Supplementary methods and analysis from "*Dominant bee species and floral abundance drive parasite temporal dynamics in plant-pollinator communities*", Graystock *et al.*

Broad multiplex PCR panels to diagnose major bee parasites

We first screened samples for three groups of taxa known to contain common pollinator parasites, trypanosomatids, Microsporidians and *Apicystis*, in multiplex [1]. Samples determined to be positive for either Trypanosome or Microsporidia were then used in further multiplex assays to determine the presence of trypanosomes common in North American bees (*Crithidia bombi, C. expoeki*) or Microsporidians (*Nosema bombi, N. ceranae*) respectively. *Apicystis bombi* is the only *Apicystis* species reported in bees, so further multiplexes were not performed on these positives. In addition to this multiplex, we ran a host control on all bee samples using Apidae general primers [2] which we found to amplify across the broad range of hosts used here. For all Primers, subsets of positives were sequenced to confirm correct amplification. Primers, reagent concentrations, and thermal cycling conditions are shown in Supplementary Table 1.

Trypanosomatid multiplex to diagnose two common Crithidia parasite species

Samples found to be positive for trypanosomatids in the broad multiplex were then further screened in a multiplex designed to indicate single and dual infections of *C. bombi* and *C. expoeki*, which was developed as part of previously published project [3]. Primers, reagent concentrations, and thermal cycling conditions are shown in Supplementary Table 1.

Microsporidia multiplex to diagnose two common Nosema parasite species

Samples found to be positive for Microsporidia in the broad multiplex were then further screened in a duplex designed to indicate single and dual infections of *N. bombi* and *N. ceranae.* Although most of the genetic data associated with the Microsporidia on GenBank is based on portions of the small subunit region (16S), we were interested in using less variable regions that were highly discernable in each species. Using a modified version of primers NoscRNAPol-F2 (5’-GGGTTCCCTAAACCTGGTGGTTT-3’ and NoscRNAPol-R2 (5’-TCACATGACCTGGTGCTCCTTCT -3’) that amplify a >600 bp region of largest subunit of the protein-coding DNA-dependent, RNA polymerase II (RPB1) [4], we obtained sequences of *N. bombi* (MG494263) and *N. ceranae* (MN175395). These were aligned with available *N. ceranae* (XM_002995356) and *N. apis* (JX213670) sequences from GenBank in Geneious v.6.1.8 (Biomatters, Auckland, NZ). With the aid of the Primer 3 plug-in [5], we selected suitable priming regions unique to *N. bombi* or *N. ceranae.*

Potential primers were then examined to ensure that they would not produce amplicons for non-target species and that amplicons for each species could be visually differentiated by routine electrophoresis based on their size differential. Representative sequences of a variety of Microsporidia (*N. apis*: DQ996230, DQ996232, JX213663, JX213665, JX213751, JX213670, HQ457438, HQ457435, HQ457436; *N. bombycis:* JX213751; *N. disstriae:* HQ457438; *N. empoascae:* DQ996232; *N. fumiferanae:* HQ457438; *N. granulosis:* DQ996233; *N. lymantriae:* JX213749; *N.* sp.: HQ457436, HQ457437; *N. trichoplusiae:* DQ996234; *Varimorpha necatrix:* DQ996236), were screened to ensure primer specificity. A final set of differential primers was selected from those that had similar melting temperatures and minimal interactions when combined in a single reaction. The novel primer set NB185F (5’- ACTAAGCCAATGTTCCACGTT -3’) and NB185R (5’-CCAGTAAACCCACTTTCACAGAT -3’) produces an amplicon 185 bp long if *N. bombi* DNA is present, and NC288F (5’- TGAGGGAGAATTAACCGAGGC-3’) plus NC288R (5’-AGCATCCCTTCCATAACAATAGATG-3’) produces an amplicon 288 bp in the presence of *N. ceranae* DNA.

Before being applied to the samples in this experiment, primer sets were tested in PCR both singly and in combination with positives and negatives verified by microscopy to ensure accurate diagnosis. Sequences of *N. ceranae* obtained with the NC288F-NC288R primer set were deposited on Genbank (MG494264, MG494265; 242 bp with primer regions trimmed), but because *N. bombi* sequences obtained with NB185F-NB185R were < 200 bp, they were not eligible for deposition. A representative sequence (141 bp with the primer regions trimmed) is 5’-GGGTACATGAACAAGATCAAAAAGATTTTAGAATGTGTGTGCTACTATTGTTCAAAAATAAAAATTGACAAGAAATCTTTGAAGAAAGACTTGAATTTTGTATGGAATGCTTGTAAAGCTAAAGCAGTTTGTGAAGGAGAA-3’ (Internal Sample Numbers AS107, WC066). Extracted DNA and slide-mounted tissues are archived at the USDA-Pollinating Insects Research Unit in Logan, Utah. Primers, reagent concentrations, and thermal cycling conditions are shown in Supplementary Table 1.

Supplementary Table 1 | PCR mixes and conditions for the detection of the various parasites.

Primers & source	Assay mix								Thermal cycling			Amplicon size (bp)
	dNTP (mM)	$MgCl_2$ (mM)	5xbuffer (µl)	Taq (U)	Primer F (µM)	Primer R (µM)	Template (µl)	Total volume (µl)	1 - Denaturing Min | Temp	2 - Replication Sec | Temp	3- Elongation Min | Temp	
Broad multiplex *Trypanosomatids*$_{TA}$ *,* *Microsporidia*$_{MA}$ *& Apicystis*$_{AB}$ 1 *CB-SSUrRNA-F2 (5-3): CTTTTGACGAACAACTGCCCTATC* *CB18SR2 (5-3): TGCTCCTTTGTTATCCCATGCT* *MSporF2 (5-3): AGTGGTGCATGGCCGTTTTC* *MSporDegR (5-3): GGTGTGTRCAAAGAACAGGG* *Apicyst357F (5-3): AGCGATGGATGTCTTGGGTC* *Apicyst357R (5-3): CCTAGTTAGTTTCTTTTCCTCCGC*	0.4	2.5	2.6	1	0.8 TA 0.8 MA 0.8 AB	0.8 TA 0.8 MA 0.8 AB	1	10	2 | 94	10x 30 | 94 30 | 60 45 | 72 30x 30 | 94 30 | 57 45 | 72	5 | 72	584TA 270MA 357AB
Crithidia Multiplex *C. sp,*$_{C}$ *C. bombi*$_{CB}$ *and C. expoeki*$_{CE}$ 3 *Crith18SF (5-3): TACCACTTCTACGGAGGGCA* *CB18SR2 (5-3): TGCTCCTTTGTTATCCCATGCT* *CB279F (5-3): ATACTCATATTTTAGTGTGGGCTGT* *CB279R (5-3): AACAAAACAAATGCATTACAATAACTA* *CE163F (5-3): TGTACTATGATGTCGTATTGAGGT* *CE163R (5-3): ATACAAATGGCAATAAAACATGTAAAA*	0.4	2.5	2.6	1	0.8 C 0.8 CB 0.8 CE	0.8 C 0.8 CB 0.8 CE	1	10	2 | 94	40x 45 | 94 45 | 57 60 | 72	7 | 72	470C 279CB 163CE
Nosema Duplex *N. bombi*$_{NB}$ *and N. ceranae*$_{NC}$ (This study) *NB185F (5-3): ACTAAGCCAATGTTCCACGTT* *NB185R (5-3): CCAGTAAACCCACTTTCACAGAT* *NC288F (5-3): TGAGGGAGAATTAACCGAGGC* *NC288R (5-3): AGCATCCCTTCCATAACAATAGATG*	0.4	2.5	2.6	1	0.8 NC 0.8 NB	0.8 NC 0.8 NB	1	10	2 | 94	40x 45 | 94 45 | 57 60 | 72	5 | 72	288NC 185NB
Host control *Apidae* 2 *ApidaeF(5-3): AGATGGGGGCATTCGTATTG* *ApidaeR(5-3): ATCTGATCGCCTTCGAACCT*	0.2	1.5	2	1.25	0.2	0.2	1	10	2 | 94	35x 60 | 94 60 | 57 60 | 72	5 | 72	130

Supplementary Table 2 | Parasite prevalence among the 89 species of flowers that were screened. (*n* = 2,631 individual flowers were screened in total.)

Plant species	**Samples screened**	**Percent positive with *Nosema bombi***	**Percent positive with *Nosema ceranae***	**Percent positive with *Crithidia bombi***	**Percent positive with *Crithidia expoeki***	**Percent positive with Neogregarines**
Achillea millefolium	3	0.0	0.0	0.0	0.0	0.0
Alliaria petiolata	1	0.0	0.0	0.0	0.0	0.0
Anaphalis margaritacea	2	0.0	0.0	0.0	0.0	0.0
Anemone nemorosa	2	0.0	50.0	0.0	0.0	0.0
Apocynum cannabinum	16	0.0	0.0	6.3	0.0	0.0
Asclepias incarnata	2	0.0	0.0	0.0	0.0	0.0
Asclepias syriaca	12	0.0	0.0	0.0	0.0	0.0
Brassica rapa	12	16.7	0.0	8.3	0.0	25.0
Calystegia sepium	3	0.0	0.0	0.0	0.0	0.0
Centaurea stoebe	265	2.3	0.8	6.0	2.3	6.0
Cerastium fontanum	2	0.0	0.0	0.0	0.0	0.0
Cichorium intybus	15	6.7	0.0	0.0	0.0	0.0
Cirsium arvense	35	0.0	0.0	5.7	0.0	0.0
Cirsium vulgare	8	0.0	0.0	0.0	0.0	0.0
Clematis virginiana	3	0.0	0.0	0.0	0.0	0.0
Clinopodium vulgare	18	0.0	0.0	0.0	0.0	0.0
Cornus racemosa	2	0.0	0.0	0.0	0.0	0.0
Daucus carota	79	5.1	1.3	1.3	2.5	5.1
Dianthus armeria	15	0.0	0.0	0.0	0.0	0.0
Dipsacus fullonum	53	0.0	0.0	5.7	1.9	0.0
Doellingeria umbellata	23	4.3	0.0	0.0	0.0	0.0
Epilobium ciliatum	2	0.0	0.0	0.0	0.0	0.0
Erigeron annuus	35	2.9	2.9	0.0	2.9	2.9
Erigeron sp.	2	0.0	0.0	0.0	0.0	0.0
Eupatorium perfoliatum	4	0.0	0.0	0.0	0.0	0.0
Eutrochium maculatum	13	0.0	0.0	0.0	0.0	0.0
Fragaria virginiana	56	5.4	1.8	5.4	0.0	0.0
Galium mollugo	5	0.0	0.0	0.0	0.0	0.0
Glechoma hederacea	3	0.0	0.0	0.0	0.0	0.0
Hesperis matronalis	3	0.0	0.0	0.0	0.0	0.0
Hieracium aurantiacum	3	33.3	33.3	0.0	0.0	0.0
Hieracium caespitosum	27	0.0	3.7	3.7	0.0	7.4
Hieracium pilosella	6	0.0	0.0	0.0	0.0	0.0
Hieracium scabrum	47	2.1	0.0	4.3	0.0	6.4
Hieracium sp.	29	6.9	0.0	3.4	6.9	3.4

Hypericum perforatum	15	0.0	0.0	0.0	0.0	0.0
Impatiens capensis	8	0.0	0.0	0.0	0.0	0.0
Leucanthemum vulgare	100	5.0	2.0	1.0	5.0	2.0
Linaria vulgaris	3	0.0	0.0	0.0	0.0	0.0
Lobelia siphilitica	3	0.0	0.0	0.0	0.0	0.0
Lonicera morrowii	12	0.0	0.0	16.7	0.0	0.0
Lotus corniculatus	161	1.9	0.6	4.3	0.0	1.2
Lychnis flos-cuculi	50	8.0	2.0	10.0	0.0	6.0
Lycopus americanus	2	0.0	0.0	0.0	0.0	0.0
Lysimachia ciliata	2	0.0	0.0	0.0	0.0	0.0
Lythrum salicaria	107	0.0	0.0	0.9	0.0	0.0
Malva moschata	10	0.0	0.0	0.0	0.0	0.0
Melilotus albus	37	0.0	0.0	5.4	5.4	0.0
Melilotus officinalis	22	0.0	0.0	18.2	0.0	0.0
Mentha arvensis	28	3.6	3.6	0.0	0.0	7.1
Monarda fistulosa	53	0.0	0.0	0.0	0.0	1.9
Oxalis stricta	5	0.0	0.0	0.0	0.0	0.0
Pastinaca sativa	8	0.0	0.0	25.0	0.0	0.0
Penstemon digitalis	127	1.6	1.6	4.7	0.8	4.7
Plantago lanceolata	7	0.0	0.0	0.0	0.0	0.0
Potentilla canadensis	14	0.0	0.0	0.0	0.0	0.0
Potentilla recta	109	1.8	0.0	2.8	0.9	0.0
Potentilla simplex	5	0.0	0.0	0.0	0.0	0.0
Prunella vulgaris	36	0.0	0.0	0.0	0.0	0.0
Pycnanthemum tenuifolium	79	0.0	0.0	0.0	0.0	0.0
Ranunculus acris	184	1.6	0.0	1.6	1.6	4.9
Rosa multiflora	58	0.0	0.0	3.4	1.7	0.0
Rubus allegheniensis	78	1.3	0.0	1.3	1.3	1.3
Rubus hispidus	8	0.0	0.0	0.0	0.0	0.0
Rudbeckia hirta	18	0.0	0.0	5.6	0.0	0.0
Rumex crispus	1	0.0	0.0	0.0	0.0	0.0
Salix sp.	23	0.0	0.0	0.0	0.0	0.0
Silphium perfoliatum	16	0.0	0.0	0.0	0.0	0.0
Sisyrinchium angustifolium	3	0.0	0.0	0.0	0.0	0.0
Sisyrinchium montanum	17	0.0	0.0	0.0	0.0	23.5
Solidago graminifolia	44	0.0	0.0	0.0	0.0	0.0
Solidago juncea	64	6.3	0.0	1.6	0.0	3.1
Solidago nemoralis	28	0.0	0.0	0.0	3.6	0.0
Solidago rugosa	37	2.7	0.0	0.0	2.7	5.4
Stellaria pubera	24	4.2	4.2	4.2	0.0	20.8
Stellaria sp.	8	0.0	0.0	0.0	0.0	37.5

Symphyotrichum ericoides	19	0.0	0.0	5.3	0.0	0.0
Symphyotrichum lateriflorum	24	4.2	0.0	4.2	0.0	0.0
Symphyotrichum novae-angliae	3	0.0	0.0	0.0	0.0	0.0
Symphyotrichum novae-belgii	13	0.0	0.0	0.0	0.0	0.0
Taraxacum officinale	27	0.0	0.0	0.0	3.7	3.7
Trifolium aureum	3	0.0	0.0	0.0	33.3	0.0
Trifolium pratense	10	0.0	0.0	0.0	0.0	0.0
Trifolium repens	33	3.0	3.0	12.1	3.0	6.1
Veronica officinalis	4	0.0	0.0	25.0	0.0	0.0
Veronica persica	24	0.0	0.0	12.5	0.0	0.0
Veronica serpyllifolia	10	0.0	0.0	0.0	0.0	0.0
Vicia cracca	26	3.8	0.0	0.0	0.0	0.0
Vicia tetrasperma	8	0.0	12.5	0.0	0.0	25.0

Supplementary Table 3 | Parasite prevalence among the 110 species of bees that were screened. (*n* = 2,685 individual bees were screened in total.)

Bee species	**Samples screened**	**Percent positive with *Nosema bombi***	**Percent positive with *Nosema ceranae***	**Percent positive with *Crithidia bombi***	**Percent positive with *Crithidia expoeki***	**Percent positive with *Neogregarines***
Agapostemon splendens	1	0.0	0.0	0.0	0.0	0.0
Agapostemon virescens	6	0.0	0.0	0.0	0.0	0.0
Andrena carlini	7	0.0	0.0	0.0	0.0	14.3
Andrena crataegi	2	0.0	0.0	0.0	0.0	0.0
Andrena cressonii	4	0.0	0.0	0.0	0.0	0.0
Andrena forbessi	3	0.0	0.0	0.0	0.0	0.0
Andrena frigida	1	0.0	0.0	0.0	0.0	0.0
Andrena hippotes	3	0.0	0.0	0.0	0.0	0.0
Andrena hirticincta	4	0.0	0.0	0.0	0.0	0.0
Andrena imitatrix	2	0.0	0.0	0.0	0.0	0.0
Andrena milwaukeensis	2	0.0	0.0	0.0	0.0	0.0
Andrena nasonii	44	0.0	0.0	0.0	0.0	13.6
Andrena nivalis	4	0.0	50.0	0.0	0.0	0.0
Andrena nuda	1	0.0	0.0	0.0	0.0	0.0
Andrena perplexa	10	0.0	0.0	0.0	0.0	0.0
Andrena platyparia	1	0.0	0.0	0.0	0.0	0.0
Andrena pruni	6	0.0	0.0	0.0	0.0	16.7
Andrena rugosa	1	0.0	0.0	0.0	0.0	0.0
Andrena simplex	2	0.0	0.0	0.0	0.0	50.0
Andrena spp.	8	0.0	0.0	0.0	0.0	0.0
Andrena wilkella	50	0.0	2.0	0.0	0.0	2.0
Anthidiellum notatum	1	0.0	0.0	0.0	0.0	0.0
Anthidium manicatum	1	0.0	0.0	0.0	0.0	0.0
Anthophora bomboides	1	0.0	0.0	0.0	0.0	0.0
Anthophora terminalis	17	0.0	0.0	0.0	0.0	5.9
Apis mellifera	632	0.9	18.8	0.3	0.5	4.0
Augochlora pura	20	0.0	0.0	10.0	0.0	15.0
Augochlorella aurata	79	0.0	0.0	1.3	0.0	1.3
Augochloropsis fulgida	8	0.0	0.0	0.0	0.0	0.0
Bombus bimaculatus	56	1.8	0.0	10.7	12.5	1.8
Bombus borealis	5	0.0	0.0	0.0	0.0	0.0
Bombus fervidus	9	0.0	11.1	0.0	0.0	22.2
Bombus griseocollis	45	0.0	0.0	22.2	2.2	0.0
Bombus impatiens	345	0.0	0.9	11.0	1.4	9.6
Bombus perplexus	2	50.0	50.0	0.0	0.0	0.0

Bombus rufocinctus	1	0.0	0.0	0.0	0.0	0.0
Bombus sandersoni	16	6.3	0.0	0.0	6.3	0.0
Bombus ternarius	4	0.0	0.0	0.0	0.0	0.0
Bombus vagans	22	0.0	0.0	4.5	27.3	18.2
Ceratina calcarata	142	0.0	0.0	0.7	0.0	2.8
Ceratina dupla	142	0.0	0.0	0.0	0.0	1.4
Ceratina mikmaqi	154	0.0	0.6	1.9	0.0	0.6
Ceratina spp.	28	0.0	3.6	0.0	0.0	0.0
Ceratina strenua	10	0.0	0.0	0.0	0.0	0.0
Coelioxys banksi	1	0.0	0.0	0.0	0.0	0.0
Coelioxys modesta	1	0.0	0.0	0.0	0.0	0.0
Coelioxys moesta	2	0.0	0.0	0.0	0.0	0.0
Coelioxys rufitarsis	1	0.0	0.0	0.0	0.0	100.0
Colletes inaequalis	1	0.0	0.0	0.0	0.0	0.0
Colletes simulans	3	0.0	0.0	33.3	0.0	0.0
Colletes solidaginis	1	0.0	0.0	0.0	0.0	0.0
Halictus confusus	12	0.0	0.0	0.0	0.0	0.0
Halictus ligatus	41	0.0	0.0	0.0	0.0	0.0
Halictus rubicundus	10	0.0	0.0	0.0	0.0	10.0
Heriades carinatus	14	0.0	0.0	0.0	0.0	0.0
Heriades spp.	3	0.0	0.0	0.0	0.0	0.0
Hoplitis pilosifrons	5	0.0	0.0	0.0	0.0	0.0
Hoplitis producta	8	0.0	0.0	0.0	0.0	37.5
Hoplitis simplex	1	0.0	0.0	0.0	0.0	0.0
Hoplitis spoliata	1	0.0	0.0	0.0	0.0	0.0
Hoplitis spp.	1	0.0	0.0	0.0	0.0	0.0
Hylaeus affinis	9	0.0	0.0	0.0	0.0	0.0
Hylaeus affinis/modestus group	8	0.0	0.0	0.0	0.0	0.0
Hylaeus annulatus	11	0.0	0.0	0.0	0.0	0.0
Hylaeus illinoisensis	39	0.0	0.0	0.0	0.0	5.1
Hylaeus mesillae	21	0.0	0.0	0.0	0.0	0.0
Hylaeus sp. 1	3	0.0	0.0	0.0	0.0	0.0
Hylaeus spp.	33	0.0	0.0	0.0	0.0	3.0
Lasioglossum albipenne	20	0.0	0.0	0.0	0.0	0.0
Lasioglossum coeruleum	1	0.0	0.0	0.0	0.0	0.0
Lasioglossum coriaceum	16	0.0	0.0	0.0	0.0	0.0
Lasioglossum cressonii	28	0.0	0.0	0.0	0.0	0.0
Lasioglossum dreisbachi	1	0.0	0.0	0.0	0.0	0.0
Lasioglossum leucozonium	23	0.0	0.0	0.0	0.0	4.3
Lasioglossum lineatulum	2	0.0	0.0	0.0	0.0	0.0
Lasioglossum macoupinense	1	0.0	0.0	0.0	0.0	0.0

Lasioglossum michiganense	1	0.0	0.0	0.0	0.0	100.0
Lasioglossum mitchelli	3	0.0	0.0	0.0	0.0	0.0
Lasioglossum nigroviride	2	0.0	0.0	0.0	0.0	0.0
Lasioglossum nymphaearum	4	0.0	0.0	0.0	0.0	0.0
Lasioglossum obscurum	3	0.0	0.0	0.0	0.0	0.0
Lasioglossum pectinatum	1	0.0	0.0	0.0	0.0	0.0
Lasioglossum quebecense	4	0.0	0.0	0.0	0.0	0.0
Lasioglossum spp.	126	0.0	0.0	0.0	0.0	0.8
Lasioglossum versans	3	0.0	0.0	0.0	0.0	0.0
Lasioglossum versatum	141	0.0	0.7	0.0	0.0	0.7
Lasioglossum weemsi	3	0.0	0.0	0.0	0.0	0.0
Lasioglossum zonulum	37	0.0	0.0	2.7	2.7	0.0
Megachile brevis	1	0.0	0.0	0.0	0.0	0.0
Megachile campanulae	7	0.0	0.0	0.0	0.0	0.0
Megachile centuncularis	3	0.0	0.0	0.0	0.0	0.0
Megachile gemula	2	0.0	0.0	0.0	0.0	50.0
Megachile latimanus	2	0.0	0.0	0.0	0.0	50.0
Megachile mendica	7	0.0	0.0	0.0	0.0	0.0
Megachile montivaga	9	0.0	0.0	11.1	0.0	0.0
Megachile pugnata	2	0.0	0.0	0.0	0.0	0.0
Megachile relativa	7	0.0	0.0	0.0	0.0	14.3
Megachile rotundata	1	0.0	0.0	0.0	0.0	0.0
Megachile sculpturalis	3	0.0	0.0	0.0	0.0	33.3
Melissodes desponsa	4	0.0	0.0	0.0	0.0	0.0
Melissodes druriella	4	0.0	0.0	0.0	0.0	0.0
Melissodes spp.	4	0.0	0.0	0.0	0.0	0.0
Melissodes subillata	3	0.0	0.0	0.0	0.0	0.0
Nomada luteoloides	1	0.0	0.0	0.0	0.0	0.0
Nomada pygmaea group	1	0.0	0.0	0.0	0.0	0.0
Nomada sp. 1	1	0.0	0.0	0.0	0.0	0.0
Nomada sp. 2	2	0.0	0.0	0.0	0.0	0.0
Nomada sp. 3	1	0.0	0.0	0.0	0.0	0.0
Nomada sp. 4	3	0.0	0.0	0.0	0.0	0.0
Nomada spp.	1	0.0	0.0	0.0	0.0	0.0
Osmia atriventris	1	0.0	0.0	0.0	0.0	0.0
Osmia bucephala	1	0.0	0.0	0.0	0.0	0.0
Osmia georgica	1	0.0	0.0	0.0	0.0	0.0
Osmia nigriventris	2	0.0	0.0	0.0	0.0	0.0
Osmia pumila	1	0.0	0.0	0.0	0.0	0.0
Pseudopanurgus andrenoides	2	0.0	0.0	0.0	0.0	0.0
Sphecodes aroniae	1	0.0	0.0	0.0	0.0	0.0

Sphecodes carolinas	1	0.0	0.0	0.0	0.0	0.0
Stelis lateralis	1	0.0	0.0	0.0	0.0	0.0
Xylocopa virginica	40	0.0	2.5	2.5	5.0	10.0

Supplementary Table 4 | Effects of week number on the prevalence of parasite groups/species in the pollinator community. GLMMs were fitted with parasite prevalence as binomial response, week number as predictor, and site as random factor. Significance of week number were evaluated using likelihood ratio tests. To account for multiple testing given the number of parasite groups/species, we used a Bonferroni-corrected significance level of $\alpha = 0.05/7 = 0.0071$. Significant positive effects are shown in blue. Durbin-Watson tests using scaled residuals were also conducted to check for temporal autocorrelation; a significant temporal autocorrelation would have invalidated the use of a non-autoregressive model like GLMM. The last parasite group refers to all four parasite species and neogregarines combined. Parasite groups/species with less than 20 positive samples were excluded from the analysis. Sample size was n = 2,672.

Parasite	**Likelihood ratio test**			**DW test for temporal autocorr.**	
	Coef. est.	χ^2_1	**p-value**	**DW**	**p-value**
Microsporidia	0.65	17	< 0.001	2.0	0.97
Trypanosomatids	0.11	45	< 0.001	2.4	0.39
N. bombi		< 20 positives			
N. ceranae	0.068	14	< 0.001	2.0	0.93
C. bombi	0.17	39	< 0.001	1.9	0.8
C. expoeki	0.071	2.9	0.087	1.5	0.24
Neogregarines	0.055	7.6	0.0059	1.8	0.58
Combined	0.092	56	< 0.001	1.6	0.36

Supplementary Table 5 | Effects of week number on the prevalence of parasite groups/species in the floral community. GLMMs were fitted with parasite prevalence as binomial response, week number as predictor, and site as random factor. Significance of week number were evaluated using likelihood ratio tests. To account for multiple testing given the number of parasite groups/species, we used a Bonferroni-corrected significance level of $\alpha = 0.05/7 = 0.0071$. Significant negative effects are shown in red. Durbin-Watson tests using scaled residuals were also conducted to check for temporal autocorrelation. Parasite groups/species with less than 20 positive samples were excluded from the analysis.

Parasite	**Likelihood ratio test**			**DW test for temporal autocorr.**	
	Coef. est.	χ^{2}_{1}		**Coef. est.**	χ^{2}_{1}
Microsporidia	-0.028	2.9	0.090	1.5	0.28
Trypanosomatids	-0.017	1.6	0.21	2.7	0.11
N. bombi	-0.019	0.50	0.48	2.4	0.3
N. ceranae		< 20 positives			
C. bombi	-0.035	2.8	0.092	2.0	0.93
C. expoeki	-0.017	0.26	0.61	2.0	0.92
Neogregarines	-0.036	2.8	0.096	1.6	0.42
Combined	-0.038	8.3	0.0040	2.2	0.58

Supplementary Table 6 | Effects of bee genus and its interaction with week number on the prevalence of parasite groups/species in the pollinator community. GLMMs were fitted with parasite prevalence in each genus as binomial response, week number (shifted), pollinator genus and their interaction as predictors, and site as random factor. To account for multiple testing, we used a Bonferroni-corrected significance level of $\alpha = 0.05/7 = 0.0071$. Significance of predictors were evaluated using likelihood ratio tests. Significant effects are shown in fuschia. Note that none of the *Ceratina* samples tested positive for *C. expoeki* and were hence excluded from the *C. expoeki* analysis, since they would have otherwise led to model degeneracy. Sample size was n = 2,196 for *C. expoeki*, and n = 2,672 for all other parasite groups/species.

Parasite	**Week * genus**		**Genus**	
	χ^2_1	p-value	χ^2_1	p-value
Microsporidia	1.4	0.85	200	< 0.001
Trypanosomatids	35	< 0.001	160	< 0.001
N. ceranae	2.2	0.70	230	< 0.001
C. bombi	15	0.0057	140	< 0.001
C. expoeki	8.2	0.042	28	< 0.001
Neogregarines	4.3	0.37	47	< 0.001
Combined	31	< 0.001	230	< 0.001

Supplementary Table 7 | Post-hoc pairwise contrasts for the main effects of bee genus. Results were based on the same models used in Supplementary Table 6. p-values were calculated using the simultaneous inference procedure by Hothorn, Bretz and Westfall (2008), which incorporated corrections for multiple testing given the number of contrasts. In addition, we used a Bonferroni-corrected significance level of α = 0.05/7 = 0.0071 to account for the number of parasite groups/species. Significant positive and negative contrasts are shown in blue and red respectively.

Parasite	Pairwise contrast	Coef. est.	z	p-value
Microsporidia	*Apis* - *Bombus*	1.5	6.4	< 0.001
	Apis - *Ceratina*	4.2	5.2	< 0.001
	Apis - *Lasioglossum*	2.4	6.6	< 0.001
	Apis - Others	2.4	8.2	< 0.001
	Bombus - *Ceratina*	2.7	3.2	0.0090
	Bombus - *Lasioglossum*	0.91	2.2	0.15
	Bombus - Others	0.88	2.6	0.066
	Ceratina - *Lasioglossum*	-1.8	-2.0	0.23
	Ceratina - Others	-1.8	-2.1	0.18
	Lasioglossum - Others	-0.035	-0.078	1.0
Trypanosomatids	*Apis* - *Bombus*	-1.7	-7.0	< 0.001
	Apis - *Ceratina*	1.0	2.3	0.15
	Apis - *Lasioglossum*	0.91	2.1	0.22
	Apis - Others	0.67	1.8	0.37
	Bombus - *Ceratina*	2.7	6.6	< 0.001
	Bombus - *Lasioglossum*	2.6	6.5	< 0.001
	Bombus - Others	2.4	7.1	< 0.001
	Ceratina - *Lasioglossum*	-0.11	-0.20	1.0
	Ceratina - Others	-0.34	-0.68	0.96
	Lasioglossum - Others	-0.23	-0.47	0.99
N. ceranae	*Apis* - *Bombus*	3.0	6.4	< 0.001
	Apis - *Ceratina*	4.0	5.0	< 0.001
	Apis - *Lasioglossum*	4.6	4.0	< 0.001
	Apis - Others	3.5	6.7	< 0.001
	Bombus - *Ceratina*	1.1	1.2	0.74
	Bombus - *Lasioglossum*	1.6	1.3	0.64
	Bombus - Others	0.48	0.71	0.95
	Ceratina - *Lasioglossum*	0.57	0.41	0.99
	Ceratina - Others	-0.59	-0.62	0.97
	Lasioglossum - Others	-1.2	-0.93	0.87
C. bombi	*Apis* - *Bombus*	-4.5	-4.2	< 0.001
	Apis - *Ceratina*	-1.3	-1.1	0.78
	Apis - *Lasioglossum*	0.46	0.20	1.0
	Apis - Others	-1.2	-0.93	0.87
	Bombus - *Ceratina*	3.2	5.1	< 0.001
	Bombus - *Lasioglossum*	5.0	2.3	0.11
	Bombus - Others	3.3	4.8	< 0.001
	Ceratina - *Lasioglossum*	1.8	0.82	0.91
	Ceratina - Others	0.17	0.19	1.0
	Lasioglossum - Others	-1.6	-0.74	0.94
C. expoeki	*Apis* - *Bombus*	-2.1	-2.9	0.015
	Apis - *Ceratina*		No positive *Ceratina* samples	
	Apis - *Lasioglossum*	1.5	0.71	0.88
	Apis - Others	1.3	0.85	0.81

	Bombus - *Ceratina*	No positive *Ceratina* samples		
	Bombus - *Lasioglossum*	3.7	1.8	0.25
	Bombus - Others	3.4	.5	0.048
	Ceratina - *Lasioglossum*	No positive *Ceratina* samples		
	Ceratina - Others	No positive *Ceratina* samples		
	Lasioglossum - Others	-0.26	0.11	1.0
Neogregarines	*Apis* - *Bombus*	-0.89	-3.2	0.010
	Apis - *Ceratina*	1.1	2.4	0.12
	Apis - *Lasioglossum*	1.4	2.4	0.093
	Apis - Others	-0.33	-1.1	0.77
	Bombus - *Ceratina*	2.0	4.5	< 0.001
	Bombus - *Lasioglossum*	2.3	4.1	< 0.001
	Bombus - Others	0.56	2.2	0.16
	Ceratina - *Lasioglossum*	0.31	0.46	0.99
	Ceratina - Others	-1.4	-3.1	0.013
	Lasioglossum - Others	-1.7	-3.1	0.015
Combined	*Apis* - *Bombus*	-0.21	-1.4	0.60
	Apis - *Ceratina*	2.3	7.7	< 0.001
	Apis - *Lasioglossum*	2.7	6.9	< 0.001
	Apis - Others	1.4	6.8	< 0.001
	Bombus - *Ceratina*	2.5	8.4	< 0.001
	Bombus - *Lasioglossum*	2.9	7.4	< 0.001
	Bombus - Others	1.6	7.8	< 0.001
	Ceratina - *Lasioglossum*	0.41	0.85	0.90
	Ceratina - Others	-0.98	-3.0	0.022
	Lasioglossum - Others	-1.4	-3.3	0.0068

Supplementary Table 8 | Effects of week number on parasite prevalence in different bee genera. Results were based on the same models used in Supplementary Table 6. p-values were calculated using the simultaneous inference procedure by Hothorn, Bretz and Westfall (2008), which incorporated corrections for multiple testing given the number of genera. In addition, we used a Bonferroni-corrected significance level of $\alpha = 0.05/7 = 0.0071$ to account for the number of parasite groups/species. Significant positive and negative effects are shown in blue and red respectively.

Parasite	Genus	Coef. est.	z	p-value
Microsporidia	*Apis*	-0.079	-3.5	0.002
	Bombus	-0.037	-0.73	0.96
	Ceratina	-0.15	-0.81	0.93
	Lasioglossum	-0.070	-0.80	0.94
	Others	-0.022	-0.35	1.0
Trypanosomatids	*Apis*	-0.093	-2.3	0.094
	Bombus	0.065	2.0	0.21
	Ceratina	-0.14	-1.5	0.49
	Lasioglossum	0.034	0.32	1.0
	Others	0.26	4.9	< 0.001
N. ceranae	*Apis*	-0.098	-4.1	< 0.001
	Bombus	0.049	0.38	1
	Ceratina	-0.145	-0.80	0.94
	Lasioglossum	-0.098	-0.36	1.0
	Others	0.00041	0.004	1.0
C. bombi	*Apis*	-0.23	-1.7	0.37
	Bombus	0.13	2.7	0.038
	Ceratina	-0.16	-1.3	0.69
	Lasioglossum	0.51	1.1	0.80
	Others	0.27	2.6	0.043
C. expoeki	*Apis*	-0.099	-0.10	0.88
	Bombus	-0.10	-0.11	0.25
	Ceratina	No positive *Ceratina* samples		
	Lasioglossum	0.50	0.5	0.70
	Others	0.32	0.32	0.33
Neogregarines	*Apis*	-0.067	-1.5	0.50
	Bombus	0.030	0.65	0.97
	Ceratina	0.072	0.89	0.90
	Lasioglossum	-0.043	-0.32	1.0
	Others	0.039	0.94	0.88
Combined	*Apis*	-0.11	-4.8	< 0.001
	Bombus	0.057	1.9	0.25
	Ceratina	-0.026	-0.40	1.00
	Lasioglossum	0.064	0.60	0.98
	Others	0.076	2.1	0.16

Supplementary Table 9 | Effects of bee diversity (Shannon index) on parasite prevalence in the bee community. GLMMs were fitted with parasite prevalence as binomial response, Shannon index as predictor, and site as random factor. We considered parasite prevalence based on all bee genera, as well as without *Apis* and *Bombus*. Significance of pollinator diversity were evaluated using likelihood ratio tests. To account for multiple testing, we used a Bonferroni-corrected significance level of $\alpha = 0.05/7 = 0.0071$ for prevalence based on all genera, and $\alpha = 0.05/4 = 0.13$ for prevalence without Apis and Bombus. Significant negative effects are shown in red. Sample size was n = 2,446 for all bee genera, and 1,390 without *Apis* and *Bombus*.

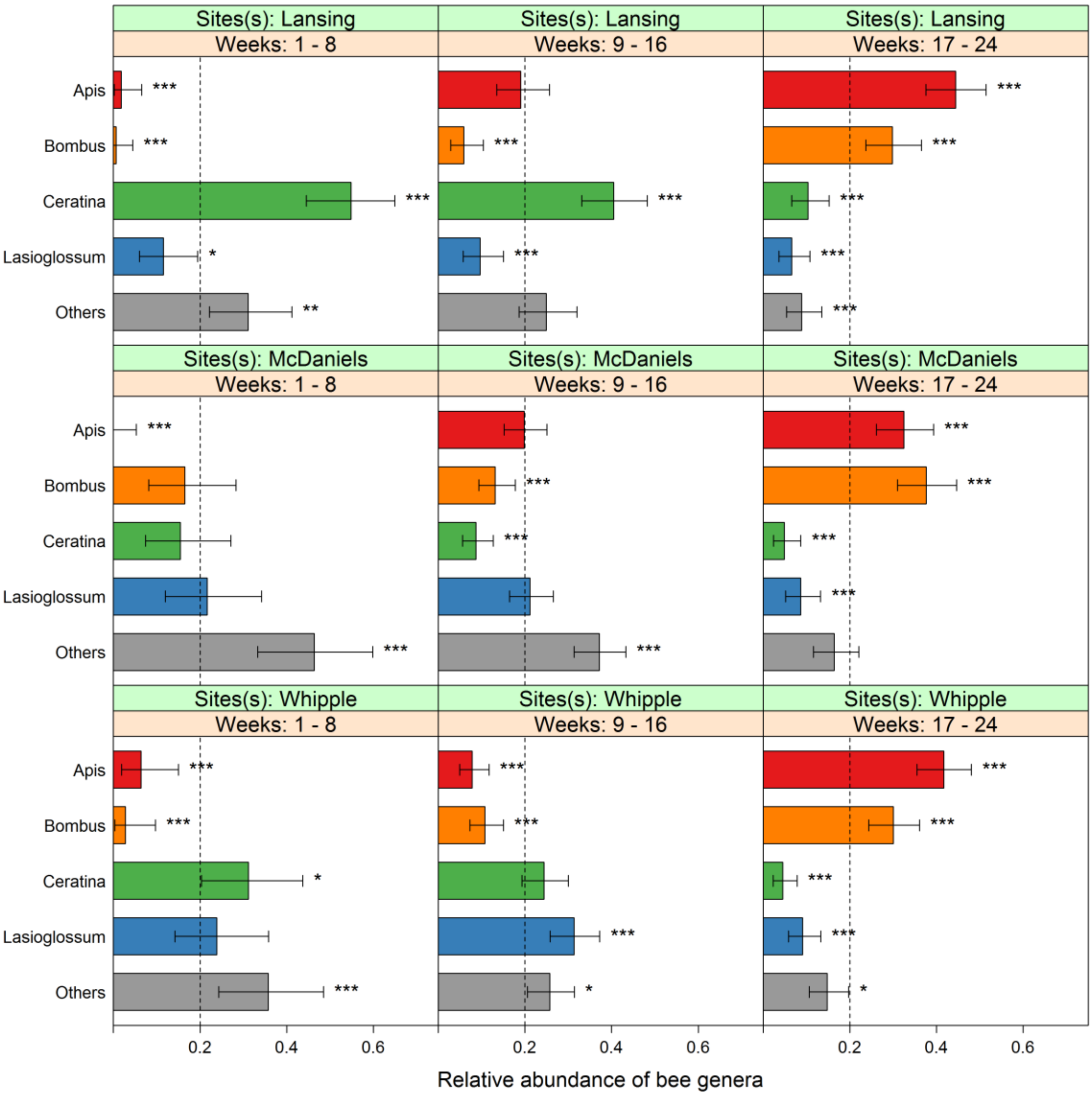
	All bee genera			**Without *Apis* and *Bombus***		
Parasite	**Coef. est.**	χ^2_1	**p-value**	**Coef. est.**	χ^2_1	**p-value**
Microsporidia	-0.41	7.4	0.0065	0.52	0.54	0.46
Trypanosomatids	-0.74	21	< 0.001	-1.8	22	< 0.001
N. bombi		< 20 positives			< 20 positives	
N. ceranae	-0.64	13	< 0.001		< 20 positives	
C. bombi	-1.1	21	< 0.001		< 20 positives	
C. expoeki	-0.0056	0.00016	0.99		< 20 positives	
Neogregarines	-0.37	3.6	0.060	0.020	0.0014	0.97
Combined	-0.69	34	< 0.001	-0.64	2.6	0.11

Supplementary Table 10 | Effects of floral diversity (Shannon index) on parasite prevalence in the floral community. GLMMs were fitted with parasite prevalence as binomial response, Shannon index as predictor, and site as random factor. Significance of floral diversity were evaluated using likelihood ratio tests. To account for multiple testing, we used a Bonferroni-corrected significance level of $\alpha = 0.05/7 = 0.0071$. Sample size was n = 2,624.

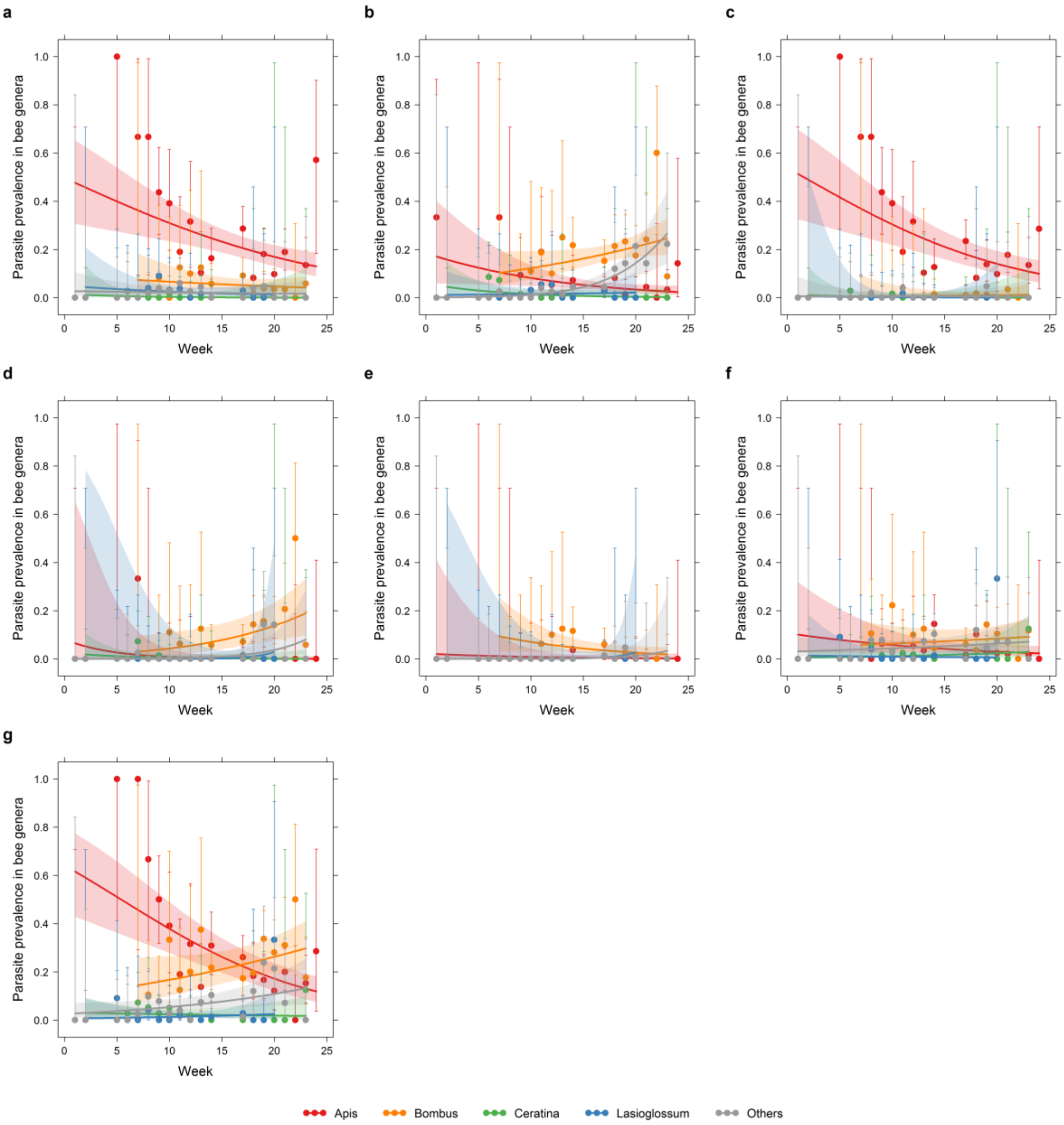
Parasite	**Coef. est.**	χ^2_1	**p-value**
Microsporidia	0.34	4.0	0.045
Trypanosomatids	-0.15	1.1	0.30
N. bombi	0.088	0.10	0.75
N. ceranae		< 20 positives	
C. bombi	-0.090	0.16	0.69
C. expoeki	0.063	0.031	0.86
Neogregarines	-0.56	6.3	0.012
Combined	-0.16	1.3	0.25

Supplementary Table 11 | Effects of total floral abundance on parasite prevalence in the floral community. GLMMs were fitted with parasite prevalence as binomial response, $\log_{10}$(mean total floral abundance per quadrat) as predictor, and site as random factor. Significance of floral abundance were evaluated using likelihood ratio tests. To account for multiple testing, we used a Bonferroni-corrected significance level of $\alpha = 0.05/7 = 0.0071$. Significant negative effects are shown in red. Sample size was $n = 2{,}624$.

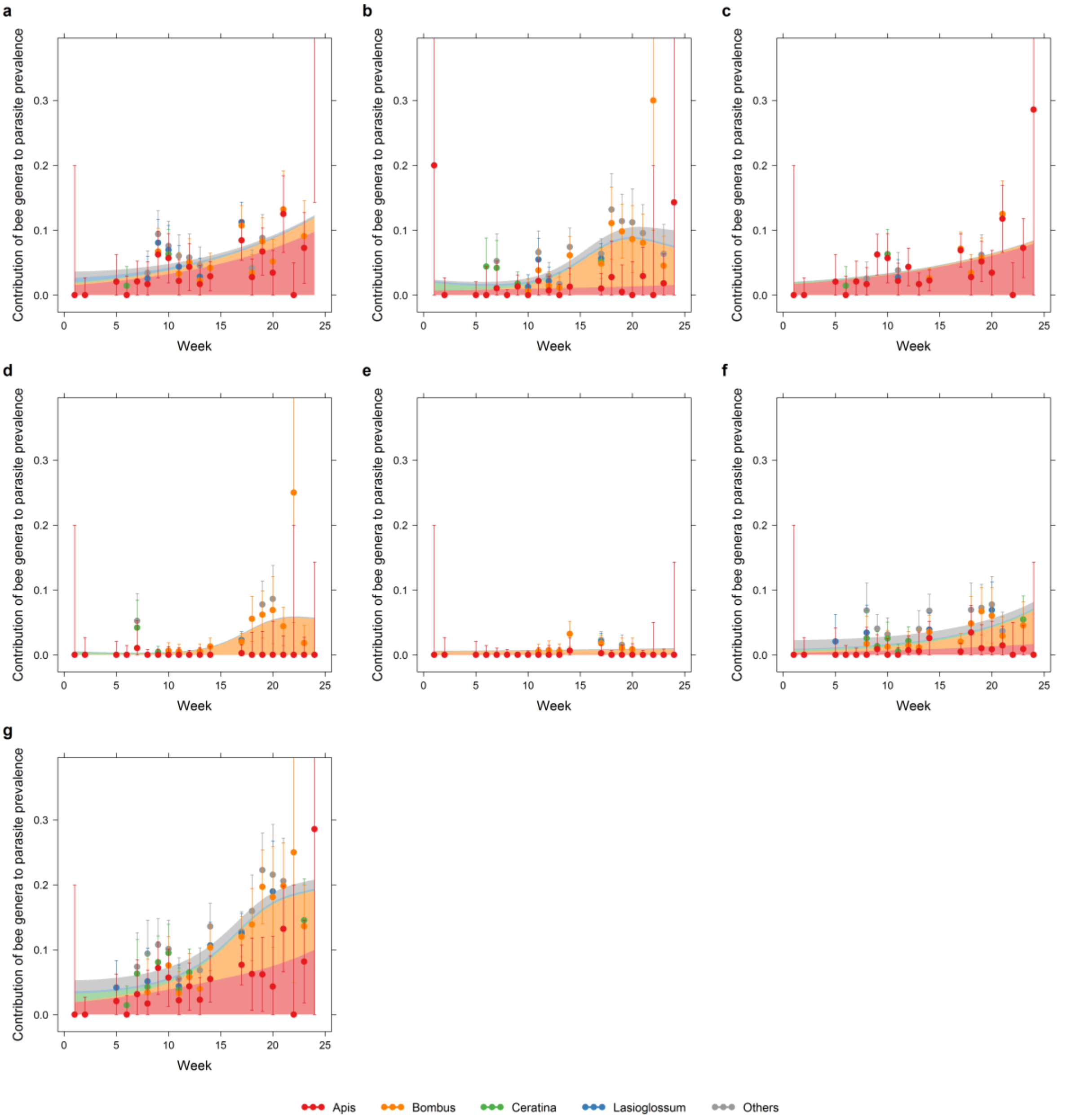
Parasite	Coef. est.	χ^2_1	p-value
Microsporidia	-0.26	2.2	0.14
Trypanosomatids	-0.17	1.2	0.27
N. bombi	-0.23	0.68	0.41
N. ceranae		< 20 positives	
C. bombi	-0.41	3.3	0.068
C. expoeki	-0.40	1.2	0.28
Neogregarines	-0.19	0.74	0.39
Combined	-0.39	8.0	0.0046



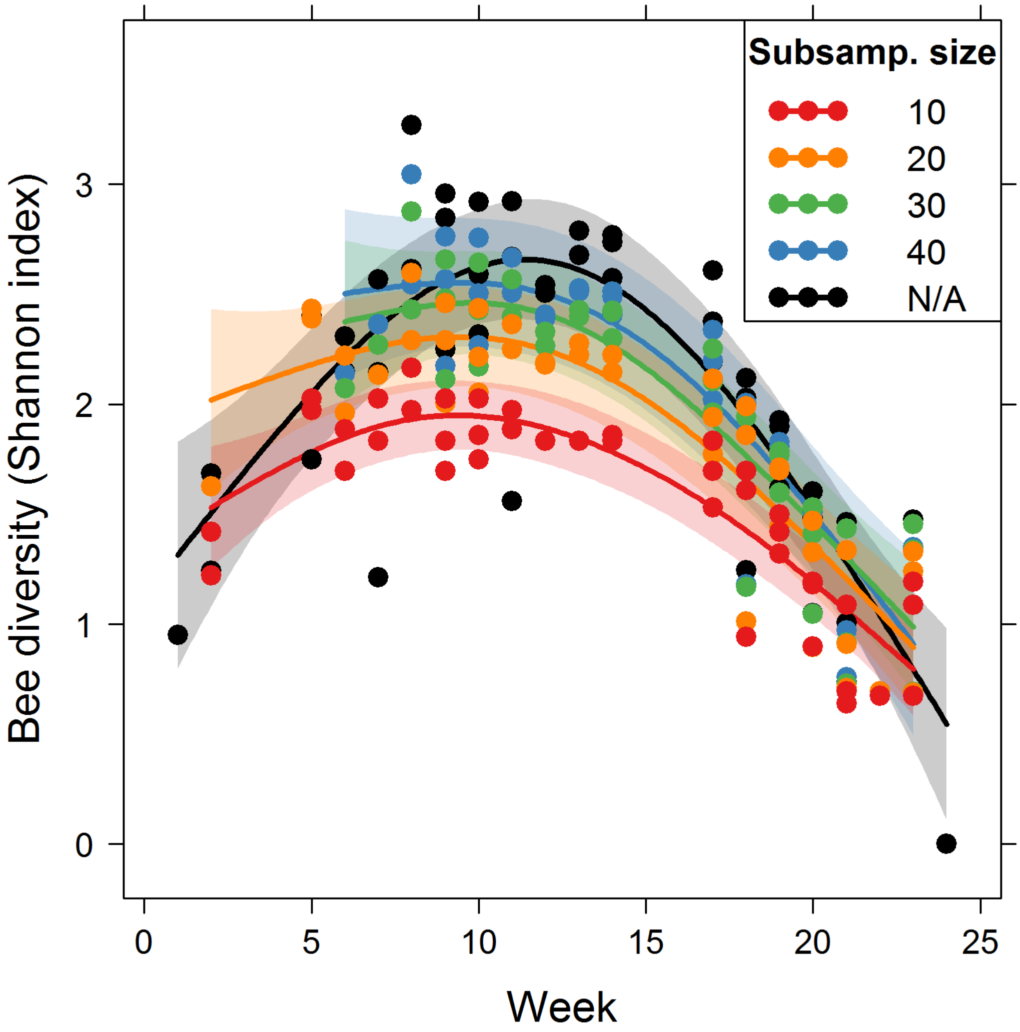
Supplementary Fig. 1 | Relative abundance of the four most common bee genera, in three 8-week periods of the field season. For each genus, post-hoc evaluations of the deviation from the null hypothesis (of equal multinomial proportions) were conducted using exact binomial tests with Bonferroni correction. 99% confidence intervals are presented here in accordance with this correction. Error bars are 95% Clopper-Pearson confidence intervals. Sample sizes are *n* = 164, 289, 349 for the three periods at Lansing, *n* = 97, 449, 348 at McDaniels, and *n* = 109, 447, 420 at Whipple.



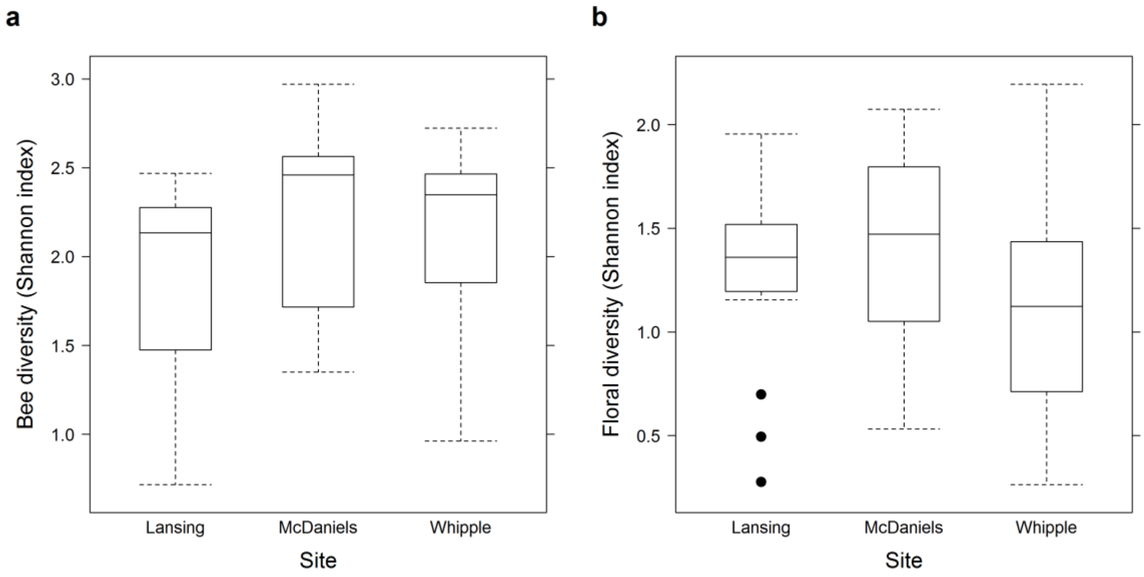
Supplementary Fig. 2 | Parasite prevalence in different bee genera across the season. Parasite species/groups shown here are (**a**) microsporidians, (**b**) trypanosomatids, (**c**) *N. ceranae*, (**d**) *C. bombi*, (**e**) *C. expoeki*, (**f**) neogregarines and (**g**) the four parasite species and neogregarines combined. Curves and confidence bands were fitted using binomial GLMMs with genus, week number and their interactions as predictors, and site as a random factor. To reduce plot clutter, points and error bars shown here are based on combining data from all three sites each week. Error bars are 95% Clopper-Pearson confidence intervals.



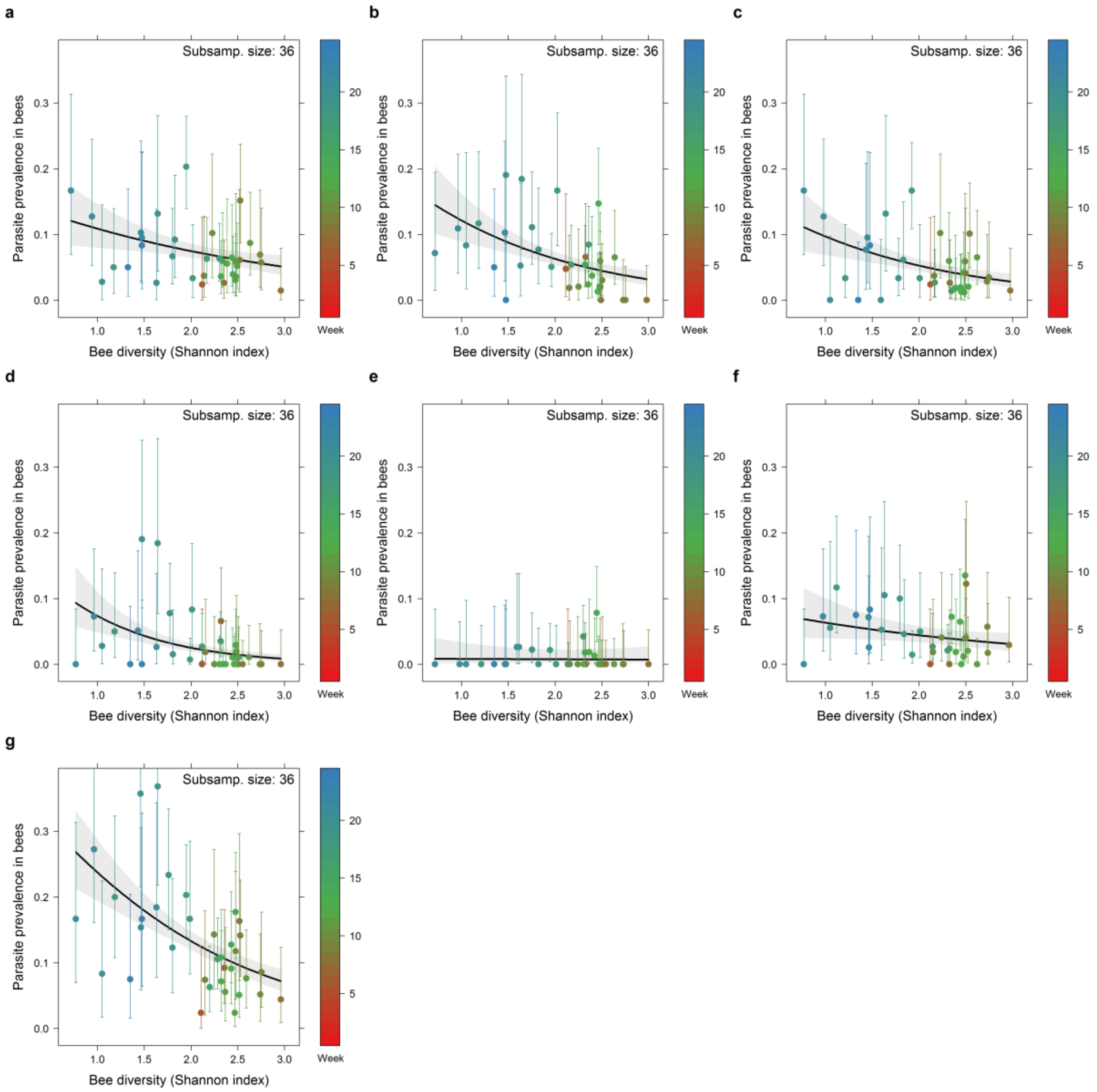
Supplementary Fig. 3 | Contributions from each bee genus to overall prevalence of parasites in the community across the season. Parasite species/groups shown here are (**a**) microsporidians, (**b**) trypanosomatids, (**c**) *N. ceranae*, (**d**) *C. bombi*, (**e**) *C. expoeki*, (**f**) neogregarines and (**g**) the four parasite species and neogregarines combined. Contributions were defined as (relative abundance of genus) × (parasite prevalence in genus), and plotted as stacked smoothing splines fitted using GAM with site as a random factor. Error bars are 95% Clopper-Pearson confidence intervals.



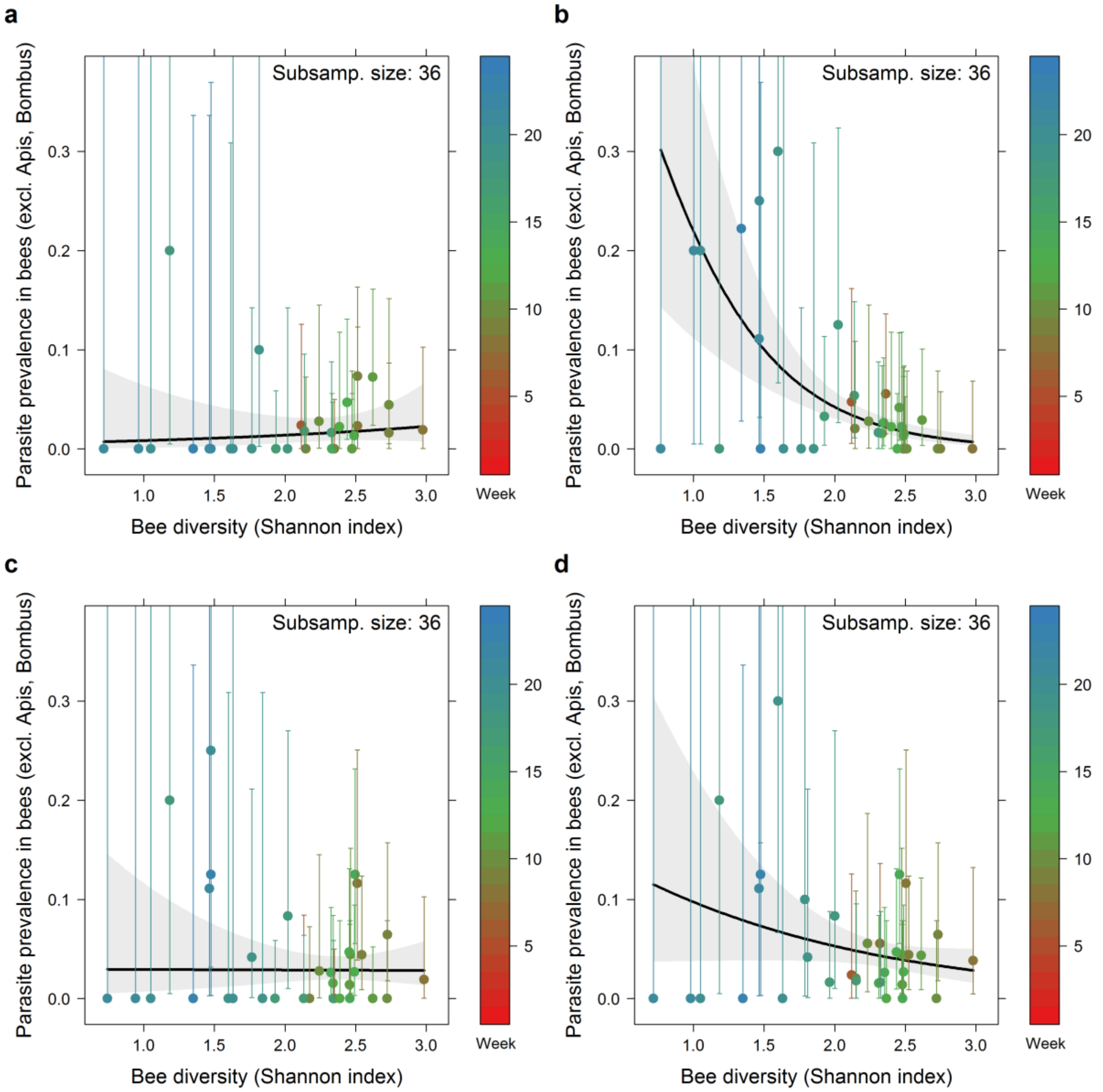
Supplementary Fig. 4 | Bee diversity at different site and weeks, with and without rarefaction. Smaller subsample sizes allowed more site/week samples to be included, especially those from earlier weeks, but at the expense of reducing the strength of any temporal trends. Curves shown here are smoothing splines fitted using GAM with site as a random factor.



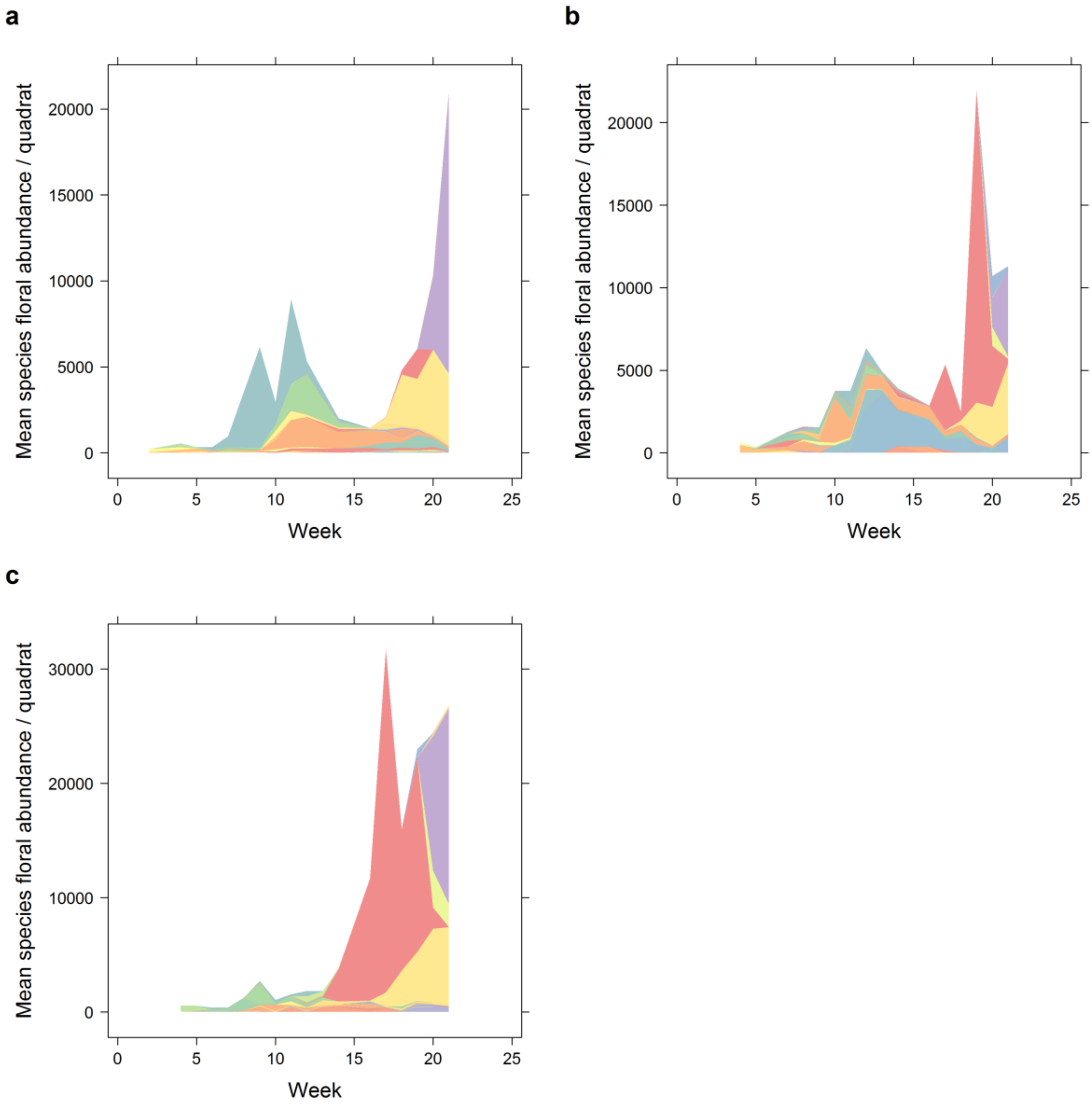
Supplementary Fig. 5 | Variation in bee and floral diversities across sites. Shannon indices for the (**a**) bee and (**b**) flower communities were calculated using bee samples and site floral surveys respectively, with different weeks as replicates.



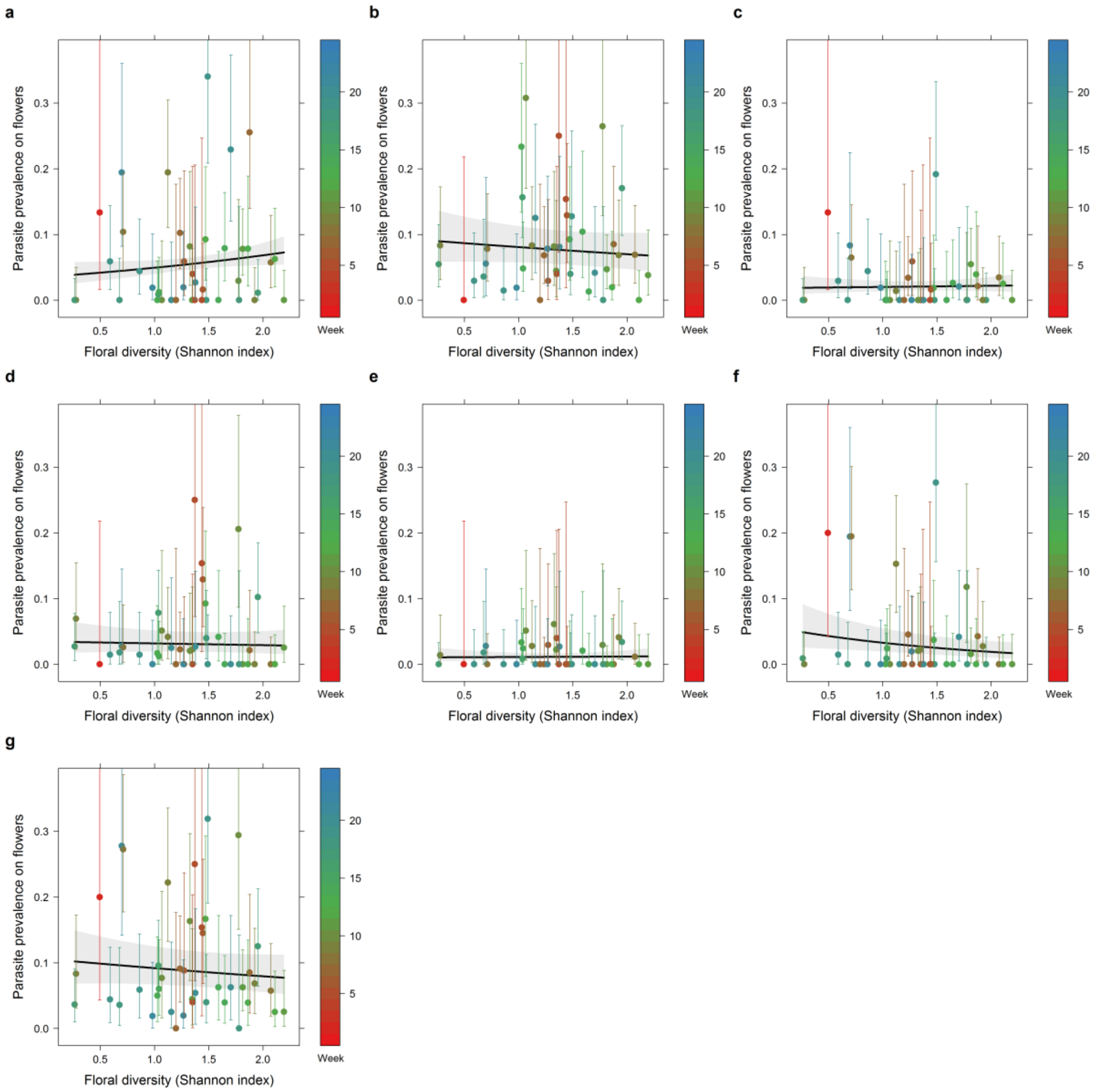
Supplementary Fig. 6 | Association between the prevalence of different parasite groups/species in bees and bee diversity. Parasite species/groups shown here are (**a**) microsporidians, (**b**) trypanosomatids, (**c**) *N. ceranae*, (**d**) *C. bombi*, (**e**) *C. expoeki*, (**f**) neogregarines and (**g**) the four parasite species and neogregarines combined. Colour indicates week number. Curves were fitted using binomial GLMMs with site as a random factor. Error bars are 95% Clopper-Pearson confidence intervals.



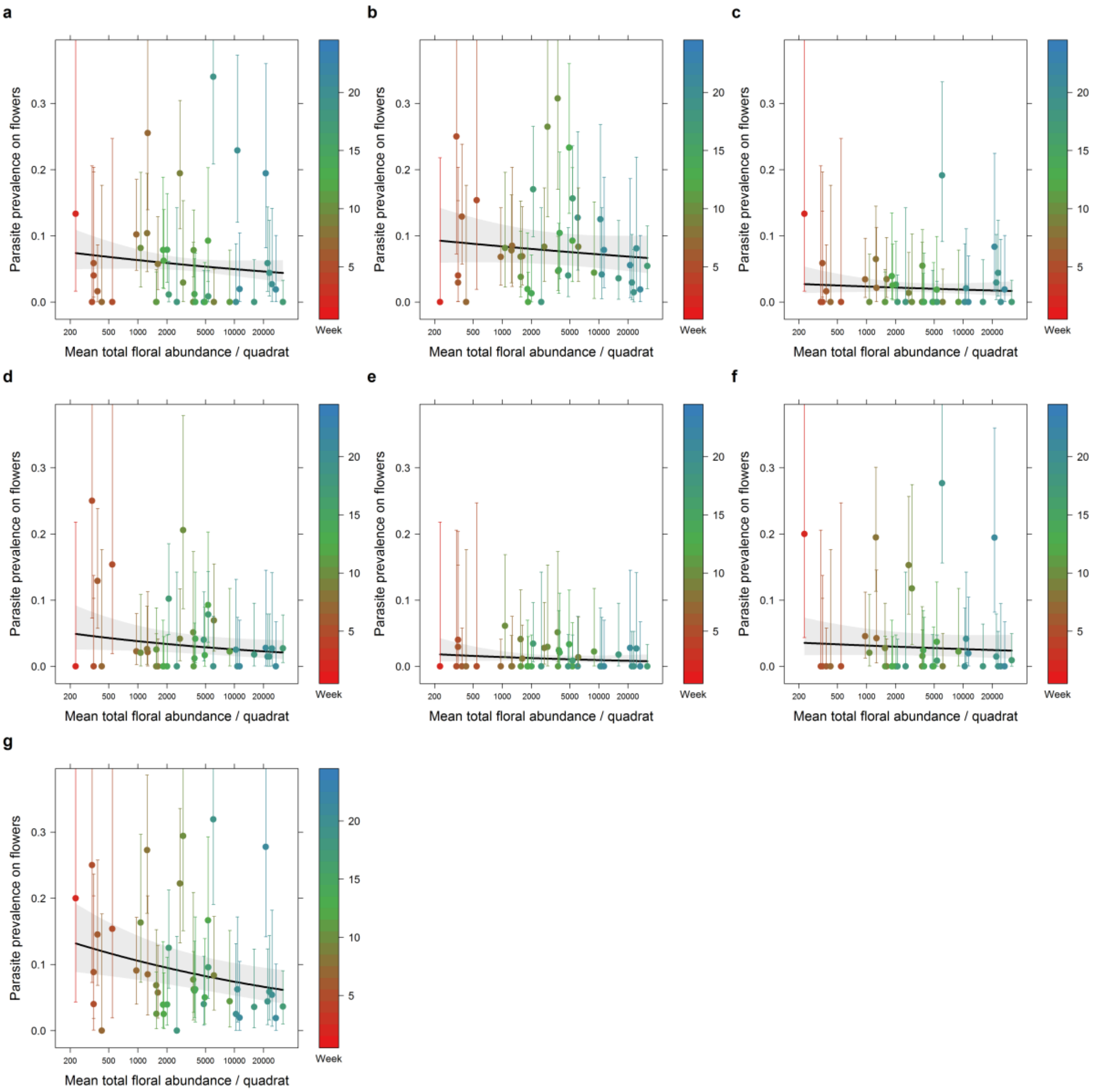
Supplementary Fig. 7 | Association between the prevalence of different parasite groups/species in bees (excluding *Apis* and *Bombus*) and pollinator diversity. Parasite species/groups shown here are (**a**) microsporidians, (**b**) trypanosomatids, (**c**) neogregarines and (**d**) the four parasite species and neogregarines combined. Colour indicates week number. Curves were fitted using binomial GLMMs with site as a random factor. Error bars are 95% Clopper-Pearson confidence intervals.



Supplementary Fig. 8 | Species floral abundances across the season. Mean floral abundances per quadrat were evaluated for each plant species at (**a**) Lansing, (**b**) McDaniels and (**c**) Whipple, and shown as stacked plots.



Supplementary Fig. 9 | Association between the prevalence of different parasite groups/species on flowers and floral diversity. Parasite species/groups shown here are (**a**) microsporidians, (**b**) trypanosomatids, (**c**) *N. bombi*, (**d**) *C. bombi*, (**e**) *C. expoeki*, (**f**) neogregarines and (**g**) the four parasite species and neogregarines combined. Colour indicates week number. Curves were fitted using binomial GLMMs with site as a random factor. Error bars are 95% Clopper-Pearson confidence intervals.



Supplementary Fig. 10 | Association between the prevalence of different parasite groups/species on flowers and total floral abundance. Parasite species/groups shown here are (**a**) microsporidians, (**b**) trypanosomatids, (**c**) *N. bombi*, (**d**) *C. bombi*, (**e**) *C. expoeki*, (**f**) neogregarines and (**g**) the four parasite species and neogregarines combined. Colour indicates week number. Curves were fitted using binomial GLMMs with site as a random factor. Error bars are 95% Clopper-Pearson confidence intervals.

Supplementary References

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