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Electronic Appendix part A. Species data used in analyses. The column headed sqrt cbc contains the square root of the overall Common Birds Census population trend (as used in the analyses).

	Species	sqrt cbc	Migrant status	niche breadth	LN niche position	LN Body Size	Annual productivity	Total brain residuals
Barn Swallow	*(Hirundo rustica)*	0.98	Migrant	87.99	-1.42	2.95	9.0	-0.09
Black-billed Magpie	*(Pica pica)*	1.35	Resident	85.13	-0.63	5.36	6.0	0.15
Blackbird	*(Turdus merula)*	0.77	Resident	92.56	-0.98	4.56	12.0	-0.10
Blackcap	*(Sylvia atricapilla)*	1.48	Migrant	82.92	-0.61	2.92	7.5	0.01
Blue Tit	*(Parus caeruleus)*	1.15	Resident	90.42	-0.95	2.38	10.0	0.19
Carrion Crow	*(Corvus corone)*	1.47	Resident	103.63	-1.76	6.18	4.5	0.02
Chaffinch	*(Fringilla coelebs)*	1.13	Resident	99.82	-1.79	3.10	4.5	0.00
Chiffchaff	*(Phylloscopus collybita)*	0.99	Migrant	81.44	-0.53	2.12	11.0	-0.01
Common Bullfinch	*(Pyrrhula pyrrhula)*	0.74	Resident	94.39	-0.64	3.14	9.0	0.08
Common Cuckoo	*(Cuculus canorus)*	1.08	Migrant	108.65	-1.24	4.71	12.5	0.04
Common Linnet	*(Carduelis cannabina)*	0.77	Resident	85.55	-0.89	2.93	12.5	0.03
Common Moorhen	*(Gallinula chloropus)*	1.02	Resident	77.66	-0.58	5.85	14.0	-0.17
Common Starling	*(Sturnus vulgaris)*	0.77	Resident	89.51	-0.63	4.39	11.0	-0.04
Common Whitethroat	*(Sylvia communis)*	0.79	Migrant	78.58	-0.64	2.67	4.5	0.05
Corn Bunting	*(Emberiza calandra)*	0.62	Resident	64.88	0.09	3.84	10.0	-0.09
Eurasian Jackdaw	*(Corvus monedula)*	1.26	Resident	83.95	-1.25	5.41	5.0	0.05
Eurasian Tree Sparrow	*(Passer montanus)*	0.41	Resident	65.55	-0.38	3.08	12.5	-0.09
Eurasian Treecreeper	*(Certhia familiaris)*	0.95	Resident	99.29	-0.33	2.21	11.0	0.10
European Goldfinch	*(Carduelis carduelis)*	1.26	Resident	83.25	-0.92	2.74	10.0	0.08
European Greenfinch	*(Carduelis chloris)*	1.01	Resident	82.64	-0.66	3.32	10.0	0.02
European Robin	*(Erithacus rubecula)*	1.16	Resident	98.08	-1.13	2.87	10.0	0.00
European Turtle Dove	*(Streptopelia turtur)*	0.59	Migrant	73.68	0.06	5.04	3.8	-0.04
Garden Warbler	*(Sylvia borin)*	0.72	Migrant	87.65	-0.50	2.90	4.5	-0.10
Great Tit	*(Parus major)*	1.33	Resident	89.42	-0.94	2.93	10.5	0.14
Grey Partridge	*(Perdix perdix)*	0.51	Resident	69.26	-0.32	5.95	15.0	-0.34
Hedge Accentor	*(Prunella modularis)*	0.82	Resident	87.98	-0.88	2.92	10.0	0.03
Lesser Whitethroat	*(Sylvia curruca)*	1.01	Migrant	69.12	-0.31	2.52	5.0	-0.03
Long-tailed Tit	*(Aegithalos caudatus)*	1.52	Resident	81.86	-0.60	2.08	10.0	0.09
Mallard	*(Anas platyrhynchos)*	1.52	Resident	95.20	-1.06	6.94	11.0	-0.17
Mistle Thrush	*(Turdus viscivorus)*	0.73	Resident	95.60	-1.11	4.78	8.0	
Northern Lapwing	*(Vanellus vanellus)*	0.79	Resident	97.44	-1.06	5.39	4.0	-0.01
Pied Wagtail	*(Motacilla alba)*	1.28	Resident	98.17	-1.58	3.01	11.0	-0.08
Reed Bunting	*(Emberiza schoeniclus)*	0.85	Resident	93.82	-0.45	2.96	6.8	0.00
Sedge Warbler	*(Acrocephalus schoenobaenus)*	0.62	Migrant	84.88	-0.30	2.46	5.5	-0.05
Skylark	*(Alauda arvensis)*	0.71	Resident	107.43	-0.89	3.59	12.0	-0.06
Song Thrush	*(Turdus philomelos)*	0.61	Resident	102.51	-1.20	4.30	10.0	-0.08
Stock Pigeon	*(Columba oenas)*	1.62	Resident	76.29	-0.65	5.67	5.0	-0.12
Willow Warbler	*(Phylloscopus trochilus)*	0.88	Migrant	114.44	-1.13	2.18	6.0	-0.06
Winter Wren	*(Troglodytes troglodytes)*	1.41	Resident	100.53	-1.38	2.19	6.5	0.07
Yellowhammer	*(Emberiza citrinella)*	0.86	Resident	73.52	-0.55	3.29	8.0	-0.07

Electronic Appendix part B. Calculation of brain-body residuals (relative brain size)

Brain-body residual values can fall into multiple groups as a result of ‘grade-shifts’, where the slopes of the allometry between taxonomic groups are similar, but the intercepts differ (Gould 1975; Wang *et al.* 2002; Burish *et al.* 2004). To test for the presence of a grade shift, the mean residual values for passerines and non-passerines were compared. Secondly, the residuals from a subset of UK farmland birds within the Mlikovsky dataset (n= 70) were recalculated for Passeriformes and non-Passeriformes, and these were tested for a phylogenetic bias. This is a larger set of species than were used for calculating CBC indices in an attempt to obtain the most accurate relationship between body and brain weight.

Significant phylogenetic effects between passerines and non-passerines were detected in overall brain size ($F_{1,67} = 9.37$, $p = 0.003$) Recalculated residuals for both overall brain size within passerines and non-passerines removed this bias (brain $F_{1,67} = 0.004$, $p = 0.95$), and were used in the analyses. Significant phylogenetic differences in residuals were found between passerines and non-passerines in telencephalon residuals ($F_{1,41} = 10.41$, $p = 0.002$), but not in the other brain components (brain stem $F_{1,41} = 0.17$, $p = 0.68$; cerebellum $F_{1,41} = 1.81$, $p = 0.19$; optical lobes $F_{1,41} = 2.85$, $p = 1.10$). Recalculating the residuals for telencephalon size removed the difference between the two taxonomic group ($F_{1,41} = 0.11$, $p = 0.74$).

Hypotheses for brain size evolution generally follow one of the following arguments. Brain size is essentially a consequence of body size evolution. Larger bodied species have larger brains. As we used brain body residuals rather than brain size alone, we should have accounted for this. However, a related argument with brain and body size is that secondary reduction in body size often results in a larger relative brain size (the Chihuahua fallacy). This could effectively be what is happening with passerines and explain the grade-shift between passerine and non-passerine brain-body allometries. However, by calculating residuals separately for passerines and non-passerines, we should have accounted for this.

Electronic Appendix part C.

PGLS can be shown to be exactly equivalent to the widely used method of independent contrasts for a completely resolved phylogeny and the assumption that traits evolve by a 'Brownian motion' model of evolution (Rohlf 2001). Under the assumption of Brownian motion, the expected trait covariance between any two species is directly proportional to the amount of shared evolutionary history. This equals the length of the branches connecting the root of the phylogenetic tree to their most recent common ancestor. If this assumed model of Brownian motion is incorrect (e.g. if closely related species are not more similar in traits than two randomly chosen species), then a statistical model incorporating phylogenetic information may not fit the data as well as one assuming that traits evolved independently (phylogenetic independence). However, the covariance matrix can be modified in PGLS to accommodate the degree to which trait evolution deviates from Brownian motion, using a measure of phylogenetic correlation, λ, derived by Pagel (1999; see also Freckleton *et al.* 2002). λ is a multiplier of the off-diagonal elements of the covariance matrix (i.e. those quantifying the degree of relatedness between species), with λ normally varying between 0 and 1. If the covariance matrix is constructed assuming a Brownian motion model of evolution then $\lambda = 1$ retains that model, while $\lambda = 0$ specifies phylogenetic independence. The maximum likelihood value of λ can be estimated by fitting PGLS models with different values of λ and finding the value that minimises the log-likelihood. This best-fitting model can be used as a basis for inference, while the value of λ associated with it can be used as a metric of the degree of phylogenetic correlation in the data (Freckleton et al. 2002).