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Supplementary material

Supplementary materials

DNA extraction

Ethanol was removed from the samples by freeze-drying to prevent loss of DNA from the vials, and dried samples were stored at -80 °C until DNA extraction. DNA was extracted using a precipitation and re-suspension method adapted from Bramwell *et al*. (1995), with modifications recommended by Lever *et al.* (2015). Lysis buffer (30 mM Tris, 30 mM EDTA, pH 8) was added at room temperature and mixed by vortex. Samples were quickly re-frozen in liquid nitrogen to lyse cells and then briefly thawed in a 37 °C water bath. A mixture of two different beads (0.2 g ceramic beads 1.4 mm and 0.3 g garnet beads 0.7 mm) was added and samples were shaken at 30 Hz for 3 x 40 s using a TissueLyser II (Qiagen, Hilden Germany). To 19-parts sample solution, 1 part SDS solution (10% w/v) and 0.1 parts proteinase K (20 mg/ml) were added, and samples incubated for 4 h in a shaking incubator at 55 °C to continue lysis and protein digestion. Sample temperature was raised to 65 °C and to each 5 part sample solution, 1 part of 5 M NaCl solution was added and mixed by inversion, then 0.8 parts warm CTAB solution (hexadecyltrimethylammonium bromide, 10% w/v) added and mixed. Samples were then incubated at 65 °C for 10 min, and placed on ice for two subsequent extractions of DNA using chloroform:isoamyl alcohol (chl:iaa, 24:1). In the first extraction, 1 part chl:iaa solution was added to 1 part of sample solution and mixed briefly by vortex. The mixture was centrifuged for 5 min at 14 000 x g at 4 °C and the top aqueous layer removed and retained on ice. An equal volume of chl:iaa solution was added to the removed aqueous layer and briefly vortexed. The mixture was again centrifuged for 5 min at 14 000 x g at 4 °C, the resultant top aqueous layer removed (noting the volume of supernatant removed) and retained on ice. 1 µl of linear polyacrylamide solution (GenElute LPA, Sigma-Aldrich) was added to the removed

supernatant to promote precipitation of DNA. To the 1 part volume of aqueous layer obtained, 0.7 parts of ice-cold isopropanol was added and mixed by inversion. Samples were incubated in the dark at 4 °C overnight to allow DNA precipitation. After precipitation, DNA was pelleted by centrifugation at 4 °C, 21000 x g, for 30 minutes. Supernatant was removed, and DNA pellet was washed with ice-cold 70 % ethanol and centrifuged at 21000 x g and 4 °C for 10 min at 4 °C. Ethanol was removed and the pellet air-dried for 5 min, before being resuspended in TE buffer and mixed by flicking to minimise DNA degradation. Samples were stored at -80 °C until further processing.

To create a positive control sample carrying an assemblage of relevant invertebrate taxa, DNA was extracted from ≥ 15 mg of tissue from frozen specimens of *Drosophila melanogaster*, *Bombyx mori*, *Daphnia pulex*, *Apis mellifera, Tribolium castaneum* and *Eisenia fetida*, using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany) following manufacturers' instructions. Extracted DNA was quantified using the QuantiFluor ONE dsDNA system (Promega, Southampton, UK) following the manufacturer's protocol and diluted to 0.5 ng/µL. Samples in which the original DNA concentration was below 0.5 ng/µL were left at that concentration (i.e. not diluted).

Molecular confirmation of bird species

To confirm that each faecal sample originated from common cuckoo, avian COI DNA was amplified and sequenced from the DNA extracts. Polymerase chain reaction (PCR) was carried out with the primer pair AvMiF1 (5'-CCCCCGACATAGCATTCC-3') and BirdR1 (5'-ACGTGGGAGATAATTCCAAATCCTG-3') (Hebert *et al.* 2004, Kerr *et al.* 2009). This primer pair targets a ~290 base pair (bp) region of the avian COI gene and was selected following an assay to assess the performance of several avian

COI primer pairs in amplifying DNA from positive control faecal samples from cuckoo, and sympatric species including meadow pipit *Anthus pratensis*, carrion crow *Corvus corone*, common wood pigeon *Columba palumbus* and Eurasian magpie *Pica pica* (supplementary materials Figure A2). Amplification of avian COI DNA from faecal samples took place in total volume of 20 µl and contained final concentrations of 1x GoTaq Green Flexi-buffer (Promega), 2 mM $MgCl_2$, 250 µM each dNTP (Thermo Scientific, Paisley, UK) and 600 nM each of AvMiF1 and BirdR1 primers (Eurofins Genomics, Ebersberg, Germany), 0.5 mg Bovine Serum Albumin (BSA; NEB, Ipswich, MA, USA), 0.667 U GoTaq G2 Flexi DNA Polymerase (Promega) and 3 µL (i.e. 3-30 ng) of template DNA. The following touch-up cycling programme was used: After an initial denaturing step of 94 °C for 5 min, this was followed by 5 cycles of 94 °C for 1 min, 45 °C for 40 s, 72 °C for 1 min; 10 cycles of 94 °C for 1 min, 48 °C for 40 s, 72 °C for 1 min; 35 cycles of 94 °C for 1 min, 51 °C for 40 s, 72 °C for 1 min and then a final extension for 5 min at 72 °C and a temperature hold at 4 °C. Samples that did not amplify successfully using these conditions (typically due to presence of natural inhibitors in the DNA extract) were amplified through the use of two rounds of PCRs each consisting of final concentrations of 1x Qiagen Multiplex PCR Master Mix (Qiagen), 0.5 µM of each primer (AvMiF1 and BirdR1) and 0.1 volume of Q-solution. For the first PCR of 15 cycles, 0.25 ng DNA were added to a final volume of 10 µL and then 2 µL of this reaction was added to a second PCR of 25 cycles with a reaction volume of 25 µL. Both PCRs used an initial heat activation of 95 °C for 15 min, followed by a three step cycling protocol for 10 (PCR 1) or 25 cycles (PCR 2), respectively, at 94 °C for 30 s, 57 °C for 90 s and 72 °C for 90 s followed by a final extension step at 72 °C for 10 min.

PCR products were visualised on agarose gel to ensure amplification of expected sequence length, and were then purified using QIAquick gel extraction kit (Qiagen) following the manufacturer's instructions. Purified PCR products were Sanger sequenced against AvMiF1 primer (Eurofins Genomics) and the resulting sequences entered as queries into the Barcode of Life Database (BOLD) version 4 (Ratnasingham & Hebert 2007), searching species-level barcodes. Faecal samples were identified as common cuckoo if their tested avian COI DNA sequence matched database sequences from this species with ≥98% similarity (following Clare *et al.* 2011 and King *et al.* 2015).

DNA amplification for diet analysis and sequencing

DNA sequencing of a 157 base pair length region of the mitochondial cytochrome-b oxidase I (COI) gene was used to identify prey taxa from faecal samples. In total, 43 COI gene amplicon libraries were prepared: 38 faecal samples, three extraction blanks, one positive control and one PCR negative control). Libraries were prepared by PCR amplification of a 157 bp region of the COI gene found in animal mitochondrial DNA (mtDNA) using the universal 'mini-barcode' primers ZBJ-ArtF1c (5'-AGATATTGGAACWTTATATTTTA TTTTTGG-3') and ZBJ-ArtR2c (5'-WACTAATCAATTWCCAAATCCTCC-3') (Zeale *et al.* 2011). These primers were selected based on their ability to amplify degraded DNA and provide species-level taxonomic assignments for 13 arthropod orders (Zeale *et al*. 2011, Trevelline *et al.* 2016) and were modified by the addition of 5' overhang adapter sequences complementary to the Illumina multiplex indexing primers used in downstream sequencing protocols (Illumina 2013). For each sample, three independent PCR reactions were carried out in a total volume of 25 µl and with final concentrations of 1x NEBNext High-Fidelity PCR Master Mix (NEB), and 200 nM each of dZBJ-ArtF1c and

ZBJ-ArtR2c primers (Integrated DNA Technologies, Leuven, Belgium), 1 µg BSA and 2.5 ng of template DNA. The reactions were prepared on ice and the PCR programme comprised an initial denaturing step of 98 °C for 3 min, then 25 cycles of 98 °C for 10 s, 55 °C for 30 s, 72 °C for 30 s; and final extension at 72 °C for 5 min and a hold at 4 °C.

Extraction blanks and three negative PCR controls were also included in the amplifications to check for contamination, and the mixture of invertebrate DNA of known taxa were included as positive controls.

Libraries were purified by magnetic bead clean-up (DeAngelis *et al.* 1995; Jolivet & Foley 2015) according to Illumina 16S metagenomic sequencing library protocol (Illumina 2013). Dual indices and Illumina sequencing adapters from the Illumina Nextera XT index kit v2 indexes sets A, B and D (Illumina Inc., San Diego, CA, USA) were added to the target amplicons (each replicate sample received one of the three indices) in a second PCR step using NEBNext High-Fidelity 2x PCR Master Mix. Cycle conditions were 95 °C for 3 min, the 15 cycles of 95 °C for 30 s, 55 °C for 30 s, 72 °C for 30 s; and final extension at 72 °C for 5 min and a hold at 4 °C. Libraries were again purified using a magnetic bead clean-up as above, subsequently quantified using the QuantiFluor ONE dsDNA System, diluted to 4nM and pooled in equimolar concentrations. The library size and quality of the final pool was assessed with a HS D100 Screentape (Agilent, Stockport, UK) on a TapeStation 2200 (Agilent).

High-throughput sequencing

Sequencing of all amplified DNA (PCR products) from i) cuckoo faecal samples, ii) controls and iii) blanks was carried out on the Illumina MiSeq platform (Illumina) at

Exeter Sequencing Service (University of Exeter, UK), using the v3 paired-end 300 bp kit, following manufacturer's instructions.

Sequencing data analysis

DNA sequence reads from Illumina MiSeq runs were de-multiplexed according to the 5' adaptor used in each replicate PCR of DNA from each faecal sample. In the R package Dada2 (Callahan *et al.* 2016), reads were truncated at 200 bp, with the first 30 and 24 bp removed of the forward and reverse reads, respectively, to remove primer sequence. Sequences were also truncated where the Phred Q-score of a base first registered as Q35 or lower (truncQ=35), which translates to a base-call error rate of ~3 per 10,000 bases (Ewing & Green 1998, Trevelline *et al*. 2016). Reads containing bases recorded as N were removed, as required by Dada2, as were reads with more than two expected errors (maxEE=c(2,2)). Reads were de-replicated in Dada2, which was used to identify amplicon sequence variants (ASVs).

Diet analysis

In order to estimate the completeness of dietary diversity captured by the sampling effort, accumulation curves and asymptotic richness estimates for number of taxonomic families detected were generated in R 3.5.0 using the library VEGAN (functions: specaccum, method = random, permutations = 1000; specpool index = chao, Oksanen *et al.* 2019).

Appendix

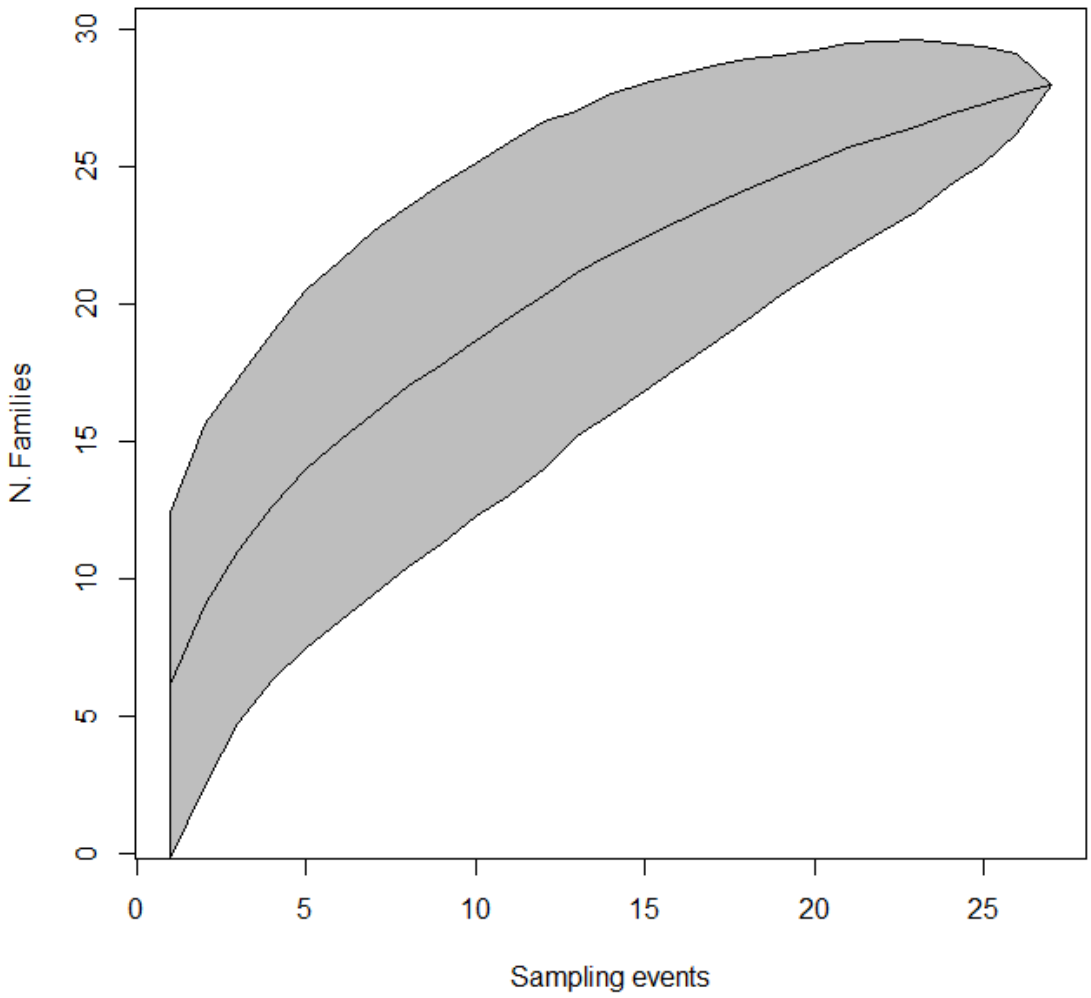

Figure A1. Accumulation curve for number of insect families (excluding taxa of extremely small body size predicted to be consumed by or contaminants of prey) detected in successive faecal sampling events (n = 27) from cuckoos in Dartmoor National Park.

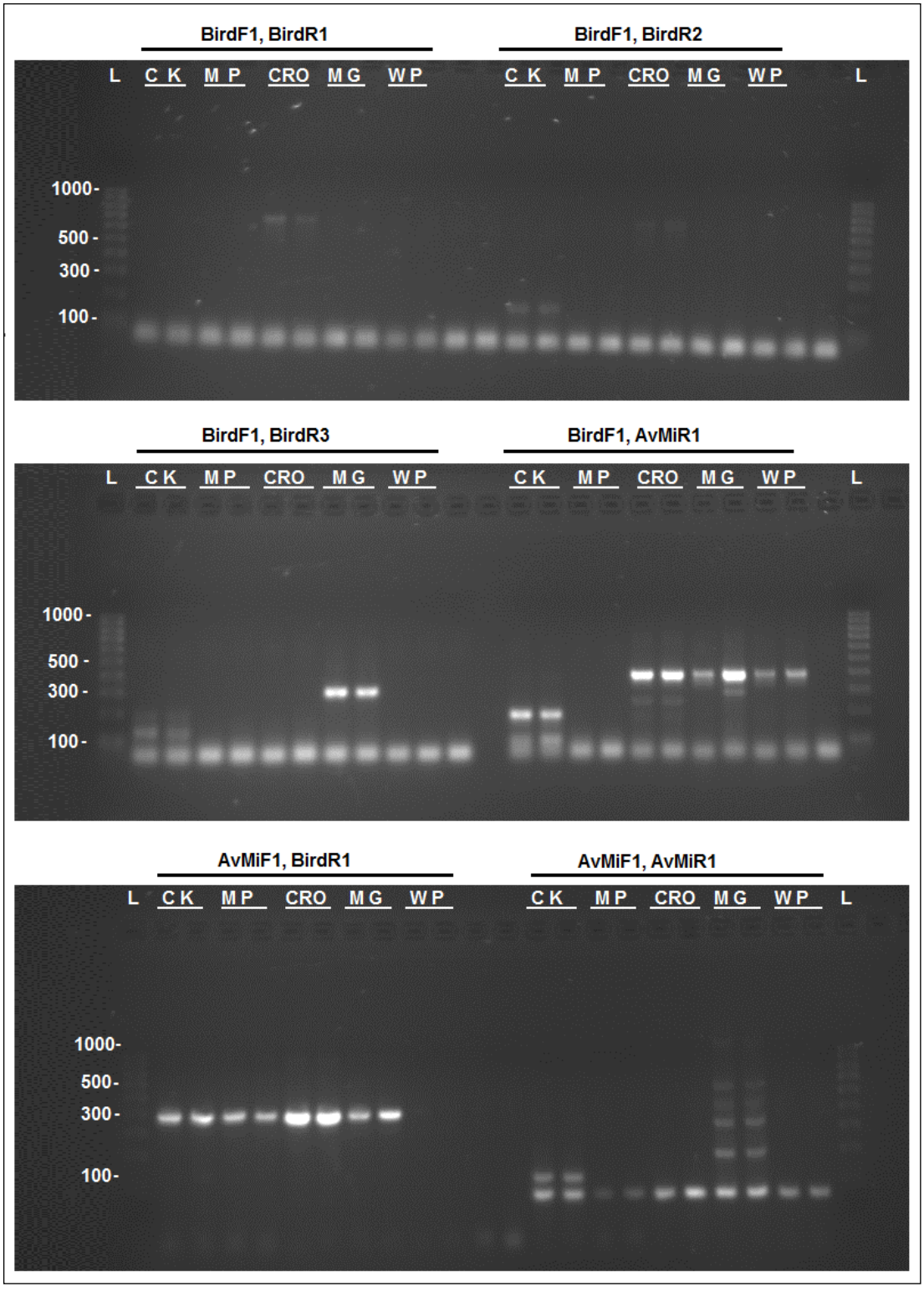

Figure A2. Gel image showing amplification of avian COI DNA from faeces of cuckoo *Cuculus canorus* (CK) meadow pipit *Anthus pratensis* (MP), carrion crow *Corvus corone* (CRO), magpie *Pica pica* (MG) and woodpigeon *Columba palumbus* (WP), by the primer pairs BirdF1/BirdR1, BirdF1/BirdR2, BirdF1/BirdR3, BirdF1/AvMiR1, AvMiF1/BirdR1, and AvMiF1/AvMiR1. L = molecular-weight size marker (100 bp DNA

ladder), numbers are molecule length in base pairs bp. Primer sequences BirdF1 (5'-TTCTCCAACCACAAAGACATTGGCAC-3'), BirdR1 (5'-ACGTGGG-AGATAATTCCAAATCCTG-3'), BirdR2 (5'-ACTACATGTGAGATGATTCCGAATCC-AG-3'), BirdR3 (5'-AGGAGTTTGCTAGTACGATGCC-3') (Hebert *et al.* 2004), AvMiF1 (5'-CCCCCGACATAGCATTCC-3'), AvMiR1 (5'-ACTGAAGCTCCGGCATG-GGC-3') (Kerr *et al.* 2009).

Table A1. Number of reads and amplicon sequence variants (ASVs) detected by high-throughput sequencing of each PCR replicate in diet analysis and Table 1.

Sampling event	Replicate	Species-matched ASVs	Total ASVs	Species-matched reads	Total reads
171	171A	14	18	24419	25791
172	172_P_A	6	6	11188	11188
175	175_B	14	15	12227	12233
175	175_D	5	6	5376	5412
176	176_A	15	18	26976	27052
176	176_B	8	9	23411	23599
178	178_A	18	20	21114	21197
178	178_B	14	14	20984	20984
180	180_A	4	7	11248	11633
181	181_A	15	15	29946	29946
181	181_B	17	17	32906	32906
186	186_A	7	7	17112	17112
189	189_A	4	4	10551	10551
190	190_B	16	17	33977	34006
192	192_A	12	12	56963	56963
192	192_B	18	18	107165	107165
195	195_A	14	17	9951	10224
195	195_B	9	9	56309	56309
195	196_ci_A	17	25	60938	61786
195	196_ci_B	20	34	36481	37807
195	197_A	17	22	46107	46327
195	197_B	14	15	36417	36514
201	201_A	12	12	22489	22489
201	201_B	21	21	63426	63426
201	202_A	21	21	39770	39770
201	202_B	20	20	38164	38164
201	203_A	15	15	13814	13814
204	204_A	12	14	15141	15363
204	205_B	8	12	286426	286863
204	205_D	7	15	103823	104403

206	206_A	8	8	27569	27569
206	206_B	11	11	48471	48471
207	207_A	12	12	23902	23902
209	209_A	6	30	261	28575
209	209_B	14	38	1726	42664
210	210_A	4	11	4314	9630
210	210_B	4	12	5494	8779
211	211_A	9	12	20140	21735
211	211_B	7	8	10115	10229
212	212_A	11	15	5517	11820
212	212_B	9	12	14156	15405
215	215_A	14	14	42896	42896
215	215_B	11	11	63818	63818
216	216_B	4	5	36452	40709
217	217_A	9	9	11741	11741
217	217_B	4	4	12038	12038
220	220_A	12	13	42561	42563
220	220_B	18	23	146020	147889
223	223_A	30	30	13197	13197
225	225_A	14	14	11731	11731
225	225_B	3	3	12120	12120
500	500_A	8	8	11443	11443
500	500_B	10	10	23668	23668

Table A2. In order to assess whether inclusion of sample replicates affected frequencies of occurrence of taxa, we repeated calculation of frequencies with i) a reduced sample of the original data that excluded four faecal samples for which chart-visualised composition of taxonomic families suggested strong differences in sequenced assemblage between their two PCR replicates (n = 23 sampling events). Asterisks denote taxa with no UK records, assumed to represent closely related UK taxa.

Class	Order	Family	Species	Freq (%)
Insecta	Lepidoptera			73.9
	'Large Lepidoptera'			65.2
		Lasiocampidae		60.9
			Euthrix potatoria	52.2
			*Pernattia chlorophragma**	47.8
			*Tolype mayelisae**	4.3
		Limacodidae	*Euclea nanina**	47.8
		Nymphalidae		47.8
			*Napeogenes sylphis**	47.8
			*Pierella luna**	4.3
		Geometridae		17.4

		*Casbia rhodoptila**	8.7
		Petrophora chlorosata	8.7
		*Pseudoterpna coronillaria**	4.3
	Erebidae		8.7
		*Achaea janata**	4.3
		*Pharga pholausalis**	4.3
	Lycaenidae	*Polyommatus dizinensis**	4.3
	Noctuidae	*Xestia agathina*	8.7
Orthoptera	Acrididae	*Omocestus viridulus*	56.5
Diptera			56.5
'Large Diptera'			52.2
	Rhagionidae		39.1
		Rhagio scolopaceus	21.7
		Rhagio tringarius	17.4
	Tipulidae		26.1
		Tipula paludosa	26.1
		Tipula luna	4.3
	Limoniidae	*Limonia nubeculosa*	4.3
	Pediciidae	*Tricyphona immaculata*	8.7
Coleoptera			13.0
	Scarabaeidae	*Phyllopertha horticola*	8.7
	Staphylinidae	*Ocypus aeneocephalus*	4.3
Hemiptera			8.7
	Miridae	*Lygocoris rugicollis*	4.3
	Psyllidae	*Cacopsylla melanoneura*	4.3
Plecoptera	Leuctridae	*Leuctra hippopus*	4.3
'Small Lepidoptera'	Oecophoridae		65.2
		*Callimima lophoptera**	4.3
		*Cosmaresta callichrysa**	4.3
		*Eulechria sp.**	47.8
		*Ioptera demica**	0.0
		*Phloeocetis sp.**	21.7
	Glyphipterigidae	*Glyphipterix fuscoviridella*	8.7
	Thyrididae	*Dysodia sica*	0.0
	Tortricidae	*Crocidosema plebejana**	4.3
	Ypsolophidae	*Ochsenheimeria urella*	4.3
'Small Diptera'	Chloropidae		30.4
		*Apallates coxendix**	17.4
		Tricimba sp.	13.0
	Culicidae		8.7
		*Aedes fowleri**	4.3
		*Ochlerotatus hungaricus**	4.3
	Anthomyiidae	*Hylemya variata*	4.3
	Bibionidae	*Dilophus febrilis*	4.3

		Psychodidae	*Psychoda trinodulosa*	4.3
Arachnida	Sarcoptiformes			21.7
		Chamobatidae	*Chamobates pusillus*	13.0
		Crotoniidae	*Platynothrus peltifer*	8.7
		Punctoribatidae	*Punctoribates punctum*	4.3
Bdelloidea	*Incertae sedis*	Philodinidae	*Macrotrachela quadricornifera*	4.3
Eutardigrada	Parachaela			13.0
		Hypsibiidae	*Isohypsibius sattleri*	8.7
		Macrobiotidae	*Murrayon dianeae*	4.3
			No match	52.2

Table A3. In order to assess whether inclusion of sample replicates affected frequencies of occurrence of taxa, we repeated calculation of frequencies with a reduced sample of the original data that excluded faecal samples where only one PCR replicate showed library DNA concentration of >2 ng/μL ahead of sequencing. (n = 18 sampling events). Asterisks denote taxa with no UK records, assumed to represent closely related UK taxa.

Class	Order	Family	Species	Freq (%)
Insecta	Lepidoptera			88.9
	'Large Lepidoptera'			83.3
		Lasiocampidae		72.2
			Euthrix potatoria	61.1
			*Pernattia chlorophragma**	50.0
			*Tolype mayelisae**	11.1
		Nymphalidae		55.6
			*Napeogenes sylphis**	50.0
			*Pierella luna**	5.6
		Limacodidae	*Euclea nanina**	50.0
		Erebidae		11.1
			*Achaea janata**	5.6
			*Pharga pholausalis**	5.6
		Geometridae		22.2
			*Casbia rhodoptila**	11.1
			Petrophora chlorosata	11.1
			*Pseudoterpna coronillaria**	5.6
		Lycaenidae	*Polyommatus dizinensis**	11.1
		Noctuidae	*Xestia agathina*	11.1
	Orthoptera	Acrididae	*Omocestus viridulus*	55.6
	Diptera			61.1
	‘Large Diptera’			61.1
		Rhagionidae		50.0
			Rhagio scolopaceus	27.8
			Rhagio tringarius	27.8

		Tipulidae		22.2
			Tipula paludosa	22.2
			Tipula luna	5.6
		Limoniidae	*Limonia nubeculosa*	5.6
		Pediciidae	*Tricyphona immaculata*	5.6
	Coleoptera			16.7
		Scarabaeidae	*Phyllopertha horticola*	11.1
		Staphylinidae	*Ocypus aeneocephalus*	5.6
	Hemiptera			11.1
		Miridae	*Lygocoris rugicollis*	5.6
		Psyllidae	*Cacopsylla melanoneura*	5.6
	Plecoptera	Leuctridae	*Leuctra hippopus*	5.6
	'Small Lepidoptera'	Oecophoridae		66.7
			*Callimima lophoptera**	5.6
			*Cosmaresta callichrysa**	5.6
			*Eulechria sp.**	50.0
			*Ioptera demica**	5.6
			*Phloeocetis sp.**	22.2
		Glyphipterigidae	*Glyphipterix fuscoviridella*	11.1
		Thyrididae	*Dysodia sica*	5.6
		Tortricidae	*Crocidosema plebejana**	5.6
		Ypsolophidae	*Ochsenheimeria urella*	5.6
	'Small Diptera'	Chloropidae		27.8
			*Apallates coxendix**	16.7
			Tricimba sp.	11.1
		Culicidae		16.7
			*Aedes fowleri**	11.1
			*Ochlerotatus hungaricus**	5.6
		Anthomyiidae	*Hylemya variata*	5.6
		Bibionidae	*Dilophus febrilis*	0.0
		Psychodidae	*Psychoda trinodulosa*	0.0
Arachnida	Sarcoptiformes			22.2
		Chamobatidae	*Chamobates pusillus*	11.1
		Crotoniidae	*Platynothrus peltifer*	11.1
		Punctoribatidae	*Punctoribates punctum*	5.6
Bdelloidea	Incertae_sedis	Philodinidae	*Macrotrachela quadricornifera*	5.6
Eutardigrada	Parachaela			16.7
		Hypsibiidae	*Isohypsibius sattleri*	11.1
		Macrobiotidae	*Murrayon dianeae*	5.6
			No match	55.6

Table A4. Frequency of occurrence of eukaryote taxa matched with ≥98% to DNA sequences in the Barcode of Life Database (BOLD), in clusters of co-occurrent faecal samples ('sampling events' n = 27) from common cuckoo adults in Dartmoor National Park, UK in 2016-17 breeding seasons, as detected by Illumina MiSeq amplicon sequencing. Asterisks denote species-level matches with no previous UK records assumed here to represent closely-related UK-occurring taxa. Footnotes denote cases where a matched taxon had no UK records but field observations suggest the most likely species or genus being taken as prey by cuckoos.

Class	Order	Family	Species	Freq (%)
Insecta	**Lepidoptera**			77.8
	'Large Lepidoptera'			70.4
		Lasiocampidae		66.7
			Euthrix potatoria	51.9
			*Pernattia chlorophragma**	51.9
			*Tolype mayelisae**	7.4
		Limacodidae[1]	*Euclea nanina**	51.9
		Nymphalidae[2]		51.9
			*Napeogenes sylphis**	51.9
			*Pierella luna**	3.7
		Geometridae		14.8
			*Casbia rhodoptila**	7.4
			Petrophora chlorosata	7.4
			*Pseudoterpna coronillaria**[3]	3.7
		Erebidae		7.4
			*Achaea janata**	3.7
			*Pharga pholausalis**	3.7
		Lycaenidae	*Polyommatus dizinensis**	7.4
		Noctuidae	*Xestia agathina*	7.4
	Orthoptera	Acrididae	*Omocestus viridulus*	59.3
	Diptera			59.3
	'Large Diptera'			55.6
		Rhagionidae		44.4
			Rhagio scolopaceus	22.2
			Rhagio tringarius	25.9
		Tipulidae		22.2
			Tipula paludosa	22.2
			Tipula luna	3.7
		Limoniidae	*Limonia nubeculosa*	3.7
		Pediciidae	*Tricyphona immaculata*	7.4
		'Craneflies'	(Tipulidae, Limoniidae, Pediciidae)	29.6

	Coleoptera			11.1
		Scarabaeidae	*Phyllopertha horticola*	7.4
		Staphylinidae	*Ocypus aeneocephalus*	3.7
	Hemiptera			7.4
		Miridae	*Lygocoris rugicollis*	3.7
		Psyllidae	*Cacopsylla melanoneura*	3.7
	Plecoptera	Leuctridae	*Leuctra hippopus*	3.7

Small invertebrates and non-animals of probable non-diet origin:

Insecta	'Small Lepidoptera'	Oecophoridae		66.7
			*Callimima lophoptera**	3.7
			*Cosmaresta callichrysa**	3.7
			*Eulechria sp.**	51.9
			*Ioptera demica**	3.7
			*Phloeocetis sp.**	18.5
		Glyphipterigidae	*Glyphipterix fuscoviridella*	7.4
		Thyrididae*	*Dysodia sica*	3.7
		Tortricidae	*Crocidosema plebejana**	3.7
		Ypsolophidae	*Ochsenheimeria urella*	3.7
	'Small Diptera'	Chloropidae		29.6
			*Apallates coxendix**	14.8
			Tricimba sp.	14.8
		Culicidae		11.1
			*Aedes fowleri**	7.4
			*Ochlerotatus hungaricus**	3.7
		Anthomyiidae	*Hylemya variata*	3.7
		Bibionidae	*Dilophus febrilis*	3.7
		Psychodidae	*Psychoda trinodulosa*	3.7
Arachnida	**Sarcoptiformes**			18.5
		Chamobatidae	*Chamobates pusillus*	11.1
		Crotoniidae	*Platynothrus peltifer*	7.4
		Punctoribatidae	*Punctoribates punctum*	3.7
Bdelloidea (Rotifera)	***Incertae sedis***	Philodinidae	*Macrotrachela quadricornifera*	3.7
Eutardigrada (Tardigrada)	**Parachaela**			11.1
		Hypsibiidae	*Isohypsibius sattleri*	7.4

	Macrobiotidae	*Murrayon dianeae*	3.7
		No match	51.9

[1] Superfamily Zygaenoidea, most likely *Zygaena spp.*
[2] *Coenonympha pamphilus*
[3] *Pseudoterpna pruinata*

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