

SUPPLEMENTARY INFORMATION

APPENDIX 1

Table of samples and haplotypes. Sample id; haplotypes for 537bp of cytochrome b, 358bp of glyceraldehyde-3-phosphate dehydrogenase intron 11; 808 bp of ND2, 661 bp of COI and 2026 bp of concatenated mtDNA; latitude, longitude and island of trapping.

ID	Haplotypes			ND2	COI	Concatenated mtDNA	Latitude	Longitude	Island
	cytb	g3pdh (allele 1)	g3pdh (allele 2)						
SSA03	cytb-1	g3pdh-1	g3pdh-1	ND2-2	-	-	39.744286	3.170699	Mallorca
SSA04	cytb-1	g3pdh-1	g3pdh-1	ND2-1	COI-1	multi-1	39.748944	3.177025	Mallorca
SSA06	cytb-1	g3pdh-1	g3pdh-1	ND2-3	-	-	39.470166	3.280321	Mallorca
SSA07	cytb-1	g3pdh-1	g3pdh-1	ND2-2	-	-	39.470778	3.280451	Mallorca
SSA08	cytb-1	g3pdh-1	g3pdh-1	ND2-2	-	-	39.751638	3.182741	Mallorca
SSA09	cytb-1	g3pdh-1	g3pdh-1	ND2-2	-	-	39.469254	3.281154	Mallorca
SSA10	cytb-1	g3pdh-1	g3pdh-1	ND2-1	COI-1	multi-1	39.469254	3.281154	Mallorca
SSA11	cytb-1	g3pdh-1	g3pdh-1	ND2-2	COI-1	multi-2	39.471162	3.282045	Mallorca
SSA12	cytb-2	g3pdh-1	g3pdh-1	ND2-2	COI-1	multi-3	39.472109	3.281514	Mallorca
SSA13	cytb-1	g3pdh-1	g3pdh-1	ND2-1	COI-1	multi-1	39.472109	3.281514	Mallorca
SSA14	cytb-1	g3pdh-1	g3pdh-1	ND2-1	-	-	39.472109	3.281514	Mallorca
SSA15	cytb-1	-	-	ND2-1	-	-	39.472109	3.281514	Mallorca
SSA17	cytb-1	g3pdh-1	g3pdh-1	ND2-1	COI-1	multi-1	39.473225	3.282031	Mallorca
SSA18	cytb-3	g3pdh-2	g3pdh-2	ND2-4	-	-	42.772675	10.169999	Elba
SSA21	cytb-4	g3pdh-2	g3pdh-2	ND2-4	COI-2	multi-4	42.778167	10.171948	Elba
SSA22	cytb-3	g3pdh-2	g3pdh-2	ND2-4	COI-2	multi-7	42.77883	10.169613	Elba
SSA23	cytb-3	-	-	ND2-4	COI-2	multi-7	40.053778	9.570469	Sardinia
SSA24	cytb-3	g3pdh-2	g3pdh-2	ND2-5	COI-2	multi-8	40.053778	9.570469	Sardinia
SSA25	cytb-3	g3pdh-3	g3pdh-4	ND2-4	-	-	40.053778	9.570469	Sardinia
SSA26	cytb-3	g3pdh-2	g3pdh-2	ND2-4	-	-	40.053778	9.570469	Sardinia
SSA27	cytb-4	g3pdh-2	g3pdh-2	ND2-4	COI-2	multi-4	40.053778	9.570469	Sardinia
SSA29	cytb-4	g3pdh-2	g3pdh-2	ND2-4	-	-	40.053778	9.570469	Sardinia
SSA30	cytb-3	g3pdh-2	g3pdh-2	ND2-4	-	-	40.053778	9.570469	Sardinia
SSA31	cytb-3	g3pdh-3	g3pdh-3	ND2-4	-	-	42.778832	10.169613	Elba
SSA32	cytb-3	-	-	-	-	-	40.856249	9.167481	Sardinia
SSA33	cytb-4	g3pdh-2	g3pdh-2	ND2-4	COI-2	multi-4	40.852627	9.173701	Sardinia
SSA34	cytb-3	g3pdh-3	g3pdh-3	ND2-4	-	-	40.766178	9.427426	Sardinia
SSA35	cytb-3	g3pdh-2	g3pdh-2	ND2-4	-	-	40.713228	9.369324	Sardinia
SSA36	cytb-4	g3pdh-2	g3pdh-5	ND2-6	COI-2	multi-5	40.986329	9.161331	Sardinia
SSA37	cytb-4	g3pdh-2	g3pdh-2	ND2-4	COI-2	multi-4	40.502995	8.396651	Sardinia
SSA38	cytb-4	g3pdh-2	g3pdh-2	ND2-7	-	-	40.502995	8.396651	Sardinia
SSA39	cytb-4	g3pdh-6	g3pdh-6	ND2-4	COI-2	multi-4	40.347701	8.904704	Sardinia
SSA40	cytb-3	g3pdh-3	g3pdh-4	ND2-4	COI-2	multi-7	40.479583	8.600801	Sardinia
SSA41	cytb-3	g3pdh-2	g3pdh-2	ND2-8	COI-2	multi-6	40.661428	9.116621	Sardinia
SSA42	cytb-3	-	-	ND2-9	-	-	39.254478	9.399521	Sardinia
SSA43	cytb-4	-	-	ND2-4	-	-	39.255831	9.404547	Sardinia
SSA44	cytb-4	-	-	ND2-4	-	-	39.307357	8.439455	Sardinia
SSA45	cytb-4	g3pdh-3	g3pdh-3	ND2-4	COI-2	multi-4	39.307357	8.439455	Sardinia
SSA46	cytb-4	-	-	ND2-4	-	-	39.360791	8.439504	Sardinia
SSA47	cytb-3	g3pdh-5	g3pdh-5	ND2-4	COI-2	multi-7	39.384091	8.394254	Sardinia
SSA48	cytb-4	g3pdh-2	g3pdh-2	ND2-4	COI-2	multi-4	39.396183	8.397611	Sardinia
SSA49	cytb-4	g3pdh-2	g3pdh-2	ND2-10	-	-	39.396183	8.397611	Sardinia
SSA50	cytb-3	g3pdh-2	g3pdh-2	-	-	-	42.621343	9.416281	Corsica

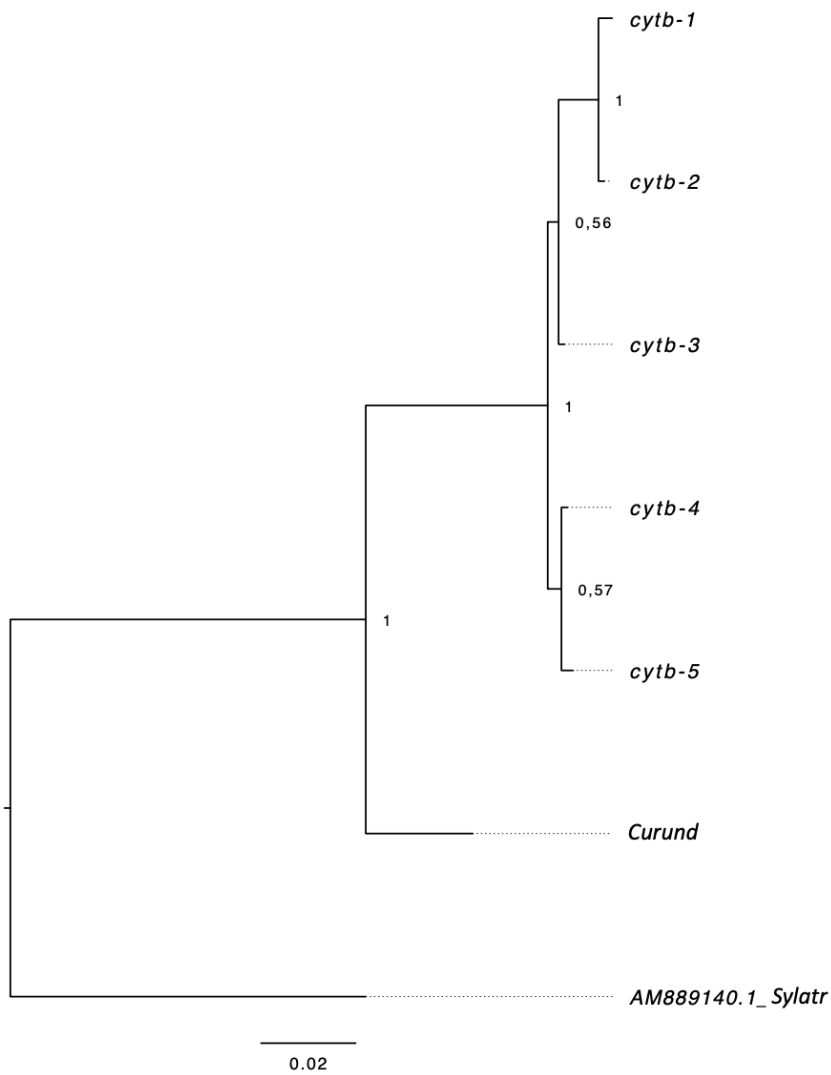
Haplotypes

ID	cytb	g3pdh		ND2	COI	Concatenated		Latitude	Longitude	Island
		(allele 1)	(allele 2)			mtDNA				
SSA51	cytb-3	<i>g3pdh-7</i>	<i>g3pdh-7</i>	ND2-4	COI-2	<i>multi-7</i>		42.621343	9.416281	Corsica
SSA52	cytb-3	<i>g3pdh-6</i>	<i>g3pdh-6</i>	ND2-4	-	-		42.343863	9.175694	Corsica
SSA53	cytb-3	-	-	ND2-4	-	-		42.462384	9.211615	Corsica
SSA54	cytb-3	<i>g3pdh-2</i>	<i>g3pdh-5</i>	ND2-4	-	-		42.559956	8.944973	Corsica
SSA55	cytb-3	-	-	ND2-4	-	-		42.220507	8.826005	Corsica
SSA56	cytb-4	<i>g3pdh-2</i>	<i>g3pdh-7</i>	ND2-4	COI-2	<i>multi-4</i>		42.043016	9.039547	Corsica
SSA57	cytb-3	<i>g3pdh-3</i>	<i>g3pdh-3</i>	ND2-4	-	-		42.175148	9.163639	Corsica
SSA58	cytb-3	<i>g3pdh-3</i>	<i>g3pdh-3</i>	ND2-11	-	-		42.175148	9.163639	Corsica
SSA61	cytb-3	<i>g3pdh-3</i>	<i>g3pdh-3</i>	ND2-12	-	-		42.56073	8.721843	Corsica
SSA62	cytb-3	<i>g3pdh-3</i>	<i>g3pdh-3</i>	-	COI-2	-		42.569054	8.719259	Corsica
SSA63	cytb-3	<i>g3pdh-2</i>	<i>g3pdh-2</i>	-	-	-		42.571837	8.719137	Corsica
SSA64	cytb-3	<i>g3pdh-7</i>	<i>g3pdh-7</i>	-	-	-		42.325901	9.166712	Corsica
SSA65	cytb-4	<i>g3pdh-2</i>	<i>g3pdh-7</i>	ND2-4	COI-2	<i>multi-4</i>		42.325901	9.166712	Corsica
SSA66	cytb-4	<i>g3pdh-2</i>	<i>g3pdh-7</i>	-	-	-		39.798407	9.499367	Sardinia
SSA67	cytb-5	<i>g3pdh-2</i>	<i>g3pdh-2</i>	ND2-4	-	-		39.798407	9.499367	Sardinia
SSA68	cytb-3	<i>g3pdh-3</i>	<i>g3pdh-3</i>	-	-	-		39.798407	9.499367	Sardinia
SSA69	cytb-4	<i>g3pdh-2</i>	<i>g3pdh-5</i>	-	-	-		39.798407	9.499367	Sardinia
SSA71	cytb-3	<i>g3pdh-3</i>	<i>g3pdh-4</i>	-	-	-		39.798407	9.499367	Sardinia
SSA88	cytb-4	<i>g3pdh-6</i>	<i>g3pdh-6</i>	-	-	-		39.798407	9.499367	Sardinia

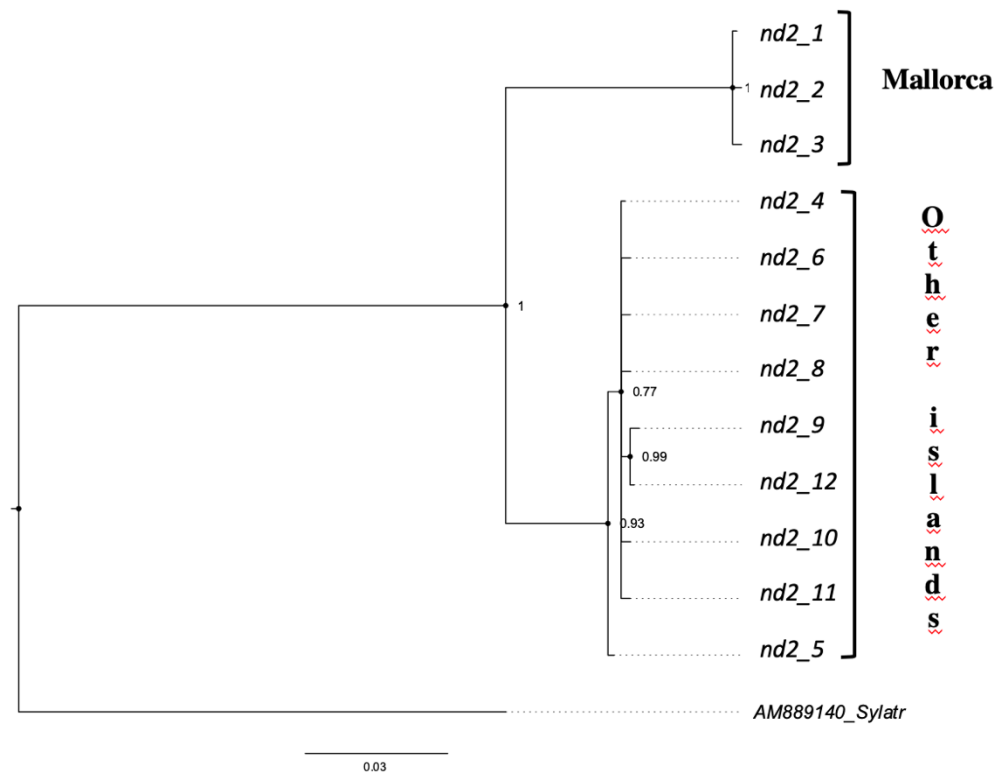
APPENDIX 2

50% majority consensus rule Bayesian Inference trees. Bayesian Posterior Probabilities of each node are reported.

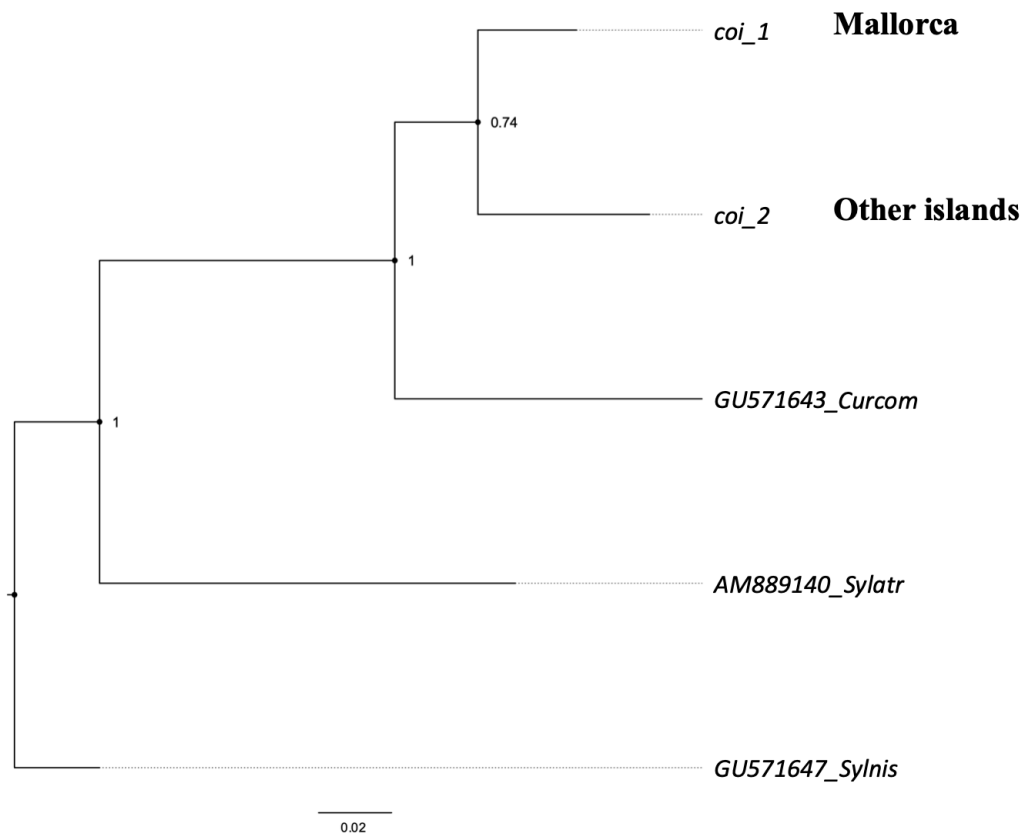
a) Bayesian tree of 537bp *cytochrome b* fragment haplotypes. *Curruca undata* (*Curund*) and *Sylvia atricapilla* (*Sylatr*) were used as outgroup.



b) Bayesian tree of ND2 haplotypes. *Sylvia atricapilla* (*Sylatr*) was used as outgroup.



c) Bayesian tree of COI haplotypes. b) Bayesian tree of ND2 haplotypes. *Curruca undata* (*Curund*) and *Sylvia atricapilla* (*Sylatr*) were used as outgroup.



APPENDIX 3

Analyses of Molecular Variance results and fixation indices. Each island (Mallorca, Sardinia, Corsica and Elba) was defined as a single population, groups were defined as taxa breeding ranges (Mallorca for *Curruca balearica*, Sardinia, Corsica and Elba for *Curruca sarda*).

Small negative values of variance components and percentage of variation are biased estimates of actual null values, due to a corresponding absence of genetic structure at the corresponding level; in these cases no P-values are calculated.

a) Cytochrome b (*cytb*)

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation	P-value	Fixation indices
Among groups	1	51.567	2.46108	90.48	P=0.2522	$\Phi_{CT} = 0.90478$
Among populations within groups	2	1.707	0.05155	1.9	P=0.0225	$\Phi_{SC} = 0.19904$
Within populations	58	12.033	0.20746	7.63	P<0.0001	$\Phi_{ST} = 0.90478$

b) Glyceraldehyde-3-phosphate dehydrogenase intron 11 (G3PDH)

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation	P-value	Fixation indices
Among groups	1	33.369	0.88460	70.78	P=0.25611	$\Phi_{CT} = 0.70777$
Among populations within groups	2	0.968	0.00589	0.47	P=0.37928	$\Phi_{SC} = 0.01613$
Within populations	102	36.654	0.35935	28.75	P<0.00001	$\Phi_{ST} = 0.71248$

c) Cytochrome c oxidase (COI)

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation	P-value	Fixation indices
Among groups	1	162	18	100		
Among populations within groups	2	0	0	0		
Within populations	20	0	0	0		

d) NADH dehydrogenase subunit 2 (ND2)

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation	P-value	Fixation indices
Among groups	1	655.181	29.828	99.09		$\Phi_{CT} = 0.99086$
Among populations within groups	2	0.234	-0.01629	-0.05		$\Phi_{SC} = -0.05918$
Within populations	52	15.158	0.2915	0.97		$\Phi_{ST} = 0.99032$

e) Concatenated sequences

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation	P-value	Fixation indices
Among groups	1	425.429	47.9968	99.16		$\Phi_{CT} = 0.99164$
Among populations within groups	2	0.132	-0.11739	-0.24		$\Phi_{SC} = -0.29018$
Within populations	19	9.917	0.5193	1.08		$\Phi_{ST} = 0.98922$