

1 Need for mate recognition promotes avian-perceived
2 plumage sexual dichromatism in true thrushes (genus:
3 *Turdus*)

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7 **Abstract**

8 Ecological conditions limiting the time to find a compatible mate or increasing the difficulty in doing so
9 likely promote the evolution of traits used for species and mate recognition. Here, we tested this species
10 recognition hypothesis for promoting plumage sexual dichromatism in the true thrushes (*Turdus*), a large
11 and diverse genus of passerine birds. We used receptor-noise limited models of avian vision to quantify
12 avian-perceived chromatic and achromatic visual contrasts between male and female plumage patches
13 and tested the influence of breeding timing, spacing, and sympatry with other *Turdus* species on plumage
14 dimorphism. As predicted, we found that 1) true thrush species with migratory behaviour have greater
15 plumage sexual dimorphism than non-migratory species, 2) species with longer breeding seasons have less
16 sexual dichromatism, and 3) the number of *Turdus* thrush species breeding in sympatry is associated with
17 more plumage dimorphism. These results suggest that conspecific recognition systems, including species
18 and mate recognition, play a prominent role in the evolution of thrush plumage sexual dimorphism.

19 **Keywords**

20 *dichromatism, plumage, species recognition, chromatic, achromatic*

21 **Introduction**

22 Species recognition is necessary in sexually reproducing lineages for individuals to find compatible mates
23 and produce viable offspring [1,2]. Conspicuous traits signaling species and sex identity increase the
24 ease and speed of species recognition by reducing the effort, error, and time involved when searching
25 for compatible mates and lessen the likelihood of mating with heterospecifics [3]. Alternatively, traits
26 used in species and mate recognition may also serve as signals of status to conspecifics and reduce costly
27 conflicts over resources and mates [4]. Accordingly, distinct traits facilitating species-specific recognition
28 should be more likely to arise and be maintained when closely-related species are more sympatric, when

29 the time to find a breeding mate is limited, when potential mates are not encountered often, and when
30 competition for mates and resources is higher [1].

31 In birds, plumage colour is a highly conspicuous trait signaling species and (often) sex identity [5,6]
32 . Plumage sexual dichromatism, or the distinct set of differences in the appearance of male and female
33 feather colours, is common in birds and usually attributed to different natural and sexual selection pres-
34 sures on males and females [7–11]. Fundamentally, plumage sexual dichromatism results in a visibly per-
35 ceivable trait useful for recognizing an individual's species, sex, and (sometimes) age (e.g., in species with
36 sex-specific delayed plumage maturation, see [12]). Therefore, plumage sexual dichromatism reduces the
37 time and effort necessary to identify a suitable mate [13,14]. Evidence in favor of this recognition hypoth-
38 esis for sexual dichromatism includes a positive association of greater plumage sexual dichromatism with
39 migratory behaviour and shorter breeding seasons [9]. Specifically, bird species that migrate to and from
40 their breeding territories and have large geographic ranges tend to have greater plumage sexual dichro-
41 matism than species that do not migrate and have limited breeding ranges [10,15–17]. Additionally, bird
42 species that reside on mainland continents and have larger breeding ranges often have greater plumage
43 colour elaboration and sexual dichromatism than species living on islands with limited breeding ranges
44 [18–23].

45 Moreover, plumage sexual dichromatism likely plays a role in hybridization avoidance via reproductive
46 character displacement to facilitate species and mate recognition. For example, in European *Ficedula* fly-
47 catchers, female choice selects for divergent male plumage colouration across populations and species,
48 leading to character displacement and reduced rates of interspecific hybridization [24–26]. More broadly
49 and across taxa, greater plumage dichromatism is positively correlated with transitions from allopatry to
50 parapatry and increases in geographic range overlaps among passerine sister species pairs [27]. Plumage
51 sexual dichromatism has also been found to be positively associated with species richness among sister
52 species pairs, and dichromatism mainly increases through changes in male plumage [28], suggesting that
53 female choice and male-male competition lead to concurrent changes in male plumage colour and spe-
54 ciation events. Further, plumage sexual dichromatism is positively associated with greater interspecific
55 plumage colour evolution rate and divergence in *Tyrannida* suboscines [29]. Therefore, plumage sexual
56 dichromatism may be a selected trait for facilitating species and mate recognition when closely-related
57 species have sympatric breeding ranges [5,30].

58 True thrushes (genus: *Turdus*) are an exceptionally diverse genus of passerine birds consisting of about
59 ~86 species distributed across the globe (Fig. 1). Plumage sexual dimorphism and migratory behaviours
60 vary substantially between species and sexual dichromatism has evolved multiple times in thrushes across
61 the world [31,32]. Interestingly, there have been several documented cases of hybridization in *Turdus*
62 thrushes, and there is a large hybrid zone between four *Turdus* species (*T. atrogularis*, *T. eunomus*, *T. nau-*
63 *manni*, *T. ruficollis*) in north-central Asia [33], indicating that some sympatric *Turdus* species successfully
64 interbreed. Therefore, the true thrushes are an ideal passerine clade for examining the species recognition
65 hypothesis for plumage sexual dimorphism.

66 Overall, ecological conditions that increase the time and degree of difficulty in finding a suitable con-
67 specific mate should select for phenotypic traits that reliably signal species and sex identity. Taken to-

68 gether, across various bird lineages, greater plumage dichromatism is present in species that are i) migra-
 69 tory rather than nonmigratory, ii) have shorter breeding seasons, ii) live on mainlands rather than islands,
 70 iv) have larger breeding ranges (distributions), and v) breed in sympatry with more closely-related species
 71 suggests that circumstances where rapid species recognition is challenging strongly favour the evolution
 72 and maintenance of prominent plumage sexual dichromatism in birds. Here, we test these predictions of
 73 the species recognition hypothesis for sexually-dimorphic avian plumage. To this end, we evaluate the
 74 potential influences of breeding timing, spacing, and sympatry on plumage dichromatism in the *Turdus*
 75 thrushes.

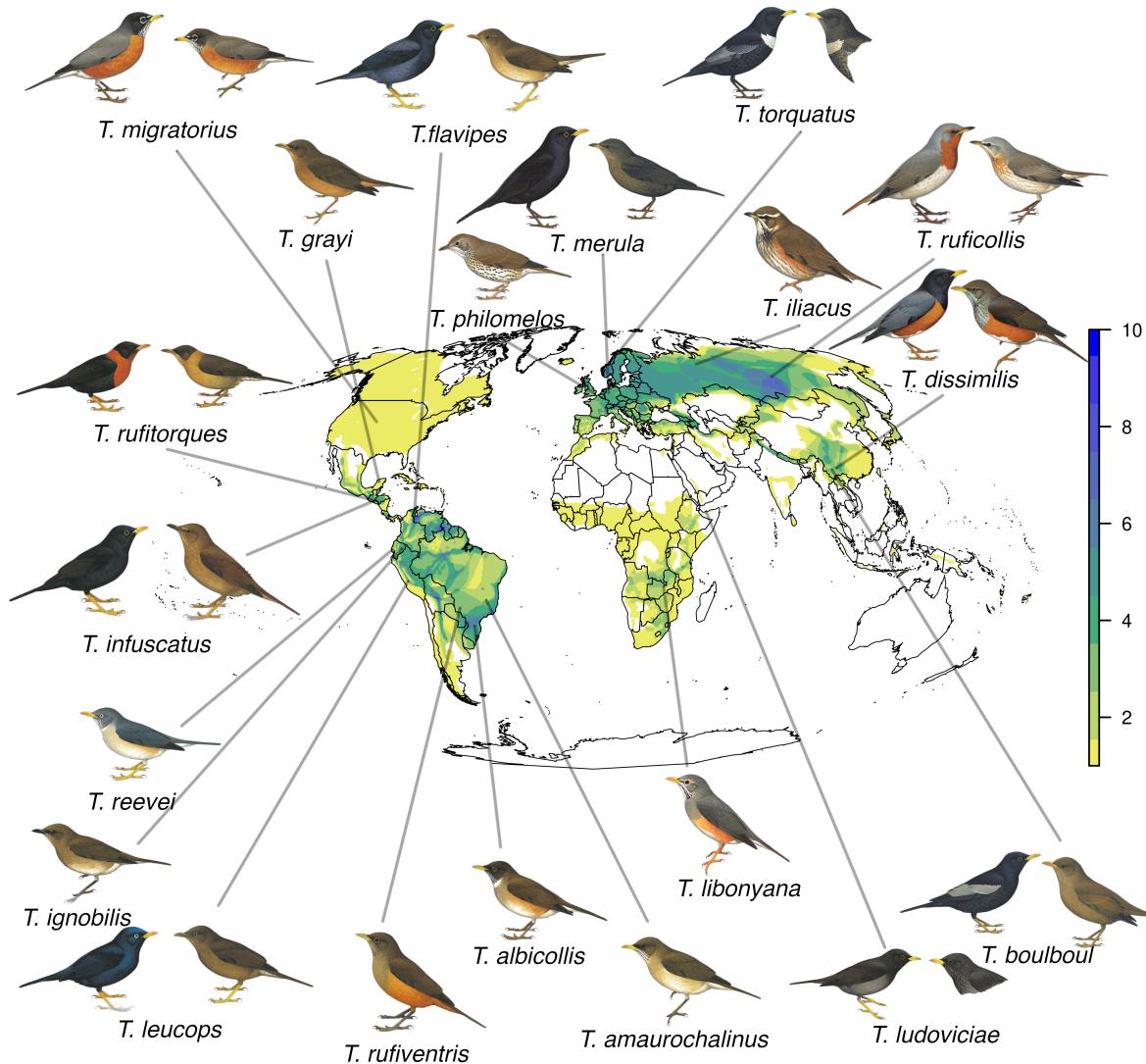


Figure 1: Breeding ranges of all recognized *Turdus* species from BirdLife International. Colors indicate the number of *Turdus* thrush species in sympatry with overlapping breeding ranges. Illustrations © HBW Alive/Lynx Edicions

76 Methods

77 Initial pre-registration of the study's methods and analyses are available on [Open Science Framework](#).

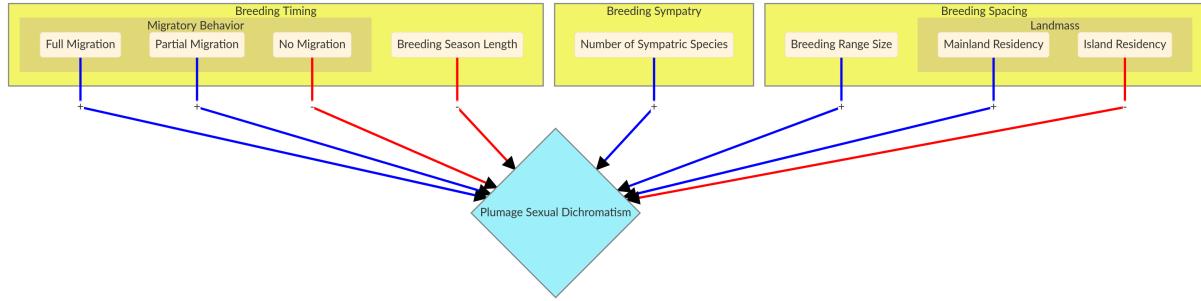


Figure 2: Hypotheses and predictions for each model. Arrow colours indicate predicted correlation, positive (blue) and negative (red).

78 **Plumage sexual dichromatism**

79 A total of N=77 *Turdus* thrush species (approximately ~89% of all known true thrush species) were sam-
 80 pled for plumage spectral reflectance using prepared bird skin specimens at the American Museum of
 81 Natural History in New York City and the Field Museum in Chicago. Reflectance measurements spanning
 82 300-700nm were taken in triplicate from the belly, breast, throat, crown and mantle plumage patches [34]
 83 of each individual. N=3 male and N=3 female individuals were measured for most species (exceptions: *T.*
 84 *lawrencii*, N=2 males and N=2 females; *T. swalesi*, N=1 male and N=1 female). Reflectance spectra were
 85 measured using a 400 μm fiber optic reflection probe fitted with a rubber stopper to maintain a consis-
 86 tent measuring distance of 3 mm and area of 2 mm^2 at a 90° angle to the surface of the feather patch.
 87 Measurements were taken using a JAZ spectrometer with a pulsed-xenon light source (Ocean Optics,
 88 Dunedin, USA) and we used a diffuse 99% reflectance white standard (Spectralon WS-1-SL, Labsphere,
 89 North Sutton NH, USA).

90 We applied a receptor-noise limited visual model [35] of the European Blackbird (*T. merula*) visual sys-
 91 tem [36] in the *pavo* [37] package in R v4.0.0 [38] to calculate avian-perceived chromatic and achromatic
 92 visual contrast (in units of “Just-Noticeable Differences”, or JNDs) of male vs. female plumage patches for
 93 all sampled *Turdus* species. Chromatic and achromatic JNDs were calculated for male-female pairs within
 94 each species (i.e., N=9 JND values calculated per patch for each species where N=3 males and N=3 fe-
 95 males sampled), and then JND values were averaged for each species’ respective plumage patches. Under
 96 ideal laboratory conditions, 1 JND is generally considered to be the discriminable threshold past which
 97 an observer is predicted to be able to perceive the two colors as different. However, natural light envi-
 98 ronments vary both spatially and temporally [39], bringing into question the accuracy of a 1 JND thresh-
 99 old for generalizing visual contrast under natural conditions. Therefore, we calculated the total number
 100 of sexually-dichromatic plumage patches per species (out of N=5 measured patches) as the number of
 101 plumage patches with average JND values > 1, 2, or 3 to account for uncertainty in visual discrimination
 102 thresholds due to variation in psychophysical and ambient lighting conditions affecting the strength of
 103 between-sex plumage visual contrast [40]. Additionally, we modeled the number of divergent plumage
 104 patches (JND >1, 2, and 3) within sexes and between different sympatric species under different levels
 105 of breeding range overlap (10% increments between 0-90%).

106 **Life History Data**

107 **Breeding Timing Model**

108 We collected data on migration behaviour and breeding season length from *Thrushes* [31] and the *Hand-
109 book of the Birds of the World* [41]. We assigned three different kinds of migratory behaviour: 1) *full
110 migration* when a species description clearly stated that a species “migrates”, 2) *partial migration* when a
111 species was described to have “altitudinal migration”, “latitudinal migration” or “movement during non-
112 breeding season”, or 3) *sedentary* when a species was described as “resident” or “sedentary”. Breeding
113 season length was defined as the number of months the species breeds each year.

114 **Breeding Sympatry Model**

115 Species’ breeding ranges were acquired from *BirdLife International* [42]. We calculated congener breeding
116 range overlaps (as percentages) using the *letsR* package in R [43]. We then calculated the number of sym-
117 patric species as the number of congeners with breeding ranges that overlap >30% with the focal species’
118 breeding range [27]. Comparisons of the number of sexually-dimorphic plumage patches vs. the number
119 of sympatric species among different breeding range overlap thresholds are provided in Supplementary
120 Figure 2.

121 **Breeding Spacing Model**

122 Species’ breeding range sizes (in km²) were acquired using the *BirdLife International* breeding range maps.
123 Species’ island vs. mainland residence was also determined using breeding ranges from *BirdLife Interna-
124 tional*. Mainland residence was assigned if the species had a breeding range on any continent and Japan.
125 Island residence was assigned to species having a breeding range limited to a non-continental landmass
126 entirely surrounded by an oceanic body of water.

127 **Statistical modeling**

128 We used phylogenetically-corrected Bayesian multilevel logistic regression models using the *brms* v2.13.0
129 package [44] in R v4.0.0 [38] where responses, the number of sexually-dichromatic patches >1, 2, and
130 3 chromatic and achromatic JNDs, were modelled as binomial trials (N=5 plumage patch “trials”) to test
131 for associations with breeding timing, breeding sympathy and breeding spacing. For all phylogenetically-
132 corrected models, we used the *Turdus* phylogeny from Nylander et al. (2008) [45] to create a covariance
133 matrix of species’ phylogenetic relationships. All models used a dataset of N=67 out of the *Turdus* species
134 for which all the types of data (see above) were available.

135 Our *breeding timing* models included the following predictors: z-scores of breeding season length
136 (mean-centered by $\mu = 5.4$ months, and scaled by one standard deviation $\sigma = 2.3$ months), migratory
137 behaviour (no migration as the reference category versus partial or full migration), and their interaction.
138 *Breeding sympathy* models included the number of sympatric species with greater than 30% breeding range
139 overlap as the only predictor of the probability of having a sexually-dichromatic plumage patch. *Breeding*

spacing models included \log_e transformed breeding range size (km²) and breeding landmass (mainland as the reference category versus island). We also ran null models (intercept only) for all responses. All models' intercepts and response standard deviations were assigned a weak prior (Student T: df = 3, location = 0, scale = 10), and predictor coefficients were assigned flat priors. We ran each model for 6,000 iterations across 6 chains and assessed Markov Chain Monte Carlo (MCMC) convergence using the Gelman-Rubin diagnostic (Rhat) [46]. We then performed k-fold cross-validation [47] to refit each model K=16 times. For each k-fold, the training dataset included a randomly selected set of $N - N \frac{1}{K}$ or $N \approx 63$ species, and the testing dataset included $N \frac{1}{K}$ or $N \approx 4$ species not included in the training dataset. Finally, we compared differences between the models' expected log pointwise predictive densities (ELPD) to assess which model(s) best predicted the probability of having a sexually-dichromatic plumage patch. [47].

Models' predictor effects were assessed using 90% highest-density intervals of the posterior distributions and probability of direction, the proportion of the posterior distribution that shares the same sign (positive or negative) as the posterior median [48], to provide estimates of the probability of that a predictor has an entirely positive or negative effect on the presence of sexually-dimorphic plumage patches. We assume predictor estimates with a probability of direction ≥ 0.90 to be indicative of a true existence of a predictor's effect on sexually-dimorphic plumage patches [48].

Results

Avian visual modeling

Among $N=77$ *Turdus* species, the following proportion have sexually monomorphic plumage (combined achromatic and chromatic JND thresholds): 1.3% ($n=1$ species) have no sexually-dimorphic patches > 1 JND, 44% ($n=34$ species) have no dimorphic patches > 2 JND, and 63% ($n=49$ species) have no dimorphic patches > 3 JND (Table S1). Conversely, 98.7% ($n=78$ species) have at least one sexually-dimorphic plumage patch > 1 JND, 56% ($n=43$ species) have at least one plumage patch > 2 JND, and 37% ($n=28$ species) have at least one patch > 3 JND (Table S1). Additional proportions of *Turdus* species with sexually-dimorphic achromatic or chromatic plumage patches are available in Table S2. When comparing within sexes between sympatric species (i.e., at least a 30% overlap in breeding ranges: $n=39$ species with at least one sympatric species and a median of $n=6$ sympatric species per focal species), the median number of avian-discriminable plumage patches between species is 1 or greater for all achromatic and chromatic JND thresholds except for sympatric females at a chromatic JND threshold > 3 (Fig. S1).

Model comparisons

We obtained $N \geq 4000$ effective posterior samples for each model parameter and all models' Markov Chains (MCMC) successfully converged (Rhat = 1 for all models' parameters) (Supplementary Figure 3, 4). All *breeding sympathy*, *breeding timing*, and *breeding spacing* models performed similarly well and substantially better than *intercept only* models in predicting the probability of having a sexually-dimorphic plumage patch with achromatic JND values > 1 , 2, or 3 (Table 1; all models predicting achromatic plumage

175 patches had ELPD values within 4, following the convention of Burnham and Anderson (2002)[49]).
176 Among models predicting the probability of having a sexually-dichromatic plumage patch with chromatic
177 JND values >1, 2, or 3, all *breeding sympatry*, *breeding timing*, and *breeding spacing* models performed much
178 better than *intercept only* models, and *breeding sympatry* models had the top predictive performance (Ta-
179 ble 1; *breeding sympatry* models all have ELPD =0, only the *breeding spacing* models predicting dichromatic
180 plumage patches with had similar predictive performance).

181 **Achromatic plumage sexual dimorphism predictors**

182 All model predictors' effect estimates are provided as the posterior median odds-ratio (OR) and 90%
183 highest-density interval (HDI) in Table 2. Among predictors of achromatic sexually-dimorphic plumage
184 patches, only predictors included in the *breeding timing* model have predictors with probability of direction
185 (*pd*) values ≥ 0.90 (Table 2). Specifically, longer breeding season length was associated with lower odds of
186 a species having a sexually-dimorphic plumage patch with achromatic JND > 2 (breeding season length,
187 OR [90% HDI] = 0.10 [0.01, 1.1], 89.5% decrease in odds per 2.3-month increase in breeding season) and
188 JND > 3 (breeding season length, OR [90% HDI] = 0.25 [0.03, 1.5], 75% decrease in odds per 2.3-month
189 increase in breeding season). Additionally, full migratory behaviour, rather than no migratory behaviour,
190 was associated with greater odds of a species having a sexually-dimorphic plumage patch with achromatic
191 JND > 1 (full migration, OR [90% HDI] = 4.97 [0.95, 24.4]), JND > 2 (full migration, OR [90% HDI] = 66.5
192 [3.2, 1802.4]) and JND > 3 (OR [90% HDI] = 22.3 [1.6, 307.9]). Finally, both full and partial migratory
193 behaviour, rather than no migration behaviour, in conjunction with longer breeding season lengths are
194 associated with greater odds of a species having a sexually-dimorphic plumage patch with achromatic
195 JND > 1 (breeding season length x full migration, OR [90% HDI] = 4.84 [0.67, 39.6]), JND > 2 (breeding
196 season length x full migration, OR = 66.3 [0.59, 11415.7]; breeding season length x partial migration, OR
197 [90% HDI] = 20.7 [0.9, 589.1]) and JND > 3 (breeding season length x partial migration, OR [90% HDI] =
198 8.28 [0.76, 109.1]).

199 **Chromatic plumage sexual dimorphism predictors**

200 Among predictors of *breeding timing* models predicting chromatic sexually-dimorphic plumage patches,
201 longer breeding season length was associated with lower odds of a species having a plumage patch with
202 chromatic JND > 2 (OR [90% HDI] = 0.14 [0.01, 1.42], 86% reduction in odds per 2.3 month increase in
203 breeding season), and both full and partial migratory behaviour rather than no migration are associated
204 with greater odds of a species having a plumage patch JND > 1 (partial migration, OR [90% HDI] = 2.2
205 [0.94, 4.9]), JND > 2 (full migration, OR [90% HDI] = 80.51 [2.8, 3432.9]) and JND > 3 (partial migration,
206 OR [90% HDI] = 71.2 [0.32, 59062.9]; full migration, OR [90% HDI] = 234.7 [0.51, 300382.6]). For
207 *breeding spacing models*, island residency rather than mainland residency was associated with lower odds
208 of having a plumage patch > 1 chromatic JND (island, OR [90% HDI] = 0.27 [0.09, 0.89]). Finally, more
209 *Turdus* species in sympatry was associated with higher odds of a species having a chromatic plumage
210 patch with JND > 1 (number of sympatric species, OR [90% HDI] = 1.4 [1.18, 1.67], 40% increase in odds

per each additional sympatric species), JND > 2 (sympatric species, OR [90% HDI] = 1.59 [1.01, 2.52],
 59% increase in odds per each additional sympatric species), and JND > 3 (sympatric species, OR [90%
 HDI] = 2.11 [1.03, 4.46], 111% increase in odds per each additional sympatric species).

Table 1: Expected log pointwise predictive densities (ELPD) differences and kfold information criterion values of models (ELPD Difference \pm standard error (kfold IC \pm standard error)). Values closest to zero indicate greater model prediction performance.

Plumage Metric	JND Threshold	Model			
		Breeding Sympatry	Breeding Timing	Breeding Spacing	Intercept Only
Achromatic					
	1 JND	0 \pm 0 (-122.17 \pm 0.67)	-2.51 \pm 2.49 (-124.68 \pm 2.38)	-2.59 \pm 1.01 (-124.76 \pm 1.04)	-21.69 \pm 7.36 (-143.87 \pm 7.51)
	2 JND	0 \pm 0 (-98.94 \pm 7.56)	-1.19 \pm 3.95 (-100.13 \pm 9.22)	-0.7 \pm 1.34 (-99.64 \pm 7.92)	-52.42 \pm 12.67 (-151.36 \pm 13.4)
	3 JND	-0.04 \pm 1.4 (-85.4 \pm 8.91)	-1.7 \pm 4.41 (-87.07 \pm 10.71)	0 \pm 0 (-85.37 \pm 8.76)	-28.54 \pm 10.02 (-113.91 \pm 13.65)
Chromatic					
	1 JND	0 \pm 0 (-115.75 \pm 2.95)	-5.67 \pm 3.55 (-121.42 \pm 2.28)	-2.73 \pm 3.4 (-118.49 \pm 2.67)	-14.8 \pm 7.22 (-130.55 \pm 7.05)
	2 JND	0 \pm 0 (-88.47 \pm 8.77)	-3.8 \pm 4.46 (-92.27 \pm 10.01)	-3.32 \pm 5.29 (-91.79 \pm 10.91)	-50.53 \pm 14.49 (-139 \pm 16.77)
	3 JND	0 \pm 0 (-62.77 \pm 10.41)	-8 \pm 4.32 (-70.77 \pm 12.29)	-4.43 \pm 3.9 (-67.2 \pm 11.72)	-47.63 \pm 15.34 (-110.4 \pm 20.01)

Table 2: Model predictor effect estimates (posterior median odds ratio and 90% highest-density interval) on the presence of a plumage patch with achromatic or chromatic visual contrast values > 1 , 2, and 3 JND. Model effects with a probability of direction (pd) value ≥ 0.90 are bolded in **red** for a negative effect and **blue** for a positive effect on plumage dichromatism. Phylogenetic signal (λ) for each model is provided as the median and 90% credible interval of the intraclass correlation coefficient among species.

Model	Parameter	Achromatic, JND > 1	Achromatic, JND > 2	Achromatic, JND > 3	Chromatic, JND > 1	Chromatic, JND > 2	Chromatic, JND > 3
Breeding Timing							
	Intercept	0 (0, 0.54), pd = 0.98	0 (0, 0.19), pd = 0.99	0 (0, 0.19), pd = 0.99	0.41 (0.05, 2.79), pd = 0.78	0 (0, 1.73), pd = 0.95	0 (0, 1.37), pd = 0.96
	Breeding Season Length	0.1 (0.01, 1.05), pd = 0.97	0.25 (0.03, 1.49), pd = 0.91	0.25 (0.03, 1.49), pd = 0.91	0.89 (0.56, 1.4), pd = 0.66	0.14 (0.01, 1.42), pd = 0.94	0.08 (0, 9.14), pd = 0.83
	Partial Migration vs. No Migration	0.56 (0.31, 2.75), pd = 0.53	4.11 (0.3, 61.54), pd = 0.83	3.65 (0.44, 33.64), pd = 0.85	2.2 (0.24, 4.89), pd = 0.94	6.7 (0.42, 134.8), pd = 0.88	71.16 (0.32, 59062.92), pd = 0.92
	Full Migration vs. No Migration	4.37 (0.95, 24.41), pd = 0.96	66.52 (3.19, 1802.4), pd = 0.99	22.34 (1.59, 307.9), pd = 0.98	2.29 (0.69, 7.31), pd = 0.88	80.31 (2.81, 343.86), pd = 0.99	234.71 (0.51, 200382.62), pd = 0.95
	Breeding Season Length x Partial Migration	1.34 (0.48, 3.92), pd = 0.68	20.71 (0.87, 589.09), pd = 0.96	8.28 (0.76, 109.11), pd = 0.94	1.39 (0.65, 31.32), pd = 0.76	9.03 (0.44, 251.36), pd = 0.9	34.46 (0.08, 68228.71), pd = 0.85
	Breeding Season Length x Full Migration	4.34 (0.67, 39.63), pd = 0.9	66.3 (0.59, 11415.7), pd = 0.93	16.41 (0.27, 824.69), pd = 0.89	1.68 (0.31, 8.33), pd = 0.7	160.6 (0.84, 67791.13), pd = 0.95	433.67 (0.01, 371945.69), pd = 0.85
	Phylogenetic Signal λ , Median (90% Credible Interval)	0.29 (0.16, 0.43)	0.72 (0.56, 0.86)	0.61 (0.42, 0.8)	0.17 (0.08, 0.28)	0.74 (0.57, 0.88)	0.89 (0.77, 0.97)
Breeding Spacing							
	Intercept	0 (0, 2.44), pd = 0.95	0 (0, 0.14), pd = 0.98	0 (0, 0.14), pd = 0.98	0.51 (0.03, 9.7), pd = 0.65	0 (0, 7.63), pd = 0.92	0 (0, 8.19), pd = 0.91
	Island vs. Mainland	1.08 (0.25, 4.79), pd = 0.54	0.53 (0.01, 17.83), pd = 0.61	0.92 (0.05, 19.32), pd = 0.52	0.27 (0.09, 0.89), pd = 0.97	0.03 (0, 3.99), pd = 0.89	0.04 (0, 67.59), pd = 0.77
	Breeding Range Size	1.08 (0.88, 1.32), pd = 0.75	1.23 (0.76, 2.01), pd = 0.77	1.3 (0.87, 1.93), pd = 0.87	1.02 (0.87, 1.19), pd = 0.58	1.24 (0.75, 2.05), pd = 0.77	1.26 (0.54, 2.99), pd = 0.69
	Phylogenetic Signal λ , Median (90% Credible Interval)	0.27 (0.15, 0.41)	0.71 (0.56, 0.85)	0.6 (0.42, 0.77)	0.15 (0.07, 0.25)	0.72 (0.55, 0.86)	0.85 (0.71, 0.95)
Breeding Sympatry							
	Intercept	0.41 (0.03, 5.83), pd = 0.72	0 (0, 0.98), pd = 0.95	0 (0, 0.34), pd = 0.98	0.25 (0.04, 1.35), pd = 0.91	0 (0, 1.12), pd = 0.95	0 (0, 0.29), pd = 0.98
	Number of Sympatric Species ($\geq 30\%$ Breeding Range Overlap)	1.03 (0.84, 1.27), pd = 0.61	1.15 (0.74, 1.75), pd = 0.71	1.13 (0.76, 1.63), pd = 0.71	1.4 (1.18, 1.67), pd = 0.99	1.59 (1.01, 2.52), pd = 0.96	2.11 (1.03, 4.46), pd = 0.97
	Phylogenetic Signal λ , Median (90% Credible Interval)	0.26 (0.14, 0.39)	0.7 (0.54, 0.83)	0.59 (0.41, 0.77)	0.13 (0.06, 0.23)	0.69 (0.52, 0.83)	0.82 (0.67, 0.94)

214 **Discussion**

215 Our results provide comparative correlative evidence in support of predictions of the species recognition
216 hypothesis for plumage sexual dimorphism in true thrushes. We used a receptor-noise limited model of
217 *Turdus merula* vision [35,36] to measure avian-perceivable visual contrast of plumage colours and found
218 that the odds of plumage sexual dimorphism are much greater for *Turdus* thrush species that have full or
219 partial migration rather than no migration, have relatively short breeding seasons, and are in sympatry
220 with many other true thrush species (Table 1,2). Our results align with prior comparative studies of avian
221 plumage sexual dimorphism where strong associations of sexual dichromatism with greater migratory
222 behaviour [10] and more sympatric taxa [27] were found among many species of different passerine
223 families.

224 Further, we determined that sympatric *Turdus* species have distinguishable plumage colouration dif-
225 ferences from one another when measuring plumage appearance from the avian visual perspective (Fig.
226 S1). Therefore, plumage sexual dichromatism may have evolved to facilitate species and mate recognition
227 in species breeding under greater sympatry with other true thrushes. However, we cannot directly deter-
228 mine here if plumage sexual dimorphism in sympatric *Turdus* species is the result of reproductive character
229 displacement. Namely, we do not know if past changes in species' plumage sexual dimorphism occurred
230 before or during periods of sympatry with other *Turdus* species. Regardless, present-day plumage sexual
231 dimorphism and perceivable differences in plumage colouration between sympatric species likely reduces
232 the challenge of finding compatible mates.

233 Previous studies have found that closely-related sympatric species tend to have more similar plumage
234 appearance than expected if plumage colouration patterns had evolved to facilitate species recognition
235 via reproductive character displacement [50,51]. The potential lack of major plumage colour divergence
236 among closely-related sympatric species may be attributable to constraints imposed by a shared light en-
237 vironment on colour signal efficiency [52], or similar natural selection pressures (e.g., predators, parasites,
238 and weather). Generally, despite greater similarity in plumage appearance in comparison to allopatric
239 species, closely-related sympatric species can still have substantially different and biologically-relevant
240 differences in achromatic or chromatic interspecific visual contrast of plumage patches when measuring
241 plumage colouration differences from the avian visual perspective (as we have found in our analyses).

242 **Conclusions**

243 Patterns of plumage sexual dimorphism in true thrushes (*Turdus*) are consistent with select predictions
244 of the species recognition hypothesis for plumage sexual dimorphism. Migratory behaviour and limited
245 breeding seasons reduce the amount of time available to find a mate, and greater plumage sexual dimor-
246 phism may help migratory species find compatible mates more rapidly. Greater plumage sexual dimor-
247 phism in *Turdus* species under sympatry with other true thrush species also supports the possibility that
248 increased plumage sexual dichromatism may be the result of reproductive character displacement. There-
249 fore, greater plumage sexual dimorphism likely reduces species recognition errors and hybridization.

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