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Appendix 1

Methods

Cleaning protocols

The householders involved in the study were responsible for cleaning the feeding stations. We prescribed a set of cleaning protocols for householders to follow, which were based on typical cleaning practices of bird feeding participants in New Zealand (Galbraith et al. 2014). This was in an attempt to ensure our results would be relevant, as far as was possible, to the current feeding situation. In terms of the frequency of cleaning, the majority of feeding respondents (63%) cleaned structures used in feeding at least once a month, with 43% overall cleaning at least once a week. Most respondents that cleaned feeding structures used water to do so (84.2%), rather than using detergent (20%) or a disinfectant (1.1%), with 46.3% also scrubbing structures to clean them. On this basis, we asked householders to thoroughly scrub the surface of the table and the feeders with water once every two weeks, rinsing with clean water and allowing to dry. We asked that cleaning be done before feeding in the morning, or after the food was all gone, to minimise disruption. In addition, we asked householders to brush away any build up of debris from the stations on a daily basis. Householders were provided with a bucket, gloves, and scrubbing brushes to be used solely for cleaning the stations. We also requested householders remove any bird baths from their gardens for the duration of the study.

Salmonella spp. screening methods

Screening was conducted at Gribbles Veterinary Pathology, Auckland, New Zealand. Cloacal swabs were inoculated onto Xylose-Lysine-Desoxycholate (XLD) and Hektoen agars, and Selenite F and/or Rappaport (RVS) selective broths, incubated aerobically at 35–37°C overnight. Enrichment broths were subcultured onto XLD and Hektoen agars and incubated for a further 18 h aerobically at 35–37°C. All suspect colonies were identified using Microbact MB12A biochemical identification kits or MALDI-TOF (matrix assisted laser desorption/ionisation-time of flight mass spectrometry). These were confirmed serologically at the Enteric Reference Laboratory at the Institute of Environmental Science and Research (ESR), Wellington, New Zealand.

Chlamydophila psittaci screening methods

Chlamydophila psittaci screening was performed at Massey Equine Parentage and Animal Genetic Services Centre, Palmerston North, New Zealand. Genomic DNA was extracted from dry cloacal swabs. The swab was added to 100 µl of deionised water, left to sit for 5 min and then vortexed. The swab was removed and the remaining liquid spun at 12000 rpm for 3 min. The supernatant was discarded leaving 10 µl in the tube, to which 40 µl of Instagene matrix (Bio-Rad) and 1 µl of Proteinase K 20 mg ml^{-1} (New England Biolabs) were added. This solution was incubated for 1 h at 56°C, boiled for 8 min, vortexed, and spun at 12000 rpm for 3 min. The samples were run with a control sample of 460 bp segment of the genome of the *Chlamydophila* family was amplified using PCR with the primers, forward 5'-TGATGAGGCATGCAAGTC-3' and reverse 5'-TTACCTGGTACGCTCAAAT-3' (Robertson et al 2009). This primer set targets the 16S rRNA gene product, designed through the comparison of the GenBank sequences of *C. muridarum* (D85718), *C. suis* (U73110), *C. trachomatis* (D85722), Cp abortus (U61766), Cp caviae (D85708), Cp felis (D85701), Cp pecorum (D85717), Cp pneumoniae (L06108) and Cp psittaci (AB285329). PCR was performed by mixing 2 µl of 10 Firepol Blend Mastermix including 10 mM $MgCl_2$ (Solis BioDyne), 1 µl of 100× BSA 10 mg ml^{-1} (New England Biolabs), 0.4 µl of each of the forward and reverse primers, and 2 µl DNA. This was made up to a 10 µl volume and run on an Applied Biosystems Genamp 2700 thermal cycler. The 16SG PCR reactions were subjected to an initial denaturing period of 10 min at 96°C, followed by 40× cycles of 94°C for 30 s, 58°C (annealing temperature) for 30 s and 72°C for 30 s. This was followed by a final extension period of 2 min at 72°C. After PCR, 8 µl of amplified product was loaded on to a 1.5% agarose gel containing ethidium bromide, subjected to electrophoresis for 10 min and photographed using UV transillumination (UVP Transilluminator).

Gastrointestinal parasite screening methods

We used the faecal floatation method to assess endoparasite loads. Water was added to the faecal sample until the vials was ca ¾ full, and then vigorously stirred with a clean wooden stick until thoroughly blended. They were then centrifuged for 5 min at 2000 rpm to separate out the particulate matter. The supernatant was removed with a sterile pipette before an aqueous solution of $ZnSO_4$ (2.4 mol l^{-1}; specific gravity 1.18) was added to bring the volume to 2 ml. The sample was then gently mixed with a clean wooden stick and centrifuged for a further 5 min. $ZnSO_4$ was added in drops to the sample to form a convex meniscus. A cover slip was placed on this and left for 5 min. The cover slip was then transferred to a glass slide and screened under a microscope for the presence of coccidia and gastrointestinal helminth eggs. Where parasites were detected, we counted eggs/oocysts in the field of view at 10 randomly selected places on the slide under a low power magnification (40×) as an index of infection intensity.

References

Galbraith, J. A., Beggs, J. R., Jones, D. N., McNaughton, E. J., Krull, C. R. and Stanley, M. C. 2014. Risks and drivers of wild bird feeding in urban areas of New Zealand. – Biol. Conserv. 180: 64–74.

Appendix 2

Table A1. Summary of initial generalized linear mixed model (GLMM) results testing the effect of an experimental feeding regime on pathogen and parasite measures at urban study properties in northern Auckland, New Zealand, with interaction terms included for all models.

Response variable	Host species	Model error structure[†]	Experimental group (reference level: feeding)			Season (reference level: autumn)			Experimental group × season interaction (reference level: feeding, autumn)		
			Non-feeding			Spring			Non-feeding, Spring		
			β	χ^2	p	β	χ^2	p	β	χ^2	p
Salmonella spp. (prevalence)	House sparrow	B[‡]	-0.602	-0.53	0.60	0.289	0.28	0.78	0.636	0.29	0.77
Pox-like lesions (prevalence)	House sparrow	B	-0.336	0.04	0.84	**-3.053**	**42.2**	**<0.001*****	1.403	1.93	0.16
	Silvereye	B[‡]	-0.022	-0.03	0.98	1.098	1.36	0.17	-0.481	-0.32	0.75
	Eurasian blackbird	B[‡]	-0.816	-0.60	0.55	-0.022	-0.02	0.99	0.218	0.08	0.94
Mites (prevalence)	House sparrow	B	-0.225	1.26	0.26	**0.544**	**5.79**	**0.02***	0.945	1.29	0.26
	Silvereye	B	0.085	0.30	0.58	**1.204**	**12.0**	**<0.001*****	0.213	0.07	0.78
	Eurasian blackbird	B[‡]	-0.973	-0.93	0.36	**2.646**	**2.66**	**<0.01****	-0.180	-0.09	0.93
Mites (abundance)	House sparrow	NB	-0.066	2.74	0.10	**1.456**	**11.8**	**<0.001*****	1.522	1.98	0.16
	Silvereye	NB	0.710	1.40	0.24	**1.286**	**8.80**	**<0.01****	-0.495	0.61	0.43
	Eurasian blackbird	NB	-1.135	2.28	0.13	**5.167**	**18.3**	**<0.001*****	-0.988	0.25	0.62
Lice (prevalence)	House sparrow	B	0.397	0.01	0.94	**-0.414**	**4.59**	**0.03***	-1.396	2.29	0.13
	Silvereye	B	-0.183	0.41	0.52	**-2.780**	**4.58**	**0.03***	2.128	2.32	0.13
	Eurasian blackbird	B[‡]	-0.232	-0.19	0.85	-0.713	-0.77	0.44	-0.345	-0.19	0.85
Lice (abundance)	House sparrow	NB	**-0.728**	**4.86**	**0.03***	-0.136	1.17	0.28	-1.505	1.63	0.20
	Silvereye	NB	0.167	0.54	0.46	**-2.803**	**7.31**	**<0.01****	1.633	1.36	0.24
	Eurasian blackbird	NB	2.885	0.05	0.83	1.151	0.70	0.40	-4.043	2.79	0.09 •
Helminths (prevalence)	House sparrow	B	-1.008	1.08	0.30	**0.869**	**4.91**	**0.03***	0.676	0.33	0.57
	Silvereye	B	0.450	3.32	0.07 •	0.422	3.44	0.06 •	0.657	0.48	0.49
	Eurasian blackbird	B	0.143	0.01	0.92	**1.609**	**5.08**	**0.02***	-0.366	0.08	0.78
Helminths (abundance)	House sparrow	NB	-0.025	0.01	0.94	1.407	2.28	0.13	0.192	0.01	0.93
	Silvereye	NB	1.400	3.26	0.07 •	-0.283	0.13	0.72	0.090	0.004	0.95
	Eurasian blackbird	NB	-2.768	3.42	0.06 •	-0.432	0.22	0.64	1.824	0.97	0.32
Coccidia (prevalence)	House sparrow	B	0.182	0.001	0.97	**1.119**	**15.0**	**<0.001*****	-0.313	0.32	0.57
	Silvereye	B	0.141	0.74	0.39	**1.534**	**5.94**	**0.01***	-0.995	1.42	0.23
	Eurasian blackbird	B	0.310	0.09	0.77	1.099	1.08	0.30	-1.003	0.67	0.41
Coccidia (abundance)	House sparrow	NB	-0.423	0.13	0.72	0.591	2.28	0.13	0.473	0.21	0.65
	Silvereye	NB	1.255	1.42	0.23	**1.929**	**10.9**	**<0.001*****	-0.941	1.40	0.24
	Eurasian blackbird	NB	-0.662	0.27	0.60	-1.167	0.86	0.35	0.195	0.01	0.94

Parameter estimates (β) are presented for each model term at the reference levels stated, along with χ^2-test statistics from likelihood ratio tests (LRT). Significant LRTs are highlighted in bold. Significance of χ^2-test statistics: •, $p < 0.10$; *, $p < 0.05$; **, $p < 0.01$; and ***, $p < 0.001$.

[†]Error structure: B = binomial, NB = negative binomial.

[‡]Modelled using Bayesian GLMM methods: binary input variables were standardized (centered with a mean of 0) for analysis; Cauchy's prior applied to fixed effects of the model; test statistic presented for model terms is Wald-Z.

Table A2. Summary of initial generalized linear mixed model (GLMM) results testing the effect of an experimental feeding regime on bird body condition measures at urban study properties in northern Auckland, New Zealand, with interaction terms included for all models.

Response variable	Species	Model error structure †	Experimental group (reference level: feeding)			Season (reference level: autumn)			Time of day‡ (min after sunrise)			Experimental group × season interaction (reference level: feeding, autumn)		
			Non-feeding			Spring						Non-feeding, Spring		
			β	χ^2	p	β	χ^2	p	β	χ^2	p	β	χ^2	p
SMI (log-transformed)	House sparrow	N	0.037	2.19	0.14	0.010	0.08	0.78	**0.00006**	**6.05**	**0.01***	**-0.040**	**5.78**	**0.02***
	Silvereye	N	0.004	0.01	0.91	**-0.030**	**4.29**	**0.04***	0.00008	3.14	0.08 •	-0.002	0.03	0.85
	Eurasian blackbird	N	0.003	0.05	0.82	**-0.046**	**12.1**	**<0.001 *****	**0.0001**	**11.2**	**<0.001*** **	-0.015	0.28	0.59
Fat score	House sparrow	M	0.142	0.77	0.38	0.365	0.98	0.32	**0.002**	**12.3**	**<0.001*** **	-0.596	2.31	0.13
	Silvereye	M	-0.326	3.51	0.06 •	0.348	0.11	0.74	**0.005**	**17.5**	**<0.001*** **	-0.903	1.82	0.18
	Eurasian blackbird #	M	-0.050	0.29	0.59	-0.303	0.96	0.33	0.002	2.96	0.09 •	-0.463	0.23	0.63

Parameter estimates (β) are presented for each model term at the reference levels stated, along with χ^2-test statistics from likelihood ratio tests (LRT). Significant LRTs are highlighted in bold. Significance χ^2-test statistics: •, $p < 0.10$; *, $p < 0.05$; **, $p < 0.01$; and ***, $p < 0.001$.

† Error structure: M = multinomial, N = normal.

‡ Included in the models as a control variable.

Note model fitted as a CLM without the property ID random term, as random effect variance parameter = 0.

Appendix 3

Table A3. Summary of pathogen and parasite prevalence and abundance results for birds captured at urban study properties in northern Auckland, New Zealand, during an experimental feeding study.

Parasite group	Host species	Autumn						Spring					
		Feeding properties			Non-feeding properties			Feeding properties			Non-feeding properties		
		N	Prevalence %	Abundance	N	Prevalence %	Abundance	N	Prevalence %	Abundance	N	Prevalence %	Abundance
Salmonella spp.	Sparrow	54	1.85 (0.05–9.89)		48	0.00 (0.00–7.40)		56	1.79 (0.05–9.55)		53	1.89 (0.05–10.07)	
Pox-like lesions	Sparrow	173	27.17 (20.69–34.44)		53	18.87 (9.44–31.97)		126	1.59 (0.19–5.62)		68	4.41 (0.92–12.36)	
	Silvereye	21	0.00 (0.00–16.11)		40	5.00 (0.61–16.92)		87	12.64 (6.48–21.50)		30	10.00 (2.11–26.53)	
	Blackbird	22	4.55 (0.12–22.84)		23	0.00 (0.00–14.82)		27	3.70 (0.09–18.97)		11	0.00 (0.00–28.49)	
Mites	Sparrow	89	7.87 (3.22–15.54)	0.11 ± 0.04	47	6.38 (1.34–17.54)	0.11 ± 0.07	78	12.82 (6.32–22.32)	0.49 ± 0.21	56	23.21 (12.98–36.42)	2.09 ± 0.88
	Silvereye	17	41.18 (18.44–67.08)	2.35 ± 1.14	37	43.24 (27.10–60.51)	4.78 ± 2.26	70	70.00 (57.87–80.38)	8.51 ± 1.26	29	75.86 (56.46–89.70)	10.55 ± 1.90
	Blackbird	9	0.00 (0.00–33.63)	0.00 ± 0.00	21	0.00 (0.00–16.11)	0.00 ± 0.00	17	58.82 (32.92–81.56)	8.35 ± 3.94	10	30.00 (6.67–65.25)	3.10 ± 2.77
Lice	Sparrow	89	13.48 (7.17–22.37)	0.57 ± 0.24	47	19.15 (9.15–33.26)	0.28 ± 0.10	78	8.97 (3.68–17.62)	0.50 ± 0.25	56	3.57 (0.44–12.31)	0.05 ± 0.04
	Silvereye	17	17.65 (3.80–43.43)	0.24 ± 0.14	36	16.22 (6.19–32.01)	0.31 ± 0.13	69	1.43 (0.04–7.70)	0.01 ± 0.01	29	10.34 (2.19–27.35)	0.10 ± 0.06
	Blackbird	9	22.22 (2.81–60.01)	1.00 ± 0.88	21	19.05 (5.45–41.91)	0.86 ± 0.47	17	11.76 (1.46–36.44)	2.76 ± 2.64	10	0.00 (0.00–30.85)	0.00 ± 0.00
Helminths	Sparrow	122	5.74 (2.34–11.46)	1.11 ± 0.74	46	2.17 (0.06–11.53)	1.09 ± 1.09	71	12.68 (5.96–22.70)	4.55 ± 2.17	53	6.1 (2.3–12.7)	5.38 ± 5.15
	Silvereye	19	15.79 (3.38–39.58)	2.47 ± 1.98	31	22.58 (9.59–41.10)	10.03 ± 7.49	59	22.03 (12.29–34.73)	1.86 ± 0.76	26	33.3 (21.4–47.1)	8.27 ± 4.01
	Blackbird	12	16.67 (2.09–48.41)	18.92 ± 13.52	16	28.0 (12.1–49.4)	1.19 ± 0.83	14	34.6 (17.2–55.7)	12.29 ± 6.11	9	28.0 (12.1–49.4)	4.78 ± 2.39
Coccidia	Sparrow	122	23.77 (16.53–32.32)	58.63 ± 19.33	46	35.4 (26.0–45.6)	38.39 ± 21.24	71	32.6 (26.1–65.1)	105.89 ± 34.11	53	35.4 (26.0–45.6)	111.28 ± 43.80
	Silvereye	19	57.89 (33.50–79.75)	8.00 ± 3.80	31	66.7 (52.9–78.6)	36.71 ± 20.05	59	79.5 (68.8–87.8)	63.81 ± 23.97	26	66.7 (52.9–78.6)	92.50 ± 40.76
	Blackbird	12	25.00 (5.49–57.19)	143.00 ± 113.94	16	32.0 (14.9–53.5)	73.75 ± 59.67	14	38.5 (20.2–59.4)	44.50 ± 28.13	9	32.0 (14.9–53.5)	27.89 ± 17.69

Appendix 4

Table A4. Summary of body condition measures for birds captured at urban study properties in northern Auckland, New Zealand, during an experimental feeding study. The scaled mass index (SMI) is mass corrected for body size (using tarsal length). Fat score is a visual estimate of fat deposition in the furculum measured using a scale of 0 (no fat) to 5 (fat extending over pectoral muscle).

Body condition measure	Species	Autumn				Spring				Overall			
		Feeding properties		Non-feeding properties		Feeding properties		Non-feeding properties		Feeding properties		Non-feeding properties	
		N	Mean ± SE	N	Mean ± SE	N	Mean ± SE	N	Mean ± SE	N	Mean ± SE	N	Mean ± SE
SMI	Sparrow	177	27.45 ± 0.16	54	28.62 ± 0.33	128	27.93 ± 0.22	68	27.82 ± 0.20	305	27.65 ± 0.13	122	28.18 ± 0.19
	Silvereye	21	11.88 ± 0.25	41	11.97 ± 0.14	87	11.74 ± 0.11	30	11.59 ± 0.18	108	11.77 ± 0.10	71	11.81 ± 0.11
	Blackbird	24	94.72 ± 1.44	23	94.81 ± 1.15	27	91.49 ± 1.23	11	90.91 ± 2.09	51	93.01 ± 0.96	34	93.55 ± 1.06
Fat score	Sparrow	171	2.47 ± 0.08	53	2.62 ± 0.16	126	2.79 ± 0.10	67	2.60 ± 0.12	297	2.61 ± 0.06	120	2.61 ± 0.09
	Silvereye	21	2.24 ± 0.26	40	2.03 ± 0.12	87	2.52 ± 0.11	29	1.83 ± 0.18	108	2.46 ± 0.10	69	1.94 ± 0.10
	Blackbird	21	1.29 ± 0.14	22	1.32 ± 0.21	27	1.22 ± 0.10	11	1.09 ± 0.16	48	1.25 ± 0.08	33	1.24 ± 0.15

Appendix 5

Table A5. Generalized linear mixed model (GLMM) result summary testing for a relationship between parasite and body condition measures, for parasite variables that were influenced by the experimental feeding regime.

Response variable	Host species	Predictor variable	β	χ^2	p
Lice abundance	House sparrow	SMI	-0.106	0.46	0.50
		Fat 1	-0.554	5.19	0.39
		Fat 2	-2.015		
		Fat 3	-1.343		
		Fat 4	-0.651		
		Fat 5	0.062		
Helminth prevalence	Silvereye	SMI	0.216	1.07	0.30
		Fat 1	0.223	7.45	0.19
		Fat 2	-0.779		
		Fat 3	-0.331		
		Fat 4	-0.390		
		Fat 5	0.676		
Helminth abundance	Silvereye	SMI	-0.236	0.49	0.48
		Fat 1	2.860	3.56	0.61
		Fat 2	1.925		
		Fat 3	2.201		
		Fat 4	1.082		
		Fat 5	2.240		
	Eurasian blackbird	SMI	-0.115	0.89	0.35
		Fat 1	0.287	0.61	0.89
		Fat 2	-0.575		
		Fat 3*	0.618		

Parameter estimates (β) are presented for each predictor variable (or levels thereof), along with χ^2-test statistics for whole effects from likelihood ratio tests (LRT). Reference level for fat score is 0.
Error structure of models as per Table 1.
*Fat score categories 3 and 4 were combined for analysis, as the small number of observations in category 4 was causing singularity.