

Supplementary material

Appendix 1: Materials and methods

Phylogenetic analysis

A time-dated phylogeny was estimated in BEAST 1.8.2 (Drummond et al. 2012) using sequence data from Alström et al. (2011). We included 30 species in this study (Supplementary material Appendix 2, Table A1). We analysed 1–3 individuals per species, with *Aegithalos caudatus*, *Leptopoecile sophiae*, *Phylloscopus lorenzii* and *Phylloscopus reguloides* as outgroups, based on Alström et al. (2014). Appropriate substitution models for the nuclear introns were determined based on the Bayesian Information Criterion calculated by jModelTest version 0.1.1 (Posada 2008a, b): ODC HKY+G, myo HKY, GAPDH HKY + I. For cytochrome b (cytb) the GTR + G model was used. An uncorrelated relaxed lognormal clock (Drummond et al. 2006) was applied to all loci, with the mean rate for cytb set to 0.0105 substitutions/site/lineage (following Weir & Schluter 2008) and the rates for the other loci estimated. A ‘birth-death incomplete sampling’ tree prior was applied. Two independent runs of 100 x 10⁶ generations were run. The MCMC output was analysed in Tracer version 1.5.0 in the BEAST package to evaluate whether valid estimates of the posterior distribution of the parameters had been obtained. The first 50% of the generations were discarded as ‘burn-in’. Trees were summarized using TreeAnnotator version 1.7.4 in the BEAST package, choosing ‘maximum clade credibility tree’ and ‘mean heights’, and displayed in FigTree version 1.4.0 (Rambaut, 2012).

References

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Appendix 2: Supplementary figures and tables

Table A1. Measurements of song traits. Mean and standard deviation of song measurements for each taxon are shown, as well as Blomberg's K with P value for each variable. N : number of individuals measured for each taxon. n : number of songs measured for each taxon. numnote: number of notes, duration: strophe duration, longnote: duration of the longest note, peakfreq: frequency with the largest amplitude, highfreq: the highest frequency, lowfreq: the lowest frequency, bandwidth: frequency bandwidth measured as difference between highfreq and lowfreq.

Taxa	N	n	numnote	duration (s)	longnote (s)	peakfreq (Hz)	highfreq (Hz)	lowfreq (Hz)	bandwidth (Hz)
<i>Urosphena neumanni</i>	2	2	3.00±0.00	0.52±0.48	0.32±0.24	3445±24	4522±62	2756±487	1766±426
<i>Urosphena pallidipes</i>	2	2	6.00±0.00	0.87±0.10	0.14±0.05	4592±202	6933±61	1981±0	4952±61
<i>Urosphena squameiceps</i>	4	4	48.00±21.68	3.35±0.38	0.05±0.03	8245±658	10077±472	7278±519	2800±891
<i>Urosphena whiteheadi</i>	5	6	3.50±0.50	0.58±0.44	0.16±0.14	8921±745	9790±638	8383±896	1407±352
<i>Tesia cyaniventer</i>	5	12	9.75±3.89	2.42±1.03	0.16±0.05	3761±951	4859±1284	1809±314	3050±1208
<i>Tesia olivea</i>	4	4	19.25±3.40	3.61±1.45	0.15±0.01	5041±650	7386±874	1873±83	5513±817
<i>Tesia everetti</i>	4	6	8.17±0.75	1.91±1.76	0.16±0.05	3772±428	6000±552	1435±265	4565±637
<i>Tesia superciliaris</i>	5	5	10.80±1.92	1.66±0.44	0.18±0.08	3870±351	5960±940	1671±490	4289±1301

Table A1. Continued

Taxa	<i>N</i>	<i>n</i>	numnote	duration (s)	longnote (s)	peakfreq (Hz)	highfreq (Hz)	lowfreq (Hz)	bandwidth (Hz)
<i>Cettia cetti</i>	5	7	6.43±3.87	1.25±0.83	0.12±0.03	4297±1083	8170±780	1673±474	6497±1190
<i>Cettia brunnifrons</i>	5	5	8.60±1.14	1.70±0.20	0.46±0.06	5436±641	9578±788	465±255	9113±807
<i>Cettia castaneocoronata</i>	5	5	4.60±1.14	0.70±0.07	0.17±0.09	5339±602	6735±231	3118±665	3617±872
<i>Cettia major</i>	3	3	7.00±1.00	1.60±0.18	0.16±0.00	4416±235	5340±172	2153±376	3187±524
<i>Phyllergates cucullatus</i>	5	14	9.79±4.00	1.08±0.33	0.27±0.52	4619±706	5586±1018	3808±765	1778±876
<i>Horornis canturians</i>	4	5	10.20±4.27	1.43±0.20	0.32±0.40	2512±463	4651±670	654±131	3996±748
<i>Horornis seebohmi</i>	5	6	8.50±0.45	2.18±0.30	0.71±0.07	3644±608	5871±626	1392±197	4479±605
<i>Horornis ruficapilla</i>	3	7	6.14±1.57	1.54±0.22	0.60±0.05	3438±901	5475±582	1353±397	4122±525
<i>Horornis haddeni</i>	2	6	4.00±0.89	1.96±0.66	0.86±0.14	2170±696	3172±636	1091±222	2082±781
<i>Horornis parens</i>	3	10	5.40±0.70	1.71±0.20	0.74±0.14	3292±562	4745±644	1920±840	2825±1001
<i>Horornis carolinae</i>	2	4	3.25±0.96	1.27±0.12	0.89±0.09	2556±262	3208±247	1722±472	1486±447
<i>Horornis annae</i>	1	3	3.00±2.00	1.55±0.26	1.19±0.08	2242±1600	3502±1766	746±277	2756±1492

Table A1. Continued

Taxa	<i>N</i>	<i>n</i>	numnote	duration (s)	longnote (s)	peakfreq (Hz)	highfreq (Hz)	lowfreq (Hz)	bandwidth (Hz)
<i>Horornis diphone</i>	5	10	5.40±1.58	1.60±0.37	0.87±0.32	2086±390	3497±1049	803±259	2693±842
<i>Horornis brunnescens</i>	4	5	50.60±37.07	11.41±3.08	1.69±0.29	4585±239	5581±415	2790±812	2791±433
<i>Horornis acanthizoides</i>	4	4	69.50±39.37	25.41±6.33	1.40±0.49	5233±1242	7364±569	3562±632	3802±854
<i>Horornis flavolivacea</i>	5	5	4.00±0.71	1.38±0.09	0.87±0.10	4137±365	6701±352	2515±485	4186±690
<i>Horornis vulcania</i>	5	5	3.20±0.84	1.45±0.27	0.88±0.35	3478±677	5305±952	1929±433	3376±776
<i>Horornis fortipes</i>	5	10	4.80±0.92	2.15±0.25	1.25±0.13	3494±498	5624±781	1653±161	3971±772
<i>Tickellia hodgsoni</i>	5	11	15.45±8.15	1.34±0.33	0.19±0.06	5852±632	7814±1595	3359±1644	4456±3001
<i>Abroscopus superciliaris</i>	5	8	4.50±0.93	0.81±0.19	0.19±0.07	4496±611	5480±509	2939±192	2541±584
<i>Abroscopus albogularis</i>	5	5	12.20±2.39	0.76±0.14	0.05±0.01	4868±229	5374±302	4427±270	947±136
<i>Abroscopus schisticeps</i>	1	2	16.00±7.07	0.85±0.39	0.05±0.01	6536±121	6976±122	3660±914	3316±1035
<i>K (P)</i>			0.60 (0.06)	0.82 (0.02)	2.42 (0.00)	1.14 (0.00)	0.76 (0.01)	1.00 (0.00)	0.62 (0.03)

Table A2. Correlation coefficients between song variables. Correlation coefficients between phylogenetic independent contrasts are shown in the upper triangle. Abbreviation for song traits are given in the legend to Table S1.

	numnote	duration	longnote	peakfreq	highfreq	lowfreq	bandwidth
numnote		0.81	-0.25	0.49	0.45	0.24	0.28
duration	0.73		0.19	0.25	0.24	0.10	0.22
longnote	-0.19	0.43		-0.34	-0.31	-0.29	-0.10
peakfreq	0.47	0.00	-0.59		0.88	0.65	0.34
highfreq	0.44	0.08	-0.48	0.90		0.32	0.69
lowfreq	0.31	-0.06	-0.46	0.74	0.46		-0.33
bandwidth	0.18	0.28	0.06	0.07	0.43	-0.48	

Correlation coefficients with absolute values greater than 0.5 are indicated in bold.

Table A3. Phylogenetic principal component analysis of strophe duration and number of notes.

	PC1	PC2
Loadings:		
numnote	0.97	-0.26
duration	0.93	0.36
% total variance	90.7	9.3

Table A4. Phylogenetic principal component analysis of peak frequency, highest frequency and lowest frequency.

	PC1	PC2
Loadings:		
peakfreq	0.82	0.54
highfreq	0.55	0.83
lowfreq	0.97	-0.26
% total variance	77.2	22.0

Table A5. Correlations between song variables and predictor variables. Correlation coefficients r and P values of regressions are shown, results using phylogenetic independent contrasts (PICs) are shown after the results of non-phylogenetic analysis. Abbreviation for song traits are the same as in Table S1.

Song trait	Latitude		Migration		Tarsus length	
	r (P)	r (P) PICs	r (P)	r (P) PICs	r (P)	r (P) PICs
peakfreq	0.19 (0.30)	0.18 (0.34)	0.12 (0.53)	-0.03 (0.86)	-0.76 (0.00)	-0.67 (0.00)
highfreq	0.35 (0.06)	0.36 (0.05)	0.27 (0.15)	0.11 (0.57)	-0.63 (0.00)	-0.55 (0.00)
lowfreq	-0.07 (0.72)	-0.10 (0.60)	-0.10 (0.61)	-0.17 (0.37)	-0.59 (0.00)	-0.44 (0.02)
bandwidth	0.41 (0.02)	0.43 (0.02)	0.33 (0.07)	0.20 (0.28)	0.11 (0.58)	-0.14 (0.47)
numnote	0.53 (0.00)	0.54 (0.00)	0.44 (0.02)	0.42 (0.02)	-0.33 (0.07)	-0.32 (0.09)
duration	0.34 (0.07)	0.30 (0.11)	0.41 (0.02)	0.29 (0.11)	0.14 (0.47)	-0.12 (0.54)
longnote	0.17 (0.37)	-0.32 (0.08)	-0.04 (0.85)	-0.21 (0.27)	0.54 (0.00)	0.19 (0.33)

Significant results ($P < 0.05$) are indicated in bold.

Table A6. Correlation coefficient between predictor variables. Correlation coefficients between phylogenetic independent contrasts are shown in the upper triangle.

	Latitude	Migration	Tarsus length
Latitude		0.85	-0.18
Migration	0.82		0.10
Tarsus	-0.18	0.04	

Correlation coefficients with absolute values greater than 0.5 are indicated in bold.

Table A7. Comparison between regressions of song length on different combinations of predictor variables. Slopes and significance are shown. Models are displayed from left to right in the order of ΔAICc values, only models with ΔAICc less than 2.5 from the best model are shown.

Predictor	Slope (<i>P</i>)			
Latitude	0.04 (0.01)		0.03 (0.30)	
Migration		0.77 (0.01)	0.35 (0.48)	0.78 (0.01)
Tarsus				-0.05 (0.38)
ΔAICc	0.00	0.64	2.11	2.43

Significant variables ($P < 0.05$) are indicated in bold.

Table A8. Comparison between regressions of contrasts of song length on different combinations of predictor variables. Slopes and significance of slope are shown. Models are displayed from left to right in the order of ΔAICc values, only models with ΔAICc less than 2.5 from the best model are shown.

Predictor	Slope (<i>P</i>)				
Latitude	0.03 (0.01)	0.03 (0.02)			
Migration			0.62 (0.02)	0.58 (0.03)	-0.01 (0.97)
Tarsus		-0.07 (0.33)	-0.11 (0.10)		0.03 (0.16)
ΔAICc	0.00	1.49	1.80	2.17	2.50

Significant variables ($P < 0.05$) are indicated in bold.

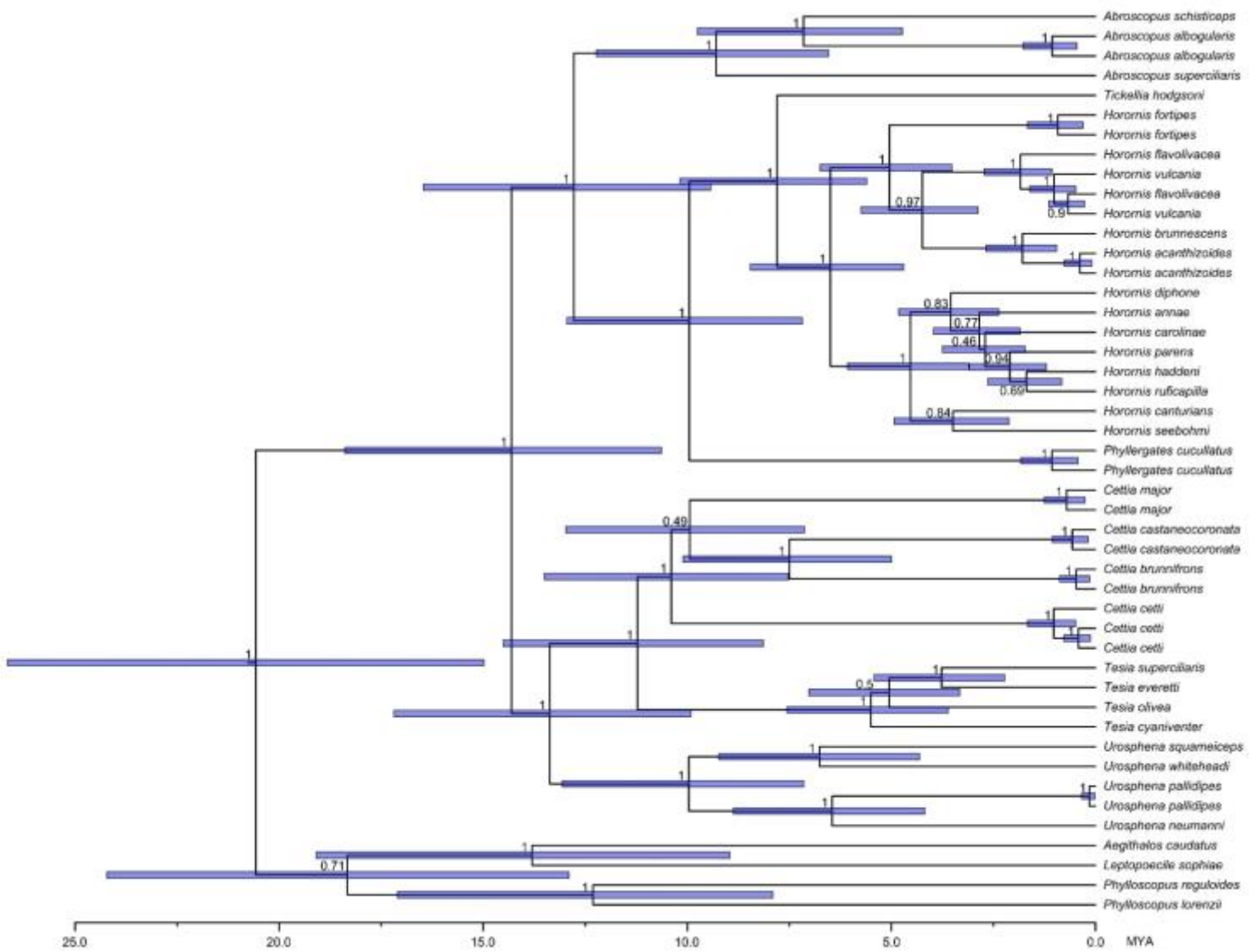


Figure A1. Phylogeny of Cettiidae family, bars at the nodes represent 95% highest posterior density (HPD) intervals of node ages, and Bayesian posterior probability are indicated near the nodes.

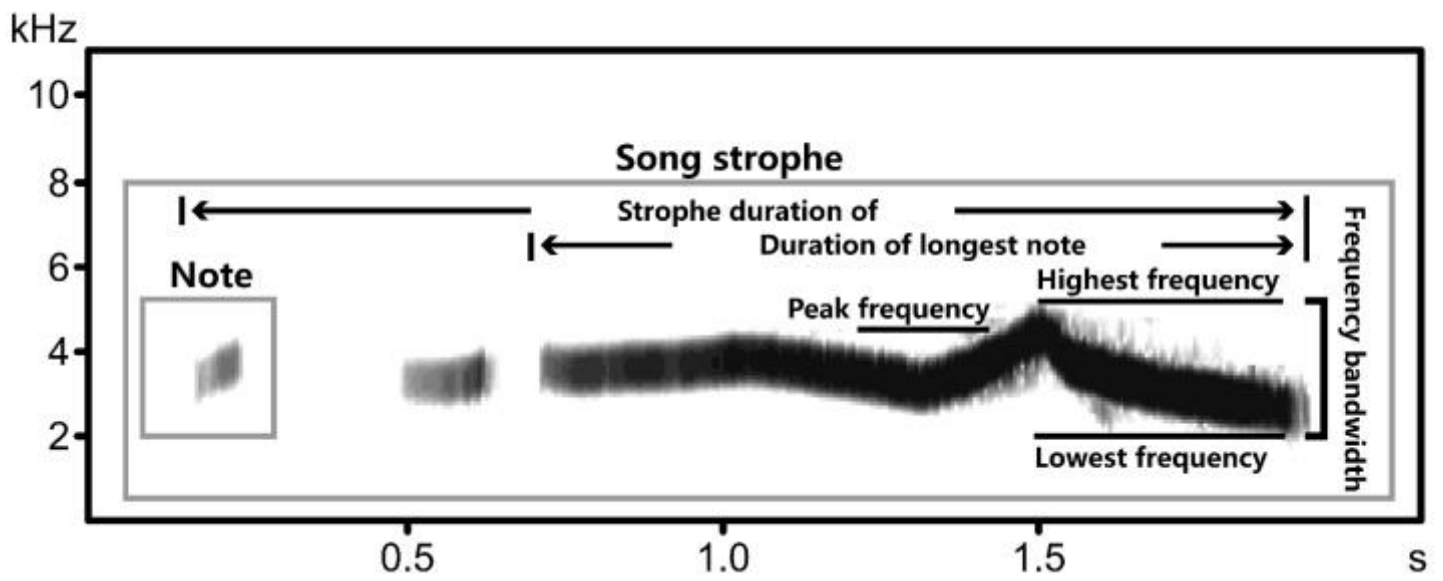


Figure A2. Song terminology, using one song strophe from *Horornis vulcania* as an example.