

Table S1. The list of sequences retrieved from GenBank and used in the phylogenetic reconstruction based on the dataset 1 (concatenated alignment of *cytb*+*ApoB*+*BRCA1*) and dataset 2 (*ApoB*+*BRCA1*). The asterics mark our own sequences obtained in the previous studies.

Species, specimens and name in the concatenation	Voucher / GB AccNo			Dataset where the sequences were used
	<i>cytb</i>	<i>apoB</i>	<i>brca1</i>	
<i>C. sicula</i> 1	IZEA2943 / DQ521040	IZEA4001 / EF524965	IZEA4001 / EF525095	dataset 1, dataset 2
<i>C. sicula</i> 2	IZEA4000 / DQ975241	IZEA4000 / EF524924	IZEA4000 / EF525061	dataset 1, dataset 2
<i>C. canariensis</i>	IZEA4285 / DQ521042	IZEA2331 / EF525043	IZEA2331 / EF525160	dataset 1, dataset 2
<i>C. tarfayensis</i>	IZEA7807 / DQ975242	IZEA7807 / EF525049	IZEA7807 / EF525165	dataset 1, dataset 2
<i>C. obscurior</i>	SBP_P662 / KC684129	sp1_SBP_P1277 / EF525034	sp1_SBP_P1277 / EF525152	dataset 1, dataset 2
<i>C. cf. obscurior</i>	sp2_SBP_R24051 / EF524779-EF524671	sp2_SBP_R24051 / EF525028	sp2_SBP_R24051 / EF525146	dataset 1, dataset 2
<i>C. eburnea</i>	sp3_ZFMK_2011.0074 / KC684152	sp3_SBP_DV0055 / EF525031	sp3_SBP_DV0055 / EF525149	dataset 1, dataset 2
<i>C. zimmermanni</i>	IZEA2053 / DQ521041	IZEA2053 / EF524942	IZEA2053 / EF525076	dataset 1, dataset 2
<i>C. musseri</i>	IZEA4398 / FJ813927	IZEA4398 / EF524921	IZEA4398 / EF525059	dataset 1, dataset 2
<i>C. rhoditis</i>	LSUMZ_36973 / MK607726	IZEA4407 / EF524989	IZEA440 / EF525116	dataset 1, dataset 2
<i>C. levicula</i>		IZEAC2686 / EF524986	IZEAC2686 / EF525113	dataset 2
<i>C. elongate</i> Balease	FMNH210551 / KY771752	FMNH210551 / KY771389	FMNH210551 / KY771566	dataset 1, dataset 2
<i>C. elongata</i> Rorekatimbo	FMNH213155 / KY771737	FMNH213155 / KY771429	FMNH213155 / KY771555	dataset 1, dataset 2
<i>C. elongata</i> Daco	LSUMZ36924 / KY771718	LSUMZ36924 / KY771452	LSUMZ36924 / KY771594	dataset 1, dataset 2
<i>C. bottegi</i>	ZMMU S189291 (1924) / MW286413*	ZMMU S189291 (1924) / MW381907*	ZMMU S189291 (1924) / MW410123*	dataset 1, dataset 2
<i>C. macmillani</i>	ZMMU S166029 (734) / EU742601*	ZMMU S166031 (741) / MW381902*	ZMMU S166031 (741) / MW410118*	dataset 1, dataset 2
<i>C. harena</i>	ZMMU S192706 (2316) /.MW286415*	ZMMU S192706 (2316) /.MW381906*	ZMMU S192706 (2316) /.MW410122*	dataset 1, dataset 2
<i>C. yaldeni</i>	ZMMU S165342 (spB30) /.EU742595*	ZMMU S165342 (spB30) /.MW381914*	ZMMU S165342 (spB30) /.MW410129*	dataset 1, dataset 2
<i>C. baileyi</i>	ZMMU S172690 (1089) / EU742596*	ZMMU S172690 (1089) / MW381908*	ZMMU S172690 (1089) / MW410124*	dataset 1, dataset 2
<i>C. glassi</i>	ZMMU S190445 (2103) / MW286416*	ZMMU S190445 (2103) / *MW381909	ZMMU S190445 (2103) / MW410125*	dataset 1, dataset 2
<i>C. thalia</i>	ZMMU S165166 (473) / MW286431*	ZMMU S165165 (468) / MW381912*	ZMMU S165165 (468) / MW410128*	dataset 1, dataset 2
<i>C. mdumai</i> 1	FMNH211327 / KP062148	FMNH211327 / KP061863	FMNH211327 / KP061937	dataset 1, dataset 2
<i>C. mdumai</i> 2	FMNH211333 / KP062140	FMNH211333 / KP061861	FMNH211333 / KP061930	dataset 1, dataset 2
<i>C. monax</i> 1	FMNH192521 / KP062007	FMNH192521 / KP061873	FMNH192521 / KP061939	dataset 1, dataset 2

Table S2. Original primers designed for amplification and sequencing of short fragments of *cytb*, *ApoB* and *BRCA1* in *Crocidura serezyensis*, *C. arispa* and *C. ramona*.

№	primer	sequence (5'-3')
<i>cytb</i>		
1	L910b	CCACTTCTTCATATAGCYAAACAAC
2	L312a	GGCTCYTAYATATWCCTYGAAACATG
3	L416a	CMTTCTGAGGAGCAACAGTCATTACTAA
4	H647b	TAGTARGGRTGGAARGGRATCTTGTC
5	H670b	TGYCCCTAGRATATCTTTRATRGTATA
6	H352a_arispa	CGGTRGCTATAACTGAGAATAAGAGTA
<i>ApoB</i>		
7	F238b	CCATCYCAGTTRTCAATATTGAAACAT
8	R327a	CCAGAACCCAGGATGGTAAAGT
<i>BRCA1</i>		
10	R262b	ATACATCATCACTTCTAGAAAACCAATCATT
11	R400a	GATCACTGGCCATTAAATCTTCTTTCTCTG
12	F164a	CCTATATGGAAGAAGAAAACYGAACAAACA
13	F606a	CACAAACACCCCTTCACAAATAAAT
14	F330a	CCATGATGCAGGGTCTAATTCAAATACA
15	R636a	GGACCAAGGCTYGAYGTAATTCTTCTTTTA

Table S3. Models for the mitochondrial *cytb* gene, *ApoB* and *BRCA1* genes employed in the maximum likelihood and Bayesian analyses.

	1 st codon positions	2 nd codon position	3 rd codon position
<i>ApoB</i> + <i>BRCA1</i>	HKY+G	K3Pu+G (GTR+G in MrBayes)	HKY+G
<i>cytb</i>	TIM2e+I+G (GTRe+I+G in BEAST)	TN+G	TIM2+I+G (GTR+I+G in BEAST) (GTR2+G in datasets II and III)