

## **Supplementary Material**

### **Helping decisions and kin recognition in long-tailed tits: is call similarity used to direct help towards kin?**

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Issue theme: Signal detection, acceptance thresholds, and the evolution of social recognition systems.

**Table S1.** Definitions of the acoustic parameters used to analyse long-tailed tit churr calls. Frequency parameters are the mean of multiple measurements taken at five time points across the signal.

Call parameter	Definition
Duration (ms)	Total time between start and end of the call.
Fundamental frequency (Hz)	Frequency of pure-tone signals and common denominator frequency of harmonic signals.
Max. fundamental frequency (Hz)	Maximum fundamental frequency across the call.
Weiner Entropy	Uniformity of the signal (noisiness).
Bandwidth (Hz)	Frequency difference between the first and final maximum intensity of the signal.
Number of repeats	Number of element repetitions in second syllable

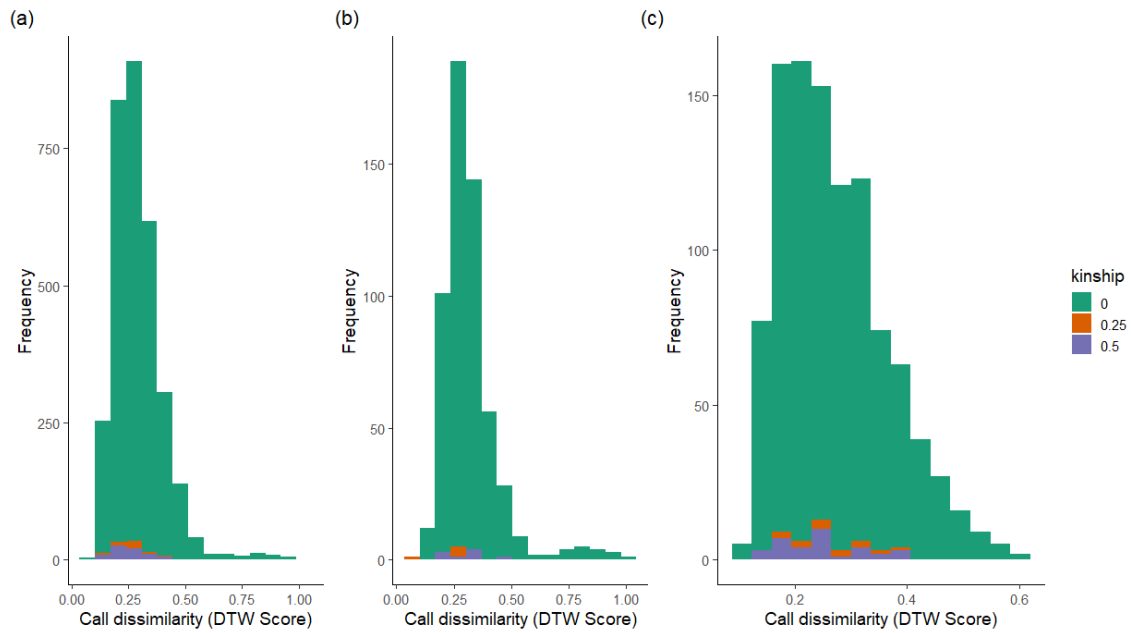
**Table S2.** Within-year repeatability, or effect of year calls were recorded, on variation in long-tailed tit churr call parameters ( $n = 907$  calls over 3 years).

Call parameter	$R \pm SE$	CI	p
Duration (ms)	$0 \pm 0.07$	0, 0.06	1
Number of repeats	$0.02 \pm 0.04$	0, 0.12	0.37
Fundamental frequency (Hz)	$0.04 \pm 0.05$	0, 0.16	0.39
Maximum fundamental frequency (Hz)	$0.01 \pm 0.7$	0, 0.22	0.4
Bandwidth (Hz)	$0.05 \pm 0.05$	0, 0.18	0.17
Weiner Entropy	$0 \pm 0.01$	0, 0.04	1

**Table S3.** Sex differences in long-tailed tit churr call parameters, tested using Gaussian (continuous data) or Poisson (count data) GLMMs ( $n = 907$  calls over 3 years).

Call parameter	Est.	df	t / z	p
Log Duration (ms)	-0.03	48.91	-0.92	0.36
Number of repeats	-0.05	-	-0.99	0.32
Fundamental frequency (Hz)	-2.89	49.81	-0.04	0.97
Maximum fundamental frequency (Hz)	-36.26	51.10	-0.47	0.64
Bandwidth (Hz)	-64.28	50.95	-1.65	0.11
Weiner Entropy	0.01	50.03	1.89	0.06

**Fig. S1.** Distributions of dissimilarity in long-tailed tit churr calls among (a) both sexes ( $n = 80$ ), (b) males ( $n = 46$ ), and (c) females ( $n = 34$ ) of three levels of kinship: first-order kin (purple bars,  $n = 71$  dyads), second-order kin (orange bars,  $n = 32$  dyads) and non-kin (green bars,  $n = 3057$  dyads), measured using dynamic-time warping analysis (DTW).



**Table S4.** GLMM outputs reporting the dissimilarity of long-tailed tit churr calls among helper-breeder dyads: (i) helpers and related ( $r \geq 0.25$ ) breeding males they helped ( $n = 9$ ); (ii) helpers and unrelated breeding males they helped ( $n = 8$ ) and (iii) helpers and unrelated breeding males within helping range ( $\leq 750\text{m}$ ) that they did not help ( $n = 218$ ). Call dissimilarity was measured using dynamic time warping analysis (DTW).

<i>AIC</i>	<i>residual df</i>	<i>N</i>		
-676	285	291		
<i>Fixed effects</i>		<i>Estimate ± SE</i>	<i>t</i>	<i>p</i>
<i>Reference: Helpers and helped relatives</i>				
(Intercept)		-1.57 ± 0.12	-13.54	<0.001
Helpers and helped non-relatives		-0.04 ± 0.14	-0.29	0.77
Helpers and unrelated breeders not helped		0.20 ± 0.10	2.02	0.04
<i>Reference: Helpers and helped non-relatives</i>				
(Intercept)		-1.61 ± 0.11	-14.54	<0.001
Helpers and unrelated breeders not helped		0.24 ± 0.09	2.52	0.01
<i>Random effects</i>		<i>Variance ± SD</i>		
Helper ( $N = 19$ )		0.02 ± 0.14		
Residual		0.09 ± 0.31		

**Table S5.** The relationship between the provisioning rate of long-tailed tit helpers ( $n = 41$  observation periods, 14 helpers, 11 nests) and the genetic relatedness, kinship and call dissimilarity of helpers to breeding males. Test statistics and significance terms are reported after backward step-wise removal of predictor variables. All biologically meaningful two-way interaction terms were also tested, and were included in the final model if they improved model fit ( $\Delta AIC > 2$ ).

Model	Predictor variable	$\Delta AIC$	$df$	$\chi^2$	$p$
Genetic relatedness	Genetic relatedness	1.22	1, 6	0.77	0.38
	Brood size	0.94	1, 8	1.06	0.3
	Group size	2.44	1, 7	4.44	0.04
	Nestling age	2.57	1, 5	4.57	0.03
	Genetic relatedness: group size	3.94	1, 9	5.94	0.01
Kinship	Kinship	3.69	1, 6	5.68	0.02
	Brood size	1.96	1, 8	0.03	0.85
	Group size	0.58	1, 7	2.59	0.11
	Nestling age	2.57	1, 5	4.57	0.03
	Kinship: group size	9.61	1, 9	11.61	< 0.001
Call dissimilarity	Call dissimilarity	1.99	1, 8	0.01	0.9
	Brood size	0.74	1, 7	1.26	0.26
	Group size	0.52	1, 6	2.52	0.11
	Nestling age	2.57	1, 5	4.57	0.03