

Conservation of interaction partners between related plants varies widely across communities and between plant families - Supporting Information

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1 Supporting information 1: Sources for networks

Table S1: Original sources for each network used in our analyses.

Network	Network type	Original source
M_PL_001	Pollination	(Arroyo <i>et al.</i> , 1982)
M_PL_002	Pollination	(Arroyo <i>et al.</i> , 1982)
M_PL_003	Pollination	(Arroyo <i>et al.</i> , 1982)
M_PL_004	Pollination	(Barrett & Helenurm, 1987)
M_PL_005	Pollination	(Clements & Long, 1923)
M_PL_006	Pollination	(Dicks & Corbet, 2012)
M_PL_007	Pollination	(Dicks & Corbet, 2012)
M_PL_008	Pollination	(Dupont <i>et al.</i> , 2003)
M_PL_009	Pollination	(Elberling & Olesen, 1999)
M_PL_010	Pollination	Elberling, H. & Olesen, J. M. Unpublished.
M_PL_011	Pollination	(Olesen <i>et al.</i> , 2002)
M_PL_012	Pollination	Olesen, J. M. Unpublished.
M_PL_013	Pollination	(Ollerton <i>et al.</i> , 2003)
M_PL_014	Pollination	(Hocking, 1968)
M_PL_015	Pollination	(Petanidou, 1991)
M_PL_016	Pollination	(Herrera, 1988)
M_PL_017	Pollination	(Mommott, 2002)
M_PL_018	Pollination	Olesen, J. M. Unpublished.
M_PL_019	Pollination	(Inouye & Pyke, 1988)
M_PL_020	Pollination	(Kevan, 1970)
M_PL_021	Pollination	(Kakutani <i>et al.</i> , 1990a)
M_PL_022	Pollination	(Medan <i>et al.</i> , 2002)
M_PL_023	Pollination	(Medan <i>et al.</i> , 2002)
M_PL_024	Pollination	(Martin, 1965)
M_PL_025	Pollination	(Motten, 1986)
M_PL_026	Pollination	(McMullen, 1993)
M_PL_027	Pollination	(Primack, 1983)
M_PL_028	Pollination	(Primack, 1983)
M_PL_029	Pollination	(Primack, 1983)
M_PL_030	Pollination	(Ramirez, 1992)
M_PL_031	Pollination	(Ramirez, 1989)

Network	Network type	Original source
M_PL_032	Pollination	(Schemske <i>et al.</i> , 1978)
M_PL_033	Pollination	(Small, 1982)
M_PL_034	Pollination	(Dmitrieva <i>et al.</i> , 1997)
M_PL_035	Pollination	(Percival, 1974)
M_PL_036	Pollination	Olesen, J. M. Unpublished.
M_PL_037	Pollination	(Montero, 2005)
M_PL_038	Pollination	(Montero, 2005)
M_PL_039	Pollination	(Stald, 2003)
M_PL_040	Pollination	(Ingversen, 2006)
M_PL_041	Pollination	(Ingversen, 2006)
M_PL_042	Pollination	(Philipp <i>et al.</i> , 2016)
M_PL_043	Pollination	(Montero, 2005)
M_PL_044	Pollination	(Kato, 2000)
M_PL_045	Pollination	(Lundgren & Olesen, 2005)
M_PL_046	Pollination	(Bundgaard, 2003)
M_PL_047	Pollination	(Dupont & Olesen, 2009)
M_PL_048	Pollination	(Dupont & Olesen, 2009)
M_PL_049	Pollination	(Bek, 2006)
M_PL_050	Pollination	(Stald, 2003)
M_PL_051	Pollination	(Vázquez & Simberloff, 2002)
M_PL_052	Pollination	(Witt, 1998)
M_PL_053	Pollination	(Yamazaki & Kato, 2003)
M_PL_054	Pollination	(Kakutani <i>et al.</i> , 1990b)
M_PL_055	Pollination	(Kato, 1996)
M_PL_056	Pollination	(Kato <i>et al.</i> , 1993)
M_PL_057	Pollination	(Inoue <i>et al.</i> , 1990)
M_PL_058	Pollination	(Bartomeus <i>et al.</i> , 2008)
M_PL_059	Pollination	(Bezerra <i>et al.</i> , 2009)
Basset	Herbivory	(Basset & Samuelson, 1996)
Bluthgen	Herbivory	(Blüthgen <i>et al.</i> , 2006)
Bodner	Herbivory	(Bodner <i>et al.</i> , 2010)
Coley	Herbivory	(Coley <i>et al.</i> , 2006)
Ibanez	Herbivory	(Ibanez <i>et al.</i> , 2013)
Joern_altuda	Herbivory	(Joern, 1979)
Joern_marathon	Herbivory	(Joern, 1979)
Novotny	Herbivory	(Novotny <i>et al.</i> , 2012)
Peralta	Herbivory	(Peralta, 2016)
Sheldon	Herbivory	(Sheldon & Rogers, 1978)
Ueckert	Herbivory	(Ueckert & Hansen, 1971)

Supporting information 2: 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).

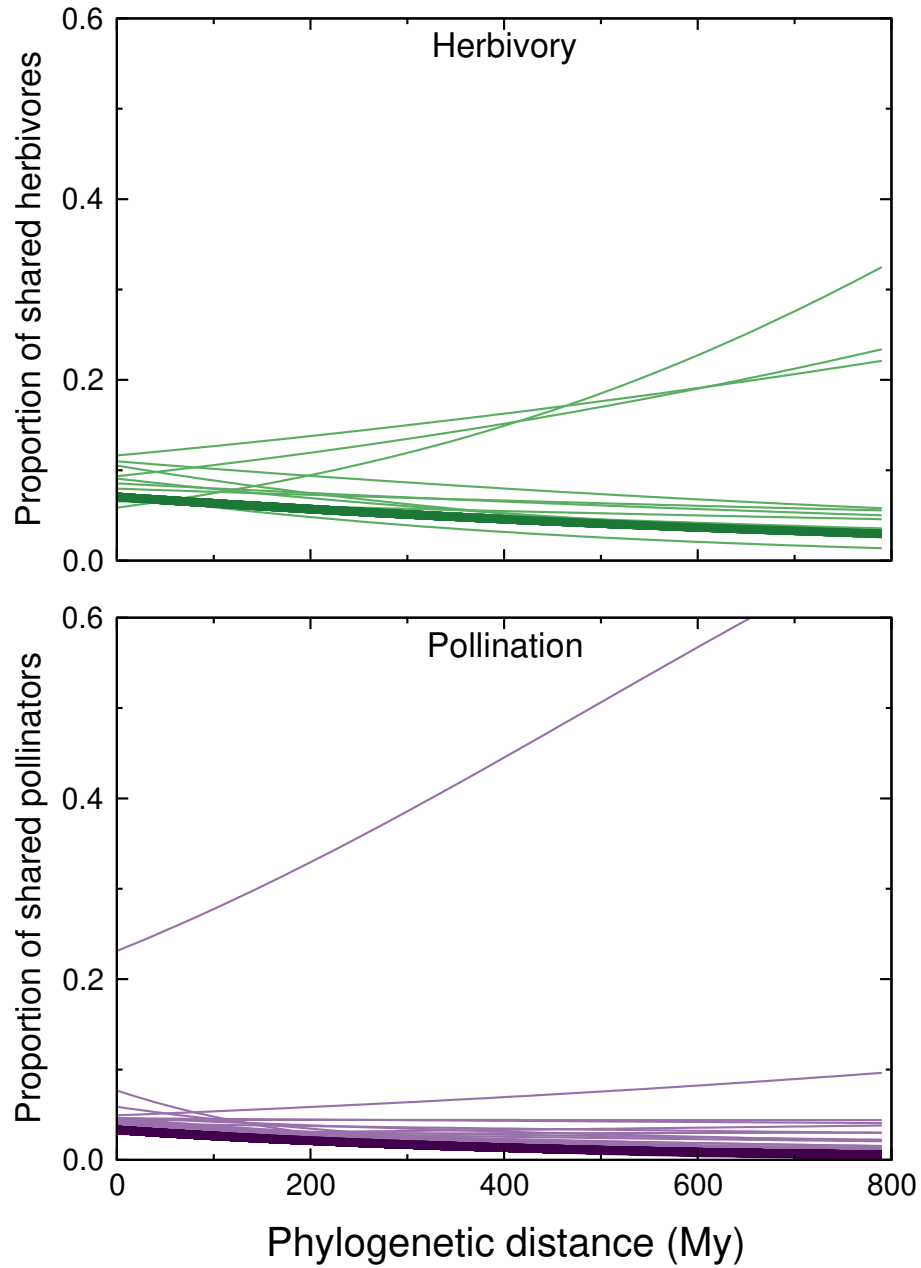


Figure S1: When considering niche overlap as the proportion of shared interaction partners rather than both the number of interaction partners that are shared and not shared, there is much less variability between networks. The overall trends (thicker, darker lines) observed are also much weaker than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

Supporting information 3: 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;

- ⁵² **M)** Ibanez, Joern_altuda, Joern_marathon, Peralta, Sheldon;
⁵³ **N)** Ueckert, Basset, Bluthgen, Bodner, Coley, Novotny.

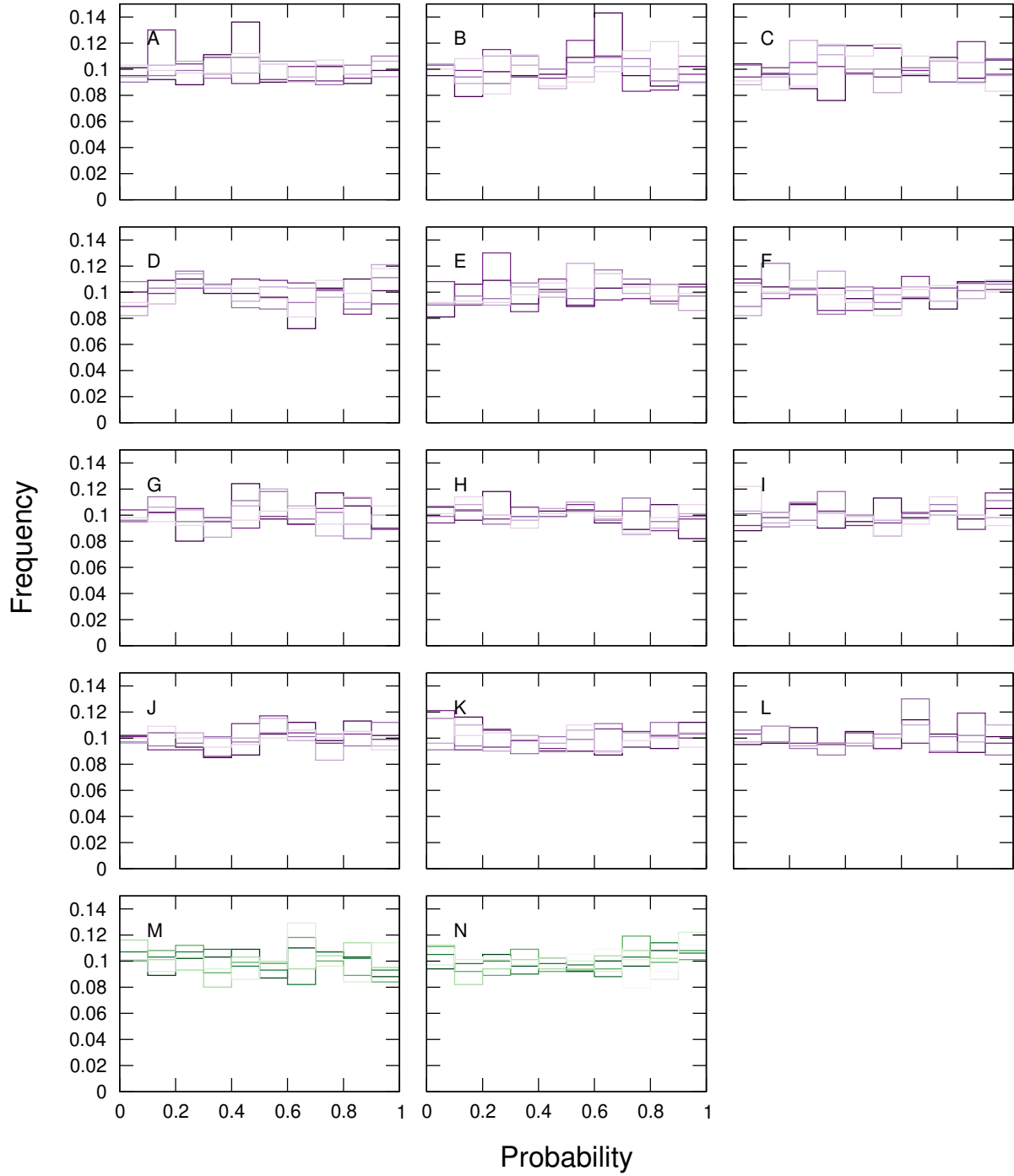


Figure S2: Nearly uniform distributions of p -values where obtained when comparing the strength of the relationship between niche overlap and phylogenetic distance in 999 permutations of each network in our dataset with 500 permutations of each permuted network. Each line in each panel represents the 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.

Supporting information 4: 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*.

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