

Supplementary information for:

Covariation among reproductive traits in flowering plants shape their interactions with pollinators

Jose B. Lanuza*, Romina Rader, Jamie Stavert, Liam K. Kendall, Manu E. Saunders and Ignasi Bartomeus

*Corresponding author E-mail: barragansljose@gmail.com

This pdf includes:

Appendix S1 (text)

Tables S1 to S5

Figures S1 to S10

Appendix S1

Description of the traits compiled in this study

Here we describe the different individual traits that have been included in the database:

Reproductive biology traits

- Breeding system: All species were classified in hermaphrodite, dioecious and monoecious species. Intermediate breeding systems or more complex ones were also annotated but all the species were divided into these three main categories for simplicity of the analysis.
- Selfing level: We recorded the selfing level of the different species with both quantitative and qualitative data. The qualitative data was divided in four main categories, high selfers (76% to 100% of selfing), medium selfers (26% to 75%), low selfers (1% to 25%) and none (0%) which was for the species that were unable to self-pollinate. The quantitative column of selfing had a high percentage of missing values (68%) but we were able to solve this by converting the four categories from the qualitative column to numerical. For this, we considered the mean value of the different categories, that is the categories of ‘none’, ‘low’, ‘medium’ and ‘high’ represented 0%, 13%, 50.5% and 88% of selfing, respectively. This reduced the percentage of missing of this column from 68% to 35% and allowed the imputation of this variable.
- Compatibility system: The different species were divided in three main categories in order to know their ability to self-pollinate. These categories were self-compatible, partially self-compatible and self-incompatible species. The field of selfing level is partly complementary to the compatibility system but is important to note that not all the self-compatible species or partially self-compatible species will self-pollinate.

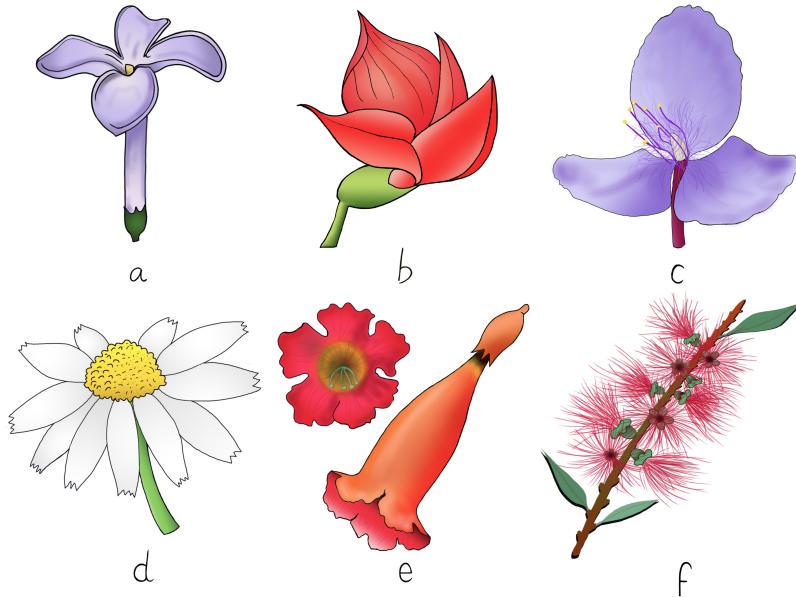
Floral traits

- Flower symmetry: Depending on the possible number of identical divisions of a flower,

plant species were classified into zygomorphic (bilaterally symmetrical with only two identical parts) and actinomorphic (radially symmetrical with more than three identical parts).

- Flower and inflorescence size: We searched for flower length and flower and inflorescence width (mm) for all species. When possible, we calculated the not found measurements with the help of online images and the software ImageJ. Note that for species with compound flowers (e.g., Asteraceae) or similar floral structures with flower heads with many small flowers we considered the inflorescence as the floral unit. For each species this is indicated in the dataset with the field of “info_level” where the measurement level is specified as capitulum or flower level. Note that for some Asteraceae species information about the disc and ray floret is also provided in the database but these were not included in our analyses.
- Flower number per plant: We compiled information about the number of flowers per plant for all species. However, this field was rare to find and we also used online images of the different species in order to calculate rough numbers of flowers per plant. We referenced all the filled fields in order to be able to follow the images that were used for these counts. It is important to note, that these numbers are not pretended to be the exact number of flowers per species but an approximate indicator of the reproductive investment for the different species that allow the macroecological analysis of this field.
- Ovule number: We searched for the number of ovules per flower for all the different species. The number of ovules of Asteraceae species are considered as the total number of ovules per capitulum. Many species were filled by genus or family level because the number of ovules of some taxonomic groups is considered to be mostly constant (e.g., Lamiaceae, Boraginaceae or Apiaceae).
- Flower morphology: We looked for images and illustrations of the flowers from the different species on the floras and available resources in order to categorize the flower

shape. We divided the flowers in 8 main different categories: open, bowl, tube, campanulate, funnelform, papilionaceous, brush and capitulum. However, we ended up grouping all flowers on the following 6 morphological groups for analyses: tube, papilionaceous, open, capitulum, campanulate and brush (Supplementary Information Text Fig. 1).



Supplementary Information Text Fig. 1. Main floral morphologies considered in this study. All species were grouped within these categories for analysis: (a) tube, (b) papilionaceous, (c) open, (d) capitulum, (e) campanulate and (f) brush.

- Style length: We searched for the length of the style (the pistil excluding the ovary and the stigma) in millimeters for all plant species. When the information about style length was missing, we tried to calculate it from images and illustrations from online resources (e.g., floras).
- Nectar provision: We recorded the presence and absence of nectar for all species. In addition, we also searched for microlitres and milligrams of nectar per flower. For species that did not have nectar information but belonged to a family that is considered as ‘nectarless’, this trait was recorded at family level and the species was recorded with ‘absence’ of nectar. This was done exclusively for well documented nectarless taxonomical

groups. For the field of microlitres of nectar, we considered single measurements of nectar standing crop. Despite the timing and methodology of the different quantitative measurements of nectar differed across studies, these fields allowed us to have an approximate idea of the reproductive investment of the different plant species to attract pollinators.

- Pollen grains per flower: For each species, we searched for the total number of pollen grains per flower. Because this fields was rarely available, we also tried to recover from pollen:ovule ratio information the total number of pollen grains by multiplying it by the average ovule number found for each species.

Other life history traits

- Life form, life span and plant height: We divided the different plant species in 4 main categories: herbs, vines, shrubs and trees. Moreover, we also divided the species between short-lived species (annual, biennial and short-lived perennials) and perennial species (long-lived). Finally, we also searched for the average height (m) of the different species and annotated the maximum and minimum height when possible. We conducted the average between the maximum and minimum height to get an approximate average height of the species when the average was not indicated.

Table S1. List of the 28 plant-pollinator studies used to build the plant trait database. Each study is shown with the first author that conducted the study, number of networks or metawebs that contains, type of information that contains (weighted or unweighted), the structure (web or metaweb), year of publication and digital object identifier or permanent link for each study.

First author	Year	Web N.	Network type	DOI
Arroyo-Correa	2019	3	Weighted web	https://doi.org/10.1111/1365-2745.13332
Bartomeus	2008	6	Weighted web	https://doi.org/10.1007/s00442-007-0946-1
Bartomeus	2008	16	Weighted web	https://github.com/ibartomeus/BeeFunData
Bek	2006	1	Unweighted web	Unpublished, Master thesis
Bundgaard	2003	1	Weighted web	Unpublished, Master thesis
Burkle	2013	1	Weighted web	https://doi.org/10.1126/science.1232728
Dicks	2002	2	Weighted web	https://doi.org/10.1046/j.0021-8790.2001.00572.x
Dupont	2003	3	Weighted web	https://doi.org/10.1111/j.1365-2656.2008.01501.x
Elberling	1999	1	Weighted web	https://doi.org/10.1111/j.1600-0587.1999.tb00507.x
Fang	2008	1	Weighted web	https://doi.org/10.1111/1749-4877.12190
Inouye	1988	1	Weighted web	https://doi.org/10.1111/j.1442-9993.1988.tb00968.x
Inouye	1990	1	Weighted metaweb	http://hdl.handle.net/2433/156099

(continued)

First author	Year	Web N.	Network type	DOI
Kaiser-Bunbury	2017	8	Weighted web	https://doi.org/10.1038/nature21071
Kaiser-Bunbury	2011	6	Weighted web	https://doi.org/10.1111/j.1365-2745.2010.01732.x
Kaiser-Bunbury	2010	2	Weighted web	https://doi.org/10.1016/j.ppees.2009.04.001
Kato	2000	1	Unweighted web	http://hdl.handle.net/2433/156116
Kevan	1970	1	Unweighted web	https://doi.org/10.2307/2258569
Lundgren	2005	1	Weighted web	https://doi.org/10.1657/1523-0430(2005)037[0514:TDAHCW]2.0.CO;2
McMullen	1993	1	Unweighted metaweb	https://biostor.org/reference/244737
Olesen	2002	2	Weighted web	https://doi.org/10.1046/j.1472-4642.2002.00148.x
Peralta	2006	4	Weighted web	https://doi.org/10.1111/ele.13510
Primack	1983	3	Unweighted metaweb	https://doi.org/10.1080/0028825X.1983.10428561
Ramirez	1989	1	Unweighted web	https://doi.org/10.2307/2388282
Ramirez	1992	1	Unweighted metaweb	https://doi.org/10.1111/j.1095-8339.1992.tb00294.x
Robertson	1929	1	Unweighted metaweb	https://doi.org/10.5962/bhl.title.11538
Small	1976	1	Weighted web	/13960/t4km08d21

(continued)

First author	Year	Web N.	Network type	DOI
Souza	2017	1	Weighted web	https://doi.org/10.1111/1365-2745.12978
Traveset	2013	1	Weighted metaweb	https://doi.org/10.1098/rspb.2012.3040

Table S2. Statistical association between the different categorical variables and the first three main axes of trait variation with the full set of species.

Functional traits	Sum Sq	F value	Pr(>F)	PC
Breeding system	304.59	119.50	0.00	PC1
Compatibility system	89.12	23.31	0.00	PC1
Lifespan	35.65	27.97	0.00	PC1
Life form	565.87	222.00	0.00	PC1
Flower shape	132.24	20.75	0.00	PC1
Flower symmetry	0.37	0.29	0.59	PC1
Nectar provision	0.38	0.29	0.59	PC1
Breeding system	304.59	119.50	0.00	PC2
Compatibility system	89.12	23.31	0.00	PC2
Lifespan	35.65	27.97	0.00	PC2
Life form	565.87	222.00	0.00	PC2
Flower shape	132.24	20.75	0.00	PC2
Flower symmetry	0.37	0.29	0.59	PC2
Nectar provision	0.38	0.29	0.59	PC2

Table S3. Loadings of the first three axes of trait variation of the phylogenetic informed principal component analysis with the full set of species.

	PC1	PC2	PC3
Autonomous selfing	0.03	0.85	-0.51
Flowers per plant	0.75	-0.27	-0.24
Flower width	-0.67	-0.38	-0.30
Style length	-0.34	-0.37	-0.66
Ovule number	-0.53	0.00	-0.02
Plant height	0.56	-0.40	-0.46
Explained variation	26.72	25.08	19.17

Table S4. Loadings of the first three axes of trait variation of the phylogenetic informed principal component analysis with the subset of species with data of nectar and pollen quantity.

	PC1	PC2	PC3
Autonomous selfing	-0.05	0.78	0.37
Flowers per plant	0.53	-0.49	0.42
Flower width	-0.74	-0.27	-0.13
Style length	-0.60	-0.30	0.11
Ovule number	-0.59	0.11	-0.08
Plant height	0.26	-0.60	0.47
Microlitres of Nectar per flower	-0.49	0.05	0.71
Pollen per flower	-0.29	-0.45	-0.13
Explained variation	23.42	21.13	14.84

Table S5. Phylogenetic signal of the different quantitative traits.

Functional traits	Lambda	P-value
Autonomous selfing	0.34	0.00
Flower number	0.69	0.00
Inflorescence width	0.57	0.00
Flower width	0.73	0.00
Flower length	0.75	0.00
Style length	0.49	0.00
Ovule number	1.00	0.00
Plant height	0.96	0.00
Nectar per flower (μ l)	0.14	0.00
Pollen grains per flower	1.00	0.00

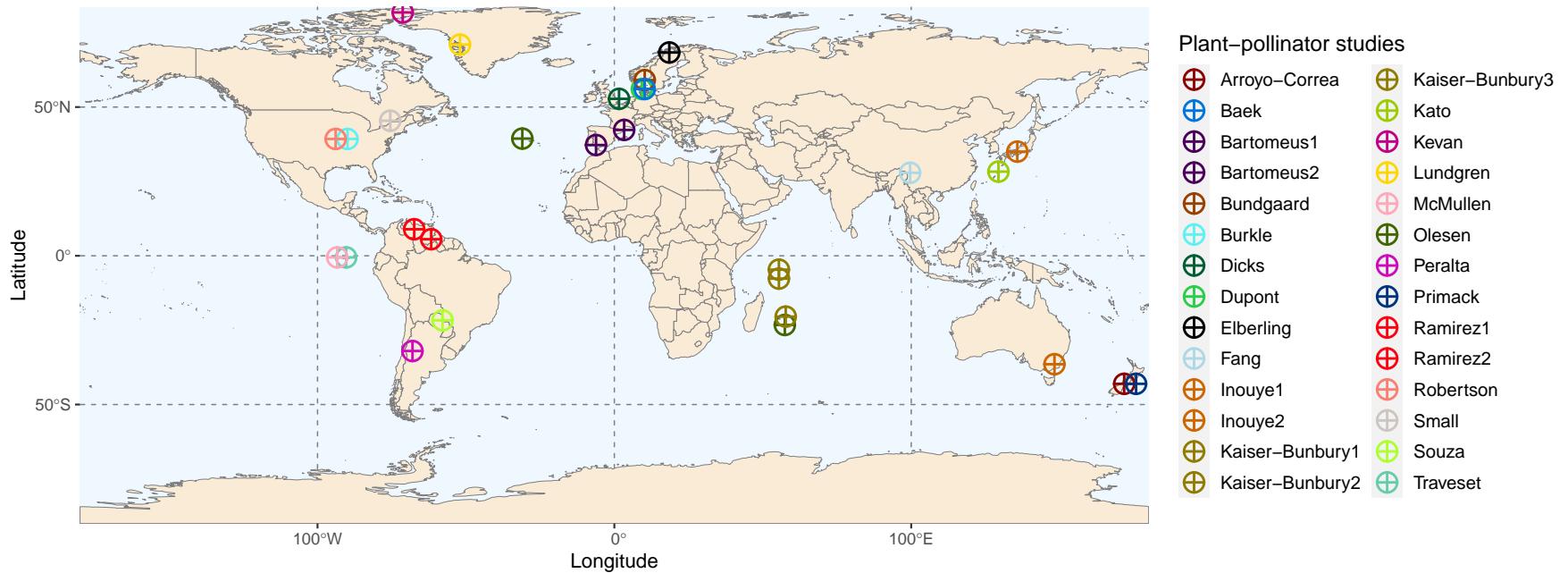


Fig. S1. Map with the different locations of the plant-pollinator studies used in this work to explore worldwide patterns at the meso-scale level. Note that for visualization purposes studies from the same authors are shown with the same colour.

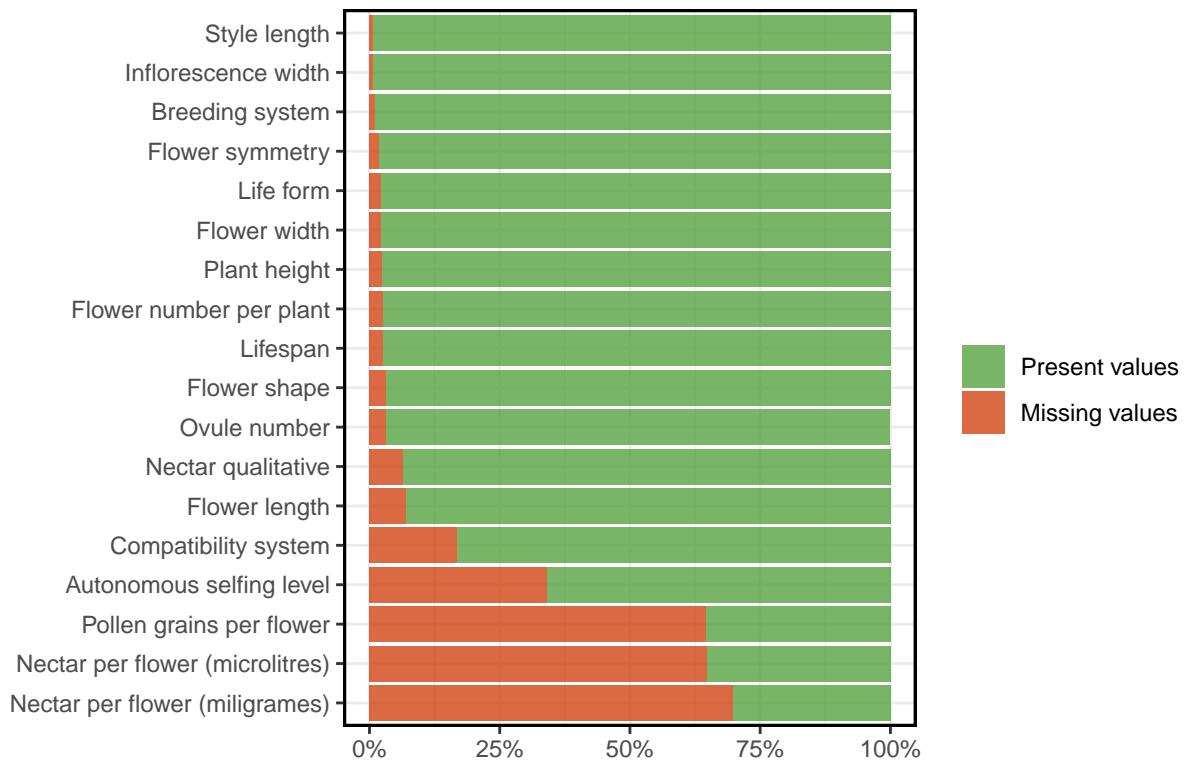


Fig. S2. Percentage of present and missing values of the different plant traits.

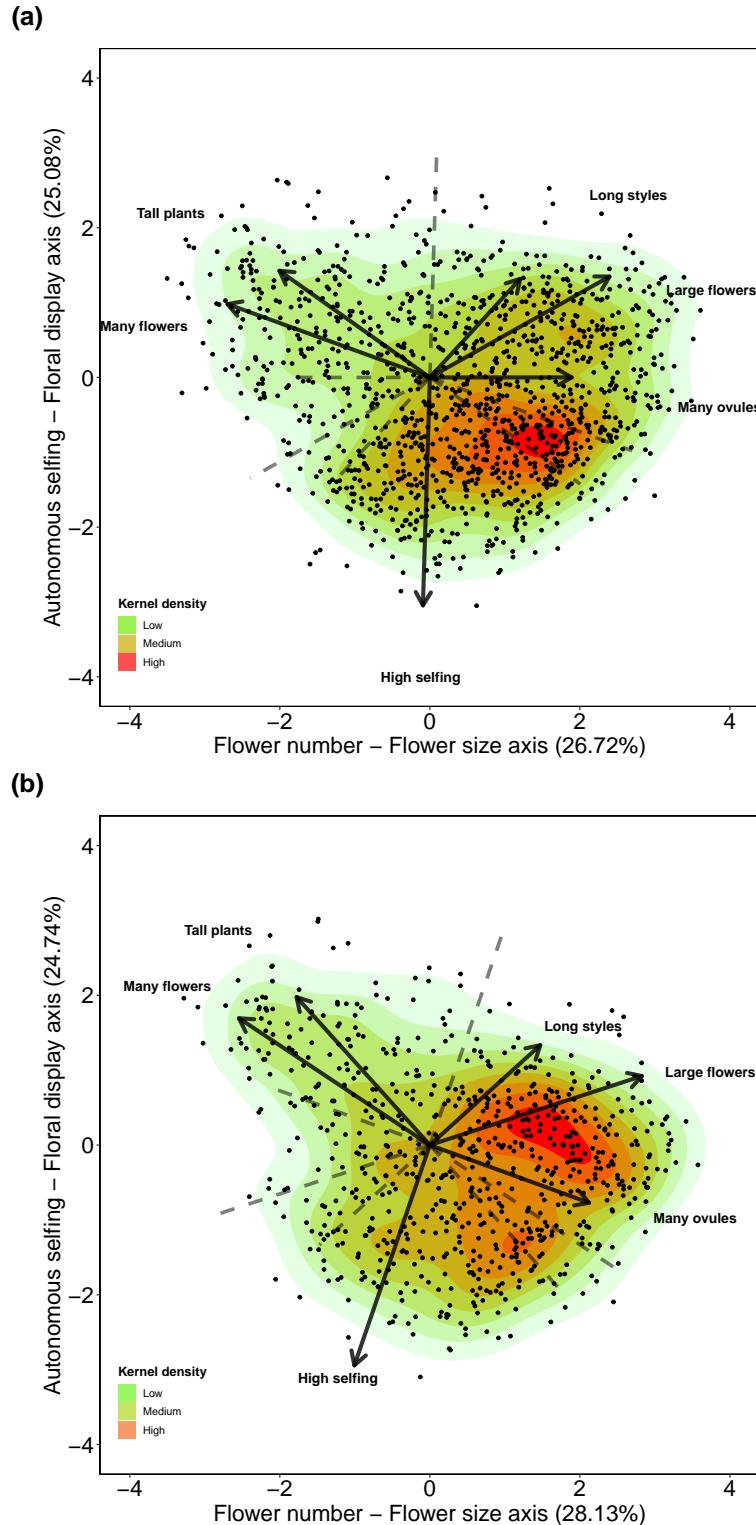


Fig. S3. Comparison of the phylogenetic informed principal component analysis for the dataset with data imputation and without data imputation. Panel 'a' shows the reproductive spectrum of trait variation for the full dataset with data imputation and panel 'b' shows the reproductive spectrum for the dataset without data imputation where the species with missing trait data were excluded from the analysis.

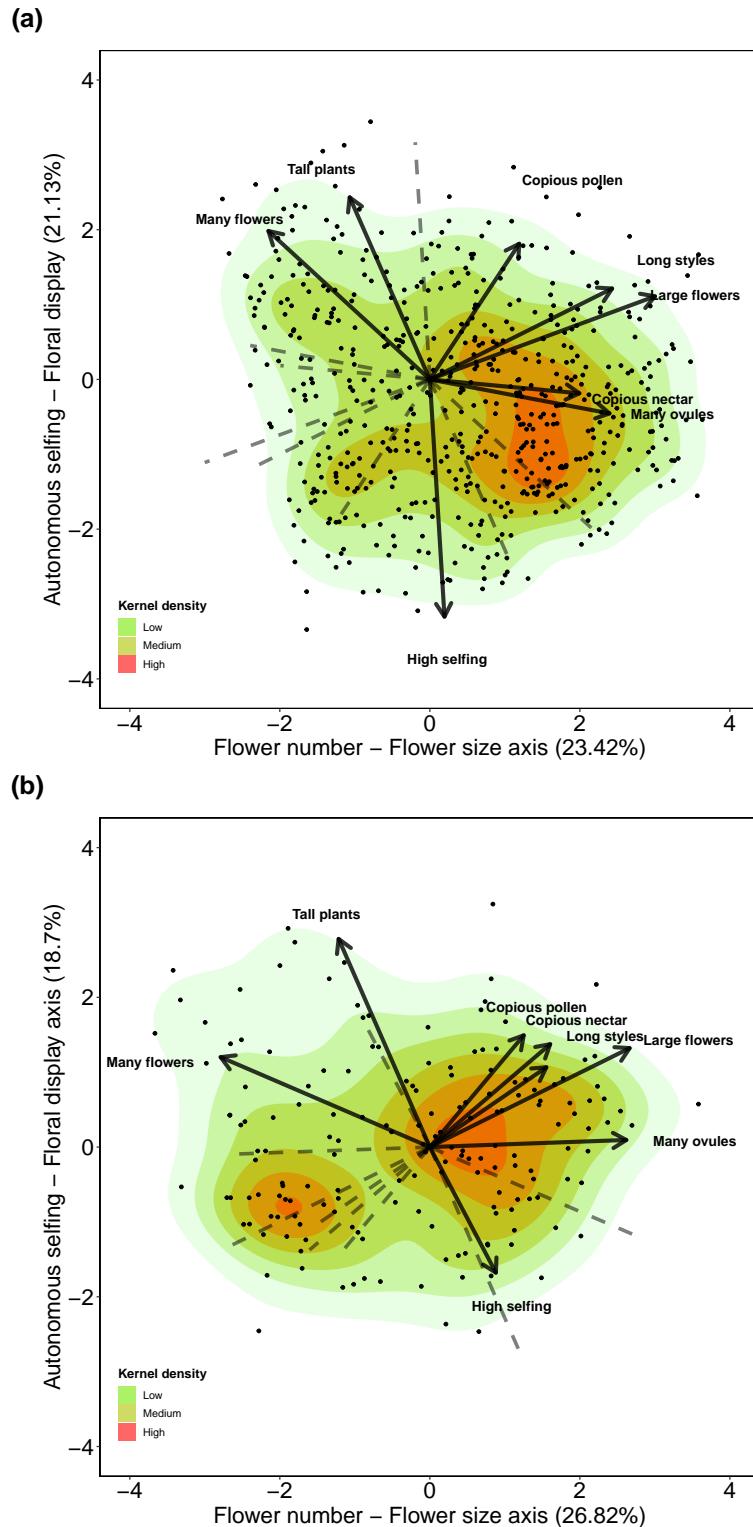


Fig. S4. Comparison of the phylogenetic informed principal component analysis for the subset of species that had information of floral rewards with data imputation and without data imputation. Panel A shows the reproductive spectrum of trait variation for the dataset with data imputation and panel B shows the reproductive spectrum for the dataset excluding species with missing trait data

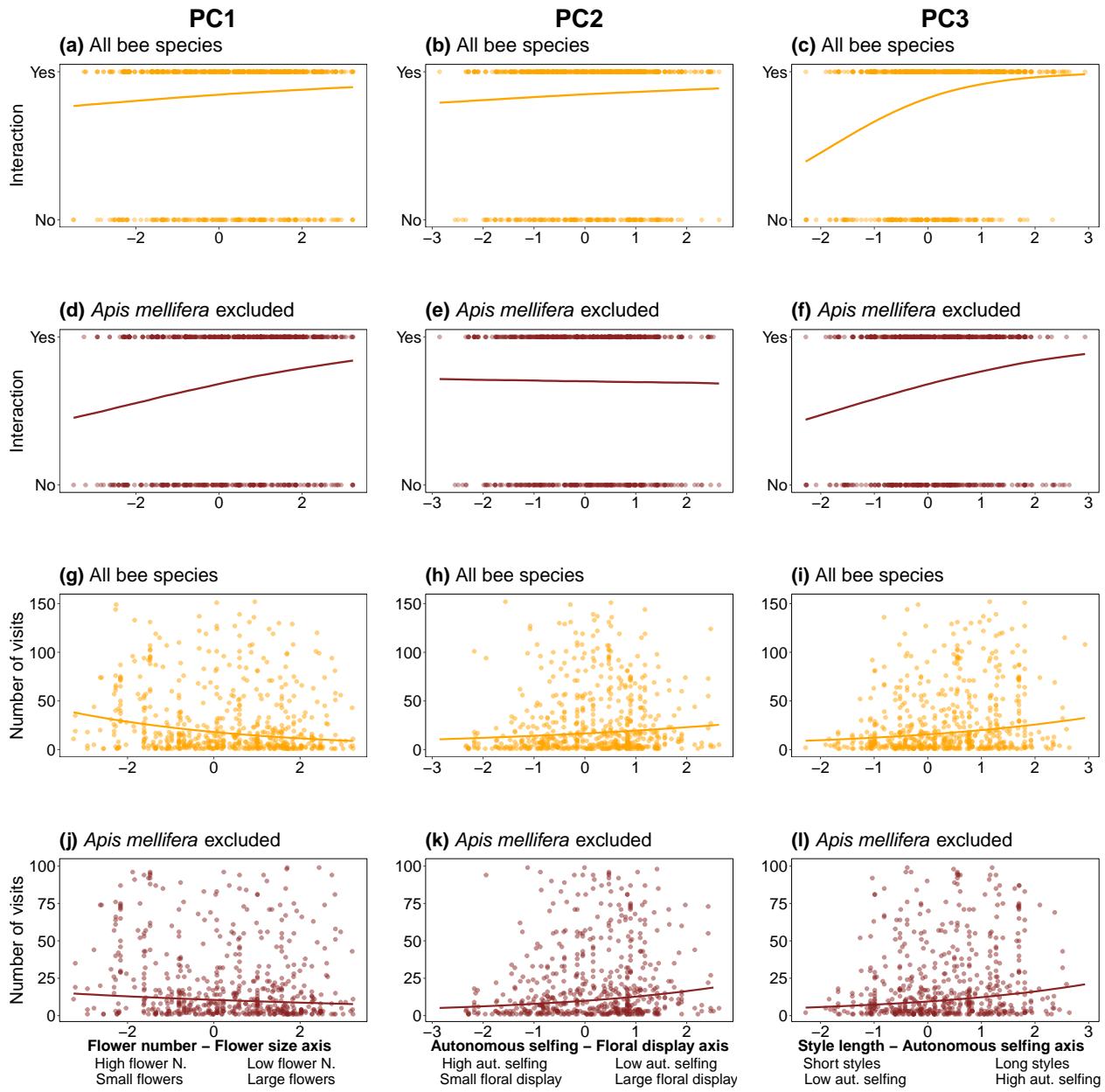


Fig. S5. Fitted posterior estimates of the interaction (yes/no) and number of visits made by bees including and excluding honey bees on the main axes of trait variation. The superior panel (plots a, b c, d, e and f) shows the comparison for presence-absence and the lower panel (plots g, h, i, j, k and l) the comparison for visitation rates.

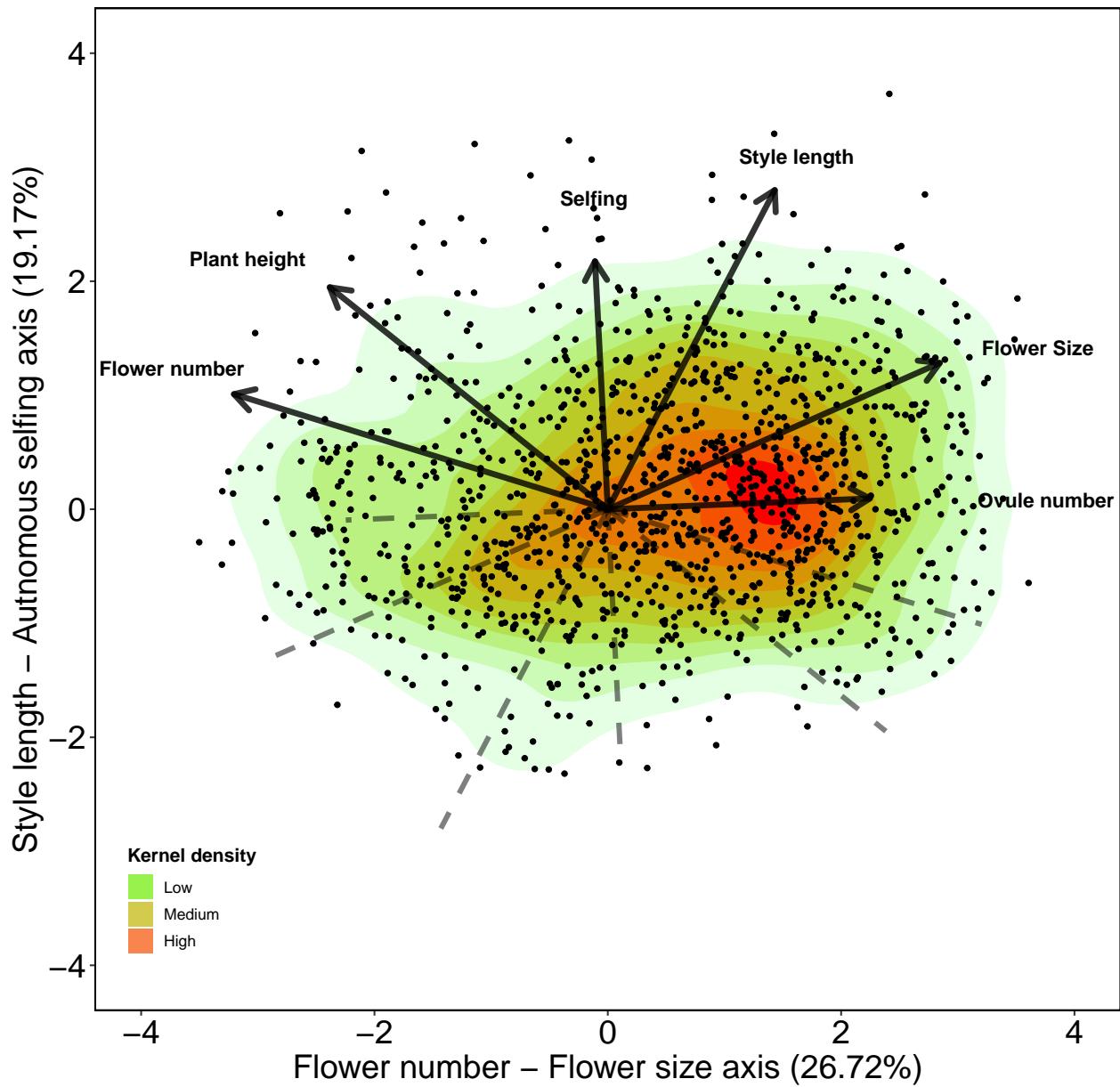


Fig. S6. Phylogenetically informed principal component analysis (pPCA) for all plant species with the first (flower number - flower size axis) and third (style length - autonomous selfing) principal component that explained most trait variation.

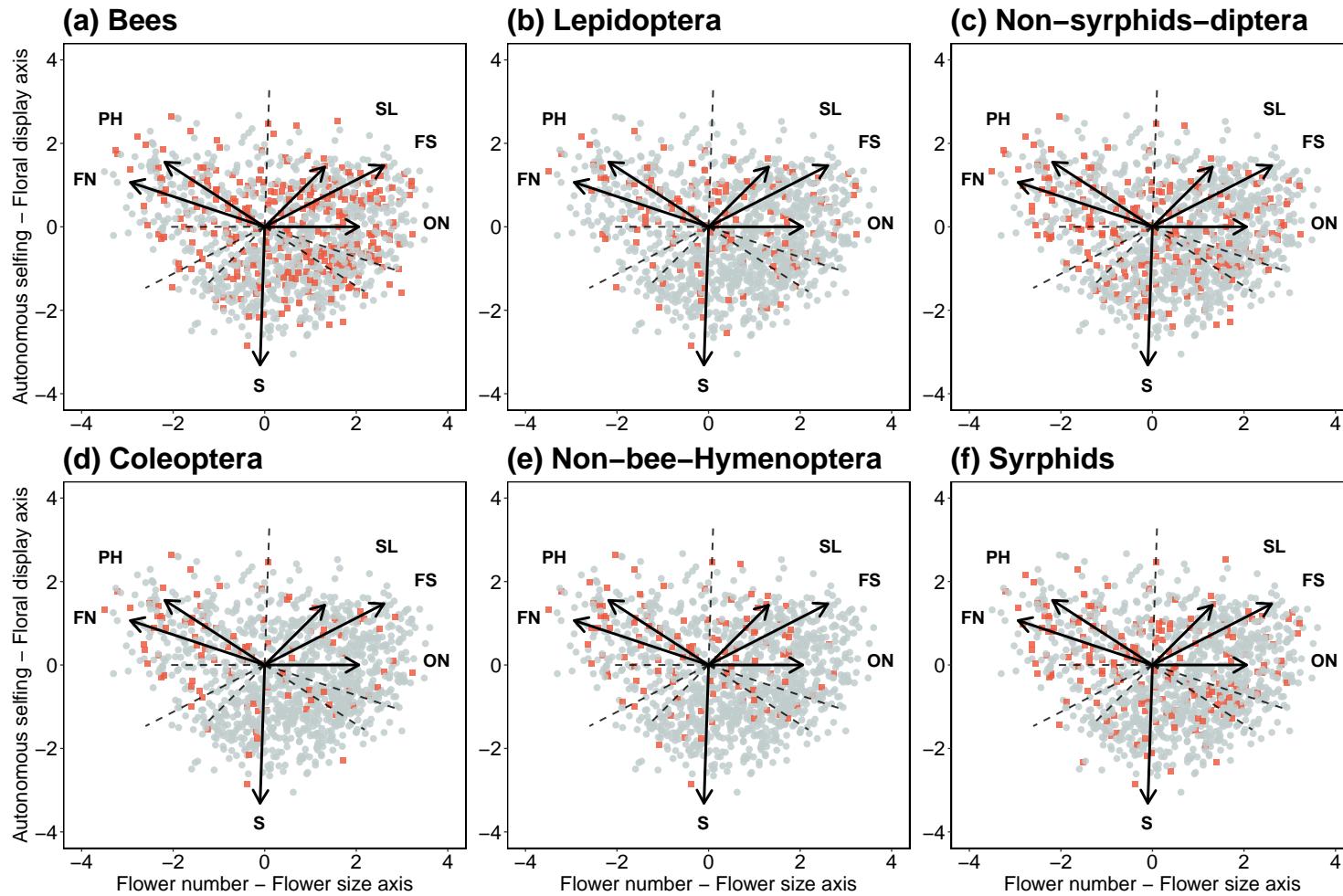


Fig. S7. Location in the trait space of the plants that were visited by each of the different pollinator guilds. The red square indicates that the pollinator guild has been observed in that specific plant. Note that the interactions used to represent the plant-pollinator guild connection are a subset of the total interactions considered in this study as indicated in the Network analysis section (see main text).

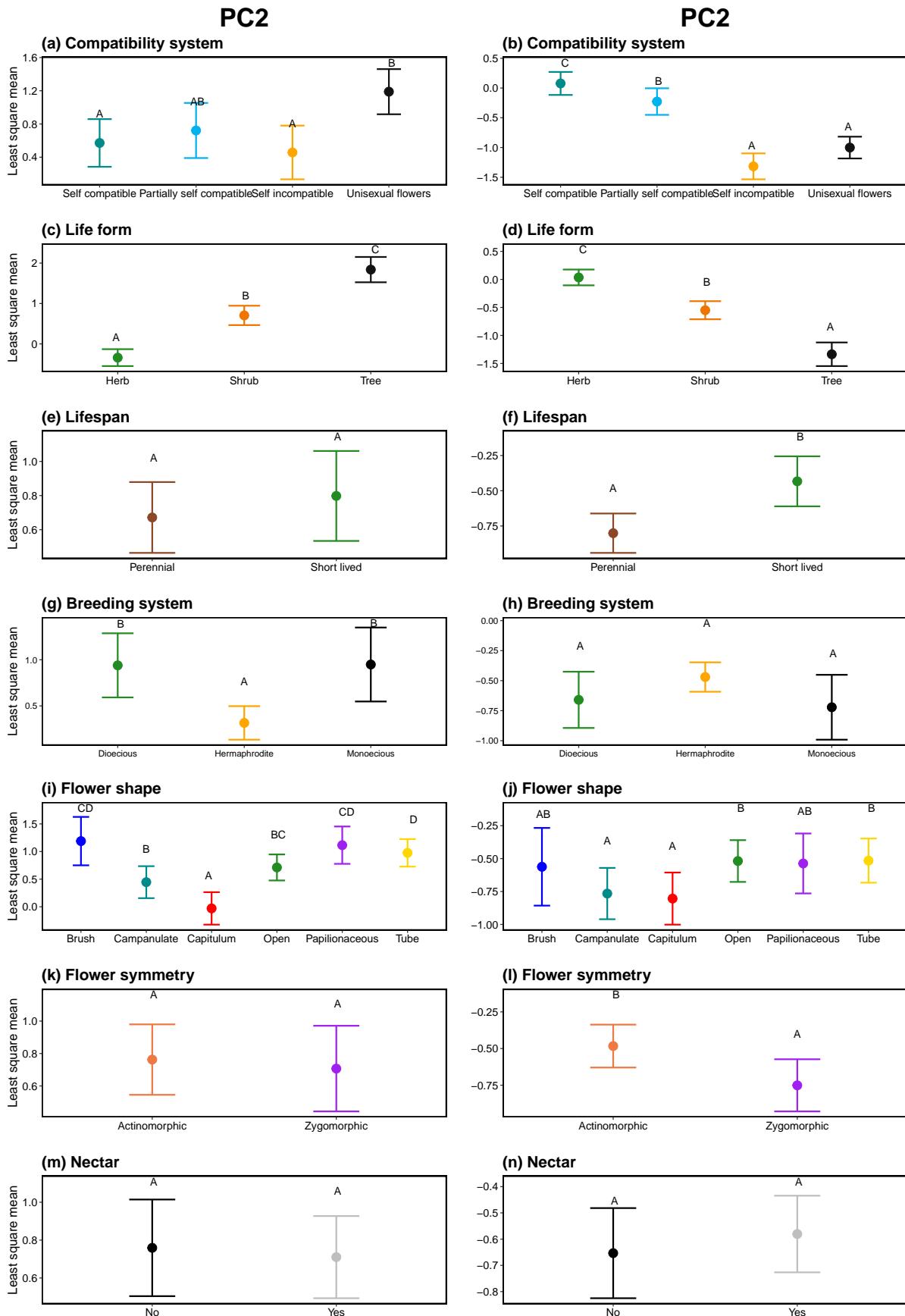


Fig. S8. Statistical comparison of the different categories of qualitative traits on the main two axes of trait variation with the full set of species. Categories that differ significantly are denoted with a different letter.

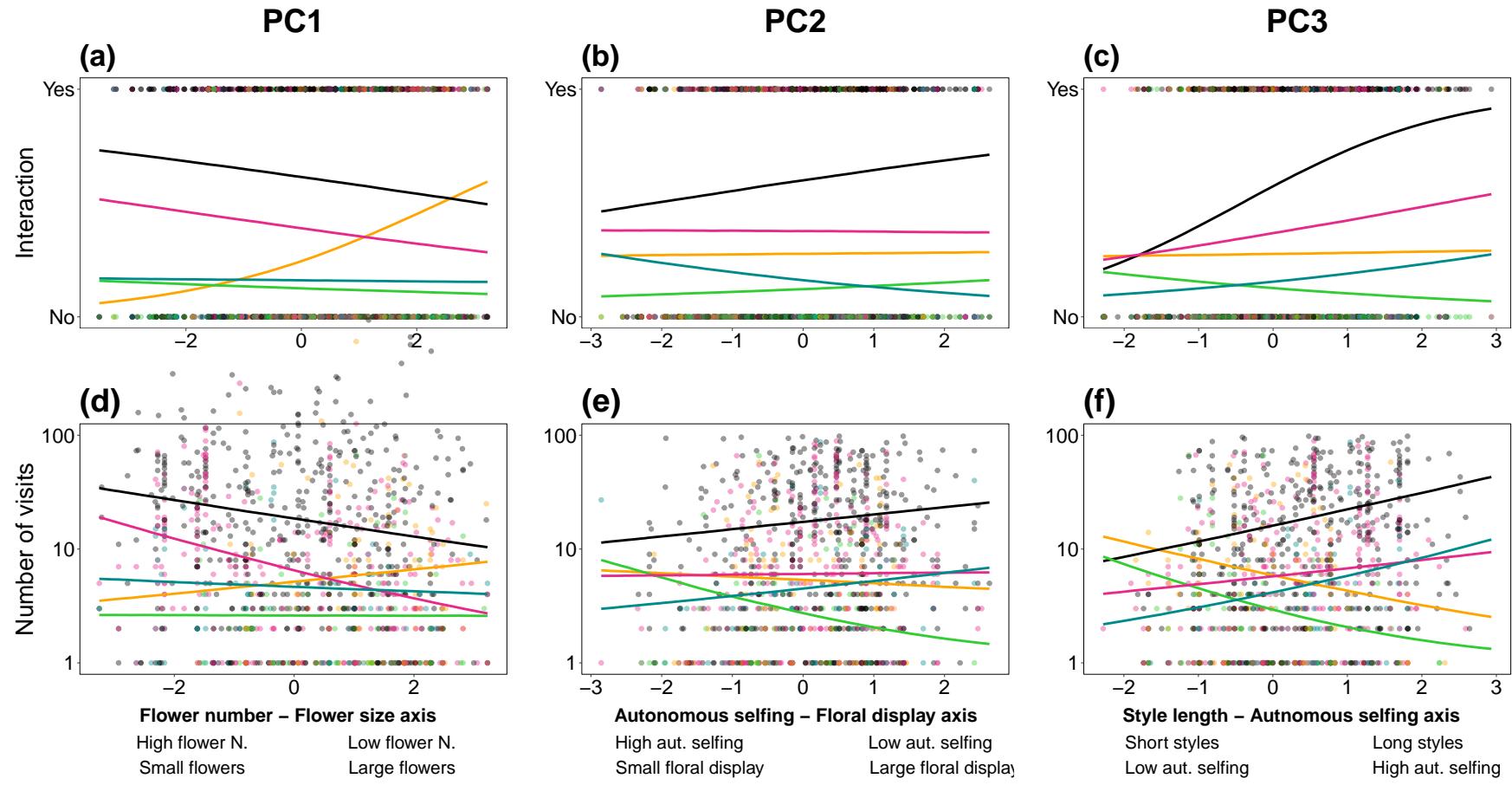


Fig. S9. Interaction (yes/no) and visitation rate of the main bee families on the main axes of trait variation. Fitted posterior estimates of the presence-absence of interaction (plots a, b and c) and visitation rate (plots e, f and g) of Andrenidae, Apidae, Colletidae, Halictidae and Megachilidae across PC1, PC2 and PC3. For visualization purposes, the response variable of number of visits was log-transformed (Y-axis of lower panel).

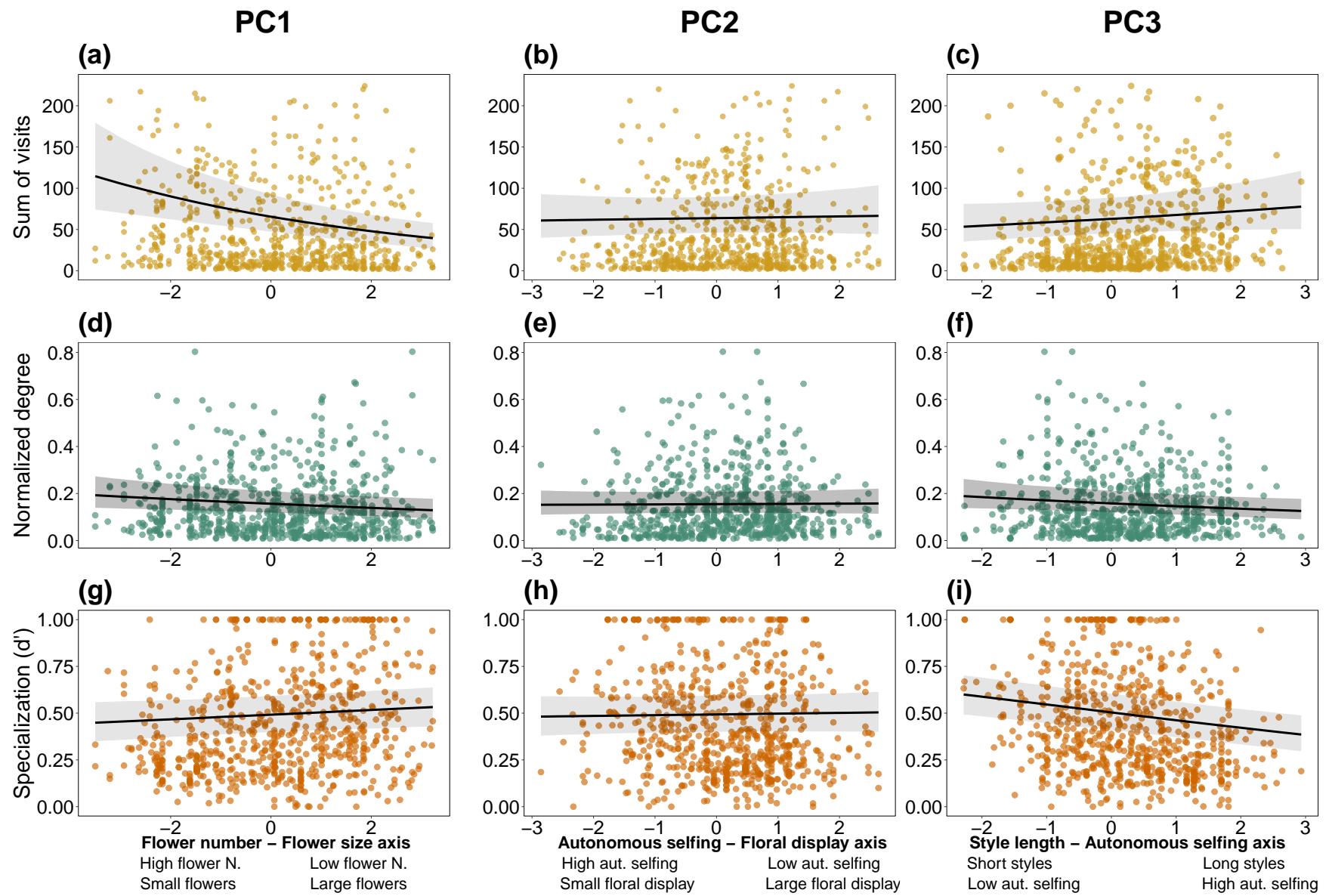


Fig. S10. Association between the main axes of trait variation (showed on different columns) and the distinct plant species level network metrics (showed on different rows). The x-axis shows the most illustrative trait extremes of the trait continuum. Note that the plots are coloured by the different network metrics.