

598 **Supplement: Sparse positive and negative weak interactions drive plant
599 species performance in a diverse community**

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625 **A Appendix**

626 **A.1 Data Exploration**

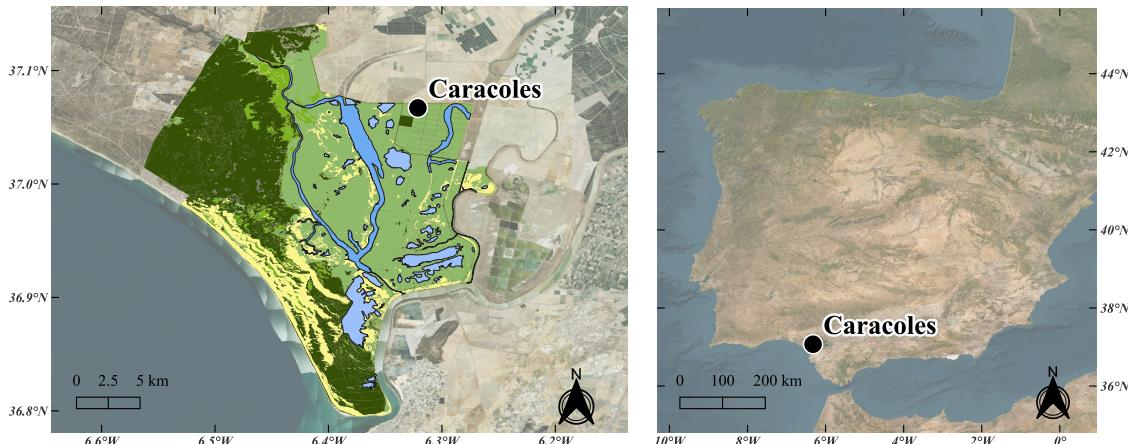


Figure S1: Geographical locations of Caracoles Ranch (2680 ha) within Doñana National Park in Spain. The vegetal categorisation of the Park is visible on the left, with forest in dark green, grassland in light green and a mixture of both with different shades of green. Sandy area are designated with pale orange. Bodies of water are in blue and river in lighter blue.

627 **A.2 Field limitations**

628 The study of complex systems can have limitations despite the use of advanced
629 statistical tools and thorough field experiments. One limitation is that estimating
630 interactions between trophic guilds can be improved with more precise and time-
631 consuming field techniques (see appendix Fig. S23 to see when all years are

lumped together). For instance, the effect of pollinators on a plant's fecundity can be estimated based on pollen deposition or flowering trait matching, which requires the collection of flower heads and pollinator individuals (Campbell, 1985; Vázquez and Simberloff, 2002; B. Lanuza et al., 2023). Similarly, the impact of herbivores on plants can be estimated based on leaf damages, which requires visual assessment of multiple leaves from a plant individual (Kempel et al., 2023). Besides alternative measurements, monitoring the community continuously, manually or with monitoring systems, would account for the time we are not observing a direct interaction. While these techniques would enhance the accuracy of estimating the impact of higher trophic guilds on plants, their feasibility in terms of time and resources at a complex scale is questionable.

References

- D. R. Campbell (Mar. 1985). “Pollen and gene dispersal: the influences of competition for pollination”. In: *Evolution* 39 (2), pp. 418–431
- Diego P. Vázquez and Daniel Simberloff (2002). “Ecological Specialization and Susceptibility to Disturbance: Conjectures and Refutations”. In: *American Naturalist* 159 (6), pp. 606–623
- Jose B. Lanuza et al. (2023). “Covariation among reproductive traits in flowering plants shapes their interactions with pollinators”. In: *Functional Ecology*
- Anne Kempel et al. (Mar. 2023). “From bottom-up to top-down control of invertebrate herbivores in a retrogressive chronosequence”. In: *Ecology Letters* 26 (3), pp. 411–424

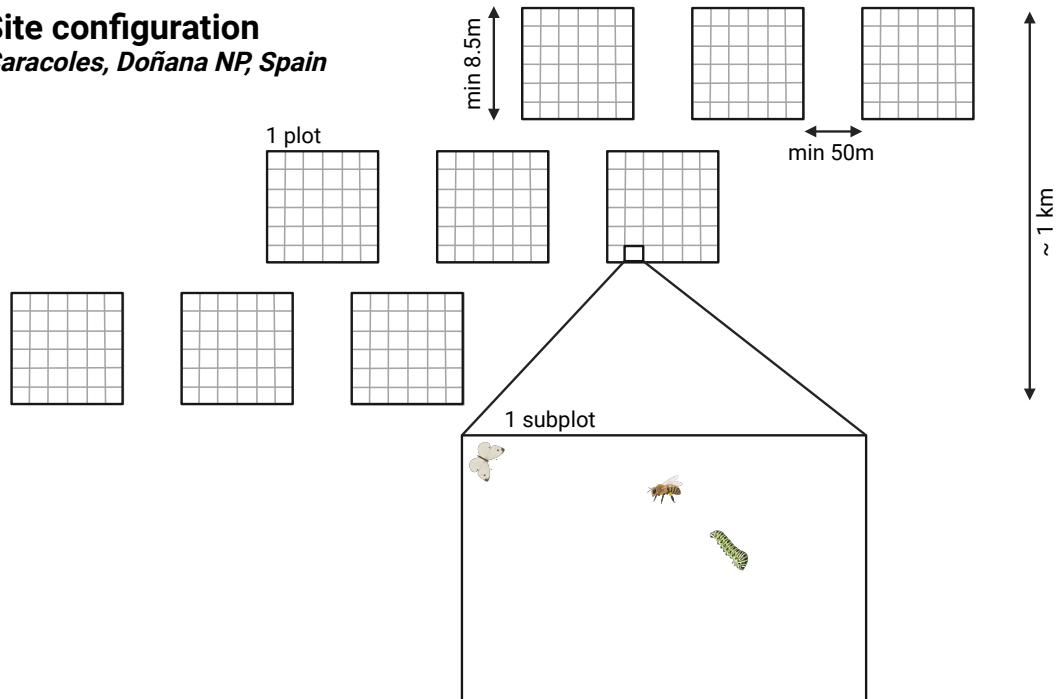
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655 A.3 Extended results

656 Figures similar to main figures, with all years, focal species and grouping levels.

Site configuration

Caracoles, Doñana NP, Spain



Data collection

Focal plant species	year	plot/ subplot	# flower	# seed	Plant neighbours	Floral visitor		Herbivore	
LEMA	2019	6-B6	2	60	HOMA CETE	1	2	1	1
LEMA					CHFU	1	1	1	1


 # flower x mean seeds per flower at time t in that subplot
 OR
 # flower x mean seeds per flower at time t in that plot

Number of individual at peak flower of LEMA
 Number of visits of the focal in that subplot over one year t
 Number of individuals on that focal in that subplot over one year

Figure S2: Site configuration and translation of observations into data table. See dataspike output file docs/input.html to see details about the different tables and their variables.

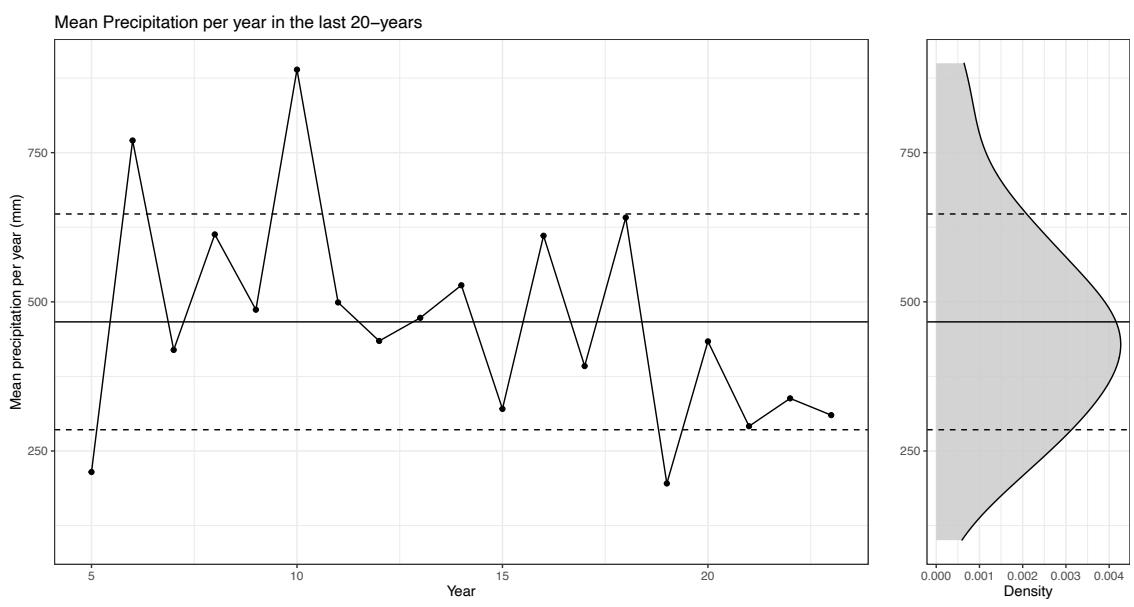


Figure S3: Annual precipitation in Caracoles in the last 20 years. Raw data taken from (Pesquera, 2023)

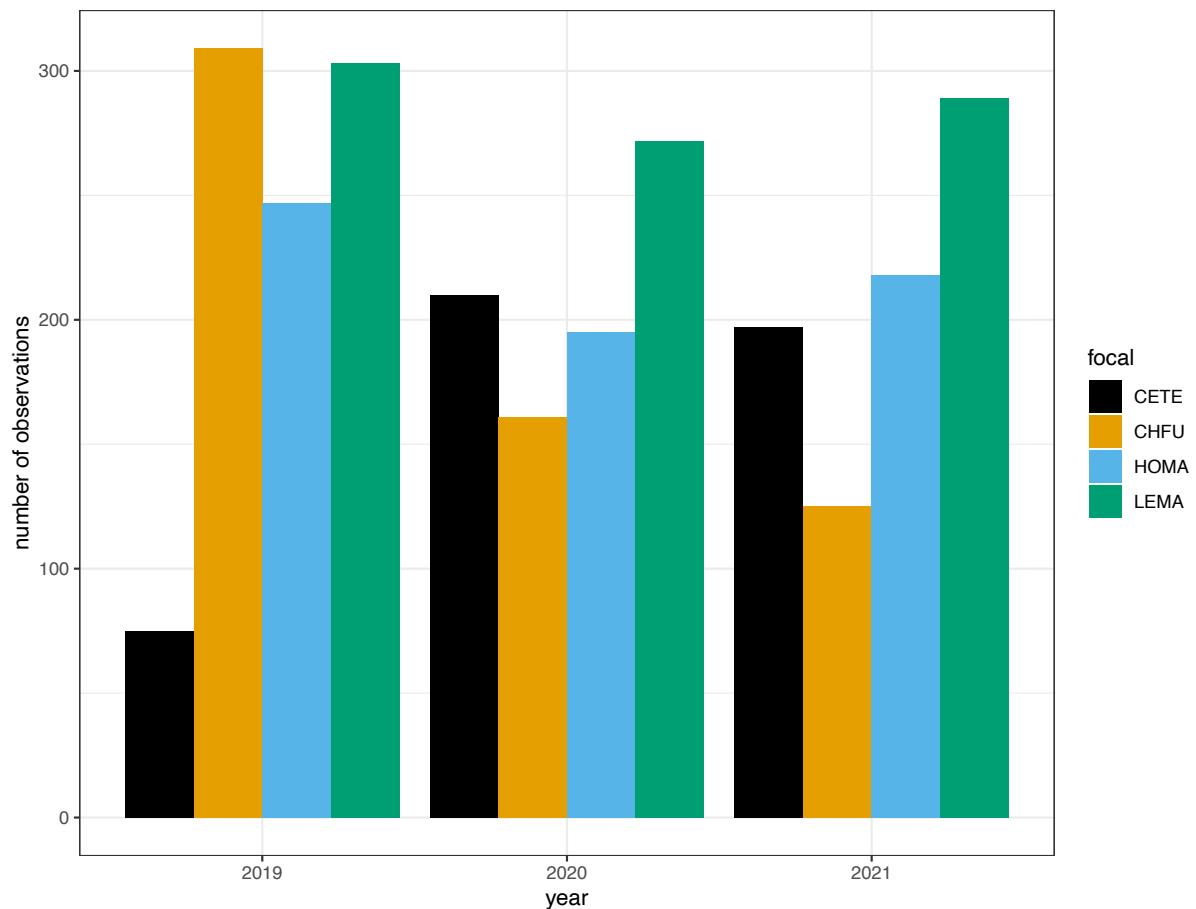


Figure S4: Number of times each focal plant species was surveyed.

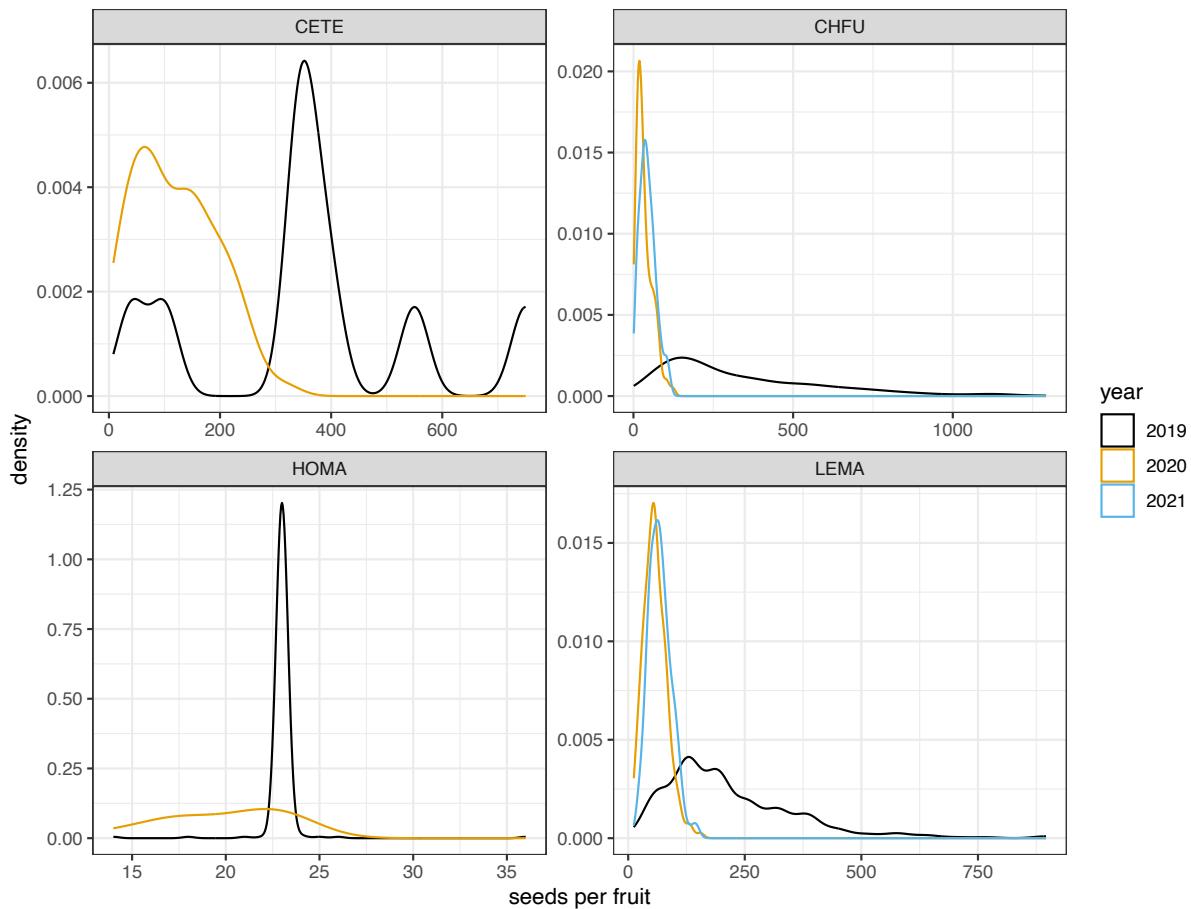


Figure S5: Distribution of seed production per flower for each focal species. In following step, we modified the following distribution: CETE 2019; CETE 2021; CHFU 2019; LEMA 2019; HOMA 2019, HOMA 2021. For these combinations, we improve the distribution of seeds per individual by sampling the mean number of seeds per flower found for the same plot or, if possible, subplot across all years; see next figure.

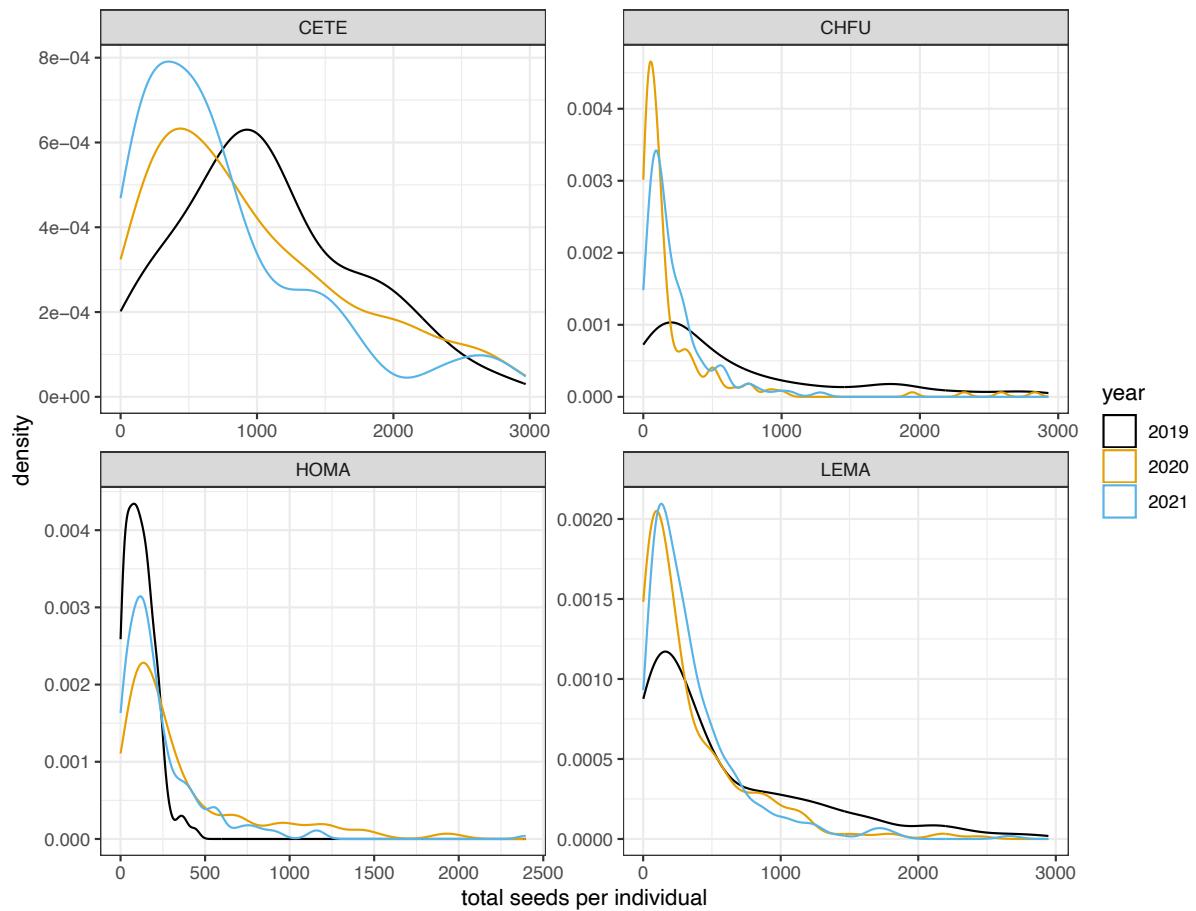


Figure S6: Distribution of seed production per individual for each focal and each year. We removed observations above 3000 seeds per individual to aid visualisation.

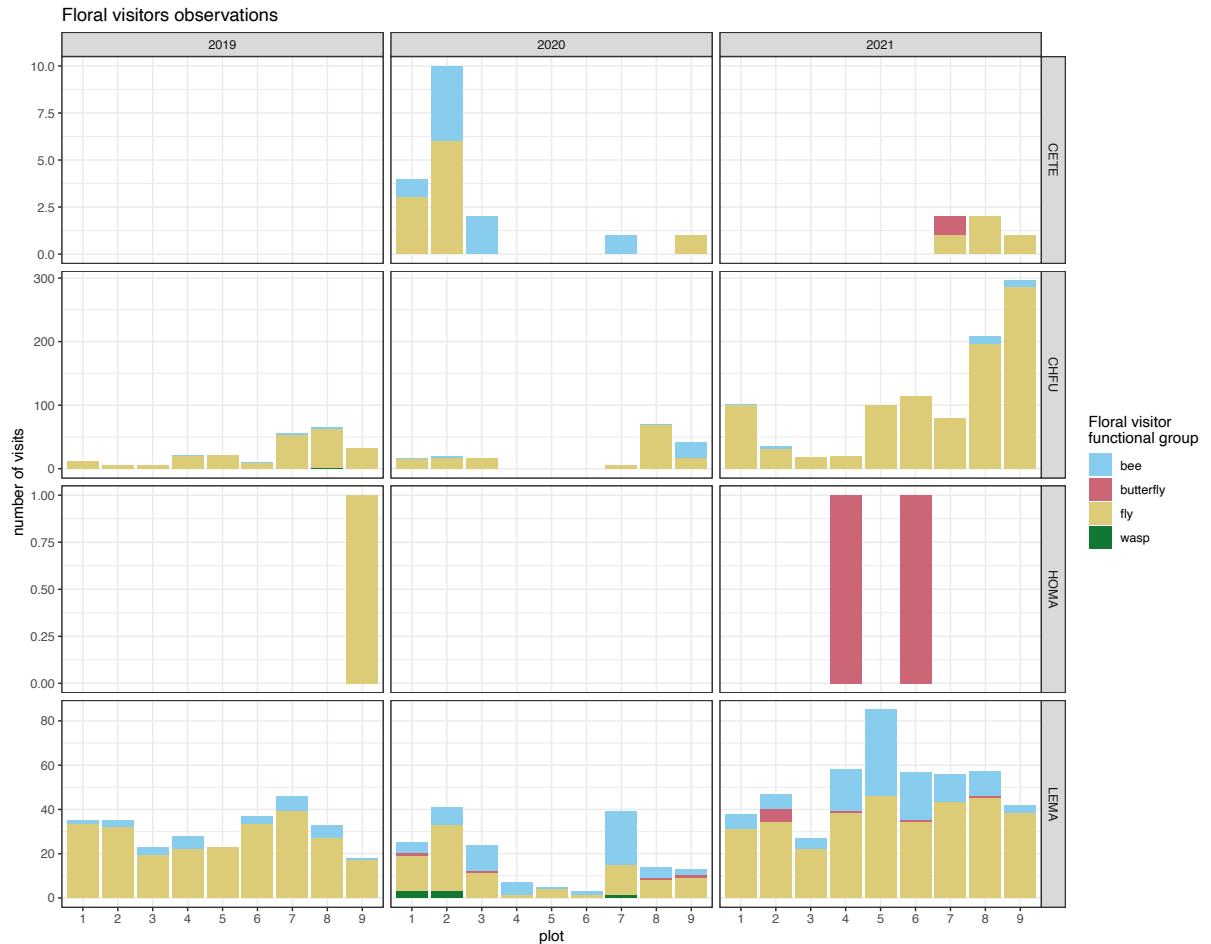


Figure S7: Number of observations of interaction between a focal species and a pollinator. Observations for HOMA were not considered as it is a wind-pollinated plant.



Figure S8: Number of observations of interaction between a focal species and a herbivore.

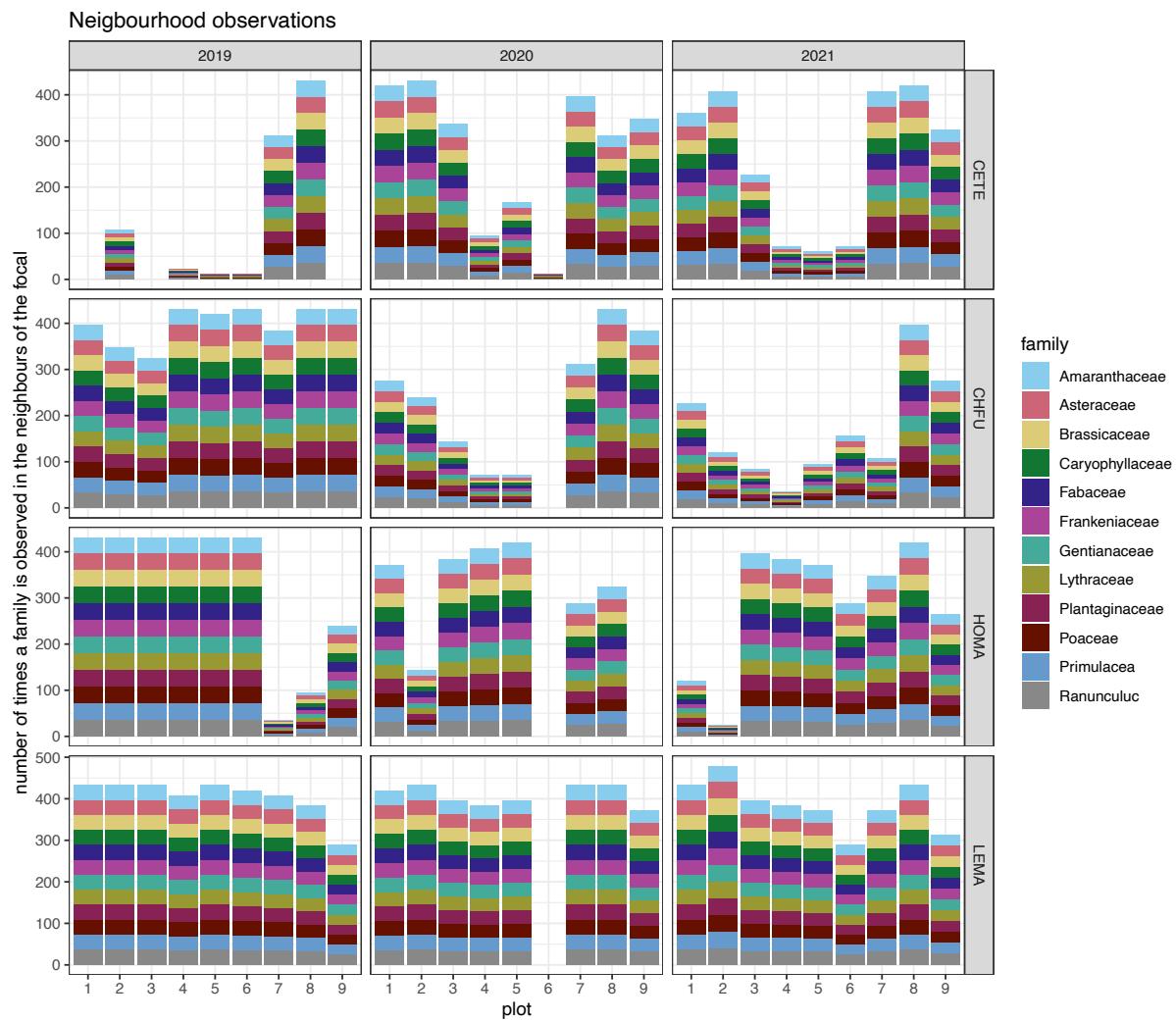


Figure S9: Number of times a family is observed in the neighbours of the focal.

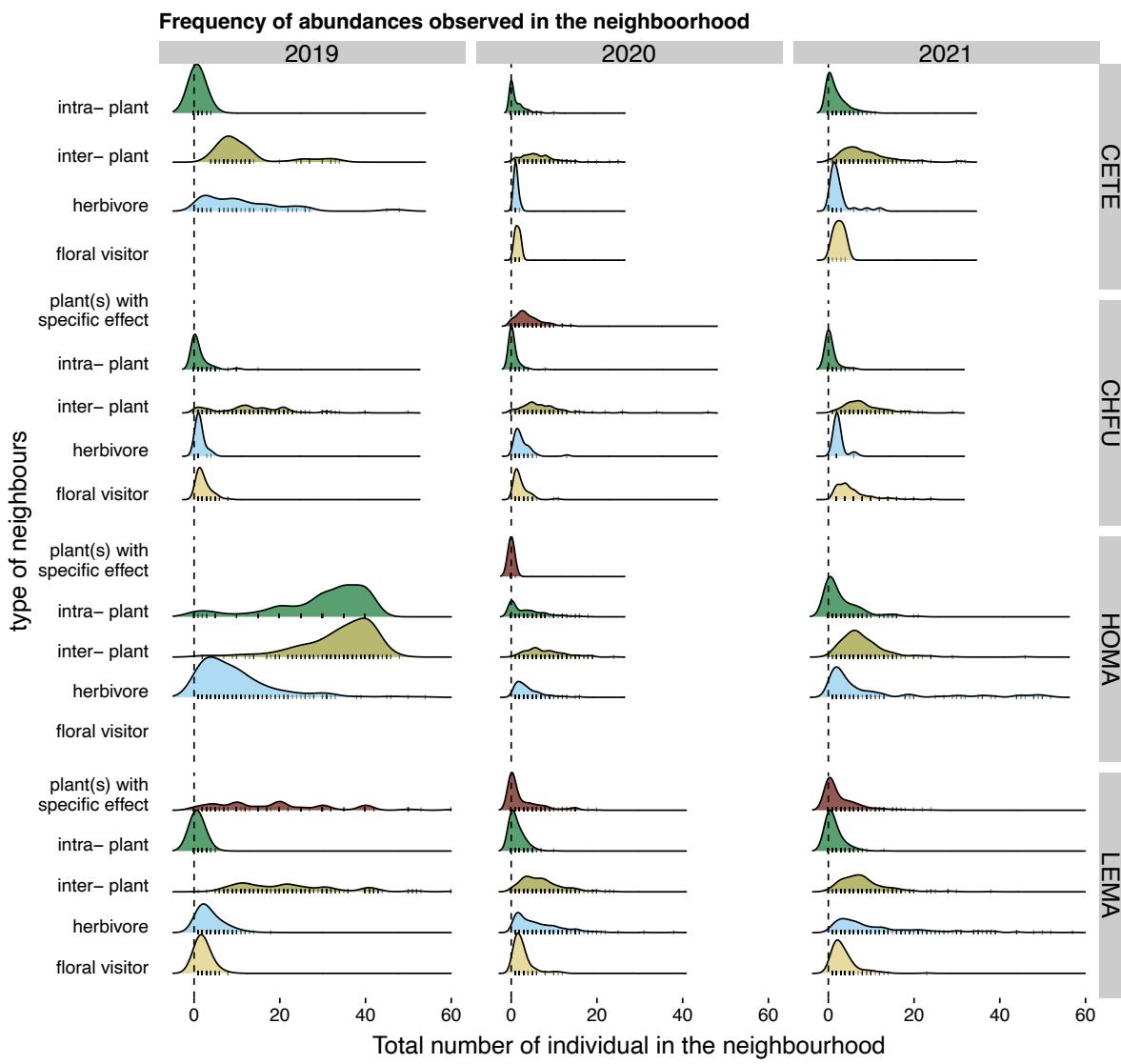


Figure S10: Kernels displaying frequency distributions of field observations per trophic level, focal species and year. We considered 30971 observations of plant neighbour individuals, 2312 observations of pollinators and 4787 observations of herbivores.

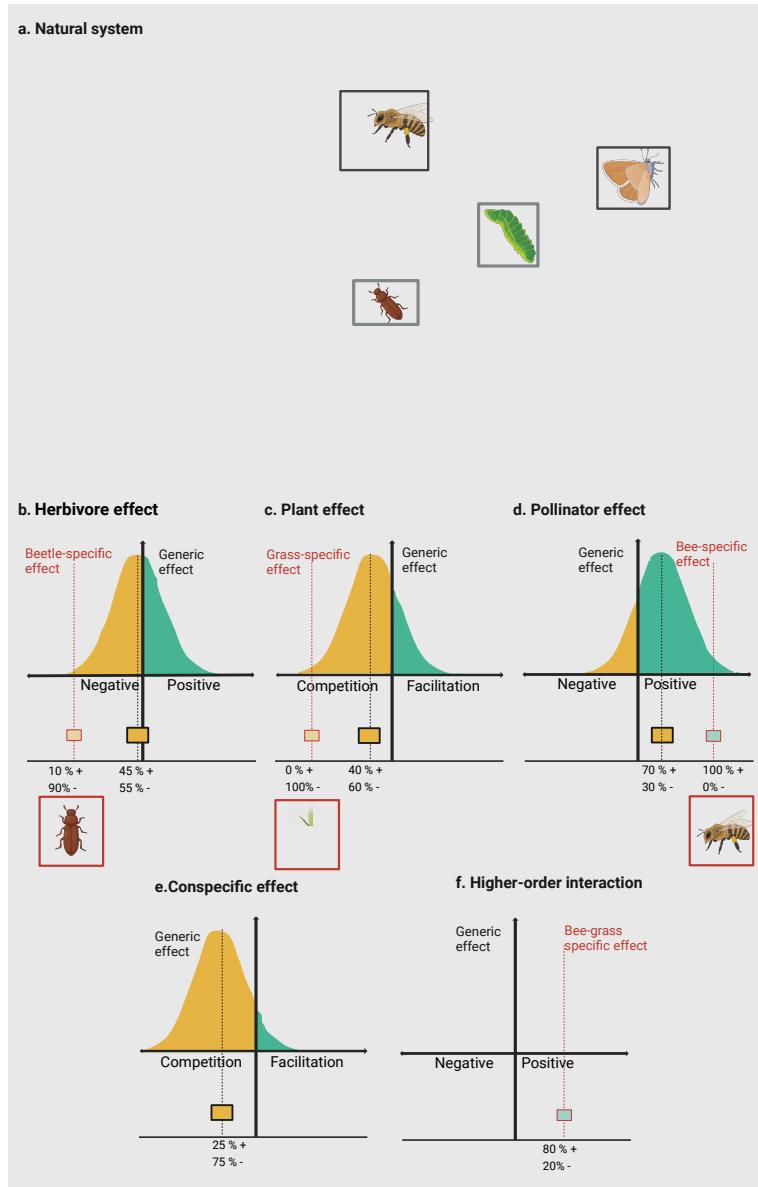


Figure S11: Extended version o Fig.1: Study system and methodological illustration Depiction of the four annual plant species studied: *Chamaemelum fuscatum* (CHFU), *Leontodon maroccanus* (LEMA), *Hordeum marinum* (HOMA), and *Centaurium tenuiflorum* (CETE), from left to right. **Panel e** shows the quantification of the intraspecific effect as a generic effect, and **panel f** shows higher-order interactions, which are only estimated when relevant; that is, they have a specific effect divergent from 0. Credit to Nerea Montesperez for the illustration.

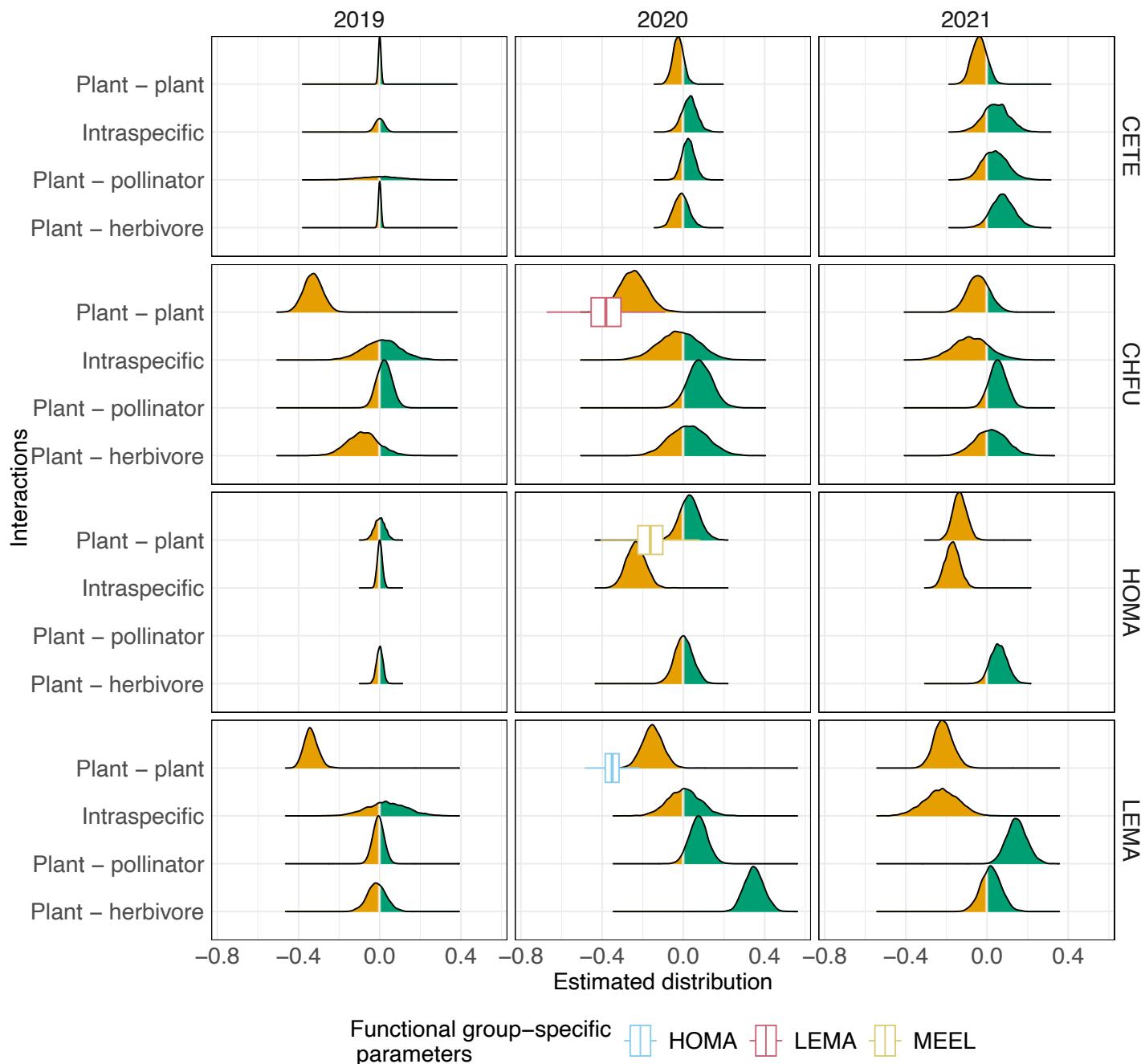


Figure S12: Distribution of generic species interactions and their group-specific interaction if relevant. Showing neighbours grouped by species.

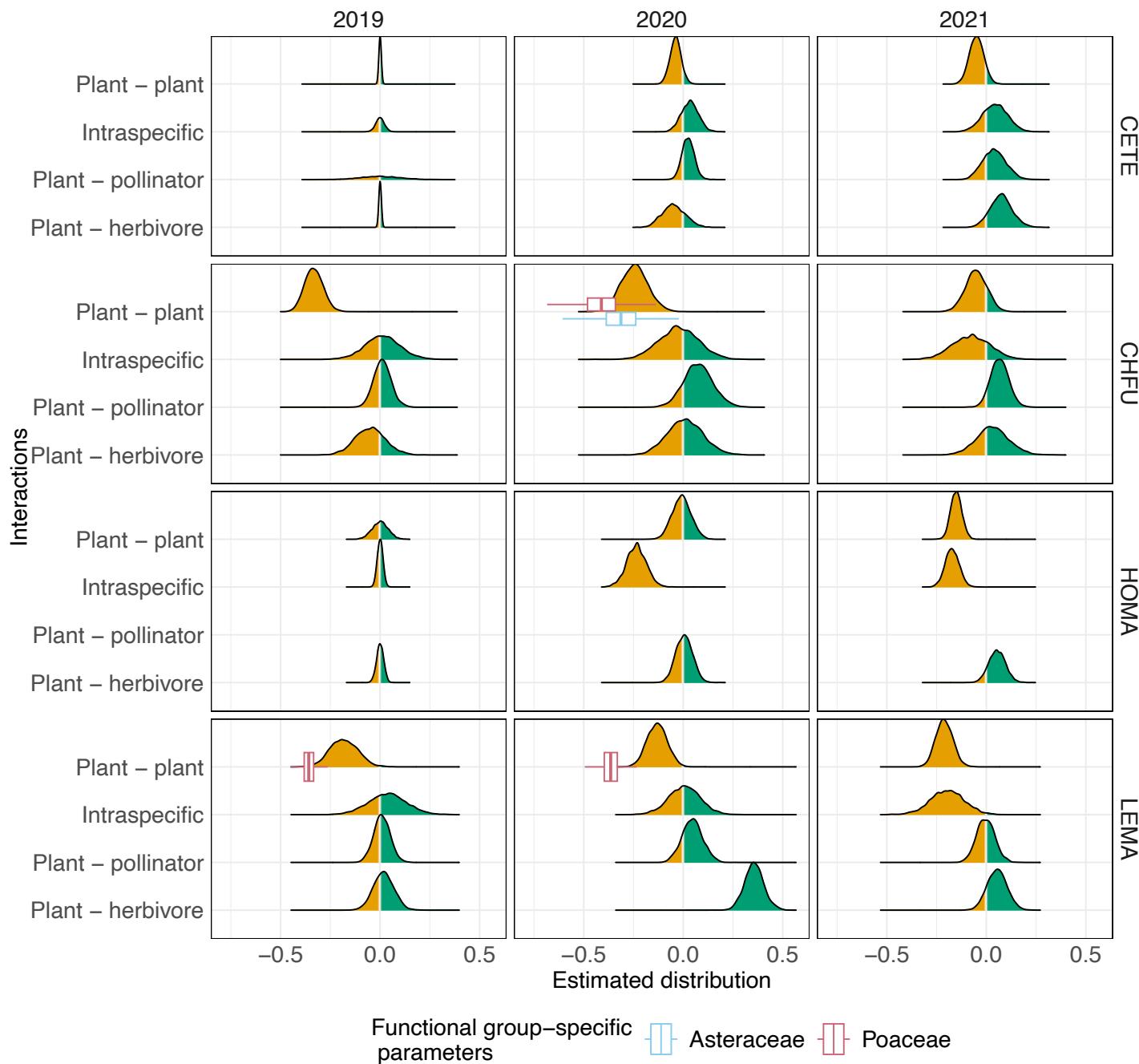


Figure S13: Distribution of generic species interactions and their family-specific interaction if relevant. Showing neighbours grouped by family.

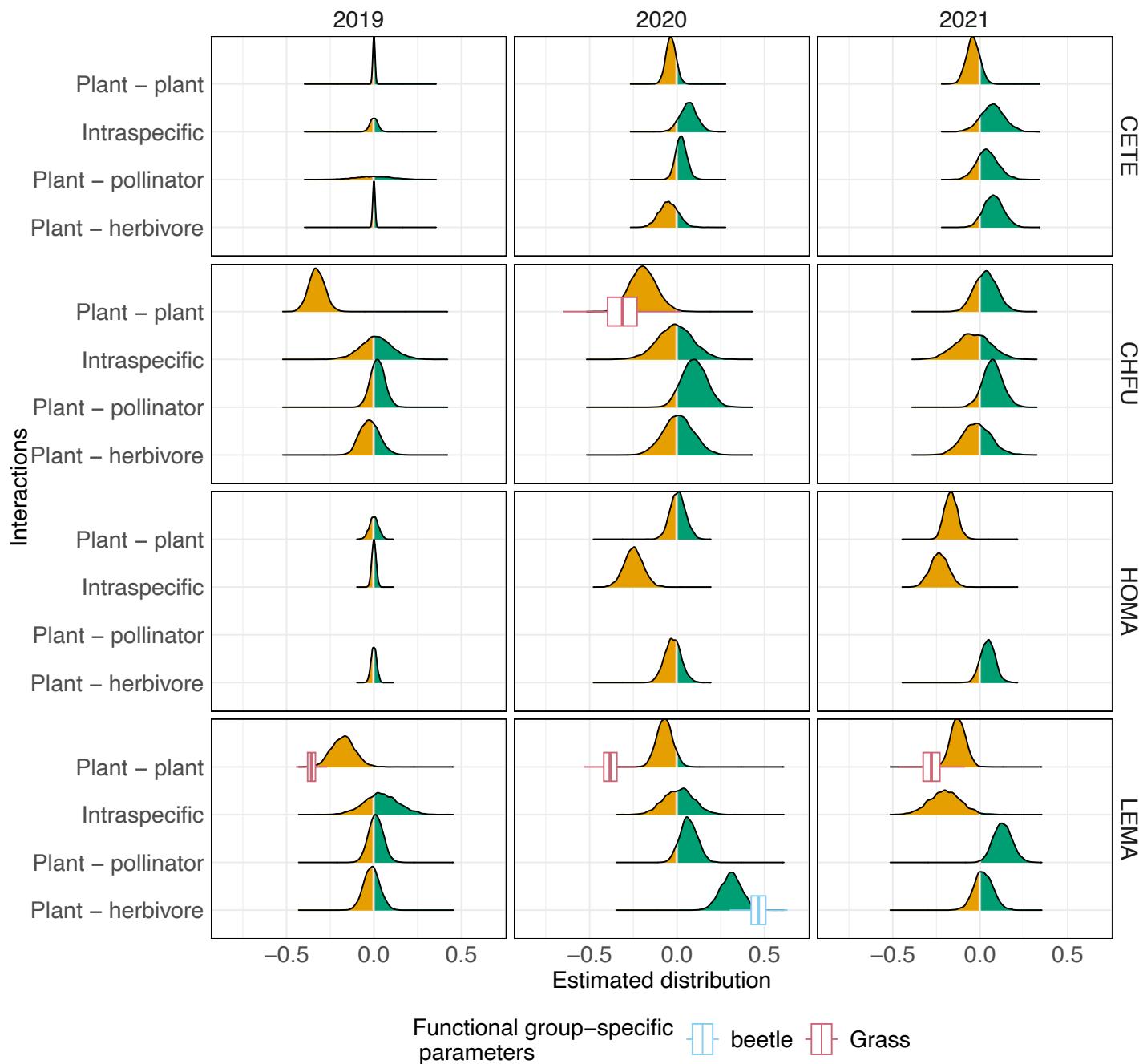


Figure S14: Distribution of generic species interactions and their functional group-specific interaction if relevant. Showing neighbours grouped by functional group.

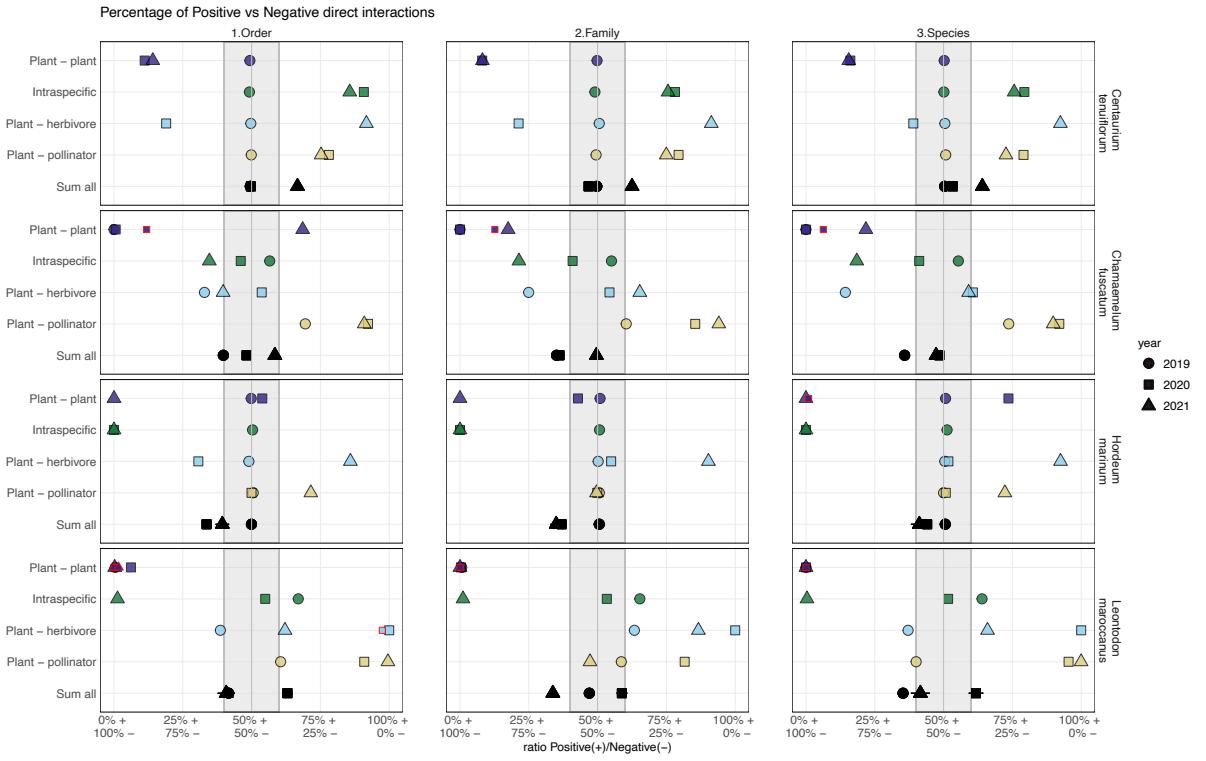


Figure S15: Percentage of positive vs negative interactions, depends on the focal species and type of direct interactions. Interactions display the full spectrum of potential interaction, from purely positive (LEMA, plant - pollinators, 2021) to purely negative (HOMA, plant - plant, 2021) or neutral (CHFU, plant-herbivore, 2020). Pollinators have consistently positive effects on plant species. Conversely, plants experienced mainly competitive interactions between them. Plant group-specific interactions are always strongly competitive when present (e.g., LEMA and CHFU). **Yet, overall, interactions are equally positive and negative;** they vary across the spectrum depending on the annual condition, focal species, and higher trophic level (black filling). The points encircled in red are group-specific interactions acting on the generic interaction designated by their filling. The grey area designates the interactions not distinctly governed by either positive or negative signs and are thus called neutral.

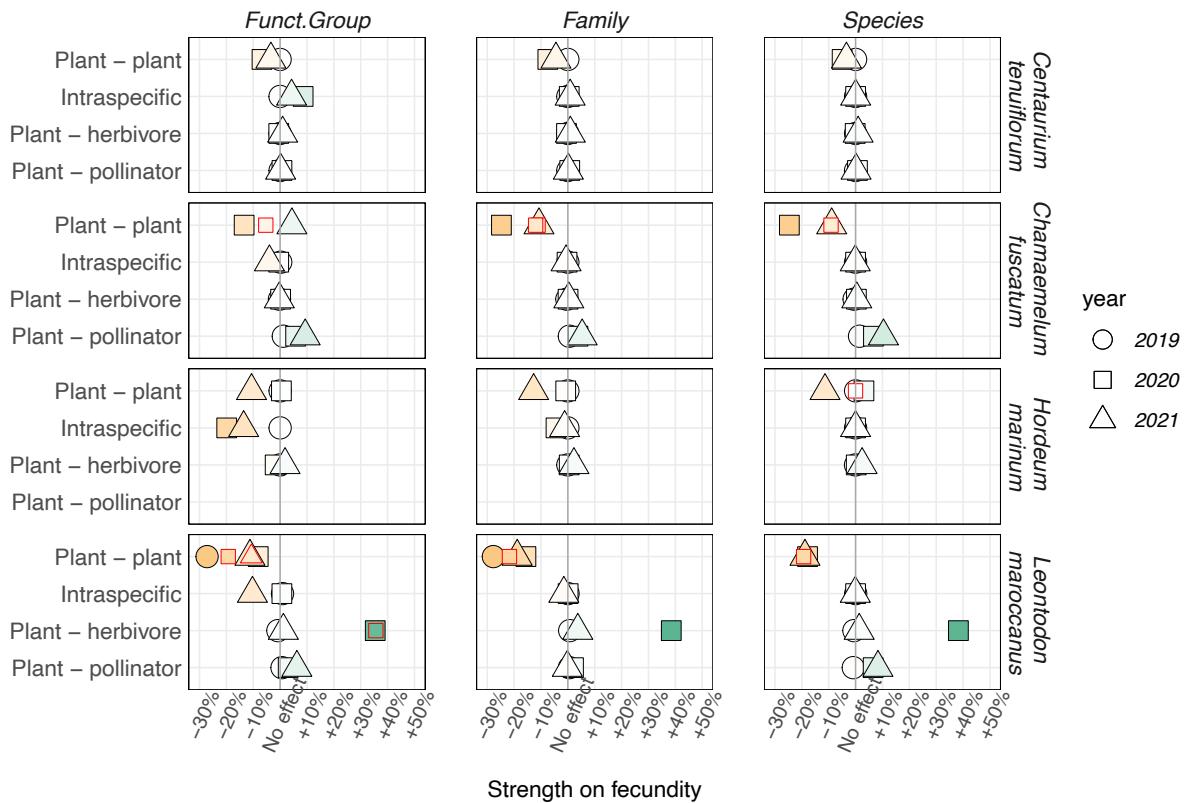


Figure S16: Strength of mean interactions depends on the focal species and type of direct generic interactions. Interactions display the full spectrum of potential interaction, from purely positive (LEMA, plant - pollinator, 2021) to purely negative (HOMA, plant - plant, 2021) or neutral (CHFU, plant-herbivore, 2020). Pollinators have consistently positive effects on plant species. Conversely, plants experienced mainly competitive interactions between them. Plant group-specific interactions are always strongly competitive when present (e.g., LEMA and CHFU). Overall, interactions are equally positive and negative. They vary across the spectrum depending on the annual condition, focal species, and trophic level. The points encircled in red are group-specific interactions acting on the generic interaction designated by their filling. Showing neighbours grouped by family.

focal	year	complexity level	number of plants	number of plant HOIs	number of herbivores	number of herbivore HOIs	number of pollinators	number of pollinator HOIs	number of plants selected	name(s) of plants selected	number of herbivores selected	name(s) of herbivores selected
LEMA	2019	functional group	2	3	4	12	2	6	1	Grass	0	NA
LEMA	2019	family	8	36	8	47	8	53	1	Poaceae	0	NA
LEMA	2019	species	16	136	12	78	22	183	0		0	NA
LEMA	2020	functional group	2	3	7	16	4	12	1	Grass	1	beetle
LEMA	2020	family	9	45	12	70	17	86	1	Poaceae	0	NA
LEMA	2020	species	19	190	18	129	27	171	1	HOMA	0	NA
LEMA	2021	functional group	2	3	4	12	3	9	1	Grass	0	NA
LEMA	2021	family	8	36	7	32	11	58	0		0	NA
LEMA	2021	species	17	153	13	76	27	184	0		0	NA
CFU	2019	functional group	2	3	4	10	3	7	0		0	NA
CFU	2019	family	8	36	6	13	9	34	0		0	NA
CFU	2019	species	13	91	8	19	19	78	0		0	NA
CFU	2020	functional group	2	3	4	10	2	6	1	Grass	0	NA
CFU	2020	family	9	45	6	23	9	40	2	Asteraceae, Poaceae	0	NA
CFU	2020	species	19	190	8	37	15	95	1	LEMA	0	NA
CFU	2021	functional group	2	3	2	4	2	6	0		0	NA
CFU	2021	family	8	36	2	8	9	51	0		0	NA
CFU	2021	species	17	153	3	22	15	115	0		0	NA
HOMA	2019	functional group	2	3	4	12	NA	NA	0		0	NA
HOMA	2019	family	12	78	12	54	NA	NA	0		0	NA
HOMA	2019	species	24	300	20	104	NA	NA	0		0	NA
HOMA	2020	functional group	2	3	4	12	NA	NA	0		0	NA
HOMA	2020	family	12	78	6	38	NA	NA	0		0	NA
HOMA	2020	species	24	300	10	87	NA	NA	0		0	NA
HOMA	2021	functional group	2	3	4	12	NA	NA	0		0	NA
HOMA	2021	family	12	78	5	26	NA	NA	0		0	NA
HOMA	2021	species	24	300	9	61	NA	NA	0		0	NA
CETE	2019	functional group	2	3	1	3	NA	NA	0		0	NA
CETE	2019	family	12	78	2	10	NA	NA	0		0	NA
CETE	2019	species	24	300	2	14	NA	NA	0		0	NA
CETE	2020	functional group	2	3	2	4	2	6	0		0	NA
CETE	2020	family	12	78	2	7	5	16	0		0	NA
CETE	2020	species	24	300	1	10	6	26	0		0	NA
CETE	2021	functional group	2	3	1	3	2	3	0		0	NA
CETE	2021	family	12	78	2	9	3	7	0		0	NA
CETE	2021	species	24	300	3	18	4	9	0		0	NA

Figure S17: Parameters included compared to 56 potential interactions observed for a specific focal, grouping and year. The column for a specific trophic level is not represented if no group-specific interactions were selected in that trophic level, such as pollinators.

focal	year	complexity level	parameter	positive perc	positive perc_hat	median estimate	ten estimate	ninety estimate	median estimate hat	ten estimate hat	ninety estimate hat
CETE	2019	functional G	Intraspecific	0.492	0	-0.00038	-0.02496	0.02440	NA	NA	NA
CETE	2019	functional G	Plant - plant	0.49375	0	-0.00004	-0.00368	0.00365	NA	NA	NA
CETE	2019	functional G	Plant - herbivore	0.497	0	-0.00003	-0.00423	0.00407	NA	NA	NA
CETE	2019	functional G	Plant - floral visitor	0.49875	0	-0.00029	-0.12281	0.12135	NA	NA	NA
CETE	2019	family	Intraspecific	0.49025	0	-0.00054	-0.02452	0.02488	NA	NA	NA
CETE	2019	family	Plant - plant	0.498	0	-0.00001	-0.00378	0.00377	NA	NA	NA
CETE	2019	family	Plant - herbivore	0.506	0	0.00007	-0.00427	0.00422	NA	NA	NA
CETE	2019	family	Plant - floral visitor	0.4945	0	-0.00113	-0.11394	0.11438	NA	NA	NA
CETE	2019	species	Intraspecific	0.50125	0	0.00005	-0.02533	0.02568	NA	NA	NA
CETE	2019	species	Plant - plant	0.50225	0	0.00002	-0.00368	0.00374	NA	NA	NA
CETE	2019	species	Plant - herbivore	0.50475	0	0.00004	-0.00410	0.00420	NA	NA	NA
CETE	2019	species	Plant - floral visitor	0.50775	0	0.00191	-0.11755	0.11935	NA	NA	NA
CETE	2020	functional G	Intraspecific	0.90775	0	0.06550	0.00785	0.12106	NA	NA	NA
CETE	2020	functional G	Plant - plant	0.1115	0	-0.03491	-0.06711	-0.00117	NA	NA	NA
CETE	2020	functional G	Plant - herbivore	0.1895	0	-0.04809	-0.11078	0.01563	NA	NA	NA
CETE	2020	functional G	Plant - floral visitor	0.78075	0	0.02322	-0.01153	0.06147	NA	NA	NA
CETE	2020	family	Intraspecific	0.78125	0	0.03365	-0.01755	0.08346	NA	NA	NA
CETE	2020	family	Plant - plant	0.08075	0	-0.03803	-0.07067	-0.00663	NA	NA	NA
CETE	2020	family	Plant - herbivore	0.213	0	-0.04936	-0.11663	0.02299	NA	NA	NA
CETE	2020	family	Plant - floral visitor	0.79425	0	0.02451	-0.01033	0.05981	NA	NA	NA
CETE	2020	species	Intraspecific	0.7935	0	0.03062	-0.01325	0.07154	NA	NA	NA
CETE	2020	species	Plant - plant	0.16125	0	-0.02548	-0.05539	0.00477	NA	NA	NA
CETE	2020	species	Plant - herbivore	0.39	0	-0.01011	-0.05290	0.03325	NA	NA	NA
CETE	2020	species	Plant - floral visitor	0.7905	0	0.02397	-0.01071	0.06054	NA	NA	NA
CETE	2021	functional G	Intraspecific	0.8565	0	0.07132	-0.00724	0.14859	NA	NA	NA
CETE	2021	functional G	Plant - plant	0.141	0	-0.04120	-0.08528	0.00350	NA	NA	NA
CETE	2021	functional G	Plant - herbivore	0.917	0	0.07542	0.01259	0.14199	NA	NA	NA
CETE	2021	functional G	Plant - floral visitor	0.7525	0	0.03908	-0.02908	0.11526	NA	NA	NA
CETE	2021	family	Intraspecific	0.756	0	0.04415	-0.02788	0.11730	NA	NA	NA
CETE	2021	family	Plant - plant	0.0815	0	-0.04897	-0.09028	-0.00767	NA	NA	NA
CETE	2021	family	Plant - herbivore	0.91325	0	0.07468	0.01070	0.13926	NA	NA	NA
CETE	2021	family	Plant - floral visitor	0.74975	0	0.03891	-0.02785	0.11053	NA	NA	NA
CETE	2021	species	Intraspecific	0.7565	0	0.04358	-0.02910	0.11872	NA	NA	NA
CETE	2021	species	Plant - plant	0.1555	0	-0.03809	-0.08073	0.00591	NA	NA	NA

CETE	2021	species	Plant - herbivore	0.9245	0	0.07655	0.01376	0.14224	NA	NA	NA
CETE	2021	species	Plant - floral visitor	0.72675	0	0.03747	-0.03237	0.11045	NA	NA	NA
LEMA	2019	functional G	Intraspecific	0.6695	0	0.04024	-0.07015	0.15757	NA	NA	NA
LEMA	2019	functional G	Plant - plant	0.0045	0.00175	-0.17543	-0.25513	-0.09831	-0.17946	-0.25398	-0.10801
LEMA	2019	functional G	Plant - herbivore	0.3865	0	-0.01219	-0.06449	0.04093	NA	NA	NA
LEMA	2019	functional G	Plant - floral visitor	0.6055	0	0.01038	-0.03652	0.05950	NA	NA	NA
LEMA	2019	family	Intraspecific	0.6535	0	0.03767	-0.07498	0.14902	NA	NA	NA
LEMA	2019	family	Plant - plant	0.0065	0.00125	-0.18392	-0.26268	-0.09994	-0.17462	-0.25017	-0.10079
LEMA	2019	family	Plant - herbivore	0.63375	0	0.01716	-0.04179	0.07836	NA	NA	NA
LEMA	2019	family	Plant - floral visitor	0.58625	0	0.00820	-0.03759	0.05674	NA	NA	NA
LEMA	2019	species	Intraspecific	0.63975	0	0.03298	-0.07924	0.14912	NA	NA	NA
LEMA	2019	species	Plant - plant	0	0	-0.34057	-0.37680	-0.29953	NA	NA	NA
LEMA	2019	species	Plant - herbivore	0.371	0	-0.01522	-0.06627	0.03940	NA	NA	NA
LEMA	2019	species	Plant - floral visitor	0.40025	0	-0.00650	-0.03770	0.02438	NA	NA	NA
LEMA	2020	functional G	Intraspecific	0.5495	0	0.01167	-0.09091	0.11037	NA	NA	NA
LEMA	2020	functional G	Plant - plant	0.0615	0	-0.07105	-0.12382	-0.01826	-0.31112	-0.37338	-0.24771
LEMA	2020	functional G	Plant - herbivore	1	0.97525	0.30929	0.23720	0.37910	0.15659	0.067825	0.247252
LEMA	2020	functional G	Plant - floral visitor	0.90925	0	0.06453	0.00798	0.12527	NA	NA	NA
LEMA	2020	family	Intraspecific	0.5335	0	0.00679	-0.08543	0.09732	NA	NA	NA
LEMA	2020	family	Plant - plant	0.00325	0	-0.13116	-0.19080	-0.07166	-0.23243	-0.29725	-0.17093
LEMA	2020	family	Plant - herbivore	1	0	0.35629	0.30195	0.41169	NA	NA	NA
LEMA	2020	family	Plant - floral visitor	0.8165	0	0.04606	-0.01378	0.10811	NA	NA	NA
LEMA	2020	species	Intraspecific	0.5165	0	0.00290	-0.08838	0.09631	NA	NA	NA
LEMA	2020	species	Plant - plant	5.00E-04	0	-0.15279	-0.21048	-0.09380	-0.19783	-0.25915	-0.13728
LEMA	2020	species	Plant - herbivore	1	0	0.34731	0.29313	0.40429	NA	NA	NA
LEMA	2020	species	Plant - floral visitor	0.95425	0	0.07371	0.02164	0.12513	NA	NA	NA
LEMA	2021	functional G	Intraspecific	0.01275	0	-0.20037	-0.30568	-0.09555	NA	NA	NA
LEMA	2021	functional G	Plant - plant	0.0025	0.01675	-0.12633	-0.17401	-0.07647	-0.15132	-0.22968	-0.0738
LEMA	2021	functional G	Plant - herbivore	0.62125	0	0.01726	-0.04232	0.08145	NA	NA	NA
LEMA	2021	functional G	Plant - floral visitor	0.99525	0	0.12809	0.06805	0.19054	NA	NA	NA
LEMA	2021	family	Intraspecific	0.011	0	-0.19624	-0.29232	-0.09646	NA	NA	NA
LEMA	2021	family	Plant - plant	0	0	-0.21164	-0.26046	-0.16057	NA	NA	NA
LEMA	2021	family	Plant - herbivore	0.86625	0	0.05409	-0.00355	0.11194	NA	NA	NA
LEMA	2021	family	Plant - floral visitor	0.4725	0	-0.00346	-0.05525	0.04911	NA	NA	NA
LEMA	2021	species	Intraspecific	0.00375	0	-0.22431	-0.32561	-0.12520	NA	NA	NA
LEMA	2021	species	Plant - plant	0	0	-0.21663	-0.26669	-0.15950	NA	NA	NA
LEMA	2021	species	Plant - herbivore	0.65975	0	0.01898	-0.03748	0.07796	NA	NA	NA

LEMA	2021	species	Plant - floral visitor	0.99975	0	0.14547	0.08863	0.20436	NA	NA	NA
HOMA	2019	functional	G Intraspecific	0.5035	0	0.00013	-0.01386	0.01484	NA	NA	NA
HOMA	2019	functional	G Plant - plant	0.4985	0	-0.0006	-0.03053	0.03059	NA	NA	NA
HOMA	2019	functional	G Plant - herbivore	0.49	0	-0.00039	-0.01886	0.01801	NA	NA	NA
HOMA	2019	functional	G Plant - floral visitor	0.50575	0	0.00122	-0.11846	0.11867	NA	NA	NA
HOMA	2019	family	Intraspecific	0.507	0	0.00034	-0.01642	0.01658	NA	NA	NA
HOMA	2019	family	Plant - plant	0.509	0	0.00068	-0.04757	0.04759	NA	NA	NA
HOMA	2019	family	Plant - herbivore	0.502	0	0.00009	-0.02104	0.02081	NA	NA	NA
HOMA	2019	family	Plant - floral visitor	0.50625	0	0.00150	-0.11819	0.11708	NA	NA	NA
HOMA	2019	species	Intraspecific	0.51275	0	0.00034	-0.01344	0.01457	NA	NA	NA
HOMA	2019	species	Plant - plant	0.50725	0	0.00044	-0.03019	0.03110	NA	NA	NA
HOMA	2019	species	Plant - herbivore	0.5045	0	0.00015	-0.01890	0.01775	NA	NA	NA
HOMA	2019	species	Plant - floral visitor	0.5	0	0.00001	-0.11391	0.11574	NA	NA	NA
HOMA	2020	functional	G Intraspecific	0	0	-0.24829	-0.31147	-0.18441	NA	NA	NA
HOMA	2020	functional	G Plant - plant	0.53875	0	0.00471	-0.04634	0.05563	NA	NA	NA
HOMA	2020	functional	G Plant - herbivore	0.3065	0	-0.02386	-0.07868	0.03081	NA	NA	NA
HOMA	2020	functional	G Plant - floral visitor	0.49975	0	-0.00001	-0.11227	0.11560	NA	NA	NA
HOMA	2020	family	Intraspecific	0	0	-0.23497	-0.29071	-0.17694	NA	NA	NA
HOMA	2020	family	Plant - plant	0.42875	0	-0.00777	-0.06396	0.04834	NA	NA	NA
HOMA	2020	family	Plant - herbivore	0.54925	0	0.00490	-0.04309	0.05477	NA	NA	NA
HOMA	2020	family	Plant - floral visitor	0.49875	0	-0.00053	-0.11949	0.11914	NA	NA	NA
HOMA	2020	species	Intraspecific	0	0	-0.23453	-0.28840	-0.17783	NA	NA	NA
HOMA	2020	species	Plant - plant	0.73575	0.00975	0.02970	-0.02540	0.08622	-0.19319	-0.2874	-0.09977
HOMA	2020	species	Plant - herbivore	0.5175	0	0.00182	-0.04792	0.05521	NA	NA	NA
HOMA	2020	species	Plant - floral visitor	0.508	0	0.00226	-0.11451	0.11812	NA	NA	NA
HOMA	2021	functional	G Intraspecific	0	0	-0.23345	-0.29301	-0.17233	NA	NA	NA
HOMA	2021	functional	G Plant - plant	0	0	-0.16697	-0.20876	-0.12461	NA	NA	NA
HOMA	2021	functional	G Plant - herbivore	0.859	0	0.04435	-0.00403	0.09030	NA	NA	NA
HOMA	2021	functional	G Plant - floral visitor	0.71525	0	0.03167	-0.03283	0.09819	NA	NA	NA
HOMA	2021	family	Intraspecific	0	0	-0.17234	-0.21203	-0.13027	NA	NA	NA
HOMA	2021	family	Plant - plant	0	0	-0.15107	-0.18319	-0.11724	NA	NA	NA
HOMA	2021	family	Plant - herbivore	0.90275	0	0.05385	0.00540	0.10285	NA	NA	NA
HOMA	2021	family	Plant - floral visitor	0.496	0	-0.00101	-0.11510	0.11116	NA	NA	NA
HOMA	2021	species	Intraspecific	0	0	-0.17036	-0.21254	-0.12908	NA	NA	NA
HOMA	2021	species	Plant - plant	0	0	-0.13446	-0.17288	-0.09374	NA	NA	NA
HOMA	2021	species	Plant - herbivore	0.925	0	0.05694	0.01021	0.10585	NA	NA	NA
HOMA	2021	species	Plant - floral visitor	0.72275	0	0.03331	-0.03115	0.10439	NA	NA	NA

CHFU	2019	functional	G Intraspecific	0.56575	0	0.01404	-0.08838	0.11936	NA	NA	NA
CHFU	2019	functional	G Plant - plant	0	0	-0.32792	-0.37898	-0.27341	NA	NA	NA
CHFU	2019	functional	G Plant - herbivore	0.32875	0	-0.02501	-0.08770	0.04265	NA	NA	NA
CHFU	2019	functional	G Plant - floral visitor	0.695	0	0.02061	-0.02533	0.06769	NA	NA	NA
CHFU	2019	family	Intraspecific	0.5505	0	0.01173	-0.08826	0.11474	NA	NA	NA
CHFU	2019	family	Plant - plant	0	0	-0.33425	-0.38494	-0.27863	NA	NA	NA
CHFU	2019	family	Plant - herbivore	0.2495	0	-0.04951	-0.13673	0.03754	NA	NA	NA
CHFU	2019	family	Plant - floral visitor	0.604	0	0.01084	-0.03718	0.06127	NA	NA	NA
CHFU	2019	species	Intraspecific	0.55375	0	0.01162	-0.09495	0.11422	NA	NA	NA
CHFU	2019	species	Plant - plant	0	0	-0.32838	-0.38145	-0.27502	NA	NA	NA
CHFU	2019	species	Plant - herbivore	0.14325	0	-0.08281	-0.17241	0.01030	NA	NA	NA
CHFU	2019	species	Plant - floral visitor	0.73675	0	0.02263	-0.01982	0.06512	NA	NA	NA
CHFU	2020	functional	G Intraspecific	0.4605	0	-0.09977	-0.12644	0.10751	NA	NA	NA
CHFU	2020	functional	G Plant - plant	0.006	0.1185	-0.19495	-0.28188	-0.10504	-0.11815	-0.23783	-0.00068
CHFU	2020	functional	G Plant - herbivore	0.53675	0	0.00778	-0.09079	0.10990	NA	NA	NA
CHFU	2020	functional	G Plant - floral visitor	0.923	0	0.09778	0.01681	0.18064	NA	NA	NA
CHFU	2020	family	Intraspecific	0.40925	0	-0.02351	-0.14079	0.09218	NA	NA	NA
CHFU	2020	family	Plant - plant	0.00025	0.126875	-0.24507	-0.32381	-0.16759	-0.11794	-0.23746	0.003222
CHFU	2020	family	Plant - herbivore	0.54325	0	0.01044	-0.09334	0.11379	NA	NA	NA
CHFU	2020	family	Plant - floral visitor	0.85475	0	0.07567	-0.00855	0.16069	NA	NA	NA
CHFU	2020	species	Intraspecific	0.4115	0	-0.02199	-0.13970	0.09244	NA	NA	NA
CHFU	2020	species	Plant - plant	0	0.063	-0.24647	-0.32530	-0.16852	-0.13193	-0.23601	-0.03136
CHFU	2020	species	Plant - herbivore	0.6065	0	0.02523	-0.08214	0.13439	NA	NA	NA
CHFU	2020	species	Plant - floral visitor	0.9205	0	0.08054	0.01404	0.15083	NA	NA	NA
CHFU	2021	functional	G Intraspecific	0.3465	0	-0.04148	-0.15671	0.07393	NA	NA	NA
CHFU	2021	functional	G Plant - plant	0.6855	0	0.03208	-0.04221	0.10565	NA	NA	NA
CHFU	2021	functional	G Plant - herbivore	0.3965	0	-0.02134	-0.11243	0.07438	NA	NA	NA
CHFU	2021	functional	G Plant - floral visitor	0.90925	0	0.07125	0.00923	0.13648	NA	NA	NA
CHFU	2021	family	Intraspecific	0.21425	0	-0.07552	-0.18767	0.03300	NA	NA	NA
CHFU	2021	family	Plant - plant	0.175	0	-0.05167	-0.11365	0.01284	NA	NA	NA
CHFU	2021	family	Plant - herbivore	0.65325	0	0.02981	-0.06166	0.12731	NA	NA	NA
CHFU	2021	family	Plant - floral visitor	0.9405	0	0.06665	0.01483	0.11846	NA	NA	NA
CHFU	2021	species	Intraspecific	0.18475	0	-0.07974	-0.18337	0.02486	NA	NA	NA
CHFU	2021	species	Plant - plant	0.21775	0	-0.04271	-0.10391	0.02100	NA	NA	NA
CHFU	2021	species	Plant - herbivore	0.591	0	0.01877	-0.07055	0.10753	NA	NA	NA
CHFU	2021	species	Plant - floral visitor	0.89825	0	0.05305	0.00390	0.10204	NA	NA	NA

Table S1: Percentage of positive value for each interaction type for each focal, year and level of complexity. The mean, median, variance, 10% and 90% interval are also displayed. The "hat" designated group-specific parameters and their summed values.

659 **A.4 Bayesian sparse approach - details**

660 **A.4.1 Motivation**

661 As noted in the introduction of this paper, model overfitting is a major challenge
662 with individual performance models that incorporate too many parameters. Given
663 the severity of this challenge we felt it important to highlight the steps taken to
664 overcome it. Most notably, the use of a sparse modelling approach can avoid
665 overfitting when quantifying species interactions by using sparse estimation of
666 parameters (O'Hara and Sillanpää, 2009; Hastie, Tibshirani, and Wainwright, 2015).
667 We used this approach to infer simplicity by focusing only on the parameters that
668 are actively affecting a response variable, such as fecundity (Hastie, Tibshirani,
669 and Wainwright, 2015). Using sparse matrices does not eliminate parameters
670 due to their lack of information but rather evaluates which parameters have the
671 most relevant information about a system to answer a question (Piironen and
672 Vehtari, 2017). While it leads to conclusions specific to a system, it also brings out
673 generalities about types of ecological systems (Weiss-Lehman et al., 2022). For
674 instance, in this study we found that plant interactions are dominantly negative,
675 and grass individuals (Poaceae family) reinforced such competition, a conclusion
676 we speculate could be occurring in other grassland ecosystems as the Poaceae
677 family has distinct ecological strategies (Huang et al., 2024). An alternative to
678 this approach is to estimate all observed interactions and approximate the others,
679 which provides flexibility to field experience and relaxes concerns about unobserved
680 interactions (Bimler et al., 2023). However, the sparse matrix similarly relaxes the
681 requirement of field observation while facilitating convergence.

682 **A.4.2 Origin**

683 Weiss-Lehman et al. (2022) recently extended a Bayesian-Sparse modelling approach
684 for application with annual plant performance models such as the one used in this
685 study. By adopting this approach, we can consider numerous parameters without
686 overfitting our models. This Bayesian approach defines an interaction coefficient
687 according to a probability distribution rather than a constant value. By estimating
688 distributions, we can include natural variation in all of our parameters. The sparsity

689 approach then involves selecting the relevant parameters driving individual fecundity
690 by defining a 'sparse' matrix, which is one with many zero values, as is common in
691 most interaction datasets. To create this underlying matrix, we populated a matrix
692 composed of all plausible interactions between plants, pollinators and herbivores.
693 As most pairs were not observed, the matrix is 'sparse', meeting the requirements of
694 this approach. Based on this matrix, we are then able to define the net interaction
695 coefficients (e.g., α_{ij}) of a focal species i as the sum of a generic value per focal
696 species ($\bar{a}_{i,0}$) and a group-specific value for the neighbours j ($\hat{a}_{i,j}$) (fig. 2).

697 Additionally, we extended the approach to include higher-order interactions. To
698 do this, we used the approach detailed above but using an average effect specific
699 to each plant species pair set to 0. We set the generic HOI effect to 0 to maintain
700 reasonable parameter complexity and allowed only group-specific HOIs. That
701 is, for a focal species i , interacting with a set S of plant neighbours, the sparsity
702 approach defines S number of average effect \bar{b} , all set to zero, and S^2 number
703 of group-specific effects which can have a negative, positive or null effect of the
704 fecundity of i . Similar to pairwise interactions, the relevance of group-specific HOIs
705 is evaluated in the preliminary fit via shrinkage priors to include only relevant HOIs
706 in the final model (see Appendix, section A.4 for further details and equations).
707 We thus identify the relevant HOIs within plants and across trophic levels, that
708 is any significant effect from a herbivore or pollinator group on a plant pairwise
709 interactions.

710 **A.4.3 Plant-plant pairwise interactions**

711 According to the Sparsity approach, the plant-plant pairwise effect of species j on
712 species i is :

$$\alpha_{ij,t} = \bar{a}_{Plt,i0,t} + \hat{a}_{Plt,ij,t} \quad (\text{S1})$$

713 with $\bar{a}_{Plt,i0,t}$ the average effect of plant neighbours on individuals of species i and
714 $\hat{a}_{Plt,ij,t}$ the deviation from this average effect associated with species or group j .
715 The preliminary analysis determines if $\hat{a}_{Plt,ij,t}$ is statistically different than 0, in
716 which case it is included in the final model. For the intraspecific interaction (i.e.,
717 $i = j$), the $\bar{a}_{Plt,ii,t}$ is automatically set to zero, as the $\hat{a}_{Plt,ii,t}$ is always included in
718 the final model.

719 **A.4.4 Plant - herbivore/pollinator pairwise interactions**

720 Similarly, the plant-herbivore/pollinator pairwise effect of species m/l on species i
721 is defined by:

$$\alpha_{Herb,im,t} = \bar{a}_{Herb,i0,t} + \hat{a}_{Herb,im,t} \quad (\text{S2})$$

722 with $\bar{g}_{Herb,i0,t}$ the effect of an average herbivore individual on individuals of species
723 i and $\hat{g}_{Herb,im,t}$ the deviation from this average effect associated with group or
724 species m , during the growing season t . The same equation applies to $\alpha_{Pol,il,t}$.

725 **A.4.5 Higher-order interactions**

726 The sparse approach was extended to higher-order interactions, except that the
727 average effect specific to each plant species pair is set to 0. We defined the generic
728 HOIs effect to zero to maintain reasonable parameter complexity and allowed only
729 group-specific HOIs. That is, for a focal species i , interacting with a set S of plant
730 neighbours, the sparsity approach defines S number of average effect \bar{b} , all set to
731 zero, and S^2 number of group-specific effects which can have a negative, positive
732 or null effect of the fecundity of i . For the species pair i (focal) and j , the HOI is
733 defined as:

$$\beta_{H,ijk,t} = \bar{b}_{i0,t} + \hat{b}_{ijk,t} \quad (\text{S3})$$

734 with $\bar{b}_{i0,t} = 0$ the effect of an average hetero-specific interaction on species pairs
735 i, j and $\hat{b}_{ijk,t}$ the deviation from this average effect associated with species k . Here,
736 k is interchangeable with m and l , which designated the effect of a herbivore
737 and a pollinator on a plant-pairwise interaction. In the case of HOIs with a
738 pollinator($\beta_{Pol,ijl}$)/herbivore ($\beta_{H,ijm}$) changing the per capita effect of one plant on
739 another, the number of group-specific effects ($\hat{b}_{i,j,j}$ or $\hat{b}_{i,j,m}$) is $SPol$ or SH .

740 **A.4.6 Sparsity-inducing priors**

741 For each element defining the interacting parameters, we employ sparsity-inducing
 742 priors (i.e., sparsity is the property of being scattered), more specifically regularised
 743 horseshoe priors, to define both the average effect (*element*) and the deviation
 744 (*element*) (Weiss-Lehman et al., 2022). That is, in the preliminary fit, each
 745 parameter follows a specific prior distribution as follows:

$$\begin{aligned} \bar{\text{element}} &\sim N(0, \tau \tilde{\delta}_{0,j}) \\ \hat{\text{element}} &\sim N(0, \tau \delta_{e,j}) \end{aligned} \quad (\text{S4})$$

746 with τ the global tendency of the model towards sparsity. The sparsity of the
 747 model is set by the value of τ , with smaller values setting the priors for the deviation
 748 (group-specific parameter-*element*) more tightly centred on 0. Conversely, $\tilde{\delta}$ sets the
 749 deviation from 0, enabling group-specific parameters to bring the model away from
 750 sparsity. A higher individual $\tilde{\delta}$ term designated a wider prior for that group-specific
 751 parameter, leading to the inclusion in the final fit of that group-specific deviation
 752 from the average (Weiss-Lehman et al., 2022). In the regularized horseshoe prior,
 753 these $\tilde{\delta}$ terms are defined as

$$\begin{aligned} \tilde{\delta}_j &= \frac{c\delta_j}{\sqrt{c^2 + \tau\delta_j^2}} \\ \delta_j &\sim \text{half-Cauchy}(0, 1) \\ c^2 &\sim \text{inverse-delta}\left(\frac{v}{2}, \frac{vs^2}{2}\right) \end{aligned} \quad (\text{S5})$$

754 We followed the definition of these parameters by (Piironen and Vehtari, 2017;
 755 Weiss-Lehman et al., 2022): $\tilde{\delta}_j$ is the combination of a half-Cauchy and inverse-
 756 gamma distribution, which causes large coefficients to be shrunk towards 0 by a
 757 Student's t distribution with v degrees of freedom and a scale of s^2 . They set v to 4
 758 and s^2 to 2. They similarly set the global shrinkage parameter τ to a half-Cauchy
 759 prior with a scaled parameter equal to 1 ($\tau \sim \text{half-Cauchy}(0, 1)$).

760 **A.4.7 Intrinsic performance**

761 In both fits, the intrinsic fecundity of the focal species was defined as:

$$\lambda_i \sim \bar{\lambda}_i U_{i,t} \quad (\text{S6})$$

762 with $\bar{\lambda}_i$, the normalized intrinsic fecundity, defined by a normal prior $N(0, 1)$ with
 763 a range between 0 and 1; and $U_{i,t}$ the mean fecundity observed for focal species
 764 i at time t . This additional step in estimating the intrinsic fecundity assures the
 765 inclusion of a realistic intrinsic fecundity consistent with observations.

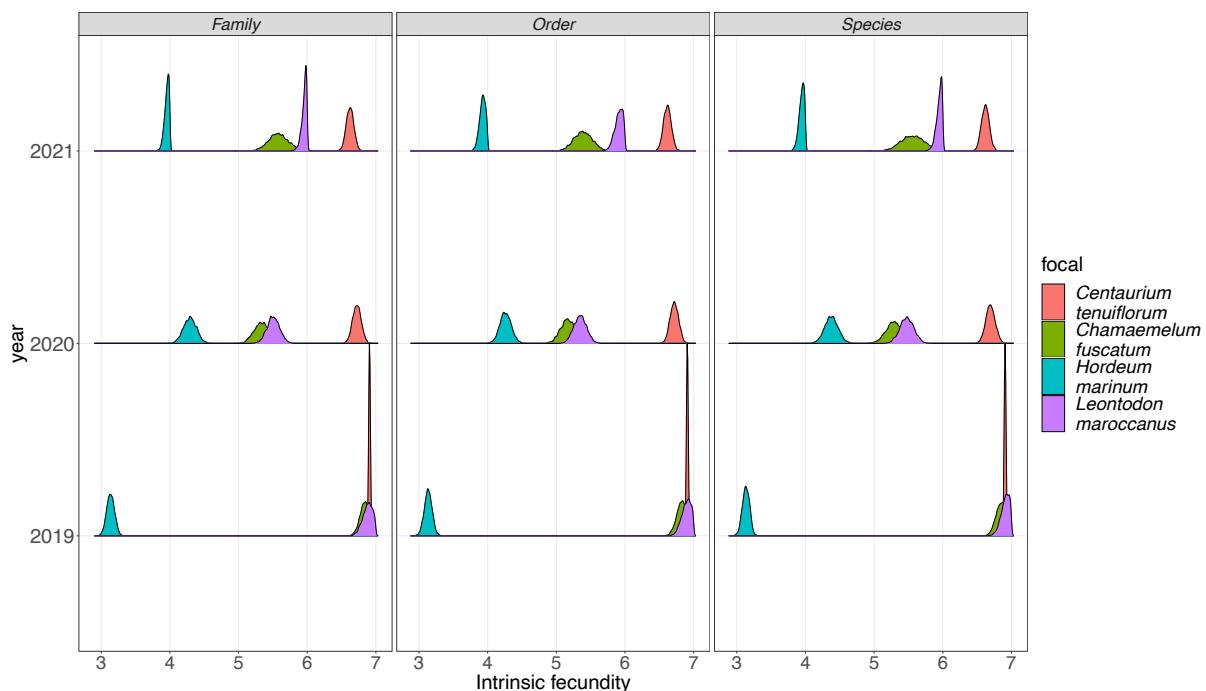


Figure S18: Intrinsic performance estimates for each year and focal species (log). The estimates for the season 2020 and 2021 are consistent. The 2019 season shows the response to the flooding that happened in 2018.

766 **A.4.8 Bayesian initial values**

767 All initial values of parameters were set to randomly draw between -2 and 2,
768 respecting the parameters' range for the initial fit. The final fit had specific initial
769 values for parameters $\bar{\lambda}_i$, $\bar{a}_{i,0}$, and α_{ii} , randomly drawn from a normal distribution
770 defined by the preliminary estimation of their mean and standard deviation.

771 **A.4.9 Bayesian priors**

772 To check the definition of our priors, we ran the preliminary and final model with
773 null data. That is, with all observations equal to zero. We can see that the priors
774 converge and adopt normal distributions within the given range of values.

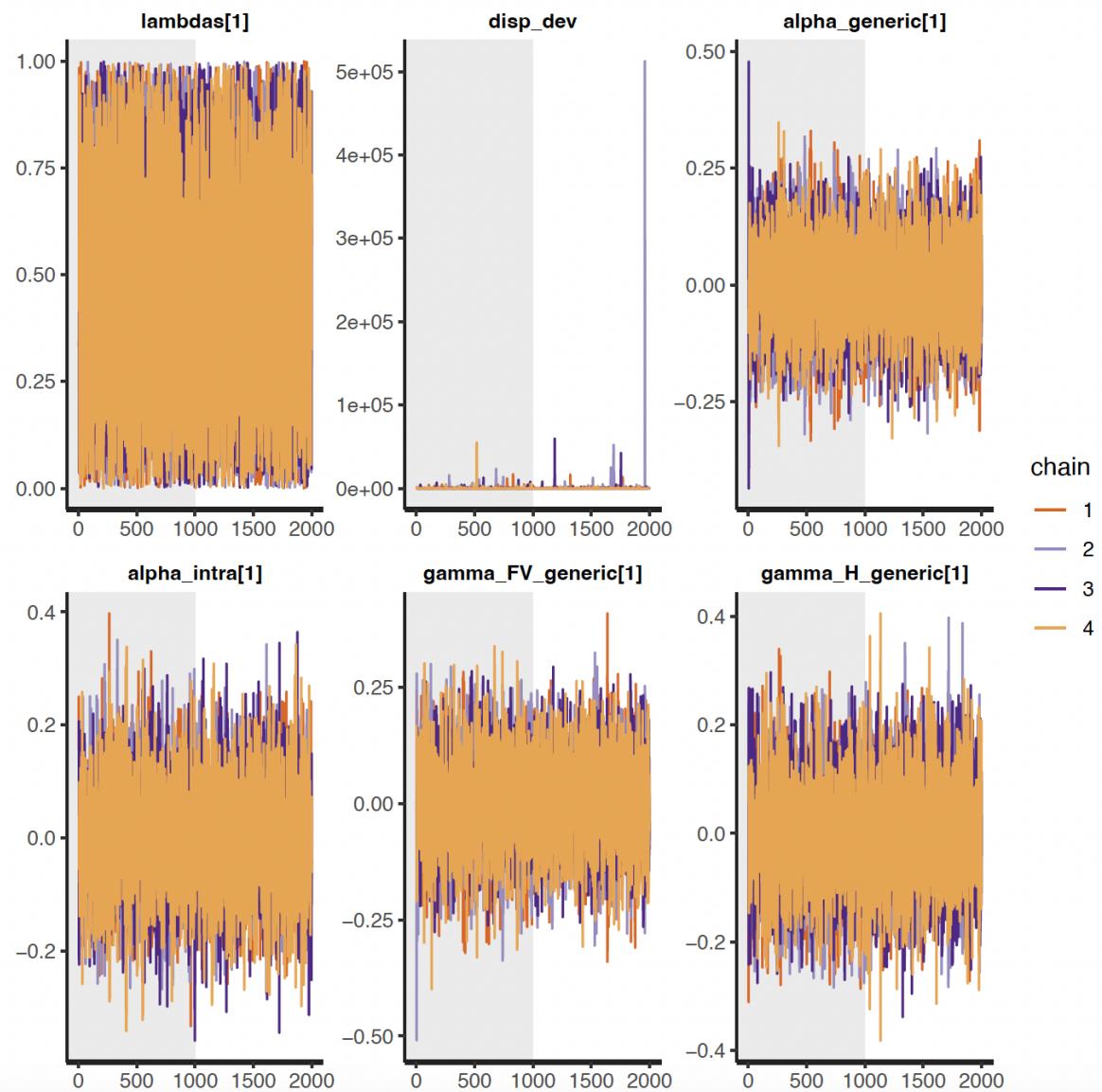


Figure S19: Trace plot for generic parameters of the preliminary fit model for the empty dataset. We can see that the priors converge and adopt normal distributions.

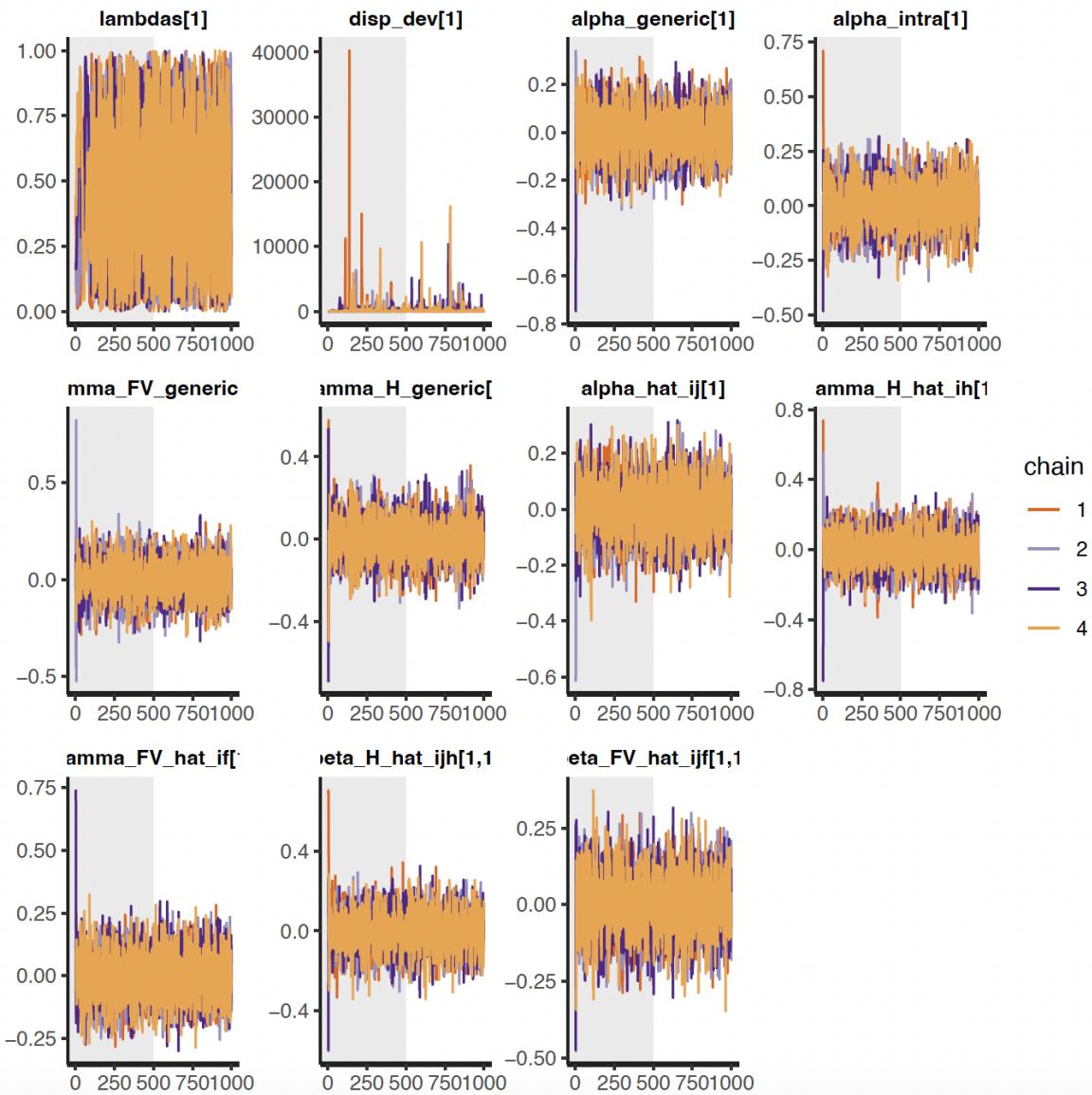


Figure S20: Trace plot for generic parameters and the first specific parameters for each trophic level of the final fit model for the empty dataset. We can see that the priors converge and adopt normal distributions.

775 **A.4.10 Model behaviour check**

776 The graphs of behaviours concerning each parameter and post-predictive checks can
777 be accessed in the supplementary file called "Supp_ModelsBehavior.pdf". For each
778 model, we checked for convergence using the Gelman–Rubin diagnostic ($Rhat$),
779 the precision of parameter estimates using the effective sample size ($Neff$) and
780 other behavioural statistics. All models' diagnostics follow Bayesian norms (e.g.,
781 $Rhat < 1.1$, $Neff > 500$).

782 The explanatory powers of the final fitted models were evaluated according
783 to Root mean squared deviance (RMSD) (Thomas, Yen, and Vesk, 2019) and
784 the leave-one-out approximation (Vehtari, Gelman, and Gabry, 2017). RMSD
785 is a measure of accuracy, defined as the square root of the mean of the squared
786 differences between observed data and model predictions (Thomas, Yen, and Vesk,
787 2019). While RMSD does not have an official threshold besides "the lower the
788 better", we compared it with the predictive range of the model for the minimum,
789 median and high abundance of neighbours. We supplement the RMSD with two
790 metrics looking at the predictive power of the models by estimating the effective
791 number of parameters and the theoretical expected log pointwise predictive density
792 for a new dataset ($p - loo$ and $elpd_{loo}$ in the "loo" R package version 2.7.0 Vehtari
793 et al., 2024). Finally, we compared the final fits of one focal and year across the
794 different grouping of neighbours by comparing their relative $elpd_{loo}$ ("loo" R
795 package version 2.7.0 Vehtari et al., 2024, tab.S3).

796 We computed the following metrics:

- 797 • Convergence using the Gelman–Rubin diagnostic ($Rhat$). The $Rhat$ can
798 be extracted from the stan fit object directly. Bayesian norms require
799 $\max(Rhat) < 1.1$.
- 800 • Precision of parameter estimates using the effective sample size ($Neff$). The
801 $Neff$ can be extracted from the stan fit object directly. Bayesian norms require
802 $\min(Neff) > 500$.
- 803 • Root mean squared deviance (RMSD) is a measure of accuracy, defined as the
804 square root of the mean of the squared differences between observed data(x)

805 and model predictions(y). We computed RMSD according to Thomas, Yen,
806 and Vesk (2019).

- 807 • Effective number of parameters ($p - loo$ in the "loo" R package version 2.7.0
808 Vehtari et al., 2024). When $p_{loo} < N$, with N the number of parameters
809 estimated in the model, we can assume that the model behaves well. On the
810 opposite, a model with $p_{loo} > N$ would describe a specification in the model.
- 811 • The theoretical expected log pointwise predictive density for a new dataset
812 ($elpd_{loo}$ in the "loo" R package version 2.7.0 Vehtari et al., 2024). $elpd_{loo}$ is
813 the log probability of the ability of the model to predict a new dataset.
- 814 • Diagnostic for Pareto smoothed importance sampling called L in the "loo" R
815 package version 2.7.0 Vehtari et al., 2024. The Pareto k diagnostic assesses
816 the extent to which removing a single observation from the overall distribution
817 affects the posterior distribution. If omitting an observation significantly alters
818 the posterior distribution, then it indicates that importance sampling may not
819 be able to provide a reliable estimate (Vehtari, Gelman, and Gabry, 2017).
820 When $k < \min(1 - 1/\log_{10}(S), 0.7)$, with S the number of observations,
821 describes a model with relatively good in-sample predictive power.

Table S2: Model behaviour for each final model. $Rhat < 1.1$ and $Neff > 100$ are necessary conditions to ensure the good behaviour of the model. Evaluated according to Root mean squared deviance (Thomas, Yen, and Vesk, [2019]) and the leave-one-out approximation (Vehtari, Gelman, and Gabry, [2017]).

focal	year	complexity	nparameter	n. obs	Rhat	Neff	mean fec observed	sdfec obs	min/maxsd	mean/rmsd	min/maxsd	Sim/Bias	Rrequired	Requiredsd	perc.R	Pearo	Prace/Check	elpdia/o	elpdiao/e
LFEMA	2019	class	6	290	1.00	1602.89	537.78	577.68	668.58	623.25	713.93	148.25	0.15	0.00	3.8+0.4	Good specification	2170.0447	11.0535502	
LFEMA	2019	family	6	290	1.00	1441.70	537.78	577.68	667.43	631.33	711.53	1625.15	0.21	0.14	0.00	3.6+0.3	Good specification	-2166.8816	11.0249541
LFEMA	2019	species	5	290	1.00	1244.77	537.78	577.68	658.69	624.79	690.37	1012.89	0.21	0.13	0.00	3.6+0.4	Good specification	-2170.8583	10.149976
LFEMA	2020	class	7	270	1.00	1203.80	332.91	422.90	589.45	492.84	929.38	391.34	0.68	0.22	0.00	3.5+0.8	Good specification	-1755.2685	18.7840841
LFEMA	2020	family	6	270	1.00	1382.40	332.91	422.90	575.25	491.70	876.22	471.00	0.63	0.23	0.00	5.2+0.7	Good specification	-1755.8812	18.84363942
LFEMA	2020	species	6	270	1.00	1540.43	332.91	422.90	575.82	497.80	810.96	442.71	0.64	0.23	0.00	5.3+0.7	Good specification	-1757.9581	18.787557
LFEMA	2021	class	6	288	1.00	1420.74	349.92	361.33	362.27	354.02	378.93	618.61	0.07	0.05	0.00	5.6+2.2	Good specification	-1931.4485	15.661019
LFEMA	2021	family	5	288	1.00	1237.38	349.92	361.33	361.53	356.42	376.34	1161.64	0.05	0.03	0.00	4.2+0.9	Good specification	-1932.2387	15.590784
LFEMA	2021	species	5	288	1.01	1452.76	349.92	361.33	364.10	355.16	391.23	778.32	0.09	0.05	0.00	4.3+1.1	Good specification	-1927.7544	15.590784
CFHU	2019	class	5	252	1.00	1320.45	682.80	698.43	752.90	734.07	802.69	482.17	0.18	0.10	0.00	3.1+0.3	Good specification	-2190.0785	8.88578332
CFHU	2019	family	5	252	1.00	1511.82	682.80	698.43	751.08	731.26	790.98	528.32	0.18	0.10	0.00	3.1+0.3	Good specification	-2186.5689	8.89044684
CFHU	2019	species	5	252	1.00	1496.75	682.80	698.43	751.59	733.43	799.83	531.29	0.19	0.10	0.00	3.3+0.3	Good specification	-2189.2002	8.8961045
CFHU	2020	class	6	159	1.00	1671.32	176.86	266.57	251.12	297.48	243.05	0.04	0.04	0.01	3.6+0.7	Good specification	-978.03149	16.757671	
CFHU	2020	family	7	159	1.00	1298.88	176.86	255.33	274.57	259.00	308.31	354.57	0.07	0.06	0.00	3.6+0.6	Good specification	-971.84939	16.5402644
CFHU	2020	species	6	159	1.01	1479.55	176.86	255.33	275.91	255.04	420.18	299.16	0.08	0.08	0.00	3.9+0.7	Good specification	-973.56896	16.5204564
CFHU	2021	class	5	125	1.00	1832.95	254.14	307.84	305.06	325.78	327.46	122.22	0.02	0.02	0.00	3.8+0.7	Good specification	-812.92078	11.2282523
CFHU	2021	family	5	125	1.00	1418.84	254.14	304.51	304.51	300.13	325.09	13.52	0.04	0.04	0.00	3.9+0.8	Good specification	-811.95779	11.3502227
CFHU	2021	species	5	125	1.01	1280.18	254.14	307.84	302.59	296.33	319.16	8.20	0.03	0.03	0.00	4.2+0.8	Good specification	-812.62477	11.2448888
HODMA	2019	class	4	247	1.01	1375.10	122.24	97.51	97.87	97.13	103.04	0.60	0.01	0.00	3.2+0.3	Good specification	-1457.0558	12.066629	
HODMA	2019	family	4	247	1.00	1348.77	122.24	97.51	97.86	97.11	103.76	1.07	0.01	0.00	3.1+0.3	Good specification	-1436.9407	12.0405615	
HODMA	2019	species	4	247	1.00	1366.83	122.24	97.51	97.86	106.27	139.00	0.01	0.01	0.00	3.3+0.4	Good specification	-1437.0801	12.0922732	
HODMA	2020	class	4	194	1.00	1292.21	326.44	355.33	350.38	348.06	368.31	5.80	0.04	0.04	0.00	3.6+0.6	Good specification	-131.518211	15.5767959
HODMA	2020	family	4	194	1.00	1311.81	326.44	355.33	350.39	348.06	363.89	4.88	0.04	0.04	0.00	3.8+0.6	Good specification	-131.518259	15.584090
HODMA	2020	species	4	194	1.00	1505.15	326.44	355.23	350.32	348.08	368.97	2.46	0.04	0.03	0.00	3.7+0.6	Good specification	-131.5183985	15.55683938
HODMA	2021	class	5	218	1.00	1625.34	220.37	235.04	231.79	227.70	255.71	0.28	0.02	0.02	0.00	4.4+0.8	Good specification	-139.7236	16.164229
HODMA	2021	family	4	218	1.00	1338.68	220.37	235.04	231.10	227.34	240.28	0.47	0.02	0.02	0.00	4.8+1.3	Good specification	-139.5588	16.1616614
HODMA	2021	species	5	218	1.01	1418.77	220.37	235.04	231.36	227.31	250.08	0.14	0.03	0.01	5.1+1.3	Good specification	-139.58546	16.1755026	
CETE	2019	class	4	68	1.00	1717.42	1167.37	699.66	703.03	68.593	899.16	354.24	0.03	0.03	0.00	3.1+1.1	Good specification	-540.72431	5.8329247
CETE	2019	family	4	68	1.01	1431.07	1167.37	699.66	702.31	68.576	851.17	219.53	0.03	0.04	0.00	3.2+1.2	Good specification	-540.72431	5.9246756
CETE	2019	species	4	68	1.00	1397.93	1167.37	699.66	702.55	68.04	913.25	260.53	0.03	0.01	0.01	3.2+1.2	Good specification	-540.71675	5.90295473
CETE	2020	class	5	187	1.00	1325.16	109.41	805.44	805.21	793.28	913.83	190.02	0.02	0.03	0.00	3+0.4	Good specification	-1481.2673	10.80977
CETE	2020	family	5	187	1.01	1507.74	109.41	805.44	805.12	793.54	883.73	229.71	0.02	0.02	0.00	3+0.4	Good specification	-1481.2581	10.8958923
CETE	2020	species	5	187	1.00	1737.77	109.41	805.44	806.31	793.95	930.61	160.80	0.02	0.03	0.00	3+0.4	Good specification	-1481.4591	10.8894184
CETE	2021	class	5	186	1.01	1765.27	746.61	619.63	62.95	708.02	422.22	0.01	0.01	0.00	2.8+0.5	Good specification	-1481.3563	11.0588975	
CETE	2021	family	5	186	1.00	1320.89	746.61	619.63	621.90	614.24	680.01	22.19	0.01	0.01	0.00	2.7+0.4	Good specification	-1481.2771	11.096935
CETE	2021	species	5	186	1.00	1346.37	746.61	619.63	621.96	613.98	738.71	38.02	0.01	0.00	2.7+0.4	Good specification	-1481.2771	11.0670526	

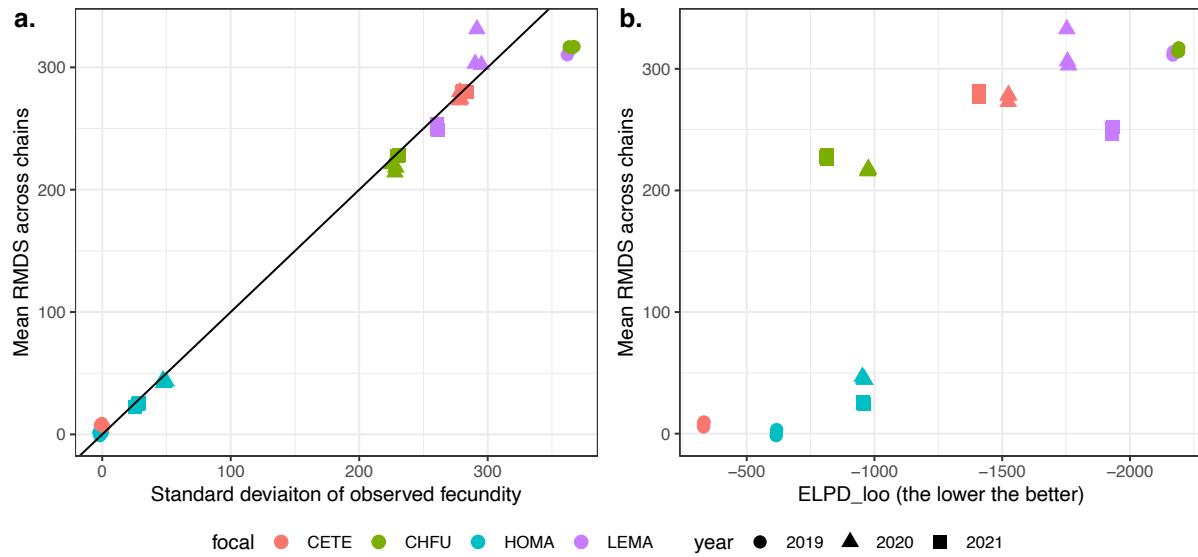


Figure S21: Relationships between the mean RMDS of each model and (a) the standard deviation of the observed fecundity; (b) the $elpd_{loo}$ of the model. For panel (a), models with a RMDS lower than the standard deviation have a good explanatory power. All models are close to the standard deviation, showing that all model are either good (i.e., $sd(x) > mean(rmds)$) or moderately good (i.e., $sd(x) > mean(rmds)$) at explaining the data. Panel (b) shows the relation between a model's RMDS and its $elpd_{loo}$. Models with small RMDS have concurrently high $elpd_{loo}$.

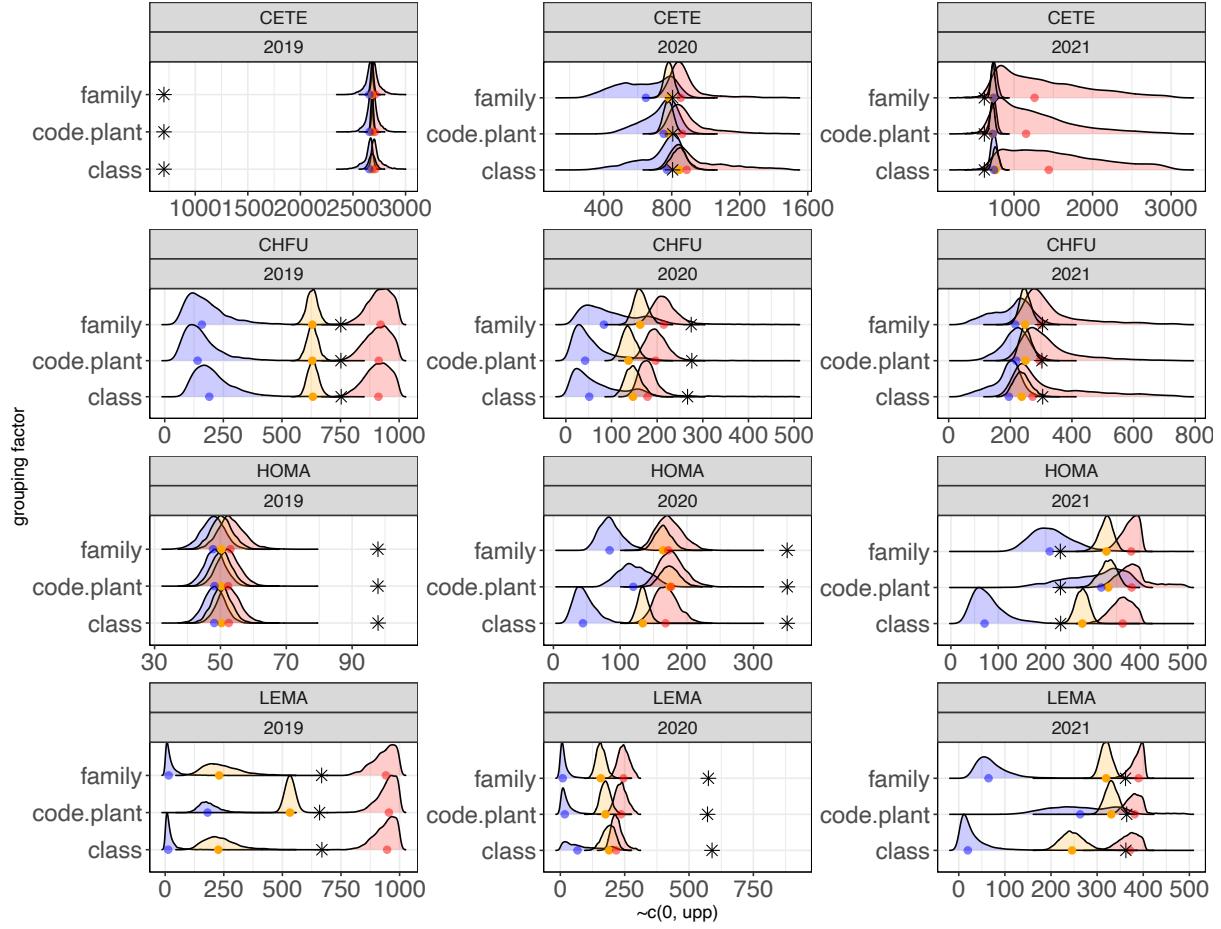


Figure S22: Representation of the deterministic explanatory power of each model (e.g., LEMA in 2020 with neighbours grouped as Family) with RMSD. The position of the mean RMSD compared to the three fecundity ranges (x-axis) shows the explanatory power of the model. Rows show a focal species; columns are years, and the y-axis is the grouping factors. The blue distribution is the fecundity range of the focal computed when the neighbourhood has a maximum effect (high abundance) and inversely for the red distribution. The orange distribution is the fecundity range of the focal computed when the neighbourhood has an average effect (mean abundance and median impact). The mean RMDS and its lower and upper quantiles are computed across chains for each model in black. A low RMDS is "better", especially if it is lower than the red distribution, showing that the model can distinguish between a scenario with high and low abundance of neighbours. For instance, for LEMA - 2021 -family, RMSD is in the blue violin, showing a low bias compared to the predicted mean and maximum range of fecundity. Inversely, for the model LEMA - 2020 -family, the RMDS is in the red violin, showing a higher bias and a limited explanatory power. This figure helps to relate the unit of the RMSD with the response variable.

822 **A.4.11 Model comparison**

823 For one focal species and one year, we compared the model when the neighbourhood
824 was gathered according to three different grouping factors: functional class, family
825 and species. We use the *loo_compare* function (*loo_compare* in the "loo" R
826 package version 2.7.0 Vehtari et al., 2024), which compares the $elpd_{loo}$ (i.e., log
827 probability of the ability of the model to predict a new dataset). From $elpd_{loo}$, we
828 can compare multiple model fits of one dataset (here between different groups of
829 the neighbourhood: class, family or species) by comparing the $elpd_{diff}$. SE_{diff}
830 is the standard error of component-wise differences of $elpd_{loo}$ for two models.
831 If $SE_{diff} * 1.96 < elpd_{diff}$, then the models are significantly different (Vehtari,
832 Gelman, and Gabry, 2017).

Table S3: Model comparison using the "loo" R package version 2.7.0 Vehtari et al., [2024] Overall, no grouping factor is selected. Only "class" (or functional grouping) is selected as a significantly inferior model in three occurrences.

focal	year	model	$elpd_{diff}$	$se_{elpd_{diff}}$	$elpd_{loo}$	$se_{elpd_{loo}}$	p_{loo}	$se_{p_{loo}}$	looc	se_{looc}	sign.int	significance
LEMA	2019	Family	0	0	-2169.882	11.025	3.598	0.334	4339.763	22.050	0.000	not significantly diff
LEMA	2019	Class	-0.1631665	0.56925593	-2170.045	11.055	3.757	0.354	4340.089	22.111	1.116	not significantly diff
LEMA	2019	Species	-0.9767104	1.29718669	-2170.858	10.795	3.626	0.368	4341.717	21.590	2.542	not significantly diff
LEMA	2020	Class	0	0	-1755.269	18.784	5.533	0.805	3510.537	37.568	0.000	not significantly diff
LEMA	2020	Family	-0.6126776	2.89091611	-1755.881	18.848	5.250	0.680	3511.762	37.697	5.666	not significantly diff
LEMA	2020	Species	-2.1265758	3.21356922	-1757.395	18.879	5.345	0.651	3514.790	37.758	6.299	not significantly diff
LEMA	2021	Species	0	0	-1927.754	15.370	4.310	1.092	3855.509	30.741	0.000	not significantly diff
LEMA	2021	Family	-4.4842677	2.93144727	-1932.239	15.891	4.185	0.901	3864.477	31.782	5.746	not significantly diff
LEMA	2021	Class	-5.394096	1.56065354	-1933.148	15.663	5.649	1.976	3866.297	31.326	3.059	significantly diff
CHFU	2019	Species	0	0	-2189.200	8.896	3.260	0.327	4378.400	17.792	0.000	not significantly diff
CHFU	2019	Family	-0.3687258	0.40252402	-2189.569	8.899	3.118	0.335	4379.138	17.798	0.789	not significantly diff
CHFU	2019	Class	-0.8783294	0.56609209	-2190.079	8.886	3.080	0.283	4380.157	17.772	1.110	not significantly diff
CHFU	2020	Family	0	0	-971.849	16.540	3.584	0.598	1943.699	33.081	0.000	not significantly diff
CHFU	2020	Species	-1.5195767	0.90557773	-973.369	16.820	3.887	0.723	1946.738	33.641	1.775	not significantly diff
CHFU	2020	Class	-6.1821055	1.55774287	-978.031	16.758	3.601	0.711	1956.063	33.515	3.053	significantly diff
CHFU	2021	Family	0	0	-811.958	11.335	3.931	0.765	1623.916	22.670	0.000	not significantly diff
CHFU	2021	Species	-0.6669801	1.06003738	-812.625	11.245	4.217	0.770	1625.250	22.490	2.078	not significantly diff
CHFU	2021	Class	-0.9629905	1.51836295	-812.921	11.223	3.776	0.711	1625.842	22.446	2.976	not significantly diff
HOMA	2019	Family	0	0	-1436.941	12.041	3.139	0.338	2873.881	24.081	0.000	not significantly diff
HOMA	2019	Class	-0.11151345	0.12023234	-1437.056	12.067	3.195	0.348	2874.112	24.133	0.236	not significantly diff
HOMA	2019	Species	-0.139459	0.07414302	-1437.080	12.092	3.259	0.363	2874.160	24.185	0.145	not significantly diff
HOMA	2020	Class	0	0	-1315.821	15.577	3.646	0.575	2631.642	31.154	0.000	not significantly diff
HOMA	2020	Family	-0.0748174	0.17231429	-1315.896	15.584	3.801	0.603	2631.792	31.168	0.338	not significantly diff
HOMA	2020	Species	-0.0774048	0.07946359	-1315.899	15.557	3.749	0.596	2631.797	31.114	0.156	not significantly diff
HOMA	2021	Family	0	0	-1393.588	16.162	4.830	1.255	2787.176	32.323	0.000	not significantly diff
HOMA	2021	Class	-0.1354742	0.80630568	-1393.724	16.116	4.358	0.841	2787.447	32.233	1.580	not significantly diff
HOMA	2021	Species	-0.2664159	0.23837223	-1393.855	16.176	5.062	1.273	2787.709	32.351	0.467	not significantly diff
CETE	2019	Class	0	0	-540.714	5.853	3.129	1.104	1081.427	11.706	0.000	not significantly diff
CETE	2019	Species	-0.00304	0.07103122	-540.717	5.903	3.160	1.151	1081.433	11.806	0.139	not significantly diff
CETE	2019	Family	-0.010598	0.10226118	-540.724	5.925	3.195	1.162	1081.449	11.849	0.200	not significantly diff
CETE	2020	Family	0	0	-1481.258	10.896	2.961	0.393	2962.516	21.792	0.000	not significantly diff
CETE	2020	Class	-0.009196	0.04468646	-1481.267	10.881	2.956	0.387	2962.535	21.762	0.088	not significantly diff
CETE	2020	Species	-0.2009627	0.138892	-1481.459	10.889	3.026	0.399	2962.918	21.779	0.272	not significantly diff
CETE	2021	Species	0	0	-1418.273	11.067	2.721	0.437	2836.545	22.134	0.000	not significantly diff
CETE	2021	Family	-0.0043675	0.04307259	-1418.277	11.097	2.737	0.431	2836.554	22.194	0.084	not significantly diff
CETE	2021	Class	-0.0835341	0.02128665	-1418.356	11.059	2.822	0.461	2836.713	22.118	0.042	significantly diff

833 **A.4.12 All years together**

834 To evaluate if the estimation of generic interactions are consistent when lumping all
 835 years of observed data together, we ran the model without dividing the dataset per
 836 year. All main findings hold, and estimations of generic interactions are similar.

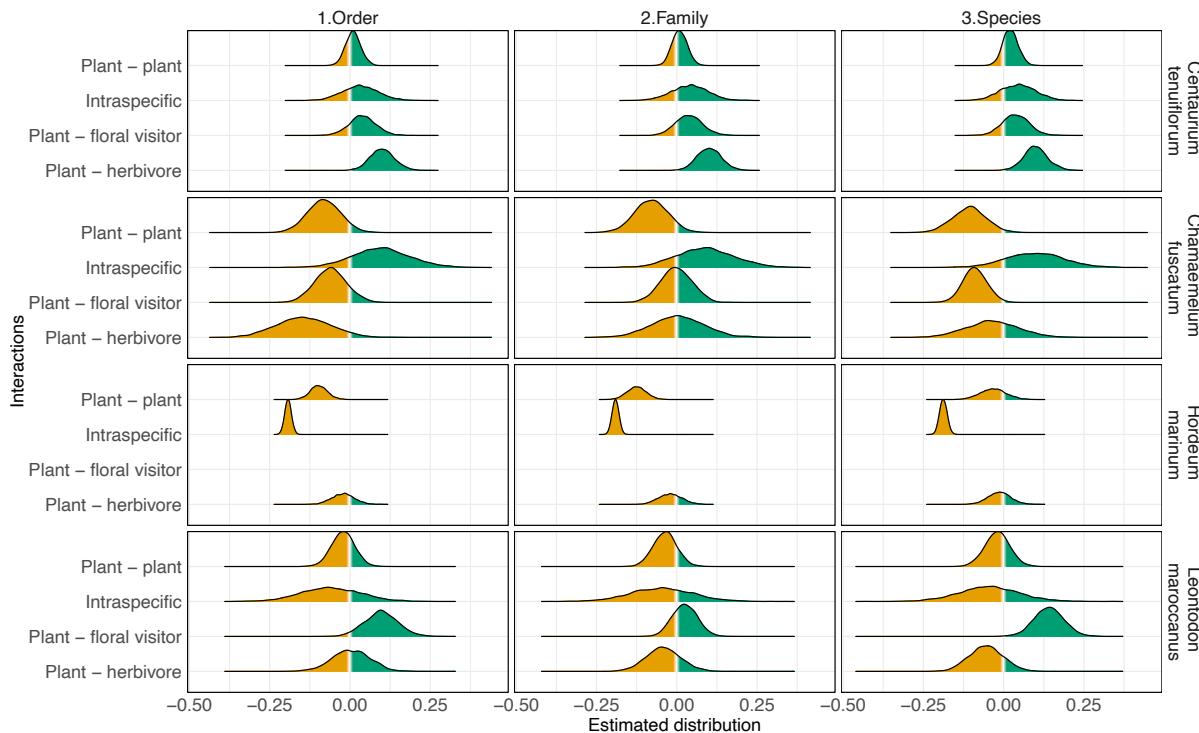


Figure S23: Estimates of generic interactions for each focal when all years are lumped together. Main findings hold, with plant-plant interactions stronger and more competitive overall. Yet, plant-herbivores interactions do not show a strong positive effect for LEMA as observed for 2020 in fig. 3. All distributions resemble the distributions computed for each year (fig. S12, fig. S13, and fig. S14). The year 2019 has slightly narrower distributions, especially for CETE and HOMA, probably due to the lower number of neighbourhood surveys (fig. S4).

837 **A.4.13 With simulated data**

838 To evaluate the theoretical framework developed, we computed a simulated commu-
839 nity based on pre-defined interaction coefficients, abundances of plant neighbours,
840 and individuals of a higher trophic level; here, we considered pollinators and
841 herbivores. Based on these parameters, the distribution of a focal plant species
842 (named K1) potentially interacting with 5 plant neighbours, 5 pollinators, and 5
843 herbivores was drawn. This simulated fecundity and the community abundances
844 were used to evaluate the behaviour of the theoretical framework (identical to the
845 main results) around two main challenges.

846 The first challenge was to include HOIs and a Ricker population model (Ricker,
847 1954), which allowed for multispecies interactions and facilitation, respectively. For
848 the model fitting, we checked for convergence using the Gelman–Rubin diagnostic
849 (Rhat), the precision of parameter estimates using the effective sample size (Neff)
850 and other behavioural statistics. All models' diagnostics follow Bayesian norms
851 (e.g., Rhat was equal to $1.006827 < 1.1$, Neff was equal to $360.97 > 100$).

852 The second challenge concerned the Sparsity approach. Including HOIs and
853 higher-trophic levels increased exponentially the number of parameters included in
854 the individual fitness model. Fortunately, Weiss-Lehman et al. (2022) specifically
855 developed the Bayesian-Sparse approach to tackle the challenge of handling many
856 parameters. Nevertheless, we checked the correct detection of group-specific
857 parameters by running the preliminary and final fit. The preliminary fit identifies
858 the group-specific interactions relevant to the correct fit of the individual fitness
859 model. As a result, the preliminary fits of the HOIs model identify all plant-specific
860 pairwise interactions as relevant effects for individual fecundity.

861 For both challenges, we compared parameters estimated with the initial parame-
862 ters set to compute the simulated community (fig. S24). We judged the accuracy
863 (closeness to the set values) of the estimation of the parameters to be good. Indeed,
864 the distributions of the estimations accurately centred around the set values.

865 **References**

866 R. B. O'Hara and M. J. Sillanpää (Mar. 2009). “A review of Bayesian variable
867 selection methods: what, how and which”. In: *Bayesian Anal* 4 (1), pp. 85–117

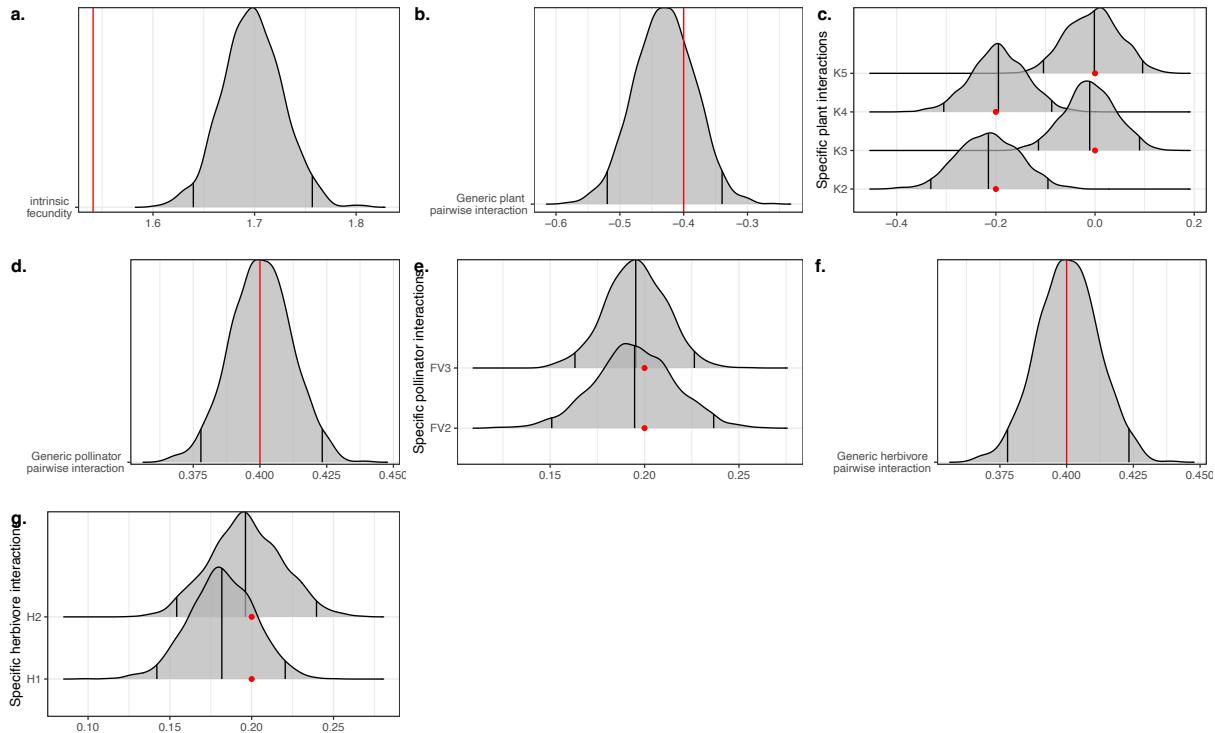


Figure S24: Distribution of the estimated parameters compared to the set parameters (red point or line) of the simulated community for focal plant K1. Each model leads to different estimations. **a** Intrinsic fecundity distributions of focal K1 for each model. **b** Plant generic pairwise interaction distributions with the focal K1. **c** Plant-specific pairwise interaction distributions. **d** Pollinator pairwise interaction distributions with the focal K1. **e** Pollinator-specific pairwise interaction distributions. **f** Herbivore pairwise interactions distributions with the focal K1. **g** Herbivore-specific pairwise interaction distributions.

- 868 Trevor Hastie, Robert Tibshirani, and Martin Wainwright (Jan. 2015). “Statistical
 869 learning with sparsity: The lasso and generalizations”. In: *Statistical Learning*
 870 with Sparsity: The Lasso and Generalizations, pp. 1–337
- 871 Aki Vehtari, Andrew Gelman, and Jonah Gabry (Sept. 2017). “Practical Bayesian
 872 model evaluation using leave-one-out cross-validation and WAIC”. in: *Statistics*
 873 and Computing 27 (5), pp. 1413–1432
- 874 Juho Piironen and Aki Vehtari (2017). “Sparsity information and regularization in
 875 the horseshoe and other shrinkage priors”. In: *Electronic Journal of Statistics* 11.2,

- 876 pp. 5018–5051
- 877 Freya M. Thomas, Jian D.L. Yen, and Peter A. Vesk (Feb. 2019). “Using functional
878 traits to predict species growth trajectories, and cross-validation to evaluate these
879 models for ecological prediction”. In: *Ecology and Evolution* 9 (4), pp. 1554–1566
- 880 Christopher P. Weiss-Lehman et al. (May 2022). “Disentangling key species inter-
881 actions in diverse and heterogeneous communities: A Bayesian sparse modelling
882 approach”. In: *Ecology Letters* 25 (5), pp. 1263–1276
- 883 Malyon D Bimler et al. (Feb. 2023). “Estimating interaction strengths for diverse
884 horizontal systems using performance data”. In: *Methods in Ecology and Evolution*
885 00, pp. 1–13
- 886 Kailing Huang et al. (May 2024). “Why are graminoid species more dominant?
887 Trait-mediated plant–soil feedbacks shape community composition”. In: *Ecology*,
888 e4295

889