

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

4

5 **Abstract**

6 Ecological conditions limiting the time to find a compatible mate or increasing the difficulty in doing so
7 likely promote the evolution of traits used for species and mate recognition. Conspicuous traits that
8 signal an individual's species, sex, and breeding status reduce the challenge of identifying a compati-
9 ble conspecific mate, and should be more common in migratory rather than sedentary species, species
10 with shorter breeding seasons, and species breeding under high sympatry with many closely-related het-
11 erospecifics. Here, we tested this recognition hypothesis for promoting plumage sexual dichromatism
12 in the true thrushes (*Turdus* spp.), a large and diverse genus of passerine birds. We used receptor-noise
13 limited models of avian vision to quantify avian-perceived chromatic and achromatic visual contrasts
14 between male and female plumage patches and tested the influence of breeding season length, spatial
15 distribution, and sympatry with other *Turdus* species on plumage dichromatism. As predicted, we found
16 that 1) true thrush species with migratory behaviour have greater plumage sexual dichromatism than
17 non-migratory species, 2) species with longer breeding seasons have less plumage sexual dichromatism,
18 and 3) greater numbers of *Turdus* thrush species breeding in sympatry is associated with more plumage
19 sexual dichromatism. These results suggest that social recognition systems, including species and mate
20 recognition, play a prominent role in the evolution of plumage sexual dichromatism in true thrushes.

21 **Keywords**

22 *achromatic, chromatic, dichromatism, plumage, mate recognition*

23 **Introduction**

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

30 arise and be maintained under conditions that increase both the difficulty of finding a compatible mate
31 and degree of resource competition among conspecifics and closely-related species. Conditions likely to
32 favour traits signaling individuals' species, sex, and breeding status include higher sympatry with many
33 closely-related species, limited time to find compatible breeding mates, and lower rates of encounter with
34 potential breeding mates [1].

35 In birds, plumage colour is a highly conspicuous trait signaling species and (often) sex identity [5,6].
36 Plumage sexual dichromatism, or the distinct set of differences in the appearance of male and female
37 feather colours and patterns, is common in birds and is usually attributed to different natural and sex-
38 ual selection pressures on males and females [7–11]. Plumage sexual dichromatism results in a visibly
39 perceivable trait useful for recognizing an individual's species, sex, and breeding status (e.g., in species
40 with sex-specific delayed plumage maturation, see [12]), reducing the time and effort expended to iden-
41 tify a suitable mate [13,14]. Evidence in favour of this recognition hypothesis for sexual dichromatism in
42 birds includes a positive association of greater plumage sexual dichromatism with migratory behaviour
43 and shorter breeding seasons [9], both of which reduce the amount of time available to search and find
44 suitable mates and successfully breed. Additional support for the recognition hypothesis includes a con-
45 sistent pattern of greater plumage sexual dichromatism and plumage colour elaboration in avian species
46 that reside on mainland continents and have large geographic ranges in comparison to species that do
47 not migrate, reside on islands, and have limited breeding ranges [10,15–23].

48 Moreover, plumage sexual dichromatism likely plays a role in hybridization avoidance via reproduc-
49 tive character displacement to facilitate species and mate recognition, especially among closely-related
50 species. For example, in *Ficedula* flycatchers, female choice selects for divergent male plumage coloura-
51 tion across populations and species, leading to male character displacement and reduced rates of in-
52 terspecific hybridization [24–26]. More broadly and across taxa, greater plumage dichromatism is posi-
53 tively associated with higher breeding sympathy with closely-related heterospecifics. Among a large sam-
54 ple of passerine sister species pairs, transitions from allopatry to parapatry and increases in geographic
55 range overlaps are positively correlated with greater plumage dichromatism [27]. Greater plumage sexual
56 dichromatism has also been found to be positively associated with greater avian species divergence and
57 richness [28,29]. Among passerine sister species pairs, more pronounced changes in male rather than
58 female plumage colouration in sexually-dichromatic species suggest that female choice and male-male
59 competition often lead to concurrent increases in sexual dichromatism and speciation events [28]. There-
60 fore, plumage sexual dichromatism may be a selected trait for facilitating species and mate recognition
61 when closely-related species have sympatric breeding ranges [5,30].

62 True thrushes (*Turdus* spp.) are an exceptionally diverse monophyletic genus of passerine birds con-
63 sisting of about ~86 species distributed across the globe (Fig. 1). The true thrushes are an ideal passerine
64 clade for examining the recognition hypothesis for plumage sexual dichromatism because plumage sexual
65 dichromatism and migratory behaviours vary substantially between species and sexual dichromatism has
66 evolved multiple times in thrushes across the world [31,32]. Hybridization also occurs in some, but not
67 all, *Turdus* species, indicating that some sympatric *Turdus* species can successfully interbreed. A partic-
68 ular well-documented example of hybridization in true thrushes occurs at large hybrid zone between

69 four *Turdus* species (*T. atrogularis*, *T. eunomus*, *T. naumanni*, *T. ruficollis*) in north-central Asia [33]. Fur-
70 ther, plumage sexual dichromatism in true thrushes often coincides with age and breeding status in male
71 thrushes. Delayed plumage maturation in males is common among true thrushes [34–36], where males
72 have “female-like” plumage colouration during their first breeding season and develop typical breeding
73 adult male plumage for subsequent breeding seasons. The presence of delayed plumage maturation and
74 distinct juvenal plumage may serve as a signal of a young male’s sexual immaturity in order to reduce
75 levels conspecific aggression from older adults [36] and also suggests that female thrushes prefer older
76 males with prominent adult plumage as breeding mates.

77 Overall, ecological conditions that increase the time and degree of difficulty in finding a suitable con-
78 specific mate should select for phenotypic traits that reliably signal species and sex identity. Across
79 various bird lineages, greater plumage dichromatism is present in species that are i) migratory rather than
80 nonmigratory, ii) have shorter breeding seasons, iii) live on mainlands rather than islands, iv) have larger
81 breeding ranges (distributions), and v) breed in sympatry with more closely-related species. These pat-
82 terns suggest that ecological circumstances where rapid and accurate mate recognition is challenging
83 strongly favour the evolution and maintenance of prominent plumage sexual dichromatism in birds. Here,
84 we test these predictions of the recognition hypothesis for plumage sexual dichromatism by evaluating
85 the potential influences of breeding timing, spacing, and sympatry on plumage dichromatism in *Turdus*
86 thrushes (Fig. 2).

87 Methods

88 Plumage sexual dichromatism

89 A total of N=77 *Turdus* thrush species (approximately ~89% of all known true thrush species) were sam-
90 pled for plumage spectral reflectance using prepared bird skin specimens at the American Museum of
91 Natural History in New York City and the Field Museum in Chicago, USA. Reflectance measurements
92 spanning 300-700nm were taken in triplicate from the belly, breast, throat, crown, and mantle plumage
93 patches [37] of each individual. N=3 male and N=3 female individuals were measured for most species
94 (exceptions: *T. lawrencii*, N=2 males and N=2 females; *T. swalesi*, N=1 male and N=1 female). Reflectance
95 spectra were measured using a 400 µm fiber optic reflection probe fitted with a rubber stopper to main-
96 tain a consistent measuring distance of 3 mm and area of 2 mm² at a 90° angle to the surface of the
97 feather patch. Measurements were taken using a JAZ spectrometer with a pulsed-xenon light source
98 (Ocean Optics, Dunedin, USA) and we used a diffuse 99% reflectance white standard (Spectralon WS-1-
99 SL, Labsphere, North Sutton NH, USA).

100 We applied a receptor-noise limited visual model [38] of the European Blackbird (*T. merula*) visual sys-
101 tem [39] in the *pavo* [40] package in R v4.0.0 [41] to calculate avian-perceived chromatic and achromatic
102 visual contrast (in units of “Just-Noticeable Differences”, or JNDs) of male vs. female plumage patches for
103 all sampled *Turdus* species. Chromatic and achromatic JNDs were calculated for male-female pairs within
104 each species (i.e., N=9 JND values calculated per patch for each species where N=3 males and N=3 fe-

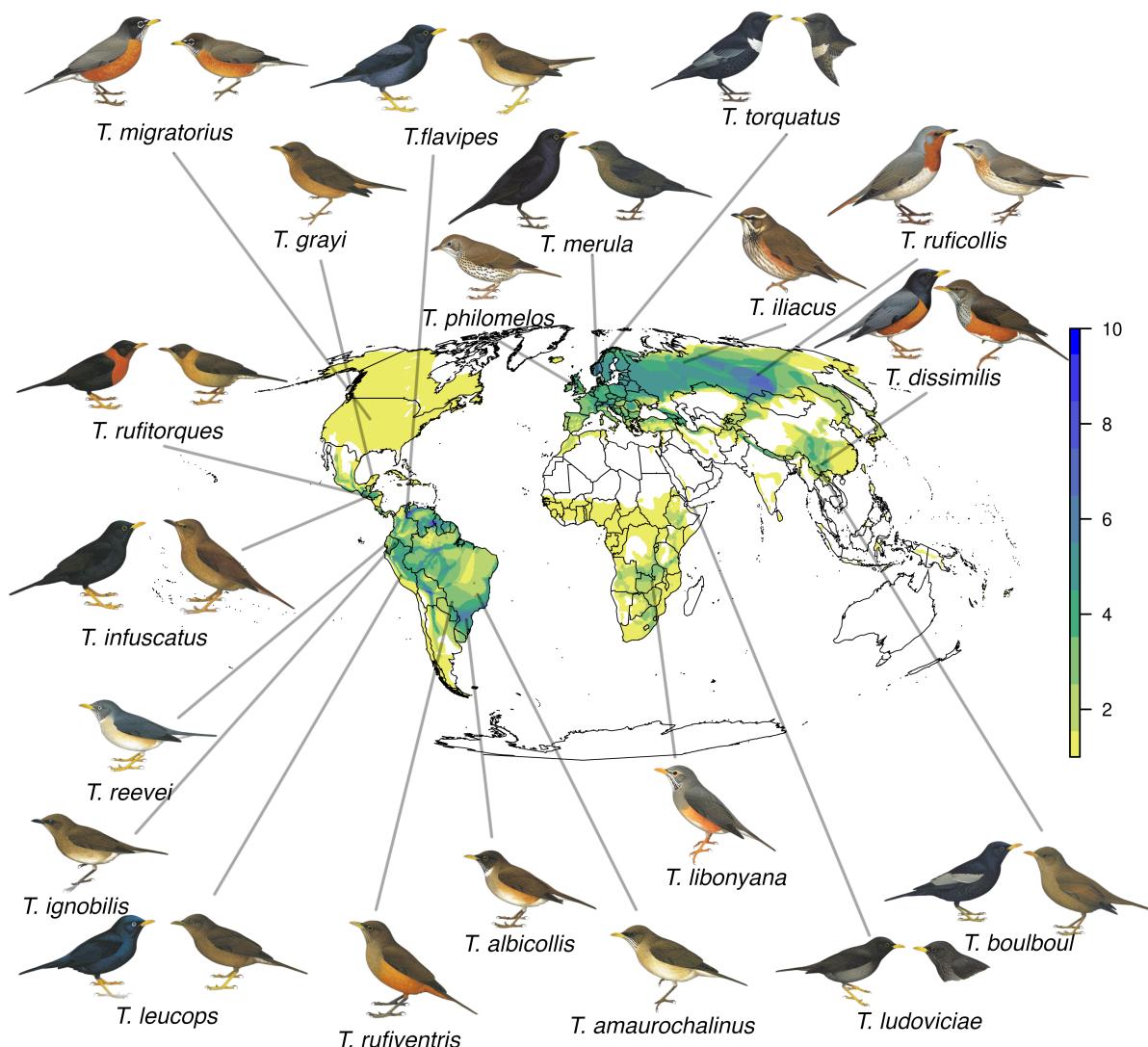


Figure 1: Breeding ranges of all recognized *Turdus* species from BirdLife International, with representative species' males and females shown for species with plumage sexual dichromatism. The color scale indicates the number of *Turdus* thrush species in sympatry with overlapping breeding ranges. Illustrations used with permission from HBW Alive/Lynx Edicions

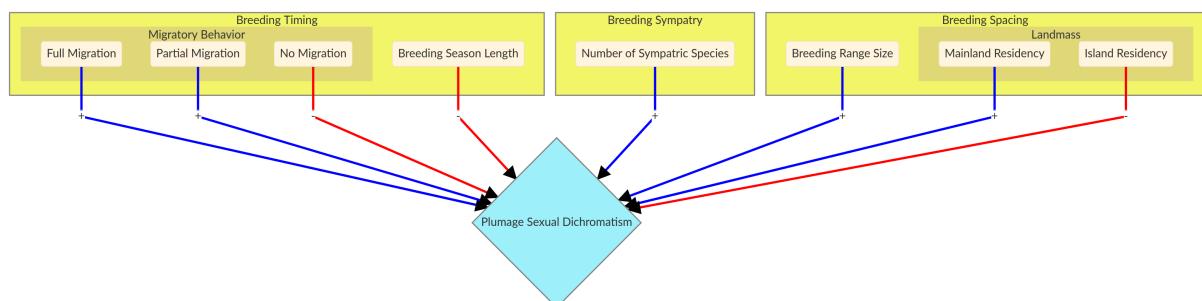


Figure 2: Hypotheses and predictions for each model (large yellow boxes). Arrow colours indicate predicted correlation, positive (blue) and negative (red)

105 males sampled), and then JND values were averaged for each species' respective plumage patches. Under
106 ideal laboratory conditions, 1 JND is generally considered to be the discriminable threshold past which
107 an observer is predicted to be able to perceive the two colours as different. However, natural light envi-
108 ronments vary both spatially and temporally [42], bringing into question the accuracy of a 1 JND thresh-
109 old for generalizing visual contrast under natural conditions. Therefore, we calculated the total number
110 of sexually-dichromatic plumage patches per species (out of N=5 measured patches) as the number of
111 plumage patches with average JND values > 1, 2, or 3 to account for uncertainty in visual discrimination
112 thresholds due to variation in psychophysical and ambient lighting conditions affecting the strength of
113 between-sex plumage visual contrast [43]. Additionally, we modeled the number of divergent plumage
114 patches (at the three different JND thresholds listed above) within sexes and between different sympatric
115 species under different levels of breeding range overlap (10% increments between 0-90%; Fig. S1).

116 **Life History Data**

117 **Breeding Timing Model**

118 We collected data on migration behaviour and breeding season length from *Thrushes* [31] and the Hand-
119 book of the Birds of the World [44]. We assigned three different kinds of migratory behaviour: 1) full
120 migration when a species description clearly stated that a species "migrates", 2) partial migration when a
121 species was described to have "altitudinal migration", "latitudinal migration" or "movement during non-
122 breeding season", or 3) sedentary when a species was described as "resident" or "sedentary". Breeding
123 season length was defined as the number of months the species breeds each year.

124 **Breeding Sympatry Model**

125 Species' breeding ranges were acquired from *BirdLife International* [45]. We calculated congener breeding
126 range overlaps (as percentages) using the *letsR* package in R [46]. We then calculated the number of sym-
127 patric species as the number of congeners with breeding ranges that overlap >30% with the focal species'
128 breeding range [27]. Comparisons of the number of sexually-dimorphic plumage patches vs. the number
129 of sympatric species among different breeding range overlap thresholds are provided in Supplementary
130 Figure 2.

131 **Breeding Spacing Model**

132 Species' breeding range sizes (in km²) were acquired using the *BirdLife International* breeding range maps.
133 Species' island vs. mainland residence was also determined using breeding ranges from *BirdLife Interna-*
134 *tional*. Mainland residence was assigned if the species had a breeding range on any continent and Japan.
135 Island residence was assigned to species having a breeding range limited to a non-continental landmass
136 entirely surrounded by a marine body of water.

137 **Statistical modeling**

138 We used phylogenetically-corrected Bayesian multilevel logistic regression models using the *brms* v2.13.0
139 package [47] in R v4.0.0 [41]. We modeled plumage sexual dichromatism responses as the number of
140 sexually-dichromatic patches > 1, 2, or 3 chromatic and achromatic JNDs. Plumage dichromatism re-
141 sponses were modeled as binomial trials (N=5 plumage patch “trials”) to test for associations with breed-
142 ing timing, breeding sympatry and breeding spacing. For all phylogenetically-corrected models, we used
143 the *Turdus* molecular phylogeny from Nylander et al. (2008) [48] to create a covariance matrix of species’
144 phylogenetic relationships. All models used a dataset of N=67 out of the *Turdus* species for which all the
145 types of data (see above) were available.

146 Our *breeding timing* models included the following predictors: z-scores of breeding season length
147 (mean-centered by $\mu = 5.4$ months, and scaled by one standard deviation $\sigma = 2.3$ months), migratory
148 behaviour (no migration as the reference category versus partial or full migration), and their interaction.
149 *Breeding sympatry* models included the number of sympatric species with greater than 30% breeding range
150 overlap as the only predictor of the probability of having a sexually-dichromatic plumage patch. *Breeding*
151 *spacing* models included \log_e transformed breeding range size (km²) and breeding landmass (mainland
152 as the reference category versus island). We also ran null models (intercept only) for all responses. All
153 models’ intercepts and response standard deviations were assigned a weakly informative prior (Student
154 T: df = 3, location = 0, scale = 10) [49], and predictor coefficients were assigned flat uninformative priors.
155 We ran each model for 6,000 iterations across 6 chains and assessed Markov Chain Monte Carlo (MCMC)
156 convergence using the Gelman-Rubin diagnostic (Rhat) [49]. We then performed k-fold cross-validation
157 [50] to assess each model’s accuracy in predicting plumage sexual dichromatism of randomly-selected
158 samples of *Turdus* thrush species, refitting each model K=16 times. For each k-fold, the training dataset
159 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
160 $N \approx 4$ species not included in the training dataset. Finally, we compared differences between the models’
161 expected log pointwise predictive densities (ELPD) to assess which model(s) best predicted the probability
162 of having a sexually-dichromatic plumage patch. [50].

163 Models’ predictor effects were assessed using 90% highest-density intervals of the posterior distribu-
164 tions and probability of direction, the proportion of the posterior distribution that shares the same sign
165 (positive or negative) as the posterior median [51], to provide estimates of the probability of that a predic-
166 tor has an entirely positive or negative effect on the presence of sexually-dimorphic plumage patches. We
167 assume predictor estimates with a probability of direction ≥ 0.90 to be indicative of a reliable existence
168 of a predictor’s effect on sexually-dimorphic plumage patches [51].

169 **Results**

170 **Avian visual modeling**

171 Among N=77 *Turdus* species, the following proportion have sexually monomorphic plumage (combined
172 achromatic and chromatic JND thresholds): 1.3% (n=1 species) have no sexually-dimorphic patches > 1

173 JND, 44% (n=34 species) have no dimorphic patches > 2 JND, and 63% (n=49 species) have no dimorphic
174 patches > 3 JND (Table S1). Additional proportions of *Turdus* species with sexually-dimorphic achromatic
175 or chromatic plumage patches are available in Table S2. When comparing within sexes between sympatric
176 species (i.e., following [27] at least a 30% overlap in breeding ranges: n=39 species with at least one
177 sympatric species and a median of n=6 sympatric species per focal species), the median number of avian-
178 discriminable plumage patches between species is 1 or greater for all three achromatic and chromatic
179 JND thresholds except for sympatric females at a chromatic JND threshold > 3 (Fig. S1).

180 **Model comparisons**

181 *Breeding sympatry*, *breeding timing*, and *breeding spacing* performed considerably better than *intercept-only*
182 (null models) in predicting the probability of a species having a sexually-dimorphic plumage patch. We
183 obtained N ≥ 4000 effective posterior samples for each model parameter and all models' Markov Chains
184 (MCMC) successfully converged (Rhat = 1 for all models' parameters). All *breeding sympatry*, *breeding tim-*
185 *ing*, and *breeding spacing* models performed similarly well and substantially better than *intercept only* mod-
186 els in predicting the probability of having a sexually-dimorphic plumage patch with achromatic JND values
187 > 1, 2, or 3 (Table 1; all models predicting achromatic plumage patches had ELPD values within 4, follow-
188 ing the convention of [52]). Among models predicting the probability of having a sexually-dichromatic
189 plumage patch with chromatic JND values >1, 2, or 3, all *breeding sympatry*, *breeding timing*, and *breeding*
190 *spacing* models performed much better than *intercept only* models, and *breeding sympatry* models had the
191 top predictive performance (Table 1; *breeding sympatry* models all have ELPD =0, only the *breeding spacing*
192 models predicting dichromatic plumage patches had similar predictive performance).

193 **Achromatic plumage sexual dichromatism predictors**

194 Migratory behaviour and shorter breeding season lengths were strongly associated with greater odds of
195 a species having achromatic plumage sexual dichromatism. All model predictors' effect estimates are pro-
196 vided as the posterior median odds-ratio (OR) and 90% highest-density interval (HDI) in Table 2. Among
197 predictors of achromatic sexually-dimorphic plumage patches, only predictors included in the *breeding*
198 *timing* model have predictors with probability of direction (pd) values ≥ 0.90 (Table 2). Specifically, longer
199 breeding season length was associated with lower odds of a species having a sexually-dimorphic plumage
200 patch with achromatic JND > 2 (breeding season length, OR [90% HDI] = 0.10 [0.01, 1.1], 89.5% decrease
201 in odds per 2.3-month increase in breeding season) and JND > 3 (breeding season length, OR [90% HDI]
202 = 0.25 [0.03, 1.5], 75% decrease in odds per 2.3-month increase in breeding season). Additionally, full
203 migratory behaviour, rather than no migratory behaviour, was associated with greater odds of a species
204 having a sexually-dimorphic plumage patch with achromatic JND > 1 (full migration, OR [90% HDI] = 4.97
205 [0.95, 24.4]), JND > 2 (full migration, OR [90% HDI] = 66.5 [3.2, 1802.4]) and JND > 3 (OR [90% HDI] =
206 22.3 [1.6, 307.9]). Finally, both full and partial migratory behaviour, rather than no migration behaviour,
207 in conjunction with longer breeding season lengths are associated with greater odds of a species having
208 a sexually-dimorphic plumage patch with achromatic JND > 1 (breeding season length x full migration,

209 OR [90% HDI] = 4.84 [0.67, 39.6]), JND > 2 (breeding season length x full migration, OR = 66.3 [0.59,
 210 11415.7]; breeding season length x partial migration, OR [90% HDI] = 20.7 [0.9, 589.1]) and JND > 3
 211 (breeding season length x partial migration, OR [90% HDI] = 8.28 [0.76, 109.1]).

212 ***Chromatic plumage sexual dichromatism predictors***

213 Migratory behaviour, shorter breeding season lengths, and larger numbers of sympatric *Turdus* species
 214 were strongly associated with greater odds of a species having chromatic plumage sexual dichromatism.
 215 Among predictors of *breeding timing* models predicting chromatic sexually-dimorphic plumage patches,
 216 longer breeding season length was associated with lower odds of a species having a plumage patch with
 217 chromatic JND > 2 (OR [90% HDI] = 0.14 [0.01, 1.42], 86% reduction in odds per 2.3 month increase
 218 in breeding season). Both full and partial migratory behaviour rather than no migration are associated
 219 with greater odds of a species having a plumage patch JND > 1 (partial migration, OR [90% HDI] = 2.2
 220 [0.94, 4.9]), JND > 2 (full migration, OR [90% HDI] = 80.51 [2.8, 3432.9]) and JND > 3 (partial migration,
 221 OR [90% HDI] = 71.2 [0.32, 59062.9]; full migration, OR [90% HDI] = 234.7 [0.51, 300382.6]). For
 222 *breeding spacing models*, island residency rather than mainland residency was associated with lower odds
 223 of having a plumage patch > 1 chromatic JND (island, OR [90% HDI] = 0.27 [0.09, 0.89]). Finally, more
 224 *Turdus* species in sympatry was associated with higher odds of a species having a sexually-dimorphic
 225 chromatic plumage patch with JND > 1 (number of sympatric species, OR [90% HDI] = 1.4 [1.18, 1.67],
 226 40% increase in odds per each additional sympatric species), JND > 2 (sympatric species, OR [90% HDI]
 227 = 1.59 [1.01, 2.52], 59% increase in odds per each additional sympatric species), and JND > 3 (sympatric
 228 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.

| | | Model | | | |
|-------------------|---------------|------------------------------------|---------------------------------------|---------------------------------------|--|
| Plumage Metric | JND Threshold | Breeding Sympathy | 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) |

229 **Discussion**

230 Our results provide comparative correlative evidence in support of predictions of the recognition hypothesis
231 for plumage sexual dichromatism in true thrushes. We used a receptor-noise limited model of *Turdus*
232 *merula* vision [38,39] to measure avian-perceivable visual contrast of plumage colours and found that the
233 odds of plumage sexual dichromatism are much greater for *Turdus* thrush species that have full or partial
234 migration rather than no migration, have relatively short breeding seasons, and are in sympatry with many
235 other true thrush species (Table 1,2). Our results align with prior comparative studies of avian plumage
236 sexual dichromatism where strong associations of sexual dichromatism with greater migratory behaviour
237 [10] and more sympatric taxa [27] were found among many species of different passerine families.

238 Further, we determined that sympatric *Turdus* species have distinguishable plumage colouration differences
239 from one another when measuring plumage appearance from the avian visual perspective (Fig. S1).
240 Divergent plumage colouration within sexes between closely-related species indicates that plumage sexual
241 dichromatism may have evolved to facilitate species and mate recognition in *Turdus* species breeding
242 under higher sympatry with other true thrushes. However, we cannot directly determine if the plumage
243 sexual dichromatism in sympatric *Turdus* species is the result of reproductive character displacement. We
244 do not know if past changes in species' plumage sexual dichromatism occurred before or during periods of
245 sympatry with other *Turdus* species. Regardless, present-day plumage sexual dichromatism and perceivable
246 differences in plumage colouration between sympatric species likely reduces the challenge of finding
247 compatible mates by signaling an individual's sex, breeding status, and species. For example, the four
248 species *Turdus* hybrid zone in north-central Asia [33] is a particularly striking example where reproductive
249 character displacement has likely occurred and all four species exhibit strong plumage sexual dichromatism
250 (Fig. S3). Comparing within sexes between sister species pairs of *T.ruficollis* and *T.atrogularis*, and
251 *T.naumanni* and *T.eunomus* [48], plumage patterns of the species pairs are nearly identical except for a divergence
252 in colour. *T.ruficollis* and *T.atrogularis* share similar facial and throat colouring patterns, with the
253 main difference being red colouration in *T.ruficollis* in opposition to the black colouration of *T.atrogularis*.
254 In the second species pair, *T.naumanni* has red ventral plumage colouration and *T.eunomus* has black ventral
255 plumage colouration.

256 Previous studies have found that closely-related sympatric species tend to have more similar plumage
257 appearance than expected if plumage colouration patterns had evolved to facilitate species recognition
258 via reproductive character displacement [53,54]. The potential lack of major plumage colour divergence
259 among closely-related sympatric species may be attributable to constraints imposed by a shared light environment
260 on colour signal efficiency [55], or similar natural selection pressures (e.g., predators, parasites,
261 and weather). Generally, despite greater similarity in plumage appearance in comparison to allopatric
262 species, closely-related sympatric species can still have substantially different and biologically-relevant
263 differences in achromatic or chromatic interspecific visual contrast of plumage patches when measuring
264 plumage colouration differences from the avian visual perspective (as we have found in our analyses).

265 **Conclusions**

266 Patterns of plumage sexual dichromatism in true thrushes (*Turdus*) are consistent with select predictions
267 of the recognition hypothesis for plumage sexual dichromatism. Migratory behaviour and limited breed-
268 ing seasons reduce the amount of time available to find a mate, and greater plumage sexual dichromatism
269 may help migratory species find compatible mates more rapidly. Greater plumage sexual dichromatism
270 in *Turdus* species under sympatry with other true thrush species also supports the possibility that in-
271 creased plumage sexual dichromatism may be the result of reproductive character displacement. There-
272 fore, greater plumage sexual dichromatism likely increases the speed and accuracy of finding a compatible
273 breeding mate, reduces species and mate recognition errors, and decreases hybridization.

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1 Supplementary Material: Rapid mate recognition promotes
2 greater avian-perceived plumage sexual dichromatism in
3 true thrushes (genus: *Turdus*)

4

5 **Supplementary Tables and Figures**

| Characteristic | Achromatic & Chromatic JND > 1, N = 77 ¹ | Achromatic & Chromatic JND > 2, N = 77 ¹ | Achromatic & Chromatic JND > 3, N = 77 ¹ |
|--|--|--|--|
| Number of Sexually-Dimorphic Plumage Patches | | | |
| 0 | 1 (1.3%) | 34 (44%) | 49 (64%) |
| 1 | 4 (5.2%) | 14 (18%) | 10 (13%) |
| 2 | 11 (14%) | 7 (9.1%) | 2 (2.6%) |
| 3 | 10 (13%) | 3 (3.9%) | 2 (2.6%) |
| 4 | 10 (13%) | 1 (1.3%) | 7 (9.1%) |
| 5 | 12 (16%) | 4 (5.2%) | 0 (0%) |
| 6 | 8 (10%) | 3 (3.9%) | 0 (0%) |
| 7 | 4 (5.2%) | 4 (5.2%) | 3 (3.9%) |
| 8 | 5 (6.5%) | 1 (1.3%) | 1 (1.3%) |
| 9 | 5 (6.5%) | 1 (1.3%) | 1 (1.3%) |
| 10 | 7 (9.1%) | 5 (6.5%) | 2 (2.6%) |

¹ Statistics presented: n (%)

Table S1: Number of sexually-dimorphic plumage patches for combined achromatic and chromatic just noticeable differences (JND) thresholds by number of *Turdus* thrush species (% of species).

| Characteristic | Achromatic > 1 JND, N = 77 ¹ | Achromatic > 2 JND, N = 77 ¹ | Achromatic > 3 JND, N = 77 ¹ | Chromatic > 1 JND, N = 77 ¹ | Chromatic > 2 JND, N = 77 ¹ | Chromatic > 3 JND, N = 77 ¹ |
|--|---|---|---|--|--|--|
| Number of Sexually-Dimorphic Plumage Patches | | | | | | |
| 0 | 8 (10%) | 41 (53%) | 51 (66%) | 6 (7.8%) | 47 (61%) | 61 (79%) |
| 1 | 19 (25%) | 10 (13%) | 10 (13%) | 15 (19%) | 11 (14%) | 5 (6.5%) |
| 2 | 14 (18%) | 9 (12%) | 4 (5.2%) | 22 (29%) | 5 (6.5%) | 3 (3.9%) |
| 3 | 11 (14%) | 5 (6.5%) | 7 (9.1%) | 11 (14%) | 7 (9.1%) | 2 (2.6%) |
| 4 | 11 (14%) | 5 (6.5%) | 3 (3.9%) | 14 (18%) | 1 (1.3%) | 2 (2.6%) |
| 5 | 14 (18%) | 7 (9.1%) | 2 (2.6%) | 9 (12%) | 6 (7.8%) | 4 (5.2%) |

¹ Statistics presented: n (%)

Table S2: Number of sexually-dimorphic plumage patches for separate achromatic and chromatic just noticeable differences (JND) thresholds by number of *Turdus* thrush species (% of species).

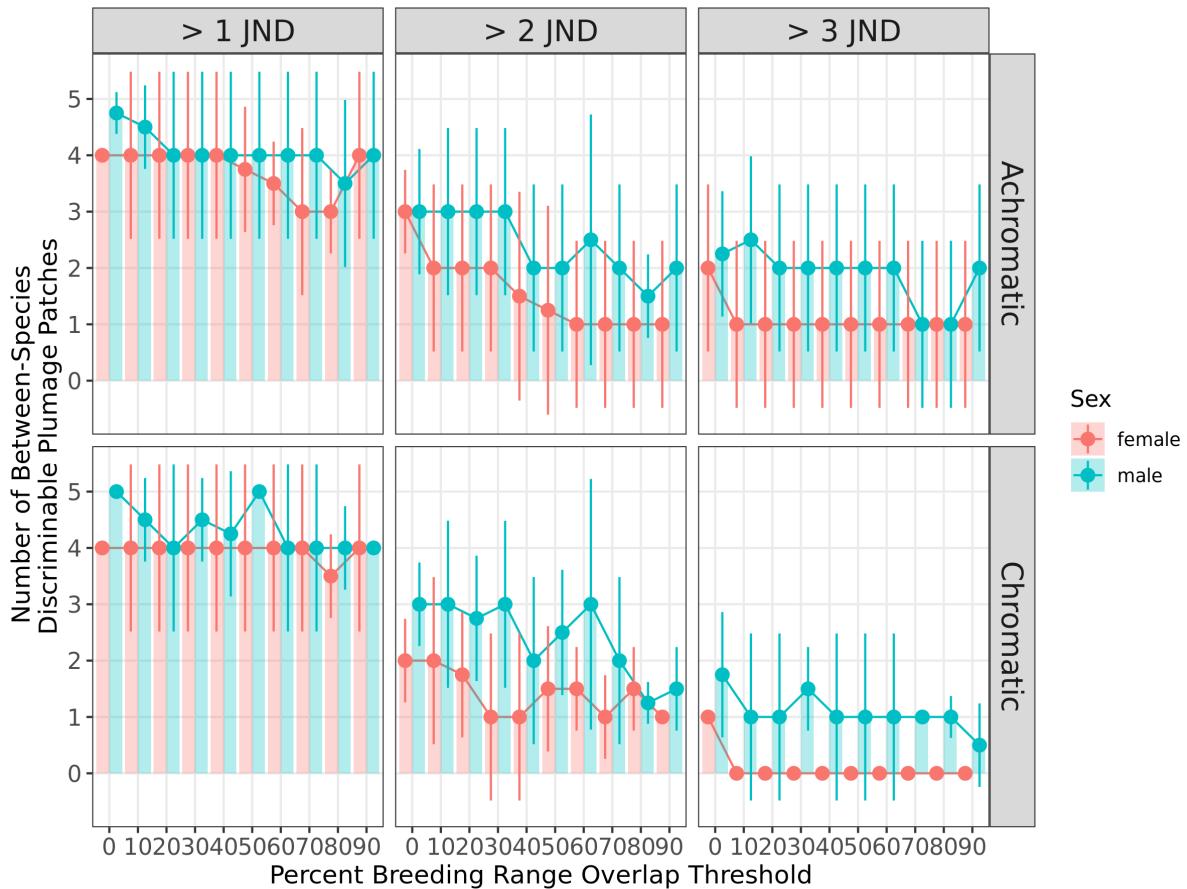


Fig S1: Median ± median absolute deviation of number of distinguishable plumage patches by just noticeable differences (JND) thresholds of 1, 2, and 3 between male and female *Turdus* thrush species in sympatry at various breeding range overlaps (percent).

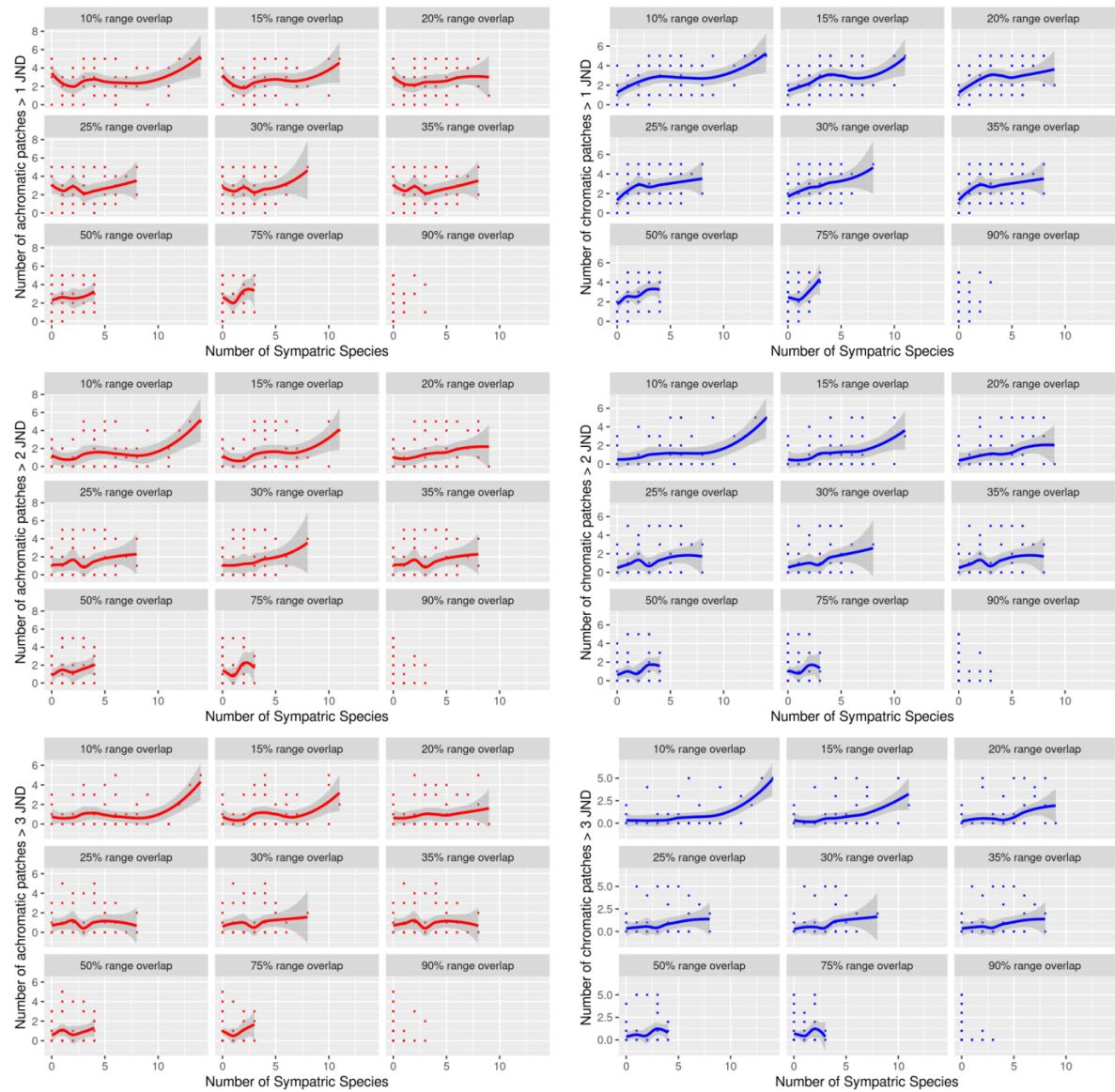


Fig S2: Number of sexually-dichromatic chromatic and achromatic plumage patches versus number of sympatric *Turdus* species, faceted by sympathy overlap thresholds (0-90%). Lines are Loess nonlinear regression fits with no correction for phylogenetic relatedness among species.

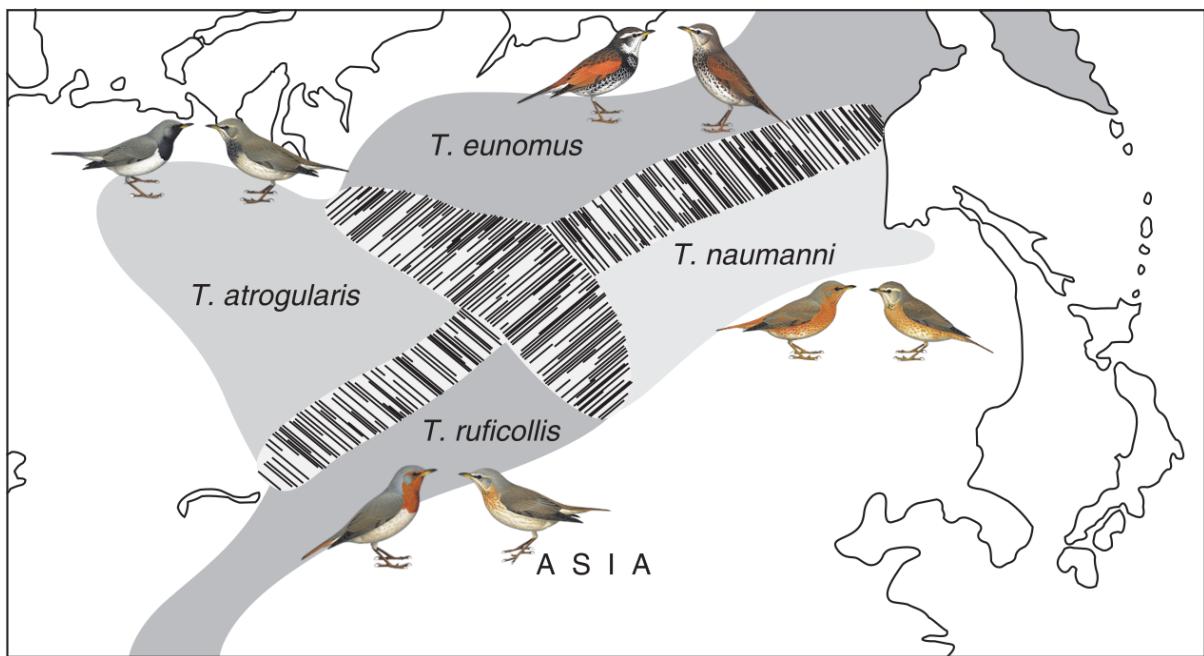


Fig S3: Four species hybrid zone in north-central Asia (*T. atrogularis*, *T. ruficollis*, *T. eunomus*, and *T. naumannii*). Map is from [1]. Illustrations © HBW Alive/Lynx Edicions.

⁶ References

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⁸