

## Supporting Information

### **Common birds combine pest control and seed dispersal in apple orchards through a hybrid interaction network.**

Daniel García<sup>1,2</sup>, Beatriz Rumeu<sup>1,2,3</sup>, Juan Carlos Illera<sup>2</sup>, Marcos Miñarro<sup>4</sup>, Gemma Palomar<sup>5,6</sup> & Juan Pedro González-Varo<sup>1,2,3</sup>

1- Depto. de Biología de Organismos y Sistemas, Universidad de Oviedo, Oviedo E-33071, Spain

2- Biodiversity Research Institute (CSIC-Oviedo University-Principality of Asturias), University of Oviedo, Campus of Mieres, Mieres E-33600, Spain.

3- Depto. de Biología – IVAGRO, Universidad de Cádiz, Puerto Real E-11510, Spain

4- Servicio Regional de Investigación y Desarrollo Agroalimentario (SERIDA), Villaviciosa E-33300, Spain

5- Depto. de Genética, Fisiología y Microbiología, Universidad Complutense de Madrid, Madrid E28040, Spain

6- Institute of Environmental Sciences, Jagiellonian University, Kraków 30-387, Poland.

\* Author for correspondence (danielgarcia@uniovi.es)

**Table S1.** Number of individual birds of different species sampled at field censuses, mist-netting, dropping content visual analysis, dropping content analysis after DNA extraction, and DNA-metabarcoding analysis. DNA extraction and metabarcoding subsamples were chosen to represent as many as possible bird species (with a minimum sample size of 3 individuals) according to their capture frequency and aiming to cover the different capture sites and dates across the whole year. The consideration of bird species as legitimate seed disperser (LSD) is also shown.

Species	Sp. acronym	Census	Mist-netting	Dropping content	DNA extraction	DNA metabarcoding	LSD <sup>a</sup>
<i>Acrocephalus scirpaceus</i>	Acr sci	0	1	1	1	0	-
<i>Aegithalos caudatus</i>	Aeg cau	16	51	49	37	35	-
<i>Anthus pratensis</i>	Ant pra	0	1	1	0	0	-
<i>Anthus trivialis</i>	Ant tri	0	1	1	0	0	-
<i>Carduelis carduelis</i>	Car car	28	35	35	14	13	-
<i>Certhia brachydactyla</i>	Cer bra	10	13	10	10	9	- <sup>b</sup>
<i>Cettia cetti</i>	Cet cet	2	0	0	0	0	-
<i>Chloris chloris</i>	Chl chl	12	11	11	11	11	-
<i>Cisticola juncidis</i>	Cis jun	7	0	0	0	0	-
<i>Columba palumbus</i>	Col pal	2	0	0	0	0	+
<i>Cyanistes caeruleus</i>	Cya cae	61	46	45	37	31	-
<i>Curruca communis</i>	Cur com	0	2	2	2	0	+
<i>Dendrocopos major</i>	Den maj	12	4	3	3	3	+
<i>Emberiza cirrus</i>	Emb cir	0	3	3	1	0	-
<i>Erithacus rubecula</i>	Eri rub	143	203	199	106	76	+
<i>Ficedula hypoleuca</i>	Fic hyp	9	14	14	14	12	+
<i>Fringilla coelebs</i>	Fri coe	35	36	35	22	20	+ <sup>c</sup>
<i>Garrulus glandarius</i>	Gar glan	23	2	2	1	0	+
<i>Hippolais polyglotta</i>	Hip pol	3	1	1	0	0	-
<i>Hirundo rustica</i>	Hir rus	0	1	1	0	0	-
<i>Lanius collurio</i>	Lan col	4	8	7	7	7	+
<i>Motacilla cinerea</i>	Mot cin	1	3	3	1	0	-
<i>Muscicapa striata</i>	Mus str	2	4	4	4	3	+
<i>Nannus troglodytes</i>	Nan tro	56	11	11	11	11	- <sup>d</sup>
<i>Oriolus oriolus</i>	Ori ori	6	3	3	4	3	+
<i>Parus major</i>	Par maj	61	136	116	79	60	-
<i>Passer domesticus</i>	Pas dom	1	1	1	0	0	-

Table S1 (cont.).

Species	Sp. acronym	Census	Mist-netting	Dropping content	DNA extraction	DNA metabarcoding	LSD <sup>a</sup>
<i>Periparus ater</i>	Per ate	2	7	7	7	7	-
<i>Phoenicurus ochruros</i>	Pho och	0	1	1	0	0	+
<i>Phoenicurus phoenicurus</i>	Pho pho	0	1	1	1	0	+
<i>Phylloscopus collybita</i>	Phy col	2	36	32	27	26	+
<i>Phylloscopus ibericus</i>	Phy ibe	3	1	1	-	0	+
<i>Phylloscopus trochilus</i>	Phy tro	0	6	6	6	5	+
<i>Picus sharpei</i>	Pic sha	3	4	4	4	4	+
<i>Pyrrhula pyrrhula</i>	Pyr pyr	8	19	14	11	10	-
<i>Regulus ignicapilla</i>	Reg ign	17	17	15	15	15	- <sup>e</sup>
<i>Saxicola rubicola</i>	Sax rub	0	2	2	0	0	-
<i>Serinus serinus</i>	Ser ser	17	30	29	16	17	-
<i>Sturnus vulgaris</i>	Stu vul	47	0	0	0	0	+
<i>Sylvia atricapilla</i>	Syl atr	124	197	195	128	75	+
<i>Sylvia borin</i>	Syl bor	1	4	4	4	4	+
<i>Turdus iliacus</i>	Tur ili	50	3	3	3	3	+
<i>Turdus merula</i>	Tur mer	95	102	95	68	57	+
<i>Turdus philomelos</i>	Tur phi	47	48	48	35	33	+
<i>Turdus pilaris</i>	Tur pil	0	1	1	0	0	+
<b>Totals</b>		<b>910</b>	<b>1070</b>	<b>1016</b>	<b>690</b>	<b>550</b>	

a- Status by Simmons, B. I., Sutherland, W. J., Dicks, L. V., Albrecht, J., Farwig, N., García, D., ... & González-Varo, J. P. (2018). Moving from frugivory to seed dispersal: Incorporating the functional outcomes of interactions in plant–frugivore networks. *Journal of Animal Ecology*, 87(4), 995-1007

b- Status checked after Harrap, S. (2020). Short-toed Treecreeper (*Certhia brachydactyla*), version 1.0. In Birds of the World (J. del Hoyo, A. Elliott, J. Sargatal, D. A. Christie, and E. de Juana, Editors). Cornell Lab of Ornithology, Ithaca, NY, USA.

c- Considered LSD of ivy *Hedera helix* given the occurrence of intact seeds in the fecal analysis.

d- Status checked after Kroodsma, D. E., D. Brewer, D. A. Christie, and J. S. Marks (2020). Eurasian Wren (*Troglodytes troglodytes*), version 1.0. In Birds of the World (J. del Hoyo, A. Elliott, J. Sargatal, D. A. Christie, and E. de Juana, Editors). Cornell Lab of Ornithology, Ithaca, NY, USA.

e- Status checked after Martens, J. and M. Päckert (2020). Common Firecrest (*Regulus ignicapilla*), version 1.0. In Birds of the World (J. del Hoyo, A. Elliott, J. Sargatal, D. A. Christie, and E. de Juana, Editors). Cornell Lab of Ornithology, Ithaca, NY, USA

**Table S2.** Relative abundance of ripe fruits of different plant species sampled across the three study sites and the whole year.

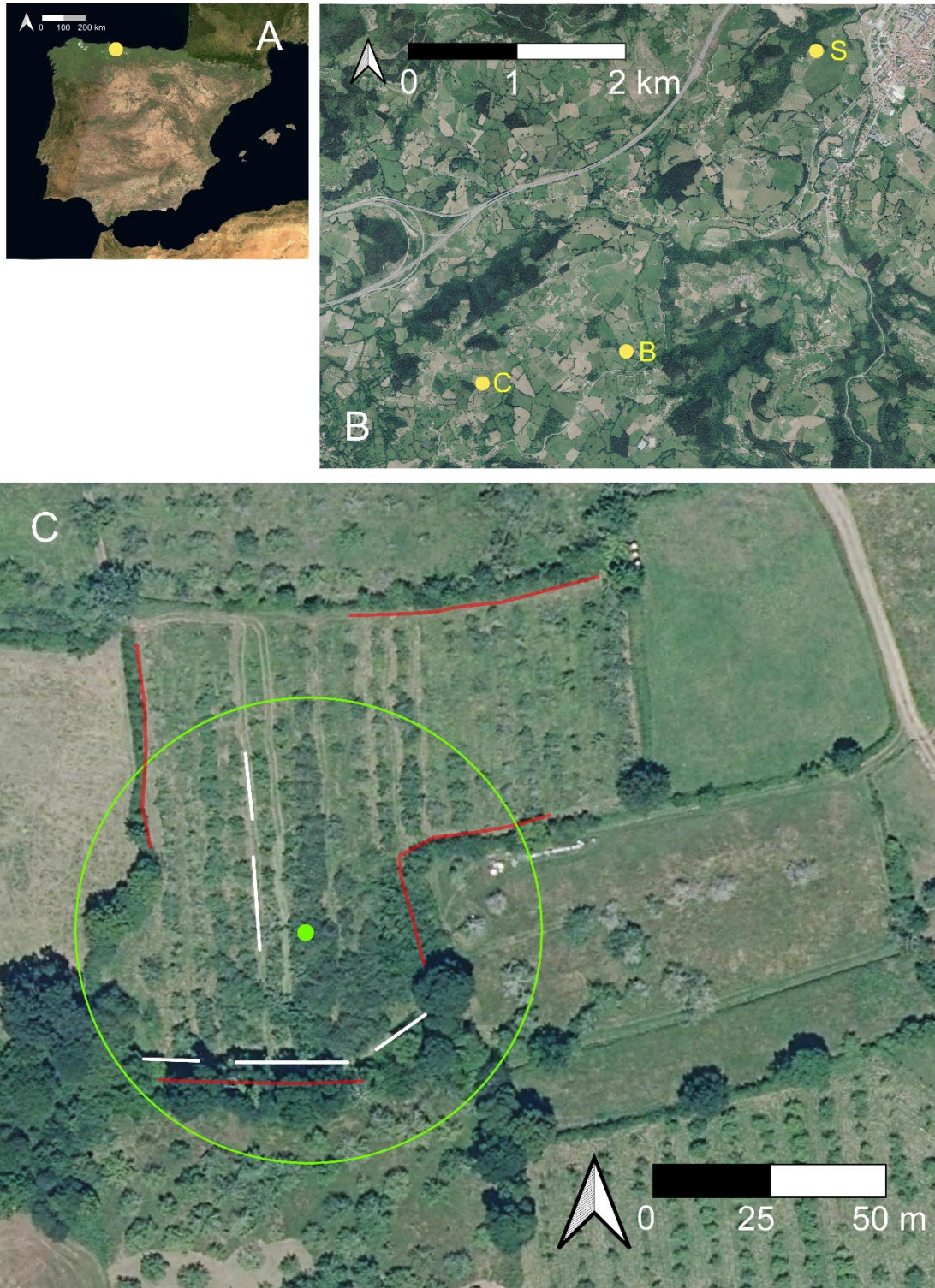
Species	No. fruiting plants	No. fruits	Relative abundance (prop.)
<i>Arum maculatum</i>	1	35	1.49E-05
<i>Bryonia dioica</i>	8	2436	1.04E-03
<i>Cornus sanguinea</i>	159	154684	6.60E-02
<i>Crataegus monogyna</i>	5	143	6.10E-05
<i>Euonymus europaeus</i>	100	55757	2.38E-02
<i>Hedera helix</i>	132	873410	3.73E-01
<i>Ilex aquifolium</i>	8	13963	5.96E-03
<i>Iris foetidissima</i> *	3	620	1.75E-05
<i>Laurus nobilis</i>	75	316842	1.35E-01
<i>Ligustrum vulgare</i>	4	108	4.61E-05
<i>Lonicera periclymenum</i>	15	784	3.34E-04
<i>Phytolacca americana</i>	5	47	2.01E-05
<i>Prunus spinosa</i>	65	20730	8.84E-03
<i>Rhamnus alaternus</i>	12	4668	1.99E-03
<i>Rosa canina</i>	225	45589	1.94E-02
<i>Rubia peregrina</i>	108	7842	3.35E-03
<i>Rubus fruticosus</i> **	230	207282	8.84E-02
<i>Ruscus aculeatus</i>	488	24687	1.05E-02
<i>Sambucus nigra</i>	83	263679	1.12E-01
<i>Smilax aspera</i>	299	345475	1.47E-01
<i>Solanum dulcamara</i>	9	283	1.21E-04
<i>Solanum nigrum</i>	1	41	1.49E-05
<i>Tamus communis</i>	42	3402	1.45E-03
<i>Viscum album</i>	20	2181	9.30E-04

\* *Iris foetidissima* fruit unit considered here is the capsule that contains, on average, 25 red fleshy-like mimetic seeds

\*\* *Rubus fruticosus* fruit unit considered here is the bramble (i.e. polydrupe), composed, on average, by 30 one-seeded drupes.

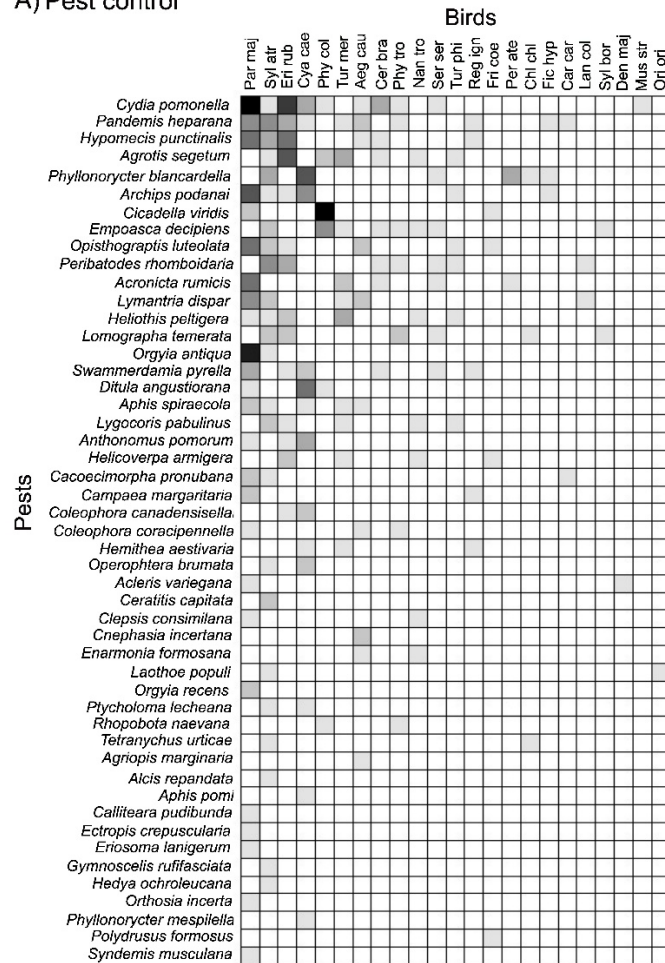
**Table S3.** Results of Gamma-family (log link) Generalized Linear Mixed Models evaluating the effects of bird species relative abundance (percentage of individuals), body mass (g) and diet diversity (inverse Simpson Index) on bird species centrality measures on the hybrid (pest control and seed dispersal) interaction network. All predictors were standardized prior to analysis. Models included the variance ( $\pm$ SD) estimate for taxonomic identity factors included as random effects. Marginal and conditional (in parentheses) R<sup>2</sup> values are also given.

Response variables	<b>Weighted degree</b> (Gamma, log)				<b>Harmonic closeness</b> (Gamma, log)				<b>Betweenness</b> (Gamma, log)			
	R <sup>2</sup> = 0.560 (0.681)				R <sup>2</sup> = 0.653 (0.814)				R <sup>2</sup> = 0.608 (0.608)			
Predictors	Estimate	SE/SD	t	P	Estimate	SE/SD	t	P	Estimate	SE/SD	t	P
Intercept	-3.242	0.235	-13.77	<0.001	-0.879	0.041	-21.64	<0.001	4.610	0.215	21.43	<0.001
Relative abundance	0.976	0.198	4.91	<0.001	0.186	0.027	6.81	<0.001	1.178	0.298	3.94	<0.001
Body mass	-0.097	0.208	-0.46	0.640	0.011	0.032	0.33	0.740	-0.378	0.207	-1.83	0.068
Diet diversity	-0.075	0.241	-0.31	0.754	-0.041	0.033	-1.22	0.223	0.0172	0.299	0.06	0.953
Genus [Family] (random)	0.151	0.389			0.004	0.067			0.000	0.000		
Family (random)	0.041	0.203			0.003	0.052			0.000	0.000		

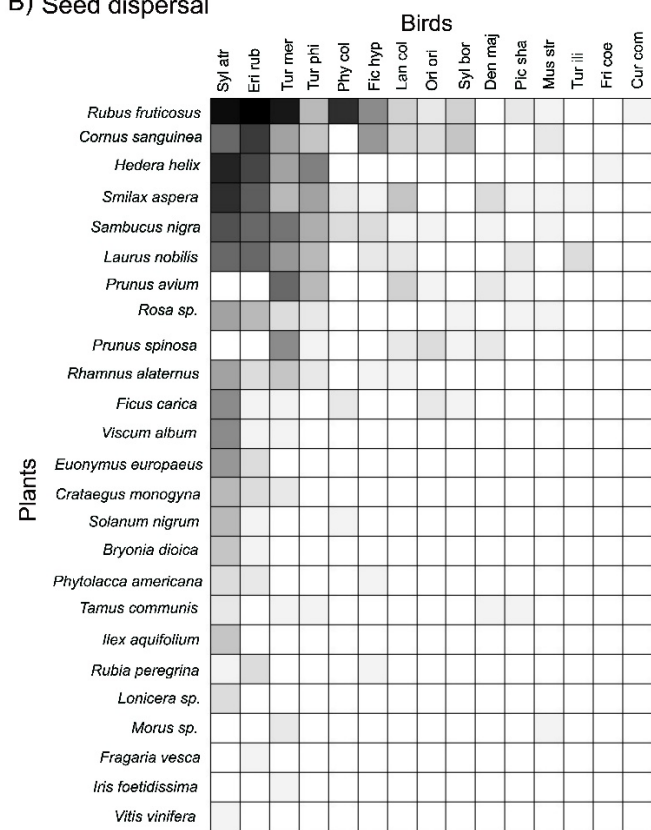


**Figure S1.** A) Location of the study sites in northern Spain. B) View of study sites (S: Sorribes,  $43^{\circ} 28' 44''$  N,  $5^{\circ} 26' 54''$  W, 25 m asl; B: Bustariega,  $43^{\circ} 27' 22''$  N,  $5^{\circ} 27' 69''$  W, 97 m asl; and C: Camoca,  $43^{\circ} 27' 10''$  N,  $5^{\circ} 28' 58''$  W, 85 m asl) in the region, highlighting the variegated landscape composed of a fine-grain mosaic with anthropogenic patches (pasture meadows, timber plantations, apple orchards, other crops and urban settlements) and seminatural-woody habitats (like hedgerows and native forest patches). C) Aerial view of Camoca site representing the 50-m radius point-count plot for bird censuses (green circle), location of settlement of mist-nets for bird capture (white lines) and transects for counts of fleshy-fruits along woody hedgerows and forest patches surrounding apple orchard (red lines).

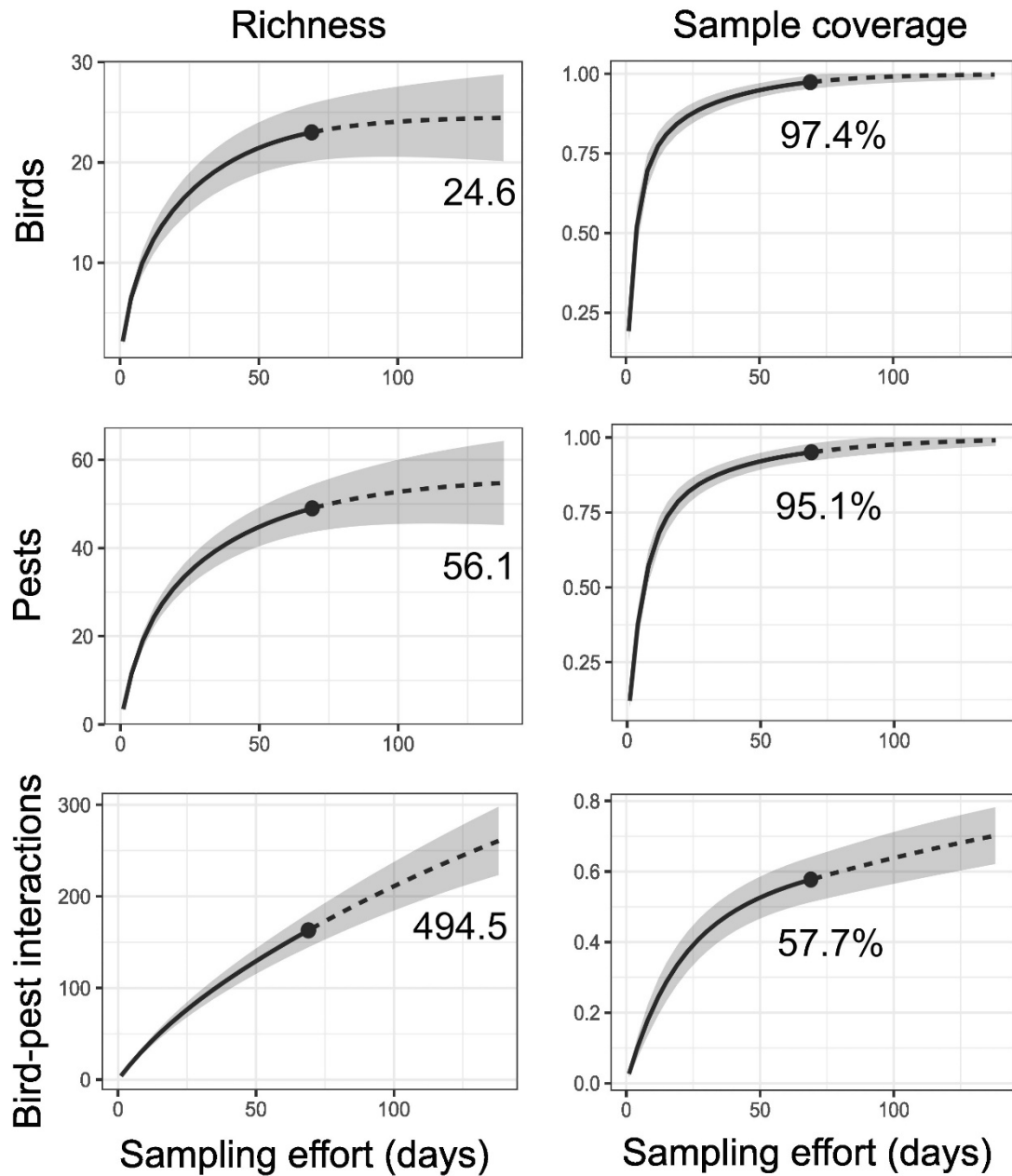
A) Pest control



B) Seed dispersal

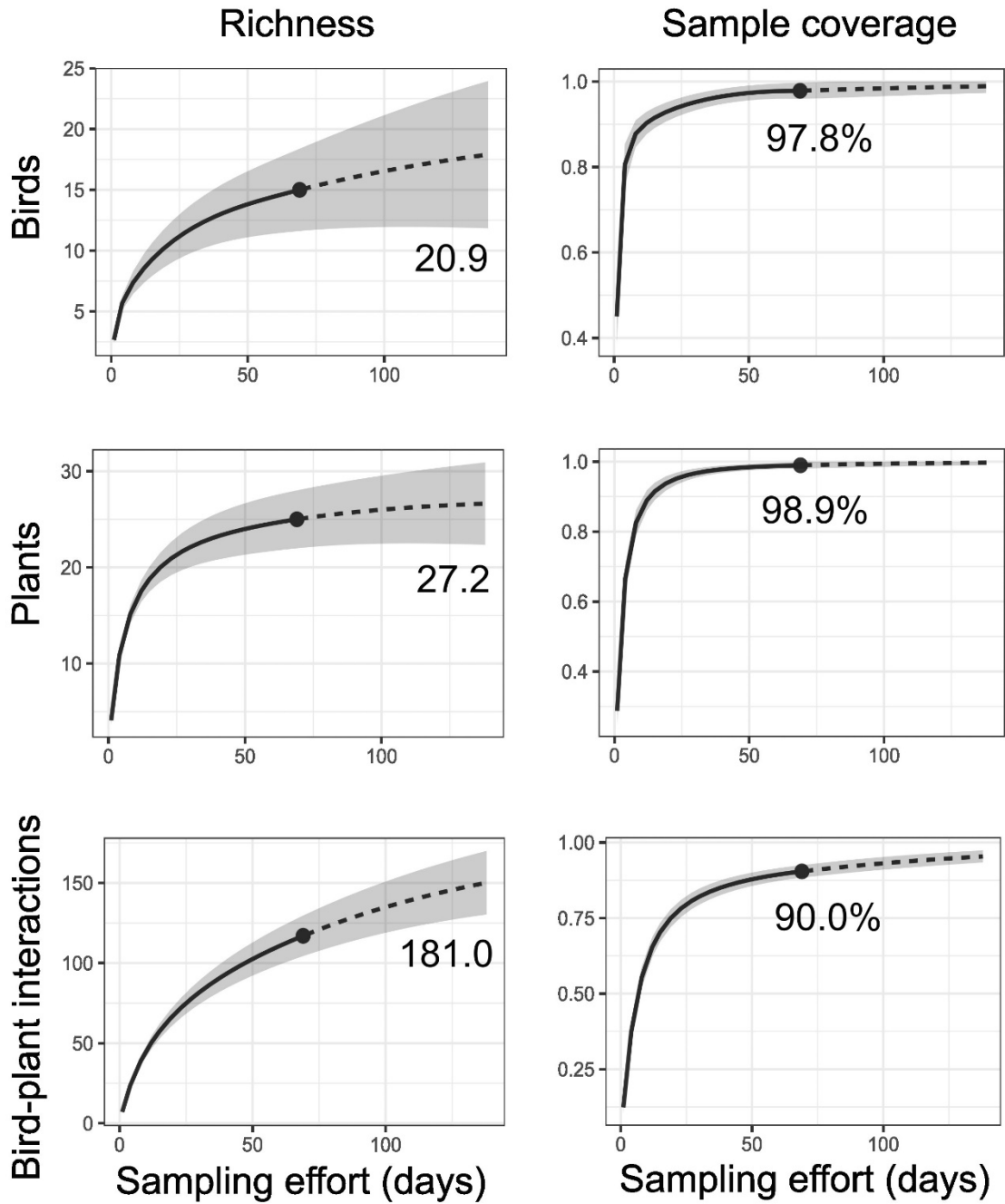


**Figure S2.** Representation of bird-pest (A) and bird-plant (B) interaction matrix underpinning, respectively, pest-control and seed dispersal networks. Actual interactions between species pairs are depicted in grey-to-black squares, with darkness proportional to the frequency of occurrence. See Table S1 for bird species acronyms.

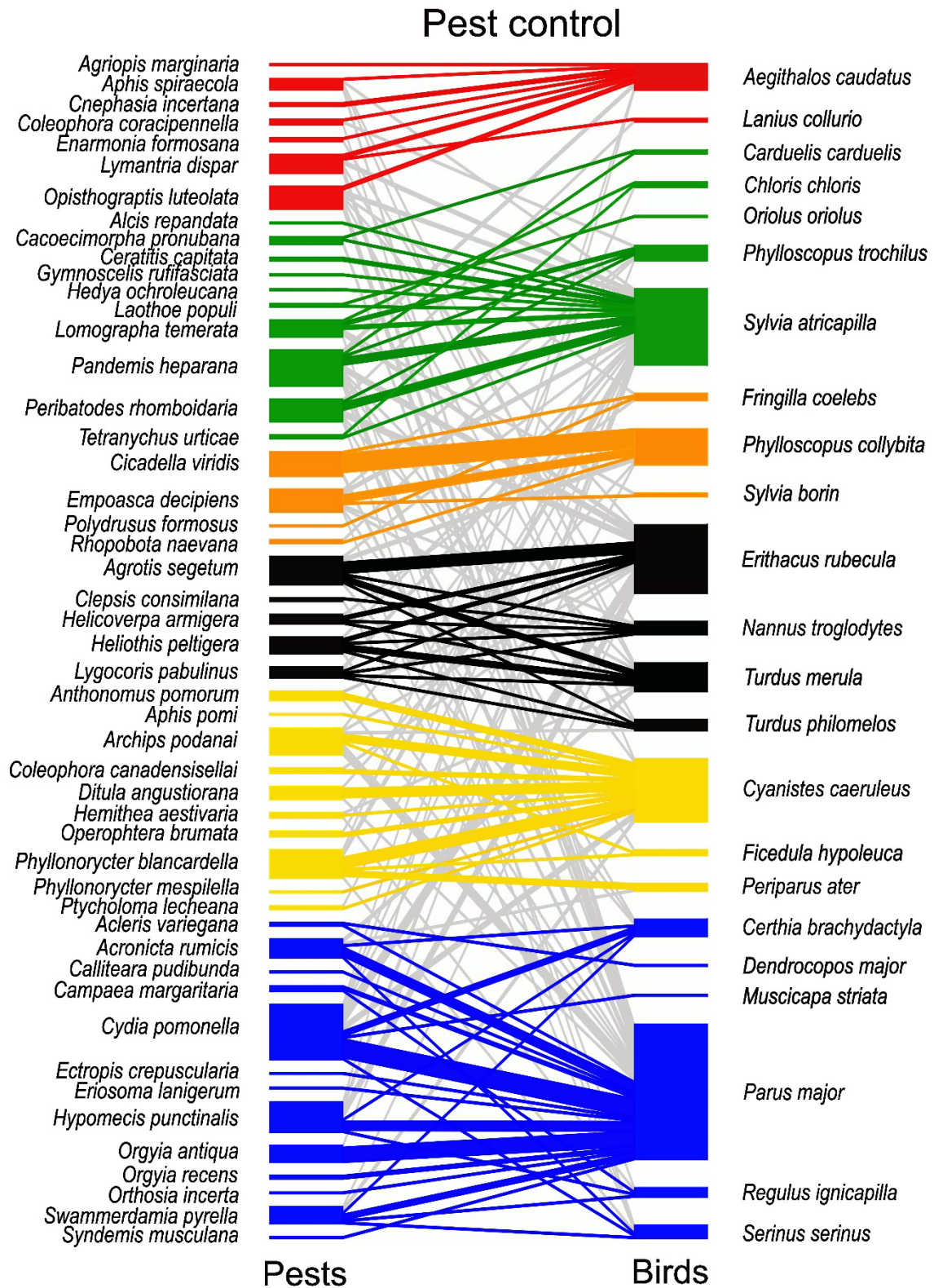


**Figure S3.** Cumulative curves of birds, apple pest arthropods, and bird-pest interactions richness and sample coverage, per sampling effort unit (mist-netting days). Dot symbol represents the observed value and the dashed line the extrapolated values expected with higher sampling effort. Shaded area represents 95% confidence intervals. Asymptotic values are shown for richness. Sample coverage values indicate the percentages of the total number of observations belonging to the set of species (or interactions) detected in the sample, and it is interpreted as an estimate of sample completeness.

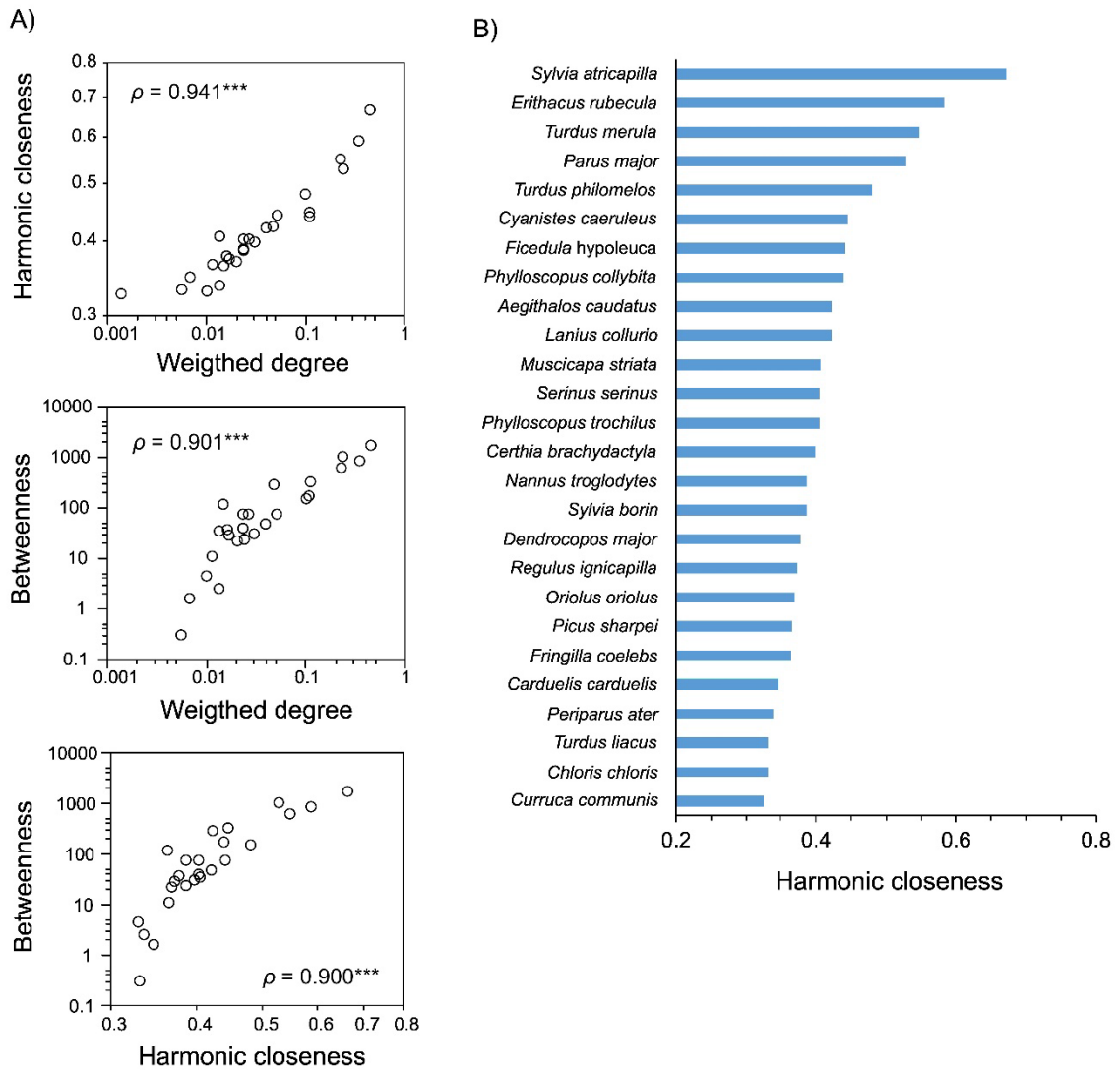




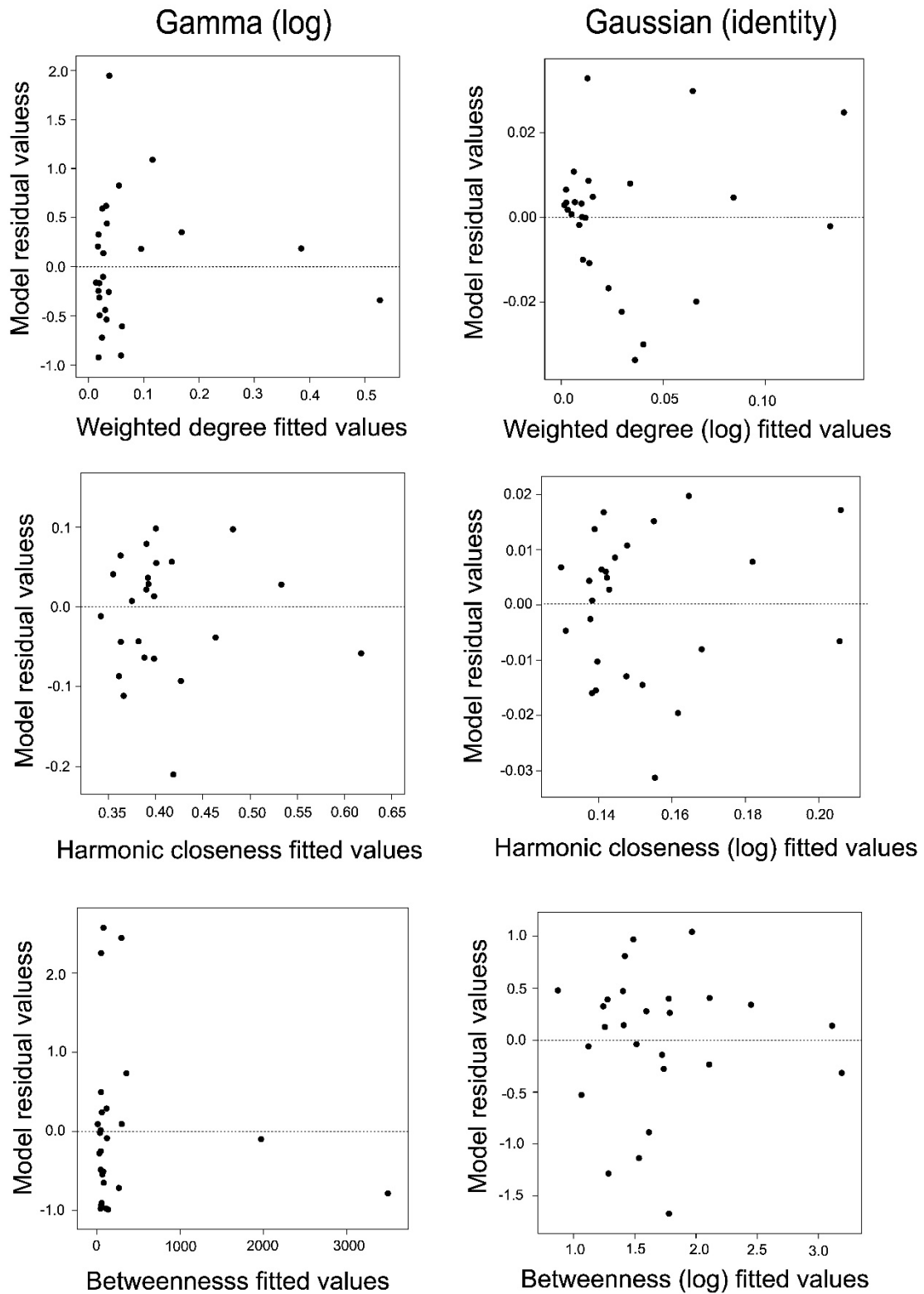
**Figure S4.** Cumulative curves of birds, fleshy-fruited plants, and bird-plant interactions richness and sample coverage, per sampling effort unit (mist-netting days). Dot symbol represents the observed value and the dashed line the extrapolated values expected with higher sampling effort. Shaded area represents 95% confidence intervals. Asymptotic values are shown for richness. Sample coverage values indicate the percentages of the total number of observations belonging to the set of species (or interactions) detected in the sample, and it is interpreted as an estimate of sample completeness.



**Figure S5.** Detailed representation of bipartite networks between pests and birds (pest control). Rectangles in columns correspond to different species, with rectangle height being proportional to species interaction frequencies. Links between rectangles represent paired interactions between species, with link width being proportional to the proportion of interactions. Species and interactions are ordered to highlight modularity (different colors indicate species and links conforming different modules).



**Figure S6.** A) Bivariate representations of centrality measures (weighted degree, harmonic closeness and betweenness, in logarithmic scale) of different bird species. Values of Spearman's correlation coefficient between measures ( $\rho$ ) and their degrees of significance (\*\*\*:  $P < 0.001$ ) are shown. B) Example of distribution of centrality values (harmonic closeness) across bird species.



**Figure S7.** Plots of residual vs fitted values corresponding to different centrality measures (weighted degree, harmonic closeness and betweenness) used as response variables in different Generalized Linear Mixed Models considering Gamma (log link) or Gaussian (identity link, log-transformed data) as distribution family, and bird species relative abundance (percentage of individuals), body mass (g) and diet diversity (inverse Simpson Index) as fixed predictors (see also Table 2 in the main text and Table S3).