SUPPLEMENTARY MATERIAL

APPENDIX S1

Supplementary methods

Supplementary figures (S1) and tables (S1-S9)

APPENDIX S1

SUPPLEMENTARY METHODS

Compiling sister species datasets

We generated two datasets of avian sister species pairs. First, we assembled a dataset of passerine sister pairs for which we could collect detailed data on plumage colouration using spectrophotometric measurements. To do this, we compiled a list of sister pairs from published phylogenetic trees of passerine families or genera generated using mtDNA. We only included trees in which (i) > 70% of taxa had been sampled, and (ii) node support was high, with either posterior probability > 95% or ML bootstrap support > 70%. When several phylogenies were presented in a paper, we only selected sister species resolved in all trees. When nodal support varied with the method of phylogenetic reconstruction, ML bootstrap values took precedence. We assumed that consensus trees and trees based on concatenated molecular datasets provided the most reliable source of phylogenetic information and thus, whenever possible, we assessed nodal support based on the values given in these trees. Sister pair ages were generated by building a time-calibrated phylogenetic tree using multiple mitochondrial cytochrome (cyt) *b* sequences per species (where possible; see below). The resulting dataset contained 144 species pairs and is referred to as dataset 1 throughout.

Second, to assess the links between speciation, sympatry and sexual selection on a broader scale, we assembled data for a larger set of sister pairs sampled from across the avian radiation (including non-passerines). Following previous analyses (Pigot et al. 2016), sister pairs and their divergence times (My) were extracted from the Jetz et al. (2012) time-calibrated phylogenies, using the Hackett et al. (2008) backbone topology and focusing on trees containing only those species represented by genetic data (n = 6,670). Using a random sample of 100 trees, we generated a single MCC tree with median node heights and extracted sister pairs from across the tree, excluding pairs containing pelagic species with poorly defined breeding distributions (n = 69) and pairs from poorly sampled genera (sampling <70%; n = 723), which are unlikely to represent true sister species (Pigot et al. 2016). The resulting dataset contained 1306 sister species pairs. We report the results produced using pairs sampled from the MCC tree, but as these results are subject to phylogenetic uncertainty, we re-ran our analyses on pairs extracted from each of the 100 sampled trees and also report median values across all replicate trees. Aside from differences in sample size and taxonomic scope, this larger dataset was comparable to the first, except that it included many species for which we were unable to obtain spectrophotometric measurements of colour. Thus, for all species included in all replicate trees, we quantified dichromatism using human visual estimates

of sex-differences in colouration based on illustrations (see below). We refer to this larger dataset as dataset 2 throughout the text.

Estimating passerine-only sister species ages

To build a time-calibrated tree for passerine-only sister species, we searched GenBank for available cyt-*b* sequences, excluding those <400 bp in length and all sequences that were excessively divergent from other conspecific sequences, which are likely to represent nuclear copies of the cyt-*b* gene (i.e. 'numts'). For species represented by multiple sequences, we pruned out those sequences originating from similar localities/subspecies that had identical (or extremely similar) sequence identity. For the remaining species in the dataset we included a single representative cyt *b* sequence and where a choice of sequences was available for a given species, we chose the longest. The resulting dataset contained 288 bird species (i.e. 144 sister species pairs) represented by 556 cyt-*b* sequences, with 86/288 species represented by more than one sequence. We aligned the chosen sequences using MAFFT (Katoh et al. 2002) and built the phylogeny with BEAST v1.7.4 (Drummond et al. 2012) using an uncorrelated lognormal relaxed-clock model with a Yule prior on branch lengths and a GTR-gamma model set to a mean rate of 1.05% sequence evolution per lineage per million years (Weir and Schluter 2008). As cyt-*b* is inappropriate for inferring deeper phylogenetic relationships, we used backbone constraints to define *a priori* all the known species pairs and genera in our sample. We conducted four runs (each 20 million generations sampled every 5000 generations) and combined the samples from each run after first checking for convergence and removing the first 25% as burn in. To produce a dated phylogeny, we generated a maximum clade credibility (MCC) tree using TREEANNOTATOR (Drummond et al. 2012), with node ages equal to the median age across all posterior trees.

Quantifying sexual dichromatism

Spectrophotometric measurements of dichromatism

For the 144 pairs of passerine bird species in our smaller dataset, we quantified sexual dichromatism objectively using measurements of plumage colour collected using a spectrophotometer. By using colour data derived from a spectrophotometer, this allows us to assess the links between plumage dichromatism and speciation/sympatry whilst avoiding the problems associated with human misrepresentation of avian colour (Cuthill et al. 1999). All spectrophotometer measurements were collected using an Ocean Optics (Dunedin, Florida) USB2000 spectrophotometer and a PX-2-pulsed Xenon light source with the spectrophotometer probe at 90^{o}

to the feather's surface. Measurements were standardized to a WS-1 white standard, considered to reflect more than 98% of light with 250–1500 nm wavelength.

To measure plumage colouration, we took five replicate spectrophotometric measurements at six body regions (crown, throat, belly, wing coverts, back and tail) from three male and three female adult specimens of each species (where possible) in full breeding plumage. For each reflectance reading, the reflectance data were averaged into 19 bins covering 20 nm of the spectrum between 320 and 700 nm, the approximate visible spectrum of most avian species (Hart 2001). Reflectance scores are highly correlated at similar wavelengths, so we used principal components analysis (PCA) to collapse reflectance values into fewer independent axes of variation capable of summarising spectrum shape (Endler 1990; Cuthill et al. 1999). Some previous comparative studies (e.g. Stoddard and Prum 2008) have instead modelled the spectral sensitivity of the avian eye but this involves making assumptions about colour perception in numerous species for which data on spectral sensitivity are lacking (Borges et al. 2015). We note that our PCA analysis is a widely-used procedure for handling spectral data (Endler and Théry 1996; Bennett et al. 1997; Hunt et al. 1999; Macedonia 2001; Stein and Uy 2006; Seddon et al. 2013; Dunn et al. 2015), and previous studies comparing the outputs with those of visual models have yielded qualitatively similar estimates of colour and dichromatism (Armenta et al. 2008; Stoddard and Prum 2008) and dichromatism (Armenta et al. 2008). We used the first three PCs, which together explained over 99% of the variance spectrum shape (Table S1) and broadly correspond to variation in brightness (PC1), chroma/hue (PC2 and PC3) across spectra. To calculate dichromatism we averaged replicate measurements within a patch for each sex and then summed the Euclidean distances between male and female scores for each patch (Seddon et al. 2013). A dichromatism score of zero indicates identical colouration in both sexes (monochromatism) with higher positive values indicating greater degree of dichromatism. To improve normality, dichromatism scores were log-transformed. Finally, to calculate pair-level scores, we used the average score of both species.

Human scores of dichromatism

It is not yet feasible to obtain spectrophotometric measures of plumage colour for thousands of species, so for all species in dataset 2 (n = 5681, including all species occurring in replicate trees) we scored sexual dichromatism from handbook illustrations (del Hoyo et al. 1992–2011). Specifically, we used standard methodology (Owens and Bennett 1994; Owens and Hartley 1998) to score the difference in plumage coloration between the sexes over five body regions (head, nape-rump-back, throat-belly, tail, and wings) for each species in our sample. Each region was scored separately using three scores: 0, no difference between the sexes; 1, difference between the sexes only in shade or intensity of color; 2, difference in colour or pattern between the sexes. The dichromatism scores for all five body regions were then summed to give species-specific scores of

plumage dichromatism on a scale from 0 (monochromatic) to 10 (maximum dichromatism). Unlike spectrophotometric scores of dichromatism, our human scores of dichromatism were not log-transformed because of issues associated with the log-transformation of count data (O'Hara and Kotze 2010). As before, pair-level scores were calculated by taking the average score of both species.

Human observers may underestimate the extent of sexual dichromatism in birds because of an inability to perceive signals in ultraviolet wavelengths (Cuthill et al. 1999). Nevertheless, among the species common to both datasets (n = 281), spectrophotometric and human-derived estimates of dichromatism were highly correlated (Spearman's r = 0.69, P < 0.001), adding to a growing body of evidence that human scores can provide useful estimates of plumage dichromatism (Armenta et al. 2008; Seddon et al. 2010). Furthermore, our results were similar irrespective of whether spectrophotometric or human visual estimates of dichromatism were used, suggesting that our conclusions are robust to the particular approach used to quantify dichromatism.

Additional predictors of geographic range overlap

Latitude. Species' latitudinal centroids were estimated using the R package PBSmapping. Following previous studies (e.g. Weir and Schluter 2007), we then used average (absolute) centroid values to estimate the midpoint latitudinal position of sister pairs.

Migration and territoriality. Following previous studies (Salisbury et al. 2012; Pigot and Tobias 2015; Cooney et al. 2016), we used descriptions in *The Handbook of the Birds of the World* series (del Hoyo et al. 1992–2011) to score species according to levels of migratory tendency (1 = sedentary, 2 = short-distance migrants, 3 = long-distance migrants) and territoriality (1 = permanent year-round territoriality, 2 = seasonal or weak territoriality, 3 = non-territorial). For both variables, we then used the mean score of species within each pair to provide a simple index capturing the relative level of migratory behavior or territoriality in a sister pair. For further details and justification of traits and scoring method see Pigot and Tobias (2015).

Body size. Body mass values were extracted from 'EltonTraits 1.0' (Wilman et al. 2014) and log-transformed before taking the average for each sister pair.

Geographic realm. Each sister pair was unambiguously assigned to a particular geographic realm (Africa, Eurasia, Oceania, North America, South America) based on the dominant geographic position of their breeding range distributions.

Simulating birth-death trees

Birth-death trees with lag time correction were simulated using the R package TreeSim (Stadler 2011) and custom code. For dataset 1, trees were simulated for 15 time units (max sister pair age =

11.7 My) using speciation rate values ranging from 0 to 0.15 in 0.01 intervals, and from 0.15 to 0.90 in 0.05 intervals. For speciation rates ≤ 0.4, simulated extinction fractions ranged from 0, 0.05, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 0.95, 0.99. For speciation rates > 0.4, the same extinction rates were used provided net diversification rate (speciation – extinction) < 0.45. For dataset 2, trees were simulated for 50 time units (max sister pair age = 49.3 My) using similar parameter values except that for speciation rates > 0.15, the same extinction rates were used provided net diversification rate ≤ 0.15. This type of restriction was necessary for computational reasons given the excessively large tree sizes, but should not bias our likelihood search because such trees are unrealistically large. For each set speciation and extinction rates, 21 values of lag time were used (0, 0.1, 0.2…1.9, 2). For each set of sister pair age distributions, the probability density function was obtained using the LOCFIT package in R, and the probability of given pair age equals the probability density at the corresponding point in the simulated distribution. For a given set of slope and intercept parameters describing the change in speciation and extinction rates with increasing dichromatism, the likelihood was obtained by multiplying the probabilities of each sister species age, derived from the appropriate simulated distribution. More details of the simulation approach and model fitting can be found in Weir and Schluter (2007) and Seddon et al. (2013).

References

Armenta, J. K., P. O. Dunn, and L. A. Whittingham. 2008. Quantifying avian sexual dichromatism: a comparison of methods. J. Exp. Biol. 211:2423-2430.

Bennett, A. T., I. C. Cuthill, J. C. Partridge, and K. Lunau. 1997. Ultraviolet plumage colors predict mate preferences in starlings. Proc. Natl. Acad. Sci. U.S.A. 94:8618-8621.

Borges, R., I. Khan, W. E. Johnson, M. T. P. Gilbert, G. Zhang, E. D. Jarvis, S. J. O'Brien, and A. Antunes. 2015. Gene loss, adaptive evolution and the co-evolution of plumage coloration genes with opsins in birds. BMC Genomics 16:751.

Cooney, C. R., N. Seddon, and J. A. Tobias. 2016. Widespread correlations between climatic niche evolution and species diversification in birds. J. Anim. Ecol. 85:869-878.

Cuthill, I. C., A. T. D. Bennett, J. C. Partridge, and E. J. Maier. 1999. Plumage reflectance and the objective assessment of avian sexual dichromatism. Am. Nat. 153:183-200.

del Hoyo, J., A. Elliott, J. Sargatal, and D. A. Christe. 1992–2011. The Handbook of the Birds of the World, vols 1-16. Lynx Edicions, Barcelona.

Drummond, A. J., M. A. Suchard, D. Xie, and A. Rambaut. 2012. Bayesian phylogenetics with BEAUti and the BEAST 1.7. Mol. Biol. Evol. 29:1969-1973.

Dunn, P. O., J. K. Armenta, and L. A. Whittingham. 2015. Natural and sexual selection act on different axes of variation in avian plumage color. Science Advances 1:e1400155.

Endler, J. A. 1990. On the measurement and classification of colour in studies of animal colour patterns. Biol. J. Linn. Soc. 41:315-352.

Endler, J. A. and M. Théry. 1996. Interacting effects of lek placement, display behavior, ambient light, and color patterns in three Neotropical forest-dwelling birds. Am. Nat. 148:421-452.

Hackett, S. J., R. T. Kimball, S. Reddy, R. C. K. Bowie, E. L. Braun, M. J. Braun, J. L. Chojnowski, W. A. Cox, K. L. Han, J. Harshman, C. J. Huddleston, B. D. Marks, K. J. Miglia, W. S. Moore, F. H.

198 Sheldon, D. W. Steadman, C. C. Witt, and T. Yuri. 2008. A phylogenomic study of birds
199 reveals their evolutionary history. Science 320:1763-1768.
200 Hart, N. S. 2001. The visual ecology of avian photoreceptors. Progress in Retinal and Eye Research
201 20:675-703.
202 Hunt, S., I. C. Cuthill, A. T. Bennett, and R. Griffiths. 1999. Preferences for ultraviolet partners in the
203 blue tit. Anim. Behav. 58:809-815.
204 Jetz, W., G. H. Thomas, J. B. Joy, K. Hartmann, and A. O. Mooers. 2012. The global diversity of birds
205 in space and time. Nature 491:444-448.
206 Katoh, K., K. Misawa, K. Kuma, and T. Miyata. 2002. MAFFT: a novel method for rapid multiple
207 sequence alignment based on fast Fourier transform. Nucleic Acids Res. 30:3059-3066.
208 Macedonia, J. M. 2001. Habitat light, colour variation, and ultraviolet reflectance in the Grand
209 Cayman anole, *Anolis conspersus*. Biol. J. Linn. Soc. 73:299-320.
210 O'Hara, R. B. and D. J. Kotze. 2010. Do not log-transform count data. Methods in Ecology and
211 Evolution 1:118-122.
212 Owens, I. P. F. and P. M. Bennett. 1994. Mortality costs of parental care and sexual dimorphism in
213 birds. Proc. R. Soc. London Ser. B 257:1-8.
214 Owens, I. P. F. and I. R. Hartley. 1998. Sexual dimorphism in birds: why are there so many different
215 forms of dimorphism? Proc. R. Soc. London Ser. B 265:397-407.
216 Pigot, A. L. and J. A. Tobias. 2015. Dispersal and the transition to sympatry in vertebrates. Proc. R.
217 Soc. London Ser. B 282:20141929.
218 Pigot, A. L., J. A. Tobias, and W. Jetz. 2016. Energetic constraints on species coexistence in birds.
219 PLoS Biol. 14:e1002407.
220 Salisbury, C. L., N. Seddon, C. R. Cooney, and J. A. Tobias. 2012. The latitudinal gradient in dispersal
221 constraints: ecological specialisation drives diversification in tropical birds. Ecol. Lett.
222 15:847-855.
223 Seddon, N., C. A. Botero, J. A. Tobias, P. O. Dunn, H. E. Macgregor, D. R. Rubenstein, J. A. Uy, J. T.
224 Weir, L. A. Whittingham, and R. J. Safran. 2013. Sexual selection accelerates signal evolution
225 during speciation in birds. Proc. R. Soc. London Ser. B 280:20131065.
226 Seddon, N., J. A. Tobias, M. Eaton, and A. Ödeen. 2010. Human vision can provide a valid proxy for
227 avian perception of sexual dichromatism. Auk 127:283-292.
228 Stadler, T. 2011. Simulating trees with a fixed number of extant species. Syst. Biol. 60:676-684.
229 Stein, A. C. and J. A. C. Uy. 2006. Plumage brightness predicts male mating success in the lekking
230 golden-collared manakin, Manacus vitellinus. Behav. Ecol. 17:41-47.
231 Stoddard, M. C. and R. O. Prum. 2008. Evolution of avian plumage color in a tetrahedral color space:
232 a phylogenetic analysis of New World buntings. Am. Nat. 171:755-776.
233 Weir, J. T. and D. Schluter. 2007. The latitudinal gradient in recent speciation and extinction rates of
234 birds and mammals. Science 315:1574-1576.
235 Weir, J. T. and D. Schluter. 2008. Calibrating the avian molecular clock. Mol. Ecol. 17:2321-2328.
236 Wilman, H., J. Belmaker, J. Simpson, C. de la Rosa, M. M. Rivadeneira, and W. Jetz. 2014. EltonTraits
237 1.0: species-level foraging attributes of the world's birds and mammals. Ecology 95:2027.
238

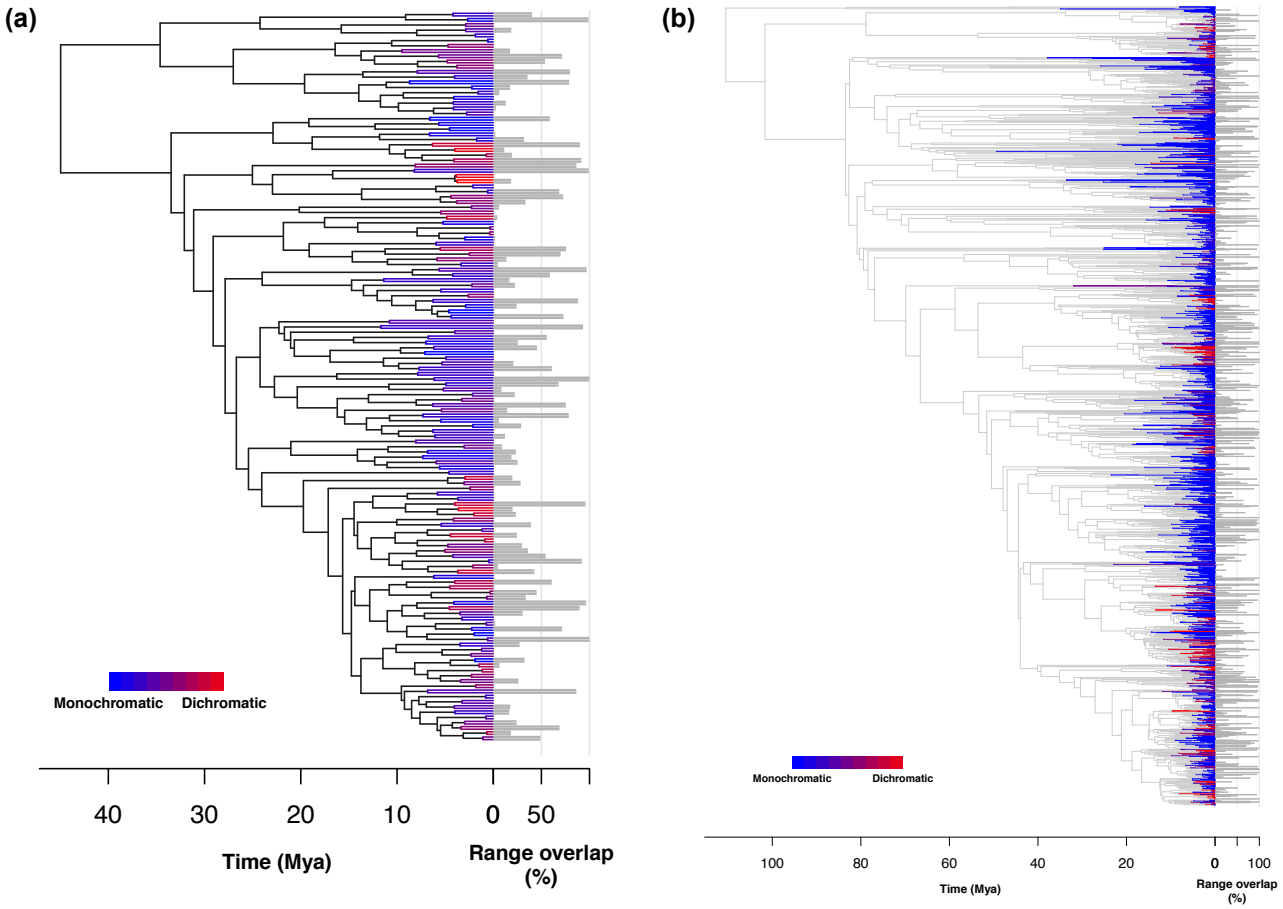

Figure S1. Plot showing the variation in evolutionary age, extent of range overlap and level of sexual dichromatism across avian sister species pairs with respect to the underlying phylogeny. In (a) dichromatism is estimated for a set of passerine sister pairs using spectrophotometric measurements of plumage (dataset 1; n = 144 species pairs), whereas in (b) estimates are based on human scores of dichromatism for a broader sample of passerine and non-passerine pairs (dataset 2; n = 1306 species pairs).

Table S1. Principal component (PC) loadings and importance values for reflectance measurements of plumage colour (n = 61920) collapsed into 20nm bins.

Wavelength bin (nm)	PC1	PC2	PC3
320-340	0.21	0.26	–0.54
340-360	0.22	0.23	–0.43
360-380	0.23	0.23	–0.29
380-400	0.23	0.25	–0.09
400-420	0.23	0.26	0.09
420-440	0.23	0.25	0.22
440-460	0.23	0.23	0.31
460-480	0.23	0.20	0.36
480-500	0.23	0.15	0.35
500-520	0.24	0.03	0.15
520-540	0.24	–0.08	0.00
540-560	0.24	–0.14	–0.03
560-580	0.24	–0.19	–0.03
580-600	0.23	–0.23	–0.04
600-620	0.23	–0.26	–0.03
620-640	0.23	–0.28	–0.03
640-660	0.22	–0.29	–0.02
660-680	0.22	–0.30	–0.02
680-700	0.22	–0.31	–0.01
Standard deviation	4.04	1.43	0.67
Proportion of variance	0.86	0.11	0.02
Cumulative proportion	0.86	0.97	0.99

Table S2. Critical ΔAICc values for models testing the association between diversification and parapatry/sympatry rates and dichromatism across alternative sister pair datasets.

	Dataset 1	Dataset 2
Parameter	**Critical ΔAICc**	**Critical ΔAICc**
Diversification models		
Speciation rate	3.66	18.05
Extinction rate	–1.42	3.37
Allopatry / sympatry models		
Sympatry rate (>0%)	1.80	8.32
Sympatry rate (>5%)	1.87	8.45
Sympatry rate (>10%)	2.55	8.03
Sympatry rate (>20%)	3.26	8.63
Sympatry rate (>30%)	4.13	9.04
Sympatry rate (>40%)	1.86	8.21
Sympatry rate (>50%)	0.68	7.90
Sympatry rate (>60%)	0.78	4.57
Sympatry rate (>70%)	1.05	3.07
Sympatry rate (>80%)	1.35	4.26
Allopatry / parapatry / sympatry models		
Parapatry rate (0-20%)	1.86	10.47
Parapatry rate (5-25%)	2.27	8.36
Parapatry rate (10-30%)	3.07	9.63
Sympatry rate (>20%)	4.04	11.84
Sympatry rate (>25%)	3.13	8.61
Sympatry rate (>30%)	3.09	7.10

Values correspond to the 95th percentile ($\alpha = 0.05$) of the null distribution of ΔAICc values generated by fitting models to simulated datasets (n = 100; see Methods). Net slope refers to the slope of net diversification rates (i.e. speciation rate – extinction rate).

Table S3. Median parameter values of speciation and extinction rates across gradients of increasing sexual dichromatism estimated using datasets of avian sister pairs (n = 1283 – 1321) sampled from 100 posterior trees.

Parameter	Estimate	ΔAICc
Speciation intercept	0.07	–
Speciation slope	0.03	12.33
Extinction intercept	0.02	–
Extinction slope	–0.10	–1.15
Net intercept	0.06	–
Net slope	0.04	16.43

Dichromatism values were re-scaled (0-1) prior to model fitting. ΔAICc values quantify the improvement in model fit (positive values) compared to constant-rate models in which the focal slope parameter(s) were constrained to be zero.

Table S4. PGLS models of the relationship between age and sexual dichromatism across avian sister pairs.

Term	Estimate	SE	*t*	*P*
Dataset 1				
Intercept	4.568	0.924	4.943	<0.001
Dichromatism	–0.631	0.405	–1.559	0.121
Dataset 2				
Intercept	14.491	4.456	3.252	0.001
Dichromatism	0.312	0.197	1.592	0.112

Spec dataset: R^2 = 0.01; Pagel's λ = 0.76. Human dataset: R^2 < 0.01; Pagel's λ = 1.00.

Table S5. Models of the relationship between sympatry rate and sexual dichromatism across sister pairs of birds under alternative range overlap thresholds used to assign sympatry.

Threshold (%)	*N* (allo/sym)	Hazard ratio [95% CI]	ΔAICc
Dataset 1			
>0	43 / 97	1.86 [1.19, 2.92]	5.39*
>5	54 / 86	1.78 [1.14, 2.78]	4.27*
>10	60 / 80	1.81 [1.14, 2.85]	4.22*
>20	76 / 64	1.41 [0.87, 2.28]	–0.19
>30	92 / 48	1.28 [0.73, 2.23]	–1.33
>40	100 / 40	1.38 [0.75, 2.51]	–1.01
>50	105 / 35	1.23 [0.64, 2.37]	–1.68
>60	110 / 30	1.40 [0.70, 2.79]	–1.18
>70	116 / 24	1.30 [0.59, 2.85]	–1.64
>80	125 / 15	1.47 [0.56, 3.88]	–1.46
Dataset 2			
>0	600 / 706	1..38 [1.19, 1.60]	14.95*
>5	750 / 556	1.53 [1.30, 1.80]	22.29*
>10	804 / 502	1.50 [1.27, 1.78]	18.09*
>20	883 / 423	1.44 [1.20, 1.74]	11.87*
>30	938 / 368	1.42 [1.16, 1.73]	8.88
>40	994 / 312	1.35 [1.09, 1.68]	4.88
>50	1035 / 271	1.44 [1.15, 1.82]	6.94
>60	1075 / 231	1.36 [1.06, 1.75]	3.40
>70	1112 / 194	1.27 [0.96, 1.68]	0.69
>80	1150 / 156	1.18 [0.86, 1.62]	–1.05

Hazard ratios refer to the ratio of transition rates per unit change in dichromatism. To aid comparison, dichromatism values were standardised prior to analysis. ΔAICc values quantify the improvement in model fit (positive values) compared to constant-rate models. Asterisks (*) denote significant (α = 0.05) ΔAICc values compared to null expectations. allo = allopatric; sym = sympatric.

Table S6. Median parameter values for the relationship between sympatry rate and sexual dichromatism (under alternative range overlap thresholds) using datasets of avian sister pairs (n = 1283 – 1321) sampled from 100 posterior trees.

Threshold	Hazard ratio [95% CI]	ΔAICc
0	1.43 [1.23, 1.66]	18.31*
5	1.53 [1.29, 1.80]	21.31*
10	1.50 [1.27, 1.78]	17.99*
20	1.43 [1.18, 1.73]	10.71*
30	1.37 [1.12, 1.68]	6.57
40	1.31 [1.05, 1.64]	3.37
50	1.39 [1.09, 1.76]	4.74
60	1.31 [1.01, 1.70]	2.03
70	1.22 [0.91, 1.63]	–0.32
80	1.12 [0.81, 1.57]	–1.56

Hazard ratios refer to the ratio of transition rates per unit change in dichromatism. ΔAICc values quantify the relative improvement in model fit (positive ΔAICc values) compared to constant-rate models. Asterisks (*) denote significant (α = 0.05) ΔAICc values compared to null expectations.

Table S7. Median parameter values for the relationships between parapatry and sympatry rate and sexual dichromatism (under alternative range overlap thresholds) using datasets of avian sister pairs (n = 1283 – 1321) sampled from 100 posterior trees.

Thresholds (%; para/sym)	*N* (allo/para/ sym)	Parameter	Hazard ratio [95% CI]	ΔAICc
0-20 / >20	607 / 280 / 434	ap	1.48 [1.27, 1.71]	22.40*
		ps	1.41 [1.05, 1.89]	3.28
5-15 / >25	755 / 166 / 400	ap	1.51 [1.29, 1.78]	20.99*
		ps	1.14 [0.79, 1.64]	–1.53
10-30 / >30	811 / 136 / 374	ap	1.49 [1.25, 1.77]	16.99*
		ps	1.04 [0.70, 1.54]	–1.85

Hazard ratios refer to the ratio of transition rates per unit change in dichromatism. To aid comparison, dichromatism values were standardised prior to analysis. ΔAICc values quantify the improvement in model fit (positive values) compared to constant-rate models. Asterisks (*) denote significant (α = 0.05) ΔAICc values compared to null expectations. allo = allopatric; para = parapatric; sym = sympatric; ap = allopatry to paraptry; ps = parapatry to sympatry.

Table S8. Multi-predictor model of variation in sympatry rate among sister pairs of birds (dataset 2; n = 1306) using alternative range overlap thresholds to define sympatry.

	>0%		>10%		>20%	
Term	**Hazard ratio**	**ΔAICc**	**Hazard ratio**	**ΔAICc**	**Hazard ratio**	**ΔAICc**
Dichromatism	1.25 [1.07, 1.46]	5.56	1.34 [1.18, 1.60]	7.56	1.29 [1.06, 1.57]	4.19
Migration	1.20 [0.95, 1.51]	0.31	1.19 [0.91, 1.54]	–0.41	1.17 [0.89, 1.56]	–0.80
Territoriality	1.33 [1.12, 1.58]	8.54	1.49 [1.22, 1.82]	13.05	1.55 [1.25, 1.92]	13.64
Latitude	1.11 [0.87, 1.42]	–1.36	1.17 [0.88, 1.55]	–0.92	1.23 [0.91, 1.66]	–0.22
Body mass	0.75 [0.61, 0.92]	5.73	0.73 [0.58, 0.92]	5.01	0.84 [0.66, 1.08]	–0.16
Pass/non-pass: Pass	1.21 [0.98, 1.49]	1.01	1.26 [0.98, 1.61]	1.34	1.35 [1.03, 1.77]	2.79
Continent: Eurasia	1.09 [0.85, 1.41]	18.28	1.01 [0.75, 1.36]	12.63	1.05 [0.76, 1.46]	10.68
Continent: North America	1.11 [0.82, 1.49]	–	1.11 [0.78, 1.58]	–	1.15 [0.78, 1.70]	–
Continent: Oceania	1.37 [0.94, 1.99]	–	1.78 [1.19, 2.68]	–	1.95 [1.27, 3.01]	–
Continent: South America	1.69 [1.33, 2.14]	–	1.55 [1.18, 2.05]	–	1.57 [1.16, 2.13]	–

Hazard ratios [95% CI] refer to the ratio of transition rates per unit change in predictor variable. ΔAICc values quantify the relative change in model fit when the focal variable was included in the model compared to when it was excluded (positive values imply improvement). Reference categories: Pass/non-pass = non-Passeriformes; Continent = Africa.

Table S9. Multi-predictor model of variation in parapatry and sympatry rate among sister pairs of birds (dataset 2; n = 1306) using alternative range overlap thresholds (%; parapatry / sympatry).

		0-20 / >20		5-25 / >25		10-30 / >30	
Parameter	**Term**	**Hazard ratio**	**ΔAICc**	**Hazard ratio**	**ΔAICc**	**Hazard ratio**	**ΔAICc**
ap	Dichromatism	1.30 [1.11, 1.51]	8.41	1.34 [1.13, 1.59]	9.05	1.32 [1.11, 1.58]	7.10
	Migration	1.17 [0.93, 1.47]	–0.23	1.20 [0.94, 1.54]	0.06	1.19 [0.91, 1.54]	–0.41
	Territoriality	1.35 [1.14, 1.60]	10.18	1.52 [1.26, 1.85]	17.11	1.50 [1.23, 1.83]	13.82
	Latitude	1.16 [0.91, 1.48]	–0.58	1.17 [0.90, 1.54]	–0.59	1.17 [0.88, 1.55]	–0.84
	Body mass	0.73 [0.60, 0.89]	7.91	0.74 [0.60, 0.92]	5.21	0.76 [0.60, 0.95]	3.64
	Pass/non-pass: Pass	1.23 [1.00, 1.52]	1.77	1.28 [1.01, 1.61]	2.32	1.31 [1.03, 1.68]	2.89
	Continent: Eurasia	1.03 [0.80, 1.32]	20.56	1.11 [0.83, 1.47]	14.35	1.00 [0.74, 1.34]	13.1
	Continent: N. America	1.12 [0.83, 1.50]	–	1.12 [0.80, 1.57]	–	1.11 [0.78, 1.58]	–
	Continent: Oceania	1.36 [0.94, 1.97]	–	1.84 [1.25, 2.73]	–	1.79 [1.20, 2.68]	–
	Continent: S. America	1.67 [1.32, 2.11]	–	1.61 [1.24, 2.11]	–	1.54 [1.17, 2.03]	–
ps	Dichromatism	1.41 [1.05, 1.89]	3.24	1.61 [0.81, 1.66]	–1.35	1.13 [0.77, 1.67]	–1.65
	Migration	1.15 [0.76, 1.75]	–1.58	0.98 [0.60, 1.60]	–2.03	1.05 [0.62, 1.79]	–2.00
	Territoriality	2.17 [1.59, 2.97]	21.93	1.63 [1.09, 2.42]	3.64	2.30 [1.48, 3.58]	11.77
	Latitude	1.59 [1.02, 2.50]	2.01	1.40 [0.81, 2.43]	–0.59	1.38 [0.77, 2.50]	–0.86
	Body mass	1.38 [0.94, 2.02]	0.71	1.59 [1.00, 2.53]	1.89	1.68 [1.01, 2.80]	1.92
	Pass/non-pass: Pass	1.52 [1.05, 2.22]	2.77	1.45 [0.90, 2.33]	0.29	1.72 [1.01, 2.94]	1.91
	Continent: Eurasia	0.84 [0.53, 1.32]	10.12	0.61 [0.33, 1.12]	5.45	0.52 [0.27, 0.99]	4.34
	Continent: N. America	1.30 [0.73, 2.32]	–	1.40 [0.63, 3.09]	–	0.97 [0.42, 2.26]	–
	Continent: Oceania	3.21 [1.38, 7.47]	–	1.79 [0.68, 4.75]	–	1.72 [0.61, 4.86]	–
	Continent: S. America	1.44 [0.94, 2.19]	–	1.08 [0.61, 1.90]	–	1.03 [0.56, 1.91]	–

Hazard ratios [95% CI] refer to the ratio of transition rates per unit change in predictor variable. ΔAICc values quantify the relative change in model fit when the focal variable was included in the model compared to when it was excluded (positive values imply improvement). Reference categories: Pass/non-pass = non-Passeriformes; Continent = Africa. ap = allopatry to paraptry; ps = parapatry to sympatry.