (connectivity) distribution as the original network. We then calculated the 95% confidence interval for each random M, by resampling the random graphs 100 times. The observed M is significant when its value remains outside of the confidence interval.

Code	System	Observed M	Random M	Lower M	Higher M	Significance
1	<i>Acraea</i>	0.413879	0.183873	0.1821033	0.1856427	yes
2	<i>Acrocercops</i>	0.489796	0.288571	0.3013686	0.2757734	yes
3	<i>Achrysocharoides</i>	0.396694	0.378926	0.3718039	0.3860481	yes
4	<i>Alnicola</i>	0.303841	0.122861	0.1215002	0.1242218	yes
5	<i>Anthidium</i>	0.108473	0.046049	0.04523081	0.04686719	yes
6	<i>Aphis</i>	0.297833	0.171935	0.1704438	0.1734262	yes
7	<i>Aquilegia</i>	0.41196	0.141404	0.1399055	0.1429025	yes
8	<i>Arceuthobium</i>	0.279838	0.104340	0.1035444	0.1051356	yes
9	<i>Arenavirus</i>	0.220604	0.078793	0.07689791	0.08068809	yes
10	<i>Aristolochia</i>	0.066724	0.040195	0.03934824	0.04104176	yes
11	<i>Arsenophonus</i>	0.705326	0.217275	0.2165139	0.2180361	yes
12	<i>Arum</i>	0.202894	0.099326	0.0981118	0.1005402	yes
13	<i>Asclepias</i>	0.069110	0.045096	0.0446504	0.0455416	yes
14	<i>Bartonella</i>	0.271640	0.152722	0.1504289	0.1550151	yes
15	<i>Betaretrovirus</i>	0.549600	0.243192	0.2396074	0.2467766	yes
16	<i>Blattabacterium</i>	0.30484	0.164704	0.1629153	0.1664927	yes
17	<i>Blepharida</i>	0.615741	0.408611	0.40467	0.412552	yes
18	<i>Blochmannia</i>	0.135206	0.051593	0.05126763	0.05191837	yes
19	<i>Botrytis</i>	0.391242	0.219130	0.2163544	0.2219056	yes
20	<i>Brachycaudus</i>	0.464302	0.283060	0.2803074	0.2858126	yes
21	<i>Bradyrhizobium</i>	0.598338	0.334626	0.3280261	0.3412259	yes
22	<i>Bruchus</i>	0.144638	0.091271	0.09021473	0.09232727	yes
23	<i>Brueelia</i>	0.0338882	0.016083	0.01561478	0.01655122	yes
24	<i>Campanula</i>	0.080096	0.040631	0.0401727	0.0410893	yes
25	<i>Campylobacter</i>	0.075800	0.053566	0.05211572	0.05501628	yes

26	<i>Ceratosolen</i>	0.535059	0.170888	0.1693603	0.1724157	yes
27	<i>Ceropegia</i>	0.277269	0.100709	0.1000469	0.1013711	yes
28	<i>Cinara</i>	0.597353	0.343887	0.3405781	0.3471959	yes
29	<i>Conophthorus</i>	0.50000	0.49999	0.499999	0.499999	yes
30	<i>Coronavirus</i>	0.300052	0.127122	0.1261332	0.1281108	yes
31	<i>Costus</i>	0.454768	0.116078	0.1151715	0.1169845	yes
32	<i>Crematogaster</i>	0.074669	0.048535	0.0458618	0.0512082	yes
33	<i>Ctenophthalmus</i>	0.0483944	0.043531	0.04280764	0.04425436	yes
34	<i>Curculio</i>	0.0229209	0.011203	0.0109183	0.0114877	yes
35	<i>Chelostoma</i>	0.545664	0.224335	0.2225256	0.2261444	yes
36	<i>Chlamydia</i>	0.035200	0.048456	0.04605698	0.05085502	no
37	<i>Chrysolina</i>	0.391837	0.206121	0.2040735	0.2081685	yes
38	<i>Dendroctonus</i>	0.188492	0.160057	0.1569410	0.1631730	yes
39	<i>Dennyus</i>	0.219164	0.098794	0.09696339	0.1006246	yes
40	<i>Dickeya</i>	0.072531	0.054228	0.05157007	0.05688593	yes
41	<i>Echium</i>	0.00000	0.0000	0.0000	0.0000	no
42	<i>Encarsia</i>	0.0593875	0.033790	0.03288809	0.03469191	yes
43	<i>Erysiphe</i>	0.550642	0.302566	0.300335	0.304797	yes
44	<i>Escovopsis</i>	0.0271003	0.011887	0.01175983	0.01201417	yes
45	<i>Ficus</i>	0.643922	0.190746	0.1898405	0.1916515	yes
46	<i>Ficus</i>	0.141869	0.044090	0.04394596	0.04423404	yes
47	<i>Flavivirus</i>	0.354394	0.104565	0.1039730	0.1051570	yes
48	<i>FoamyVirus</i>	0.279001	0.080884	0.08030329	0.08146471	yes
49	<i>Frankia</i>	0.545185	0.259390	0.2558343	0.2629457	yes
50	<i>Galerucella</i>	0.444444	0.298889	0.2920020	0.3057760	yes
51	<i>Geomydoecus</i>	0.574074	0.343333	0.3373860	0.3492800	yes
52	<i>Geosmithia</i>	0.0502959	0.043531	0.04280764	0.04425436	yes
53	<i>Gladiolus</i>	0.226952	0.088121	0.08766687	0.08857513	yes
54	<i>Glomus</i>	0.0447554	0.035005	0.03448738	0.03552262	yes
55	<i>Golovinomyces</i>	0.482699	0.357457	0.3519989	0.3629151	yes
56	<i>Goniocena</i>	0.174519	0.106346	0.1051725	0.1075195	yes
57	<i>Haemoproteus</i>	0.701591	0.369849	0.3668338	0.3728642	yes
58	<i>Hantavirus01</i>	0.317791	0.128141	0.1270647	0.1292173	yes
59	<i>Hantavirus02</i>	0.676453	0.313169	0.3099792	0.3163588	yes
60	<i>Helicobacter</i>	0.456488	0.226788	0.2247723	0.2288037	yes
61	<i>Immunodeficiencyvirus F</i>	0.0951075	0.045588	0.04497952	0.04619648	yes
62	<i>Immunodeficiencyvirus S</i>	0.239759	0.108387	0.1070446	0.1097294	yes
63	<i>Influenza A</i>	0.420174	0.149813	0.1486040	0.1510220	yes
64	<i>Influenza H5N1</i>	0.152445	0.076730	0.07581499	0.077645	yes
65	<i>Iochoroma</i>	0.00001	0.00001	0.00001	0.00001	no
66	<i>Kladothrips</i>	0.495000	0.156515	0.1542789	0.1587511	yes
67	<i>Lamellodiscus</i>	0.163265	0.098593	0.09684135	0.1003446	yes
68	<i>Lentivirus</i>	0.666667	0.603056	0.5956399	0.6104721	yes
69	<i>Lyssavirus</i>	0.214533	0.126003	0.1218809	0.1301251	yes
70	<i>Mastrevirus</i>	0.035077	0.016982	0.0163507	0.0176133	yes
71	<i>Methanobrevibacter</i>	0.419753	0.183400	0.1801870	0.1866130	yes
72	<i>Microbotryum</i>	0.183750	0.099450	0.09741603	0.1014840	yes
73	<i>Moraea</i>	0.176454	0.073815	0.07315612	0.07447388	yes
74	<i>Morbillivirus</i>	0.125850	0.074904	0.07308708	0.07672092	yes
75	<i>Mycobacterium</i>	0.013070	0.013070	0.013070	0.013070	no
76	<i>Myovirus</i>	0.203434	0.099335	0.09718299	0.1014870	yes
77	<i>Oncothrips</i>	0.468750	0.203867	0.1961079	0.2116261	yes
78	<i>Onthophagus</i>	0.00000	0.00000	0.00000	0.00000	no
79	<i>Ophraella</i>	0.444444	0.208933	0.2011832	0.2166828	yes
80	<i>Pantoea</i>	0.330835	0.195246	0.1922948	0.1981972	yes
81	<i>Phyllonorycter</i>	0.747330	0.241780	0.2404736	0.2430864	yes
82	<i>Phytomyza</i>	0.641398	0.083098	0.08290337	0.08329263	yes
83	<i>Plasmodium</i>	0.770664	0.327686	0.3267135	0.3286585	yes
84	<i>Plasmodium</i>	0.399200	0.169579	0.1683003	0.1708577	yes
85	<i>Pleistodontes</i>	0.833333	0.833333	0.833333	0.833333	yes
86	<i>Pneumocystis</i>	0.537396	0.251229	0.2474795	0.2549785	yes
87	<i>Podovirus</i>	0.414827	0.189646	0.1856816	0.1936104	yes
88	<i>Polygonia</i>	0.198962	0.079892	0.07707734	0.08270666	yes
89	<i>Pontania</i>	0.156608	0.077121	0.07491165	0.07933035	yes
90	<i>Pseudomyrmex</i>	0.350644	0.114953	0.1138356	0.1160704	yes
91	<i>Quercus</i>	0.120760	0.037129	0.03672348	0.03753452	yes
92	<i>Retrovirus</i>	0.597097	0.177273	0.176158	0.178388	yes
93	<i>Rhadinopsylla</i>	0.18402	0.125659	0.1229388	0.1283792	yes

94	<i>Rhagoletis</i>	0.689050	0.396826	0.3927664	0.4008856	yes
95	<i>Rickettsia</i>	0.301706	0.090138	0.08958427	0.09069173	yes
96	<i>SarcomaVirus</i>	0.524221	0.235900	0.2318969	0.2399031	yes
97	<i>Siphovirus</i>	0.500771	0.147593	0.1462697	0.1489163	yes
98	<i>Spinturnix</i>	0.214158	0.111255	0.1088520	0.1136580	yes
99	<i>Spiroplasma</i>	0.339340	0.134302	0.1333062	0.1352978	yes
100	<i>Spumavirus</i>	0.21875	0.108021	0.1047667	0.1112753	yes
101	<i>Stator</i>	0.085293	0.061647	0.06043836	0.06285564	yes
102	<i>Stemphylium</i>	0.134063	0.082382	0.08034486	0.08441914	yes
103	<i>Terfezia</i>	0.0354938	0.0354938	0.0354938	0.0354938	no
104	<i>Tetraopes</i>	0.024996	0.012438	0.01186642	0.01300958	yes
105	<i>Tetratrichomonas</i>	0.642857	0.480765	0.4742586	0.4872714	yes
106	<i>Thamnophis</i>	0.036691	0.027275	0.02658815	0.02796185	yes
107	<i>Timarcha</i>	0.074659	0.042537	0.04169897	0.04337503	yes
108	<i>Timema</i>	0.244946	0.161867	0.1587579	0.1649761	yes
109	<i>Trepanoma</i>	0.511673	0.110340	0.1097317	0.1109483	yes
110	<i>Trirhabda</i>	0.358739	0.163382	0.1613903	0.1653737	yes
111	<i>Trypanosoma</i>	0.581844	0.327015	0.3244767	0.3295533	yes
112	<i>Urophora</i>	0.540000	0.381150	0.3760649	0.3862351	yes
113	<i>Vidua</i>	0.524221	0.234412	0.2302701	0.2385539	yes
114	<i>Wolbachia 01</i>	0.702207	0.392330	0.3885103	0.3961497	yes
115	<i>Wolbachia 02</i>	0.512117	0.278309	0.2757735	0.2808445	yes
116	<i>Wolbachia03</i>	0.304840	0.093720	0.09320615	0.09423385	yes

Table 3. Between-module differences in per-species host range and host assemblage composition. Host range was compared with one-way ANOVAs, whereas host assemblage was compared with ADONIS.

Code	System	df	Host range		Host assemblage		
			F	P	R ²	F	P
1	<i>Acraea</i>	3,24	2.56	0.08	0.58	11.16	0.001
2	<i>Acrocercops</i>	1,5	0.57	0.48	0.60	7.40	0.001
3	<i>Achrysocharoides</i>	6,8	0.55	0.76	0.61	2.05	0.01
4	<i>Alnicola</i>	4,27	3.07	0.03	0.69	15.50	0.01
5	<i>Anthidium</i>	1,26	0.94	0.34	0.31	11.95	0.009
6	<i>Aphis</i>	5,34	0.37	0.86	0.35	3.64	0.01
7	<i>Aquilegia</i>	2,28	0.48	0.62	0.52	32.28	0.01
8	<i>Arceuthobium</i>	4,42	7.15	0.002	0.28	17.36	0.009
9	<i>Arenavirus</i>	2,16	0.21	0.81	0.97	319.96	0.0001
10	<i>Aristolochia</i>	2,33	0.44	0.66	0.11	2.12	0.04
11	<i>Arsenophonus</i>	13,95	0.00	0.99	0.99	842.00	0.0001
12	<i>Arum</i>	2,18	0.78	0.47	0.23	5.67	0.009
13	<i>Asclepias</i>	1,35	13.60	0.001	0.26	12.26	0.01
14	<i>Bartonella</i>	2,18	0.70	0.51	0.55	10.99	0.01
15	<i>Betaretrovirus</i>	5,15	0.00	0.99	0.99	300.00	0.0001
16	<i>Blattabacterium</i>	7,15	0.00	0.99	0.99	250.00	0.0001
17	<i>Blepharida</i>	11,20	0.24	0.99	0.56	2.32	0.01
18	<i>Blochmannia</i>	5,71	0.00	0.99	0.99	300.00	0.0001
19	<i>Botrytis</i>	3,19	0.40	0.76	0.59	9.16	0.01
20	<i>Brachycaudus</i>	8,20	0.87	0.56	0.95	46.34	0.009
21	<i>Bradyrhizobium</i>	6,10	0.94	0.51	0.74	4.87	0.009
22	<i>Bruchus</i>	2,22	1.81	0.19	0.14	3.68	0.009
23	<i>Brueelia</i>	2,21	0.00	0.99	0.99	63.14	0.0001
24	<i>Campanula</i>	1,35	0.95	0.33	0.17	7.03	0.01
25	<i>Campylobacter</i>	3,16	0.26	0.85	0.58	7.24	0.001
26	<i>Ceratosolen</i>	4,29	0.00	0.99	0.99	65.00	0.0001
27	<i>Ceropegia</i>	3,44	1.24	0.31	0.30	24.54	0.001
28	<i>Cinara</i>	9,18	0.41	0.92	0.82	9.13	0.01
29	<i>Conophthorus</i>	10,2	0.23	0.96	0.92	2.34	0.01
30	<i>Coronavirus</i>	5,35	0.00	0.99	0.99	300.00	0.0001
31	<i>Costus</i>	1,39	0.00	0.99	0.99	300.00	0.0001
32	<i>Crematogaster</i>	2,7	0.60	0.57	0.42	2.56	0.02
33	<i>Ctenophthalmus</i>	2,26	2.61	0.09	0.19	2.98	0.01
34	<i>Curculio</i>	5,20	5.03	0.004	0.97	116.50	0.0001
35	<i>Chelostoma</i>	5,29	1.89	0.13	0.77	19.70	0.009
36	<i>Chlamydia</i>	1,7	0.76	0.41	0.26	2.44	0.03
37	<i>Chrysolina</i>	6,25	1.21	0.33	0.16	5.54	0.009
38	<i>Dendroctonus</i>	3,14	0.63	0.61	0.11	1.98	0.02
39	<i>Dennyus</i>	3,17	0.00	0.99	0.99	65.00	0.0001
40	<i>Dickeya</i>	2,6	0.53	0.62	0.40	2.01	0.01
41	<i>Echium</i>						
42	<i>Encarsia</i>	1,21	11.36	0.003	0.87	142.52	0.0001
43	<i>Erysiphe</i>	19,40	0.29	0.99	0.66	4.09	0.009
44	<i>Escovopsis</i>	4,65	0.00	0.99	0.99	4.65	0.0001
45	<i>Ficus</i>	14,100	5.77	0.0001	0.84	38.56	0.009
46	<i>Ficus</i>	3,256	0.75	0.52	0.18	19.03	0.01
47	<i>Flavivirus</i>	5,65	3.04	0.01	0.98	878.60	0.0001
48	<i>FoamyVirus</i>	2,47	0.00	0.99	0.99	226.00	0.0001
49	<i>Frankia</i>	9,13	0.00	0.99	0.99	65.00	0.0001
50	<i>Galerucella</i>	3,6	0.56	0.66	0.73	5.40	0.01
51	<i>Geomydoecus</i>	5,9	0.00	0.99	0.99	65.00	0.0001
52	<i>Geosmithia</i>	3,10	4.77	0.02	0.70	7.96	0.009
53	<i>Gladiolus</i>	5,74	0.78	0.56	0.11	9.21	0.01
54	<i>Glomus</i>	2,32	0.80	0.46	0.25	5.48	0.01
55	<i>Golovinomyces</i>	4,11	0.25	0.98	0.49	2.68	0.01
56	<i>Gonioctena</i>	8,23	2.88	0.02	0.74	9.85	0.009
57	<i>Haemoproteus</i>	6,30	0.60	0.73	0.76	15.80	0.001
58	<i>Hantavirus01</i>	3,37	0.00	0.99	0.99	787.00	0.0001
59	<i>Hantavirus02</i>	6,23	0.00	0.99	0.99	382.00	0.0001
60	<i>Helicobacter</i>	8,28	0.33	0.95	0.78	12.12	0.001
61	<i>Immunodeficiencyvirus F</i>	2, 27	0.00	0.99	0.99	500.00	0.0001
62	<i>Immunodeficiencyvirus S</i>	3,23	0.21	0.89	0.99	568.00	0.0001
63	<i>Influenza A</i>	5,36	0.00	0.99	0.99	65.00	0.0001

64	<i>Influenza H5N1</i>	5,26	0.00	0.99	0.99	65.00	0.0001
65	<i>lochroma</i>						
66	<i>Kladothrips</i>	2,19	0.00	0.99	0.99	950.00	0.0001
67	<i>Lamellodiscus</i>	3,15	0.35	0.79	0.33	8.36	0.01
68	<i>Lentivirus</i>	6,5	0.00	0.99	0.99	65.00	0.0001
69	<i>Lyssavirus</i>	2,7	0.00	0.99	0.99	565.00	0.0001
70	<i>Mastrevirus</i>	2,11	0.00	0.99	0.99	889.00	0.0001
71	<i>Methanobrevibacter</i>	6,15	1.02	0.45	0.98	5.46	0.009
72	<i>Microbotryum</i>	4,11	0.27	0.87	0.95	54.17	0.001
73	<i>Moraea</i>	4,40	0.80	0.54	0.24	13.74	0.009
74	<i>Morbillivirus</i>	3,10	7.07	0.008	0.83	16.33	0.001
75	<i>Mycobacterium</i>	4,72	2.88	0.02	0.60	27.03	0.001
76	<i>Myovirus</i>	3,14	0.00	0.99	0.99	300.00	0.0001
77	<i>Oncothrips</i>	1,7	0.00	0.99	0.99	300.00	0.0001
78	<i>Onthophagus</i>						
79	<i>Ophraella</i>	4,7	0.53	0.72	0.25	3.31	0.03
80	<i>Pantoea</i>	4,16	0.15	0.96	0.65	7.43	0.009
81	<i>Phyllonorycter</i>	12,64	0.37	0.97	0.13	11.19	0.0009
82	<i>Phytomyza</i>	3,462	0.67	0.57	0.59	220.61	0.0001
83	<i>Plasmodium</i>	18,162	1.02	0.44	0.04	7.41	0.01
84	<i>Plasmodium</i>	4,37	1.03	0.45	0.71	22.48	0.001
85	<i>Pleistodontes</i>	15,6	0.33	0.963	0.99	36.45	0.009
86	<i>Pneumocystis</i>	8,12	0.00	0.99	0.99	870.00	0.0001
87	<i>Podovirus</i>	2,14	0.00	0.99	0.99	870.00	0.0001
88	<i>Polygonia</i>	1,11	0.93	0.34	0.63	18.02	0.009
89	<i>Pontania</i>	2,13	1.62	0.23	0.98	283.29	0.0001
90	<i>Pseudomyrmex</i>	3,31	2.31	0.10	0.33	16.03	0.009
91	<i>Quercus</i>	1,45	0.24	0.63	0.56	56.74	0.00001
92	<i>Retrovirus</i>	5,65	0.00	0.99	0.99	65.00	0.0001
93	<i>Rhadinopsylla</i>	3,12	0.37	0.78	0.35	2.16	0.01
94	<i>Rhagoletis</i>	10,19	0.40	0.93	0.95	34.09	0.001
95	<i>Rickettsia</i>	7,57	22,17	0.0001	0.94	122.36	0.0001
96	<i>SarcomaVirus</i>	2, 12	0.00	0.99	0.99	203.00	0.0001
97	<i>Siphoviorus</i>	3,41	0.00	0.99	0.99	203.00	0.0001
98	<i>Spinturnix</i>	2,12	0.75	0.49	0.70	13.83	0.01
99	<i>Spiroplasma</i>	6,40	1.79	0.13	0.70	15.45	0.001
100	<i>Spumavirus</i>	1,8	0.00	0.99	0.99	633.00	0.0001
101	<i>Stator</i>	3,18	2.89	0.06	0.66	11.92	0.01
102	<i>Stemphylium</i>	4,15	0.56	0.69	0.57	4.89	0.009
103	<i>Terfezia</i>	1,6	0.54	0.49	0.35	3.21	0.04
104	<i>Tetraopes</i>	3,11	0.00	0.99	0.99	352.00	0.0001
105	<i>Tetratrichomonas</i>	7,10	4.40	0.01	0.66	2.79	0.01
106	<i>Thamnophis</i>	1,22	4.54	0.04	0.19	5.12	0.01
107	<i>Timarcha</i>	2,23	3.96	0.03	0.51	24.7	0.001
108	<i>Timema</i>	3,12	1.12	0.38	0.18	3.24	0.01
109	<i>Treponema</i>	3,67	0.00	0.99	0.99	200.33	0.0001
110	<i>Trirhabda</i>	4,21	0.00	0.99	0.20	5.99	0.009
111	<i>Trypanosoma</i>	6,34	0.58	0.74	0.52	6.17	0.009
112	<i>Urophora</i>	3,7	0.49	0.70	0.75	8.02	0.009
113	<i>Viduae</i>	6,12	0.21	0.97	0.96	48.64	0.0001
114	<i>Wolbachia 01</i>	17,20	0.00	0.99	0.99	200.33	0.0001
115	<i>Wolbachia 02</i>	14,24	0.00	0.99	0.99	65.53	0.0001
116	<i>Wolbachia 03</i>	8,76	0.00	0.99	0.99	65.50	0.0001

Table 4. Summary of the Generalized Linear Models (N=116 systems) testing the factors affecting the Number of Modules (Poisson) and Modularity (Gaussian). Number of Modules was fitted to a Poisson distribution with log as the link function, whereas Modularity was fitted to a Normal distribution with identity as the link function. Taxonomic resolution of host use was included as a covariate only to control for its potential effect on the observed relationship.

Source	df	Num M			M		
		Likelihood Ratio	P-value	Estimate \pm 1 SE	Likelihood Ratio	P-value	Estimate \pm 1 SE
Interaction Sign	1	2.308	0.1287		0.444	0.5051	
Interaction Intimacy	1	5.921	0.0150		3.071	0.0797	
Domain	2	23.033	<.0001		1.699	0.4276	
Host range	1	30.609	<.0001	-0.392 \pm 0.173	24.629	<.0001	-0.044 \pm 0.011
Spp/ network	1	4.153	0.0416	0.011 \pm 0.006	4.673	0.0306	0.001 \pm 0.001
Taxonomic resolution	7	24.200	0.0011		7.232	0.4051	

Table 5. Between-Domain differences in the number of modules and Modularity values. N refers to the number of clades studied per kingdom.

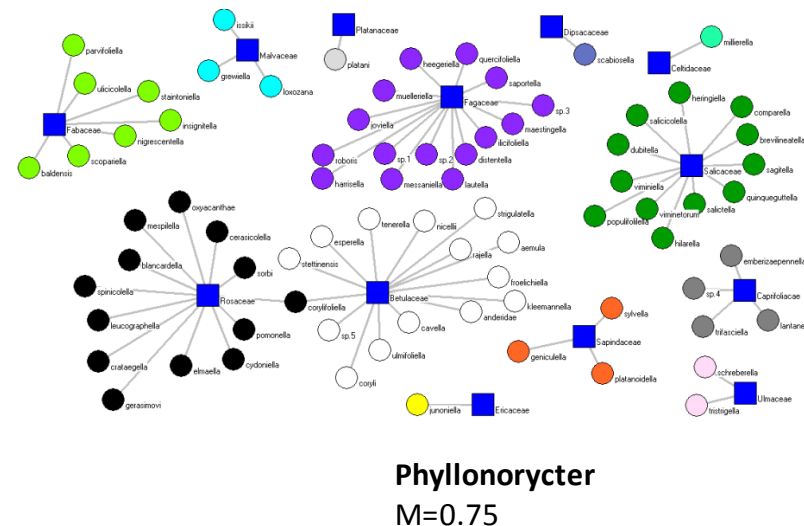
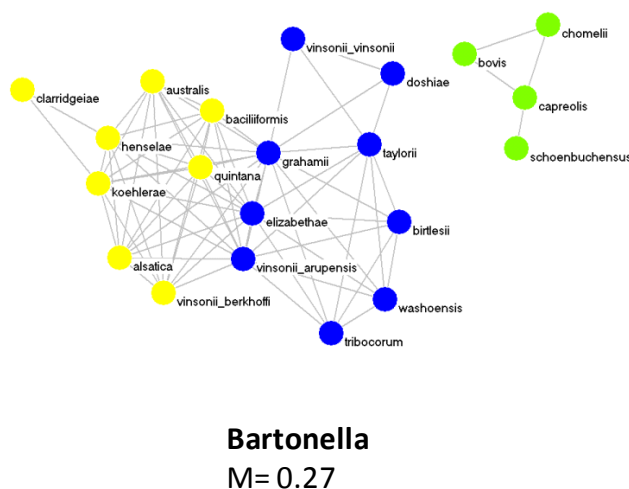
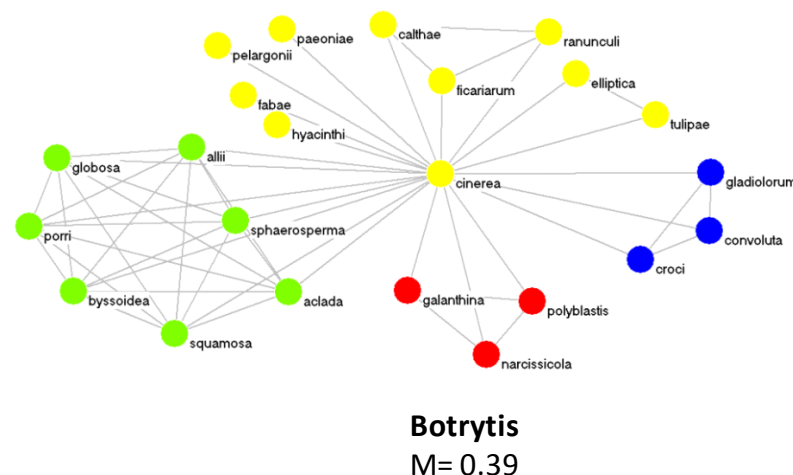
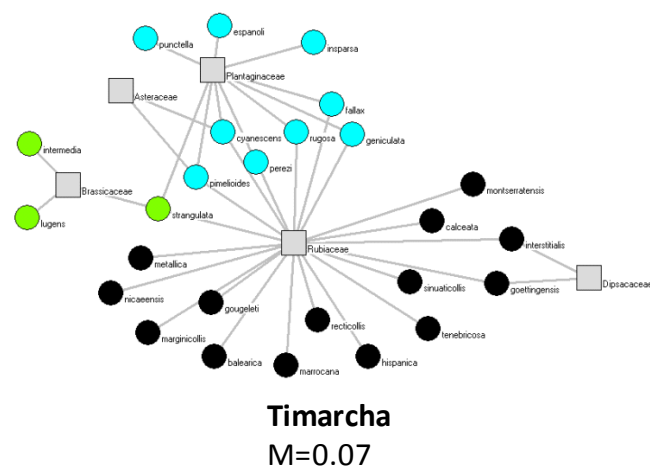
Domain	N	Number of Modules		Modularity	
		Mean	Std Err	Mean	Std Err
Eukaryote	76	5.342	0.414	0.312	0.025
Prokaryote	19	7.631	0.828	0.332	0.050
Virus	21	4.350	0.350	0.338	0.043

Table 6. Summary of the Generalized Linear Model testing the factors affecting the interactive niche conservatism across systems (N= 111 systems). Phylogenetic signal occurrence (yes *versus* no) was fitted to a binomial distribution. Sample size is the number of consumer-host associations. Taxonomic resolution of host use was included as a covariate only to control for its potential effect on the observed relationship.

Source	df	Likelihood Ratio	P-value	Estimate \pm 1 SE
Interaction Sign	1	0.425	0.5145	
Interaction Intimacy	1	0.081	0.7749	
Domain	2	3.442	0.1789	
Sample size	1	14.84	0.0001	-0.088 \pm 0.036
Host range	1	1.079	0.2992	-0.006 \pm 0.207
Taxonomic resolution	7	7.915	0.3401	

Supplementary Figures

Figure 1: Network structure of four specialist clades differing in the value of M to indicate how M decrease with the amount of species sharing hosts between different modules. In *Timarcha* there are three modules, but all of them share some hosts. In *Bartonella* one module interacts mostly with rodents (Muridae, Cricetidae, Sciuridae), second module with Cervidae and Bovidae, and the last module with Felidae, Hominidae and Canidae. In *Botrytis* there are four modules, one interacting with Iridiaceae, one with Amaryllidaceae, one with Alliaceae, and one with several plant families. Finally, in *Phyllonorycter* there are 13 modules, none sharing a single host with any other module.



Supplementary Data

Appendix 1: Data set of the overall clades used in this study.

Code	System	Domain	Kingdom	Interaction Type	Interaction Sign	Intimacy	Spp/ network	Spp/ phylogeny	Modularity	No Modules	Host range [max-min]	Phylosignal
1	Acraea	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	28	28	0.414	4	1.79 [1-5]	0.001
2	Acrocercops	Eucarya	Animalia	Leaf mining	Negative	Symbiotic	7	7	0.490	2	1.71 [1-4]	0.048
3	Achrysocharoides	Eucarya	Animalia	Parasitoid	Negative	Symbiotic	15	15	0.397	7	2.93 [1-9]	0.201
4	Alnicola	Eucarya	Fungi	Mycorrhiza	Positive	Symbiotic	32	32	0.303	6	2.43 [1-8]	0.001
5	Anthidium	Eucarya	Animalia	Pollination	Positive	Non-symbiotic	28	28	0.108	2	3.82 [1-10]	0.006
6	Aphis	Eucarya	Animalia	Sap-sucking	Negative	Non-symbiotic	40	31	0.298	6	2.93 [1-25]	0.004
7	Aquilegia	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	34	26	0.412	3	1.29 [1-5]	0.007
8	Arceuthobium	Eucarya	Plantae	Parasitism	Negative	Symbiotic	44	44	0.280	5	1.28 [1-3]	0.082
9	Arenavirus	Virus	RNA Virus	Parasitism	Negative	Symbiotic	19	19	0.221	3	1.05[1-2]	0.001
10	Aristolochia	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	37	29	0.067	3	4.65 [1-15]	0.001
11	Arsenophonus	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	109	109	0.705	14	1.00 [1-1]	0.001
12	Arum	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	21	15	0.203	3	3.19 [1-8]	0.96
13	Asclepias	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	37	37	0.061	2	7.30 [1-32]	0.023
14	Bartonella	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	21	20	0.271	3	1.57 [1-3]	0.006
15	Betaretrovirus	Virus	RNA virus	Parasitism	Negative	Symbiotic	21	21	0.550	6	1.09 [1-2]	0.018
16	Blattabacterium	Bacteria	Bacteria	Nutrition	Positive	Symbiotic	23	23	0.305	8	1.00 [1-1]	0.001
17	Blepharida	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	32	32	0.613	10	2.56 [1-11]	0.001
18	Blochmannia	Bacteria	Bacteria	Nutrition	Positive	Symbiotic	77	77	0.135	6	1.00 [1-1]	0.001
19	Botrytis	Eucarya	Fungi	Parasitism	Negative	Symbiotic	23	20	0.391	4	1.44 [1-11]	0.783
20	Brachycaudus	Eucarya	Animalia	Sap-sucking	Negative	Non-symbiotic	29	28	0.464	9	1.24 [1-4]	0.018
21	Bradyrhizobium	Bacteria	Bacteria	Nutrition	Positive	Symbiotic	17	17	0.598	7	3.08 [1-18]	0.023
22	Bruchus	Eucarya	Animalia	Seed predation	Negative	Symbiotic	31	22	0.145	3	3.96 [1-19]	0.001
23	Brueelia	Eucarya	Animalia	Parasitism	Negative	Non-symbiotic	24	24	0.117	4	1.00 [1-1]	1
24	Campanula	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	37	18	0.080	2	4.32 [1-18]	1
25	Campylobacter	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	20	20	0.076	4	3.3 [1-13]	0.503
26	Ceratosolen	Eucarya	Animalia	Pollination	Positive	Symbiotic	34	15	0.535	5	1.00 [1-1]	0.02
27	Ceropegia	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	48	20	0.277	4	1.78 [1-15]	0.92
28	Cinara	Eucarya	Animalia	Sap-sucking	Negative	Non-symbiotic	28	28	0.597	10	2.11 [1-6]	0.387
29	Conophthorus	Eucarya	Animalia	Stem-boring	Negative	Symbiotic	13		0.500	11	3.08 [1-20]	
30	Coronavirus	Virus	RNA virus	Parasitism	Negative	Symbiotic	41	41	0.300	6	1.00 [1-1]	0.001
31	Costus	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	41	41	0.455	2	1.00 [1-1]	0.00
32	Crematogaster	Eucarya	Animalia	Myrmecophytism	Positive	Symbiotic	10	10	0.075	3	8.20 [1-17]	0.619
33	Ctenophthalmus	Eucarya	Animalia	Parasitism	Negative	Non-symbiotic	29		0.048	4	11.24 [1-47]	
34	Curculio	Eucarya	Animalia	Seed predation	Negative	Symbiotic	50	20	0.022	5	1.19 [1-2]	0.99
35	Chelostoma	Eucarya	Animalia	Pollination	Positive	Non-symbiotic	35	35	0.546	6	1.37 [1-5]	0.001
36	Chlamydia	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	9	9	0.035	2	3.78 [1-12]	1
37	Chrysolina	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	32	30	0.392	7	1.03 [1-2]	0.001
38	Dendroctonus	Eucarya	Animalia	Stem boring	Negative	Symbiotic	19	18	0.188	4	6.50 [1-22]	0.024
39	Dennyus	Eucarya	Animalia	Parasitism	Negative	Non-symbiotic	21	21	0.219	4	1.00 [1-1]	0.005
40	Dickeya	Bacteria	Bacteria	Plant pathogen	Negative	Symbiotic	9	9	0.072	3	5.67 [1-14]	
41	Echium	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	25	25	0.000	.	8.78 [2-17]	.
42	Encarsia	Eucarya	Animalia	Parasitoid	Negative	Symbiotic	23	23	0.059	2	1.17 [1-2]	0.999
43	Erysiphe	Eucarya	Fungi	Plant pathogen	Negative	Symbiotic	60	31	0.551	20	2.27 [1-24]	0.651
44	Escovopsis	Eucarya	Fungi	Parasitism	Negative	Symbiotic	70	70	0.027	5	1.00 [1-1]	0.001

45	Ficus	Eucarya	Plantae	Pollination	Positive	Symbiotic	115	31	0.644	15	1.23 [1-3]	0.0001
46	Ficus	Eucarya	Plantae	Seed dispersal	Positive	Non-symbiotic	260	55	0.142	4	6.06 [1-45]	0.001
47	Flavivirus	Virus	RNA virus	Parasitism	Negative	Symbiotic	71	71	0.354	6	1.05 [1-2]	0.001
48	FoamyVirus	Virus	RNA virus	Comensalism	Positive	Symbiotic	50	50	0.279	3	1.00 [1-1]	0.001
49	Frankia	Eucarya	Fungi	N-fixing	Positive	Symbiotic	24	24	0.545	10	1.00 [1-1]	0.002
50	Galerucella	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	10	10	0.444	4	1.30 [1-3]	0.35
51	Geomydoecus	Eucarya	Animalia	Parasitism	Negative	Non-symbiotic	94	94	0.574	8	1.00 [1-1]	0.001
52	Geosmithia	Eucarya	Fungi	Parasitism	Negative	Symbiotic	14	14	0.050	4	2-06 [1-6]	0.033
53	Gladiolus	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	80		0.230	6	1.42 [1-4]	
54	Glomus	Eucarya	Fungi	Mycorrhiza	Positive	Symbiotic	25	22	0.045	3	4.17 [1-13]	0.677
55	Golovinomyces	Eucarya	Fungi	Plant pathogen	Negative	Symbiotic	16		0.483	5	2.06 [1-9]	
56	Goniocena	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	32	15	0.174	9	1.34 [1-2]	0.003
57	Haemoproteus	Eucarya	Chromalveolata	Parasitism	Negative	Symbiotic	37	37	0.702	7	1.16 [1-3]	0.0001
58	Hantavirus01	Virus	RNA virus	Parasitism	Negative	Symbiotic	41	41	0.318	4	1.00 [1-1]	0.0001
59	Hantavirus02	Virus	RNA virus	Parasitism	Negative	Symbiotic	30	30	0.676	7	1.00 [1-1]	0.0001
60	Helicobacter	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	37	27	0.456	8	1.32 [1-4]	0.001
61	Influenzavirus A	Virus	RNA virus	Parasitism	Negative	Symbiotic	42	42	0.420	6	1.00 [1-1]	0.001
62	Influenzavirus A H5N1	Virus	RNA virus	Parasitism	Negative	Symbiotic	32	32	0.152	6	1.00 [1-1]	0.99
63	Immunodeficiency F	Virus	RNA virus	Parasitism	Negative	Symbiotic	30	30	0.095	3	1.00 [1-1]	0.0001
64	Immunodeficiency S	Virus	RNA virus	Parasitism	Negative	Symbiotic	27	16	0.240	4	1.04 [1-2]	0.0001
65	Ioichroma	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	15	15	0.001	.	3.20 [1-5]	.
66	Kladothrips	Eucarya	Animalis	Gall-making	Negative	Symbiotic	21	21	0.495	3	1.00 [1-1]	0.002
67	Lamellodiscus	Eucarya	Animalia	Parasitism	Negative	Symbiotic	19	19	0.163	4	1.26 [1-3]	0.609
68	Lentivirus	Virus	RNA virus	Parasitism	Negative	Symbiotic	12	12	0.667	7	1.00 [1-1]	0.004
69	Lyssavirus	Virus	RNA virus	Parasitism	Negative	Symbiotic	10	10	0.214	3	1.00 [1-1]	0.212
70	Mastrevirus	Virus	DNA virus	Plant pathogen	Negative	Symbiotic	14	14	0.035	3	1.00 [1-1]	0.001
71	Methanobrevibacter	Archaea	Euryarchaeota	N-production	Positive	Symbiotic	22	22	0.420	7	1.68 [1-4]	0.014
72	Microbotryum	Eucarya	Fungi	Plant pathogen	Negative	Symbiotic	16	16	0.184	5	1.19 [1-2]	0.023
73	Moraea	Eucarya	Plantae	Pollination	Positive	Non-symbiotic	45	25	0.176	5	2.00 [1-7]	0.227
74	Morbillivirus	Virus	RNA virus	Parasitism	Negative	Symbiotic	14	14	0.126	4	7.07 [1-11]	0.009
75	Mycobacterium	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	77	45	0.013	5	1.52 [1-9]	1.00
76	Myovirus	Virus	DNA virus	Parasitism	Negative	Symbiotic	18	18	0.203	4	1.00 [1-1]	0.0001
77	Oncothrips	Eucarya	Animalis	Gall-making	Negative	Symbiotic	9	9	0.469	2	1.00 [1-1]	0.001
78	Onthophagus	Eucarya	Animalia	Detritivory	Positive	Non-symbiotic	27	.	0.000	.	5.55 [1-10]	.
79	Ophraella	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	12	12	0.444	4	1.00 [1-1]	0.09
80	Pontaea	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	21	21	0.331	5	1.86 [1-7]	
81	Phyllonorycter	Eucarya	Animalia	Endophyty	Negative	Symbiotic	77	77	0.747	13	1.01 [1-2]	0.001
82	Phytomyza	Eucarya	Animalia	Leaf mining	Negative	Symbiotic	466	25	0.641	4	1.10 [1-42]	0.001
83	Plasmodium	Bacteria	Chromalveolata	Parasitism	Negative	Symbiotic	181	30	0.771	18	1.46 [1-16]	0.001
84	Plasmodium	Bacteria	Chromalveolata	Parasitism	Negative	Symbiotic	42	42	0.399	5	1.57[1-9]	0.001
85	Pleistodontes	Eucarya	Animalia	Pollination	Positive	Symbiotic	22	18	0.833	16	1.09 [1-2]	0.997
86	Pneumocystis	Eucarya	Fungi	Parasitism	Negative	Symbiotic	21	21	0.537	9	1.00 [1-1]	0.001
87	Podovirus	Virus	DNA virus	Parasitism	Negative	Symbiotic	17	17	0.415	3	1.00 [1-1]	0.0001
88	Polygonia	Eucarya	Plantae	Folivory	Negative	Non-symbiotic	15	13	0.199	2	2.47 [1-7]	0.023
89	Pontania	Eucarya	Animalia	Gall-making	Negative	Symbiotic	16	16	0.157	3	1.06 [1-2]	0.040
90	Pseudomyrmex	Eucarya	Animalia	Domatia	Positive	Non-symbiotic	35	14	0.351	4	1.68 [1-6]	0.852
91	Quercus	Eucarya	Plantae	Seed dispersal	Positive	Non-symbiotic	47	11	0.121	2	1.94 [1-4]	0.76
92	Retrovirus	Virus	RNA virus	Parasitism	Negative	Symbiotic	61	61	0.597	6	1.00 [1-1]	0.001
93	Rhadinopsylla	Eucarya	Animalia	Parasitism	Negative	Non-symbiotic	16	.	0.184	3	8.75 [1-42]	.
94	Rhagoletis	Eucarya	Animalia	Seed predation	Negative	Symbiotic	30	30	0.689	11	1.03 [1-2]	0.001
95	Rickettsia	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	65	65	0.302	8	1.24 [1-3]	0.001

96	SarcomaVirus	Virus	RNA virus	Parasitism	Negative	Symbiotic	15	15	0.524	3	1.00 [1-1]	0.007
97	Siphovirus	Virus	DNA virus	Parasitism	Negative	Symbiotic	45	45	0.501	4	1.00 [1-1]	0.001
98	Spinturnix	Eucarya	Animalia	Parasitism	Negative	Non-symbiotic	15	11	0.214	3	1.40 [1-2]	0.495
99	Spiroplasma	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	47	47	0.339	7	1.60 [1-11]	0.137
100	Spumavirus	Virus	RNA virus	Parasitism	Positive	Symbiotic	10	10	0.219	2	1.00 [1-1]	0.0001
101	Stator	Eucarya	Animalia	Seed predation	Negative	Non-symbiotic	22	21	0.085	5	2.73 [1-18]	0.013
102	Stemphylium	Eucarya	Fungi	Plant pathogen	Negative	Symbiotic	25	17	0.134	5	3.70 [1-27]	0.809
103	Terfezia	Eucarya	Fungi	Mycorrhiza	Positive	Symbiotic	8	8	0.036	2	2.87 [1-7]	0.900
104	Tetraopes	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	15	15	0.025	3	1.00 [1-1]	0.990
105	Tetratrichomonas	Bacteria	Excavata	Parasitism	Negative	Symbiotic	18	18	0.643	8	2.89 [1-11]	0.120
106	Thamnophis	Eucarya	Animalia	Predation	Negative	Non-symbiotic	24	24	0.037	2	5.58 [1-11]	0.184
107	Timarcha	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	26	26	0.075	18	1.46 [1-3]	0.001
108	Timema	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	17	14	0.187	4	1.65 [1-4]	0.980
109	Treponema	Bacteria	Excavata	Nutrition	Positive	Symbiotic	71	71	0.512	4	1.00 [1-1]	0.001
110	Trirhabda	Eucarya	Animalia	Folivory	Negative	Non-symbiotic	26	24	0.359	5	1.00 [1-1]	0.001
111	Trypanosoma	Eucarya	Excavata	Parasitism	Negative	Symbiotic	41	19	0.582	7	2.61 [1-11]	0.001
112	Urophora	Eucarya	Animalia	Gall-making	Negative	Symbiotic	11	11	0.540	4	1.18 [1-3]	0.033
113	Vidua	Eucarya	Animalia	Brood parasitism	Negative	Non-symbiotic	19	19	0.524	7	1.16 [1-3]	0.001
114	Wolbachia01	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	38	38	0.702	17	1.00 [1-1]	0.001
115	Wolbachia02	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	40	40	0.512	16	1.00 [1-1]	0.001
116	Wolbachia03	Bacteria	Bacteria	Parasitism	Negative	Symbiotic	85	85	0.301	10	1.00 [1-1]	0.001

Supplementary Notes

We provide here information about each of the systems used in our study, including their current taxonomic status and some notes on their natural history. We also provide the main literature sources used to build the phylogenies and interaction networks. Finally, for some groups we thank some researchers that sent us their unpublished data.

1) **Acraea** (Animalia: Lepidoptera, Nymphalidae) is a genus of African butterflies containing around 220 species. The larvae are leaf-chewing feeding on many plant species belonging to several families. For our review, the hosts were considered at the level of plant family, since this is the lowest existing taxonomic resolution.

Reference:

K. L. Silva-Brandão, N. Wahlberg, R. Bastos Francini, A. M. L. Azeredo-Espin, K. S. Brown Jr., M. Paluch, D. C. Lees, and A. V.L. Freitas (2008). Phylogenetic relationships of butterflies of the tribe *Acraeini* (Lepidoptera, Nymphalidae, Heliconiinae) and the evolution of host plant use. *Molecular Phylogenetics and Evolution* 46: 515–531.

2) **Acrocercops** (Animalia: Lepidoptera: Gracilliridae) is a large genus of leaf-mining moths that feed on several to few tree species. We have used host genus as the taxonomic resolution in this group.

References:

Ohshima, I., K. Yoshizawa 2006. Multiple host shifts between distantly related plants, Juglandaceae and Ericaceae, in the leaf-mining moth *Acrocercops leucophaea* complex (Lepidoptera: Gracillariidae). *Mol. Phyl. Evol.* 38: 231–240.

3) **Achrysocharoides** (Animalia: Hymenoptera, Eulophidae) is a genus of parasitoid wasps with 48 described species. Most species attack leaf-mining Lepidoptera belonging to the genus *Phyllonorycter* (Gracillariidae). For our review, we used 15 European species attacking *Phyllonorycter*, and thus the hosts were considered at the level of species.

Reference:

López-Vaamonde, C., H.C.J. Godfray, S.A. West, C. Hansson and J.M. Cook (2005). The evolution of host use and unusual reproductive strategies in *Achrysocharoides* parasitoid wasps. *Journal of Evolutionary Biology* 18: 1029–1041.

4) **Alnicola** (= *Naucoria*) (Fungi: Agaricales, Cortinariaceae) is a genus of strictly temperate, obligately ectomycorrhizal fungi. *Alnicola* is a comparatively small genus with approximately 60 species mentioned in the literature. Most *Alnicola* spp. are strictly host-specific on alders (*Alnus* spp.), while a small number are mycobionts on willows (*Salix* spp.) or other hosts. For this reason, in this study the hosts were considered at the species level.

Reference:

Moreau P.A., U. Peintner and M. Gardes 2006. Phylogeny of the ectomycorrhizal mushroom genus *Alnicola* (Basidiomycota, Cortinariaceae) based on rDNA sequences with special

emphasis on host specificity and morphological characters. *Molecular Phylogenetics and Evolution* 38: 794–807.

5) **Anthidium** (Animalia: Hymenoptera, Megachilidae) is a genus of oligolectic to polylectic bees that forage for pollen and nectar in many plant species belonging to different families. The host taxonomic resolution considered in this review is plant family.

Reference:

Müller, A. 1996. Host-plant specialization in Western Palearctic Anthiine bees (Hymenoptera: Apoidea: Megachilidae). *Ecological Monographs* 66: 235–257.

6) **Aphis** (Animalia: Hemiptera, Aphididae) is a genus of generalist sap-sucking insects that feed on many different plant families. For our study, the hosts were considered at the level of plant family, since this is the lowest existing taxonomic resolution for most species.

References:

Ozdemir, I., S. Toros, A.N. Kilincer, M.O. Gürkan 2006. A Survey of Aphididae (Homoptera) on Wild Plants in Ankara, Turkey. *Ekoloji* 15: 1–6.

Turcinaviciene, J., R. Rakauskas and B.V. Pedersen 2006. Phylogenetic relationships in the “*grossulariae*” species group of the genus *Aphis* (Hemiptera: Sternorrhyncha: Aphididae): Molecular evidence. *European Journal of Entomology* 103: 597–604.

D’acier A. C., E. Jousselin, J.F. Martin, J. Y. Rasplus 2007. Phylogeny of the Genus *Aphis* Linnaeus, 1758 (Homoptera: Aphididae) inferred from mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution* 42: 598–611.

7) **Aquilegia** (Plantae: Ranunculales, Ranunculaceae) is a plant genus comprising 70 species distributed throughout the Nearctic and Palearctic. Their flowers are pollinated by several species of bees, hoverflies and hummingbirds (only in North America). For this reason, we considered the insect family as the host resolution.

References:

Eckert, C.G. and A. Schaefer 1998. Does self-pollination provide reproductive assurance in *Aquilegia canadensis* (Ranunculaceae)? *American Journal of Botany* 85: 919–924.

Huang, S.Q., L.L. Tang, Q. Yu and Y.H. Guo 2004. Temporal floral sex allocation in protogynous *Aquilegia yabeana* contrasts with protandrous species: support for the mating environment hypothesis. *Evolution* 58: 1131–1134.

Sébastien Lavergne S., M. Debussche and J. D. Thompson 2005. Limitations on reproductive success in endemic *Aquilegia viscosa* (Ranunculaceae) relative to its widespread congener *Aquilegia vulgaris*: the interplay of herbivory and pollination. *Oecologia* 142:212–220.

Brunet J. and H. R. Sweet 2006. Impact of insect pollinator group and floral display size on outcrossing rate. *Evolution* 60: 234–246.

Medrano, M., M. C. Castellanos, and C. M. Herrera 2006. Comparative floral and vegetative differentiation between two European *Aquilegia* taxa along a narrow contact zone. *Plant Systematics and Evolution* 262: 209–224.

Whittall, J. and S.A. Hodges 2007. Pollinator shifts drive increasingly long nectar spurs in columbine flowers. *Nature* 447: 706-710.

8) **Arceuthobium** (Plantae: Santalales: Viscaceae) is a plant genus comprising 44 species that parasitize members of Pinaceae and Cupressaceae in North America, Central America, Asia and Africa. Most species inhabit North America, growing on *Pinus* spp. For this review the hosts were considered at the level of genus.

References:

Nickrent, D. L. 2002. Mistletoe phylogenetics: Current relationships gained from analysis of DNA sequences. Pp. 48-57 in: Proceedings of the Western International Forest Disease Work Conference, August 14-18, 2000. Waikoloa, Hawai'i. 253 pp.

Nickrent, D.L., M.A. García, M.P. Martín, and R.L. Mathiasen 2004. A phylogeny of all species of *Arceuthobium* (Viscaceae) using nuclear and chloroplast DNA sequences. *Amer. J. Bot.* 91: 125-138

Norton, D.A. and M.A. Carpenter 1998. Mistletoes as parasites: host specificity and speciation. *Trends Ecol. Evol.* 13:101-105.

9) **Arenavirus** (RNA Virus: RNA Virus, Arenaviridae) is a genus of viruses that cause hemorrhagic fevers and neurologic disease in humans. Rodents are the natural hosts of arenaviruses. The virus–host relationship between individual arenaviruses and rodent species is relatively specific and, in the well-documented virus–rodent associations, arenaviruses are able to establish chronic infections with continuous production of virus and little or no disease in the rodent host. For our review, we have used host family as the lowest taxonomic resolution.

Reference:

Bowen, M.D., C. J. Peters, and S. T. Nichol 1997. Phylogenetic analysis of the *Arenaviridae*: Patterns of virus evolution and evidence for cospeciation between arenaviruses and their rodent hosts. *Mol. Phyl. Evol.* 8: 301-316.

10) **Aristolochia** (Plantae: Piperales, Aristolochiaceae) is a large plant genus. They are widespread and occur in a great diversity of climates in all continents except Australia. Their flowers have a specialized pollination mechanism. The plants are aromatic and their strong scent attracts insects. The inner part of the perianth tube is covered with hairs, acting as a fly-trap. These hairs then wither to release the fly, covered with pollen. Since these plants are generalist, visited by many different flies belonging to several to many Diptera families, the host resolution considered in our review was family.

References:

Neinhuis C., S. Wanke, K. W. Hilu, K. Müller, and T. Borsch 2005. Phylogeny of Aristolochiaceae based on parsimony, likelihood, and Bayesian analyses of trnL-trnF sequences. *Pl. Syst. Evol.* 250: 7-26.

Ohi-Toma, T., T. Sugawara, H. Murata, S. Wanke, C. Neinhuis and J. Murata 2006. Molecular phylogeny of *Aristolochia* sensu lato (Aristolochiaceae) based on sequences of *rbcl*, *matK*, and

phyA genes, with special reference to differentiation of chromosome numbers. Syst. Bot. 31: 481-492.

Wanke, S.J. U. 2006. Evolution of the genus *Aristolochia*: Systematics, Molecular Evolution and Ecology. Phil Diss. Technischen Universität Dresden, Germany.

Berjano R., P. L. Ortiz, M. Arista and S. Talavera 2009. Pollinators, flowering phenology and floral longevity in two Mediterranean *Aristolochia* species, with a review of flower visitor records for the genus. Plant Biology 11: 6-16.

11) **Arsenophonus** (Bacteria: Gamma Proteobacteria: Enterobacteriaceae) is a genus of insect intracellular symbionts. The genus *Arsenophonus* is striking in the diversity of symbiont types represented. The host resolution considered in our review was family.

Reference:

Nováková, E, V. Hypša, N. A Moran 2009. *Arsenophonus*, an emerging clade of intracellular symbionts with a broad host distribution. BMC Microbiology 9:143.

12) **Arum** (Plantae: Alismatales: Araceae) is a small plant genus native to Europe, northern Africa, and western Asia. The 28 species of the genus *Arum* (Araceae) attract and temporarily trap insects (mainly flies, and beetles in a few cases) during a complex pollination process. At anthesis, the appendix of the inflorescence produces heat and emits a specific odour which attracts insects. The lured insects are trapped within the floral chamber when stigmas are receptive. They will be released about 24h later after pollen emission, ensuring pollen dissemination. Since these plants are generalists, visited by many different insects belonging to many families, the host resolution considered in our review was family.

References:

Kite, G.C., W.L.A. Hetterscheid, M.J. Lewis, P.C. Boyce, J. Ollerton, E. Cocklin, A. Díaz, and M.S.J. Simmonds 1998. Inflorescence odours and pollinators of *Arum* and *Amorphophallus* (Araceae). In: S.J. Owen and P.J. Rudall (eds). Reproductive biology, pp 295-315. Royal Botanic Gardens, Kew. London, UK.

Gibernau, M., D. Macquart and G. Przetak 2004 Pollination in the Genus *Arum* – a review. Aroideana 27: 148-166.

Mansion, G., G. Rosenbaum, N. Schoenenberger, G. Bacchetta, J.A. Rosselló and E. Conti 2008. Phylogenetic analysis informed by geological history supports multiple, sequential invasions of the Mediterranean Basin by the Angiosperm family Araceae. Syst. Biol. 57: 269–285.

13) **Asclepias** (Plantae: Gentianales: Apocynaceae) is a large genus of herbaceous perennial, dicotyledonous plants. Pollination in this genus is accomplished in an unusual manner, as the pollen is grouped into complex structures called pollinia (or "pollen sacs"), rather than being individual grains or tetrads, as is typical for most plants. The feet or mouthparts of flower visiting insects such as bees, wasps and butterflies, slip into one of the five slits in each flower formed by adjacent anthers. The bases of the pollinia then mechanically attach to the insect, pulling a pair of pollen sacs free when the pollinator flies off. Pollination is effected by the reverse procedure in which one of the pollinia becomes trapped within the anther slit. Because *Asclepias* flowers are visited by many different animals, both insects and vertebrate. We consider animal family as the lowest host resolution for this system.

References:

The main source of host species were obtained from the data set called ASCLEPOL (http://www.old.uni-bayreuth.de/departments/planta2/research/pollina/as_pol_d.html) (see references therein), created by Jeff Ollerton, Sigrid Liede and Paul Forster, and maintained by the Department of Plant Systematics of the University of Bayreuth (Germany).

Ollerton, J. and S. Liede 1997. Pollination systems in the Asclepiadaceae: a survey and preliminary analysis. *Biol. J. Linn. Soc.* 62: 593-610.

Agrawal, A.A., J.P. Salminen and M. Fishbein 2009. Phylogenetic trends in phenolic metabolism of Milkweeds (*Asclepias*): evidence for escalation. *Evolution* 63: 663-673.

14) **Bartonella** (Bacteria: Apha Proteobacteria, Bartonellaceae) is a genus of facultative intracellular bacteria that cause characteristic hostrestricted hemotropic infections in mammals and are typically transmitted by blood-sucking arthropods. They produce a wide variety of human diseases, such as bartonellosis (Carrion's disease), endocarditis and bacillary angiomatosis. The number of species is unknown but the number of named species has grown quickly in the last few years. In addition to the 14 currently recognized species, several *Bartonella* strains have been recovered from a wide range of wild and domestic mammals in Europe and America. Due to the amplitude in host spectrum, we have considered for our review host family as the lowest taxonomic resolution.

References:

Houpikian P. and D. Raoult 2001. Molecular phylogeny of the genus *Bartonella*: what is the current knowledge? *FEMS Microbiology Letters* 200: 1-7.

Abbot, P., A. E. Aviles, L. Eller and L. A. Durden 2007. Mixed Infections, Cryptic Diversity, and Vector-Borne Pathogens: Evidence from *Polygenis* Fleas and *Bartonella* Species. *Appl. Environ. Microbiol.* 73: 6045-6052.

Dehlo, C. 2008. Infection-associated type IV secretion systems of *Bartonella* and their diverse roles in host cell interaction. *Cell. Microbiol.* 10: 1591-1598.

Chomel, B.B., H.J. Boulouis, E.B. Breitschwerdt, R.W. Kasten, M. Vayssier-Taussat, R. J. Birtles, J. E. Koehler and C. Dehlo 2009. Ecological fitness and strategies of adaptation of *Bartonella* species to their hosts and vectors. *Vet. Res.* 40:29.

15) **Betaretrovirus** (Virus: RNA Virus: Retroviridae) is a genus of retrovirus attacking a wide spectrum of vertebrates. They can produce mammary tumours in rodents and simians. We have used host order as the taxonomic resolution.

References:

Gifford, R., P. Kabat, J. Martin, C. Lynch, M. Tristem 2005. Evolution and Distribution of Class II-Related Endogenous Retroviruses. *J. Virol.* 79: 6478-6486.

16) **Blattabacterium** (Bacteria: Flavobacteriales: Blattabacteriaceae) is a genus of mutualistic endosymbionts existing in special bactericites of the fat bodies of several species of cockroaches. The taxonomic level used for our review has been species.

References:

Clark J W, S Hossain, C A Burnside, and S Kambhampati 2001. Coevolution between a cockroach and its bacterial endosymbiont: a biogeographical perspective. *Proc Biol Sci.* 268: 393–398.

Maekawa K., Y. C. Park b, N. Lo 2005. Phylogeny of endosymbiont bacteria harbored by the woodroach *Cryptocercus* spp. (Cryptocercidae: Blattaria): Molecular clock evidence for a late Cretaceous—early Tertiary split of Asian and American lineages. *Mol. Phyl. Evol.* 36:728-733.

17) **Blepharida** (Animalia: Coleoptera, Chrysomelidae) is a large beetle genus, mostly feeding as leaf-chewers on trees belonging to the genus *Bursera*. For this reason, the taxonomic level used for our review has been species.

References:

Becerra, J. X. and E. Venable. 1999. Macroevolution of insect-plant associations: The relevance of host biogeography to host affiliation. *PNAS USA* 96:12626-12631.

Becerra, J.X. 2002. Synchronous coadaptation in an ancient case of herbivory. *PNAS USA* 100: 12804–12807.

Becerra, J. X. 2004. Molecular Systematics of *Blepharida* beetles (Chrysomelidae: Alticinae) and relatives. *Molecular Phylogenetics and Evolution* 30: 107-117.

18) **Blochmannia** (Bacteria: Gamma Proteobacteria: Enterobacteriaceae) is a genus of mutualistic endosymbiotic bacteria providing nutrition to a wide spectrum of ant species, especially *Camponotus* species. We have used ant genus as the taxonomic resolution in this study.

References:

Degnan, P.H., A.B. Lazarus, C.D. Broch, J.J. Wernegreen 2004. Host–Symbiont Stability and Fast Evolutionary Rates in an Ant–Bacterium Association: Cospeciation of *Camponotus* Species and Their Endosymbionts, *Candidatus* Blochmannia. *Syst. Biol.* 53:95–110.

Wernegreen, J.J., S. N. Kauppinen, S. G. Brady, P. S. Ward 2009. One nutritional symbiosis began another: Phylogenetic evidence that the ant tribe Camponotini acquired *Blochmannia* by tending sap-feeding insects. *BMC Evol. Biol.* 9:292.

19) **Botrytis** (Fungi: Helotiales, Sclerotiniaceae) is a small genus of ascomycete fungi composed of species that are important pathogens of many agronomically important crops, such as grapevine, tomato, bulb flowers, and ornamental crops. Although most species are extreme specialists, the host range of the entire genus is very wide. For this reason, the taxonomic level used has been host family.

References:

Staats M., P. van Baarlen, and J. A. L. van Kan (2005). Molecular phylogeny of the plant pathogenic genus *Botrytis* and the evolution of host specificity. *Mol. Biol. Evol.*: 333–346.

20) **Brachycaudus** (Animalia: Hemiptera, Aphidae) is a medium-sized genus composed of aphid species than can be major agricultural pests. The host breadth ranges from strict monophagy to polyphagy. Thus, we have used host family as the taxonomic level in this study.

References:

Scott, J.K. and P. B. Yeoh 1998. Host range of *Brachycaudus rumexicolens* (Patch), an aphid associated with the Polygonaceae. *Biol. Control*. 13: 135-142.

Rakauska, R. and V. Juronis 2006. *Brachycaudus divaricatae* Shaposhnikov (Hemiptera: Aphididae). Changes in host specificity pose a new threat to plum farming. *Act. Zool. Lituanica* 16: 61-66.

D'Acier, A.C., G. Cocuzza, E. Jouselin, V. Cavalieri and S. Barbagallo 2008. Molecular phylogeny and systematic in the genus *Brachycaudus* (Homoptera: Aphididae): insights from a combined analysis of nuclear and mitochondrial genes. *Zoologica Scripta* 37: 175–193.

21) **Bradyrhizobium** (Bacteria: Alpha Proteobacteria: Bradyrhizobiaceae) is a genus of gram-negative soil bacteria, many of which fix nitrogen. They are traditionally associated with legumes. We have used host genus as the taxonomic resolution for host use.

References:

Rivas, R., M. Martensa, P. de Lajudiec, A. Willems 2009. Multilocus sequence analysis of the genus *Bradyrhizobium*. *Syst. Appl. Microbiol.* 32: 101–110.

Menna, P., F. Gomes Barcellos, M. Hungria 2009. Phylogeny and taxonomy of a diverse collection of *Bradyrhizobium* strains based on multilocus sequence analysis of the 16S rRNA gene, ITS region and *glnII*, *recA*, *atpD* and *dnaK* genes. *Int. J. Syst. Evol. Microbiol.* 59: 2934–2950

22) **Bruchus** (Animalia: Coleoptera, Bruchidae) is a small genus of seed-beetles feeding mostly on fabaceous seeds. They may constitute important crop pests. We have used plant species as taxonomic resolution for host use. Dr. Gael J. Kergoat (INRA, Montpellier, France) kindly helped us with host use in *Bruchus*.

References:

Kergoat, G.J., Delobel, A., Silvain, J.-F., 2004. Phylogeny and hostspecificity of European seed beetles (Coleoptera, Bruchidae), new insights from molecular and ecological data. *Mol. Phyl. Evol.* 32: 855–865.

Kergoat, G.J., Alvarez, N., Hossaert-McKey, M., Faure, N., Silvain, J.-F., 2005a. Parallels in the evolution of the two largest New and Old World seed-beetle genera (Coleoptera, Bruchidae). *Mol. Ecol.* 14: 4003–4021.

Kergoat, G.J., Silvain, J.-F., Delobel, A., Tuda, M., Anton, K-W. 2007. Defining the limits of taxonomic conservatism in host–plant use for phytophagous insects: Molecular systematics and evolution of host–plant associations in the seed-beetle genus *Bruchus* Linnaeus (Coleoptera: Chrysomelidae: Bruchinae). *Mol. Phyl. Evol.* 43: 251–269.

De los Mozos, M. 1992. Brúquidos (Coleoptera: Bruchidae) asociados al cultivo de la lenteja (*Lens culinaris* Medikus) en Castilla-La Mancha: especies implicadas y valoración de la plaga. *Bol. San. Veg. Plagas* 18:347-353.

23) **Brueelia** (Animalia: Phthiraptera: Philopteridae) is one of the largest genera of lice. While most ischnoceran genera are restricted to a single family or order of hosts, *Brueelia* occurs on at least 41 families of birds in at least four orders. We have used host order as the taxonomic resolution for our study.

References:

Johnson, K. P., R. J. Adams, and D. H. Clayton. 2001. The phylogeny of the louse species *Brueelia* does not reflect host phylogeny. *Biol. J. Linn. Soc.* 77: 233–247.

Bueter, C., J. Weckstein, K. P. Johnson, J. M. Bates, and C. E. Gordon 2009. Comparative phylogenetic histories of two louse genera found on *Catharus* thrushes and other birds. *J. Parasitol.* 95: 295–307.

24) **Campanula** (Plantae: Ranunculales:Campanulaceae) is a large genus of pollination-generalist plants distributed across the Holarctic and visited by a very diverse pollinator fauna, ranging from flies and beetles to bees and even birds. We have used host family as the taxonomic resolution.

References:

Roquet C., L. Sáez, J. J. Aldasoro, A. Susanna, M.L. Alarcó, and N. García-Jacas 2008. Natural delineation, molecular phylogeny and floral evolution in *Campanula*. *Syst. Bot.* 33: 203-217.
Roquet C., I. Sanmartín, N. García-Jacas, L. Sáez, A. Susanna, N. Wikström, J. J. Aldasoro 2009. Reconstructing the history of Campanulaceae with a Bayesian approach to molecular dating and dispersal–vicariance analyses. *Mol. Phyl. Evol.* 52: 575–587.

25) **Campylobacter** (Bacteria: Epsilon Proteobacteria: Campylobacteraceae) is a small genus of motile bacteria comprising severe human and animal pathogens. We have used host family as the taxonomic resolution.

References:

- Waldenström J., T. Broman, I. Carlsson, D. Hasselquist, R. P. Achterberg, J. A. Wagenaar, B. Olsen 2002. Prevalence of *Campylobacter jejuni*, *Campylobacter lari*, and *Campylobacter coli* in Different Ecological Guilds and Taxa of Migrating Birds. *Appl. Environ. Microbiol.* 68: 5911-5917
- Korczak, B.M. , R. Stieber, S. Emler, A. P. Burnens, J. Frey, P. Kuhnert 2006 Genetic relatedness within the genus *Campylobacter* inferred from *rpoB* sequences. *Int. J. Syst. Evol. Microbiol.* 56: 937–945

26) **Ceratosolen** (Animalia: Hymenoptera: Agaonidae) is a large genus of obligate highly specialized fig-pollinating wasps. We have used *Ficus* section as the taxonomic resolution.

References:

- Kerdelhue C., I. Le Clainche, and J-Y Rasplus 1999. Molecular phylogeny of the *Ceratosolen* species pollinating *Ficus* of the Subgenus *Sycomorus sensu stricto*: Biogeographical history and origins of the species-specificity breakdown cases. *Mol. Phyl. Evol.* 11: 401-414.

Weiblen,, G.D. 2001. Phylogenetic relationships of fig wasps pollinating functionally dioecious *Ficus* based on mitochondrial DNA sequences and morphology. *Syst. Biol.* 50: 243-267.

Lopez-Vaamonde C., N. Wikström, K. M. Kjer, G. D. Weiblen, J. Y. Rasplus, C. A. Machado and J. M. Cook 2009. Molecular dating and biogeography of fig-pollinating wasps. *Mol. Phyl. Evol.* 52: 715-726.

27) **Ceropegia** (Plantae: Gentianales: Apocynaceae) is a large plant genus with over 180 species pollinated by several fly families. The pollination mechanism is very interesting, flower tubes are lined with small hairs that point downward to form a trap for small flies. When flies are attracted into the flower by the odour they are prevented from escaping until the hairs wither, Pollinia of the *Ceropegia* flower are attached to the flies' bodies when they escape. We have use section as the taxonomic resolution. Dr. Jeff Ollerton (University of Northampton, UK) kindly provided some information on host use.

References:

- Ollerton, J., S. Masinde, U. Meve, M. Picker and A. Whittington 2009. Fly pollination in *Ceropegia* (Apocynaceae: Asclepiadoideae): biogeographic and phylogenetic perspectives. *Ann. Bot.* 103: 1501-1514.

Meve, U. and S. Liede-Schumann 2007. *Ceropegia* (Apocynaceae, Ceropegieae, Stapeliinae): paraphyletic but still taxonomically sound. *Ann. Miss. Bot. Gard.* 94: 392–406.

28) **Cinara** (Animalia: Hemiptera: Lachnidae) is a genus of bugs that feed exclusively on the woody parts of conifers of the Cupressaceae and Pinaceae, especially the genus *Pinus*. We have used tree species as the taxonomic resolution.

References:

Favret C. and D. J. Voegtlin 2004. Speciation by host-switching in pinyon *Cinara* (Insecta: Hemiptera: Aphididae). *Mol. Phyl. Evol.* 32: 139–151.

29) **Conophthorus** (Animalia: Coleoptera: Scolytidae) is a small genus of specialized seed predator beetles that live on pine and fir cones. We used host species as the taxonomic resolution.

References:

Anthony I. Cognato, A. I. N. E. Gillette, R. Campos Bolaños, F. A.H. Sperling 2005. Mitochondrial phylogeny of pine cone beetles (Scolytinae, *Conophthorus*) and their affiliation with geographic area and host. *Mol. Phyl. Evol.* 36: 494–508.

30) **Coronavirus** (RNAVirus: RNA virus: Coronaviridae) is a genus of animal virus primarily infecting the upper respiratory and gastrointestinal tract of mammals and birds. In humans it produces severe acute respiratory syndrome (SARS). We have used host family as the taxonomic resolution.

References:

Dong, B. Q., W. Liu,^{1†} X. H. Fan, D. Vijaykrishna, X. C. Tang, F. Gao, L. F. Li, G. J. Li, J. X. Zhang, L. Q. Yang, L. L. M. Poon, S. Y. Zhang, J. 2007. Detection of a Novel and Highly Divergent Coronavirus from Asian Leopard Cats and Chinese Ferret Badgers in Southern China. *J. Virol.* 81: 6920-6926.

Vijaykrishna, D., G. J. D. Smith, J. X. Zhang, J. S. M. Peiris, H. Chen, Y. Guan 2007. Evolutionary Insights into the Ecology of Coronaviruses. *J. Virol.* 81: 4012-4020.

Woo, P.C.Y., S.K.P. Lau, Y. Huang, K. Y. Yuen 2009. Coronavirus Diversity, Phylogeny and Interspecies Jumping. *Exp Biol. Medic.*

31) **Costus** (Plantae: Zingiberales: Costaceae) is a tropical plant genus exhibiting a specialized pollination system. In the Neotropics it is pollinated by bees or hummingbirds. We have used host family as the taxonomic resolution.

References:

Kay, K.M., P.E. Reeves, R.G. Olmstead, D. W. Schemske 2005. Rapid speciation and the evolution of hummingbird pollination in Neotropical *Costus* subgenus *Costus* (Costaceae): evidence from nrDNA ITS and ETS sequences. *Amer. J. Bot.* 92: 1899–1910.

32) **Crematogaster** (Animalia: Hymenoptera: Formicidae) subgenus *Decacrema* ants establish a mutualistic association with the *Macaranga* trees from the southeast Asia called myrmecophytism. We have used host species as the taxonomic resolution in this study.

References:

Quek, S.P., S.J. Davies, T. Itino, N.E. Pierce 2004. Codiversification in an ant-plant mutualism: stem texture and the evolution of host use in *Crematogaster* (Formicidae: Myrmicinae) inhabitants of *Macaranga* (Euphorbiaceae). *Evolution* 58: 554-570.

33) **Ctenophthalmus** (Animalia: Siphonaptera: Ctenophthalmidae) is a small genus of generalist parasitic fleas that mostly attack rodents and shrews. We used mammal species as the taxonomic resolution. Dr. Boris Krasnov (University of the Negev, Israel) kindly helped us with host use in this clade.

References:

Krasnov B. R., D. Mouillot, G. I. Shenbrot, I. S. Khokhlova, Poulin R. 2004. Geographical variation in host specificity of fleas (Siphonaptera) parasitic on small mammals: the influence of phylogeny and local environmental conditions. *Ecography* 27: 787-797.

Krasnov B. R., Poulin R., G. I. Shenbrot, D. Mouillot, I. S. Khokhlova 2005. Host specificity and geographic range in haematophagous ectoparasites. *Oikos* 108: 449-456.

Poulin R., B. R. Krasnov, G. I. Shenbrot, D. Mouillot, I. S. Khokhlova 2006. Evolution of host specificity in fleas: Is it directional and irreversible? *Int J. Parasitol.* 36: 185-191.

Whitinga, M. F., A. S. Whitinga, M. W. Hastriterb and K. Dittmara 2008. A molecular phylogeny of fleas (Insecta: Siphonaptera): origins and host associations. *Cladistics* 24: 1-8.

34) **Curculio** (Animalia: Coleoptera: Curculionidae) is a large genus of seed predators that mostly feed on seeds of fagaceous trees, like oak, chestnut, beech, etc. We have used genus as the taxonomic resolution in our data set.

References:

Hughes, J. and A. P. Vogler 2004. Ecomorphological adaptation of acorn weevils to their oviposition site. *Evolution* 58. 1971-1983.

Hughes, J. and A. P. Vogler 2004. The phylogeny of acorn weevils (genus *Curculio*) from mitochondrial and nuclear DNA sequences: the problem of incomplete data. *Mol. Phyl. Evol.* 32: 601-615.

Toju, H. and T.I. Sota 2009. Do arms races punctuate evolutionary stasis? Unified insights from phylogeny, phylogeography and microevolutionary processes. *Mol. Ecol.* 18: 3940-3954.

35) **Chelostoma** (Animalia: Hymenoptera: Megachilidae) is a medium-sized bee genus composed of both oligolectic (specialist) and polylectic (generalist) species. We have used host family as the taxonomic resolution.

References:

Claudio Sedivy, C., C. J. Praz, A. Müller, A. Widmer, and S. Dorn 2008. Patterns of host-plant choice in bees of the genus *Chelostoma*: the constraint hypothesis of host-range evolution in bees. *Evolution* 1-17.

36) **Chlamydia** (Bacteria: Chlamydiales: Chlamydiaceae) is a [genus](#) of [bacteria](#) that are obligate intracellular parasites (organisms). Many of the chlamydia species are [pathogenic](#). *Chlamydia* infections are the most common [sexually transmitted bacterial infections](#) in humans and are the leading cause of infectious blindness worldwide. Recent taxonomic and systematic studies recognize only three *Chlamydia* species, locating the remaining species in the genus *Chlamydiophila*. We have preferred to use the classical taxonomy, since the new taxonomy is not universally accepted. We used host order as the taxonomic resolution in this study.

References:

Pudjiatmoko, H.F., Y. Ochiai, T. Yamaguchi, K. Hirai 1997. Phylogenetic analysis of the genus *Chlamydia* based on 16s rRNA gene sequences. *Int. J. Syst. Bact.* 47: 425-431.
 Bush, R.M., K. D. E. Everett 2001. Molecular evolution of the *Chlamydiaceae*. *Int. J. Syst. Evol. Microbiol.* 51: 203–220.
 Van Loock, M. D. Vanrompay, B. Herrmann, J. Vander Stappen, G. Volckaert, B. M. Goddeeris, K. D. E. Everett 2003. Missing links in the divergence of *Chlamydophila abortus* from *Chlamydophila psittaci*. *Int. J. Syst. Evol. Microbiol.* 53: 761–770.
 Geens, T., A. Dewitte, N. Boon, D Vanrompay 2005. Development of a *Chlamydophila psittaci* species specific and genotype-specific real-time PCR. *Vet. Res.* 36: 787–797

37) **Chrysolina** (Animalia: Coleoptera: Chrysomelidae) is a large genus more than 400 species with a worldwide distribution excluding South America, the Australian region, and Antarctica. It is mostly composed of specialist herbivorous beetles. We have used host family as the taxonomic resolution.

References:

Garin C.F., C. Juan, E. Petitpierre 1999. Mitochondrial DNA phylogeny and the evolution of host-plant use in Palearctic *Chrysolina* (Coleoptera, Chrysomelidae) leaf beetles. *J. Mol. Evol.* 48: 435-444.

38) **Dendroctonus** (Animalia: Coleoptera: Scolytidae) is a small genus of beetles that bore through the bark of standing or fallen trees and feed on the phloem within. They encompass a wide range of resource specialization, including both extreme specialists (species restricted to a single host-plant species) and relative generalists (species able to feed-on up to 20 plant species, sometimes in several genera). We have used host species as the taxonomic resolution.

References:

Kelley, S. T. and B. D. Farrell 1998. Is specialization a dead end? The phylogeny of host use in *Dendroctonus* bark beetles (Scolytidae). *Evolution* 52: 1731-1743.

39) **Dennyus** (Animalia: Phthiraptera: Menoponidae) is a specialized small genus of lice parasitizing swiftlets (Apodidae). We have used host subfamily as the taxonomic resolution.

References:

Clayton, D.H., R.D. Price and R.D.M. Page 1996. Revision of *Dennyus* (*Collodennyus*) lice (Phthiraptera: Menoponidae) from swiftlets, with description of new taxa and a comparison of host-parasite relationships. *Syst. Entomol.* 21: 179-204.

Clayton, D.H., S.E. Bush and K.P. Johnson 2004. Ecology of congruence: past meets present. *Syst. Biol.* 53: 165-173.

40) **Dickeya** (Bacteria: Gamma Proteobacteria: Enterobacteriaceae) is a small genus of plant pathogenic bacteria attacking a wide spectrum of plant species. We have used host genus as taxonomic resolution.

References:

Parkinson, N., D. Stead, J. Bew, J. Heeney, L. Tsrer, J. Elphinstone 2009. *Dickeya* species relatedness and clade structure determined by comparison of *recA* sequences. *Int J Syst Evol Microbiol.* 59:2388-2393

41) **Echium** (Plantae: Lamiales: Boraginaceae) is a medium-size plant genus pollinated by a wide and very diverse fauna of insects. We have used host family as the taxonomic resolution. We thank Dr. Y. Dupont (University of Arrhus, Denmark) and Dr. L. Navarro (University of Vigo, Spain) for sharing their unpublished data.

References:

Gutián, J., P. Gutián and L. Navarro 1993. Tamaño del núcleo de población y polinización en *Echium plantagineum*. *Anales Jard. Bot. Madrid* 51: 65-72.

Dupont, Y.L. and C. Skov 2004. Influence of geographical distribution and floral traits on species richness of bees (Hymenoptera: Apoidea) visiting *Echium* species (Boraginaceae) of the Canary Islands. *Int. J. Pl. Sci.* 165: 377-386.

García-Maroto F., A. Mañas-Fernández, J. A. Garrido-Cárdenas, D. López Alonso, J. L. Guill-Guerrero, B. Guzmán, P. Vargas 2009. D6-Desaturase sequence evidence for explosive Pliocene radiations within the adaptive radiation of Macaronesian *Echium* (Boraginaceae). *Mol. Phyl. Evol.* 52: 563-574.

42) **Encarsia** (Animalia: Hymenoptera: Aphelinidae) is a diverse and cosmopolitan group of species with great economic importance since they are parasitoids of several insects behaving as very aggressive pests. We have used host family as the taxonomic resolution.

References:

Babcock C. S., J. M. Heraty, P. J. De Barro, F. Driver, and S. Schmidt 2001. Preliminary Phylogeny of *Encarsia* Förster (Hymenoptera: Aphelinidae) Based on Morphology and 28S rDNA. *Mol. Phyl. Evol.* 18: 306-323.

43) **Erysiphe** (Fungi: Erysiphales: Erysiphaceae) is a fungal genus composed of many specialist species and several extremely generalists. Many of the species in this genus are plant pathogens which cause powdery mildew. We have used host family as the taxonomic resolution.

References:

Okamoto, J., Limkaisang, S., Nojima, H., Takamatsu, S. 2002. Powdery Mildew of Prairie Gentian: Characteristics, Molecular Phylogeny and Pathogenicity. *J. Gen. Pl. Pathol.* 68: 200-207.

Francis, S.A., B.C. Roden, M.J. Adams, J. Weiland, M.J.C. Asher 2007. Comparison of ITS sequences from UK and North American sugar-beet powdery mildews and the designation of *Erysiphe betae*. *Mycol. Res.* 111: 204-212.

Braun, U., Takamatsu, S., Heluta, V., Limkasisang, S., Divarangkoon, R., Cook, R., Boyle, H. 2006. Phylogeny and taxonomy of powdery mildew fungi of *Erysiphe* sect. *Uncinula* on *Carpinus* species. *Mycol. Progr.* 5: 139-153

44) **Escovopsis** (Fungi: Hypocreales: Not assigned) is a medium-sized microfungus genus establishing a very complex symbiosis with several species of attine ants. The fungi parasitize the obligate mutualistic fungus cultivated by the ants. A fourth symbiont in the attine symbiosis, a filamentous bacterium (actinomycete), is cultured by the ants on specialized body surfaces to derive antibiotics that inhibit the growth of *Escovopsis*. This fungus can attack the cultivates of several ant genus, and this has been the taxonomic resolution used in our study.

References:

Currie C. R., B. Wong, A. E. Stuart, T. R. Schultz, S. A. Rehner, U. G. Mueller, G.-H. Sung, J. W. Spatafora, N. A. Straus 2003. Ancient tripartite coevolution in the Attine ant-microbe symbiosis. *Science* 299: 386-388.

Cafaro, M.J. C.R. Currie 2005. Phylogenetic analysis of mutualistic filamentous bacteria associated with fungus-growing ants. *Can. J. Microbiol.* 51: 441-446.

Gerardo N.M., U. G Mueller, C. R Currie 2006. Complex host-pathogen coevolution in the *Apterostigma* fungus-growing ant-microbe symbiosis. *BMC Evolutionary Biology* 6: 88.

Gerardo N. M., S. R. Jacobs, C. R. Currie, U. G. Mueller 2006. Ancient Host-Pathogen Associations Maintained by Specificity of Chemotaxis and Antibiosis. *Plos Biol.* 8:e235.

Poulsen M, Erhardt DP, Molinaro DJ, Lin T-L, Currie CR (2007) Antagonistic bacterial interactions help shape host-symbiont dynamics within the fungus-growing ant-microbe mutualism. *PLoS ONE* 2: e960.

45) **Ficus** (Plantae: Rosales: Moraceae) is a large plant genus distributed over all subtropical and tropical regions in the world. Fig trees have a very specialized pollination systems, with the highly modified inflorescence, or syconia, being pollinated by wasp species of the family Agaonidae that also prey upon the developing seeds. We have used wasp genus as the taxonomic resolution.

References:

- Herrer, E.A., C. A. Machado, E. Bermingham, J.D. Nason, D.M. Windsor, S.S. McCafferty, W. Van Houten and K. Bachmann 1999. Molecular phylogenies of figs and their pollinator wasps. *J. Biogeogr.* 23: 521-530.
- Weiblen, G.D. and G.L. Bush 2002. Speciation in fig pollinators and parasites. *Mol. Ecol.* 11: 1573-1578.
- Jousselin, E., J. Y. Rasplus and F. Kjellberg 2003. Convergence and coevolution in a mutualism: evidence from a molecular phylogeny of *Ficus*. *Evolution* 57: 1255-1269.
- Machado C. A., E. Jousselin, F. Kjellberg, S. G. Compton and E. A. Herre. 2001. Phylogenetic relationships, historical biogeography and character evolution of fig-pollinating wasps. *Proc. Roy. Soc. London B* 268: 685-694.
- Rønsted N., G. D. Weiblen, J. M. Cook, N. Salamin, C. A. Machado, V. Savolainen 2005. 60 million years of co-divergence in the fig–wasp symbiosis. *Proc. Roy. Soc. London B* 272: 2593–2599.
- Rhett D. Harrison, R.D., J.-Y. Rasplus 2006. Dispersal of fig pollinators in Asian tropical rain forests. *J. Trop. Ecol.* 22: 631-639.
- Rønsted N., G. Salvo. V. Savolainen 2007. Biogeographical and phylogenetic origins of African fig species (*Ficus* section *Galoglychia*). *Mol. Phyl. Evol.* 43: 190-201.
- Rønsted N., G. D. Weiblen, V. Savolainen, J. M. Cook 2008. Phylogeny, biogeography, and ecology of *Ficus* section *Malvanthera* (Moraceae). *Mol. Phyl. Evol.* 44: 12-22.
- Erasmus, J. C., S. van Noort, E. Jousselin, J. M. Greeff. 2007. Molecular phylogeny of fig wasp pollinators (Agaonidae, Hymenoptera) of *Ficus* section *Galoglychia*. *Zool. Scripta* 36: 61–78.
- Rønsted N., G.D. Weiblen, W.L. Clement, N.J.C. Zerega, V. Savolainen 2008. Reconstructing the phylogeny of figs (*Ficus*, Moraceae) to reveal the history of the fig pollination mutualism. *Symbiosis* 45.
- Jousselin, E., S. van Noort, V. Berry, J.-Y. Rasplus, Nina Rønsted, J. C. Erasmus, J. M. Greeff 2008. One fig to bind them all. Host conservatism in a fig wasp community unraveled by cospeciation analyses among pollinating and nonpollinating fig wasps. *Evolution* 62: 1777–1797.

46) **Ficus** (Plantae: Rosales: Moraceae) is a large plant genus distributed over the whole subtropical and tropical regions in the world. Fig trees have a very generalized dispersal system, with birds, bats and many different mammals acting as effective dispersers. We have used host family as the taxonomic resolution.

References:

- Shanahan, M., S. So, S.G. Compton and R. Corlett 2001. Fig-eating by vertebrate frugivores : a global review. *Biol. Rev.*, 76: 529-572.
- Lomáscolo, S.B., P. Speranza, R. T. Kimball 2008. Correlated evolution of fig size and color supports the dispersal syndromes hypothesis. *Oecologia* 156:783–796.
- Kendrick, E. L., L. A. Shipley, A. E. Hagerman, L. M. Kelley 2009. Fruit and fibre: the nutritional value of figs for a small tropical ruminant, the blue duiker (*Cephalophus monticola*). *Afr. J. Ecol.* 47: 556–566.

47) **Flavivirus** (Virus: RNA Virus: Flaviviridae) is a group of ubiquitous pathogenic viruses producing some very important diseases like the [West Nile virus](#), [dengue virus](#), [Tick-borne Encephalitis Virus](#), [Yellow Fever Virus](#), and several other [viruses](#) which may cause [encephalitis](#). Order was used as the taxonomic resolution.

References:

Kuno, G., G.J. J. Chang, K. R. Tsuchiya, N. Karabatsos, C.B. Cropp 1998. Phylogeny of the Genus *Flavivirus*. J. Virol. 72: 73-83.

Billoir, F., R. de Chesse, Hugues Tolou, P. de Micco, E. A. Gould, X. de Lamballerie 2000. Phylogeny of the genus *Flavivirus* using complete coding sequences of arthropod-borne viruses and viruses with no known vector. J. Gen. Virol. 81: 781-790.

48) Foamy virus (Virus: RNA Virus: Retroviridae) is a group of are ubiquitous, non-pathogenic retroviruses that infect all primates. We have used host family as the taxonomic resolution.

References:

Switzer, W. M., M. Salemi, V. Shanmugam, F. Gao, M. Cong, C. Kuiken, V. Bhullar, B. E. Beer, D. Vallet, A. Gautier-Hion, Z. Tooze, F. Villinger, E. C. Holmes, W Heneine 2005. Ancient co-speciation of simian foamy viruses and primates. Nature 434:376-380.

49) Frankia (Bacteria: Actinomycetales: Frankiaceae) is a small genus of nitrogen fixing filamentous bacteria that live in symbiosis with actinorhizal plants. Bacteria of this genus form root nodules. We have used host family as the taxonomic resolution in this study.

References:

Cournoyer, B., M. Gouy, P. Normand 1993. Molecular phylogeny of the symbiotic actinomycetes of the genus *Frankia* matches host-plant infection processes. Mol. Biol. Evol. 10: 1303-1316.

Michael L. Clawson, M.L., A. Bourret, D. R. Benson 2004. Assessing the phylogeny of *Frankia*-actinorhizal plant nitrogen-fixing root nodule symbioses with *Frankia* 16S rRNA and glutamine synthetase gene sequences. Mol. Phyl. Evol. 31: 131-138.

50) Galerucella (Animalia: Coleoptera:Chrysomelidae) is a very small genus of specialist herbivorous beetles. We have used host family as the taxonomic resolution in this study.

References:

Borghuis, A., J. van Groenendael, O. Madsen, J. Ouborg 2009. Phylogenetic analyses of the leaf beetle genus *Galerucella*: Evidence for host switching at speciation? Mol. Phyl. Evol. 53: 361–367.

51) Geomydoecus (Animalia: Phthiraptera: Trichodectidae) is a medium-sized lice genus associated to pocket gophers (Rodentia: Geomyidae). They are extremely host specific. We used host genus as the taxonomic resolution in this study.

References:

Page, R.D.M., R.D. Price, R.A. Hellenthal 1995. Phylogeny of *Geomydoecus* and *Thomomydoecus* pocket gopher lice (Phthiraptera: Trichodectidae) inferred from cladistic analysis of adult and first instar morphology. Syst. Entomol. 20: 129-143.

Clayton, D.H., S.E. Bush, K. P. Johnson 2004. Ecology of Congruence: Past Meets Present. Syst. Biol. 53:165–173.

52) **Geosmithia** (Fungi: Hypocreales: Trichocomaceae) is a small genus of little studied, dry-spored fungi that occur in galleries built by many phloeophagous bark beetles. These fungi can cause canker in several species of trees. We have used host genus as the taxonomic resolution in this study.

References:

Miroslav Kolarík, M., A Kubátová, Jirí Hulcr, S. Pazoutová 2008. *Geosmithia* Fungi are highly diverse and consistent bark beetle associates: Evidence from their community structure in temperate Europe. *Microbial Ecol.* 55: 65-80.

53) **Gladiolus** (Plantae: Asparagales: Iridaceae) is a large genus of plants with a moderately generalized pollination system. We have used host family as the taxonomic resolution.

References

Goldblatt, P., J.C. Manning, P. Berhardt 2001. Radiation of pollination systems in *Gladiolus* (Iridaceae: Crocoideae) in Southern Africa. *Ann. Missouri Bot. Gard.* 88: 713-734.

54) **Glomus** (Fungi: Glomerales: Glomeraceae) is a genus of arbuscular mycorrhizal (AM) fungi, and all species form symbiotic relationships (mycorrhizas) with plant roots. *Glomus* is the largest genus of AM fungi, with *ca.* 90 species described, but as currently defined is non-monophyletic. We have used host family as the taxonomic resolution.

References:

Schwarzott, D. C. Walker, A. Schüßler 2001. *Glomus*, the largest genus of the arbuscular mycorrhizal fungi (Glomales), is nonmonophyletic. *Mol. Phyl. Evol.* 21: 190-197.

Chethan Kumar, K.V., K.R. Chandrashekar, R. Lakshmipathy 2008. Variation in Arbuscular Mycorrhizal Fungi and Phosphatase Activity Associated with *Sida cardifolia* in Karnataka. *World J. Agri. Sci.* 4: 770-774

55) **Golovinomyces** (Fungi: Erysiphales: Erysiphaceae) is a genus of obligately parasitic fungi of plants, which cause powdery mildew diseases on many angiosperm species. With the exception of the dormant stage, their life cycle completely depends on living hosts, from which they obtain nutrients without killing the host cells and without which they are unable to survive. We have used host family as the taxonomic resolution.

References:

Matsuda S., S. Takamatsu 2003. Evolution of host-parasite relationships of *Golovinomyces* (Ascomycete: Erysiphaceae) inferred from nuclear rDNA sequences. *Mol. Phyl. Evol.* 27: 314-327.

Takamatsu, S., S. Matsuda 2004. Estimation of molecular clocks for ITS and 28S rDNA in Erysiphales. *Mycoscience* 45: 340-344.

Takamatsu, S., S. Matsuda, S. Niinomi, M. Havrylenko 2006. Molecular phylogeny supports a Northern Hemisphere origin of *Golovinomyces* (Ascomycota: Erysiphales). *Mycol. Res.* 110: 1093-11.

56) **Gonioctena** (Animalia: Coleoptera: Chrysomelidae) is a medium-sized beetle genus. Each species feeds, as larva and adult, on one or a few plant species, mostly of Salicaceae. However, the genus as a whole uses a great diversity of plant families. Host genus was the taxonomic resolution.

References:

Mardulyn, P., M.C. Milinkovitch, J.M. Pasteels 1997. Phylogenetic analyses of DNA and allozyme data suggest that *Gonioctena* leaf beetles (Coleoptera; Chrysomelidae) experienced convergent evolution in their history of host-plant family shifts. Syst. Biol. 46: 722-747.

57) **Haemoproteus** (Chromalveolata: Haemosporida: Haemoproteidae) is a genus of blood parasites infecting many different vertebrate species and causing blood disease. This system includes only bird parasites (=Avian haematozoa). We have used host family as the taxonomic resolution.

References:

Beadell, J.S., R. Covas, C. Gebhard, F. Ishtiaq, M. Melo, B. K. Schmidt, S. L. Perkins, G. R. Graves, R. C. Fleischer 2009. Host associations and evolutionary relationships of avian blood parasites from West Africa. Int. J. Parasitol. 39: 257–266

58) **Hantavirus01** (Virus: RNA Virus: Bunyaviridae) are single-stranded negative-sense RNA Viruses parasitizing rodents and other small mammals. Hantaviruses are not vector borne but rather are transmitted directly or indirectly between hosts during aggressive interactions or through the inhalation of infectious aerosols released in urine and feces. The taxonomic resolution used in this study was rodent subfamilies.

References:

Ramsden, C., E. C. Holmes, M. A. Charleston 2009. Hantavirus Evolution in Relation to Its Rodent and Insectivore Hosts: No Evidence for Codivergence. Mol. Biol. Evol. 26: 143–153.

59) **Hantavirus02** (Virus: RNA Virus: Bunyaviridae) are single-stranded negative-sense RNA Viruses parasitizing Insectivora and other small mammals. Hantaviruses are not vector borne but rather are transmitted directly or indirectly between hosts during aggressive interactions or through the inhalation of infectious aerosols released in urine and feces. The taxonomic resolution used in this study was rodent subfamilies.

References:

Arai, S., S. D. Ohdachi, M. Asakawa, H. J. Kang, G. Mocz, J. Arikawa, N. Okabe, R. Yanagihara 2008. Molecular phylogeny of a newfound hantavirus in the Japanese shrew mole (*Urotrichus talpoides*). PNAS 105: 16296–16301.

60) **Helicobacter** (Bacteria: Epsilon Proteobacteria: Helicobacteraceae) is a genus of pathogenic bacteria living in the gastrointestinal tract of humans and several other animal species, including cats, dogs, monkeys, sheep, pigs, rodents, birds, cheetahs and poultry. Some species infects up to 50% of the human population. Some strains of this bacterium are pathogenic to humans as it is strongly associated with peptic ulcers, chronic gastritis, duodenitis, and stomach cancer. We have used host family as the taxonomic resolution.

References:

Jie-Song, H., Z. Peng-Yuan, H. Bow 1999. Species differentiation and identification in the genus of *Helicobacter*. *World J. Gastroenterol* 5: 7-9.

Mikkonen T.P., R. I. Kärenlampi, M. L. Hänninen 2004. Phylogenetic analysis of gastric and enterohepatic *Helicobacter* species based on partial HSP60 gene sequences. *Int. J. Syst. Evol. Microbiol.* 54: 753–758.

Dewhirst, F.E., Z. Shen, M. S. Scimeca, L. N. Stokes, T. Boumenna, T. Chen, B. J. Paster, J. G. Fox 2005. Discordant 16S and 23S rRNA Gene Phylogenies for the Genus *Helicobacter*: Implications for Phylogenetic Inference. *J. Bacteriol.* 187: 6106-6118

61) Feline **Immunodeficiency virus** (Virus: RNA Virus: Retroviridae) are feline lentiviruses that infect a wide variety of carnivorous species. The taxonomic resolution used in this study was host species.

References:

Bown, E.W., N. Yuhki, C. Parcker, S.J. O'Brien 1994. A Lion Lentivirus related to feline immunodeficiency virus: Epidemiologic and Phylogenetic Aspects. *J. Virol.* 68: 5953-5968.

62) Simian **Immunodeficiency virus** (Virus: RNA Virus: Retroviridae) are primate lentiviruses that infect a wide variety of both nonhuman (SIV) and human (HIV) primate species in sub-Saharan Africa and produce several severe diseases like AIDS. The taxonomic resolution used in this study was primate subfamilies.

References:

Bibollet-Ruche F., E. Bailes, F. Gao, X. Pourrut, K. L. Barlow, J. P. Clewley, J. M. Mwenda, D. K. Langat, G. K. Chege, H. M. McClure, E. Mpoudi-Ngole, E. Delaporte, M. Peeters, G. M. Shaw, P. M. Sharp, B. H. Hahn 2004. New Simian Immunodeficiency Virus Infecting De Brazza's Monkeys (*Cercopithecus neglectus*): Evidence for a *Cercopithecus* Monkey Virus Clade. *J. Virol.* 78: 7748–7762.

63) **Influenza A virus** (Virus: RNA Virus: Orthomyxoviridae) can infect a variety of avian and mammalian hosts, including humans. Host genus was the taxonomic resolution used.

References:

Ito, T., O.T. Gorman, Y. Kawaoka, W.J. Bean, R.G. Webster 1991. Evolutionary analysis of the Influenza A virus M gene with comparison of the M1 and M2 proteins. *J. Virol.* 65: 5491-5498.

Webster, R.G., W.J. Bean, O.T. Gorman, T.M. Chambers, Y. Kawaoka 1992. Evolution and Ecology of Influenza A Viruses. *Microbiol. Rev.* 56: 152-179.

Subbarao, E.K., W. London, B. R. Murphy 1993. A single amino acid in the PB2 gene of Influenza A virus is a determinant of host range. *J. Virol.* 67: 1761-1764.

Yang, Z. 2000. Maximum likelihood estimation on large phylogenies and analysis of adaptive evolution in human Influenza Virus A. *J. Mol. Evol.* 51:423–432.

64) **Influenza H5N1 virus** (Virus: RNA Virus: Orthomyxoviridae) can infect a variety of avian and mammalian hosts, including humans. Host genus was the taxonomic resolution.

References

Pattanaik B., A. K. Pateriya, R. Khandia, C. Tosh, S. Nagarajan, S. Gounalan, H. V. Murugkar, B. P. Shankar, N. Shrivastava, P. Behera, S. Bhagat, J. S. M. Peiris, H. K. Pradhan. 2006. Phylogenetic analysis revealed genetic similarity of the H5N1 avian influenza viruses isolated from HPAI outbreaks in chickens in Maharashtra, India with those isolated from swan in Italy and Iran in 2006. *Current Science* 91: 77-81.

Wertheim J. O., M. Worobey 2007. A challenge to the ancient origin of SIVagm based on African green monkey mitochondrial genomes. *PLoS Pathog* 3(: e95

65) **Ioichroma** (Eucarya: Plantae: Solanales: Solanaceae) is a South-American plant genus displaying specialized tubular flowers that are pollinated by a diverse assemblage of insects and birds. We have used host family as the taxonomic resolution.

References:

DeWitt Smith S., S. J. Hall, P. R. Izquierdo, D. A. Baum 2008. Comparative pollination biology of sympatric and allopatric Andean *Ioichroma* (Solanaceae). *Ann. Missouri Bot. Gard.* 95: 600–617.

66) **Kladothrips** (Animalia: Tysanoptera: Phlaeothripidae) is a small genus of gall-making thrips that live on *Acacia* species. We have used *Acacia* section as the taxonomical resolution.

References:

McLeish, M.J., T. W Chapman, M. P. Schwarz 2007. Host-driven diversification of gall-inducing *Acacia* thrips and the aridification of Australia. *BMC Biology* 5:3

67) **Lamellodiscus** (Animalia: Dactylogyridea: Diplectanidae) is a genus of monogenean parasites of the fish belonging to the family Sparidae. We have used host genus as the taxonomic resolution.

References:

Desdevises, Y., S. Morand, O. Jousson, P. Legendre 2002. Coevolution between *Lamellodiscus* (Monogenea: Diplectanidae) and Sparidae (Teleostei): the study of a complex host-parasite system. *Evolution* 56: 2459–2471.

Desdevises, Y., S. Morand, O. Jousson, P. Legendre 2002. Evolution and determinants of host specificity in the genus *Lamellodiscus*(Monogenea). *Biol. J. Linn. Soc.:* 77: 431–443

Poisot T., O. Verneau, Y. Desdevises 2008. Genetic diversity within *Lamellodiscus* (Monogenea, Diplectanidae). *Eur. Sci. Fund.*

68) Primate **Lentivirus** (Virus: RNA Virus: Retroviridae) (PLS) is a genus of highly pathogenic viruses related to the human Immunodeficiency and Simian Immunodeficiency viruses (HIV and SIV). We have used host genus as the taxonomic resolution.

References

Charleston, M.A., D.L. Robertson, 2002. Preferential host switching by Primate Lentiviruses can account for phylogenetic similarity with the Primate phylogeny. *Syst. Biol.* 51:528–535.

69) **Lyssavirus** (Virus: RNA Virus: Rhabdoviridae) is a genus of virus transmitting rabies to canids and other carnivores. We have used host family as the taxonomic resolution.

References:

Jackson A. P., M. A. Charleston 2004. A Cophylogenetic Perspective of RNA–Virus Evolution. *Mol. Biol. Evol.* 21: 45–57.

70) **Mastrevirus** (Virus: DNA Virus: Geminiviridae) is a genus of devastating plant pathogenic viruses that threaten crop production and cause huge economic losses. They infect mostly Poaceae, but can also attack plants from other families. We have used host family as the taxonomic resolution.

References:

Wu, B., U. Melcher, X. Guo, X. Wang, L. Fan, G. Zhou 2008. Assessment of codivergence of Mastreviruses with their plant hosts. *BMC Evol. Biol.* 8: 335.

Harkins, G.W., W. Delpont, S. Duffy, N. Wood, A. L Monjane, B. E Owor, L. Donaldson, S. Saumtally, G. Triton, R. W Briddon, D. N Shepherd, E. P Rybicki, D. P Martin, A. Varsani 2009. Experimental evidence indicating that mastreviruses probably did not co-diverge with their hosts. *Virology* 6: 104.

71) **Methanobrevibacter** (Archaea: Methanobacteriales: Methanobacteriaceae) is a small genus of obligate anaerobes and can be unambiguously differentiated from other organisms since they all produce methane as a major catabolic product. We have used host family as the taxonomic resolution.

References:

Shinzato, N., Matsumoto, T., Yamaoka, I., Oshima, T. and Yamagishi, A. 1999. Phylogenetic diversity of symbiotic methanogens living in the hindgut of the lower termite *Reticulitermes speratus* analyzed by PCR and in situ hybridization. *Appl. Environ. Microbiol.* 65: 837-840.

Tokura M, Ohkuma M, Kudo T 2000. Molecular phylogeny of methanogens associated with flagellated protists in the gut and with the gut epithelium of termites. *FEMS Microbiol. Ecol.* 33:233-240.

Dighe A.S., K Jangid, J. M González, V. J. Pidiyar, M. S Patole, D. R Ranade, Y. S. Shouche 2004. Comparison of 16S rRNA gene sequences of genus *Methanobrevibacter*. *BMC Microbiol.* 4:20.

72) **Microbotryum** (Fungi: Urediniomycetes: Microbotryaceae) is a medium-sized genus of fungi causing anther smut disease in their host plants. They parasitize a wide spectrum of plant species, outstanding members of the family Caryophyllaceae. We have used host genus as the taxonomic resolution.

References:

Refrégier, G., M Le Gac, F. Jabbour, A. Widmer, J. A Shykoff, R. Yockteng, M. E. Hood, T. Giraud 2008. Cophylogeny of the anther smut fungi and their caryophyllaceous hosts: Prevalence of

host shifts and importance of delimiting parasite species for inferring cospeciation. BMC Evol. Biol. 8: 100.

73) **Moraea** (Plantae: Asparagales: Iridaceae) is a large genus of south-african generalist-pollination plants. Their flowers are visited by many different types of insects. We have used host family as the taxonomic resolution.

References:

Goldblatt, P., V. Savolainen, O. Porteous, I. Sostaric, M. Powell, G. Reeves, J. C. Manning, T. G. Barraclough, M. W. Chase 2002. Radiation in the Cape flora and the phylogeny of peacock irises *Moraea* (Iridaceae) based on four plastid DNA regions. Mol. Phyl. Evol. 25: 341-360.
Goldblatt, P., P. Bernhardt, J. C. Manning 2005. Pollination mechanisms in the African genus *Moraea* (Iridaceae, Iridoideae): floral divergence and adaptation for pollinators. Adansonia 27: 21-46

74) **Morbillivirus** (Virus: RNA virus: Paramyxoviridae) is a highly infectious virus genus producing measles in humans and other primates, distempers in many Carnivora mammals and rinderpest in ruminants and other herbivores. We used host family as the taxonomic resolution.

References:

Harder, T.C., M. Kenter, H. Vos, K. Siebelink, W. Huisman, G. van Amerongen, C. Örvell, T. Barrett, M. J. G. Appel, A. D. M. E. Osterhaus 1996. Canine distemper virus from diseased large felids: biological properties and phylogenetic relationships Journal of General Virology 77: 397-405.

75) **Mycobacterium** (Bacteria: Actinobacteria: Mycobacteriaceae) is a large genus of aerobic and nonmotile bacteria known to cause serious diseases in mammals, including tuberculosis and leprosy. We have used host family as the taxonomic resolution.

References:

Pitulle, C., M. Dorsch, J. Kazda, J. Wolters, E. Stackebrandt 1992. Phylogeny of Rapidly Growing Members of the Genus *Mycobacterium*. Int. J. Syst. Bacteriol. 42: 337-343.

Roth, A., M. Fischer, M. E. Hamid, S. Michalke, W. Ludwig, H. Mauch 1998. Differentiation of Phylogenetically Related Slowly Growing Mycobacteria Based on 16S-23S rRNA Gene Internal Transcribed Spacer Sequences. J. Clin. Microbiol. 36: 139-147

Devulder, G., M. Pérouse de Montclos, J. P. Flandrois 2005. A multigene approach to phylogenetic analysis using the genus *Mycobacterium* as a model. Int. J. Syst. Evol Microbiol. 55: 293-302.

76) **Myovirus** (Virus: DNA virus: Myoviridae) is a genus of bacteriophages parasitizing gram-negative Enterobacteria, gram-positive cocci, gram-negative non-enterobacteria and gram-positive bacilli. We used host family as the taxonomic resolution.

References:

Pride, D.T., T. M Wassenaar, C. Ghose, M. J. Blaser 2006. Evidence of host-virus co-evolution in tetranucleotide usage patterns of bacteriophages and eukaryotic viruses. *BMC Genomics* 7:8.

77) **Oncothrips** (Animalia: Tysanoptera: Phlaeothripidae) is a small genus of gall-making thrips that live on *Acacia* species. We have used *Acacia* section as the taxonomic resolution.

References:

Morris, D.C., M.P. Schwarz, B.J. Crespi, S.J.B. Cooper 2001. Phylogenetics of gall-inducing thrips on Australian *Acacia*. *Biol. J. Linn. Soc.* 74: 73–86.

Morris, D.C., M.P. Schwarz, S.J.B. Cooper, L.A. Mound 2002. Phylogenetics of Australian *Acacia* thrips: the evolution of behaviour and ecology. *Mol. Phyl. Evol.* 25: 278–292.

78) **Onthophagus** (Animalia: Coleoptera: Scarabeidae) is a very large genus of generalist dung beetles feeding on the excrement of many different mammalian species. We have used host family as the taxonomic resolution.

References:

Martín-Piera F. 2000. Familia Scarabeidae. Pages 215-446 in Ramos Sánchez, M.A. et al. (eds) *Coleoptera, Scarabeoidea. Fauna Ibérica Vol. 14.* Museo Natl. Ciencias Nat, CSIC, Madrid.

Villalba, S., J.M. Lobo, F. Martín-Piera, R. Zardoya 2002. Phylogenetic relationships of Iberian dung beetles (Coleoptera: Scarabeinae): insights on the evolution of nesting behavior. *J. Mol. Evol.* 55: 116-126.

Moczek, A.P., T.E. Cruickshank, A. Shelby 2006. When ontogeny reveals what phylogeny hides: gain and loss of horns during development and evolution of horned beetles. *Evolution* 60: 2329-2341.

79) **Ophraella** (Animalia: Coleoptera: Chrysomelidae) is a small genus of specialist folivorous beetles living in several Asteraceous plant species as leaf chewers. Host tribe has been used as the taxonomic resolution in this study.

References:

Futuyma, D.J., J.S. Walsh, Jr, T. Morton, D.J. Funk, M. C. Keese 1994. Genetic variation in a phylogenetic context: response of two specialized beetles (Coleoptera: Chrysomelidae) to host plants of their congeners. *J. Evol. Biol.* 7: 127- 146.

Funk, D.J., D.J. Futuyma, G. Ortí, A. Meyer 1995. A history of host association and evolutionary diversification for *Ophraella* (Coleoptera: Chrysomelidae): a new evidence from mitochondrial DNA. *Evolution* 48: 1008-1017.

Funk, D.J., D.J. Futuyma, G. Ortí, A. Meyer 1995. Mitochondrial DNA sequences and multiple data sets: a phylogenetic study of phytophagous beetles (Chrysomelidae: Ophraella). *Mol. Biol. Evol.* 12: 627-640.

Futuyma, D.J., M.C. Keese, D.J. Funk 1995. Genetic constraints on macroevolution: the evolution of host affiliation in the leaf beetle genus *Ophraella*. *Evolution* 49: 797-809.

80) **Pantaea** (Bacteria: Bacteria: Enterobacteriaceae) is a small genus of bacteria including several species that are generally associated with plants, either as epiphytes or as pathogens, and some species can cause disease in humans. We have used host family as taxonomic resolution in this study.

References:

- Brady, C., I. Cleenwerck, S. Ventera, M. Vancanneyt, J. Swings, T. Coutinho 2008. Phylogeny and identification of *Pantaea* species associated with plants, humans and the natural environment based on multilocus sequence analysis (MLSA). *Syst. Appl. Microbiol.* 31: 447-460.
- Delétoile, A., D. Decré, S. Courant, V. Passet, J. Audo, P. Grimont, G. Arlet, S. Brisse 2009. Phylogeny and identification of *Pantaea* species and typing of *Pantaea agglomerans* strains by multilocus gene sequencing. *J. Clin. Microbiol.* 47: 300-310.

81) **Phyllonorycter** (Animalia: Lepidoptera: Gracilliridae) is a medium-sized genus of leaf-mining moths. We have used host family as the taxonomic resolution.

References:

- López-Vaamonde, C., H.C. J. Godfray, J.M. Cook 2003. Evolutionary dynamics of host-plant use in a genus of leaf-mining moths. *Evolution* 57: 1804-1821.

82) **Phytomyza** (Animalia: Diptera: Agromyzidae) is the largest genus of leaf-mining flies. Host use in *Phytomyza* spans much of the variation observed for the family; hosts of non-polyphagous species include plants belonging to over 40 families and four major angiosperm clades (rosids, asterids, ranunculids and monocots). Most species are highly specialized and feed on one or a few closely related plant species. We have used host family as the taxonomic resolution.

References:

- Winkler, L.S. 2008. Patterns of diversification in phytophagous insects: phylogeny and evolution of *Phytomyza* leaf-mining flies (Diptera: Agromyzidae). Ph. Diss. Univ. of Maryland.
- Winkler, L.S., Mitter, C. 2008. The phylogenetic dimension of insect-plant interactions: a review of recent evidence. Pages 240-263 in Tilmon, K.J. (ed) *Specialization, Speciation, and Radiation: The Evolutionary Biology of Herbivorous Insects*. University of California Press, Berkeley.
- Winkler, S.A. S.J. Sceffer, Mitter, C. 2009. Molecular phylogeny and systematics of leaf-mining flies (Diptera: Agromyzidae): delimitation of *Phytomyza* Fallén sensu lato and included species groups, with new insights on morphological and host-use evolution. *Syst. Entomol.* 34: 260-292.

83) **Plasmodium** (Chromalveolata: Haemosporida: Plasmodiidae) is a genus of blood parasites infecting many different vertebrate species and causing malaria. This system includes only bird parasites (=Avian haematozoa). We have used host family as the taxonomic resolution.

References:

Beadell, J.S., R. Covas, C. Gebhard, F. Ishtiaq, M. Melo, B. K. Schmidt, S. L. Perkins, G. R. Graves, R. C. Fleischer 2009. Host associations and evolutionary relationships of avian blood parasites from West Africa. *Int. J. Parasitol.* 39: 257–266

84) **Plasmodium** (Chromalveolata: Haemosporida: Plasmodiidae) is a genus of blood parasites infecting many different vertebrate species and causing malaria. This system includes parasites from mammals, birds and reptiles, including humans. We have used host family as the taxonomic resolution.

References:

Escalante, A.A., D.E. Freeland, W.E. Collins, A.A. Lal 1998. The evolution of primate malaria parasites based on the gene encoding cytochrome b from the linear mitochondrial genome (*Plasmodium*/Apicomplexa). *Proc. Natl. Acad. Sci. USA* 95: 8124–8129

Perkins, S.L., J. J. Schall 2002. A molecular phylogeny of malarial parasites recovered from cytochrome b gene sequences. *J. Parasitol.*, 88: 972–978.

Ricklefs, R.E., S. M. Fallon 2002. Diversification and host switching in avian malaria parasites. *Proc. R. Soc. Lond. B* 269: 885–892.

Ricklefs, R.E., S. M. Fallon, E. Bermingham 2004. Evolutionary relationships, cospeciation, and host switching in Avian Malaria parasites. *Syst. Bio.* 53: 111–119.

Martinsen E.S., S. L. Perkins, J. J. Schall 2008. A three-genome phylogeny of malaria parasites (*Plasmodium* and closely related genera): Evolution of life-history traits and host switches. *Mol. Phyl. Evol.* 47: 261–273.

Garamszegi, L.Z. 2009. Patterns of co-speciation and host switching in primate malaria parasites. *Malaria Journal* 8:110.

85) **Pleistodontes** (Animalia: Hymenoptera: Agaonidae) is a small genus of specialist fig-pollinating wasps from Australia. We have used host species as the taxonomic resolution.

References:

Lopez-Vaamonde, C., J. Y. Rasplus, G. D. Weiblen, J. M. Cook 2001. Molecular phylogenies of fig wasps: Partial co-cladogenesis of pollinators and parasites. *Mol. Phyl. Evol.* 21: 55–71.

Lopez-Vaamonde, C., D. J. Dixon, J. M. Cook, J. Y. Rasplus 2002. Revision of the Australian species of *Pleistodontes* (Hymenoptera: Agaonidae) fig-pollinating wasps and their host-plant associations. *Zool. J. Linn. Soc.* 136: 637–683.

86) **Pneumocystis** (Fungi: Pneumocystidomycetes: Pneumocystidaceae) is a genus of fungus causing pneumonia in primates. We have used host family as the taxonomic resolution.

References:

Hugot, J.P., C. Demanche, V. Barriel, E. Dei-Cas, J. Guillot 2003. Phylogenetic systematics and evolution of primate-derived *Pneumocystis* based on mitochondrial or nuclear DNA sequence comparison. *Syst. Biol.* 52: 735–744.

87) **Podovirus** (Virus: DNA virus: Podoviridae) is a genus of bacteriophages parasitizing gram-negative Enterobacteria, gram-positive cocci, gram-negative non-enterobacteria and gram-positive bacilli. We have used host order as the taxonomic resolution.

References:

Pride, D.T., T. M Wassenaar, C. Ghose, M. J. Blaser 2006. Evidence of host-virus co-evolution in tetranucleotide usage patterns of bacteriophages and eukaryotic viruses. *BMC Genomics* 7:8.

88) **Polygonia** (Animalia: Lepidoptera: Nymphalidae) is a small genus of folivores living a broad spectrum of host plants. We have used host family as the taxonomic resolution.

References:

Weingartner, E., N. Wahlberg, S. Nylin 2005. Dynamics of host plant use and species diversity in *Polygonia* butterflies (Nymphalidae). *J. Evol. Biol.* 18: 1-9.

89) **Pontania** (Animalia: Hymenoptera: Tenthredinidae) is a genus of specialist sawflies inducing galls in willow trees (*Salix* spp.). We have used host subgenus as the taxonomic resolution.

References:

Nyman, T., A. Widmer, H. Roininen. 2000. Evolution of gall morphology and host-plant relationships in willow-feeding sawflies (Hymenoptera: Tenthredinidae). *Evolution* 54: 526-533.

90) **Pseudomyrmex** (Animalia: Hymenoptera: Formicidae) is a large ant genus. Some species are obligate specialized acacia-ants, well known as defensive inhabitants of several Neotropical ant-plants (myrmecophytes). We have used host genus as taxonomic resolution.

References

Ward, P.S. 1993. Systematic studies on *Pseudomyrmex* acacia-ants (Hymenoptera: Formicidae: Pseudomyrmecinae). *J. Hym. Res.* 2: 117-168.

Ward, P.S. 1999. Systematics, biogeography and host plant associations of the *Pseudomyrmex viduus* group (Hymenoptera: Formicidae), *Triplaris*- and *Tachigali*-inhabiting ants. *Zool J. Linn. Soc.* 126: 451–540.

Ward, P.S., D.A. Downie 2005. The ant subfamily Pseudomyrmecinae (Hymenoptera: Formicidae): phylogeny and evolution of big-eyed arboreal ants. *Syst. Biol.* 30:310-335.

91) **Quercus** (Plantae: Fagales: Fagaceae) is a large tree genus widely distributed throughout the Northern Hemisphere. They produce specialized seeds called acorns that are mostly dispersed by rodents, squirrels and jays. We have used host family as the taxonomic resolution.

References:

Manos, P.S. 1999. Phylogeny, biogeography, and processes of molecular differentiation in *Quercus* subgenus *Quercus* (Fagaceae). *Mol. Phyl. Evol.* 12: 333-349.

92) Murine-Leukemia **Retrovirus** (Virus: RNA virus: Retroviridae) is a genus of virus highly pathogenic to many different groups of vertebrates. We have used vertebrate order as taxonomic affiliation.

Reference:

Herniou, E., J. Martin, K. Miller, J. Cook, M. Wilkinson, M. Tristem 1998. Retroviral Diversity and Distribution in Vertebrates. *J. Virol.* 72: 5955-5966.

Martin, J., E. Herniou, J. Cook, R. W. O'Neill, M. Tristem 1999. Interclass Transmission and Phyletic Host Tracking in Murine Leukemia Virus-Related Retroviruses. *J. Virol.* 73: 2442-2449.

93) **Rhadinopsylla** (Animalia: Siphonaptera: Ctenophthalmidae) is a genus of lice parasitizing rodents and shrews. We have used host genus as the taxonomic resolution. Dr. Boris Krasnov (University of the Negev, Israel) kindly helped us with host use in this clade.

94) **Rhagoletis** (Animalia: Diptera: Tephritidae) is a genus of herbivorous flies. Several *Rhagoletis* species are important agricultural pests, with their larval stages infesting fruit of apple, cherry, blueberry, currants, and walnuts. We have used host family as the taxonomic resolution.

References:

Smith, J.J., G.L. Bush 1997. Phylogeny of the Genus *Rhagoletis* (Diptera: Tephritidae) inferred from DNA sequences of mitochondrial cytochrome oxidase II. *Mol. Phyl. Evol.* 7: 33-43.

95) **Rickettsia** (Bacteria: Alpha Proteobacteria: Rickettsiaceae) is a genus of motile, Gram-negative, non-sporeforming, obligate intracellular parasites. They cause diseases such as typhus, rickettsialpox, Boutonneuse fever, African tick bite fever, Rocky Mountain spotted fever, Australian Tick Typhus, Flinders Island Spotted Fever and Queensland tick typhus. They infect a wide variety of host. We have used host class as the taxonomic resolution.

References:

Andersson, S.G.E., D. R. Stothard, P. Fuerst, C. G. Kurland 1999. Molecular Phylogeny and Rearrangement of rRNA Genes in *Rickettsia* Species. *Mol. Biol. Evol.* 16:987-995.

Roux V., D. Raoult 2000. Phylogenetic analysis of members of the genus *Rickettsia* using the gene encoding the outer-membrane protein rOmpB (*ompB*). *Int. J. Syst. Evol. Microbiol.* 50: 1449-1455.

Sekeyova, Z., V. Roux, D. Raoult 2001. Phylogeny of *Rickettsia* spp. inferred by comparing sequences of 'gene D', which encodes an intracytoplasmic protein. *Int. J. Syst. Evol. Microbiol.* 51: 1353-1360.

Perlman, S.J., M. S. Hunter, E. Zchori-Fein 2006. The emerging diversity of Rickettsia. *Proc. Roy. Soc. Lond. B* 273: 2097-2106.

Vitorino, L., I. M. Chelo, F. Bacellar, L. Zé –Ze 2007. Rickettsiae phylogeny: a multigenic approach. *Microbiol.* 153:160.168.

Weinert, L.A., J. H Werren, A. Aebi, G. N Stone, F. M Jiggins 2009. Evolution and diversity of Rickettsia bacteria. *BMC Biology* 7:6.

96) **SarcomaVirus** (Virus: RNA Virus: Retroviridae), or Avian Sarcoma Leucosis Virus (ASLV), cause a persistent, largely asymptomatic but oncogenic infection in galliform birds, frequently resulting in lymphoma. Host ranges are poorly known and transmission is by fluid exchange. We have used host family as the taxonomic resolution.

References:

Jackson A. P., M. A. Charleston 2004. A Cophylogenetic Perspective of RNA–Virus Evolution. *Mol. Biol. Evol.* 21: 45–57.

97) **Siphovirus** (Virus: DNA virus: Siphoviridae) is a genus of bacteriophages parasitizing gram-negative Enterobacteria, gram-positive cocci, gram-negative non-enterobacteria and gram-positive bacilli. We have used host class as the taxonomic resolution.

References:

Pride, D.T., T. M Wassenaar, C. Ghose, M. J. Blaser 2006. Evidence of host-virus co-evolution in tetranucleotide usage patterns of bacteriophages and eukaryotic viruses. *BMC Genomics* 7:8.

98) **Spinturnix** (Animalia: Acarina: Spinturnidae) are parasitic mites specialized as ectoparasites on bats. We have used host genus as taxonomic resolution in this study.

References:

Bruyndonckx, N., S. Dubey, M. Ruedi, P. Christe 2009. Molecular cophylogenetic relationships between European bats and their ectoparasitic mites (Acari, Spinturnicidae). *Mol. Phyl. Evol.* 51: 227-237.

99) **Spiroplasma** (Bacteria: Mollicute: Spiroplasmataceae) is a genus of bacteria without cells that parasitize a wide variety of animals and plants. They are related with Transmissible Spongiform Encephalopathies. We have used host class as the taxonomic resolution.

References:

Gasparich, G.E., R. F. Whitcomb, D. Dodge, F. E. French, J. Glass, D. L. Williamson 2004. The genus Spiroplasma and its non-helical descendants: phylogenetic classification, correlation with phenotype and roots of the Mycoplasma mycoides clade. *Int. J. Syst. Evol. Microbiol.* 54: 893-918.

Regassa L.B., G E. Gasparich 2006. Spiroplasmas: evolutionary relationships and biodiversity. *Frontiers in Bioscience* 11, 2983-3002.

100) **Spumavirus** (Virus: RNA Virus: Retroviridae) is a retrovirus that is widespread amongst primates. Infections are typically benign, asymptomatic, and lifelong. However, Spumavirus may assist other retroviruses, such as HIV, in concomitant infections through the provision of a transcriptional transactivator. We have used host family as the taxonomic resolution.

References:

Jackson A. P., M. A. Charleston 2004. A Cophylogenetic Perspective of RNA–Virus Evolution. *Mol. Biol. Evol.* 21: 45–57.

101) **Stator** (Animalia: Coleoptera: Bruchidae) is a small genus of Neotropic and Nearctic seed predator beetles living on several species of legumes. We have used host genus as the taxonomic resolution.

References:

Morse, G.E., B.D. Farrell 2005. Ecological and evolutionary diversification of the seed beetle genus *Stator* (Coleoptera: Chrysomelidae: Bruchinae). *Evolution* 59: 1315–1333.

102) **Stemphylium** (Fungi: Pleosporales: Pleosporaceae) is a small genus of plant pathogenic fungi. We have used host family as the taxonomic resolution.

References:

Câmara, M.P.S., N. R. O'Neill, P. van Berkum 2002. Phylogeny of *Stemphylium* spp. based on ITS and glyceraldehyde-3-phosphate dehydrogenase gene sequences. *Mycologia* 94: 660–672.

103) **Terfezia** (Fungi: Pezizales: Terfeziaceae), so called desert truffles, are mycorrhizal fungi mostly endemic to arid and semi-arid areas of the Mediterranean Region, where they are associated mostly with *Helianthemum* species. We have used host genus as the taxonomic resolution.

References:

Ferdman, Y., S. Aviram, N. Roth-Bejarano, J.M. Trappe, V. Kagan-Zur 2005. Phylogenetic studies of *Terfezia pfeilii* and *Choiromyces echinulatus* (Pezizales) support new genera for southern African truffles: *Kalaharituber* and *Eremiomyces*. *Mycol. Res.* 109: 237–245.

Díez, J., J.L. Manjón, F. Martín 2002. Molecular phylogeny of the mycorrhizal desert truffles (*Terfezia* and *Tirmania*), host specificity and edaphic tolerance. *Mycologia* 94: 247–259.

104) **Tetraopes** (Animalia: Coleoptera: Cerambycidae) is a small genus of beetles that are specialists on milkweeds (*Asclepias*). We used host genus as the taxonomic resolution.

References:

Farrell, B. D., and Mitter, C. 1993. Phylogenetic determinants of insect/plant community diversity. In "Species Diversity in Ecological Communities: Historical and Geographic Perspectives" (R. Ricklefs and D. Schluter, Eds.), pp. 253–266, Univ. of Chicago Press, Chicago.

Farrell, B. D., and Mitter, C. 1998.. Might *Tetraopes* (Cerambycidae) and *Asclepias* (Asclepiadaceae) have coevolved? Biol. J. Linn. Soc. 63: 553–577.

Farrell, B.D. 2001. Evolutionary Assembly of the Milkweed Fauna: Cytochrome Oxidase I and the Age of *Tetraopes* Beetles. Mol. Phyl. Evol. 18: 467–478.

105) **Tetratrichomonas** (Excavata: Tricomonadida: Trichomonadidae) is a small protist genus parasitizing a wide spectrum of vertebrate species. We used host genus as the taxonomic resolution.

References:

Cepicka I., V. Hampl, J. Kulda, J. Flegr 2006. New evolutionary lineages, unexpected diversity, and host specificity in the parabasalid genus *Tetratrichomona*. Mol. Phyl. Evol. 39: 542–551.

Delphine Gerbod, D., V. P. Edgcomb, C. Noël, P. Delgado-Viscogliosi, E. Viscogliosi 2000. Phylogenetic position of parabasalid symbionts from the termite *Calotermes flavicollis* based on small subunit rRNA sequences. Int. Microbiol. 3:165–172.

106) **Thamnophis** (Animalia: Squamata: Colubridae) is a medium-sized genus of snakes with a very generalist diet, feeding on invertebrate and many different kind of vertebrates. We have used host family as the taxonomic resolution. Dr. Juan M. Pleguezuelos (University of Granada) helped us with diet determination.

References:

Rossman, D.A., N.B. Ford, R.A. Siegel 1996. The garter snakes: evolution and ecology. Univ. of Oklahoma Press, Norman. 332 pp.

de Queiroz, A., R Lawson, J. A. Lemos-Espinal 2002. Phylogenetic Relationships of North American Garter Snakes (*Thamnophis*) Based on Four Mitochondrial Genes: How Much DNA Sequence Is Enough? Mol. Phyl. Evol. 22: 315–329.

107) **Timarcha** (Animalia: Coleoptera: Chrysomelidae) is a small genus of apterus leaf beetles. They are specialists on several plant families. We have used host family as the taxonomic resolution.

References:

Gómez-Zurita J., C. Juan, and E. Petitpierre 2000. The Evolutionary History of the Genus *Timarcha* (Coleoptera, Chrysomelidae) Inferred from Mitochondrial COII Gene and Partial 16S rDNA Sequences. Molecular Phylogenetics and Evolution 14: 304–317.

Gómez-Zurita J., T. Hunt, F Kopliku, A P. Vogler 2007. Recalibrated Tree of Leaf Beetles (Chrysomelidae) Indicates Independent Diversification of Angiosperms and Their Insect Herbivores. PLoS ONE 2(4): e360

108) **Timema** (Animalia: Phasmatodea: Timematidae) is a small genus of herbivorous walking-stick insects living on many different kind of host plants. We have used host genus as the taxonomic resolution.

References:

- Crespi, B.J., C.P.Sandoval 2000. Phylogenetic evidence for the evolution of ecological specialization in *Timema*. J. Evol. Biol. 13: 249-262.
- Nosil, P., B.J. Crespi, C. P. Sandoval 2002. Host-plant adaptation drives the parallel evolution of reproductive isolation. Nature 417: 440-443.

109) **Treponema** (Bacteria: Spirochaetales: Spirochaetaceae) is a genus of spirochetal bacteria. Although most *Treponema* species are pathogenic, we have worked with species mutualistic of termites. They provide termites with some important nutrients. We have used host family as the taxonomic resolution.

References:

- Berlanga, M., B. J. Paster, R. Guerrero 2007. Coevolution of symbiotic spirochete diversity in lower termites. Int. Microbiol. 10:133-139

110) **Trirhabda** (Animalia: Coleoptera: Chrysomelidae) is a small genus of oligophagous leaf-beetles, feeding on species in one to three host plant genera belonging to the family Asteraceae. We have used host tribe as taxonomic resolution.

References:

- Swigonová, Z., K. M. Kjer 2004. Phylogeny and host-plant association in the leaf beetle genus *Trirhabda* LeConte (Coleoptera: Chrysomelidae). Mol. Phyl. Evol. 32: 358-374.

111) **Trypanosoma** (Excavata: Kinetoplastea: Trypanosomatidae) is a genus of unicellular parasitic protozoa. They are pathogens of many different animals. They cause Chagas disease, sleeping sickness and other diseases to humans. We have used host family as taxonomic resolution.

References:

- Haag, J., C. O'h Uigin, P. Overath 1998. The molecular phylogeny of trypanosomes: evidence for an early divergence of the Salivaria. Mol. Biochem. Parasitol. 91: 37-49
- Hamilton, P.B., J. R. Stevens, M. W. Gaunt, J. Gidley, W. C. Gibson 2004. Trypanosomes are monophyletic: evidence from genes for glyceraldehyde phosphate dehydrogenase and small subunit ribosomal RNA. Int. J. Parasitol 34: 1393-1404.
- Hamilton, P. B., W. C. Gibson, J. R. Stevens 2007. Patterns of co-evolution between trypanosomes and their hosts deduced from ribosomal RNA and protein-coding gene phylogenies. Mol. Phyl. Evol. 44: 15-25.

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112) **Urophora** (Animalia: Diptera: Tephritidae) is a medium-sized Palearctic genus of flies that attack the flower heads and stems of some tribes of Compositae. Larvae develop forming galls. We used host genus as the taxonomic resolution.

References:

Brändle, M., S. Knoll, S. Eber, J. Stadler, R. Brandl 2005. Flies on thistles: support for synchronous speciation? Biol. J. Linn. Soc. 84: 775-783.

113) **Vidua** (Animalia: Passeriformes: Viduidae) are small passerine birds native to Africa. All species are brood-parasites of strildid finches (Estrildidae). We have used host genus as the taxonomic resolution.

References:

Sorenson, M.D., K.M. Sefc and R.B. Payne 2003. Speciation by host switch in brood parasitic indigobirds. Nature 424: 928-931.

114) **Wolbachia** (Bacteria: Alphaproteobacteria: Rickettsiales) is a genus of inherited bacteria which infects arthropod species, including a high proportion of insects (~60% of species). It is one of the world's most common parasitic microbes and is possibly the most common reproductive parasite in the biosphere. We have used host family as the taxonomic resolution.

References:

Werren, J.H., W. Zhang, L. Rong Guo 1995. Evolution and phylogeny of Wolbachia: reproductive parasites of arthropods. Proc. Roy. Soc. Lond. B 261: 55-71.

115) **Wolbachia** (Bacteria: Alphaproteobacteria: Rickettsiales) is a genus of inherited bacteria which infects arthropod species, including a high proportion of insects (~60% of species). It is one of the world's most common parasitic microbes and is possibly the most common reproductive parasite in the biosphere. We have used host family as the taxonomic resolution.

References:

Plantard, O., J.Y. Rasplus, G. Mondor, L. Le Clainche, M. Solignac 1999. Distribution and phylogeny of Wolbachia inducing thelytoky in Rhoditini and 'Aylacini' (Hymenoptera: Cynipidae). Insect. Mol. Biol. 8: 185-191.

116) **Wolbachia** (Bacteria: Alphaproteobacteria: Rickettsiales) is a genus of inherited bacteria which infects arthropod species, including a high proportion of insects (~60% of species). It is one of the world's most common parasitic microbes and is possibly the most common reproductive parasite in the biosphere. We have used host order as the taxonomic resolution.

References:

Kyei-Poku, G.K., D.D. Colwell, B. Benkel, K.D. Floate 2005. On the ubiquity and phylogeny of *Wolbachia* in lice. *Mol. Ecol.* 14: 285-294.