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Multi-modal signal evolution in birds: re-examining a standard proxy for sexual selection

Christopher R. Cooney[1,2*], **Hannah E. A. MacGregor**[1,3], **Nathalie Seddon**[1†] **& Joseph A. Tobias**[1,4†]

[1]*Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, UK.*
[2]*Department of Animal and Plant Sciences, University of Sheffield, Western Bank, Sheffield S10 2TN, UK.*
[3]*School of Biological Sciences, University of Bristol, Bristol BS8 1TQ, UK.*
[4]*Department of Life Sciences, Imperial College London, Silwood Park, Buckhurst Road, Ascot, Berkshire, SL5 7PY, UK.*
[†]Equal contribution

***Author for correspondence:** c.cooney@sheffield.ac.uk

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Abstract

Sexual selection is proposed to be an important driver of speciation and phenotypic diversification in animal systems. However, previous phylogenetic tests have produced conflicting results, perhaps because they have focused on a single signalling modality (visual ornaments), whereas sexual selection may act on alternative signalling modalities (e.g. acoustic ornaments). Here we compile phenotypic data from 259 avian sister species pairs to assess the relationship between visible plumage dichromatism—a standard index of sexual selection in birds—and macroevolutionary divergence in the other major avian signalling modality: song. We find evidence for a strong negative relationship between the degree of plumage dichromatism and divergence in song traits, which remains significant even when accounting for other key factors, including habitat type, ecological divergence and interspecific interactions. This negative relationship is opposite to the pattern expected by a straightforward interpretation of the sexual selection-diversification hypothesis, whereby higher levels of dichromatism indicating strong sexual selection should be related to greater levels of mating signal divergence regardless of signalling modality. Our findings imply a 'trade-off' between the elaboration of visual ornaments and the diversification of acoustic mating signals, and suggest that the effects of sexual selection on diversification can only be determined by considering multiple alternative signalling modalities.

Keywords: birds, dichromatism, divergence, plumage, sexual selection, song, trade-off

Introduction

Previous studies have provided theoretical and empirical evidence that sexual selection can stimulate the rapid divergence of traits involved in mate choice and species recognition [1, 2], supporting the longstanding view that sexual selection is an important driver of speciation and lineage diversification [3-6]. However, direct support for this hypothesis is relatively weak and inconsistent among taxa [7], with a series of studies finding no evidence of significant correlations between sexual selection and either species richness or speciation rate when studied across birds [8-11], mammals, butterflies and spiders [12], and certain fish taxa [13]. Although these observations suggest that sexual selection has limited effects on diversification at macroevolutionary scales, an alternative possibility is that standard comparative analyses are simply ineffective because they rely on crude phenotypic proxies to estimate variation in sexual selection across species.

To quantify the intensity of sexual selection, most existing large-scale studies in birds have used visible sex-differences in plumage colouration [e.g. 2, 8, 9, 10, 14, 15]. This metric—usually termed ‘plumage dichromatism’—has become a standard proxy for sexual selection because it is easily measured and positively correlated with other indices of sexual selection such as testes size, the degree of polygyny, and the frequency of extra-pair paternity [16-19]. Nonetheless, the extent to which plumage dichromatism provides an accurate and consistent estimate of the overall intensity of sexual selection across all lineages remains uncertain, not least because it focuses on a single sexual signalling modality, whereas many taxa engage in multimodal signalling [5]. Indeed, if the intensity of sexual selection targeted at one signalling modality (e.g. visual signals) trades off or is negatively correlated with the intensity of sexual selection targeted at another (e.g. acoustic signals) [3, 20], then such interactions could lead to a breakdown in the relationship between the underlying intensity of sexual selection across species and the visual traits used as proxies for sexual selection, therefore obscuring the true relationship between sexual selection and diversification [2, 8].

Progress in resolving this question has been slow because previous studies investigating the macroevolutionary consequences of sexual selection have generally focused exclusively on visual signalling traits [2, 21], leaving open the possibility that comparisons across different sexual signalling modalities may reveal contrasting patterns. Furthermore, most studies have failed to address the role of other important selection pressures potentially shaping the evolution of signal phenotypes, such as habitat differences, ecological divergence and interspecific interactions [22, 23], and have typically focused on geographically, taxonomically and/or ecologically restricted datasets, rather than sampling more broadly across major clades.

Here we address these issues by compiling data for a global sample of 259 avian species pairs from 33 passerine families to test the relationship between visible plumage dichromatism—used as a standard proxy for sexual selection in birds and other animals [7]—and macroevolutionary divergence in the other major avian signalling modality: song. We focus on birds because they offer an unequivocal example of multimodal sexual signalling in which both traits—avian plumage colouration (a visual ornament) and song (an acoustic ornament)—are known to function in inter- and intra-sexual selection in many avian taxa [5, 24-27]. In addition, the availability of complementary species-level data on avian morphological traits, ecology, biogeography and phylogeny allows us to assess the importance of plumage dichromatism in relation to a suite of key variables known to influence patterns of signal evolution.

Our analyses can be divided into three stages. First, we use published song recordings to estimate the extent of song divergence within species pairs. Second, we assess the relationship between sexual dichromatism and degree of song divergence across pairs. Third, we use multiple regression combined with model averaging techniques to assess the relative association between dichromatism and song divergence in relation to other factors. If sexual selection has reinforcing or independent effects on traits from different signalling modalities [28], we expect the relationship between plumage dichromatism and song divergence to be positive, or non-significant, respectively. Conversely, if the effects of sexual selection on traits in different signalling modalities are negatively correlated, we expect a negative relationship between plumage dichromatism and song divergence across species pairs.

Methods

SPECIES SAMPLING AND PHYLOGENETIC FRAMEWORK

We used published molecular phylogenies to select a sample of passerine species pairs for which high quality song recordings were available [see 2, 8]. Each pair consisted of sister species, i.e. pairs of lineages that represent each other’s closest relative. We note that a few of our study pairs contain species that are not true sisters, both because of incomplete sampling in published phylogenies, and because we included some near-sisters in which one member of the pair belonged to a sister clade (or both species from a polytomy). This approach is based on the assumption that comparisons between near-sisters are informative about phenotypic divergence during recent evolutionary history [2]. Overall, our sample contained 518 species from 259 species pairs (including 243 sister species and 13 near-sisters) widely distributed across the passerine radiation (Fig. S1). For full details, see the supplementary online material. To provide a phylogenetic framework for our analyses, we sampled 1000 molecular-only trees from www.birdtree.org [29], which were pruned to include only the species included in our dataset. We then used TreeAnnotator [30] to generate a maximum clade credibility (MCC) tree, which was then pruned so that each pair was represented by a single tip.

SONG DIVERGENCE

To quantify the extent of song divergence within species pairs, we downloaded songs for all species from the Macaulay Library of Natural Sounds (www.macaulaylibrary.org) and the online database

Xeno Canto (www.xeno-canto.org). We digitized sound files in Raven Pro v1.4 using standard settings, then measured seven key temporal and spectral traits that together capture important interspecific differences in overall signal structure [for full details see 31, 32]: (i) maximum frequency (kHz), (ii) minimum frequency (kHz), (iii) peak frequency (kHz; frequency in the signal with the greatest amplitude), (iv) bandwidth (kHz; maximum frequency minus minimum frequency), (v) signal duration (s), (vi) number of notes and (vii) pace (number of notes s^{-1}). For each species, at least three high-quality recordings were measured (mean 4.8 recordings per species), providing a total sample of 2476 songs. To reduce the dimensionality of the dataset, we conducted a principal components (PC) analysis on the covariance matrix of individual (log-transformed) song measurements. The first three PCs from this analysis accounted for over 83% of the variance in the original acoustic dataset, with each PC capturing a distinct component of overall signal structure (Table S1). Specifically, PC1 (41%) loaded heavily with variables related to song pitch, PC2 (24%) loaded heavily with variables related to song length, and PC3 (18%) primarily loaded with song pace. We therefore interpreted these PCs as axes of variation in song pitch (PC1), length (PC2) and pace (PC3), respectively, with variation in overall song structure captured by position in this three-dimensional acoustic space (Fig. S2). Using these PCs, we estimated within-pair song disparity for all pairs as the Euclidean distance between species' mean PC scores in terms of overall song structure (PC1-3), and in terms of song pitch, length and pace separately (Fig. 1). To assess the sensitivity of our results, we also generated an alternative version of our dataset in which within-species song disparity estimates were corrected for observed levels of intraspecific variation (see Appendix S1 for full details).

SEXUAL DICHROMATISM

To quantify the degree of sexual dichromatism within pairs, we used published [8] species-level scores of dichromatism estimated by eye from handbook illustrations (see Appendix S1 for justification). Briefly, we used standard methodology [17, 33] to score the difference in plumage colouration 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 colour; 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).

ADDITIONAL PREDICTORS OF SONG DIVERGENCE

To explore the role of other factors known to influence estimates of phenotypic (particularly song) divergence in birds, we collected data for a suite of additional explanatory variables including divergence time [34], life history and allometric effects [35], migration status [36], habitat [37, 38], breeding latitude and insularity [39, 40], interspecific interactions [41], niche divergence [42-44] and song learning [45]. Because the key habitat attribute linked to song evolution in birds is vegetation density [32] we used a score of forest dependency (i.e. degree of association with densely forested habitat). See Appendix S1 for full details of methods, data and data sources.

STATISTICAL ANALYSES

Estimating phylogenetic signal of song divergence

We used a generalised least squares (GLS) approach to test the phylogenetic signal of song divergence in our dataset. This approach, implemented in the R package *caper* [46], estimates a maximum likelihood (ML) value for phylogenetic signal (λ) [47], which typically varies between zero (trait variance is independent of phylogeny) and one (trait variance follows a Brownian motion model of evolution). In the context of analysing song divergence, a value of $\lambda = 0$ indicates that extent of song divergence within pairs is random with respect to phylogeny, whereas a value of $\lambda = 1$ implies that closely related pairs have more similar levels of song disparity than would be expected by chance. We found that ML values of λ were zero for all four measures of song divergence, with values of $\lambda = 1$ (i.e. a Brownian motion model of evolution) significantly rejected in all cases (Table S2). Results were qualitatively similar for an alternative dataset corrected for observed levels of intraspecific variation (Table S2), indicating that variation in the extent of within-pair song divergence in our dataset is unrelated to phylogeny. This allowed us to use non-phylogenetic regression techniques with more flexible error structures than currently possible in a statistical phylogenetic comparative framework, which was necessary for our dataset (see below).

Testing the relationship between predictors and extent of song divergence

To model the observed variation in estimates of within-pair song divergence, accounting for the right-skewed distribution of disparity estimates (Fig. S3), we used generalised linear models (GLMs) with a gamma error distribution and log link. Using this approach, we (i) examined the relationship between song disparity and degree of plumage dichromatism, (ii) tested for an interaction effect between dichromatism and habitat type (forest dependency) and (iii) assessed the combined influence of all predictor variables on the extent of song disparity using single and multi-predictor regression and Akaike information criterion-based model averaging [48] corrected for small sample sizes (AIC_c).

To perform model averaging, following [49] and [50], we fitted models encompassing all possible additive combinations of our predictor variables (see above), including a null (intercept-only) model, calculating the AIC_c score of each model. We then calculated the relative importance (RI) for each predictor variable as the sum of relative Akaike weights for models in which they appear. RI values scale from 0 to 1, where a variable with a score of 0 is associated with very low Akaike weights (i.e. low importance) and 1 is consistently associated with high weights (i.e. high importance). We also calculated model-averaged estimates of regression parameters and standard error values, calculated as the sum of the parameter estimates for each model including that predictor, multiplied by the relative Akaike weight of each of those models. To give further insight into the relative importance of predictor variables, we also identified the variables included in the top-ranked (i.e. best fitting) model in each case. We used this procedure to assess the effect of predictors on response variables, including overall song disparity (PC1-3), as well as separate estimates of disparity in pitch (PC1), length (PC2) and pace (PC3) separately. For multipredictor models, we restricted the dataset to include only those species pairs for which complete data for all predictors were available (246 of 259 pairs) and pseudo-R^2 values for GLMs were estimated using the method of [51]. Pair age, generation length, body mass disparity and beak disparity were ln-transformed prior to analysis and models were inspected to ensure they complied with modelling assumptions (e.g. normality of residuals). We also checked for issues related to collinearity among predictors, which we found were unlikely to affect our results (see Appendix S1 for details). To improve the interpretability of regression coefficients, predictor variables were centered and standardised prior to model fitting [52]. All analyses were conducted in R version 3.3.1 and model averaging was performed using the R package *MuMIn* [53].

Results

RELATIONSHIP BETWEEN DICHROMATISM AND EXTENT OF SONG DIVERGENCE

Our models revealed that plumage dichromatism was significantly negatively correlated with overall song divergence between species (Table S3). Species pairs with a greater degree of plumage dichromatism tended to have less divergent songs than more monochromatic species pairs (Fig. 2). Analysing patterns of divergence in each song trait separately revealed that the overall effect of dichromatism was primarily driven by significant negative relationships with divergence in song pitch (PC1) and length (PC2), with more marginal effects on song pace (PC3) (Table S3). Furthermore, including an interaction effect with forest dependency in these models revealed no significant statistical support for the hypothesis that the relationship between dichromatism and song divergence is mediated by variation in habitat type across taxa (Table S3). Rerunning analyses correcting for observed levels of intraspecific variation produced highly similar results (Table S3).

ADDITIONAL PREDICTORS OF SONG DIVERGENCE

Single predictor regression models focused on our additional predictors of song divergence identified several variables that were individually correlated with variation in song disparity across pairs (Fig. S4-S7). In terms of total song disparity (PC1-3), the strongest individual predictor was pair age (Table S4). Furthermore, variation in overall song disparity was also significantly correlated with disparity in beak morphology, with more marginal effects detected for several other variables, including forest dependency and mass disparity (Table S4). We also detected additional significant correlations between individual predictors and estimates of disparity in specific components of song structure (Table S5).

We then assessed the relative importance of all predictors using AIC_c model averaging techniques (Fig. 3). The best-supported predictor of total song disparity (PC1-3) was pair age (RI = 0.99), which exhibited a strong and highly significantly positive relationship with disparity (Table S6). However, even after accounting for this relationship, the negative effect of dichromatism remained strong (RI = 0.98) (Fig. 3). The AIC_c best model for total song disparity accounted for 17% of the total variation, and retained these two variables plus mean pair body mass, forest dependency and within-pair beak disparity mass as positive effects, and confamilial sympatry as a negative effect (Fig. 3; Table S6).

Analysing relationships in each component song trait separately revealed that predictor variables had contrasting effects depending on the axis considered (Fig. S8; Table S7). On the one hand, divergence in song pitch (PC1) was best predicted by significant effects of dichromatism (RI = 0.97), pair age (RI = 0.96), body mass (RI = 0.93), confamilial sympatry (RI = 0.92) and forest dependency (RI = 0.89), whereas divergence in song length (PC2) was best explained by significant effects of only pair age (RI = 0.92) and dichromatism (RI = 0.91). In contrast, the only significant predictor of divergence in song pace (PC3) was a positive effect of within-pair beak disparity (RI = 0.82). Overall, AIC_c top models for these variables accounted for 22%, 12% and 6% of the total variation in disparity in song pitch, length and pace, respectively (Table S8). Rerunning models accounting for intraspecific variation produced qualitatively similar results (Table S9-S11).

Discussion

Our analyses reveal that the degree of sexual dichromatism is negatively related to the extent of divergence in song structure among closely related bird species, a pattern that remained strong after accounting for a suite of potentially correlated or confounding variables, as well as for intraspecific trait variation. This contrasts with the findings of previous studies reporting evidence for significant positive correlations between indictors of sexual selection and signal divergence in birds, supporting the view that sexual selection can drive parallel divergence across multiple signals [2, 21]. However, these studies assessed patterns of divergence in visual signalling traits (i.e. plumage colouration), using proxies for the intensity of sexual selection derived from the same signalling modality (e.g. dichromatism). In contrast, we have focused across major avian signalling modalities, finding the opposite relationship: that dichromatism (a visual signal) is negatively associated with divergence in song (an acoustic signal). Our results are therefore incompatible with a straightforward interpretation of the sexual selection-diversification hypothesis, whereby higher levels of dichromatism indicating strong sexual selection should be related to greater levels of mating signal divergence regardless of signalling modality. Instead, our findings are consistent with the alternative view that negative interactions between alternative signalling modalities play an important role in shaping macroevolutionary patterns of signal evolution in birds.

One intuitive explanation for the negative correlation between plumage dichromatism and song divergence is that it reflects an underlying link between sexual selection and acoustic signal divergence in species that do not rely on visual signals. This makes sense because single-species studies have demonstrated an important role for female choice and/or male-male competition in shaping many aspects of avian acoustic signal design [24], and many avian taxa with drab or monochromatic plumage are known to possess highly elaborate acoustic signals which often provide the best means of differentiating among lineages (e.g. Old World leaf warblers; Phylloscopidae) [54]. Thus, increased sexual selection on acoustic traits relative to visual traits in monochromatic taxa provides a plausible explanation for a negative relationship between plumage dichromatism and song disparity at broad macroevolutionary scales.

A key challenge facing this interpretation is to explain why, within species, selection would favour signals from one rather than multiple signalling modalities, thus generating negative relationships across modalities at a macroevolutionary scale. It is possible that the relative costs and benefits of signalling via a given sensory modality are shaped by the prevailing environmental conditions [38], such that ecological differences among species should play a role in determining the relative prominence of one signal type over another [27]. In line with this idea, bird species inhabiting dense habitats such as reedbeds, thickets, and the understorey of forests often have more elaborate songs than visual signals. However, our models including forest dependency as an interaction term provided no support for the idea that the relationship between plumage dichromatism and song divergence is mediated by broad-scale habitat differences among taxa.

An alternative explanation is that our findings reflect the signature of evolutionary trade-offs between alternate signalling modalities. Under a resource- or cost-based trade-off scenario—such as that envisaged by Darwin [3] and later termed the ‘transfer hypothesis’ [20]—constraints on sexual selection within species make it costly for males to signal in (or females to choose between) multiple signalling modalities [55, 56], generating the potential for interspecific trade-offs in ornament elaboration (and diversification) between alternate signalling modalities [57]. This explanation relies on the assumption that investment in one signalling modality constrains investment in another, which is plausible given that avian plumage and song traits may both be costly to produce [58]. However, the energetic costs of signal production may be relatively low [59] and potentially offset by differences in how such signals are produced and displayed [27]. A different trade-off scenario is suggested by the concept of ‘redundancy’ among alternate signal types. Under a redundancy-based model, the spread of an attractive signal in one modality leads simultaneously to increased selection for detecting the novel signal and a weakening of selection for elaborate signals in alternate modalities, which occurs not because of costs associated with producing or maintaining multiple sexual signals, but because sexual selection on the latter trait is weak or non-existent, due to redundancy [60]. Such redundancy-based trade-offs can theoretically occur in the absence of any habitat differences among taxa, or resource limitation underlying the production of signalling traits. Thus, whether selection favours one signal type (e.g. song) over another (e.g. plumage) largely depends on which signal type evolved first, which may largely be due to historical contingencies [61-63].

CONTRIBUTORY FACTORS

In addition to variation in the strength and targets of sexual selection, our results support a role for several other factors in shaping patterns of acoustic signal divergence in birds. We found strong evidence for a positive relationship between species pair age and degree of song disparity, in line with previous studies [e.g. 2, 39, 64, 65], as well as the general consensus that patterns of phenotypic divergence are primarily dictated by the time available for trait differences to evolve [34, 66]. Body mass also emerged as a significant predictor of song divergence, in line with previous studies indicating positive relationships between body mass and patterns of signal evolution in birds [2, 19]. Furthermore, we found support for links between song divergence and both habitat and the degree of confamilial sympatry. First, we found evidence for increased pitch disparity in species pairs with higher levels of forest dependency, consistent with the idea of stronger (divergent) selection on acoustic traits in taxa signalling in densely vegetated habitats [37, 38]. Second, we found that pairs which co-occurred with a greater proportion of confamilial species had lower levels of song divergence than those with lower levels of overlap. This accords with the view that interactions among related species can constrain phenotypic divergence [67], in part because acoustic communities appear to ‘partition’ finite aspects of acoustic signalling space [31, 68-70]. Finally, we found that divergence in song pace was significantly positively correlated with disparity in species’ beak morphology. Previous studies have found evidence of correlated evolution of morphology and vocal signal structure in particular clades (e.g. Darwin's finches, Neotropical woodcreepers) [43, 71, 72], presumably because biophysical constraints on song production generate correlated evolution between songs and beaks. Our results in relation to beak morphology support this view, and imply that this effect holds across passerines more generally. Nonetheless, even when we accounted for these significant effects in statistical models, the strong negative association between song divergence and dichromatism was retained.

IMPLICATIONS FOR COMPARATIVE STUDIES

Our finding that dichromatism is negatively related to song divergence across a broad sample of avian species pairs has important implications for studies testing macroevolutionary hypotheses related to sexual selection. Most importantly, it implies that plumage dichromatism provides a relatively ineffective proxy for the intensity of sexual selection in taxa primarily using non-visual signals. This potential limitation of dichromatism has previously been proposed [2, 8] with reference to bird species such as the common nightingale (*Luscinia megarhynchos*), common whitethroat (*Sylvia communis*) and sedge warbler (*Acrocephalus schoenobaenus*), passerine species with largely monomorphic plumage colouration, elaborate song traits and strong sexual selection [73-75]. Our results provide broad-scale empirical support for this view, and indicate that dichromatism will underestimate sexual selection in these taxa, potentially being negatively related to the intensity of sexual selection in samples dominated by non-visual signallers. Thus, the underlying effect of sexual selection may often be obscured in comparative studies based solely on dichromatism, perhaps helping to explain the weak or non-existent correlations between dichromatism and speciation rates in birds and other taxa with multimodal signalling [7-11].

CONCLUSIONS

Taken together, our findings are consistent with the view that sexual selection plays a major role in shaping sexual signal evolution, in conjunction with ecological factors [23, 76, 77]. However, whereas most previous studies have focused on a single signalling modality, we found evidence of a negative relationship between visual and acoustic signalling in birds, supporting the more general view that negative interactions between signalling modalities can explain general patterns of signal evolution [3, 20]. Not only do these results suggest that such 'trade-offs' are important in shaping phenotypic diversity, they also indicate that phylogenetic tests based on phenotypic metrics for the intensity of sexual selection will underestimate the association between sexual selection and diversification. We conclude that the rigour and accuracy of any comparative analysis testing the effects of sexual selection will be improved by considering phenotypic proxies for sexual selection that span all relevant signalling modalities, be they visual, acoustic, or olfactory.

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Data accessibility

The full dataset has been uploaded to Dryad Data Repository, and is available via the link: https://datadryad.org/review?doi=doi:10.5061/dryad.b4p43t7.

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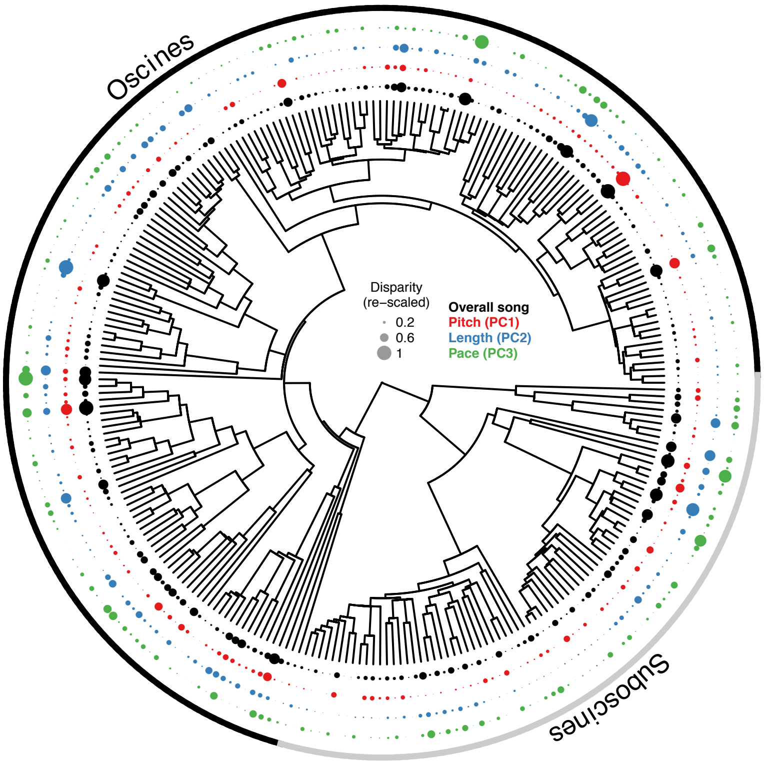
Figure and table captions

Figure 1. A phylogenetic tree of passerine species pairs (n = 259), showing within-pair disparity in overall song (PC1-3; innermost, black), pitch (PC2; red), length (PC3; blue) and pace (PC3; outermost, green). Size of points corresponds to relative within-pair song disparity. A version including species names is available in the supporting online material.

Figure 2. Scatterplot showing the relationship between total within-pair song disparity (PC1-3) and plumage dichromatism across 259 species pairs of passerine birds. Regression line (with prediction intervals, shaded) indicates the best-fitting relationship between the two variables.

Figure 3. Model averaged coefficient estimates from multipredictor GLMs predicting variation in within-pair song disparity (PC1-3) among passerine species pairs (n = 259). Points indicate the standardised effect sizes for each of the (scaled) predictor variables and lines indicate 95% confidence intervals (CI). Sizes of points represent the relative importance (RI) of each of the predictor variables, where a value of RI = 0 indicates low importance and a value of RI = 1 indicates high importance. Predictors included in the AIC_c top model are coloured (blue = negative effect; red = positive effect), with significant ($P < 0.05$) model-averaged coefficients shown in darker colours.



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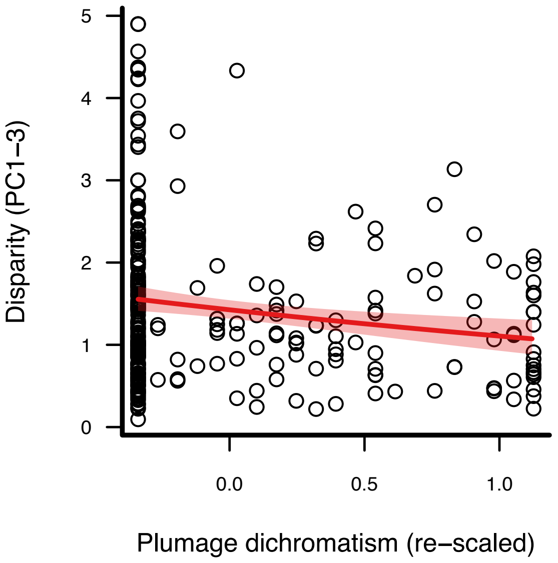

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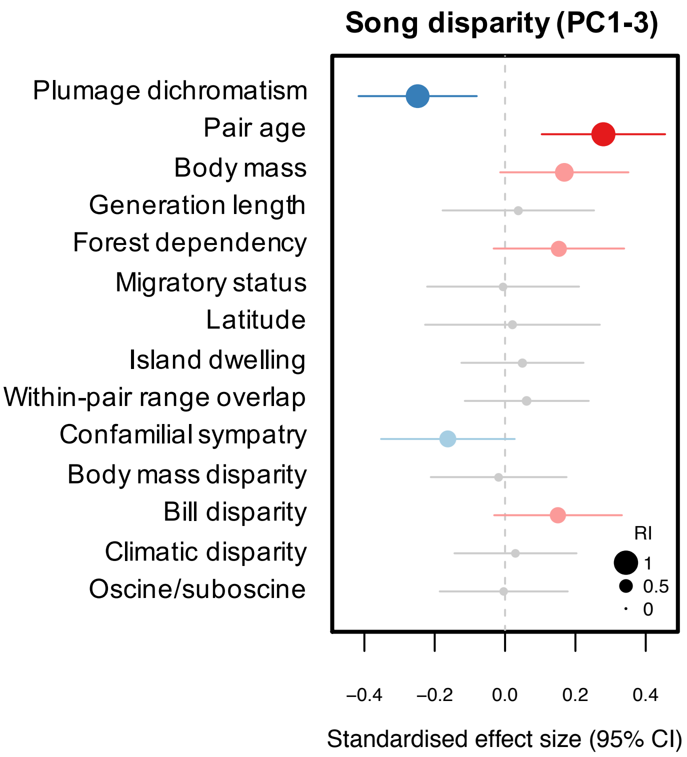

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SUPPLMENTARY MATERIAL FOR

COONEY ET AL. – MULTI-MODAL SIGNAL EVOLUTION IN BIRDS: RE-EXAMINING A STANDARD PROXY FOR SEXUAL SELECTION

APPENDIX 1

Supplementary methods

Supplementary figures (S1-S10) and tables (S1-S12)

APPENDIX 1

SUPPLMENTARY METHODS

Compiling species pair datasets

Following Seddon et al. (2013) and Cooney et al. (2017), we assembled a dataset of passerine species pairs for which we could collect detailed data on song traits. We compiled a list of species pairs from published phylogenetic trees of passerine families or genera generated using genetic data. 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 species pairs 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.

Principal component analysis of song measurements

Raw song traits were correlated across species (Table S1). Such correlations can lead to overinflated divergence estimates if each trait axis is treated as independent. Therefore, to avoid this issue and to reduce the dimensionality of our dataset, following previous studies (Tobias et al. 2014a; Tobias et al. 2014b) we conducted a principal components (PC) analysis on the covariance matrix of individual (log-transformed) song measurements. The first three PCs from this analysis accounted for over 83% of the variance in the original acoustic dataset, with each PC capturing a distinct component of overall signal structure (Table S1). Specifically, PC1 (41%) primarily loaded with variables related to song pitch, PC2 (24%) with variables related to song length, and PC3 (18%) with song pace. We chose not to retain PC4 (14%) in our analysis because of its comparatively small eigenvalue (1.006) (Kaiser 1960) and because the loadings indicated that it was primarily related to variation in minimum song frequency (loading = 0.66), which is more difficult to quantify from song spectra and therefore potentially subject to greater levels of error. By focusing exclusively on variation in the first three PCs, which are interpretable in terms of song pitch (PC1), length (PC2) and pace (PC3), respectively, our analyses are directly comparable with previous studies (e.g. Tobias et al. 2014b) using the same combination of traits (PCs) to define a three-dimensional acoustic space (Fig. S2).

Alternative dataset: accounting for intraspecific variation

Intraspecific trait variation can generate overinflated estimates of interspecific disparity, especially when sample sizes are low relative to levels of intraspecific variation and/or measurement error

(Silvestro et al. 2015). To test whether our results were sensitive to these issues, we repeated our main analyses using an alternative version of our dataset in which within-species song disparity estimates were corrected for observed levels of intraspecific variation using an approach based on ANOVA (Weir and Wheatcroft 2011; Weir et al. 2012).

Sexual dichromatism

Although it would be preferable to estimate dichromatism using more objective measurements of bird plumage colouration, such as those generated by a spectrophotometer, these types of measurements are currently unavailable for most species. However, the high correlation between spectrophotometric and human estimates of dichromatism indicate that human vision can provide a reliable estimate of avian colouration in general (Bergeron and Fuller 2018) and sexual dichromatism in particular (Armenta et al. 2008; Seddon et al. 2010). To test this assumption in our dataset, we used spectrophotometric measurements of plumage colouration from museum specimens described in (Cooney et al. 2017) to calculate objective estimates of dichromatism for species and pairs common to both datasets, following methods outlined previously (Seddon et al. 2013; Cooney et al. 2017). This resulted in dichromatism estimates for 264 species (132 pairs), which we compared to our scores based on handbook illustrations using Spearman's rank correlation. We found that estimates of dichromatism based on spec measurements and human vision were highly positively correlated (Fig. S9) across both species (Spearman's r = 0.76, P < 0.001) and species pairs (Spearman's r = 0.79, P < 0.001). Thus, we conclude that scores of dichromatism based on published illustrations are valid for our dataset, in line with previous studies (e.g. Dale et al. 2015).

Additional predictors of song divergence

To explore the role of other factors known to influence song divergence in birds, we collected data for a suite of additional explanatory variables. Details are given below.

Pair age. We generated estimates of pair age (i.e. time from the present to the most recent common ancestor) by calculating the mean height of the node connecting the pair in the (pruned) Jetz et al. (2012) phylogenies (see above).

Body mass. Estimates of body mass were extracted from Wilman et al. (2014) and we used the mean of species (ln-transformed) values to generate pair-level averages.

Generation length. Data on species' generation length, forest dependency and migratory status were compiled from BirdLife International (http://www.datazone.birdlife.org; accessed 18-10-2017), and we used the mean of species' generation length values to provide pair-level averages.

Forest dependency. In the BirdLife dataset species are assigned to one of four categories, depending on whether they "do not normally occur in forests", or exhibit "low", "medium" or "high" levels of forest dependency. To convert this into a quantitative variable capturing broad differences in habitat usage, we converted this classification system into a 4-point scoring scheme, giving each species a score of 0, 1, 2 or 3 based on whether they were recorded as having no, low, medium or high forest dependency, respectively. To capture the average level of forest dependency within a pair, we took the mean score for each pair.

Migratory status. Similarly, in the BirdLife dataset species are categorised as “not a migrant”, “nomadic”, “altitudinal migrant” or “full migrant”, so again we converted this classification system into a 2-point scoring scheme, giving each species a score of 0 (not a migrant) or 1 (nomadic, altitudinal migrant or full migrant) and then took the mean score for each pair.

Latitude. All variables relating to species’ geographical distributions are based on (breeding) range maps provided by BirdLife International and NatureServe (2016, version 9; http://www.datazone.birdlife.org). To estimate the latitudinal midpoint of each pair, we first calculated each species’ range centroids using the R package *PBSmapping* (Schnute 2015) and then took the mean of species (absolute) latitudinal values (Weir and Schluter 2007; Weir and Wheatcroft 2011; Weir et al. 2012).

Island-dwelling. To characterise species as island-dwelling, we used a high-resolution database of global geography (GSHHG version 2.3.6; http://www.soest.hawaii.edu/pwessel/gshhg/) to identify all landmasses >1 km^2 in size surrounded by ocean and smaller than Greenland (following Weigelt et al. 2013). We then overlaid species range maps on top of this dataset and calculated the proportion of species’ ranges occurring on islands. We consider species with >80% of their range occurring on islands to be primarily island dwelling and turned this into a pair-level variable by counting whether neither (0), one (1) or both (2) of the species in a pair were characterised as island dwelling.

Within-pair range overlap. To calculate range overlap between species within a pair, we took the standard approach of calculating the area of overlap between species, divided by the area of the smaller species’ range (Pigot and Tobias 2013; Tobias et al. 2014a; Cooney et al. 2017).

Confamilial sympatry. To quantify the extent of interactions with related species, we used the taxonomy of Jetz et al. (2012) and the range maps to tally up the number of same-family (confamilial) species that are sympatric with the focal species (Morinay et al. 2013), where sympatry is defined as >20% range overlap between species—a threshold commonly used to define ‘substantial’ sympatry (Tobias et al. 2014a). We then divided this number by the total number of species in the family and took the mean of these values to generate a pair-level average.

Climatic disparity. To quantify divergence in species’ climatic niches, we extracted range-wide climatic information for each species from WorldClim (http://www.worldclim.org/) using a global resolution of 10 arc minutes (~100 km^2). Following Lawson and Weir (2014), we focused on 48 climatic variables, 36 related to temperature (maximum, minimum and mean for each month of the year) and 12 to precipitation (mean for each month of the year). We then conducted a PC analysis on these (sorted) values across all species (Lawson and Weir 2014), retaining the first four PC axes that together accounted for 96% of the variation. Euclidean distances between the species' midpoint (median) values in each of the four axes were used as an overall measure of climatic divergence within a pair.

Body mass disparity. To calculate within-pair disparity in body mass, we took the absolute difference between (ln-transformed) body mass values for species within a pair.

Beak disparity. Variables relating to species' beak traits are based on a dataset of biometric measurements collected from museum specimens. For each species, we measured linear measurements of beak morphology (length, width and depth, measures at the nares) for multiple individuals per species (mean = 6.5) per sex. To quantify divergence in beak morphology, we followed the methods outlined in Pigot and Tobias (2013) and calculated beak divergence as the Euclidean distance between species mean (ln-transformed) values for all three axes.

Song learning. Finally, we identified whether species pairs belonged to the oscine (Passeri) or suboscine (Tyranni) passerine suborders, which do and do not exhibit song learning, respectively.

Collinearity among predictor variables

Collinearity among predictor variables is a potential problem in multiple regression modelling (Graham 2003). However, methods based on the type of information theoretic-based model averaging approach we employ here are generally robust to collinearity (Graham 2003; Freckleton 2011). Nonetheless, we checked for collinearity among predictors by calculating pairwise Pearson correlation coefficients (r^2) and variance inflation factors (VIF) for all variables. Only one pair of predictors (latitude and migration) showed evidence of (strong) collinearity ($r^2 = 0.75$; Table S12), and calculating VIFs for our full dataset revealed no evidence of severe (VIF > 10) or even moderate (VIF > 4) multicollinearity (range = 1.16 – 3.14; mean = 1.61), indicating that multicollinearity is unlikely to affect our results.

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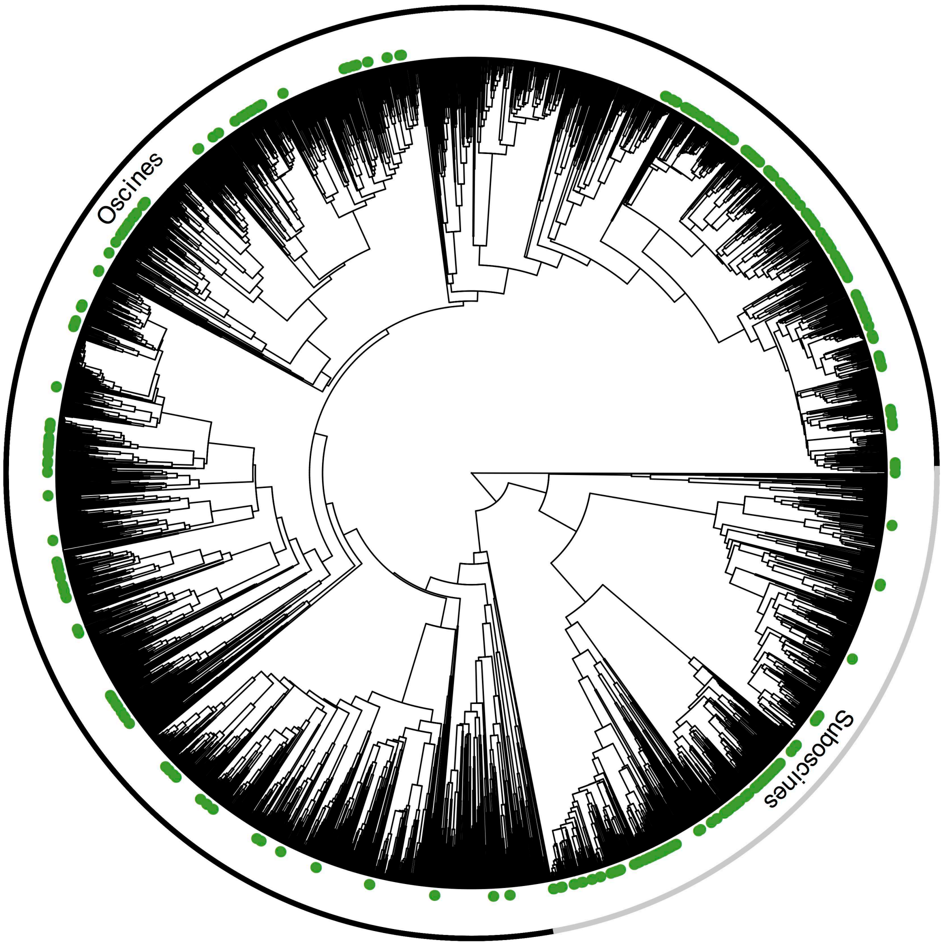

Figure S1. A representative phylogeny of passerines from Jetz et al. (2012) showing the location of species sampled in this study (green points).

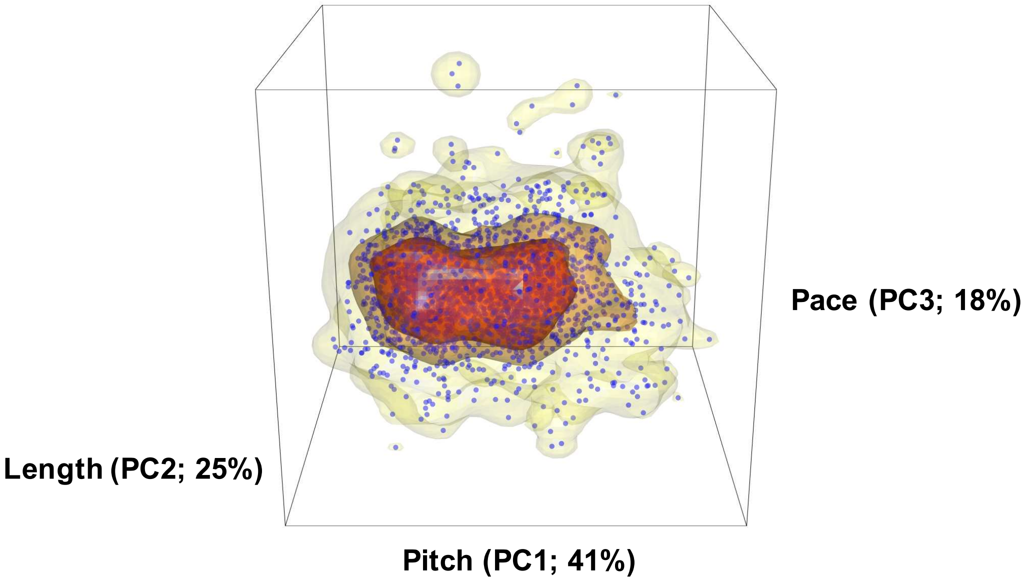

Figure S2. Plot showing the distribution of individual song recordings (n = 2476) in acoustic ‘trait space’, a defined by the first three principal component (PC) axes of variation, corresponding to variation among song in pitch (PC1), length (PC2) and pace (PC3). Coloured areas represent kernel density estimates of 50% (red), 75% (orange) and 100% (yellow) of the data (for illustrative purposes only).

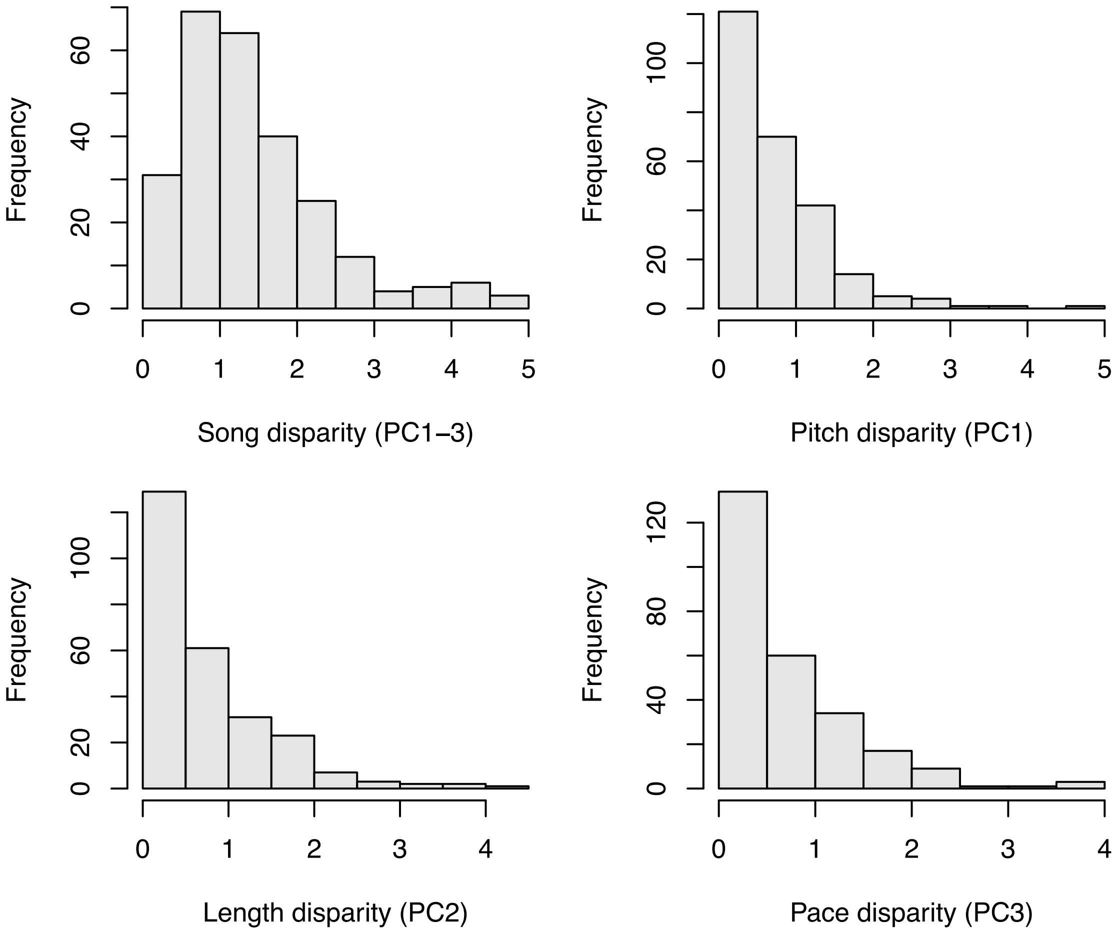

Figure S3. Histograms showing the distribution of within-pair song disparity estimates for species pairs (n = 259).

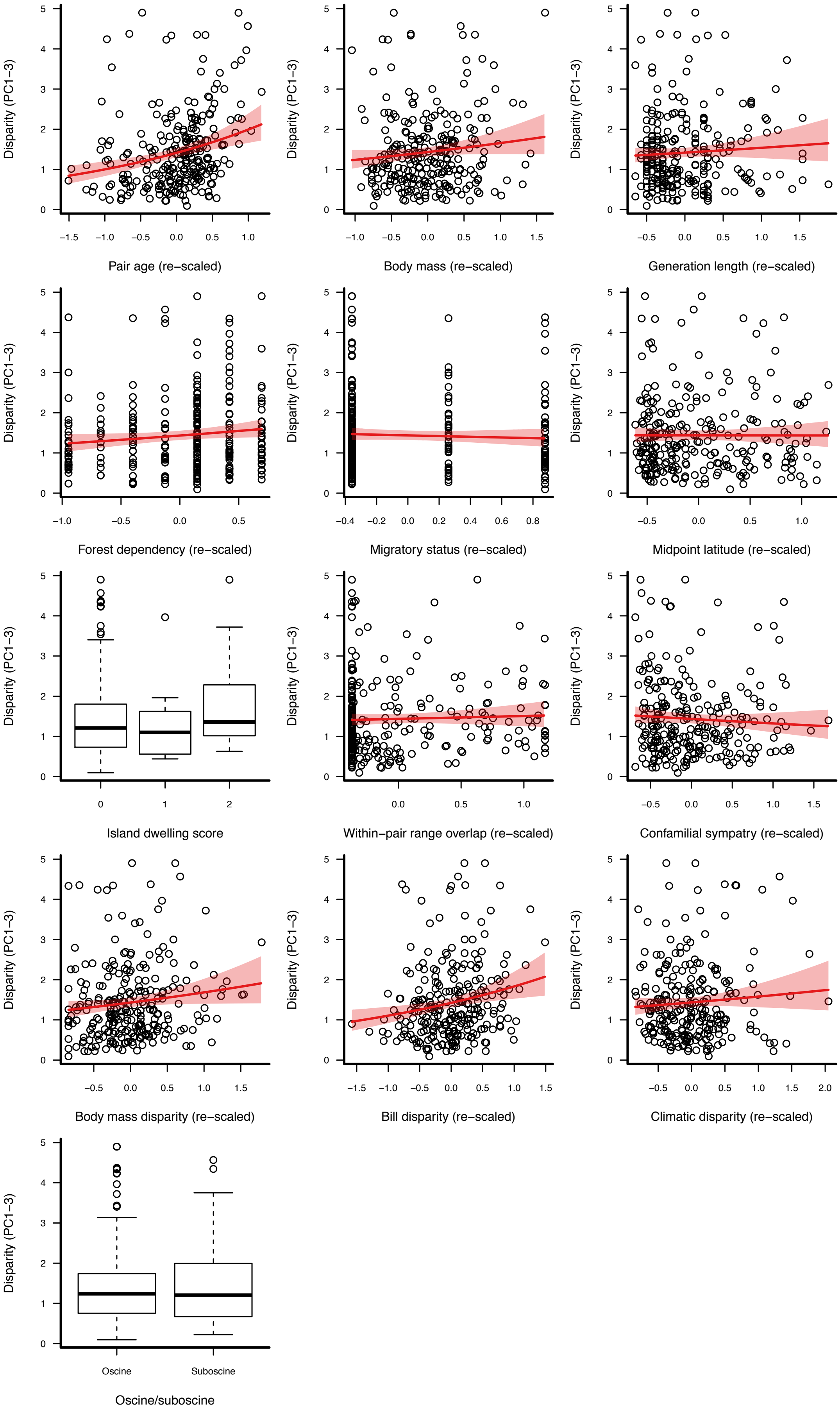

Figure S4. Plots showing the relationship between overall within-pair song disparity (PC1-3) and each of the additional predictors included in our analysis. For all continuous predictors, regressions lines (with prediction intervals, shaded) indicate the best-fitting relationship between the two variables.

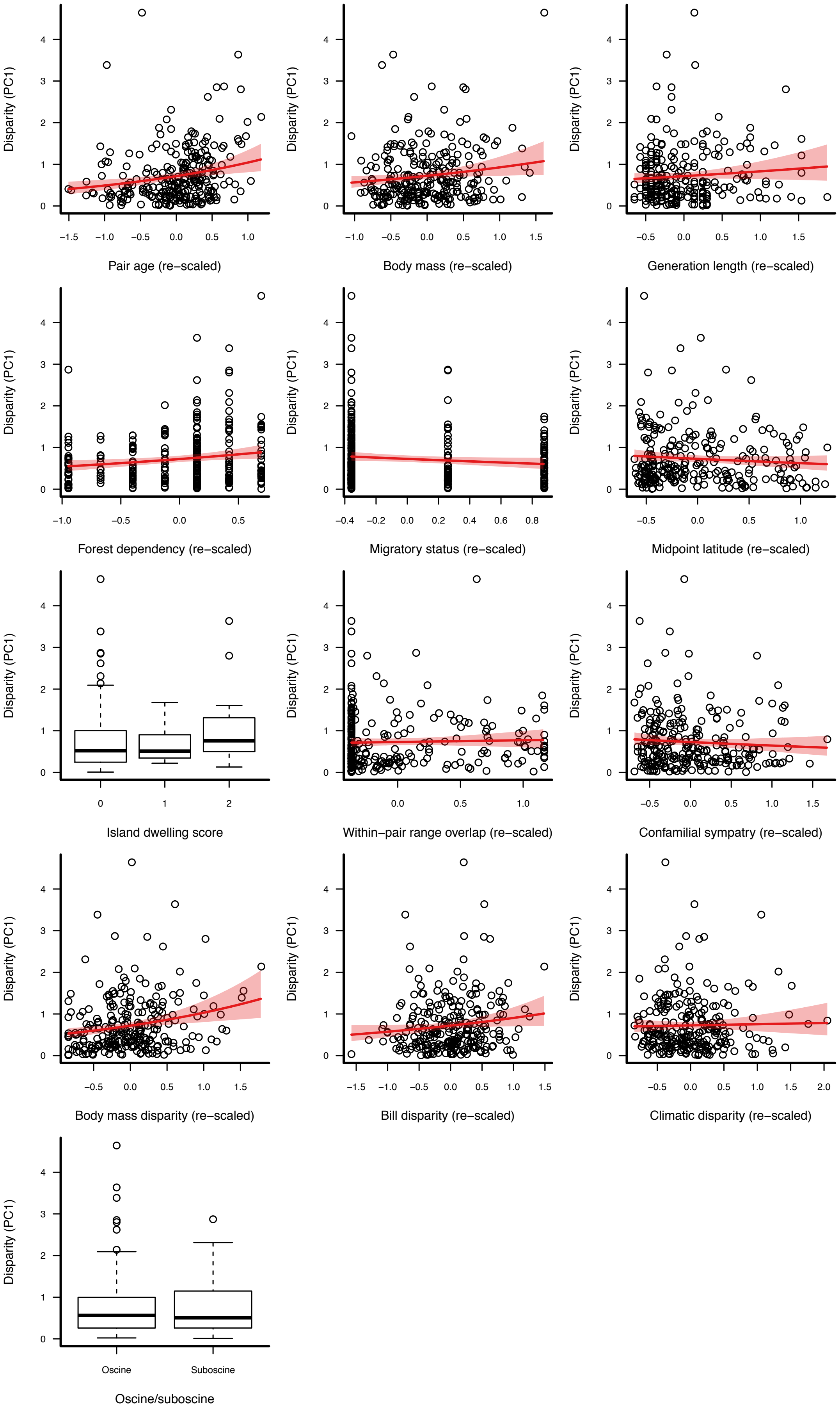

Figure S5. Plots showing the relationship between within-pair disparity in pitch (PC1) and each of the additional predictors included in our analysis. For all continuous predictors, regressions lines (with prediction intervals, shaded) indicate the best-fitting relationship between the two variables.

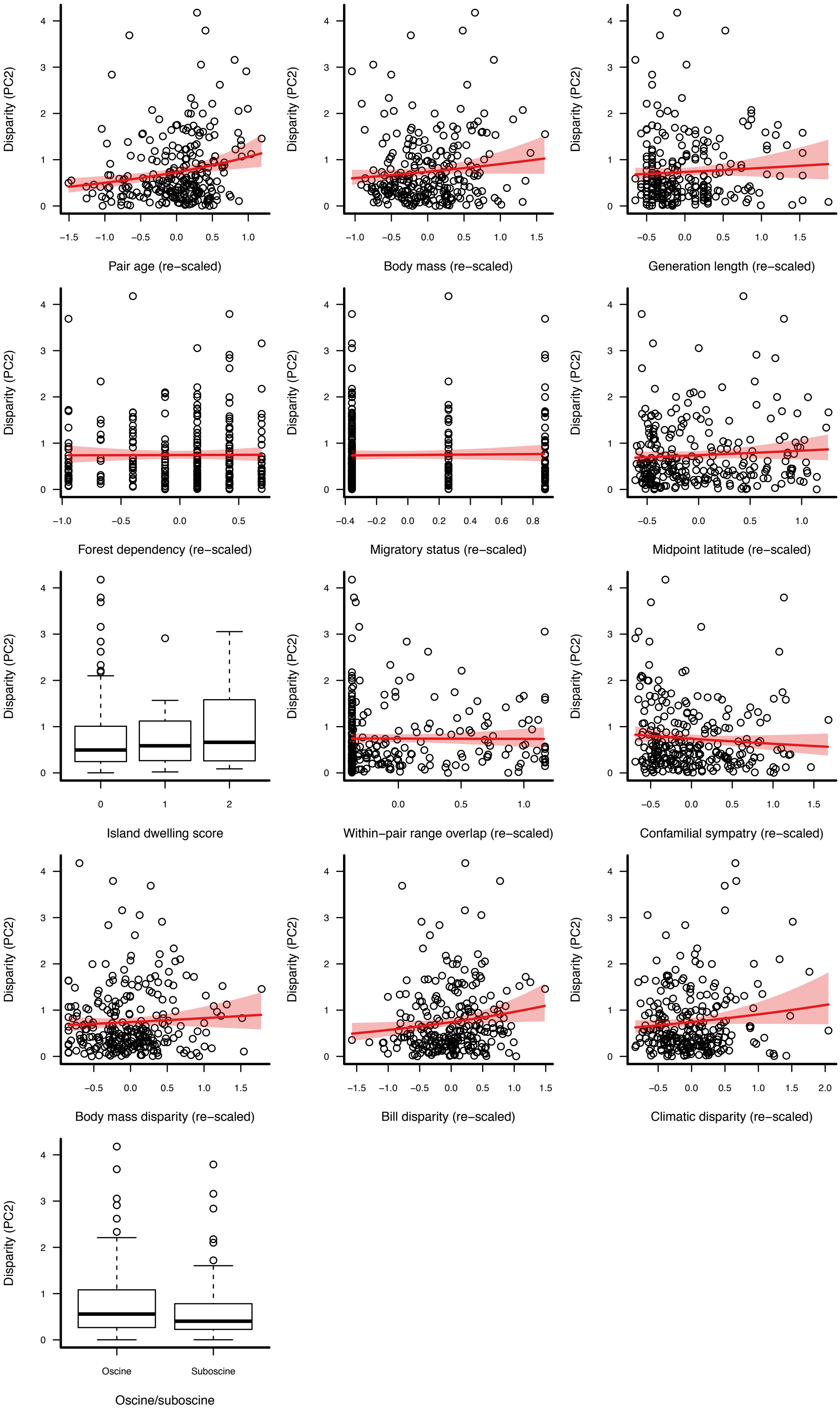

Figure S6. Plots showing the relationship between within-pair disparity in length (PC2) and each of the additional predictors included in our analysis. For all continuous predictors, regressions lines (with prediction intervals, shaded) indicate the best-fitting relationship between the two variables.

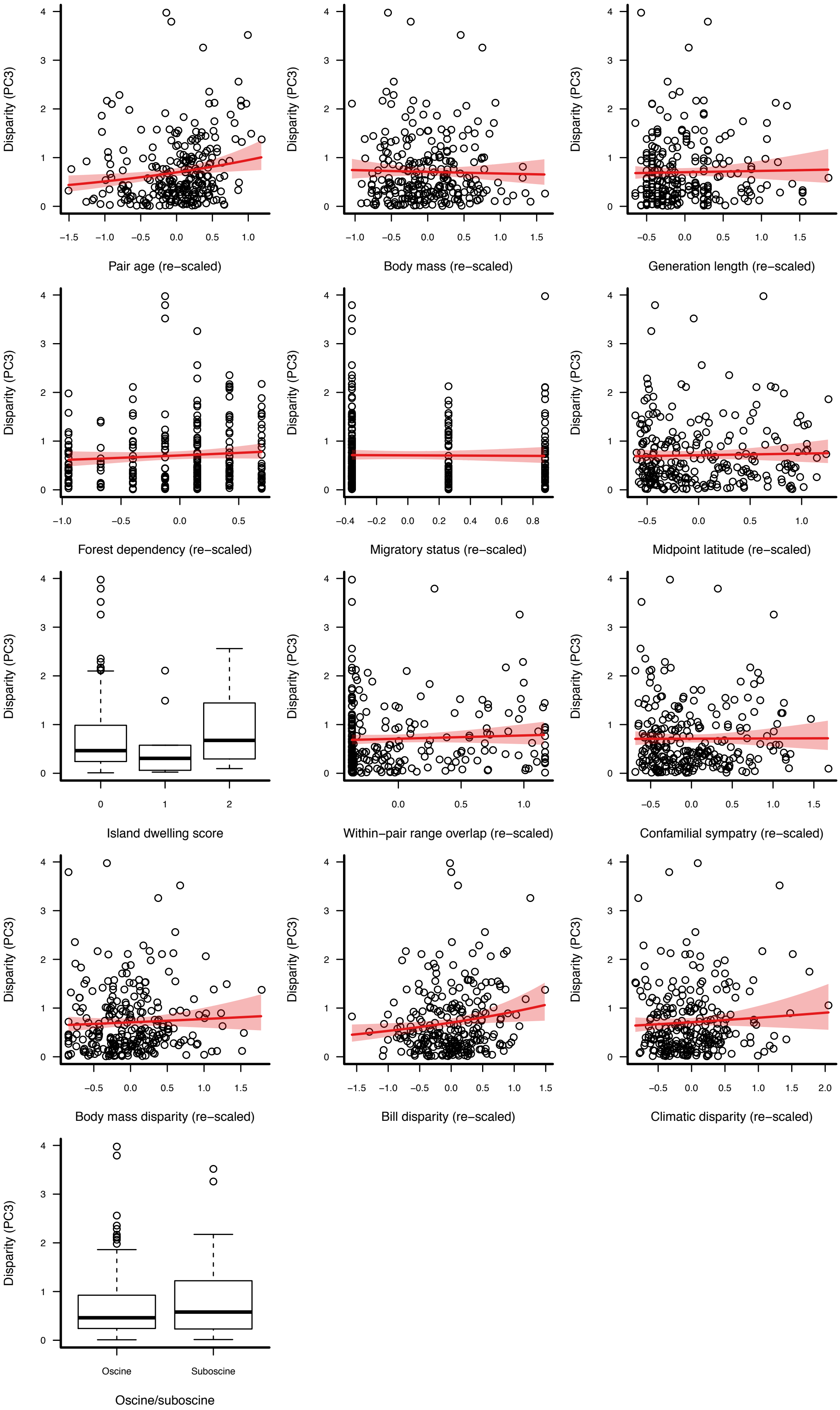

Figure S7. Plots showing the relationship between within-pair disparity in pace (PC3) and each of the additional predictors included in our analysis. For all continuous predictors, regressions lines (with prediction intervals, shaded) indicate the best-fitting relationship between the two variables.

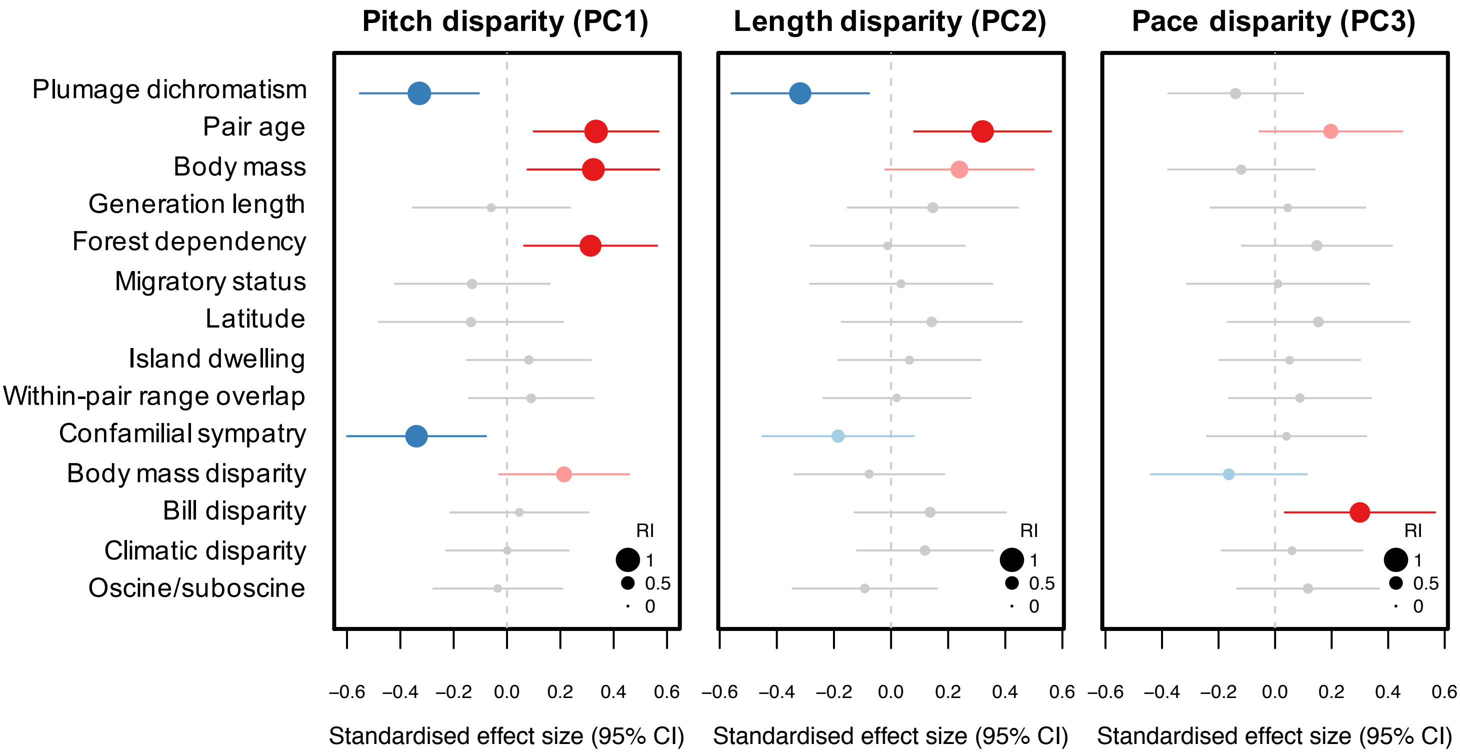

Figure S8. Model averaged coefficient estimates from multipredictor GLMs predicting variation in within-pair disparity in song pitch (PC1), length (PC2) and pace (PC3) among passerine species pairs (n = 246). Within each dataset, points indicate the standardised effect sizes for each of the (scaled) predictor variables and lines indicate 95% confidence intervals (CI). Sizes of points represent the relative importance (RI) of each of the predictor variables, where a value of RI = 0 indicates low importance and a value of RI = 1 indicates high importance. Predictors included in the AIC_c top model for each dataset are coloured (blue = negative effect; red = positive effect), with significant ($P < 0.05$) model-averaged coefficients shown in darker colours.

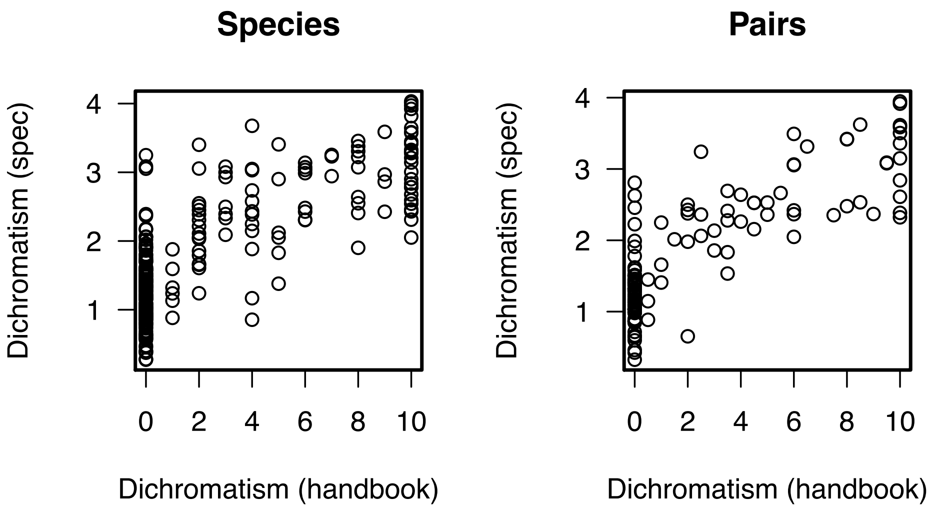

Figure S9. Scatterplots showing the relationship between dichromatism estimates based on spectrophotometric measurements of colouration from museum specimens and handbook illustrations for species (n = 264) and species pairs (n = 132) of birds.

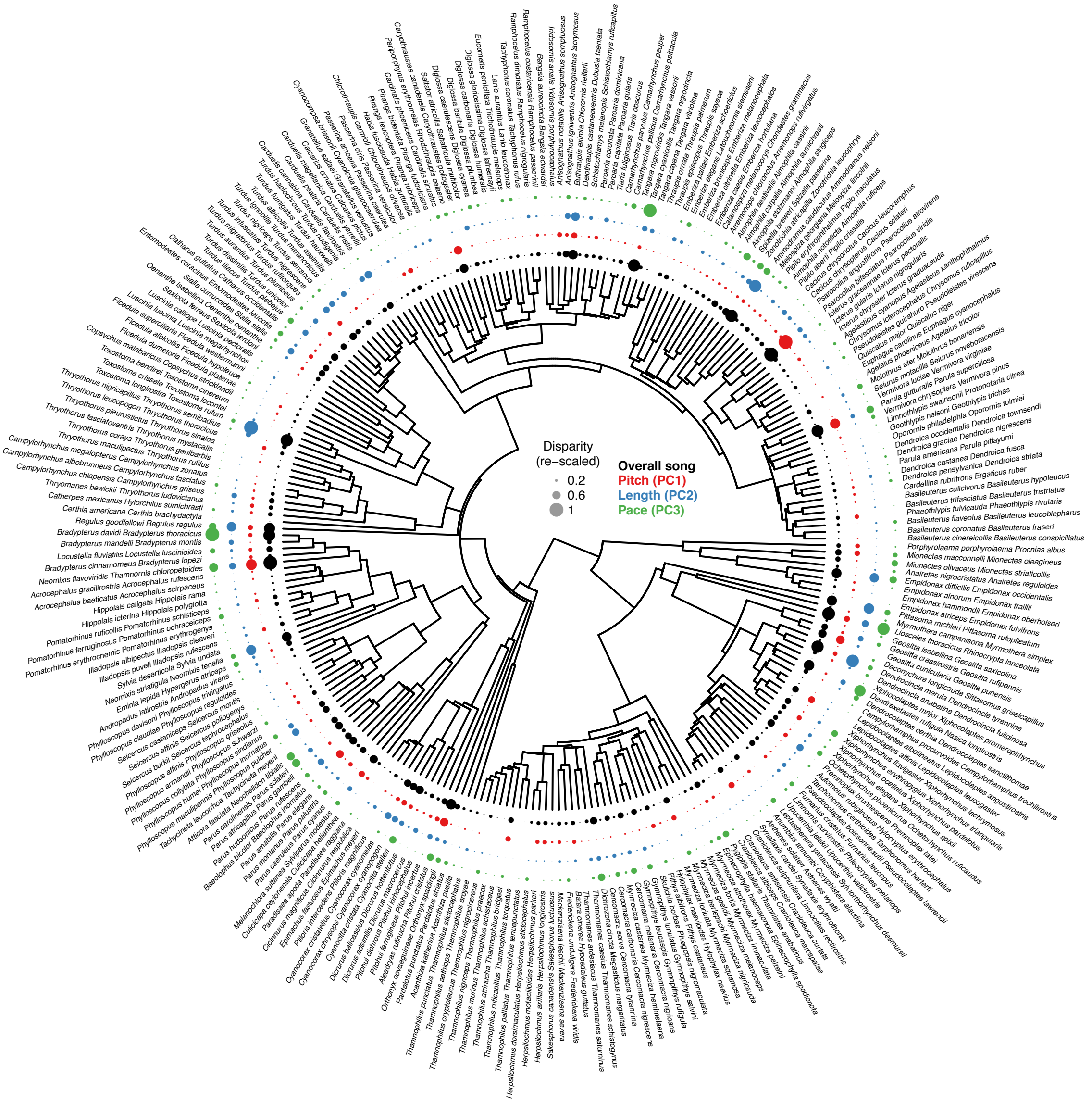

Figure S10. A phylogenetic tree of passerine species pairs (n = 259), showing within-pair disparity in overall song (PC1-3; black), pitch (PC2; red), length (PC3; blue) and pace (PC3; green).

	Pitch (PC1)	Length (PC2)	Pace (PC3)
Maximum frequency	**–0.57**	0.06	0.11
Minimum frequency	–0.27	–0.26	0.41
Peak	**–0.54**	–0.08	0.22
Bandwidth	**–0.48**	0.16	–0.07
Duration	0.12	**0.64**	0.45
Note number	–0.09	**0.70**	–0.16
Pace	–0.25	0.07	**–0.73**
Eigenvalue	2.85	1.72	1.25
Cumulative variance explained (%)	41	65	83

Table S1. Variable loadings and variance explained by the first three principal components (PCs) of an analysis of measurements of individual song recordings (n = 2476) for the species included in our analyses (n = 518). Standardised loadings of the main contributors to each component are highlighted in bold.

	Full dataset			Alternative dataset		
Variable	λ (95% CI)	P (λ = 0)	P (λ = 1)	λ (95% CI)	P (λ = 0)	P (λ = 1)
Total disparity (PC1-3)	0.00 (NA, 0.39)	1.000	<0.001	0.00 (NA, 0.29)	1.000	<0.001
Pitch disparity (PC1)	0.00 (NA, 0.09)	1.000	<0.001	0.00 (NA, 0.08)	1.000	<0.001
Length disparity (PC2)	0.00 (NA, 0.50)	1.000	<0.001	0.00 (NA, 0.14)	1.000	<0.001
Pace disparity (PC3)	0.00 (NA, 0.18)	1.000	<0.001	0.01 (NA, 0.30)	0.719	<0.001

Table S2. Maximum likelihood estimates (and 95% confidence intervals; CI) of phylogenetic signal (Pagel's lambda; λ) for each measure of within-pair song disparity across passerine species pairs (n = 259).

		Full dataset			Alternative dataset		
Response variable	Term	Estimate (SE)	*P*	R^2	Estimate (SE)	*P*	R^2
Total disparity (PC1-3)	Dichromatism	–0.25 (0.08)	0.002	0.04	–0.16 (0.06)	0.001	0.03
Pitch disparity (PC1)	Dichromatism	–0.27 (0.11)	0.015	0.03	–0.13 (0.05)	0.015	0.04
Length disparity (PC2)	Dichromatism	–0.33 (0.12)	0.005	0.04	–0.14 (0.06)	0.019	0.03
Pace disparity (PC3)	Dichromatism	–0.21 (0.12)	0.074	0.02	–0.08 (0.05)	0.137	0.01
Total disparity (PC1-3)	Dichromatism	–0.26 (0.08)	0.001	0.06	–0.17 (0.06)	0.005	0.06
	Forest dependency	0.17 (0.08)	0.039		0.15 (0.06)	0.013	
	Interaction	–0.08 (0.15)	0.585		–0.05 (0.11)	0.627	
Pitch disparity (PC1)	Dichromatism	–0.25 (0.10)	0.009	0.07	–0.14 (0.05)	0.009	0.07
	Forest dependency	0.30 (0.10)	0.006		0.13 (0.05)	0.011	
	Interaction	–0.10 (0.21)	0.633		–0.02 (0.10)	0.803	
Length disparity (PC2)	Dichromatism	–0.33 (0.12)	0.005	0.04	–0.14 (0.06)	0.019	0.04
	Forest dependency	0.02 (0.12)	0.875		0.06 (0.06)	0.311	
	Interaction	–0.10 (0.22)	0.641		–0.06 (0.11)	0.623	
Pace disparity (PC3)	Dichromatism	–0.22 (0.12)	0.065	0.02	–0.09 (0.05)	0.116	0.02
	Forest dependency	0.16 (0.12)	0.181		0.06 (0.05)	0.261	
	Interaction	–0.06 (0.22)	0.796		0.02 (0.10)	0.820	

Table S3. Standardised coefficient estimates from GLMs predicting variation in within-pair disparity in song traits among passerine species pairs (n = 259). SE, standard error. R^2, pseudo-R^2.

	Full dataset			
	N pairs	Estimate (SE)	*P*	R^2
Plumage dichromatism	259	–0.25 (0.08)	0.002	0.04
Pair age	259	0.34 (0.08)	<0.001	0.09
Body mass	259	0.15 (0.08)	0.081	0.02
Generation length	251	0.08 (0.08)	0.334	<0.01
Forest dependency	259	0.15 (0.08)	0.063	0.02
Migratory status	259	–0.06 (0.08)	0.467	<0.01
Latitude	257	0.00 (0.08)	0.987	<0.01
Island dwelling	259	0.12 (0.08)	0.150	0.01
Within-pair range overlap	257	0.05 (0.08)	0.565	<0.01
Confamilial sympatry	257	–0.08 (0.08)	0.330	0.01
Body mass disparity	259	0.16 (0.08)	0.053	0.02
Bill disparity	257	0.25 (0.08)	0.003	0.04
Climatic disparity	254	0.10 (0.08)	0.252	0.01
Oscine/suboscine	259	0.01 (0.08)	0.919	<0.01

Table S4. Standardised coefficient estimates from single predictor GLMs predicting variation in within-pair song disparity (PC1-3) among passerine species pairs (n = 259). SE, standard error. R^2, pseudo-R^2.

		Full dataset								
		Pitch disparity (PC1)			Length disparity (PC2)			Pace disparity (PC3)		
	N pairs	Estimate (SE)	*P*	R^2	Estimate (SE)	*P*	R^2	Estimate (SE)	*P*	R^2
Plumage dichromatism	259	–0.27 (011)	0.015	0.03	–0.33 (0.12)	0.001	0.04	–0.21 (0.12)	0.074	0.02
Pair age	259	0.38 (0.12)	0.001	0.07	0.37 (0.12)	0.002	0.06	0.31 (0.12)	0.010	0.04
Body mass	259	0.25 (0.11)	0.028	0.03	0.20 (0.12)	0.088	0.02	–0.05 (0.12)	0.677	<0.01
Generation length	251	0.15 (0.12)	0.203	0.01	0.11 (0.12)	0.353	0.01	0.04 (0.12)	0.741	<0.01
Forest dependency	259	0.29 (0.11)	0.008	0.04	0.01 (0.12)	0.941	<0.01	0.14 (0.12)	0.229	0.01
Migratory status	259	–0.21 (0.11)	0.060	0.02	0.03 (0.12)	0.783	<0.01	–0.02 (0.12)	0.868	<0.01
Latitude	257	–0.15 (0.11)	0.180	0.01	0.12 (0.12)	0.299	0.01	0.05 (0.12)	0.701	<0.01
Island dwelling	259	0.19 (0.11)	0.096	0.02	0.14 (0.12)	0.234	0.01	0.08 (0.12)	0.518	<0.01
Within-pair range overlap	257	0.06 (0.11)	0.621	<0.01	–0.01 (0.12)	0.937	<0.01	0.09 (0.12)	0.448	<0.01
Confamilial sympatry	257	–0.12 (0.11)	0.281	0.01	–0.16 (0.12)	0.182	0.01	0.01 (0.12)	0.954	<0.01
Body mass disparity	259	0.36 (0.11)	0.002	0.06	0.11 (0.12)	0.371	<0.01	0.09 (0.12)	0.441	<0.01
Bill disparity	257	0.23 (0.11)	0.047	0.02	0.26 (0.12)	0.030	0.03	0.28 (0.12)	0.018	0.03
Climatic disparity	254	0.04 (0.12)	0.738	<0.01	0.20 (0.12)	0.086	0.02	0.12 (0.12)	0.315	0.01
Oscine/suboscine	259	–0.01 (0.11)	0.919	<0.01	–0.14 (0.12)	0.234	0.01	0.15 (0.12)	0.215	0.01

Table S5. Standardised coefficient estimates from single predictor GLMs predicting variation in within-pair disparity in three independent axes of song variation among passerine species pairs (n = 259). SE, standard error. R^2, pseudo-R^2.

	Full dataset				
	Model averaged			AIC$_c$ top model	
	Estimate (SE)	*P*	RI	Estimate (SE)	*P*
Plumage dichromatism	-0.25 (0.09)	0.004	0.98*	-0.25 (0.08)	0.003
Pair age	0.28 (0.09)	0.002	0.99*	0.26 (0.09)	0.002
Body mass	0.17 (0.09)	0.070	0.74*	0.16 (0.09)	0.057
Generation length	0.04 (0.11)	0.731	0.29	-	-
Forest dependency	0.15 (0.09)	0.106	0.61*	0.17 (0.09)	0.064
Migratory status	-0.01 (0.11)	0.959	0.26	-	-
Latitude	0.02 (0.13)	0.868	0.28	-	-
Island dwelling	0.05 (0.09)	0.576	0.29	-	-
Within-pair range overlap	0.06 (0.09)	0.492	0.31	-	-
Confamilial sympatry	-0.16 (0.10)	0.093	0.65*	-0.18 (0.09)	0.045
Body mass disparity	-0.02 (0.10)	0.854	0.27	-	-
Bill disparity	0.15 (0.09)	0.104	0.62*	0.14 (0.09)	0.098
Climatic disparity	0.03 (0.09)	0.737	0.27	-	-
Oscine/suboscine	0.00 (0.09)	0.968	0.26	-	-

Table S6. Standardised coefficient estimates from model averaged and AIC$_c$ top model multipredictor GLMs predicting variation in within-pair song disparity (PC1-3) among passerine species pairs (n = 246). SE, standard error; RI, relative importance. Pseudo-R^2 for AIC$_c$ top model = 0.17.

	Full dataset								
	Pitch disparity (PC1)			Length disparity (PC2)			Pace disparity (PC3)		
	Estimate (SE)	*P*	RI	Estimate (SE)	*P*	RI	Estimate (SE)	*P*	RI
Plumage dichromatism	-0.33 (0.11)	0.004	0.97*	-0.32 (0.12)	0.010	0.91*	-0.14 (0.12)	0.252	0.39
Pair age	0.33 (0.12)	0.005	0.96*	0.32 (0.12)	0.009	0.92*	0.20 (0.13)	0.126	0.56*
Body mass	0.32 (0.13)	0.010	0.93*	0.24 (0.13)	0.071	0.69*	-0.12 (0.13)	0.366	0.34
Generation length	-0.06 (0.15)	0.698	0.28	0.15 (0.15)	0.337	0.38	0.04 (0.14)	0.748	0.27
Forest dependency	0.31 (0.13)	0.014	0.89*	-0.01 (0.14)	0.930	0.27	0.15 (0.13)	0.275	0.39
Migratory status	-0.13 (0.15)	0.378	0.35	0.04 (0.16)	0.829	0.28	0.01 (0.16)	0.951	0.28
Latitude	-0.13 (0.18)	0.444	0.34	0.14 (0.16)	0.375	0.36	0.15 (0.16)	0.348	0.37
Island dwelling	0.08 (0.12)	0.492	0.31	0.06 (0.13)	0.611	0.29	0.05 (0.13)	0.685	0.28
Within-pair range overlap	0.09 (0.12)	0.446	0.32	0.02 (0.13)	0.877	0.26	0.09 (0.13)	0.494	0.31
Confamilial sympatry	-0.34 (0.13)	0.011	0.92*	-0.19 (0.13)	0.172	0.49*	0.04 (0.14)	0.779	0.27
Body mass disparity	0.21 (0.12)	0.085	0.61*	-0.08 (0.13)	0.569	0.29	-0.16 (0.14)	0.245	0.42*
Bill disparity	0.05 (0.13)	0.725	0.28	0.14 (0.13)	0.309	0.38	0.30 (0.14)	0.027	0.82*
Climatic disparity	0.00 (0.12)	0.992	0.26	0.12 (0.12)	0.329	0.35	0.06 (0.13)	0.638	0.28
Oscine/suboscine	-0.03 (0.12)	0.778	0.26	-0.09 (0.13)	0.477	0.31	0.12 (0.13)	0.363	0.34

Table S7. Standardised coefficient estimates from model averaged multipredictor GLMs predicting variation in within-pair disparity in three independent axes of song variation among passerine species pairs (n = 246). SE, standard error; RI, relative importance. * Denotes predictor variables included in the AIC_c top model.

	Full dataset					
	Pitch disparity (PC1)		Length disparity (PC2)		Pace disparity (PC3)	
	Estimate (SE)	*P*	Estimate (SE)	*P*	Estimate (SE)	*P*
Plumage dichromatism	-0.34 (0.11)	0.002	-0.30 (0.12)	0.010	-	-
Pair age	0.31 (0.12)	0.007	0.34 (0.12)	0.004	0.21 (0.12)	0.095
Body mass	0.33 (0.11)	0.002	0.27 (0.12)	0.027	-	-
Generation length	-	-	-	-	-	-
Forest dependency	0.34 (0.12)	0.005	-	-	-	-
Migratory status	-	-	-	-	-	-
Latitude	-	-	-	-	-	-
Island dwelling	-	-	-	-	-	-
Within-pair range overlap	-	-	-	-	-	-
Confamilial sympatry	-0.31 (0.12)	0.010	-0.21 (0.12)	0.075	-	-
Body mass disparity	0.21 (0.12)	0.070	-	-	-0.20 (0.13)	0.131
Bill disparity	-	-	-	-	0.30 (0.13)	0.024
Climatic disparity	-	-	-	-	-	-
Oscine/suboscine	-	-	-	-	-	-

Table S8. Standardised coefficient estimates from AIC_c top models predicting variation in within-pair disparity in song traits among passerine species pairs (n = 246). SE, standard error. Pseudo-R^2 for each model: PC1 = 0.22; PC2 = 0.12; PC3 = 0.06.

	Alternative dataset				
	Model averaged			AIC$_c$ top model	
	Estimate (SE)	*P*	RI	Estimate (SE)	*P*
Plumage dichromatism	-0.16 (0.06)	0.010	0.94	-0.16 (0.06)	0.001
Pair age	0.21 (0.06)	0.001	0.99	0.20 (0.06)	0.001
Body mass	0.10 (0.07)	0.137	0.58	0.09 (0.06)	0.158
Generation length	0.03 (0.08)	0.722	0.29	-	-
Forest dependency	0.17 (0.07)	0.017	0.91	0.17 (0.06)	0.009
Migratory status	0.04 (0.08)	0.611	0.30	-	-
Latitude	0.06 (0.09)	0.497	0.34	-	-
Island dwelling	0.01 (0.07)	0.849	0.26	-	-
Within-pair range overlap	0.06 (0.07)	0.388	0.35	-	-
Confamilial sympatry	-0.15 (0.07)	0.040	0.80	-0.16 (0.07)	0.017
Body mass disparity	0.01 (0.07)	0.872	0.27	-	-
Bill disparity	0.10 (0.07)	0.124	0.58	0.09 (0.06)	0.134
Climatic disparity	0.03 (0.07)	0.647	0.28	-	-
Oscine/suboscine	0.07 (0.07)	0.298	0.40	-	-

Table S9. Standardised coefficient estimates from model averaged and AIC$_c$ top model multipredictor GLMs predicting variation in within-pair song disparity (PC1-3) using an alternative dataset of passerine species pairs (n = 246). SE, standard error; RI, relative importance. Pseudo-R^2 for AIC$_c$ top model = 0.16.

	Alternative dataset								
	Pitch disparity (PC1)			Length disparity (PC2)			Pace disparity (PC3)		
	Estimate (SE)	*P*	RI	Estimate (SE)	*P*	RI	Estimate (SE)	*P*	RI
Plumage dichromatism	-0.15 (0.05)	0.004	0.99*	-0.14 (0.06)	0.022	0.92*	-0.06 (0.06)	0.288	0.41
Pair age	0.16 (0.05)	0.004	0.99*	0.14 (0.06)	0.018	0.93*	0.10 (0.06)	0.085	0.71*
Body mass	0.15 (0.06)	0.009	0.97*	0.13 (0.07)	0.056	0.82*	-0.06 (0.06)	0.309	0.40
Generation length	-0.01 (0.07)	0.889	0.26	0.05 (0.08)	0.497	0.34	0.01 (0.07)	0.888	0.27
Forest dependency	0.16 (0.06)	0.005	0.98*	0.08 (0.07)	0.237	0.47*	0.07 (0.06)	0.264	0.44
Migratory status	0.00 (0.07)	0.970	0.26	0.04 (0.08)	0.599	0.32	0.01 (0.08)	0.928	0.29
Latitude	-0.01 (0.07)	0.885	0.26	0.09 (0.08)	0.262	0.47*	0.09 (0.07)	0.210	0.51*
Island dwelling	0.04 (0.05)	0.502	0.31	-0.01 (0.06)	0.819	0.26	0.03 (0.06)	0.579	0.30
Within-pair range overlap	0.02 (0.05)	0.702	0.27	0.03 (0.07)	0.615	0.30	0.03 (0.06)	0.597	0.29
Confamilial sympatry	-0.17 (0.06)	0.003	0.99*	-0.08 (0.07)	0.227	0.49	-0.01 (0.07)	0.911	0.27
Body mass disparity	0.10 (0.06)	0.078	0.69*	-0.04 (0.07)	0.595	0.30	-0.06 (0.06)	0.311	0.41
Bill disparity	0.01 (0.06)	0.810	0.27	0.07 (0.07)	0.319	0.41	0.14 (0.06)	0.026	0.90*
Climatic disparity	0.00 (0.05)	0.981	0.25	0.07 (0.06)	0.291	0.42	0.02 (0.06)	0.756	0.27
Oscine/suboscine	0.02 (0.06)	0.763	0.26	0.01 (0.06)	0.869	0.26	0.09 (0.06)	0.124	0.61*

Table S10. Standardised coefficient estimates from model averaged multipredictor GLMs predicting variation in within-pair disparity in song traits using an alternative dataset of passerine species pairs (n = 246). SE, standard error; RI, relative importance. * Denotes predictor variables included in the AIC$_c$ top model.

	Alternative dataset					
	Pitch disparity (PC1)		Length disparity (PC2)		Pace disparity (PC3)	
	Estimate (SE)	*P*	Estimate (SE)	*P*	Estimate (SE)	*P*
Plumage dichromatism	-0.15 (0.05)	0.003	-0.14 (0.06)	0.018	-	-
Pair age	0.15 (0.05)	0.004	0.14 (0.06)	0.018	0.09 (0.06)	0.116
Body mass	0.14 (0.05)	0.007	0.14 (0.06)	0.021	-	-
Generation length	-	-	-	-	-	-
Forest dependency	0.16 (0.05)	0.003	0.09 (0.07)	0.175	-	-
Migratory status	-	-	-	-	-	-
Latitude	-	-	-0.13 (0.07)	0.055	0.08 (0.06)	0.145
Island dwelling	-	-	-	-	-	-
Within-pair range overlap	-	-	-	-	-	-
Confamilial sympatry	-0.17 (0.05)	0.002	-	-	-	-
Body mass disparity	0.10 (0.05)	0.066	-	-	-	-
Bill disparity	-	-	-	-	0.12 (0.06)	0.036
Climatic disparity	-	-	-	-	-	-
Oscine/suboscine	-	-	-	-	0.09 (0.06)	0.098

Table S11. Standardised coefficient estimates from AIC$_c$ top models predicting variation in within-pair disparity in song traits using an alternative dataset of passerine species pairs (n = 246). SE, standard error. Pseudo-R^2 for each model: PC1 = 0.23; PC2 = 0.12; PC3 = 0.08.

	Pair age	**Body mass**	**Generation length**	**Forest dependency**	**Migratory status**	**Latitude**	**Island dwelling**	**Plumage dichromatism**	**Within-pair range overlap**	**Confamilial sympatry**	**Body mass disparity**	**Bill disparity**	**Climate disparity**
Body mass	0.03												
Generation length	0.06	0.52											
Forest dependency	0.13	0.07	0.27										
Migratory status	-0.02	-0.34	-0.31	-0.31									
Latitude	0.01	-0.29	-0.27	-0.46	0.75								
Island dwelling	0.07	0.18	0.36	0.14	-0.16	-0.18							
Plumage dichromatism	0.02	0.15	0.30	0.08	0.03	-0.05	0.06						
Within-pair range overlap	0.14	-0.01	-0.05	-0.06	0.11	0.13	0.12	-0.02					
Confamilial sympatry	0.07	0.22	0.26	0.37	-0.40	-0.55	0.11	0.09	0.10				
Body mass disparity	0.25	0.18	0.09	-0.10	-0.10	-0.05	0.13	0.02	0.04	-0.01			
Bill disparity	0.26	0.18	0.10	-0.07	-0.03	-0.02	0.13	-0.05	0.13	0.04	0.47		
Climate disparity	0.00	0.02	0.02	-0.05	0.08	0.02	-0.07	0.02	-0.41	-0.10	0.06	0.06	
Oscine/suboscine	0.03	0.04	0.10	0.25	-0.29	-0.31	-0.18	0.11	-0.04	0.33	0.01	-0.03	-0.07

Table S12. Pearson correlation coefficients (r^2) for all pairwise combinations of (standardised) predictor variables considered in our analysis