Oikos **OIK-04344**

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Appendix 1

Additional methods, species lists, additional results

Additional metrics of evolutionary isolation

In our work, evolutionary isolation of hummingbirds and plants of an observed network of interactions were estimated with an index based on Rao's quadratic entropy (QEO). Phylogenetic trees of each assemblage can be visualized in Fig. A1 (for hummingbirds) and Fig. A2 (for plants). Here we conducted additional analyses adopting different metrics of evolutionary isolation (also referred as metrics of evolutionary distinctness), equal splits (ES; Redding and Mooers 2006) and fair proportion (FP; Isaac et al. 2007). The evolutionary distinctness of a species is measured as the sum of the branch lengths separating it from the root of the tree, being branches apportioned equally among the species subtending it (FP), or divided by the number of sister lineages (ES) (Vellend et al. 2011). Values of ES and FP for each species were calculated using 'evol.distinct' function in the 'picante' package in R. We constructed matrices for each phylogenetic scenario following the same steps as described in the main text (see Methods: *Constructing probabilistic matrices*). We then re-ran the model selection procedure for each new metric.

Extended species sets

To calculate QEO, FP and ES estimates of the species we used extended species sets for hummingbirds (Table A1) and plants (Table A2) in order to reduce the chances of sub or overrepresentation of some taxons. For example, *Phaetornis eurynome* was the only member of Phaetornithinae registered in the observed network and therefore could be considered highly isolated from the other hummingbird species. But we are aware that other Phaetornithinae occur in the same region (Table A1) and take part on very similar networks of interactions (Snow and Snow 1986, Buzato et al. 2000, Maruyama et al. 2015) that eventually exchange individuals. Thus, from the perspective of other species in the observed network, *P. eurynome* is less evolutionarily unique than it would seem considering only the species of the observed network. Moreover, phylogenetic methods in community ecology are often sensitive to small species sets (Poe 1998, Munkenmuller 2012). But, although we used extended sets to calculate evolutionary isolation, the values of recorded species were transformed into values relative to their respective assemblages to construct phylogenetic scenarios. Values of each species were divided by the sum of values of all the species in the assemblage.

Results of alternative metrics

The estimates of QEO, FP and ES for each species are shown in Table A1 (for hummingbirds) and Table A2 (for plants). In Table A4 we show results of the likelihood analysis of the complete set of models considering QEO as the metric of evolutionary isolation for constructing matrices of phylogenetic scenarios. In Table A5 and Table A6 we show results of the likelihood analysis considering FP and ES respectively as the metrics of evolutionary isolation. The model composed by evolutionary histories (H–/0 scenario), morphology and phenology matching (H–/0MF) was consistently the best model considering the three metrics.

Constant value in scenarios with the intermediate isolation hypothesis

Following Vazquez et al. (2009), AIC is computed as the log-likelihoods of component vectors (species) of the probabilistic models given the observed data. The computation of AIC values is problematic for models that allow vectors with zero probabilities, such as the models that include phylogenetic scenarios with the intermediate isolation hypothesis (**μ**), because the natural logarithm of 0 is undetermined. Similar issues with log transformation of zero probabilities have emerged in many fields with several possible solutions, including parametric and non parametric data transformation (Aitchison 1982, Burbidge et al. 1988, Pawlowsky-Glahn and Buccianti 2011, Neocleus et al. 2011). For our purposes, the simplest solution is limiting the lowest possible probability by adding a small constant to all species in scenarios that include **μ** (the vectors of QEOz values of hummingbirds and plants), which works well in many situations (Atchinson 1982, Malaeb 1997, Madsen et al. 2005, Neocleus et al. 2011). An ideal constant preserves the distribution of probabilities according to the evolutionary distances among species, but excessively low values can generate biased model selection due to the log transformation of very small values. We defined this constant (c1) as ten percent of the quotient of the total probabilities of the QEOz vector divided by the total number of interactions of the observed network (**O**), thus c1= 3.5e-05. Moreover, we repeated the model selection with alternative values to verify the sensitivity of our results to this constant. Alternative values were five percent of the same quotient (c2 = 1.7e-05), 15% (c3 = 5.3e-05) and 30% (c4 = 1e-04). Results for the best models that include phylogenetic scenarios with **μ**, which were constructed with alternative constant values, are shown in Table A6. We provide R codes for obtaining the constant values as a supplement (Supplementary material Appendix 2).

Table A1. List of hummingbird species of the Serra do Mar State Park (southeastern Brazil) registered in the observed network of interactions of Vizentin-Bugoni et al. (2014, 2016) and in other studies (Snow and Snow 1986, Buzato et al. 2000, Maruyama et al. 2015), and the estimates of evolutionary isolation for each species based on Rao's quadratic entropy (QEO), fair proportion (FP), and equal splits (ES).

Hummingbird species	QEO	FP	ES
Species recorded in the observed network of interactions			
Amazilia versicolor	0.01341	10.0006	9.94274
Clytolaema rubricauda	0.09042	20.6558	21.8449
Eupetomena macroura	0.01558	10.0998	9.33322
Florisuga fusca	0.18766	27.1583	27.5569
Leucochloris albicollis	0.02197	11.4006	11.3886
Lophornis chalybeus	0.09042	20.6558	21.8449
Phaethornis eurynome	0.07127	14.0287	14.1159
Stephanoxis lalandi	0.03874	16.1819	16.683
Thalurania glaucopis	0.01877	9.85862	9.32582
Species recorded in other studies in Serra do Mar State Park			
Amazilia fimbriata	0.01255	9.78586	8.19783
Aphantochroa cirrochloris	0.01553	10.0858	9.30404
Calliphlox amethystina	0.05209	17.2995	18.1496
Chlorostilbon lucidus	0.03652	14.7103	15.6194
Glaucis hirsutus	0.06621	12.0497	12.6267
Heliomaster squamosus	0.05209	17.2995	18.1496
Hylocharis cyanus	0.01249	9.76159	8.14618
Phaethornis ruber	0.06121	12.998	12.3643
Phaethornis squalidus	0.05808	12.7036	12.0961
Ramphodon naevius	0.06621	12.0497	12.6267
Thalurania furcata	0.01877	9.85862	9.32582

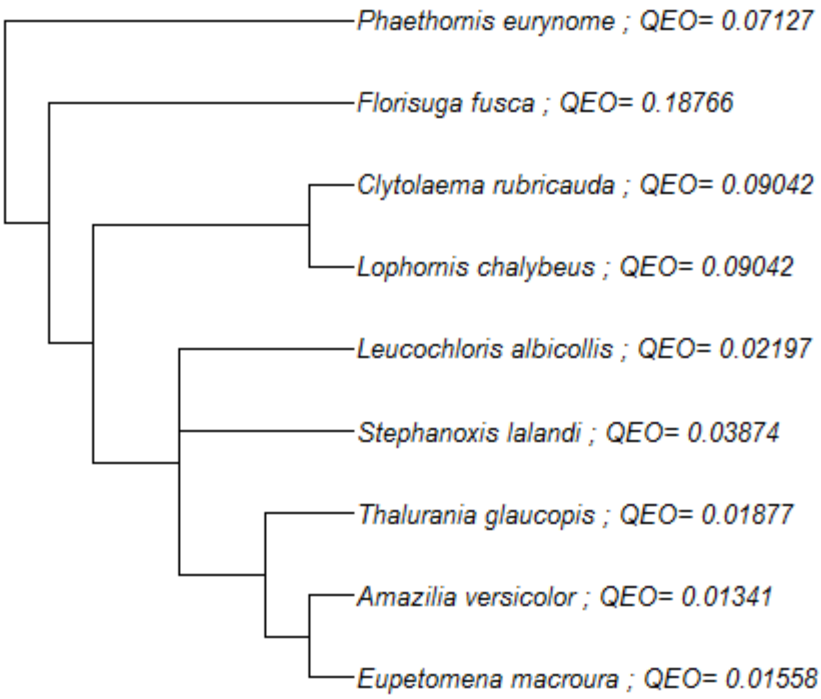

Figure A1. Phylogenetic tree of the nine hummingbird species of the Serra do Mar State Park (southeastern Brazil) registered in the observed network with their respective estimates of evolutionary isolation (QEO) calculated from the complete species set (Table A1).

Table A2. List of ornithophilous plant species of the Serra do Mar State Park (southeastern Brazil) registered in the observed network of interactions of Vizentin-Bugoni et al (2014, 2016) and in other studies (Snow and Snow 1986, Buzato et al. 2000, Maruyama et al. 2015), and the estimates of evolutionary isolation for each species based on Rao's quadratic entropy (QEO), fair proportion (FP), and equal splits (ES).

Plant species	QEO	FP	ES
Species recorded in the observed network of interactions			
Aechmea distichantha	0.00784	0.41038	0.49792
Aechmea gamosepala	0.00784	0.41038	0.49792
Aechmea nudicaulis	0.00784	0.41038	0.49792
Aechmea organensis	0.00784	0.41038	0.49792

Aechmea vanhoutteana	0.00784	0.41038	0.49792
Alstroemeria inodora	0.01987	0.14834	0.38333
Aphelandra colorata	0.00155	0.0935	0.08575
Aphelandra longiflora	0.00155	0.0935	0.08575
Besleria longimucronata	0.00342	0.11082	0.1804
Billbergia amoena	0.00784	0.41038	0.49792
Callianthe rufinerva	0.01035	0.07858	0.12865
Canna paniculata	0.01771	0.1078	0.24896
Canistrum perplexum	0.00784	0.41038	0.49792
Centropogon cornutus	0.00644	0.09301	0.14831
Edmundoa lindenii	0.00784	0.41038	0.49792
Erythrina speciosa	0.00945	0.10051	0.15365
Fuchsia regia	0.01811	0.08483	0.23229
Inga sessilis	0.00945	0.10051	0.15365
Justicia sp1	0.00155	0.0935	0.08575
Justicia sp2	0.00155	0.0935	0.08575
Lantana camara	0.00333	0.07764	0.06734
Macrocarpaea rubra	0.00672	0.07397	0.1054
Manettia cordifolia	0.00514	0.08508	0.12207
Mendoncia velloziana	0.00155	0.0935	0.08575
Mutisia speciosa	0.00756	0.07555	0.13164
Nematanthus fluminensis	0.00342	0.11082	0.1804
Nematanthus fritschii	0.00342	0.11082	0.1804
Nematanthus gregarius	0.00342	0.11082	0.1804
Nematanthus maculatus	0.00342	0.11082	0.1804
Nematanthus sericeus	0.00342	0.11082	0.1804
Nidularium innocentii	0.00784	0.41038	0.49792
Nidularium longiflorum	0.00784	0.41038	0.49792
Nidularium procerum	0.00784	0.41038	0.49792
Nidularium rutilans	0.00784	0.41038	0.49792
Psittacanthus dichrous	0.07053	0.40203	0.57292
Psychotria leiocarpa	0.00514	0.08508	0.12207
Pyrostegia venusta	0.00212	0.07082	0.05659
Sinningia cooperi	0.00342	0.11082	0.1804
Sinningia elatior	0.00342	0.11082	0.1804

Sinningia glazioviana	0.00342	0.11082	0.1804
Siphocampylus convolvulaceus	0.00644	0.09301	0.14831
Siphocampylus lauroanus	0.00644	0.09301	0.14831
Siphocampylus longipedunculatus	0.00644	0.09301	0.14831
Spirotheca rivieri	0.01035	0.07858	0.12865
Tillandsia dura	0.00784	0.41038	0.49792
Tillandsia geminiflora	0.00784	0.41038	0.49792
Tillandsia sp	0.00784	0.41038	0.49792
Tillandsia stricta	0.00784	0.41038	0.49792
Vriesea carinata	0.00784	0.41038	0.49792
Vriesea erythrodactylon	0.00784	0.41038	0.49792
Vriesea incurvata	0.00784	0.41038	0.49792
Vriesea inflata	0.00784	0.41038	0.49792
Vriesea simplex	0.00784	0.41038	0.49792
Vriesea sp	0.00784	0.41038	0.49792
Wittrockia superba	0.00784	0.41038	0.49792
Species recorded in other studies in Serra do Mar State Park			
Abutilon regnelli	0.01035	0.07858	0.12865
Aechmea coelestis	0.00784	0.41038	0.49792
Aechmea pectinata	0.00784	0.41038	0.49792
Agarista oleifolia	0.02919	0.14943	0.24740
Alstroemeria isabellana	0.01987	0.14834	0.38333
Billbergia pyramidalis	0.00784	0.41038	0.49792
Bomarea edulis	0.01987	0.14834	0.38333
Bomarea salsilloides	0.01987	0.14834	0.38333
Bromelia antiacantha	0.00784	0.41038	0.49792
Buddleja brasiliensis	0.00958	0.13890	0.19707
Camptosema scarlatinum	0.00945	0.10051	0.15365
Canistropsis seidelii	0.00784	0.41038	0.49792
Canistrum terminalis	0.00784	0.41038	0.49792
Collaea speciosa	0.00945	0.10051	0.15365
Costus arabicus	0.01003	0.10242	0.16354
Costus spiralis	0.01003	0.10242	0.16354

Dahlstedtia pinnata	0.00945	0.10051	0.15365
Dioclea sp	0.00945	0.10051	0.15365
Edmundoa ambigua	0.00784	0.41038	0.49792
Eriotheca pentaphylla	0.01035	0.07858	0.12865
Fridericia speciosa	0.00212	0.07082	0.05659
Heliconia angusta	0.00821	0.10659	0.17188
Heliconia farinosa	0.00821	0.10659	0.17188
Heliconia spathocircinata	0.00821	0.10659	0.17188
Heliconia velloziana	0.00821	0.10659	0.17188
Inga marginata	0.00945	0.10051	0.15365
Inga subnuda	0.00945	0.10051	0.15365
Justicia carnea	0.00155	0.09350	0.08575
Justicia rizzinii	0.00155	0.09350	0.08575
Lobelia fistulosa	0.00644	0.09301	0.14831
Mandevilla funiformis	0.00672	0.07397	0.10540
Manettia gracilis	0.00514	0.08508	0.12207
Marcgravia polyantha	0.01946	0.14526	0.12786
Mendoncia coccinea	0.00155	0.09350	0.08575
Mutisia campanulata	0.00756	0.07555	0.13164
Nematanthus fissus	0.00342	0.11082	0.18040
Neoregelia johannis	0.00784	0.41038	0.49792
Nidularium angustibracteatum	0.00784	0.41038	0.49792
Nidularium angustifolium	0.00784	0.41038	0.49792
Nidularium giganteum	0.00784	0.41038	0.49792
Nidularium marigoi	0.00784	0.41038	0.49792
Psychotria nuda	0.00514	0.08508	0.12207
Psychotria pubigera	0.00514	0.08508	0.12207
Quesnelia arvensis	0.00784	0.41038	0.49792
Quesnelia humilis	0.00784	0.41038	0.49792
Quesnelia marmorata	0.00784	0.41038	0.49792
Ruellia elegans	0.00155	0.09350	0.08575
Sabicea grisea	0.00514	0.08508	0.12207
Salvia balaustina	0.00781	0.13116	0.15270
Schwartzia brasiliensis	0.01946	0.14526	0.12786
Sinningia douglasii	0.00342	0.11082	0.18040

Siphocampylus betulaefolius	0.00644	0.09301	0.14831
Siphocampylus sulfureus	0.00644	0.09301	0.14831
Stachytarpheta cayennensis	0.00333	0.07764	0.06734
Tillandsia gardneri	0.00784	0.41038	0.49792
Tillandsia tenuifolia	0.00784	0.41038	0.49792
Vernonia notata	0.00756	0.07555	0.13164
Vriesea altodasserrae	0.00784	0.41038	0.49792
Vriesea ensiformis	0.00784	0.41038	0.49792
Vriesea flammea	0.00784	0.41038	0.49792
Vriesea morreniana	0.00784	0.41038	0.49792
Vriesea philippocoburgii	0.00784	0.41038	0.49792
Vriesea procera	0.00784	0.41038	0.49792
Vriesea rodigasiana	0.00784	0.41038	0.49792
Vriesea scalaris	0.00784	0.41038	0.49792
Wittrockia cyathiformis	0.00784	0.41038	0.49792

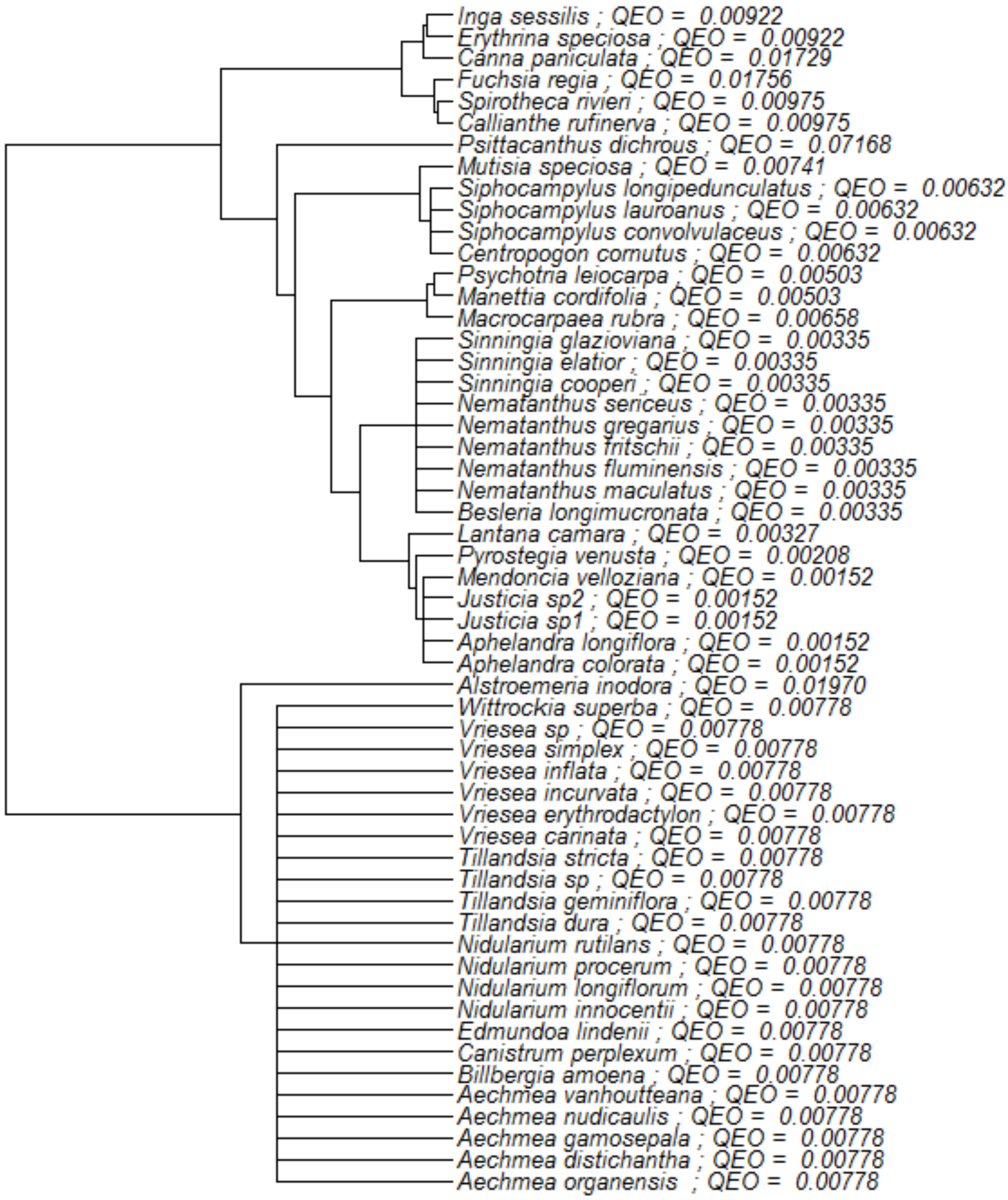

Figure A2. Phylogenetic tree of the 55 plant species of the Serra do Mar State Park (southeastern Brazil) registered in the observed network with their respective estimates of evolutionary isolation (QEO) calculated from the complete species set (Table A2).

Table A3. Results of the likelihood analysis of the models predicting interaction frequencies in the observed network, constructed from species abundances (A), morphology match (M), phenology match (F), evolutionary histories (H; phylogenetic scenarios constructed with **Rao's quadratic entropy – QEO**) and their possible combinations. Results for a model with equal probabilities between all species pairs (E) are shown for comparisons. Underlined in gray are models with lower AIC values than 10000 models with random probabilities (R; 95% CI: 12582 to 15835).

Models	AIC	ΔAIC	Weight
H-/0MF	8347	0	0.92
H-/-MF	8352	5	0.08
MF	8429	82	0
H0/-MF	8438	91	0
Hµ/0MF	8537	190	0
Hµ/-MF	8543	196	0
H-/µMF	8923	576	0
H0/µMF	9009	662	0
Hµ/µMF	9122	775	0
H-/+MF	9305	958	0
H0/+MF	9383	1036	0
Hµ/+MF	9439	1092	0
H-/0F	9874	1527	0
H-/-F	9890	1543	0
F	9903	1556	0
H0/-F	9923	1576	0
Hµ/0F	10011	1664	0
Hµ/-F	10027	1680	0
H-/+F	10337	1990	0
H+/0MF	10344	1997	0
H+/-MF	10351	2004	0
Hµ/0M	10373	2026	0
H0/+F	10379	2032	0
Hµ/-M	10390	2043	0
Hµ/+F	10440	2093	0

H-/µF	10508	2161	0
H0/µF	10539	2192	0
Hµ/µF	10649	2302	0
H-/0M	10692	2345	0
H-/-M	10709	2362	0
M	10727	2380	0
H0/-M	10748	2401	0
Hµ/+M	10795	2448	0
H+/µMF	10926	2579	0
Hµ/µM	11015	2668	0
H-/+M	11091	2744	0
H0/+M	11124	2777	0
H+/+MF	11248	2901	0
H-/µM	11333	2986	0
H0/µM	11374	3027	0
H+/0F	11435	3088	0
H+/-F	11449	3102	0
H+/+F	11974	3627	0
Hµ/+	11995	3648	0
Hµ/0	12014	3667	0
Hµ/-	12040	3693	0
H+/µF	12057	3710	0
H-/+	12251	3904	0
H0/+	12258	3911	0
H-/0	12271	3924	0
E	12278	3931	0
H-/-	12296	3949	0
H0/-	12303	3956	0
H+/0M	12305	3958	0
H+/-M	12324	3977	0
H+/+M	12648	4301	0
Hµ/µ	12697	4350	0
H-/µ	12954	4607	0
H+/µM	12958	4611	0
H0/µ	12960	4613	0

H+/+	13578	5231	0
H+/0	13598	5251	0
H+/-	13623	5276	0
H+/µ	14281	5934	0
H-/-AM	17676	9329	0
H-/0AM	17716	9369	0
H0/-AM	17742	9395	0
AM	17777	9430	0
Hµ/-AM	18041	9694	0
Hµ/0AM	18081	9734	0
H-/µAM	18205	9858	0
H-/-A	18227	9880	0
H-/0A	18264	9917	0
H0/-A	18270	9923	0
H0/µAM	18270	9923	0
A	18303	9956	0
H-/-AMF	18400	10053	0
H0/-AMF	18413	10066	0
H-/0AMF	18454	10107	0
AMF	18462	10115	0
Hµ/-A	18551	10204	0
Hµ/µAM	18572	10225	0
Hµ/+AM	18572	10225	0
Hµ/0A	18587	10240	0
H-/-AF	18752	10405	0
H0/-AF	18752	10405	0
H-/µA	18756	10409	0
AF	18797	10450	0
H0/µA	18799	10452	0
H-/0AF	18802	10455	0
H-/µAMF	18863	10516	0
H0/µAMF	18876	10529	0
Hµ/-AMF	19029	10682	0
Hµ/µA	19079	10732	0
Hµ/0AMF	19081	10734	0

H0/µAF	19220	10873	0
H-/µAF	19221	10874	0
Hµ/-AF	19342	10995	0
Hµ/0AF	19392	11045	0
Hµ/µAMF	19493	11146	0
H+/-AM	19514	11167	0
H+/0AM	19552	11205	0
H+/-AMF	19778	11431	0
Hµ/µAF	19811	11464	0
H+/0AMF	19830	11483	0
H+/-A	19873	11526	0
H+/0A	19909	11562	0
H+/-AF	20014	11667	0
H+/µAM	20038	11691	0
H+/0AF	20063	11716	0
H+/µAMF	20244	11897	0
H+/µA	20401	12054	0
H-/+AM	20402	12055	0
H0/+AM	20464	12117	0
H+/µAF	20485	12138	0
H-/+A	20848	12501	0
H0/+A	20891	12544	0
Hµ/+A	21171	12824	0
H-/+AMF	21561	13214	0
H0/+AMF	21567	13220	0
H0/+AF	21804	13457	0
H-/+AF	21807	13460	0
Hµ/+AMF	22173	13826	0
H+/+AM	22203	13856	0
Hµ/+AF	22400	14053	0
H+/+A	22493	14146	0
H+/+AMF	22881	14534	0
H+/+AF	23051	14704	0

Table A4. Results of the likelihood analysis of the models predicting interaction frequencies in the observed network, constructed from species abundances (A), morphology match (M), phenology match (F), evolutionary histories (H ; phylogenetic scenarios constructed with **fair proportion – FP**) and their possible combinations. Results for a model with equal probabilities between all species pairs (E) are shown for comparisons. Underlined in gray are models with lower AIC values than 10000 models with random probabilities (R; 95% CI: 12582 to 15835).

Models	AIC	ΔAIC	Weight
H-/0MF	8373	0	0.97
H-/-MF	8380	7	0.03
MF	8429	56	0
H0/-MF	8440	67	0
Hμ/0MF	8694	321	0
Hμ/-MF	8702	329	0
H+/0MF	9182	809	0
H+/-MF	9189	816	0
H-/+MF	9425	1052	0
H0/+MF	9489	1116	0
Hμ/+MF	9745	1372	0
H-/0F	9856	1483	0
H-/-F	9862	1489	0
F	9903	1530	0
H0/-F	9913	1540	0
Hμ/0F	10194	1821	0
Hμ/-F	10200	1827	0
H+/+MF	10270	1897	0
Hμ/-M	10550	2177	0
Hμ/0M	10556	2183	0
H+/0F	10592	2219	0
H+/-F	10598	2225	0
H-/-M	10674	2301	0
H-/0M	10680	2307	0
H0/-M	10726	2353	0
M	10727	2354	0

H-/+F	11006	2633	0
H0/+F	11057	2684	0
Hμ/+F	11309	2936	0
H+/-M	11409	3036	0
H+/0M	11415	3042	0
H+/+F	11741	3368	0
Hμ/-	12208	3835	0
Hμ/0	12214	3841	0
H-/-	12222	3849	0
H-/0	12228	3855	0
H0/-	12272	3899	0
E	12278	3905	0
Hμ/+M	12377	4004	0
H-/+M	12481	4108	0
H0/+M	12535	4162	0
H+/-	12946	4573	0
H+/0	12952	4579	0
H+/+M	13242	4869	0
Hμ/+	14049	5676	0
H-/+	14062	5689	0
H0/+	14113	5740	0
H+/+	14787	6414	0
H-/+AM	15366	6993	0
H0/+AM	15407	7034	0
H-/+AMF	15942	7569	0
H0/+AMF	15961	7588	0
H+/+AM	16004	7631	0
H-/+A	16248	7875	0
H0/+A	16285	7912	0
H+/+AMF	16375	8002	0
H-/+AF	16501	8128	0
H0/+AF	16517	8144	0
Hμ/+AMF	16647	8274	0
Hμ/+A	16653	8280	0
H+/+A	16853	8480	0

H+/+AF	16908	8535	0
Hμ/+AF	17143	8770	0
H-/0AM	17741	9368	0
AM	17777	9404	0
H-/-AM	17789	9416	0
H0/-AM	17830	9457	0
Hμ/0AM	18147	9774	0
Hμ/-AM	18195	9822	0
H-/0A	18270	9897	0
A	18303	9930	0
H-/-A	18316	9943	0
H0/-A	18353	9980	0
H+/0AM	18379	10006	0
H+/-AM	18427	10054	0
H-/0AMF	18449	10076	0
AMF	18462	10089	0
H-/-AMF	18498	10125	0
H0/-AMF	18515	10142	0
Hμ/0A	18675	10302	0
Hμ/-A	18721	10348	0
H-/0AF	18786	10413	0
AF	18797	10424	0
H-/-AF	18834	10461	0
H0/-AF	18849	10476	0
H+/0AMF	18869	10496	0
H+/0A	18875	10502	0
H+/-AMF	18918	10545	0
H+/-A	18920	10547	0
Hμ/0AMF	19110	10737	0
Hμ/-AMF	19159	10786	0
H+/0AF	19190	10817	0
H+/-AF	19238	10865	0
Hμ/0AF	19431	11058	0
Hμ/-AF	19479	11106	0
H-/μMF	20968	12595	0

H0/μMF	21023	12650	0
Hμ/μMF	21284	12911	0
H+/μMF	21739	13366	0
Hμ/μM	21842	13469	0
H-/μM	22010	13637	0
H0/μM	22056	13683	0
H-/μF	22426	14053	0
H0/μF	22478	14105	0
H+/μM	22700	14327	0
Hμ/μF	22801	14428	0
H+/μF	23166	14793	0
Hμ/μ	23681	15308	0
H-/μ	23695	15322	0
H0/μ	23745	15372	0
H+/μ	24419	16046	0
H-/μAM	32807	24434	0
H0/μAM	32847	24474	0
Hμ/μAM	33179	24806	0
Hμ/+AM	33179	24806	0
H-/μA	33210	24837	0
H0/μA	33247	24874	0
H-/μAMF	33323	24950	0
H0/μAMF	33339	24966	0
H+/μAM	33440	25067	0
H-/μAF	33595	25222	0
H0/μAF	33610	25237	0
Hμ/μA	33615	25242	0
H+/μAMF	33730	25357	0
H+/μA	33815	25442	0
Hμ/μAMF	33969	25596	0
H+/μAF	33995	25622	0
Hμ/μAF	34250	25877	0

Table A5. Results of the likelihood analysis of the models predicting interaction frequencies in the observed network, constructed from species abundances (A), morphology match (M), phenology match (F), evolutionary histories (H ; phylogenetic scenarios constructed with **equal splits – ES**) and their possible combinations. Results for a model with equal probabilities between all species pairs (E) are shown for comparisons. Underlined in gray are models with lower AIC values than 10000 models with random probabilities (R; 95% CI: 12582 to 15835).

Models	AIC	ΔAIC	Weight
H-/0MF	8370	0	0.82
H-/-MF	8373	3	0.18
MF	8429	59	0
H0/-MF	8436	66	0
Hμ/0MF	8766	396	0
Hμ/-MF	8769	399	0
H+/0MF	9278	908	0
H+/-MF	9281	911	0
H-/+MF	9319	949	0
H0/+MF	9384	1014	0
Hμ/+MF	9714	1344	0
H-/0F	9852	1482	0
H-/-F	9855	1485	0
F	9903	1533	0
H0/-F	9910	1540	0
H-/μMF	9943	1573	0
H0/μMF	10002	1632	0
Hμ/0F	10249	1879	0
Hμ/-F	10252	1882	0
H+/+MF	10253	1883	0
Hμ/μMF	10350	1980	0
Hμ/-M	10573	2203	0
Hμ/0M	10577	2207	0
H-/-M	10677	2307	0
H-/0M	10680	2310	0
H+/0F	10693	2323	0

H+/-F	10695	2325	0
M	10727	2357	0
H0/-M	10727	2357	0
H+/µMF	10823	2453	0
H-/+F	10834	2464	0
H0/+F	10888	2518	0
Hµ/+F	11203	2833	0
Hµ/µM	11292	2922	0
H-/µM	11409	3039	0
H-/µF	11422	3052	0
H0/µM	11459	3089	0
H0/µF	11477	3107	0
H+/-M	11478	3108	0
H+/0M	11482	3112	0
H+/+F	11671	3301	0
Hµ/µF	11844	3474	0
Hµ/+M	11943	3573	0
H-/+M	12027	3657	0
H0/+M	12080	3710	0
H+/µM	12199	3829	0
H-/-	12222	3852	0
Hµ/-	12226	3856	0
H-/0	12226	3856	0
Hµ/0	12230	3860	0
H+/µF	12257	3887	0
H0/-	12274	3904	0
E	12278	3908	0
H+/+M	12855	4485	0
H+/-	13032	4662	0
H+/0	13036	4666	0
H-/µ	13071	4701	0
Hµ/µ	13075	4705	0
H0/µ	13123	4753	0
H-/+	13591	5221	0
Hµ/+	13594	5224	0

H0/+	13642	5272	0
H+/μ	13881	5511	0
H+/+	14401	6031	0
H-/+AM	16915	8545	0
H0/+AM	16956	8586	0
H-/+A	17623	9253	0
H+/+AM	17624	9254	0
H0/+A	17662	9292	0
H-/0AM	17739	9369	0
H-/-AM	17769	9399	0
AM	17777	9407	0
H0/-AM	17811	9441	0
H-/+AMF	17840	9470	0
H0/+AMF	17857	9487	0
Hμ/+A	18080	9710	0
Hμ/0AM	18202	9832	0
Hμ/-AM	18231	9861	0
H-/+AF	18262	9892	0
H-/0A	18269	9899	0
H0/+AF	18278	9908	0
H-/-A	18296	9926	0
A	18303	9933	0
H+/+A	18314	9944	0
H0/-A	18334	9964	0
H+/+AMF	18336	9966	0
H-/0AMF	18447	10077	0
AMF	18462	10092	0
H+/0AM	18462	10092	0
H-/-AMF	18474	10104	0
H+/-AM	18492	10122	0
H0/-AMF	18492	10122	0
Hμ/+AMF	18556	10186	0
Hμ/0A	18726	10356	0
H+/+AF	18747	10377	0
Hμ/-A	18753	10383	0

H-/0AF	18785	10415	0
AF	18797	10427	0
H-/-AF	18810	10440	0
H0/-AF	18827	10457	0
Hμ/+AF	18946	10576	0
H+/0AMF	18951	10581	0
H+/0A	18959	10589	0
H+/-AMF	18978	10608	0
H+/-A	18986	10616	0
Hμ/0AMF	19151	10781	0
Hμ/-AMF	19178	10808	0
H+/0AF	19272	10902	0
H+/-AF	19297	10927	0
Hμ/0AF	19469	11099	0
Hμ/-AF	19495	11125	0
H-/μAM	21527	13157	0
H0/μAM	21567	13197	0
Hμ/μAM	21946	13576	0
Hμ/+AM	21946	13576	0
H-/μA	21979	13609	0
H0/μA	22018	13648	0
H+/μAM	22230	13860	0
Hμ/μA	22436	14066	0
H-/μAMF	22548	14178	0
H0/μAMF	22564	14194	0
H+/μA	22670	14300	0
H-/μAF	22818	14448	0
H0/μAF	22834	14464	0
H+/μAMF	23027	14657	0
Hμ/μAMF	23227	14857	0
H+/μAF	23299	14929	0
Hμ/μAF	23508	15138	0

Table A6. Results of the likelihood analysis with the best model and the models with lowest AIC values including the phylogenetic scenarios with the intermediate isolation hypothesis, constructed with different constant values (c1, c2, c3 and c4).

Models	AIC	ΔAIC	Weight
H-/0MF	8347	0	1
(c4)Hμ/0MF	8451	104	0
(c4)Hμ/-MF	8457	110	0
(c3)Hμ/0MF	8499	152	0
(c3)Hμ/-MF	8505	158	0
(c1)Hμ/0MF	8537	190	0
(c1)Hμ/-MF	8543	196	0
(c2)Hμ/0MF	8602	255	0
(c2)Hμ/-MF	8608	261	0
(c4)H-/μMF	8801	454	0
(c3)H-/μMF	8869	522	0
(c1)H-/μMF	8923	576	0
(c2)H-/μMF	9015	668	0

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Appendix 2

R scripts

```
##################################################################
# 1– Constructing probabilistic matrices of the phylogenetic scenarios
# 2– Likelihood analysis (Vázquez et al 2009) of models of phylogenetic scenarios
# 3– Comparing results for scenarios to a null model of random probabilities
##################################################################

### Specify the vectors with values of evolutionary isolation (e.g., QEO, FP, ES) of animals and plants.

animals_orig <- read.table("originality_animals.txt")

plants_orig <- read.table("originality_plants.txt")

### If the values were calculated from phylogenies with a higher number of species, we recommend dividing each value by the sum of the values of all species in each group (simply erase the #) in the two following lines.

# animals_orig <- animals_orig/sum(animals_orig)

# plants_orig <- plants_orig/sum(plants_orig)

### Specify the matrix of observed interaction network. It must have the same number of rows as the length of “animals_orig” and the same number of columns as the length of “plants_orig”.

obs_network <- as.matrix(read.table("matrix_of_interactions.txt"))

### Function of the standard score complement equation

invez <- function(orig, p=0.1, obs_network){ #computes the QEOz values added to a constant; p is a percentage and the default value is 10% (see Supplement 1 for details)

	z2  <- abs(scale(orig))

	inv <- ((max(z2)-z2)/max(z2))

	inv <- inv/sum(inv)

	con <- (sum(inv)/sum(obs_network)) * p # calculates the constant value

	inv <- (inv + con)/sum(inv + con)

	return(inv)

	}

constant <- function(rede_obs, p=0.1){ # computes the constant values; p is a percentage and t he default value is 10% (see Supplement 1 for details)

	const <- (1/sum(obs_network)) * p

	return(const)

	}



### Assigns values for the species according to each scenario

plants_plus <- plants_orig
```

```
animals_plus <- animals_orig

plants_minus <- 1 - plants_orig

animals_minus <- 1 - animals_orig

plants_med <- invez(plants_orig)

animals_med <- invez(animals_orig)

plants_0 <- rep(1, length(plants_orig))

animals_0 <- rep(1, length(animals_orig))


### Function to create a probabilistic matrix as a product of two vectors with probabilities

matrixmaker <- function(rows, columns){

  matrixp <- matrix(nrow = length(rows), ncol = length(columns),byrow= TRUE)

  for(i in 1:length(columns)){

    matrixp[,i]<- columns[i] * rows

  }

  matrixp <- matrixp/sum(matrixp)

 }

#########SCENARIOS WITH EVOLUTIONARY HISTORIES OF BOTH GROUPS

### SCENARIO H+/+

H_plus_plus <- matrixmaker (animals_plus, plants_plus)

 #fills the matrix elements with the multiplication of originality values of each animal-plant pair according to
H+/+ phylogenetic scenario

### SCENARIO H+/-

H_plus_minus <- matrixmaker (animals_plus, plants_minus)

### SCENARIO H-/+

H_minus_plus <- matrixmaker (animals_minus, plants_plus)

### SCENARIO H-/-

H_minus_minus <- matrixmaker(animals_minus, plants_minus)

### SCENARIO Hμ/+

H_med_plus <- matrixmaker(animals_med, plants_plus)

### SCENARIO Hμ/-

H_med_minus <- matrixmaker(animals_med, plants_minus)

### SCENARIO Hμ/μ
```

```
H_med_med <- matrixmaker(animals_med, plants_med)

### SCENARIO H+/µ

H_plus_med <- matrixmaker(animals_plus, plants_med)

### SCENARIO H-/µ

H_minus_med <- matrixmaker(animals_minus, plants_med)


#########SCENARIOS WITH NULL PROBABILITIES FOR ONE OF THE GROUPS

### SCENARIO H0/+

H_0_plus <- matrixmaker(animals_0, plants_plus)

### SCENARIO H0/-

H_0_minus <- matrixmaker(animals_0, plants_minus)

### SCENARIO H-/0

H_minus_0 <- matrixmaker(animals_minus, plants_0)

### SCENARIO H+/0

H_plus_0 <- matrixmaker(animals_plus, plants_0)

### SCENARIO Hµ/0

H_med_0 <- matrixmaker(animals_med, plants_0)

### SCENARIO H0/µ

H_0_med <- matrixmaker(animals_0, plants_med)


### Evaluating the capacity of phylogenetic scenarios in predicting observed interactions with the likelihood
analyses of Vázquez et al. (2009)

library(stats)

results <- matrix(0,ncol=3,nrow=15)

colnames(results)<-c("likelihood","AIC","Model")


# H+/+

lik <- dmultinom(obs_network, prob= H_plus_plus, log=TRUE)

aic = 2 *(-lik) + 2 * 2 # the last value in this line is the number of parameters

results[1,1]<- round(lik, digits=0)
```

```
results[1,2]<- round(aic, digits=0)
results[1,3] <- “H+/+”
# H+/-
lik <- dmultinom(obs_network, prob= H_plus_minus, log=TRUE)
aic = 2 *(-lik) + 2 * 2
results[2,1]<- round(lik, digits=0)
results[2,2]<- round(aic, digits=0)
results[2,3] <- “H+/-”
# H-/+
lik <- dmultinom(obs_network, prob= H_minus_plus, log=TRUE)
aic = 2 *(-lik) + 2 * 2
results[3,1]<- round(lik, digits=0)
results[3,2]<- round(aic, digits=0)
results[3,3] <- “H-/+”
# H-/-
lik <- dmultinom(obs_network, prob= H_minus_minus, log=TRUE)
aic = 2 *(-lik) + 2 * 2
results[4,1]<- round(lik, digits=0)
results[4,2]<- round(aic, digits=0)
results[4,3] <- “H-/-”
# Hμ/μ
lik <- dmultinom(obs_network, prob= H_med_med, log=TRUE)
aic = 2 *(-lik) + 2 * 2
results[5,1]<- round(lik, digits=0)
results[5,2]<- round(aic, digits=0)
results[5,3] <- “Hμ/μ”
# Hμ/-
lik <- dmultinom(obs_network, prob= H_med_minus, log=TRUE)
aic = 2 *(-lik) + 2 * 2
results[6,1]<- round(lik, digits=0)
results[6,2]<- round(aic, digits=0)
```

```
results[6,3] <- “Hμ/-“

# Hμ/+

lik <- dmultinom(obs_network, prob= H_med_plus, log=TRUE)

aic = 2 *(-lik) + 2 * 2

results[7,1]<- round(lik, digits=0)

results[7,2]<- round(aic, digits=0)

results[7,3] <- “Hμ/μ“

# H+/μ

lik <- dmultinom(obs_network, prob= H_plus_med, log=TRUE)

aic = 2 *(-lik) + 2 * 2

results[8,1]<- round(lik, digits=0)

results[8,2]<- round(aic, digits=0)

results[8,3] <- “H+/μ“

# H-/μ

lik <- dmultinom(obs_network, prob= H_minus_med, log=TRUE)

aic = 2 *(-lik) + 2 * 2

results[9,1]<- round(lik, digits=0)

results[9,2]<- round(aic, digits=0)

results[9,3] <- “H-/μ“

# H0/+

lik <- dmultinom(obs_network, prob = H_0_plus, log = TRUE)

aic = 2 *(-lik) + 2 * 2

results[10,1]<- round(lik, digits=0)

results[10,2]<- round(aic, digits=0)

results[10,3] <- “H0/+“

# H0/-

lik <- dmultinom(obs_network, prob = H_0_minus, log = TRUE)

aic = 2 *(-lik) + 2 * 2

results[11,1]<- round(lik, digits=0)

results[11,2]<- round(aic, digits=0)

results[11,3] <- “H0/-“
```

H-/0

lik <- dmultinom(obs_network, prob = H_minus_0, log = TRUE)

aic = 2 *(-lik) + 2 * 2

results[12,1]<- round(lik, digits=0)

results[12,2]<- round(aic, digits=0)

results[12,3] <- “H-/0“

H+/0

lik <- dmultinom(obs_network, prob = H_plus_0, log = TRUE)

aic = 2 *(-lik) + 2 * 2

results[13,1]<- round(lik, digits=0)

results[13,2]<- round(aic, digits=0)

results[13,3] <- “H+/0“

#Hμ/0

lik <- dmultinom(obs_network, prob = H_med_0, log = TRUE)

aic = 2 *(-lik) + 2 * 2

results[14,1]<- round(lik, digits=0)

results[14,2]<- round(aic, digits=0)

results[14,3] <- “Hμ/0“

#H0/μ

lik <- dmultinom(obs_network, prob = H_0_med, log = TRUE)

aic = 2 *(-lik) + 2 * 2

results[15,1]<- round(lik, digits=0)

results[15,2]<- round(aic, digits=0)

results[15,3] <- “H0/μ“

results

conf.lik.ran first tests AIC values for 10000 (default) matrices with random probabilities and then generates upper and lower limits of a 95% (default) confidence interval. The later part of this function was adapted from ‘confint’ function of the ‘bipartite’ package.

conf.lik.ran<-function(obs=obs_network, iter=10000, alpha=0.05){

    resu <- numeric(iter)

```
  for(i in 1:iter){
    ranmat= replicate(ncol(obs), runif(nrow(obs)))
    ranmat=ranmat/sum(ranmat)
    lik = dmultinom(obs, prob=ranmat, log = TRUE)
    resu[i]= 2 *(-lik) + 2 * 1 #number of parameters is set to 1
    }
xs<-sort(resu)
n<-length(xs)
lo<-xs[round(n*alpha/2)]
up<-xs[round(n*(1-alpha/2))]
med = mean(xs)
res<-list(conf_up=up,conf_low=lo,mean.r=med)
res
}
conf.lik.ran(obs_network)
```

References

Vazquez, D. P. et al. 2009b. Evaluating multiple determinants of the structure of plant-animal mutualistic networks. - Ecology 90: 2039–2046.