

Species traits, landscape quality and floral resource overlap with honeybees determine virus transmission in plant–pollinator networks

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Supplementary Table 1. Total number of screened individuals per pollinator species and number of positively tested individuals for each virus, with percentages of positive individuals shown in brackets. For each virus, the median and range (min.-max.) of absolute number of genome copies per ng of RNA are given. Here, the median and range are calculated considering the virus-positive individuals only. Deformed wing virus = DWV; black queen cell virus = BQCV.

Species	Total nr. of individuals	DWV-A			DWV-B			BQCV		
		Nr. positive	Median	Range	Nr. positive	Median	Range	Nr. positive	Median	Range
<i>Andrena humilis</i>	10	0	-	-	1 (10)	1.7×10^2	-	1 (10)	1.1×10^3	-
<i>Apis mellifera</i>	360	21 (5.8)	6.6×10^2	1.7×10^2 - 7.4×10^4	231 (64.2)	4.8×10^3	1.7×10^1 - 1.4×10^9	311 (86.4)	2.8×10^5	2.9×10^2 - 3.8×10^{11}
<i>Bombus hortorum</i>	33	3 (9.1)	8.7×10^2	2.4×10^2 - 1.0×10^3	17 (51.5)	4.4×10^3	6.9×10^2 - 5.1×10^4	25 (75.8)	2.7×10^5	1.2×10^4 - 3.8×10^6
<i>B. humilis</i>	32	4 (12.5)	6.6×10^2	4.6×10^2 - 2.1×10^3	17 (53.1)	2.1×10^3	3.0×10^2 - 3.0×10^5	23 (71.9)	1.6×10^5	2.6×10^3 - 3.5×10^8
<i>B. hypnorum</i>	9	1 (11.1)	1.4×10^3	-	5 (55.6)	3.5×10^3	1.9×10^3 - 6.6×10^4	6 (66.7)	6.8×10^5	1.0×10^4 - 9.8×10^6
<i>B. lapidarius</i>	130	3 (2.3)	7.5×10^2	5.4×10^2 - 1.2×10^3	73 (56.1)	2.7×10^3	7.7×10^1 - 2.0×10^5	113 (86.9)	3.5×10^5	3.6×10^2 - 8.2×10^7
<i>B. lucorum</i>	10	0	-	-	6 (60)	6.0×10^4	5.6×10^3 - 2.0×10^5	3 (30)	2.9×10^6	1.3×10^6 - 9.5×10^6
<i>B. pascuorum</i>	88	3 (3.4)	7.6×10^2	5.3×10^2 - 1.5×10^4	28 (31.8)	1.4×10^3	2.0×10^2 - 6.3×10^5	27 (30.7)	1.8×10^4	1.3×10^3 - 6.3×10^6
<i>B. ruderatus</i>	14	0	-	-	4 (28.6)	6.2×10^3	2.7×10^2 - 5.2×10^4	6 (42.9)	8.8×10^4	1.2×10^4 - 1.1×10^7
<i>B. subterraneus</i>	9	1 (11.1)	2.6×10^2	-	6 (66.7)	1.6×10^4	2.4×10^3 - 3.7×10^4	9 (100)	2.3×10^5	9.7×10^3 - 1.3×10^6

<i>B. sylvarum</i>	23	0	-	-	9 (39.1)	3.7×10^3	$3.2 \times 10^2 - 7.2 \times 10^4$	12 (52.2)	1.8×10^5	$4.1 \times 10^3 - 1.5 \times 10^6$
<i>B. terrestris</i>	71	5 (7.0)	8.1×10^2	$6.0 \times 10^2 - 9.7 \times 10^4$	46 (64.8)	4.3×10^3	$2.8 \times 10^2 - 2.8 \times 10^5$	45 (63.4)	1.5×10^5	$2.4 \times 10^3 - 4.0 \times 10^7$
<i>Halictus scabiosae</i>	15	0	-	-	6 (40)	9.0×10^2	$2.1 \times 10^2 - 2.4 \times 10^3$	3 (20)	5.0×10^3	$3.5 \times 10^3 - 1.2 \times 10^6$
<i>Lasioglossum glabriusculum</i>	17	1 (5.9)	6.7	-	7 (41.2)	3.7×10^2	$1.5 \times 10^2 - 2.5 \times 10^4$	6 (35.3)	2.9×10^2	$2.3 \times 10^1 - 3.7 \times 10^3$
<i>L. malachurum</i>	57	3 (5.3)	5.2×10^1	$3.4 \times 10^1 - 6.4 \times 10^1$	34 (59.6)	5.8×10^2	$4.2 \times 10^1 - 1.0 \times 10^4$	9 (15.8)	1.7×10^2	$7.2 \times 10^1 - 1.2 \times 10^4$
<i>L. morio</i>	7	0	-	-	5 (71.4)	2.5×10^2	$7.0 \times 10^1 - 8.9 \times 10^2$	0	-	-
<i>L. pauxillum</i>	67	3 (4.5)	4.0×10^1	$2.0 \times 10^1 - 1.9 \times 10^2$	28 (41.8)	6.2×10^2	$5.2 \times 10^1 - 4.8 \times 10^4$	15 (22.4)	2.9×10^2	$4.7 \times 10^1 - 5.1 \times 10^3$
<i>Melanostoma mellinum</i>	18	0	-	-	5 (27.8)	5.2×10^3	$2.2 \times 10^3 - 9.9 \times 10^3$	5 (27.8)	1.1×10^4	$9.8 \times 10^2 - 4.8 \times 10^5$
<i>Sphaerophoria philanthus</i>	8	0	-	-	1 (12.5)	1.3×10^3	-	1 (12.5)	4.7×10^3	-
<i>Syrphus vitripennis</i>	8	0	-	-	2 (25)	4.5×10^7	$3.9 \times 10^4 - 9.0 \times 10^7$	6 (75)	2.5×10^4	$8.6 \times 10^3 - 6.0 \times 10^6$

Supplementary Table 2. Twenty pollinator species were screened for three viruses, deformed wing virus A and B (DWV-A, DWV-B) and black queen cell virus (BQCV). The total number of individuals per species, and the number of landscapes in each sampling round where the specimen were collected are given.

Species	Total nr. of individuals	Nr. of landscapes in April	Nr. of landscapes in May/June	Nr. of landscapes in July
<i>Andrena humilis</i>	10	1	-	-
<i>Apis mellifera</i>	360	12	12	12
<i>Bombus hortorum</i>	33	-	4	-
<i>Bombus humilis</i>	32	-	1	3
<i>Bombus hypnorum</i>	9	-	1	-
<i>Bombus lapidarius</i>	130	-	7	7
<i>Bombus lucorum</i>	10	-	1	-
<i>Bombus pascuorum</i>	88	-	4	6
<i>Bombus ruderatus</i>	14	-	2	-
<i>Bombus subterraneus</i>	9	-	1	-
<i>Bombus sylvarum</i>	23	-	1	2
<i>Bombus terrestris</i>	71	-	-	8
<i>Halictus scabiosae</i>	15	-	1	1
<i>Lasioglossum glabriusculum</i>	17	-	-	2
<i>Lasioglossum malachurum</i>	57	-	2	4
<i>Lasioglossum morio</i>	7	-	-	1
<i>Lasioglossum pauxillum</i>	67	1	2	4
<i>Melanostoma mellinum</i>	18	2	-	-
<i>Sphaerophoria philanthus</i>	8	-	-	1
<i>Syrphus vitripennis</i>	8	-	-	1

Supplementary Table 3. Shown are the number of samples screened for viruses at each site and in each sampling round, the number of virus positive samples, the apparent virus prevalence as well as the lower and upper confidence interval (ci, 95%), calculated using the Clopper-Pearson interval. Only the data used in the statistical models is shown (i.e. sampling rounds 2 and 3, BQCV and DWV-B). BQCV = black queen cell virus and DWV-B = deformed wing virus.

Sampling round	Site	Species	No. of samples	BQCV				DWV-B			
				No. positives	Apparent prevalence	Lower ci	Upper ci	No. positives	Apparent prevalence	Lower ci	Upper ci
2	A1	<i>A. mellifera</i>	10	3	0.30	0.07	0.65	3	0.30	0.07	0.65
2	A1	<i>B. hortorum</i>	7	0	0.00	0.00	0.41	0	0.00	0.00	0.41
2	A1	<i>B. sylvarum</i>	7	1	0.14	0.00	0.58	1	0.14	0.00	0.58
2	A2	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	A2	<i>B. hortorum</i>	10	9	0.90	0.55	1.00	9	0.90	0.55	1.00
2	A2	<i>B. lapidarius</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	A2	<i>B. ruderatus</i>	7	4	0.57	0.18	0.90	4	0.57	0.18	0.90
2	A2	<i>B. subterraneus</i>	9	9	1.00	0.66	1.00	9	1.00	0.66	1.00
2	A3	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	A3	<i>B. lapidarius</i>	9	8	0.89	0.52	1.00	8	0.89	0.52	1.00
2	A3	<i>L. malachurum</i>	10	1	0.10	0.00	0.45	1	0.10	0.00	0.45
2	A4	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	A4	<i>B. lapidarius</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	A4	<i>B. ruderatus</i>	7	2	0.29	0.04	0.71	2	0.29	0.04	0.71
2	R1	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	R1	<i>L. malachurum</i>	10	2	0.20	0.03	0.56	2	0.20	0.03	0.56
2	R2	<i>A. mellifera</i>	10	5	0.50	0.19	0.81	5	0.50	0.19	0.81
2	R2	<i>B. pascuorum</i>	7	0	0.00	0.00	0.41	0	0.00	0.00	0.41
2	R3	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	R3	<i>B. pascuorum</i>	9	1	0.11	0.00	0.48	1	0.11	0.00	0.48
2	R4	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	R4	<i>B. hortorum</i>	7	7	1.00	0.59	1.00	7	1.00	0.59	1.00
2	U1	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	U1	<i>B. lapidarius</i>	9	7	0.78	0.40	0.97	7	0.78	0.40	0.97

2	U1	<i>B. pascuorum</i>	7	6	0.86	0.42	1.00	6	0.86	0.42	1.00
2	U2	<i>A. mellifera</i>	10	9	0.90	0.55	1.00	9	0.90	0.55	1.00
2	U2	<i>B. lapidarius</i>	10	5	0.50	0.19	0.81	5	0.50	0.19	0.81
2	U2	<i>L. pauxillum</i>	10	2	0.20	0.03	0.56	2	0.20	0.03	0.56
2	U3	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	U3	<i>B. lapidarius</i>	8	8	1.00	0.63	1.00	8	1.00	0.63	1.00
2	U3	<i>H. scabiosae</i>	8	2	0.25	0.03	0.65	2	0.25	0.03	0.65
2	U3	<i>L. pauxillum</i>	10	2	0.20	0.03	0.56	2	0.20	0.03	0.56
2	U4	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
2	U4	<i>B. hortorum</i>	9	9	1.00	0.66	1.00	9	1.00	0.66	1.00
2	U4	<i>B. humilis</i>	8	8	1.00	0.63	1.00	8	1.00	0.63	1.00
2	U4	<i>B. hypnorum</i>	9	6	0.67	0.30	0.93	6	0.67	0.30	0.93
2	U4	<i>B. lapidarius</i>	10	6	0.60	0.26	0.88	6	0.60	0.26	0.88
2	U4	<i>B. lucorum</i>	10	3	0.30	0.07	0.65	3	0.30	0.07	0.65
2	U4	<i>B. pascuorum</i>	10	3	0.30	0.07	0.65	3	0.30	0.07	0.65
3	A1	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	A1	<i>B. terrestris</i>	7	4	0.57	0.18	0.90	4	0.57	0.18	0.90
3	A2	<i>A. mellifera</i>	10	9	0.90	0.55	1.00	9	0.90	0.55	1.00
3	A2	<i>B. lapidarius</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	A2	<i>B. pascuorum</i>	7	0	0.00	0.00	0.41	0	0.00	0.00	0.41
3	A2	<i>B. terrestris</i>	10	4	0.40	0.12	0.74	4	0.40	0.12	0.74
3	A3	<i>A. mellifera</i>	10	7	0.70	0.35	0.93	7	0.70	0.35	0.93
3	A3	<i>B. lapidarius</i>	10	9	0.90	0.55	1.00	9	0.90	0.55	1.00
3	A3	<i>B. terrestris</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	A3	<i>L. malachurum</i>	10	1	0.10	0.00	0.45	1	0.10	0.00	0.45
3	A4	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	A4	<i>B. lapidarius</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	A4	<i>B. terrestris</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	A4	<i>L. malachurum</i>	10	5	0.50	0.19	0.81	5	0.50	0.19	0.81
3	A4	<i>S. philanthus</i>	8	1	0.13	0.00	0.53	1	0.13	0.00	0.53

3	R1	<i>A. mellifera</i>	10	7	0.70	0.35	0.93	7	0.70	0.35	0.93
3	R1	<i>B. lapidarius</i>	7	5	0.71	0.29	0.96	5	0.71	0.29	0.96
3	R1	<i>B. sylvarum</i>	7	6	0.86	0.42	1.00	6	0.86	0.42	1.00
3	R1	<i>B. terrestris</i>	10	2	0.20	0.03	0.56	2	0.20	0.03	0.56
3	R1	<i>L. malachurum</i>	10	0	0.00	0.00	0.31	0	0.00	0.00	0.31
3	R2	<i>A. mellifera</i>	10	9	0.90	0.55	1.00	9	0.90	0.55	1.00
3	R2	<i>B. lapidarius</i>	10	8	0.80	0.44	0.97	8	0.80	0.44	0.97
3	R2	<i>B. pascuorum</i>	10	2	0.20	0.03	0.56	2	0.20	0.03	0.56
3	R2	<i>B. sylvarum</i>	9	5	0.56	0.21	0.86	5	0.56	0.21	0.86
3	R2	<i>B. terrestris</i>	8	6	0.75	0.35	0.97	6	0.75	0.35	0.97
3	R2	<i>S. vitripennis</i>	8	6	0.75	0.35	0.97	6	0.75	0.35	0.97
3	R3	<i>A. mellifera</i>	10	9	0.90	0.55	1.00	9	0.90	0.55	1.00
3	R3	<i>B. pascuorum</i>	10	2	0.20	0.03	0.56	2	0.20	0.03	0.56
3	R3	<i>L. malachurum</i>	7	0	0.00	0.00	0.41	0	0.00	0.00	0.41
3	R4	<i>A. mellifera</i>	10	9	0.90	0.55	1.00	9	0.90	0.55	1.00
3	U1	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	U1	<i>B. humilis</i>	9	1	0.11	0.00	0.48	1	0.11	0.00	0.48
3	U1	<i>B. pascuorum</i>	8	1	0.13	0.00	0.53	1	0.13	0.00	0.53
3	U1	<i>B. terrestris</i>	10	4	0.40	0.12	0.74	4	0.40	0.12	0.74
3	U1	<i>L. glabriusculum</i>	7	0	0.00	0.00	0.41	0	0.00	0.00	0.41
3	U1	<i>L. pauxillum</i>	7	0	0.00	0.00	0.41	0	0.00	0.00	0.41
3	U2	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	U2	<i>B. humilis</i>	8	7	0.88	0.47	1.00	7	0.88	0.47	1.00
3	U2	<i>B. lapidarius</i>	7	7	1.00	0.59	1.00	7	1.00	0.59	1.00
3	U2	<i>B. pascuorum</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	U2	<i>B. terrestris</i>	6	5	0.83	0.36	1.00	5	0.83	0.36	1.00
3	U2	<i>L. glabriusculum</i>	10	6	0.60	0.26	0.88	6	0.60	0.26	0.88
3	U2	<i>L. pauxillum</i>	10	5	0.50	0.19	0.81	5	0.50	0.19	0.81
3	U3	<i>A. mellifera</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	U3	<i>L. pauxillum</i>	10	1	0.10	0.00	0.45	1	0.10	0.00	0.45

3	U4	<i>A. mellifera</i>	10	9	0.90	0.55	1.00	9	0.90	0.55	1.00
3	U4	<i>B. humilis</i>	7	7	1.00	0.59	1.00	7	1.00	0.59	1.00
3	U4	<i>B. lapidarius</i>	10	10	1.00	0.69	1.00	10	1.00	0.69	1.00
3	U4	<i>B. pascuorum</i>	10	2	0.20	0.03	0.56	2	0.20	0.03	0.56
3	U4	<i>H. scabiosae</i>	7	1	0.14	0.00	0.58	1	0.14	0.00	0.58
3	U4	<i>L. morio</i>	7	0	0.00	0.00	0.41	0	0.00	0.00	0.41
3	U4	<i>L. pauxillum</i>	10	0	0.00	0.00	0.31	0	0.00	0.00	0.31

Supplementary Table 4. Best ranked models ($\Delta AICc < 2$) from multi-model inference analysis investigating the effects of a species foraging patterns (i.e. community weighted mean (CWM) flower volume, CWM corolla length, specialisation (d'), resource overlap with honeybees (HB), proportion of dish flowers and weighted betweenness (Betweenness) on species virus loads (log-transformed, only virus-positive individuals). BQCV = black queen cell virus and DWV-B = deformed wing virus. Sampling round was included in all models due to the data structure (two sampling rounds in each landscape). Given are model estimates of the variables and the adjusted R^2 , AICc, delta (difference in AICc to the best model) and the Akaike weight (weight) of the respective model.

Rank	Intercept	Sampling round	Flower volume (CWM)	Corolla length (CWM)	d'	Resource overlap with HB	Dish flowers	Betweenness	Adj. R^2	AICc	delta	weight
BQCV												
1	12.00	+	-	-0.48	-	2.00	-0.71	-0.71	0.51	1328.09	0.00	0.25
2	12.10	+	-	-0.48	0.27	2.21	-0.76	-0.76	0.51	1328.28	0.20	0.22
3	12.09	+	-	-	-	1.71	-0.77	-0.77	0.51	1329.71	1.62	0.11
4	12.18	+	-	-	0.26	1.90	-0.81	-0.81	0.51	1330.09	2.00	0.09
DWV-B												
1	8.47	+	-0.27	-	0.32	0.93	-	-	0.25	1149.26	0.00	0.09
2	8.52	+	-	-	0.31	0.72	-	-	0.24	1149.62	0.36	0.07
3	8.49	+	-0.30	-	0.35	0.91	-	-0.17	0.25	1149.99	0.73	0.06
4	8.38	+	-0.26	-	-	0.69	-	-	0.24	1150.05	0.79	0.06
5	8.42	+	-	-	-	0.50	-	-	0.23	1150.27	1.01	0.05
6	8.49	+	-0.25	-0.18	0.32	1.03	-	-	0.25	1150.29	1.03	0.05
7	8.53	+	-	-0.20	0.31	0.84	-	-	0.24	1150.36	1.10	0.05
8	8.53	+	-	-	0.34	0.68	-	-0.13	0.24	1150.84	1.58	0.04
9	8.50	+	-0.28	-0.19	0.35	1.01	-	-0.17	0.25	1150.93	1.67	0.04
10	8.44	+	-	-0.20	-	0.63	-	-	0.24	1150.93	1.67	0.04
11	8.39	+	-0.24	-0.18	-	0.80	-	-	0.24	1151.01	1.75	0.04

Supplementary Table 5. Best ranked models ($\Delta AICc < 2$) from multi-model inference analysis investigating the effects of a species foraging patterns (i.e. community weighted mean (CWM) flower volume, CWM corolla length, specialisation (d'), resource overlap with honeybees (HB), proportion of dish flowers and weighted betweenness (Betweenness) on black queen cell virus (BQCV) or deformed wing virus B (DWV-B) prevalence in wild pollinators (generalised linear mixed models with binomial distribution). Sampling round was included in all models due to the data structure (two sampling rounds in each landscape). The table reports the model estimates for the variables, the AICc and delta AICc (delta) to the best model, and the Akaike weight (weight) for each model.

Rank	Intercept	Sampling round	Flower volume (CWM)	Corolla length (CWM)	d'	Resource overlap with HB	Dish flowers	Betweenness	AICc	delta	weight
BQCV											
1	0.51	+	-	-	-	1.33	-	-0.69	288.09	0.00	0.10
2	0.39	+	-0.57	-	-	1.60	-	-0.57	288.32	0.23	0.09
3	0.29	+	-0.65	-	-0.61	1.22	-	-0.56	288.61	0.52	0.07
4	0.50	+	-	-	-	1.39	-0.41	-0.57	288.84	0.75	0.07
5	0.45	+	-	-	-0.52	0.98	-	-0.69	288.93	0.84	0.06
6	0.35	+	-0.76	-	-	1.76	-	-	289.33	1.24	0.05
7	0.24	+	-0.85	-	-0.64	1.36	-	-	289.52	1.43	0.05
8	0.50	+	-	-	-	1.47	-0.60	-	289.76	1.67	0.04
9	0.44	+	-	-	-0.48	1.05	-0.39	-0.58	289.97	1.88	0.04
DWV-B											
1	-0.25	+	-	-	-	0.69	-	-	297.84	0.00	0.16
2	-0.22	+	-	-	-	0.63	-	-0.25	298.94	1.10	0.09
3	-0.14	+	-	-0.40	-	0.76	-	-0.37	299.30	1.46	0.07
4	-0.22	+	-	-0.24	-	0.79	-	-	299.42	1.59	0.07

Supplementary Table 6. Model-averaged estimates (conditional average) of best models ($\Delta AIC_c < 2$) investigating the effects of a species' traits and roles in the network (i.e. community weighted mean (CWM) flower volume, CWM corolla length, specialisation (d'), resource overlap with honeybees (HB), proportion of dish flowers and weighted betweenness (Betweenness), or the effects of species community and landscape (percentage cover of pollinator habitat (Poll. hab. %), flower Shannon diversity (H flowers), viral load in honeybees – BQCV or DWV-B – (HB load), honeybee density (HB density) and wild pollinator abundance (Poll. abundance)) on virus prevalence in wild pollinators. BQCV = black queen cell virus and DWV-B = deformed wing virus. Sampling round was included in all models due to the data structure (two sampling rounds in each landscape). Z-tests were used to derive p-values from the averaged best models. The table shows the estimates and (adjusted) standard errors (SE, Adj. SE), z and p values as well as p values corrected with the false discovery rate correction (FDR).

Response		Estimate	SE	Adj. SE	z value	p value	FDR p value
Species traits and roles models							
BQCV prevalence in wild poll.	Intercept	0.41	0.51	0.52	0.80	0.424	
	Betweenness	-0.61	0.30	0.31	1.99	0.046	0.082
	d'	-0.57	0.41	0.42	1.36	0.175	0.197
	Flower volume	-0.68	0.40	0.41	1.68	0.094	0.135
	Dish flowers	-0.46	0.33	0.33	1.39	0.165	0.197
	Resource overlap	1.36	0.46	0.46	2.93	0.003	0.013
	Sampl. round 3	-0.37	0.61	0.62	0.60	0.550	0.549
DWV-B prevalence in wild poll.	Intercept	-0.22	0.50	0.51	0.43	0.667	
	Betweenness	-0.31	0.23	0.24	1.30	0.195	0.306
	Corolla length	-0.32	0.28	0.28	1.13	0.195	0.330
	Resource overlap	0.71	0.25	0.26	2.75	0.006	0.050
	Sampl. round 3	-0.11	0.41	0.42	0.27	0.786	0.786
Community and landscape models							
BQCV prevalence in wild poll.	Intercept	1.06	0.53	0.54	1.95	0.052	
	HB preval. BQCV	0.59	0.37	0.37	1.60	0.111	0.150
	HB density	0.56	0.42	0.42	1.31	0.189	0.198
	Poll. abundance	1.42	0.44	0.44	3.2	0.001	0.006
	Poll. hab	-0.96	0.42	0.42	2.26	0.024	0.054
	Sampl. round 3	-1.50	0.72	0.73	2.02	0.043	0.082
DWV-B prevalence in wild poll.	Intercept	0.07	0.57	0.58	0.13	0.897	
	H flowers	-0.53	0.42	0.43	1.24	0.217	0.318
	HB preval DWV-B	0.42	0.32	0.32	1.31	0.189	0.306
	HB density	0.41	0.30	0.30	1.35	0.178	0.306
	Poll. abundance	0.77	0.38	0.38	2.02	0.043	0.191
	Poll. hab.	-0.44	0.43	0.43	1.01	0.310	0.359
	Sampl. round 3	-0.46	0.65	0.66	0.71	0.480	0.503

Significant results (FDR $p < 0.05$) are shown in bold.

Supplementary Table 7. The results of the similarity of percentage (SIMPER, Clarke 1993) analysis revealed that flower volume, corolla length and dish-bowl shape of visited flowers explained most of the differences in flower visitation patterns among the pollinator species assigned to the different viral load groups (given as number of viral copies per species, grouped in < 33 %, > 33 % < 66 % and > 66 % quantiles of viral loads). The contributions of the different visited flower traits are given as percentages. BQCV = black queen cell virus; DWV-B = deformed wing virus.

Comparisons	Visited flower shapes (based on community weighted means per pollinator species)								
BQCV load groups	Volume	Corolla length	Dish-bowl	Gullet	Flag	Brush	Bell-trumpet	Stalk-disk	Tube
44000 - >900000	34.93	21.40	17.83	7.95	10.68	4.08	2.06	0.98	0.09
44000 - <900000	42.80	20.58	14.65	6.67	9.90	3.97	0.93	0.49	0.00
>900000 - <900000	42.63	15.77	14.50	7.90	12.73	3.00	2.61	0.76	0.10
DWV-B load groups									
1600 - 10400	37.79	22.35	16.51	10.27	6.46	4.32	1.22	0.98	0.10
1600 - 10000	42.35	16.20	17.16	4.98	14.16	3.05	1.66	0.45	0.00
10000 - 10400	41.17	15.93	13.06	7.19	16.39	2.81	2.66	0.68	0.10

Supplementary Table 8. Best ranked models ($\Delta\text{AICc} < 2$) from multi-model inference analysis investigating the effects of percentage cover of pollinator habitat (Poll. hab. %), flower Shannon diversity (H flowers), viral load in honeybees – black queen cell virus (BQCV) or deformed wing virus B (DWV-B) – (HB load), honeybee density (HB density) and wild pollinator abundance (Poll. abundance) on BQCV or DWV-B viral load (log-transformed, only virus-positive individuals) in wild pollinators. Sampling round was included in all models due to the data structure (two sampling rounds in each landscape). The table reports the estimates of the variables, the adjusted R^2 , the AICc and delta AICc (delta) to the best model, and the Akaike weight (weight) for each model.

Rank	Intercept	Sampling round	Poll. hab. %	H flowers	HB load	HB density	Poll. abundance	Adj. R^2	AICc	delta	weight
BQCV											
1	11.72	+	-	-0.79	0.98	0.40	1.02	0.48	1346.54	0.00	0.18
2	11.14	+	-0.84	-	1.02	-	0.63	0.48	1347.27	0.73	0.13
3	11.48	+	-	-0.74	0.95	-	0.80	0.47	1347.61	1.07	0.11
4	11.29	+	-0.75	-	1.04	0.32	0.76	0.48	1347.68	1.14	0.10
5	11.41	+	-0.63	-0.54	1.00	-	0.83	0.48	1347.73	1.19	0.10
6	11.66	+	-0.51	-0.67	1.03	0.37	1.05	0.48	1347.83	1.29	0.10
7	11.30	+	-	-	0.99	0.38	0.67	0.47	1348.33	1.79	0.07
DWV-B											
1	8.47	+	-0.55	-	0.44	-	0.88	0.27	1141.44	0.00	0.12
2	8.42	+	-	-	0.44	-	0.76	0.26	1141.51	0.07	0.11
3	8.32	+	-0.68	0.39	0.40	-	0.74	0.27	1141.79	0.35	0.10
4	8.61	+	-0.65	0.45	-	-	0.88	0.27	1142.29	0.86	0.08
5	8.80	+	-0.48	-	-	-	1.05	0.26	1142.66	1.22	0.06
6	8.73	+	-	-	-	-	0.89	0.25	1142.69	1.25	0.06
7	8.31	+	-	0.28	0.42	-	0.66	0.26	1142.76	1.32	0.06
8	8.16		-0.76	0.44	0.46	-0.17	0.59	0.27	1142.93	1.49	0.06
9	8.37	+	-0.59	-	0.48	-0.12	0.79	0.27	1143.05	1.61	0.05

Supplementary Table 9. Best ranked models ($\Delta AICc < 2$) from multi-model inference analysis investigating the effects of percentage cover of pollinator habitat (Poll. hab. %), flower Shannon diversity (H flowers), viral prevalence in honeybees – black queen cell virus (BQCV) or deformed wing virus B (DWV-B) – (HB prevalence), honeybee density (HB density) and wild pollinator abundance (Poll. abundance) on BQCV or DWV-B prevalence in wild pollinators (generalised linear mixed models with binomial distribution). Sampling round was included in all models due to the data structure (two sampling rounds in each landscape). The table reports the estimates of the variables, the AICc and delta AICc to the best model, and the Akaike weight (weight) for each model.

Rank	Intercept	Sampling round	Poll. hab. %	H flowers	HB prevalence	HB density	Poll. abundance	AICc	delta	weight
BQCV										
1	1.00	+	-1.08	-	0.59	-	1.38	293.51	0.00	0.20
2	1.18	+	-1.03	-	-	-	1.58	293.77	0.26	0.18
3	0.98	+	-0.80	-	0.61	0.46	1.36	294.64	1.14	0.11
4	1.17	+	-0.76	-	-	0.43	1.57	295.01	1.50	0.09
5	0.88	+	-	-	0.59	0.86	1.07	295.48	1.97	0.07
DWV-B										
1	0.11	+	-	-	-	-	0.65	302.61	0.00	0.11
2	0.20	+	-	-	-	0.41	0.79	303.18	0.56	0.09
3	0.40	+	-	-0.56	-	-	0.93	303.39	0.78	0.08
4	-0.10	+	-	-	0.41	-	0.59	303.44	0.82	0.08
5	0.00	+	-	-	0.41	0.42	0.74	303.94	1.33	0.06
6	0.12	+	-0.44	-	-	-	0.77	304.07	1.46	0.06
7	-0.30	+	-	-	-	-	-	304.09	1.48	0.05
8	-0.49		-	-	0.48	-	-	304.28	1.66	0.05
9	0.44		-	-0.49	-	0.37	1.02	304.33	1.72	0.05
10	0.20	+	-	-0.53	0.39	-	0.86	304.34	1.73	0.05

Supplementary Table 10. Model estimates of models investigating relationships between bumblebee (*Bombus lapidarius* or *B. terrestris*) viral prevalence or load (BQCV or DWV-B) and honeybee viral prevalence or load. BQCV = black queen cell virus and DWV-B = deformed wing virus. Sampling round was included in the models of *B. lapidarius* due to the data structure (*B. lapidarius* sampled in two sampling rounds were included in the analyses; *B. terrestris* sampled in one sampling round were included in the analyses). T-tests (linear mixed models used for viral load as response variable) or z-tests (generalised linear mixed models used for viral prevalence as response variable) were used to derive p-values. The table shows the estimates and standard errors (SE), t or z values and p values.

		Estimate	SE	df	t or z value	P value
Response variable	Explanatory variables (<i>B. lapidarius</i>)					
Honeybee BQCV load	<i>B. lapidarius</i> BQCV load	0.32	0.14	8.15	2.28	0.052
	Sampling round	-3.29	0.77	86	-4.24	<0.0001
Honeybee BQCV prevalence	<i>B. lapidarius</i> BQCV prevalence	6.82	2.88		2.36	0.018
	Sampling round	-3.58	1.31		-2.73	0.006
Honeybee DWV-B load	<i>B. lapidarius</i> DWV-B load	0.53	0.16	12	3.37	0.006
	Sampling round	-1.81	0.94	100	-1.93	0.057
Honeybee DWV-B prevalence	<i>B. lapidarius</i> DWV-B prevalence	1.58	0.96		1.64	0.102
	Sampling round	-1.03	0.50		-2.08	0.037
Response variable	Explanatory variables (<i>B. terrestris</i>)					
Honeybee BQCV load	<i>B. terrestris</i> BQCV load	-0.03	0.29	6	-0.1	0.926
Honeybee BQCV prevalence	<i>B. terrestris</i> BQCV prevalence	0.79	1.88		0.42	0.676
Honeybee DWV-B load	<i>B. terrestris</i> DWV-B load	0.50	0.27	6	1.87	0.112
Honeybee DWV-B prevalence	<i>B. terrestris</i> DWV-B prevalence	2.74	0.95		2.88	0.004

Significant results (FDR $p < 0.05$) are shown in bold

Supplementary Table 11. The major land-use types and the range and mean $\pm$ SD of their percentage cover in a 500 m radius in the study landscapes.

Land-use types	Pollinator-friendly	Range (min.-max.)	Mean $\pm$ SD
Extensively managed grasslands (incl. orchards and vineyards)	Yes	0-15 %	5.1 $\pm$ 4.9
Flower strips	Yes	0-1 %	0.2 $\pm$ 0.3
Hedgerows	Yes	0-3 %	0.6 $\pm$ 0.9
Urban green space	Yes	0-72 %	22.7 $\pm$ 32.1
Urban space	No	0-25 %	8.3 $\pm$ 11.0
Arable crops	No	0-93 %	44.0 $\pm$ 34.6
Intensively managed grasslands	No	1-38 %	13.1 $\pm$ 13.7
Forest	No	0-14 %	4.5 $\pm$ 5.3

Supplementary Table 12. The table shows the primer sequences and primer names, product sizes and the references for the primers that were used for the three viral targets black queen cell virus (BQCV), deformed wing virus A and B (DWV-A, DWV-B).

Target	Primer Name	Sequence	Product size	Reference
BQCV	BQCV-qF7893 (F)	AGT GGC GGA GAT GTA TGC	294	Locke et al. (2012)
	BQCV-qB8150 (R)	GGA GGT GAA GTG GCTA TATC		
DWV-A RdRp	DWV-F8668 (F)	TTC ATT AAA GCC ACC TGG AAC ATC	136	Forsgren et al. (2009)
	DWV-B8757 (R)	TTT CCT CAT TAA CTG TGT CGT TGA		
DWV-B (VDV-1) RdRp	VDVq-F2 (8664) (F)	TAT CTT CAT TAA AAC CGC CAG GCT	140	McMahon et al. (2015)
	VDVq-R2a (8757) (R)	CTT CCT CAT TAA CTG AGT TGT TGT C		

Supplementary Table 13. The table shows the sequences of the synthetic strands used as templates for the amplification of the standard curves for the quantification of black queen cell virus (BQCV) and deformed wing virus A and B (DWV-A, DWV-B).

Synthetic strand	Sequence
BQCV (F7893-B8150)	AGTGGCGGAGATGTATGCGCTTTATCGAGGAGGAGTTCGAGTTAAAGTTGTTACTGAG AAGGGTGTGGATTTTCGTCAGAGCTACCGTTAGTCCTCAACAGACTTACGGCAGTGATG TCGCTCCTACTACTCATATCAGTACTCCTTTGGCAATAGAACAAATACCTATAAAGGG AGTCGCAGAGTTCCAAATACCGTACTATGCTCCATGTTTGTCTATCTTCGTTTAGAGCG AATTCGGAACATTTTACTATAGTTCAGGTCGGAATAATCTCGATATAGCCACTTCAC CTCC
DWV-A (F8668-B8757)	TTCATTAAAGCCACCTGGAACATCCGGTAAGCGATGGTTGTTTGACATTGAGCTGCAA GACTCGGGATGTTATCTCCTGCGTGGAATGCGTCCCGAACTTGAGATTCAATTATCAA CGACACAGTTAATGAGGAAA
DWV-B (VDVq-F2 q-R2a)	TATCTTCATTAAAACCGCCAGGCTCTTCTGGTAAGCGATGGTTGTTTGATATTGAATTA CAAGATTCAAGGATGTTATCTTTTGAGAGGGATGAGACCTGAACTTGAGATACAGTTGA CAACAACTCAGTTAATGAGGAAG

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