

Supplementary material

Appendix.1

Table A1 . Full results of phylogenetic generalized least squares analyses for **brightness of exposed patches** repeated on 100 phylogenies. For every estimate (regression coefficient, SE, F- and p-value), we provide its mean and 95% confidence interval (LCI-UCI). Reference categories are “Monogamy” for Mating, “Closed” for Nest type and “Sedentary” for Migration. The λ value (LCI-UCI) is 0.66 (0.34-1.13). N = 412 species in the PGLS analyses.

Response: brightness (PC1)	Estimate			SE			F			p		
	Mean	LCI	UCI	Mean	LCI	UCI	Mean	LCI	UCI	Mean	LCI	UCI
Intercept	-0.24	-0.85	0.23	0.38	0.26	0.57						
Diff. in Attentiveness ^[^2]	-0.10	-0.13	-0.05	0.10	0.10	0.11	1.22	0.23	1.94	0.33	0.16	0.63
Mating (Polygamy)	0.19	-0.07	0.41	0.18	0.18	0.19	1.48	0.32	2.97	0.26	0.05	0.73
Mating (Lek)	0.33	-0.09	0.55	0.32	0.22	0.35						
Body Mass [Log ₁₀]	-0.21	-0.29	-0.13	0.08	0.07	0.09	7.77	2.03	13.19	0.02	0.00	0.16
Nest type (Open)	0.14	-0.01	0.41	0.13	0.12	0.16	2.14	0.00	7.06	0.57	0.01	1.00
Migration (Partial)	0.21	0.10	0.24	0.13	0.12	0.14	3.67	0.56	4.85	0.08	0.01	0.57
Migration (Migratory)	0.35	0.14	0.41	0.14	0.13	0.15						
Diff. in Attentiveness ^[^2] *Nest Type	0.06	0.03	0.09	0.12	0.11	0.13	0.26	0.07	0.56	0.63	0.46	0.79

Table A2. Full results of phylogenetic generalized least squares analyses for **hue of exposed patches** repeated on 100 phylogenies. For every estimate (regression coefficient, SE, F- and p-value), we provide its mean and 95% confidence interval (LCI-UCI). Reference categories are “Monogamy” for Mating, “Closed” for Nest type and “Sedentary” for Migration. The λ value (LCI-UCI) is 0.74 (0.50-1.02). N = 412 species in the PGLS analyses.

Response: hue (PC2) Predictors	Estimate			SE			F			p		
	Mean	LCI	UCI	Mean	LCI	UCI	Mean	LCI	UCI	Mean	LCI	UCI
Intercept	-0.61	-1.50	-0.34	0.44	0.31	0.73						
Diff. in Attentiveness[^2]	-0.16	-0.35	-0.12	0.10	0.10	0.12	2.73	1.44	10.34	0.17	0.00	0.23
Mating (Polygamy)	0.18	0.09	0.29	0.18	0.16	0.21	4.71	2.52	9.06	0.02	0.00	0.08
Mating (Lek)	1.02	0.92	1.23	0.35	0.28	0.49						
Body Mass [Log ₁₀]	-0.21	-0.28	-0.02	0.08	0.07	0.10	8.07	0.03	11.03	0.10	0.00	0.85
Nest type (Open)	0.03	-0.04	0.19	0.13	0.11	0.15	0.43	0.01	1.57	0.67	0.21	0.94
Migration (Partial)	0.07	-0.11	0.15	0.12	0.09	0.13	6.45	2.26	9.15	0.01	0.00	0.11
Migration (Migratory)	0.42	0.18	0.51	0.13	0.10	0.14						
Diff. in Attentiveness[^2]*Nest Type	0.12	0.07	0.32	0.12	0.11	0.13	1.32	0.36	6.89	0.40	0.01	0.55

Table A3. Full results of phylogenetic generalized least squares analyses for **brightness of concealed patches** repeated on 100 phylogenies. For every estimate (regression coefficient, SE, F- and p-value), we provide its mean and 95% confidence interval (LCI-UCI). Reference categories are “Monogamy” for Mating, “Closed” for Nest type and “Sedentary” for Migration. The λ value (LCI-UCI) is 0.53 (0.16-1.11). N = 412 species in the PGLS analyses.

Response: brightness (PC1) Predictors	Estimate			SE			F			p		
	Mean	LCI	UCI	Mean	LCI	UCI	Mean	LCI	UCI	Mean	LCI	UCI
Intercept	-0.54	-1.76	0.00	0.35	0.18	0.70						
Diff. in Attentiveness ^[^2]	-0.18	-0.30	-0.15	0.10	0.09	0.13	3.17	2.09	7.20	0.08	0.01	0.15
Mating (Polygamy)	0.26	0.11	0.51	0.19	0.18	0.22	2.97	1.16	9.15	0.10	0.00	0.35
Mating (Lek)	0.61	0.30	1.18	0.33	0.29	0.45						
Body Mass [Log ₁₀]	-0.25	-0.43	-0.21	0.08	0.06	0.11	12.24	3.95	24.43	0.01	0.00	0.05
Nest type (Open)	0.10	-0.06	0.79	0.13	0.08	0.17	7.10	0.14	95.28	0.44	0.00	0.70
Migration (Partial)	0.09	-0.08	0.14	0.13	0.12	0.15	9.57	1.49	13.27	0.02	0.00	0.23
Migration (Migratory)	0.54	0.22	0.65	0.14	0.13	0.16						
Diff. in Attentiveness ^[^2] *Nest Type	0.13	0.09	0.34	0.12	0.11	0.14	1.32	0.62	6.86	0.32	0.01	0.43

Table A4 . Full results of phylogenetic generalized least squares analyses for **hue of concealed patches** repeated on 100 phylogenies. For every estimate (regression coefficient, SE, F- and p-value), we provide its mean and 95% confidence interval (LCI-UCI). Reference categories are “Monogamy” for Mating, “Closed” for Nest type and “Sedentary” for Migration. The λ value (LCI-UCI) is 0.75 (0.54-1.18). N = 412 species in the PGLS analyses.

Response: hue (PC2) Predictors	Estimate			SE			F			p		
	Mean	LCI	UCI	Mean	LCI	UCI	Mean	LCI	UCI	Mean	LCI	UCI
Intercept	-0.13	-1.04	0.50	0.39	0.31	0.54						
Diff. in Attentiveness ^[^2]	-0.05	-0.08	0.01	0.10	0.09	0.10	0.42	0.01	0.76	0.56	0.38	0.94
Mating (Polygamy)	0.04	-0.08	0.10	0.17	0.16	0.18	1.23	0.14	3.27	0.36	0.04	0.87
Mating (Lek)	0.45	0.02	0.72	0.32	0.28	0.33						
Body Mass [Log ₁₀]	-0.37	-0.55	-0.33	0.07	0.07	0.08	24.99	16.35	54.97	0.00	0.00	0.00
Nest type (Open)	0.03	-0.07	0.23	0.13	0.12	0.15	0.76	0.16	2.45	0.46	0.12	0.69
Migration (Partial)	-0.19	-0.33	-0.13	0.12	0.12	0.13	3.87	2.40	4.66	0.03	0.01	0.09
Migration (Migratory)	0.13	-0.16	0.25	0.13	0.12	0.14						
Diff. in Attentiveness ^[^2] *Nest Type	0.04	0.01	0.06	0.11	0.11	0.12	0.14	0.00	0.27	0.74	0.60	0.96

Table A5 . Sample sizes of species used in our comparative analyses given for individual taxonomic families and further split by levels of our categorical predictors (nest type, mating system, and migration strategy).

Family	Total sample size (No species)	Nest type			Mating system		Migration strategy		
		Closed	Open	Lek	Monogamy	Polygamy	Migratory	Partial	Sedentary
Aegithalidae	2	2	0	0	1	1	0	1	1
Aegithinidae	1	0	1	0	1	0	0	0	1
Alaudidae	5	1	4	0	5	0	0	3	2
Bombycillidae	1	0	1	0	1	0	1	0	0
Cardinalidae	3	0	3	0	3	0	0	1	2
Certhiidae	3	3	0	0	3	0	0	1	2
Cinclidae	1	1	0	0	1	0	0	0	1
Cisticolidae	2	2	0	0	2	0	0	0	2
Climacteridae	3	3	0	0	3	0	0	0	3
Conopophagidae	1	0	1	0	1	0	0	0	1
Corvidae	21	4	17	0	21	0	0	2	19
Cotingidae	4	0	4	2	2	0	0	0	4
Cracticidae	1	0	1	0	1	0	0	0	1
Dendrocolaptidae	3	3	0	1	2	0	0	0	3
Drepanididae	6	0	6	0	6	0	0	0	6
Emberizidae	40	6	34	0	38	2	17	11	12
Epthianuridae	1	0	1	0	1	0	0	1	0
Estrildidae	1	1	0	0	1	0	0	0	1
Eupetidae	1	0	1	0	1	0	0	0	1
Fringillidae	22	2	20	0	21	1	2	13	7
Furnariidae	2	2	0	0	2	0	0	0	2

Grallinidae	1	0	1	0	1	0	0	0	1
Hirundinidae	7	5	2	0	7	0	4	2	1
Icteridae	10	2	8	0	7	3	4	2	4
Laniidae	4	0	4	0	4	0	0	3	1
Malaconotidae	1	0	1	0	1	0	0	1	0
Maluridae	3	3	0	0	3	0	0	0	3
Meliphagidae	9	0	9	0	9	0	0	2	7
Mimidae	3	0	3	0	3	0	1	0	2
Monarchidae	4	0	4	0	4	0	0	3	1
Motacillidae	11	3	8	0	11	0	5	4	2
Muscicapidae	6	5	1	0	6	0	6	0	0
Nectariniidae	3	3	0	0	3	0	0	0	3
Neosittidae	1	0	1	0	1	0	0	0	1
Notiomystidae	1	1	0	0	0	1	0	0	1
Oriolidae	1	0	1	0	1	0	0	0	1
Orthonychidae	2	2	0	0	2	0	0	0	2
Pachycephalidae	3	0	3	0	3	0	0	1	2
Paradisaeidae	4	0	4	2	0	2	0	0	4
Paradoxornithidae	2	1	1	0	2	0	0	0	2
Paridae	14	14	0	0	14	0	0	0	14
Parulidae	29	9	20	0	27	2	17	4	8
Passeridae	7	6	1	0	7	0	0	4	3
Petroicidae	5	0	5	0	5	0	1	0	4
Philepittidae	1	1	0	1	0	0	0	0	1
Pipridae	2	0	2	1	0	1	0	0	2
Ploceidae	7	7	0	0	3	4	0	1	6
Pomatostomidae	1	1	0	0	1	0	0	0	1

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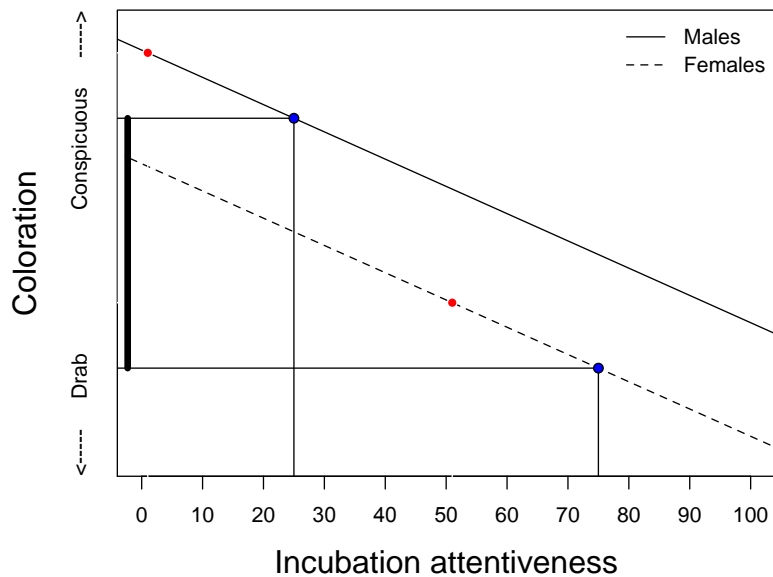
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There is one alternative that could have been used: the proportion of incubation by the sex that incubates the most (so the range would be from 0.5 to 1.0, giving an asymmetric index analogous to our absolute difference in attentiveness between the sexes). However, this index has two drawbacks:

1) For certain scenarios, it does not capture the strength of “Wallacean” selection: imagine two species, both with female-only incubation – nest attentiveness would be 40% in the first one and 80% in the second one. This index would give the value of 1 in both cases (since male would not help at all in both). However, we do expect stronger selection on the female in the second species, which has to spend 2x more time by sitting on the eggs – and indeed, this is captured by our difference index, giving the value of 40 in the first case and 80 in the second case.

2) The distribution of this index would be extremely skewed, precluding its use as a predictor in statistical analyses (Fig. A4). On the contrary, our DIFFERENCE index had acceptable distribution (see Fig. A1)

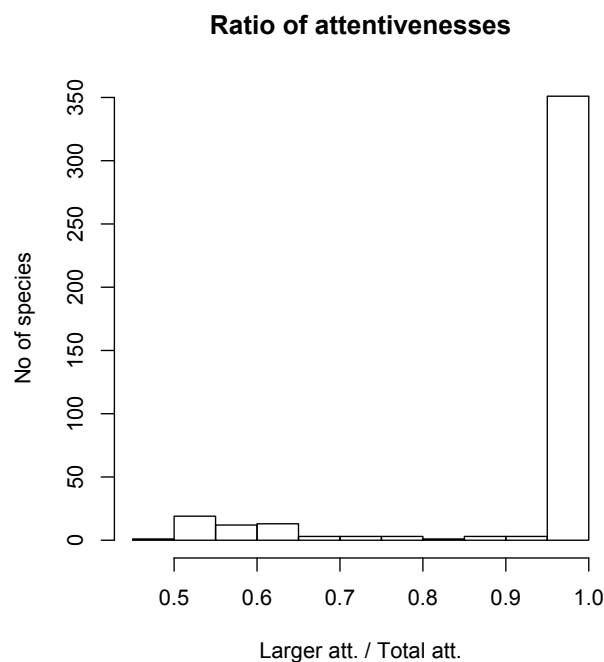


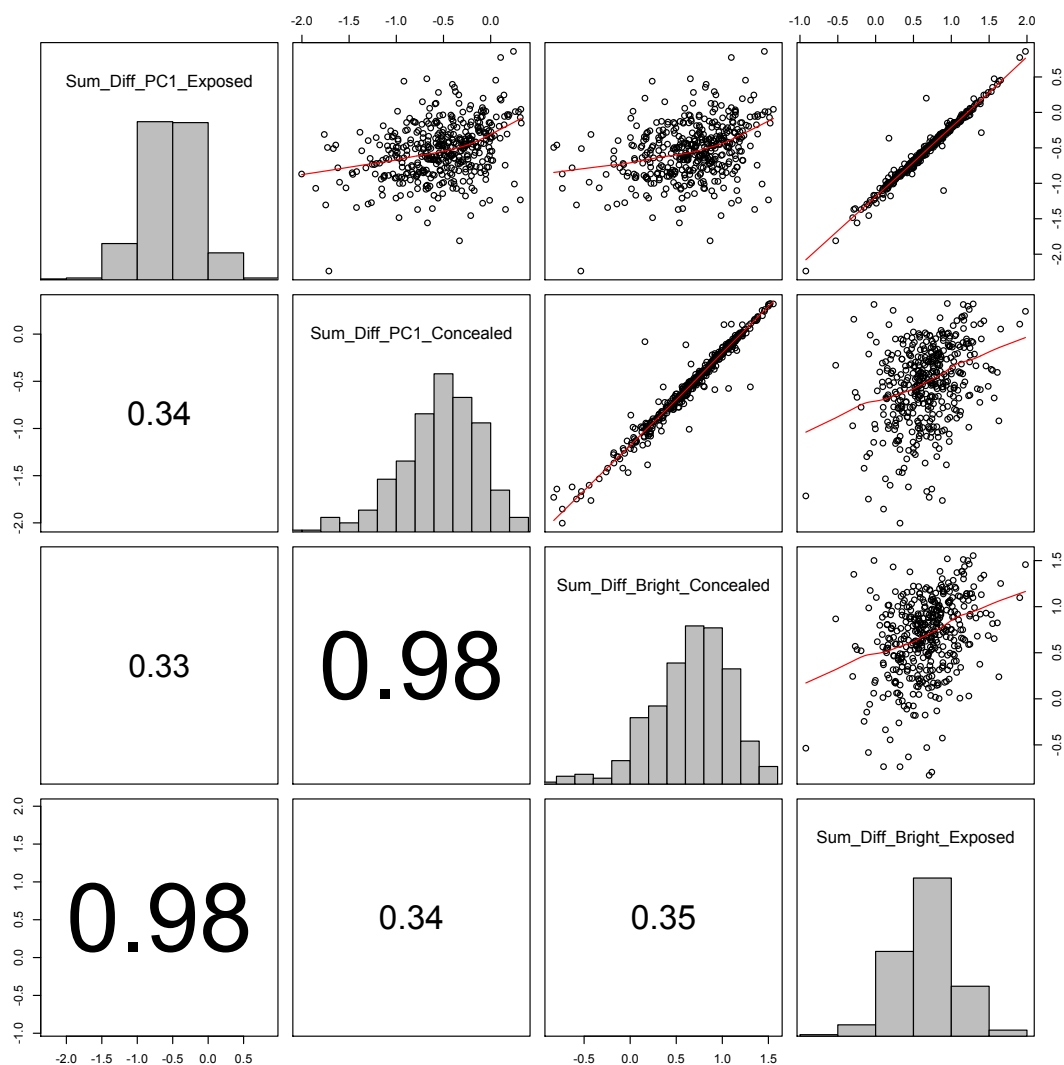
Fig. A5. Distribution of the proportion of incubation by the sex that incubates the most.

Appendix 3

Robustness of our index of sexual dichromatism

In addition to the PCA-based index of dichromatism described in the main text, we also calculated following two indexes. 1) We calculated overall brightness as the sum of reflectance values across all wavelengths (from 320 to 700 nm), separately for each patch and sex. Then we calculated absolute difference between males and females for exposed and concealed patches as in the main text (see there for details). 2) We calculated Euclidean distance between the male spectrum and the female spectrum in avian tetrahedral color space (Stoddard and Prum 2008, *Am. Nat.* 171:755-776) in pavo package (Maia et al. 2013, *Methods Ecol Evol* 4:906-913) for each patch separately. We then summed these distances for exposed (crown, mantle, cheek) and concealed patches (breast, belly) in every species.

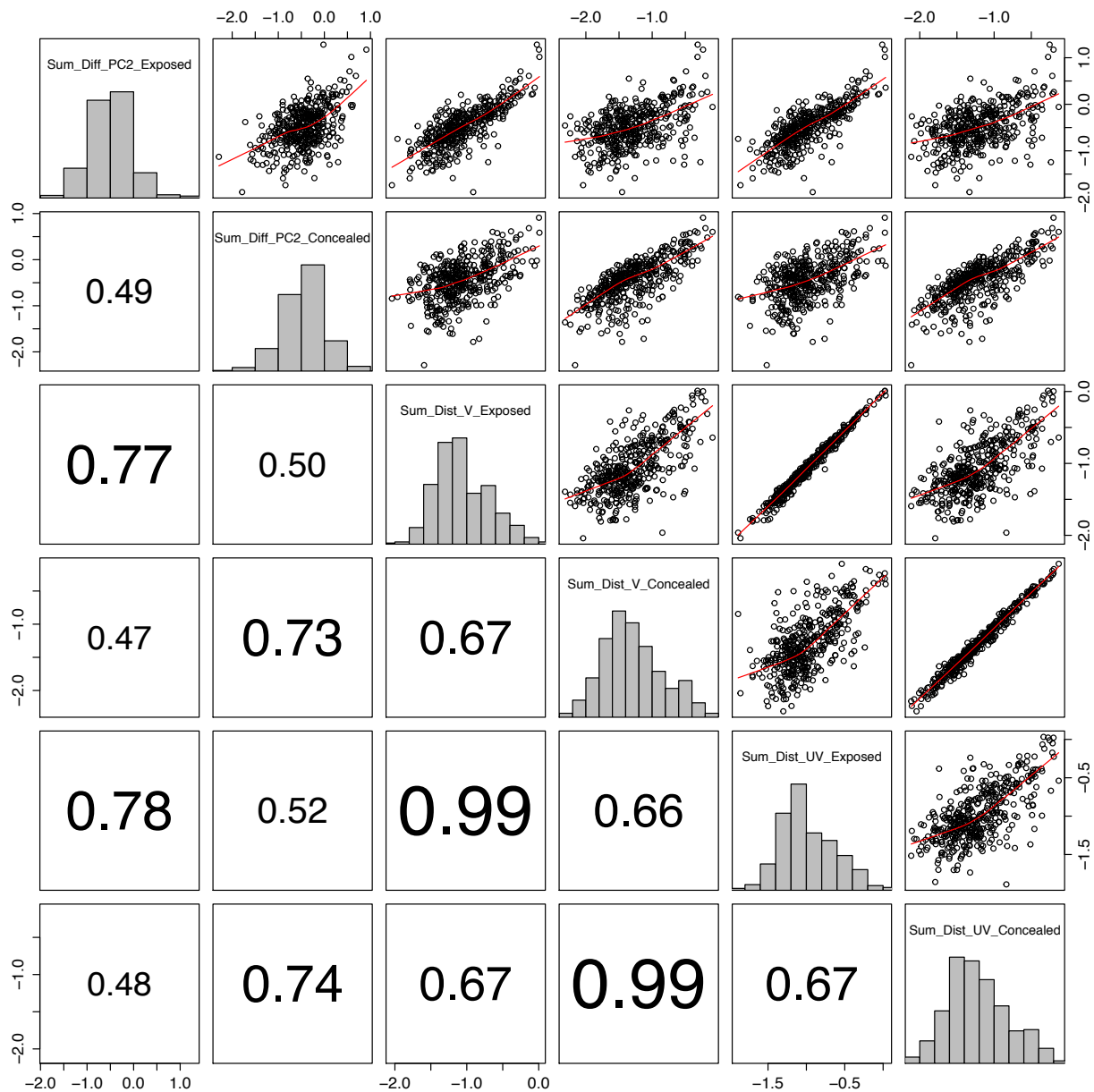
Following figure (log₁₀-transformed variables) shows very high correlations ($r = 0.98$) between the PCA-based dichromatism index of brightness (Sum_Diff_PC1) and dichromatism based on actual brightness (Sum_Diff_Bright) for both exposed and concealed patches. These results confirm that our PCA-based index of dichromatism in brightness was a very good approximation of an index based on real brightness of reflectance spectra.



Following figure (log₁₀-transformed variables) demonstrates relationships among indexes of dichromatism based on color characteristics that ignore brightness. We show that:

- Correlations between dichromatism based on the visual systems with UV-sensitive (Sum_Dist_UV) vs. V-sensitive (Sum_Dist_V) short wavelength cones are very high ($r = 0.99$).
- Correlations between dichromatism based on PCA-based index of hue (Sum_Diff_PC2) and dichromatism based on distances in the avian visual space (Sum_Dist) are reasonably high for both exposed ($r = 0.77$ and 0.78) and concealed patches ($r = 0.73$ and 0.74).

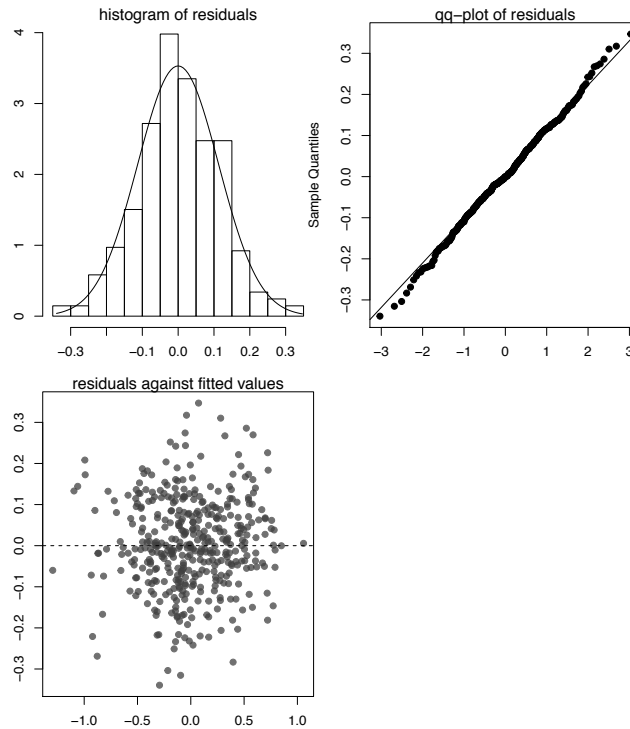
These results show that dichromatism based on PCA-based index of hue is a reasonable approximation of dichromatism based on visual space of a major group of predators using vision to locate nests (i.e. birds).



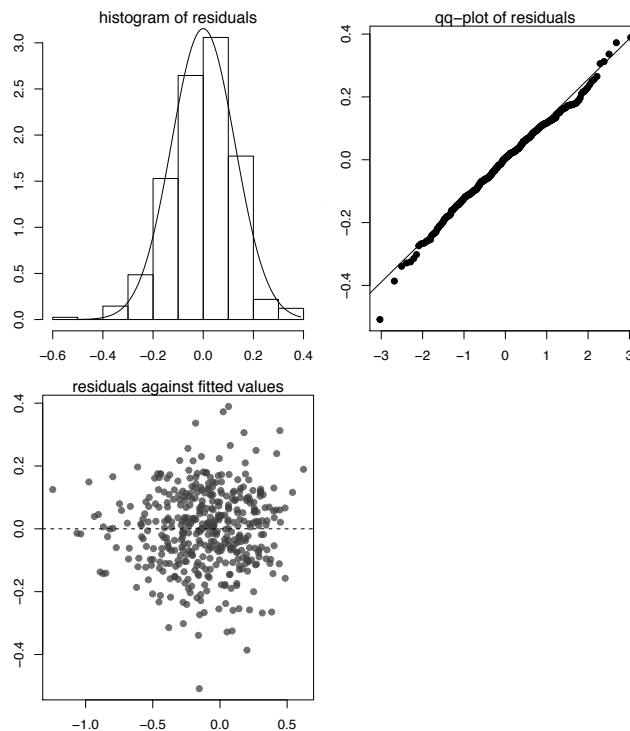
Appendix 4

Plots of residuals from the four main models presented in Tables 1 and 2 in the main text. All residuals had reasonable distribution, despite some species having quite outlying values of dichromatism (especially *Malurus cyaneus*, *M. splendens*, and *Cyanerpes lucidus*). However, apparently after \log_{10} -transformation, assumptions of the PGLS models were fulfilled.

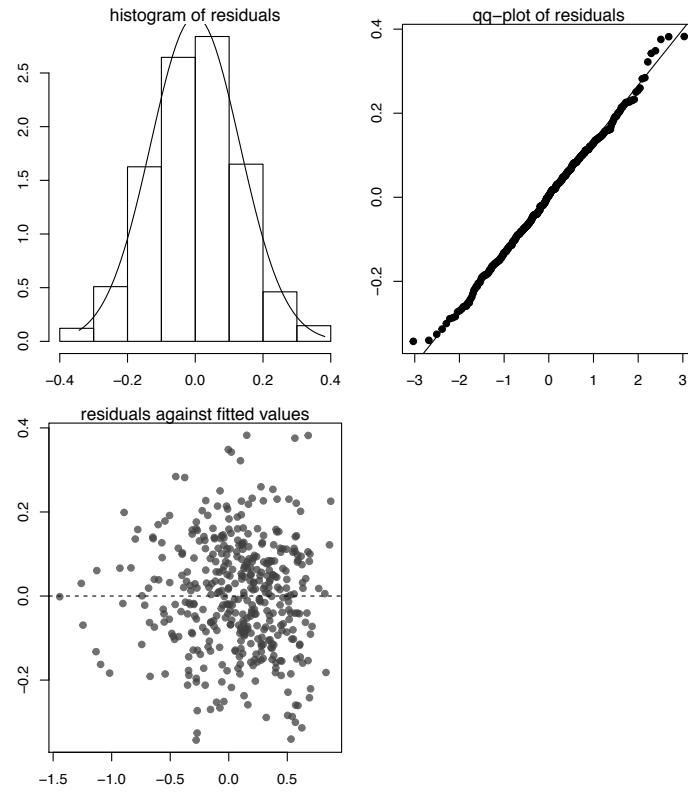
PC1 (brightness), concealed patches:



PC1 (brightness), exposed patches:



PC2 (hue), concealed patches:



PC2 (hue), exposed patches:

