

Supporting Information

Evolution of vocal performance and song complexity in island birds

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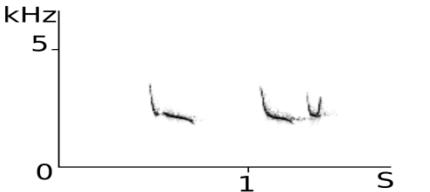
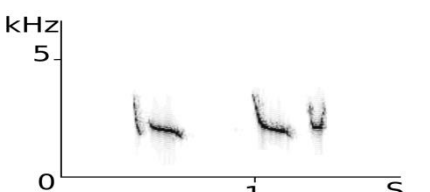
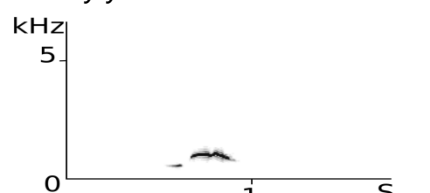
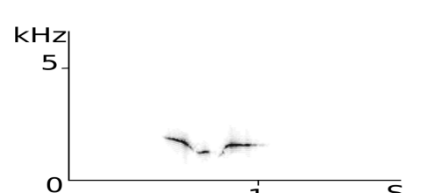
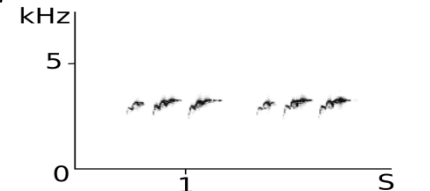
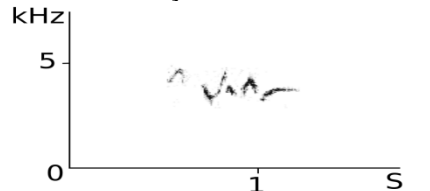
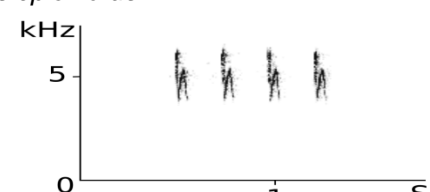
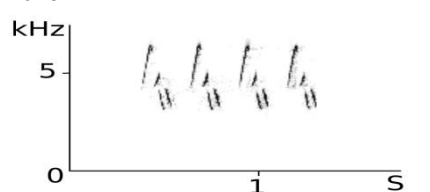
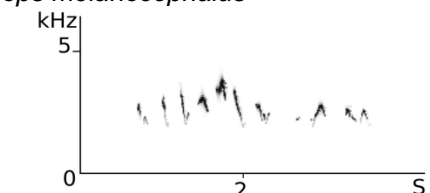
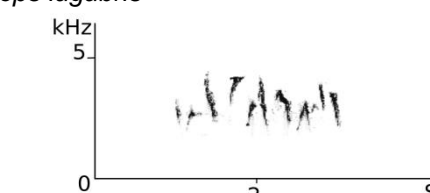
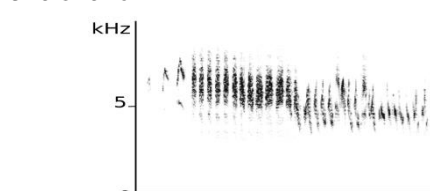
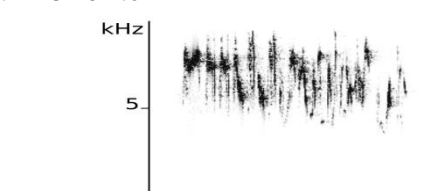
Appendix 1: Sample sites

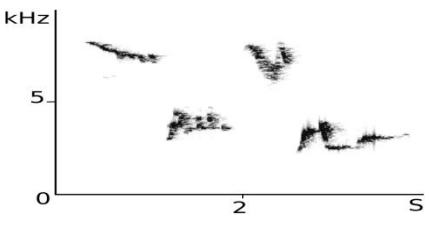
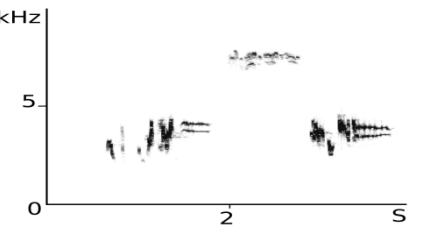
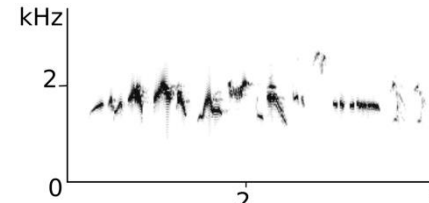
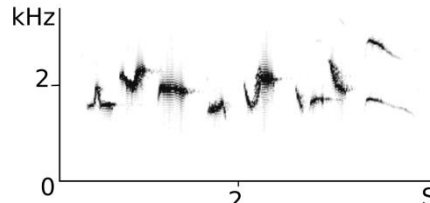
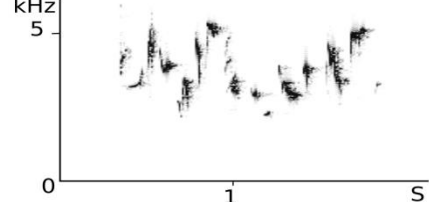
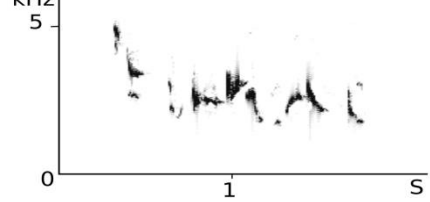
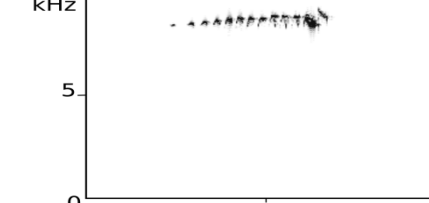
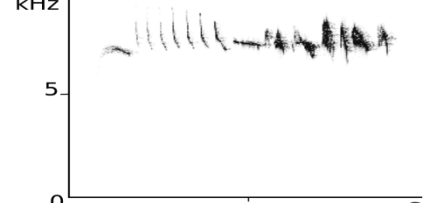
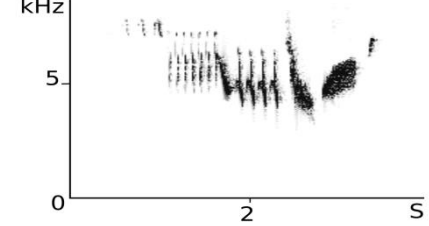
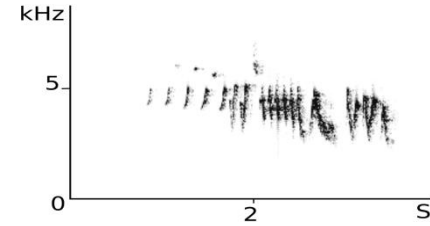
Table S1: Gazetteer with altitude above sea level (ASL) of the twelve localities (four communities) for which samples were collected. Soundscapes were characterised in two localities of each region and are described in Robert et al. (2019).

| REGION | LOCALITY | LATITUDE | LONGITUDE | ASL |
|---------------------|------------------|---------------|---------------|------|
| Madeira Island | Seixal | 32°48'55.56"N | 17°06'51.46"O | 400 |
| Madeira Island | Achada | 32°50'19.19"N | 17°11'35.70"O | 700 |
| Madeira Island | Portela | 32°45'09.81"N | 16°48'13.91"O | 500 |
| Mediterranean basin | la Rouvière | 43°39'28.23"N | 03°40'42.60"E | 290 |
| Mediterranean basin | La Verne | 43°16'40.98"N | 06°16'54.78"E | 650 |
| Mediterranean basin | Maruèjols | 43°50'07.97"N | 04°11'25.69"E | 200 |
| São Tomé Island | Chamiço | 00°19'04.54"N | 06°35'56.90"E | 600 |
| São Tomé Island | Macambrará | 00°16'30.85"N | 06°36'20.37"E | 1200 |
| São Tomé Island | Morro Esperança | 00°17'38.68"N | 06°36'39.86"E | 1000 |
| Cameroon | Mapia | 04°10'23.46"N | 09°11'57.91"E | 1950 |
| Cameroon | Bakingili Forest | 04°05'27.30"N | 09°02'39.25"E | 300 |
| Cameroon | Etome Forest | 04°03'17.09"N | 09°06'23.04"E | 400 |

Appendix 2 – Typical songs of focal species

Table S2. Spectrograms of the songtypes of the study species

| Tropical mainland | Tropical island |
|---|--|
| <p><i>Chrysococcyx chrysococcyx cupreus</i></p>  | <p><i>Chrysococcyx chrysococcyx insularum</i></p>  |
| <p><i>Oriolus brachyrynchus</i></p>  | <p><i>Oriolus crassirostris</i></p>  |
| <p><i>Terpsiphone rufiventer</i></p>  | <p><i>Terpsiphone atrochalybeia</i></p>  |
| <p><i>Urolais epichlorusⁱ</i></p>  | <p><i>Prinia mollerii</i></p>  |
| <p><i>Zosterops melanocephalus</i></p>  | <p><i>Zosterops lugubris</i></p>  |
| <p><i>Cinnyris reichenowi</i></p>  | <p><i>Anabathmis newtonii</i></p>  |

| Temperate mainland | Temperate island |
|---|--|
| <p><i>Erithacus rubecula</i></p>  | <p><i>Erithacus rubecula</i></p>  |
| <p><i>Turdus merula merula</i></p>  | <p><i>Turdus merula cabreræ</i></p>  |
| <p><i>Sylvia atricapilla atricapilla</i></p>  | <p><i>Sylvia atricapilla heinekeni</i></p>  |
| <p><i>Regulus ignicapillus</i></p>  | <p><i>Regulus madeirensis</i></p>  |
| <p><i>Fringilla coelebs coelebs</i></p>  | <p><i>Fringilla coelebs madeirensis</i></p>  |

Appendix 3: Sample size and acoustic data for each of the study species

Table S3: Summary table with the number of songs and individuals analyzed for each of the study species.

Appendix 4: Measure of acoustic parameters

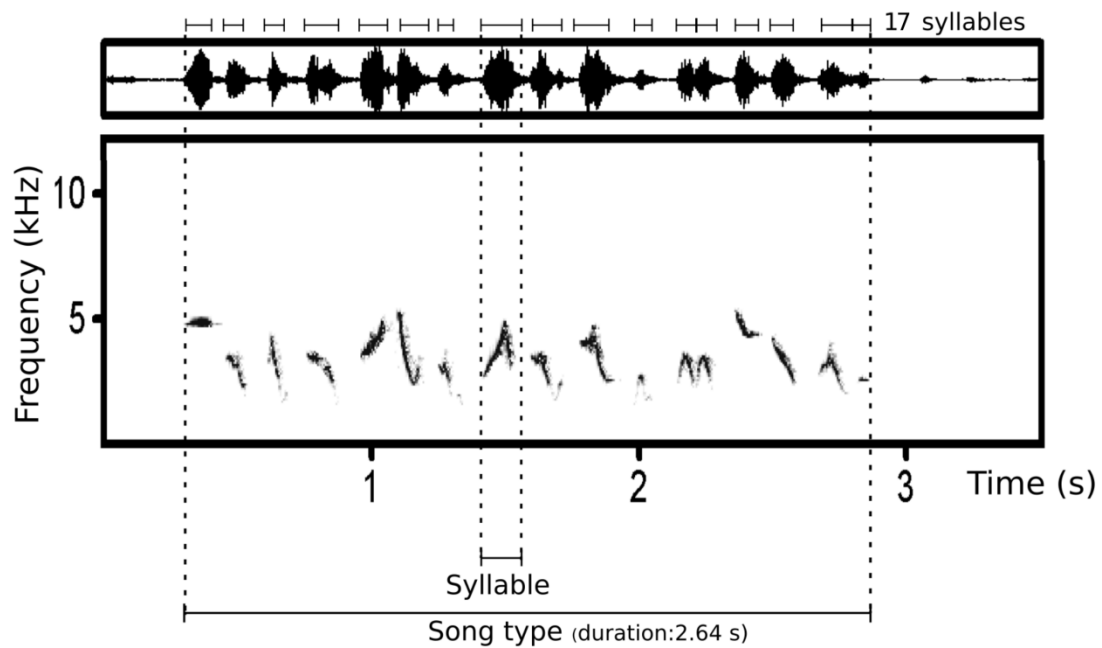


Figure S1: Spectrogram and oscillogram (above) for a song type from a Mount Cameroon speirops (*Zosterops melanocephalus*). For this song, song duration is 2.64 seconds, the number of syllables is 17, and syllable rate is $17/2.64=6.44$. The number of different syllables is 10.

Appendix 6: Correlation between variables

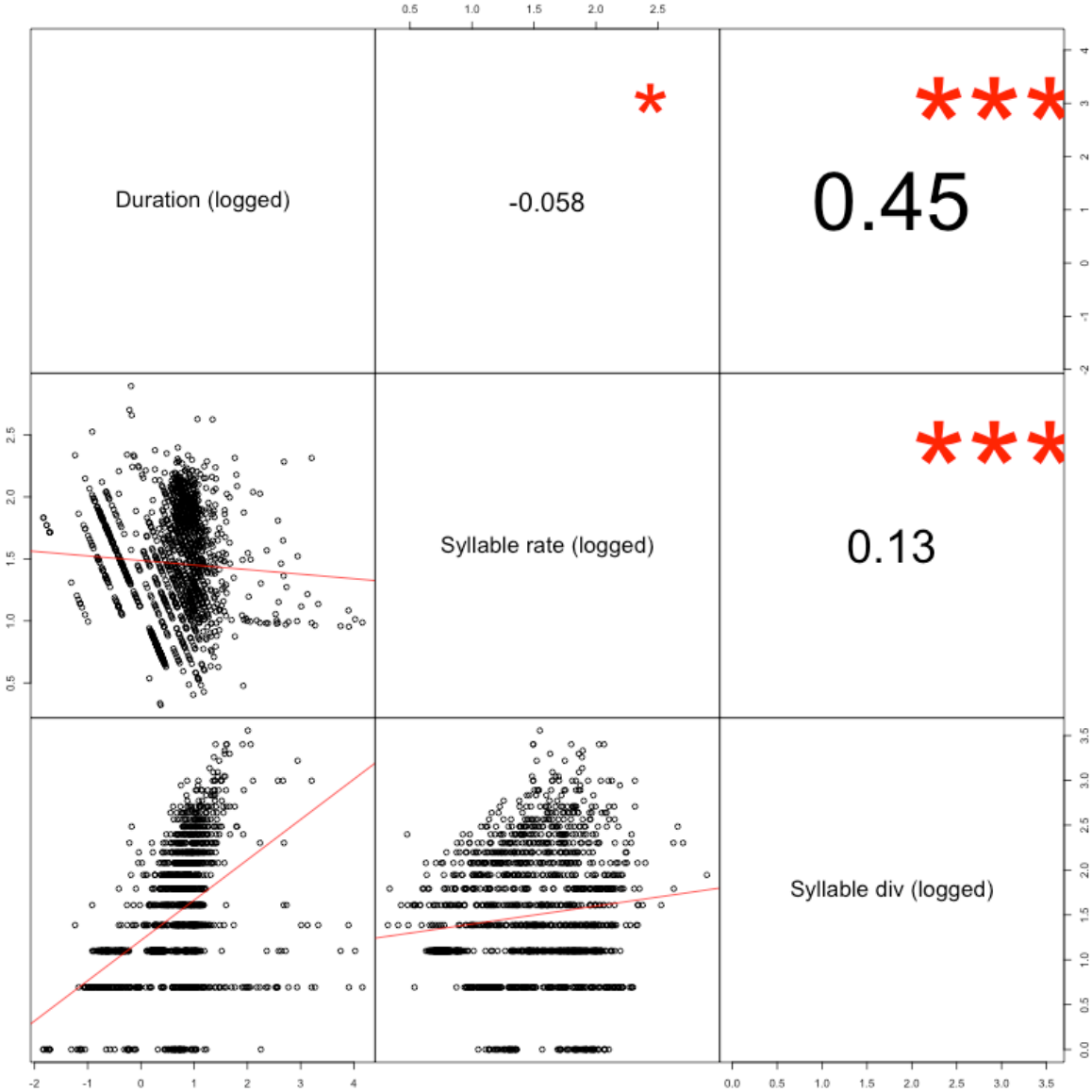


Figure S2: Correlation matrix between the three studied variables. Numbers are the values of Pearson correlation coefficient r while stars are associated p -values: * < 0.05, ** < 0.01 ***<0.001. Red lines represent fitted correlation.

Appendix 5: Accumulation curves

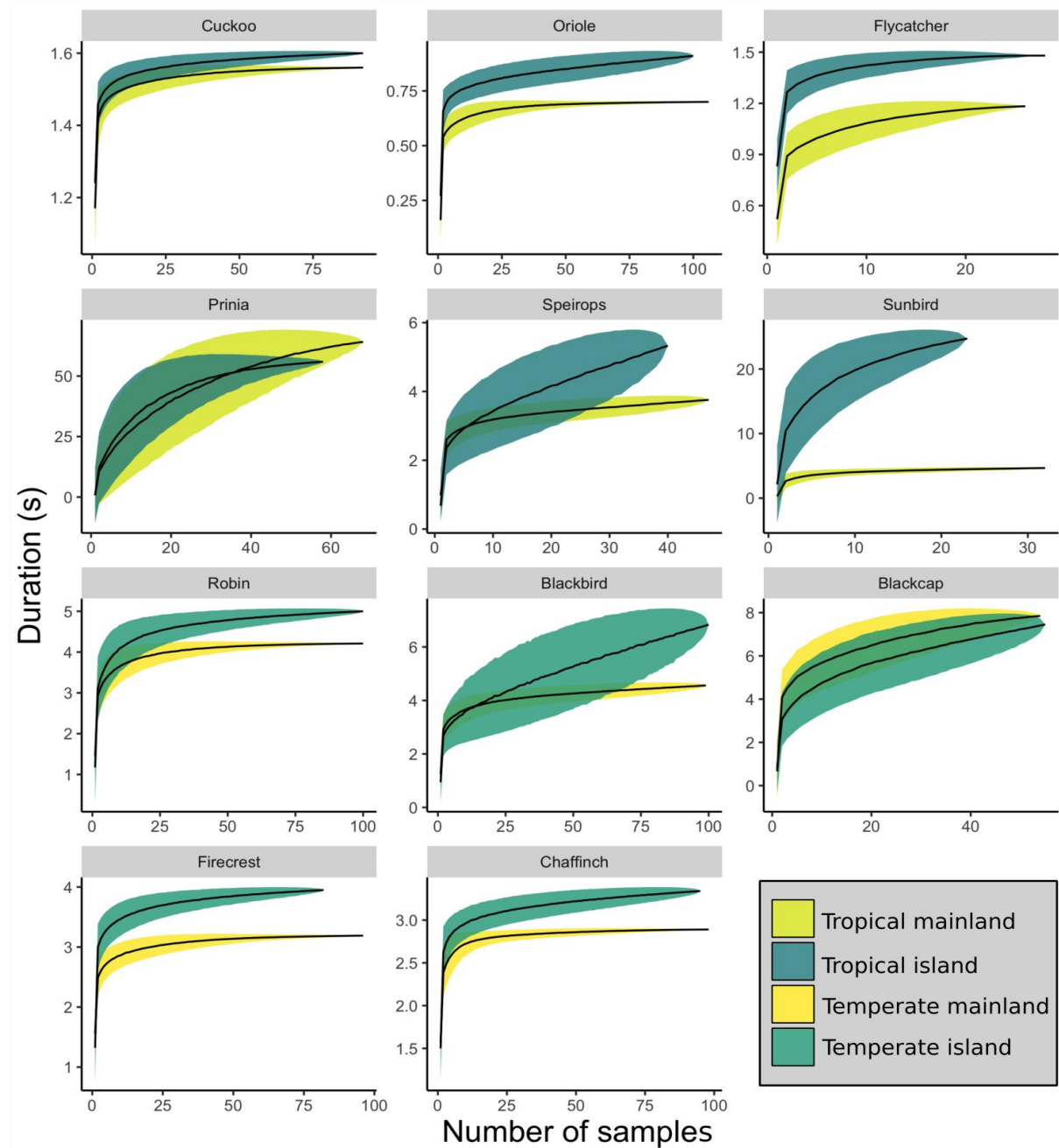


Figure S3: Accumulation curves of the mean of maximum sampled duration (line) \pm standard deviation (colored shape) of song with sampling effort (number of songs analyzed). For each different number of samples (song), we calculated the mean by taking all possible maximum in all possible combinations of this number of samples (when number of combinations was higher than 10 000, we took 10 000). Differences among species do not reflect model results (only differences in how many samples are needed to reach a plateau of maximum values).

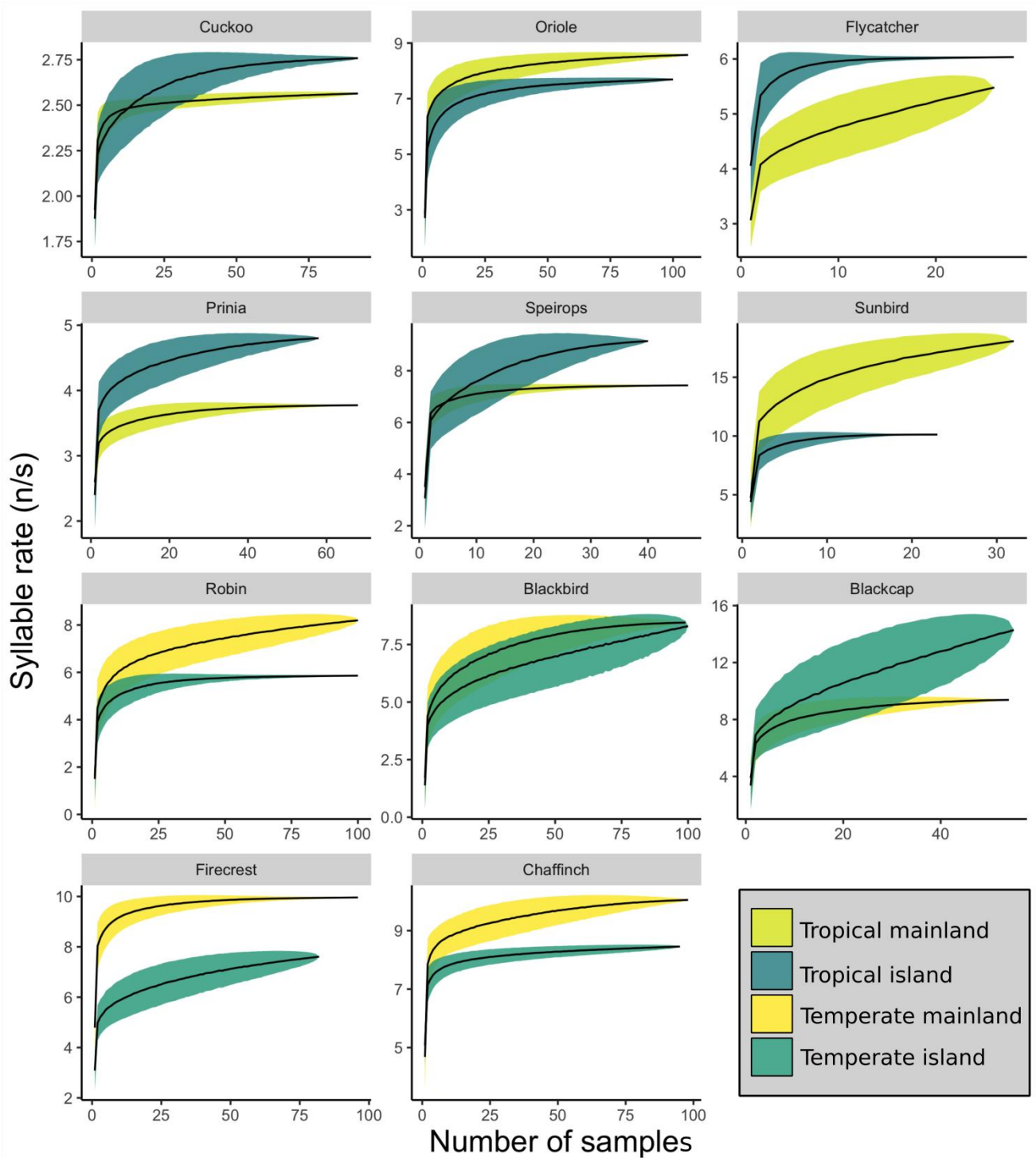


Figure S4: Accumulation curves of the mean of maximum sampled syllable rate (line) \pm standard deviation (colored shape) of song with sampling effort (number of songs analyzed). For each different number of samples (song), we calculated the mean by taking all possible maximum in all possible combinations of this number of samples (when number of combinations was higher than 10 000, we took 10 000). Differences among species do not reflect model results (only differences in how many samples are needed to reach a plateau of maximum values).

Appendix 7: Bayesian phylogenetic mixed models

In order to investigate how phylogenetic relationships among species could influence our results, we also used Bayesian phylogenetic mixed models (BPMM), using the “*MCMCglmm*” R package (Hadfield 2010; Hadfield & Nakagawa 2010).

We performed three different BPMMs on the following variables: song duration, syllable rate and syllable diversity. Similarly as for LMMs, these variables were analysed on a logarithmic scale. As our data consisted of repeated samples per individual, we included « individual » as a random effect. Proceeding as for LMMs, we tested insularity (island/mainland), latitude (tropical/temperate) and their interaction as fixed effects. We also included body mass and altitude as fixed effects.

We downloaded 10000 alternative trees from Jetz and coworkers's (2012) comprehensive bird phylogeny (downloaded from the BirdTree database: <https://birdtree.org>). We calculated posterior node probabilities in *PAUP** (Swofford 2003). All trees were identical (Figure S3) and therefore we only used one tree for the BPMM. As BirdTree phylogeny is restricted at the species level, we manually added the five insular subspecies (*Chrysococcyx cupreus insularum*, *Sylvia atricapilla heineken*, *Fringilla coelebs madeirensis*, *Erithacus rubecula rubecula* and *Turdus merula cabreræ*) on this tree by arbitrary fixing phylogenetic distances with closest continental relatives at 0.001 (maximum distance from tips to root is 84 in this ultrametric tree). For each analysis, we ran the model using 2 chains for 800000 iterations and saved posterior samples after a burn-in period of 50000, thinning every 300 iterations, resulting in an effective sample size of at least 1000. Uninformative priors were used (inverse-Wishart with belief parameters set to 0.002 and variances set to 1) for both random effect and residual variances. We assessed model convergence using the 'coda' R package (Plummer et al. 2006). For each dependent variable, we selected the best model by minimizing the deviance information criterion DIC and considered that models differing by less than 2 DIC units were equivalent.

Broadly, results of BPMM were equivalent to those presented in the main text (LMM) in terms of and fixed-effect structure of final models (Table S4). In particular, BPMM found a positive effect of insularity on syllable rate which was lower on islands. As in LMM, syllable rate was significantly affected by mass, lighter species producing faster song. Contrasting with LMM, altitude had a significant and positive (although very weak) effect on syllable rate. Song duration was not affected by altitude but it was significantly influenced by body mass, lighter species producing longer songs. Results of BPMM indicated a significant effect of interaction between “insularity” and “latitude” on song duration: song duration was longer in the tropical island than in the tropical mainland but it did not differ between the temperate island and mainland. Overall, effects of the interaction “latitude x insularity” were weaker in the BPMMs than in LMMs. This indicate that phylogenetic relationships explain a part of the significant link between our three variables and the interaction between “latitude x insularity”. Based on taxonomy proxies, most of the temperate pairs represent more recent divergence events than the tropical pairs and that probably enhance the effect of the latitude. As in LMM, BPMM indicated that syllable diversity changed with latitude and insularity (significant latitude by insularity interaction). It was lower on the temperate island than the temperate but it was higher on the tropical island than the tropical mainland. As in LMM, syllable diversity was not affected by body mass but it was significantly positively (not negatively) correlated to altitude.

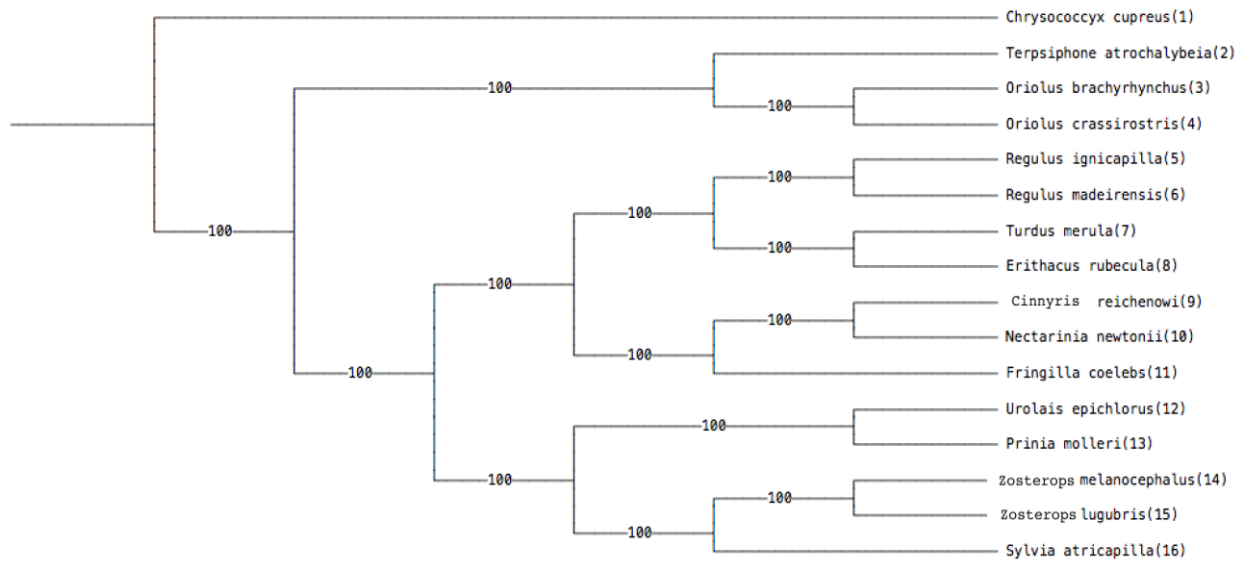


Figure S5: Consensus phylogenetic tree generated from 10000 alternative trees from Jetz and coworkers, (2012) with posterior probabilities.

Table S4: Results of the best BPMM for number of species overlapping. Terms for which the 95% credible interval did not span 0 are presented in bold characters. A probability that the posteriors encompass zero (pMCMC) is provided as a statistical test.

| | | Estimate | Lower 2.5%CI | Higher 2.5%CI | pMCMC |
|--------------------------|-------------------------------------|---------------|-----------------|------------------|------------------|
| Syllable rate (log) | Intercept | 6.02 | 5.24 | 6.74 | - |
| | Altitude | 0.0009 | 0.0004 | 0.002 | <0.01 |
| | Mass | -0.02 | -0.04 | -0.02 | <0.001 |
| | Insularity (Island) | -0.99 | -1.72 | -0.21 | 0.01 |
| | Latitude (Tropic) | -1.06 | -1.92 | -0.29 | 0.01 |
| | Insularity*latitude (Island*Tropic) | 0.41 | -0.59 | 1.41 | 0.45 |
| Song duration (log) | Intercept | 2.98 | 1.58 | 4.49 | - |
| | Altitude | 0.0009 | -0.0003 | 0.002 | 0.12 |
| | Mass | -0.02 | -0.05 | -0.004 | 0.03 |
| | Insularity (Island) | -0.34 | -1.72 | 1.21 | 0.65 |
| | Latitude (Tropic) | -1.23 | -2.75 | 0.43 | 0.14 |
| | Insularity*latitude (Island*Tropic) | 2.10 | 0.006 | 3.91 | 0.04 |
| Syllable diversity (log) | Intercept | 7.04 | 5.88 | 8.35 | - |
| | Altitude | 0.003 | 0.001 | 0.004 | <0.001 |
| | Mass | - | - | - | - |
| | Insularity (Island) | -1.35 | -2.99 | 0.39 | 0.12 |
| | Latitude (Tropic) | -5.17 | -6.96 | -3.27 | <0.001 |
| | Insularity*latitude (Island*Tropic) | 2.86 | 0.66 | 5.17 | 0.02 |

Literature cited:

- Hadfield, J. D. 2010. MCMCglmm: MCMC Methods for Multi-Response GLMMs in R. *J. Stat. Soft.* 33:1–22.
- Hadfield, J. D., & S. Nakagawa. 2010. General quantitative genetic methods for comparative biology: Phylogenies, taxonomies and multi-trait models for continuous and categorical characters. *J. Evol. Biol.* 23:494–508.
- Jetz, W., G. H. Thomas, J. B. Joy, K. Hartmann, and A. O. Mooers. 2012. The global diversity of birds in space and time. *Nature* 491:444–448.
- Plummer M, Best N, Cowles K, Vines K. 2006 CODA: convergence diagnosis and output analysis for MCMC. *R News* 6, 7–11.
- Robert, A., T. Lengagne, M. Melo, V. Gardette, S. Julien, R. Covas, D. Gomez, and C. Doutrelant. 2019. The theory of island biogeography and soundscapes: Species diversity and the organization of acoustic communities. *J. Biogeo.* 46:1901–1911.
- Swofford, D. L. 2003. PAUP*. Phylogenetic Analysis Using Parsimony (*and Other Methods). Version 4. Sinauer Associates, Sunderland, Massachusetts.