Supplemental material

Supplemental Experimental Procedures
(related to Methods, Model 1 and Table 1 in the main text).

Estimated attack risk with and without potential attacks, missing models and replacement models

Attacks were classified in the field as potential attack mark (1), clear attack mark (2), strong attack (3) and missing model (4). First, we tested whether or not the inclusion of missing moth models (values 4) and those models with markings classified as potential attacks (values 1) in the statistical analysis would change the analyses' outcomes (Table S1). Here, we used colour morph as the explanatory variable and transect ID as a random factor. Including the missing models and potential attack markings as attacks in our analyses increased model AIC values considerably in comparison to models where missing models and potential attacks were assigned as not attacked. For this reason, and to make sure that we were only counting true avian attacks, we only considered models with clear or strong beak marks as attacked in all further analyses.

Attacked and missing models were replaced with new models of the same colour to a nearby location to keep the morph frequency constant during the experiment. To test whether including or excluding attacks on the replacement models would change the analysis outcomes, we run the first model (Model 1) with and without attacks on replaced artificial moths (in the latter case, assuming that once attacked, the artificial moths died and could not be attacked again). Attacks to these replacement models are included in Model 1a (Table 1 in the main text), and not included here in Model 1b (Table S2).

Table S1 (related to Supplemental Experimental Procedures and Methods in the main text). Comparison of datasets including or excluding missing artificial moths and potential attack marks as attacks and with or without attacks on replaced artificial moths separately for each country. All datasets were tested with generalized linear mixed model fit by maximum likelihood (Laplace Approximation) and binomial family with a logit link function. Formula used was glmer(cbind(attack,time)~colour+(1|transect). Values of significance level <0.05 are bolded.

Country	Markings	Repeats included	No of obs.	df	AIC	LRT	p-value
Scotland	clear	yes	1088	2	1343.6	9.6804	**0.007905**
	all	yes	1195	2	1805.5	7.7808	**0.02044**
	clear	no	900	2	1078.6	5.1345	0.07675
	all	no	899	2	1401.5	4.1722	0.1242
Georgia	clear	no	900	2	769.0	6.0527	**0.04849**
	all	no	900	2	987.7	3.1712	0.2048
Estonia	clear	yes	968	2	705.9	0.5334	0.7659
	all	yes	1057	2	1278.2	0.9968	0.6075
	clear	no	900	2	664.6	0.3458	0.8412
	all	no	900	2	1126.2	0.2834	0.8679
Finland	clear	yes	1052	2	1133.2	2.9263	0.2315
	all	yes	1182	2	1659.8	1.4876	0.4753
	clear	no	900	2	1023.4	3.6839	0.1585
	all	no	900	2	1375.9	1.9643	0.3745

Table S2 (related to Model 1a and Table 1 in the main text). (a) Model selection and (b) estimates of the best-fitting model (Model 1b) with a dataset including only first attacks to each of the 60 models per transect (n=3600). Values of significance level <0.05 are bolded. Δ df denotes change in model degrees of freedom.

(a) Model selection	**Δ df**	**LRT**	**Pr(Chi)**	**model AIC**
colour * morph frequency				3535.2
colour + morph frequency	2	0.2056	0.9023	3531.4

The asterisk (*) denotes both main effects and interaction terms used.

(b) Model 1b

Random effects	**Variance**	**SD**		
transect within country	0.3022	0.5497		
country	0.1337	0.3657		
Fixed effects	**Estimate**	**SE**	**Z-value**	**p-value**
(Intercept): colour[w]	-3.0721	0.2109	-14.569	**<0.001**
colour[y]	-0.0979	0.0982	-0.997	0.3186
colour[r]	-0.1316	0.0990	-1.330	0.1836
morph frequency	-0.3165	0.1127	-2.808	**0.0050**

Table S3 (related to Figure 3, Figure 4, Methods and Discussion in the main text). Bird species observed within 25 meters to both sides of the transect centerline during transect counts. The table is arranged by species abundance and three most common species in each country (and in total) are bolded. Only bird species recorded to feed on insects and observed at more than one transect (out of 60) were included as potential predators in analysis (Model 4, Table 4, Figure 3, Figure 4). O=Order (Pa=Passeriformes, Co=Columbiformes, Pi=Piciformes, Ch=Charadriiformes).

O	Family	Genus	Species	EST	FIN	GEO	SCO	Total	Incl.:	Notes
Pa	*Fringillidae*	*Fringilla*	*coelebs*	**102**	19	7	**66**	**194**	yes	feed insects to the young
Pa	*Sylvidae*	*Phylloscopus*	*trochilus*	**66**	**35**	0	49	**150**	yes	
Pa	*Paridae*	*Parus*	*major*	37	**67**	**14**	28	**146**	yes	
Pa	*Muscicapidae*	*Erithacus*	*rubecula*	32	25	4	**55**	116	yes	
Pa	*Sylvidae*	*Regulus*	*regulus*	25	17	9	45	96	yes	
Pa	*Troglodytidae*	*Troglodytes*	*troglodytes*	21	0	11	**55**	87	yes	
Pa	*Muscicapidae*	*Muscicapa*	*striata*	29	15	8	24	76	yes	
Pa	*Paridae*	*Parus*	*caeruleus*	3	**54**	11	4	72	yes	
Pa	*Turdidae*	*Turdus*	*merula*	22	14	7	13	56	yes	
Pa	*Paridae*	*Parus*	*ater*	0	1	7	47	55	yes	
Pa	*Sylvidae*	*Phylloscopus*	*sibilatrix*	**45**	4	0	0	49	yes	
Pa	*Sylvidae*	*Phylloscopus*	*collybita*	41	1	0	7	49	yes	
Pa	*Emberizidae*	*Emberiza*	*citrinella*	0	18	0	23	41	yes	feed insects to the young
Pa	*Motacillidae*	*Anthus*	*trivialis*	21	12	0	5	38	yes	
Pa	*Sylvidae*	*Sylvia*	*communis*	25	0	0	11	36	yes	
Pa	*Turdidae*	*Turdus*	*philomelos*	15	7	0	10	32	yes	
Pa	*Sylvidae*	*Sylvia*	*atricapilla*	19	2	1	7	29	yes	
Pa	*Paridae*	*Parus*	*montanus*	11	13	0	4	28	yes	
Pa	*Motacillidae*	*Anthus*	*spinoletta*	0	0	**28**	0	28	yes	
Pa	*Passeridae*	*Passer*	*domesticus*	0	0	0	25	25	no	observed in one transect only
Co	*Columbidae*	*Columba*	*palumbus*	6	13	0	4	23	no	
Pa	*Prunellidae*	*Prunella*	*modularis*	3	7	2	11	23	yes	
Pa	*Sylvidae*	*Sylvia*	*borin*	20	2	0	0	22	yes	
Pa	*Sylvidae*	*Phylloscopus*	*nitidus*	0	0	**22**	0	22	yes	
Pa	*Certhiidae*	*Certhia*	*familiaris*	2	6	4	7	19	yes	
Pa	*Fringillidae*	*Carpodacus*	*erythrinus*	4	0	11	0	15	yes	feed insects to the young
Pa	*Motacillidae*	*Motacilla*	*alba*	6	1	3	2	12	yes	
Pa	*Oriolodae*	*Oriolus*	*oriolus*	11	0	0	0	11	yes	feed insects to the young[1)]
Pa	*Fringillidae*	*Pyrrhula*	*pyrrhula*	2	2	3	4	11	yes	feed insects to the young
Pa	*Fringillidae*	*Carduelis*	*cannabina*	0	0	5	6	11	yes	feed insects to the young
Pa	*Turdidae*	*Turdus*	*viscivorus*	7	0	0	1	8	yes	
Pa	*Fringillidae*	*Loxia*	*curvirostra*	1	1	2	4	8	no	specialized seed eater
Pa	*Corvidae*	*Garrulus*	*glandarius*	0	3	4	1	8	yes	
Pa	*Fringillidae*	*Carduelis*	*carduelis*	0	0	4	4	8	yes	feed insects to the young
Pa	*Sylvidae*	*Sylvia*	*curruca*	4	3	0	0	7	yes	
Pa	*Laniidae*	*Lanius*	*collurio*	3	4	0	0	7	yes	
Pa	*Paridae*	*Parus*	*cristatus*	2	5	0	0	7	yes	
Pi	*Picidae*	*Dendrocopos*	*major*	1	2	3	1	7	yes	feed on insects[2)]
Pa	*Fringillidae*	*Carduelis*	*spinus*	3	0	2	1	6	yes	feed insects to the young
Pa	*Motacillidae*	*Anthus*	*pratensis*	3	0	0	3	6	yes	
Pa	*Fringillidae*	*Serinus*	*pusillus*	0	0	6	0	6	yes	feed insects to the young?
Pa	*Muscicapidae*	*Saxicola*	*rubicola*	0	0	6	0	6	yes	
Pa	*Corvidae*	*Corvus*	*corone*	0	0	0	6	6	yes	
Pa	*Muscicapidae*	*Ficedula*	*hypoleuca*	3	2	0	0	5	yes	
Pa	*Aegithalidae*	*Aegithalos*	*caudatus*	0	5	0	0	5	yes	
Pa	*Hirundinidae*	*Riparia*	*riparia*	0	0	5	0	5	no	hunt in the air
Pa	*Muscicapidae*	*Ficedula*	*parva*	4	0	0	0	4	yes	
Pa	*Muscicapidae*	*Saxicola*	*rubetra*	2	0	1	1	4	yes	
Pa	*Corvidae*	*Nucifraga*	*caryocatactes*	0	4	0	0	4	yes	
Pa	*Hirundinidae*	*Ptyonoprogne*	*rupestris*	0	0	4	0	4	no	hunt in the air
Pa	*Fringillidae*	*Carduelis*	*chloris*	0	0	1	3	4	yes	feed insects to the young
Pa	*Sittidae*	*Sitta*	*krueperi*	0	0	3	0	3	no	missing data
Pa	*Paridae*	*Parus*	*palustris*	2	0	0	0	2	yes	
Pa	*Muscicapidae*	*Phoenicurus*	*phoenicurus*	2	0	0	0	2	yes	
Pa	*Sylvidae*	*Acrocephalus*	*schoenobaenus*	1	0	0	1	2	yes	
Pa	*Corvidae*	*Pica*	*pica*	0	1	0	1	2	yes	
Pa	*Sylvidae*	*Phylloscopus*	*sindiatus l.*	0	0	2	0	2	yes	
Pa	*Hirundinidae*	*Hirundo*	*rustica*	0	0	1	1	2	no	hunt in the air
Pa	*Alaudidae*	*Alauda*	*arvensis*	0	0	0	2	2	no	observed in one transect only
Pa	*Fringillidae*	*Coccothraustes*	*coccothraustes*	1	0	0	0	1	yes	feed insects to the young
Pa	*Corvidae*	*Corvus*	*corax*	1	0	0	0	1	yes	
Pa	*Sylvidae*	*Locustella*	*fluviatilis*	1	0	0	0	1	yes	
Pa	*Turdidae*	*Turdus*	*iliacus*	0	1	0	0	1	yes	
Ch	*Scolopacidae*	*Tringa*	*ochropus*	0	1	0	0	1	no	
Pa	*Muscicapidae*	*Monticola*	*saxatilis*	0	0	1	0	1	yes	
Pa	*Muscicapidae*	*Phoenicurus*	*ochruros*	0	0	1	0	1	yes	
Pi	*Picidae*	*Picus*	*viridis*	0	0	1	0	1	yes	feed on insects
Pa	*Emberizidae*	*Emberiza*	*schoeniclus*	0	0	0	1	1	yes	feed insects to the young

1) Milwright, R.D.P. (1998) Breeding biology of the golden oriole Oriolus oriolus in the fenland basin of eastern Britain. Bird Study, 45(3): 320-330

2) Leikola, Anto; Lokki, Juhani; Stjernberg, Torsten: Von Wright -veljesten linnut, s. 191. Otava, 2006. ISBN 951-1-18037-1

Table S4 (related to Figure 3 in the main text). Family level component loadings of the second and third principal components describing 33.7% and 8.5% of the total variation of bird communities across countries, respectively.

Bird family	PC2 loading	PC3 loading
Motacillidae	0.096621248	0.067106914
Troglotydidae	0.014708180	0.210943319
Sylvidae	0.009891431	-0.430736201
Oriolidae	0.005022655	-0.054848221
Prunellidae	0.001358338	-0.042870544
Corvidae	0.001155818	0.011587582
Picidae	-0.013150415	-0.024347383
Certhiidae	-0.014865169	0.011404222
Turdidae	-0.019693893	-0.007807002
Laniidae	-0.022166815	-0.032307565
Muscicapidae	-0.032369494	0.532307129
Fringillidae	-0.062877940	0.687239259
Paridae	-0.991991538	-0.054855828