

At a global scale, conservation of pollinators and
herbivores between related plants varies widely across
communities and between plant families
Supporting Information

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Notes S1: Sources for networks

Table S1: Original sources for each network used in our analyses. All networks beginning 'M_PL_' were collected from Ortega *et al.* (Accessed Nov. 22, 2019). Further details for unpublished networks may be found there.

Network	Network type	Country	Original source
M_PL_001	Pollination	Chile	Arroyo <i>et al.</i> (1982)
M_PL_002	Pollination	Chile	Arroyo <i>et al.</i> (1982)
M_PL_003	Pollination	Chile	Arroyo <i>et al.</i> (1982)
M_PL_004	Pollination	Canada (New Brunswick)	Barrett & Helenurm (1987)
M_PL_005	Pollination	U.S.A. (Colorado)	Clements & Long (1923)
M_PL_006	Pollination	U.K. (Norfolk)	Dicks <i>et al.</i> (2012)
M_PL_007	Pollination	U.K. (Norfolk)	Dicks <i>et al.</i> (2012)
M_PL_008	Pollination	Spain (Canary Islands)	Dupont <i>et al.</i> (2003)
M_PL_009	Pollination	Sweden	Elberling & Olesen (1999)
M_PL_010	Pollination	Denmark (Greenland)	Elberling, H. & Olesen, J. M. Unpub.
M_PL_011	Pollination	Mauritius	Olesen <i>et al.</i> (2002)
M_PL_012	Pollination	Portugal (Azores)	Olesen <i>et al.</i> (2002)
M_PL_013	Pollination	South Africa (KwaZulu-Natal)	Ollerton <i>et al.</i> (2003)
M_PL_014	Pollination	Canada (N.W.T.)	Hocking (1968)
M_PL_015	Pollination	Greece (Athens)	Petanidou (1991)
M_PL_016	Pollination	Spain (Andalucia)	Herrera (1988)
M_PL_017	Pollination	U.K. (England)	Memmott (2002)
M_PL_018	Pollination	Denmark	Olesen, J. M. Unpublished.
M_PL_019	Pollination	U.S.A. (Colorado)	Inouye & Pyke (1988)
M_PL_020	Pollination	Canada (N.W.T.)	Kevan (1970)
M_PL_021	Pollination	Japan (Kyoto)	Kato <i>et al.</i> (1990)
M_PL_022	Pollination	Argentina (Mendoza)	Medan <i>et al.</i> (2002)
M_PL_023	Pollination	Argentina (Mendoza)	Medan <i>et al.</i> (2002)
M_PL_024	Pollination	Canada (N.W.T.)	Mosquin & Martin (1967)
M_PL_025	Pollination	U.S.A. (North Carolina)	Motten (1986)
M_PL_026	Pollination	Ecuador (Galápagos Islands)	McMullen (1993)
M_PL_027	Pollination	New Zealand (South Island)	Primack (1983)
M_PL_028	Pollination	New Zealand (South Island)	Primack (1983)
M_PL_029	Pollination	New Zealand (South Island)	Primack (1983)
M_PL_030	Pollination	Venezuela	Ramirez & Brito (1992)
M_PL_031	Pollination	Venezuela	Ramirez (1989)

Network	Network type	Country	Original source
M_PL_032	Pollination	U.S.A. (Illinois)	Schemske <i>et al.</i> (1978)
M_PL_033	Pollination	Canada (Ontario)	Small (1976)
M_PL_034	Pollination	Chile	Smith-Ramírez <i>et al.</i> (2005)
M_PL_035	Pollination	Jamaica	Percival (1974)
M_PL_036	Pollination	Portugal (Azores)	Olesen, J. M. Unpublished.
M_PL_037	Pollination	Denmark	Montero (2005)
M_PL_038	Pollination	Denmark	Montero (2005)
M_PL_039	Pollination	Spain (Canary Islands)	Stald (2003)
M_PL_040	Pollination	Jamaica	Ingversen (2006)
M_PL_041	Pollination	Dominica	Ingversen (2006)
M_PL_042	Pollination	Ecuador (Galápagos Islands)	Philipp <i>et al.</i> (2006)
M_PL_043	Pollination	Denmark	Montero (2005)
M_PL_044	Pollination	Japan (Amami Islands)	Kato (2000)
M_PL_045	Pollination	Denmark (Greenland)	Lundgren & Olesen (2005)
M_PL_046	Pollination	Denmark	Bundgaard (2003)
M_PL_047	Pollination	Denmark	Dupont & Olesen (2009)
M_PL_048	Pollination	Denmark	Dupont & Olesen (2009)
M_PL_049	Pollination	Denmark	Bek (2006)
M_PL_050	Pollination	Spain (Canary Islands)	Stald (2003)
M_PL_051	Pollination	Argentina (Río Negro)	Vázquez & Simberloff (2002)
M_PL_052	Pollination	Denmark (Greenland)	Witt (1998)
M_PL_053	Pollination	Japan (Kyusu)	Yamazaki & Kato (2003)
M_PL_054	Pollination	Japan (Kyoto)	Kakutani <i>et al.</i> (1990)
M_PL_055	Pollination	Japan (Fukui Prefecture)	Kato & Miura (1996)
M_PL_056	Pollination	Japan (Yamanashi)	Kato <i>et al.</i> (1993)
M_PL_057	Pollination	Japan (Kibune)	Inoue <i>et al.</i> (1990)
M_PL_058	Pollination	Spain (Catalonia)	Bartomeus <i>et al.</i> (2008)
M_PL_059	Pollination	Brazil (Buíque)	Bezerra <i>et al.</i> (2009)
Basset	Herbivory	Papua New Guinea	Basset & Samuelson (1996)
Blüthgen	Herbivory	Malaysia (Sabah)	Blüthgen <i>et al.</i> (2006)
Bodner	Herbivory	Ecuador	Bodner <i>et al.</i> (2010)
Coley	Herbivory	Panama	Coley <i>et al.</i> (2006)
Ibanez	Herbivory	France (Central French Alps)	Ibanez <i>et al.</i> (2013)
Joern_altuda	Herbivory	U.S.A. (Texas)	Joern (1979)
Joern_marathon	Herbivory	U.S.A. (Texas)	Joern (1979)
Novotny	Herbivory	Papua New Guinea	Novotny <i>et al.</i> (2012)
Peralta	Herbivory	New Zealand (South Island)	Peralta (2016)
Sheldon	Herbivory	U.S.A. (Washington)	Sheldon & Rogers (1978)
Ueckert	Herbivory	U.S.A. (Colorado)	Ueckert & Hansen (1971)

Notes S2: R implementation of tuple-form regression

We first fit a series of regressions (one per network) relating the Jaccard dissimilarity of the interaction partners of plants i and j (J_{ij}) to the phylogenetic distance between them (δ_{ij}), using the form

$$\text{logit}(J_{ij}) \propto \beta_{\text{distance}} \delta_{ij}. \quad (1)$$

We fit these regressions using the R (R Core Team, 2016) base function “glm”, which will accept J_{ij} formatted as either a single value summarizing the probability of sharing an interaction partner *or* the numbers of shared and un-shared interaction partners (M_{ij} and U_{ij}). As we wished to use the tuple (M_{ij}, U_{ij}) as our input, the command in R was:

model=glm(cbind(M_ij,U_ij) ~ scale(delta_ij),family="binomial").

We used the same tuple-input form of the binomial regression for all subsequent regressions.

Notes S3: Repeating our analyses with proportion of shared partners

We repeated some of our analyses using the proportion of shared interaction partners as the response rather than a tuple describing the number of interaction partners that are shared and not shared. This approach is common when performing logistic regressions, but loses information about the varying weights of evidence about different plant pairs. This lost information can limit the power of the regression to detect weak trends.

Across all networks, more distantly-related plants remained less likely to share interaction partners, but this relationship was not significant in herbivory networks ($\beta_{distance} = -1.07$, $p = 0.477$; compare to $\beta_{distance} = -6.82$, $p < 0.001$ in the main text). Plants in pollination networks again tended to share fewer interaction partners overall ($\beta_{pollination} = -0.881$, $p < 0.001$; compare to $\beta_{pollination} = -1.44$, $p < 0.001$ in the main text), and the decrease in overlap with increasing phylogenetic distance was steeper than in herbivory networks ($\beta_{distance:pollination} = -26.8$, $p < 0.001$; compare to $\beta_{distance:pollination} = -18.5$, $p < 0.001$ in the main text). Thus, while we observed the same trends when treating the response as a proportion and as a tuple, the tuple format displayed these trends more clearly. This is likely because of the additional information incorporated in the tuple.

Within networks, using the proportion of shared interaction partners rather than a tuple resulted in significant relationships between phylogenetic distance and overlap in interaction partners in five herbivory networks and seven pollination networks (compare to seven and 34 networks, respectively, in the main text). In each case, the proportion of shared interaction partners decreased with increasing phylogenetic distance. Again, this demonstrates the greater power of a Jaccard regression with a tuple response to capture weak trends. The best-fit models for individual networks show much less variation when framing the response as a proportion (Fig. S1).

Notes S4: A test of connectance

To test whether the relationship between phylogenetic distance and niche overlap depended on connectance, we fit a general linear model for the slope of this relationship inferred from the glm models against connectance (C), network type (again using herbivory networks as a baseline), and their interaction:

$$\beta_{distance} \propto \beta_C \eta_N + \beta_{pollination} I_N + \beta_{C:pollination} \eta_N I_N, \quad (2)$$

where η_N is the number of plant pairs in network N for which distances could be calculated, I_N is an indicator equal to 1 if network N is a pollination network and 0 otherwise.

The strength of the relationship did not depend on network type ($\beta_{pollination}=-0.015$, $p=0.860$), connectance ($\beta_C=-0.652$, $p=0.051$), or their interaction ($\beta_{C:pollination}=0.687$, $p=0.084$). If we removed the interaction term and re-fit the model, the strength of the relationships between phylogenetic distance and niche overlap still did not depend on connectance ($\beta_C=-0.169$, $p=0.356$). We conclude that connectance does not constrain pairwise niche overlap in our dataset.

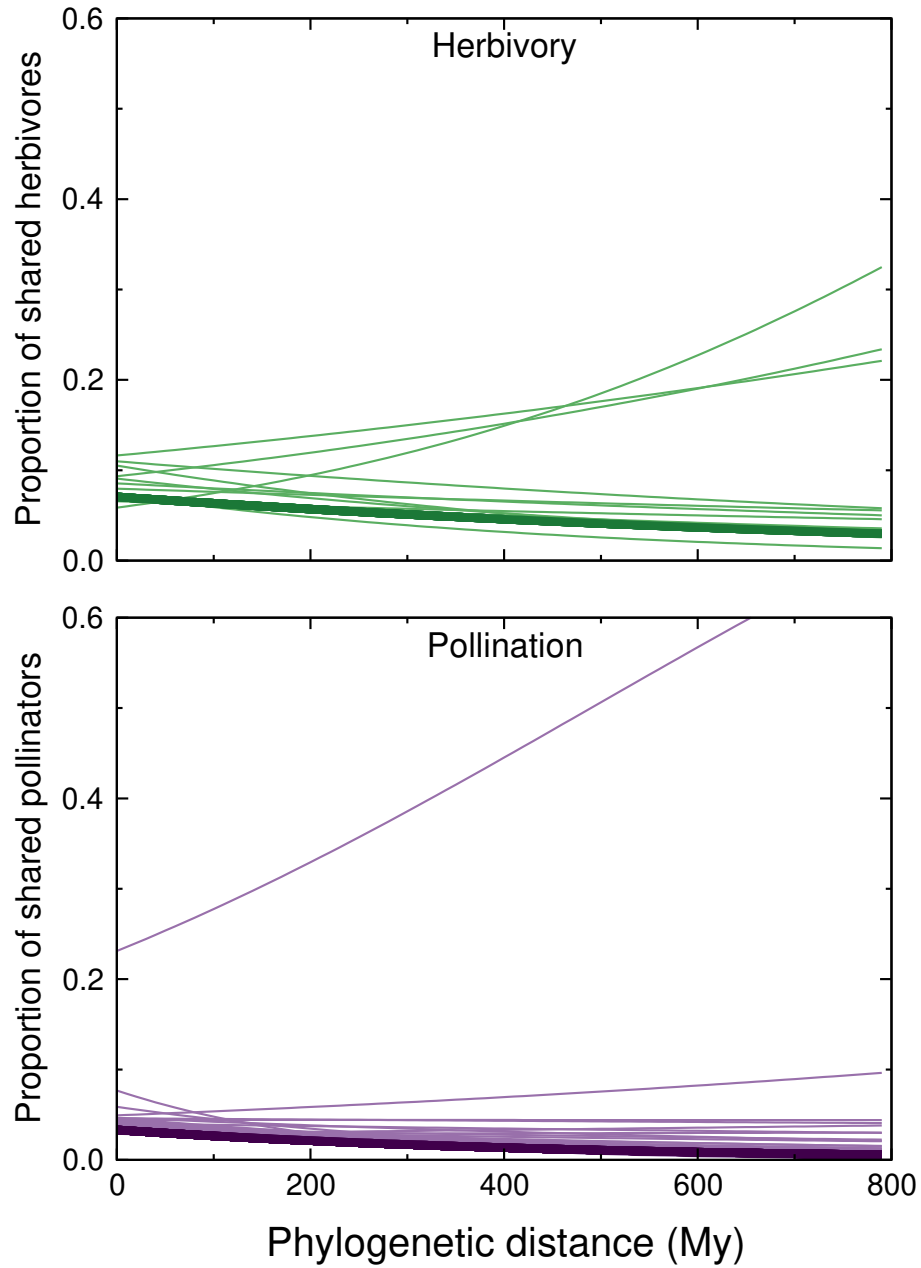


Figure S1: When considering niche overlap as the proportion of shared interaction partners rather than both the number of interaction partners that are shared and not shared, there is much less variability between networks. The overall trends (thicker, darker lines) observed are also much weaker than those detected when using all of the available information. Compare with Fig. 1, main text. Both figures are plotted on the same scale.

Notes S5: Distributions of p -values for permuted networks

Comparing the permuted networks to permutations of the permuted networks, the slope obtained from the initial permuted network showed no clear relationship to the slopes obtained from 500 permutations of the permuted network. Averaged over the 1000 permutations of each observed network, the slope of the permuted network was more extreme than 48.1-51.3% of the permutations of the permuted network. This confirms that shuffling phylogenetic distances between plant pairs destroys the relationship between distance and interaction partner overlap, and that further shuffling distances does not have a predictable effect.

Networks shown in each panel of Figure S2

All names are as in Table S1. Networks included in each panel (from darkest to lightest line colours) are:

- A) M_PL_001, M_PL_002, M_PL_003, M_PL_004, M_PL_005;
- B) M_PL_006, M_PL_007, M_PL_008, M_PL_009, M_PL_010;
- C) M_PL_011, M_PL_012, M_PL_013, M_PL_014, M_PL_015;
- D) M_PL_016, M_PL_017, M_PL_018, M_PL_019, M_PL_020;
- E) M_PL_021, M_PL_022, M_PL_023, M_PL_024, M_PL_025;
- F) M_PL_026, M_PL_027, M_PL_028, M_PL_029, M_PL_030;
- G) M_PL_031, M_PL_032, M_PL_033, M_PL_034, M_PL_035;
- H) M_PL_036, M_PL_037, M_PL_038, M_PL_039, M_PL_040;
- I) M_PL_041, M_PL_042, M_PL_043, M_PL_044, M_PL_045;
- J) M_PL_046, M_PL_047, M_PL_048, M_PL_049, M_PL_050;
- K) M_PL_051, M_PL_052, M_PL_053, M_PL_054, M_PL_055;
- L) M_PL_056, M_PL_057, M_PL_058, M_PL_059;

- M) Ibanez, Joern_altuda, Joern_marathon, Peralta, Sheldon;
N) Ueckert, Basset, Bluthgen, Bodner, Coley, Novotny.

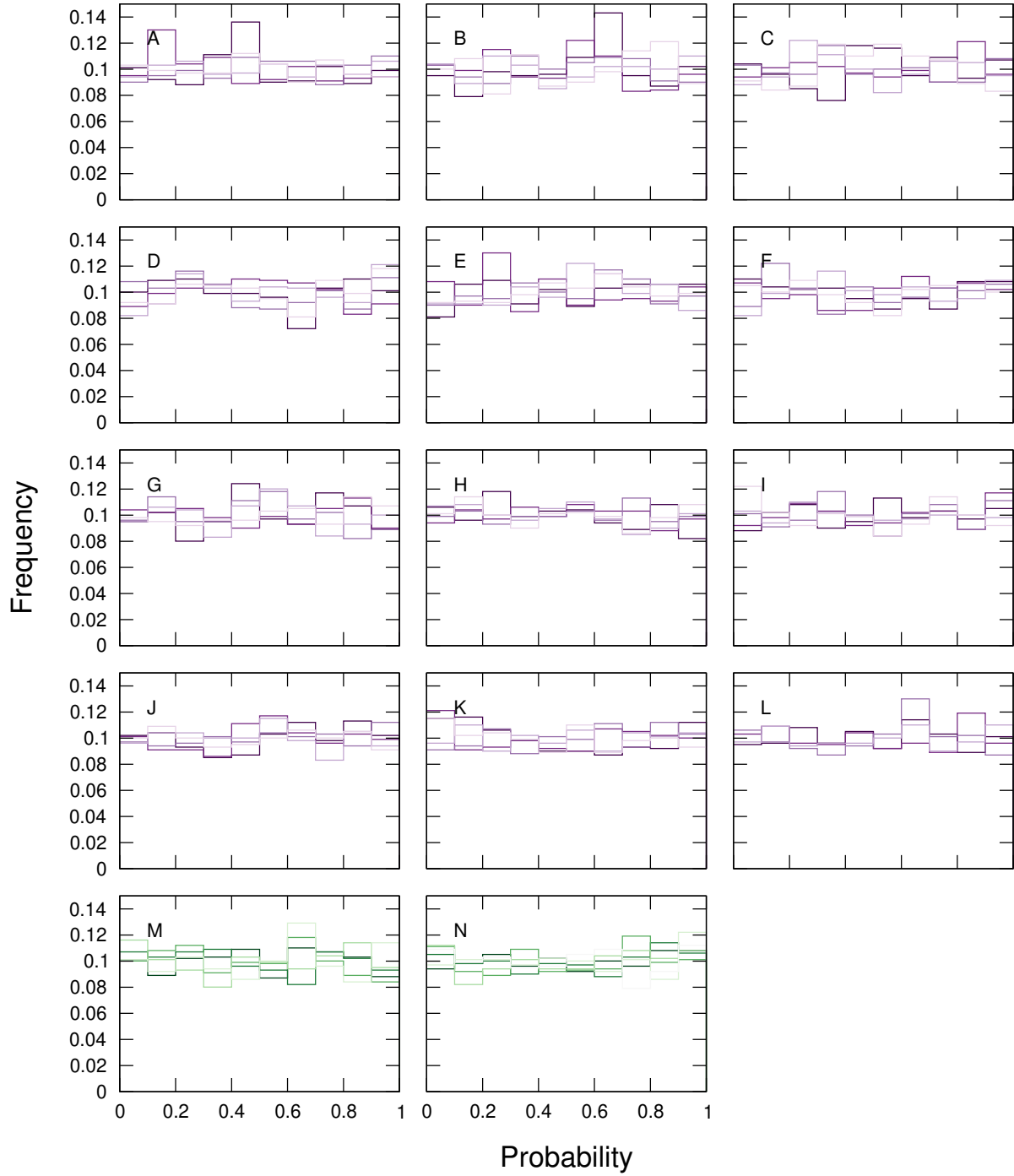


Figure S2: Nearly uniform distributions of p -values where obtained when comparing the strength of the relationship between niche overlap and phylogenetic distance in 999 permutations of each network in our dataset with 500 permutations of each permuted network. Each line in each panel represents the histogram of p -values for one network. Bins are 0.1 wide. Purple lines in panels A-L represent pollination networks while green lines in panels M-N represent plant-herbivore networks. A list of networks shown on each panel follows; see Table S1 for original sources.

Notes S6: Details of within-family regressions

Models for nine families could not be fit because there was no variation in the phylogenetic distance between plants, their numbers of shared interaction partners, or both. These families were *Amaranthaceae*, *Araliaceae*, *Cactaceae*, *Cornaceae*, *Gentianaceae*, *Liliaceae*, *Oxalidaceae*, *Rhamnaceae*, and *Zingiberaceae*. Further, we could not fit a model for *Lauraceae* in pollination networks or *Sapindaceae* in herbivory or pollination networks as only one plant pair in each network type shared any interaction partners.

Only nine families were sufficiently well-represented to fit models for shared herbivores. Five of these were also well-represented in plant-pollinator networks: *Asteraceae*, *Fabaceae*, *Melastomataceae*, *Poaceae*, and *Rubiaceae*. In total, there were 48 families which were well-represented enough to fit models for shared pollinators. Note that singular fits were obtained for *Amaranthaceae*, *Araliaceae*, *Boraginaceae*, *Campanulaceae*, *Caryophyllaceae*, *Ericaceae*, *Geraniaceae*, *Hydrangeaceae*, *Malvaceae*, *Oxalidaceae*, *Primulaceae*, *Saxifragaceae*, and *Verbenaceae*.

To account for multiple testing, we compared the p -values of the significant slopes to critical values in a sequential correlated Bonferroni test (Drezner & Drezner, 2016). This test accounts for the increased likelihood of obtaining at least one significant result by chance when conducting multiple hypothesis tests, but is less conservative and less prone to type II errors than the original Bonferroni test. All p -values remained significant after applying this test (Table S2).

Table S2: Below, we show the ranked p -values for the significant slopes in pollination and herbivory networks side-by-side with the critical values from the SCBT. Any p -value which is less than the corresponding critical value remains significant. We obtained critical values separately for the pollination and herbivory networks.

Family	Network type	p -value	Critical value
<i>Apocynaceae</i>	pollination	0.037	0.05000
<i>Rubiaceae</i>	pollination	0.026	0.03952
<i>Amaryllidaceae</i>	pollination	0.015	0.03656
<i>Apiaceae</i>	pollination	0.006	0.03300
<i>Poaceae</i>	pollination	0.003	0.03009
<i>Asteraceae</i>	pollination	<0.001	0.02784
<i>Boraginaceae</i>	pollination	<0.001	0.02610
<i>Cistaceae</i>	pollination	<0.001	0.02473
<i>Fabaceae</i>	pollination	<0.001	0.02363
<i>Lamiaceae</i>	pollination	<0.001	0.02273
<i>Lauraceae</i>	pollination	<0.001	0.02198
<i>Plantaginaceae</i>	pollination	<0.001	0.02134
<i>Polygonaceae</i>	pollination	<0.001	0.02080
<i>Ranunculaceae</i>	pollination	<0.001	0.02033
<i>Moraceae</i>	herbivory	0.046	0.05000
<i>Nothofagaceae</i>	herbivory	0.022	0.03201
<i>Pinaceae</i>	herbivory	0.020	0.02627
<i>Poaceae</i>	herbivory	0.006	0.02231
<i>Rubiaceae</i>	herbivory	<0.001	0.01952

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