

**Genetic support for the morphological identification of
larvae of Myctophidae, Gonostomatidae,
Sternopychidae and Phosichthyidae (Pisces)
from the western Mediterranean**

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Supplementary material

Table S1. – Literature containing information on larvae and adult identification characteristics of the mesopelagic fishes analysed in this study.

	Larvae	Adults
O. Myctophiformes		
F. Myctophidae		
SF. Lampanyctinae		
<i>Ceratoscopelus maderensis</i>	Tåning 1918	Lowe 1839, Tåning 1918, Hulley 1984
<i>Diaphus holti</i>	Tåning 1918	Tåning 1918, Hulley 1984
<i>Lampanyctus crocodilus</i>	Tåning 1918	Risso 1810, Tåning 1918, Hulley 1984
<i>Lampanyctus pusillus</i>	Tåning 1918, Olivar et al. 1999	Johnson 1890, Tåning 1918, Hulley 1984
<i>Lobianchia dofleinii</i>	Tåning 1918, Berdar and Cavaliere 1975	Zugmayer 1911, Tåning 1918, Hulley 1984
<i>Notoscopelus bolini</i>	Palomera 1983	Nafpaktitis 1975, Hulley 1984
<i>Notoscopelus elongatus</i>	Tåning 1918, Palomera 1983	Costa 1844, Tåning 1918, Hulley 1984
SF. Myctophinae		
<i>Benthosema glaciale</i>	Tåning 1918	Reinhardt 1837, Tåning 1918, Hulley 1984
<i>Electrona risso</i>	Tåning 1918	Cocco 1829, Tåning 1918, Hulley 1984
<i>Hygophum benoiti</i>	Tåning 1918, Olivar and Palomera 1994	Cocco 1838, Tåning 1918, Hulley 1984
<i>Hygophum hygomii</i>	Tåning 1918, Olivar and Palomera 1994	Lütken 1892, Tåning 1918, Hulley 1984
<i>Myctophum punctatum</i>	Tåning 1918	Rafinesque 1810, Tåning 1918, Hulley 1984
<i>Symbolophorus veranyi</i>	Tåning 1918	Moreau 1888, Tåning 1918, Hulley 1984
O. Stomiiformes		
F. Sternopychidae		
<i>Argyropelecus hemigymnus</i>	Jespersen and Tåning 1926	Cocco 1829, Badcock 1984
<i>Maurolicus muelleri</i>	Jespersen and Tåning 1926, Sanzo 1931	Gmelin 1789, Jespersen and Tåning 1926, Sanzo 1931
F. Gonostomatidae		
<i>Cyclothona braueri</i>	Jespersen and Tåning 1926	Jespersen and Tåning 1926
<i>Cyclothona pygmaea</i>	Jespersen and Tåning 1926	Jespersen and Tåning 1926
F. Phosichthyidae		
<i>Vinciguerria attenuata</i>	Jespersen and Tåning 1926, Sanzo 1931	Cocco 1838, Jespersen and Tåning 1926, Sanzo 1931

Table S2. – List of sequences of myctophids and stomiiforms used in the present study. Codes for the sequences from our lab are shown on the right part of the table. Apart from our results, the sequences that were used in this study and selected from GenBank (<http://www.ncbi.nlm.nih.gov/genbank>) are listed with the corresponding accession number and source. The outgroup species *BathyLAGUS euryops* was included.

Family	Species / Genus	No. Nucleotides	Genetic marker	Source Identifier	Accession number	Abbreviation
Stenoptychidae	<i>Argyroplectus hemigymnus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616410	AhA2
	<i>Argyroplectus hemigymnus</i>	650	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148085	
	<i>Argyroplectus hemigymnus</i>	651	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148086	
	<i>Argyroplectus hemigymnus</i>	651	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148087	
	<i>Argyroplectus hemigymnus</i>	652	cytochrome oxidase subunit I (COI) gene	Hastings and Burton 2010	GU440233	
	<i>Argyroplectus affinis</i>	391	mitochondrial gene for subunit 12S rRNA	Miya and Nishida 1998	D89749	
	<i>Argyroplectus staudeni</i>	391	mitochondrial gene for subunit 12S rRNA	Miya and Nishida 1998	D89748	
	<i>Argyroplectus aculeatus</i>	391	mitochondrial gene for subunit 12S rRNA	Miya and Nishida 1998	D89744	
	<i>Argyroplectus aculeatus</i>	391	mitochondrial gene for subunit 12S rRNA	Miya and Nishida 1998	D89735	
Myctophidae	<i>Benthosema glaciale</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616365	BgA1
	<i>Benthosema glaciale</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616366	BgA2
	<i>Benthosema glaciale</i>	566	cytochrome oxidase subunit I (COI) gene	This study	KC616367	BgA3
	<i>Benthosema glaciale</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616368	BgA4
	<i>Benthosema glaciale</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616369	BgA5
	<i>Benthosema glaciale</i>	648	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148097	
	<i>Benthosema glaciale</i>	648	cytochrome oxidase subunit I (COI) gene	Keskin,E., 2010	HQ167646	
	<i>Benthosema glaciale</i>	624	cytochrome oxidase subunit I (COI) gene	Sweetman, C. J., 2009	EU148098	
	<i>Cyclothonone braueri</i>	348	mitochondrial gene for subunit 12S rRNA	Miya and Nishida 1996	D84032	
	<i>Cyclothonone braueri</i>	372	mitochondrial gene for subunit 12S rRNA	This study	KC616355	CbL1
	<i>Cyclothonone braueri</i>	372	mitochondrial gene for subunit 12S rRNA	This study	KC616353	CbL2
	<i>Cyclothonone braueri</i>	372	mitochondrial gene for subunit 12S rRNA	This study	KC616356	CbL4
	<i>Cyclothonone braueri</i>	372	mitochondrial gene for subunit 12S rRNA	This study	KC616354	CbJ6
	<i>Cyclothonone pygmaea</i>	372	mitochondrial gene for subunit 12S rRNA	This study	KC616357	CpA2
	<i>Cyclothonone pygmaea</i>	349	mitochondrial gene for subunit 12S rRNA	This study	KC616358	CpA3
	<i>Cyclothonone pallida</i>	329	mitochondrial gene for subunit 12S rRNA	AB026030		
	<i>Cyclothonone alba</i>	349	mitochondrial gene for subunit 12S rRNA	Miya and Nishida 1996	D84040	
	<i>Cyclothonone pygmaea</i>	565	cytochrome oxidase subunit I (COI) gene	Miya and Nishida 1996	KC616359	CmL1
	<i>Ceratoscopelus maderensis</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616360	CmL2
	<i>Ceratoscopelus maderensis</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616361	CmL3
	<i>Ceratoscopelus maderensis</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616362	CmL4
	<i>Ceratoscopelus maderensis</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616363	CmA6
	<i>Ceratoscopelus maderensis</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616364	
	<i>Ceratoscopelus maderensis</i>	650	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148109	
	<i>Ceratoscopelus maderensis</i>	630	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148110	
	<i>Ceratoscopelus maderensis</i>	494	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	FJ164561	
	<i>Diaphus holthii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616388	DhA1
	<i>Diaphus holthii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616389	DhA2
	<i>Diaphus holthii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616390	DhA5
	<i>Diaphus holthii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616391	DhA6
	<i>Diaphus theta</i>	652	cytochrome oxidase subunit I (COI) gene	Steinke et al. 2008		
	<i>Diaphus rafinesquii</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148154	
	<i>Diaphus metopoclampus</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148151	
	<i>Electrona risso</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616411	ErT1
	<i>Hygophum benoiti</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616370	HbL1
	<i>Hygophum benoiti</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616371	HbL2
	<i>Hygophum benoiti</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616372	HbT4
	<i>Hygophum benoiti</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616373	HbA5
	<i>Hygophum benoiti</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616374	HbA6

Table S2 (cont.). – List of sequences of myctophids and stomiiforms used in the present study. Codes for the sequences from our lab are shown on the right part of the table. Apart from our results, the sequences that were used in this study and selected from GenBank (<http://www.ncbi.nlm.nih.gov/genbank>) are listed with the corresponding accession number and source. The outgroup species *BathyLAGUS euryops* was included.

Family	Species / Genus	No. Nucleotides	Genetic marker	Source Identifier	Accession number	Abbreviation
	<i>Hygophum benoiti</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616375	HbA7
	<i>Hygophum benoiti</i>	648	cytochrome oxidase subunit I (COI) gene	Keskin 2010	HQ167651	
	<i>Hygophum benoiti</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148200	
	<i>Hygophum benoiti</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148201	
	<i>Hygophum benoiti</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148202	
	<i>Hygophum hygomii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616376	HhA1
	<i>Hygophum hygomii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616377	HhA2
	<i>Hygophum hygomii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616378	HhA3
	<i>Hygophum hygomii</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148204	
	<i>Hygophum hygomii</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148205	
	<i>Hygophum hygomii</i>	831	cytochrome oxidase subunit I (COI) gene	DeVaney 2009	FJ918945	
	<i>Lampanyctus alatus</i>	594	cytochrome oxidase subunit I (COI) gene	Bucklin, A. et al., 2009	GU071738	
	<i>Lampanyctus festivus</i>	613	cytochrome oxidase subunit I (COI) gene	Gleason et al. 2010	GU441539	
	<i>Lampanyctus photonotus</i>	623	cytochrome oxidase subunit I (COI) gene	Bucklin et al. 2009	GU071732	
	<i>Lampanyctus tenuiformis</i>	595	cytochrome oxidase subunit I (COI) gene	Gruenthal et al. 2008	EU489716	
	<i>Lampanyctus tenuiformis</i>	652	cytochrome oxidase subunit I (COI) gene	Hastings and Burton 2009	GU440365	
	<i>Lampanyctus tenuiformis</i>	652	cytochrome oxidase subunit I (COI) gene	Hastings and Burton 2009	GU440366	
	<i>Lampanyctus crocodilus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616379	LcL1
	<i>Lampanyctus crocodilus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616380	LcA2
	<i>Lampanyctus crocodilus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616381	LcA3
	<i>Lampanyctus crocodilus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616382	LcA5
	<i>Lampanyctus pusillus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616383	LpL1
	<i>Lampanyctus pusillus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616384	LpL2
	<i>Lampanyctus pusillus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616385	LpA3
	<i>Lampanyctus pusillus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616386	LpA4
	<i>Lampanyctus pusillus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616387	LpL6
	<i>Lobianchia dofleinii</i>	564	cytochrome oxidase subunit I (COI) gene	This study	KF143896	LdL1
	<i>Lobianchia dofleinii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616404	LdL2
	<i>Lobianchia dofleinii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616405	LdA3
	<i>Lobianchia dofleinii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616406	LdA4
	<i>Lobianchia dofleinii</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616407	LdA5
	<i>Lobianchia sp. → Diaphus dumérili</i>	652	cytochrome oxidase subunit I (COI) gene	Vaidez-Moreno et al. 2009	GU224892	
	<i>Lobianchia sp. → Diaphus dumérili</i>	652	cytochrome oxidase subunit I (COI) gene	Vaidez-Moreno et al. 2009	GU224894	
	<i>Lobianchia sp. → Diaphus dumérili</i>	652	cytochrome oxidase subunit I (COI) gene	Vaidez-Moreno et al. 2009	GU224895	
Stenoptychidae	<i>Maurolicus muelleri</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616401	MmL1
	<i>Maurolicus muelleri</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616398	MmA2
	<i>Maurolicus muelleri</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616399	MmA3
	<i>Maurolicus muelleri</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616402	MmL4
	<i>Maurolicus muelleri</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616403	MmL5
	<i>Maurolicus muelleri</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616400	MmA6
	<i>Maurolicus muelleri</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148245	
	<i>Maurolicus muelleri</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148246	
	<i>Maurolicus muelleri</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148247	
	<i>Myctophum punctatum</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616392	MpL1
Myctophidae	<i>Myctophum punctatum</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616393	MpA2
	<i>Myctophum punctatum</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616394	MpL3
	<i>Myctophum punctatum</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616395	MpL4
	<i>Myctophum punctatum</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616396	MpA5
	<i>Myctophum punctatum</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616397	MpA6

Table S2 (cont.). – List of sequences of myctophids and stomiatiforms used in the present study. Codes for the sequences from our lab are shown on the right part of the table. Apart from our results, the sequences that were used in this study and selected from GenBank (<http://www.ncbi.nlm.nih.gov/genbank>) are listed with the corresponding accession number and source. The outgroup species *BathyLAGUS euryops* was included.

Family	Species / Genus	No. Nucleotides	Genetic marker	Source Identifier	Accession number	Abbreviation
	<i>Myctophum punctatum</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148251	
	<i>Myctophum punctatum</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148252	
	<i>Myctophum punctatum</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148253	
	<i>Notoscopelus bolini</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616408	NbA1
	<i>Notoscopelus bolini</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148275	
	<i>Notoscopelus bolini</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148276	
	<i>Notoscopelus bolini</i>	648	cytochrome oxidase subunit I (COI) gene	Keskin, E., 2010	HQ167653	
	<i>Notoscopelus elongatus</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616409	NeA1
	<i>Symbolophorus veranyi</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KF143397	SvA3
	<i>Symbolophorus veranyi</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148338	
	<i>Symbolophorus veranyi</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148339	
	<i>Symbolophorus veranyi</i>	652	cytochrome oxidase subunit I (COI) gene	Zhang et al. 2007	EU148340	
	<i>Vinciguerria attenuata</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616412	VaA1
	<i>Vinciguerria attenuata</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616413	VaA2
	<i>Vinciguerria attenuata</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616414	VaA3
	<i>Vinciguerria attenuata</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616415	VaA4
	<i>Vinciguerria attenuata</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616416	VaA5
	<i>Vinciguerria attenuata</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616417	VaA6
	<i>Vinciguerria attenuata</i>	565	cytochrome oxidase subunit I (COI) gene	This study	KC616418	VaA7
	<i>Vinciguerria attenuata</i>	307	mitochondrial gene for subunit 12S rRNA	Lopez et al. 2004	AY438704	
	<i>Vinciguerria</i> sp.	652	cytochrome oxidase subunit I (COI) gene	Bentley et al. 2013	KF929651	
Microstomatidae						

Table S3. – Distinctive features of larvae of the most abundant and frequent mesopelagic species occurring in the western Mediterranean. Sources of larval descriptions stated in Table S1.

	EYES SHAPE		HEAD	BODY SHAPE	GUT LENGTH ¹	PECTORAL FIN	
	Narrow	Ovalate-Round	Conspicuous morphology	Deep	Slender	Short Moderately long	Conspicuous features
O. Myctophiformes							
E. Myctophidae							
SF. Lampanyctinae	+ +	+ + + + +	+ + +	+ + + + +	+ + + + +	+ + + + +	
<i>Ceratoscopelus maderensis</i>			moderately deep				
<i>Diaphus holli</i>			deep, snout blunt				
<i>Lampanyctus crocodilus</i>			broad with large snout				
<i>Lampanyctus pusillus</i>			moderately deep				
<i>Lobianchia dofleini</i>			moderately deep				
<i>Notoscopelus bohini</i>			moderately deep				
<i>Notoscopelus elongatus</i>			moderately deep				
SF. Myctophictinae	+ +	+ + + + +	+ + + + +	+ + + + +	+ + + + +	+ + + + +	
<i>Benthosema glaciale</i>			large, broad				
<i>Electrona rissa</i>			broad and flat				
<i>Hygophum benoiti</i>			broad and flat				
<i>Hygophum hygomii</i>			broad and flat				
<i>Mycophthrum punctatum</i>			broad and flat				
<i>Symbolophorus veranyi</i>			broad and flat				
O. Stomiiformes							
F. Sternopychidae							
<i>Argyropelecus hemigymnus</i>	+ +	+ + + + +	+ + + + +	+ + + + +	+ + + + +	+ + + + +	
<i>Maurolicus muelleri</i>							
F. Gonostomatidae							
<i>Cyclothona braueri</i>							
<i>Cyclothona pygmaea</i>							
F. Phosichthhyidae							
<i>Vinciguerra attenuata</i>	+ +	+ + + + +	+ + + + +	+ + + + +	+ + + + +	+ + + + +	

Table S3 (cont.) – Distinctive features of larvae of the most abundant and frequent mesopelagic species occurring in the western Mediterranean. Sources of larval descriptions stated in Table S1.

	Above head	Snout or Jaws	Gut	DISTINCTIVE PIGMENTATION LOCATION	Ventral tail	Hypaxial	Dorsal tail	Caudal base	Pectoral fin
O. Myctophiformes									
E. Myctophidae	-	-	-	anus	series of spots (preflexion)	+	-	-	-
SF. Lanipanyctinae	-	-	-	lateral, swim bladder, anus	series of spots (preflexion)	-	-	-	-
<i>Ceratoscopelus maderensis</i>	-	-	-	anus	-	-	-	-	-
<i>Diaphus holli</i>	+	-	-	anus	-	-	-	-	-
<i>Lanipanyctus crocodilus</i>	-	-	-	anus, dorsal surface	-	-	-	-	-
<i>Lanipanyctus pusillus</i>	-	-	-	anus, swim bladder	-	-	-	-	-
<i>Lobianchia doffleini</i>	-	-	-	anus, swim bladder	-	-	-	-	-
<i>Notoscopelus boinii</i>	+	+	-	anus, swim bladder	-	-	-	-	-
<i>Notoscopelus elongatus</i>	+	-	-	anus	-	-	-	-	-
SF. Myctophictinae	-	-	-	-	-	-	-	-	-
<i>Benthosema glaciale</i>	-	-	-	-	-	-	-	-	-
<i>Electrona rissa</i>	-	-	-	-	-	-	-	-	-
<i>Hygophum benoiti</i>	-	-	-	lateral and anus	2-3 spots (preflexion)	-	-	-	-
<i>Hygophum hygomii</i>	-	-	-	lateral wall in prefexion, anus	1 conspicuous spot (preflexion)	-	-	-	-
<i>Mycophthrum punctatum</i>	+	+	-	ventral wall, anus	series of spots (preflexion)	+	-	-	-
<i>Symbolophorus veranyi</i>	+	+	-	lateral wall in prefexion, anus	series of spots (preflexion)	-	-	-	-
O. Stomiiformes									
F. Sternopychidae	-	-	-	-	-	-	-	-	-
<i>Argyropelecus hemigymnus</i>	-	-	-	-	-	-	-	-	-
<i>Maurolicus muelleri</i>	-	-	-	-	-	-	-	-	-
F. Gonostomatidae	-	-	-	-	-	-	-	-	-
<i>Cyclothona braueri</i>	-	-	-	-	-	-	-	-	-
C. Phosichthhyidae	-	-	-	-	-	-	-	-	-
<i>Vinciguerra attenuata</i>	-	-	-	-	-	-	-	-	-

Table S4.—Estimates of the net evolutionary divergence between species, considering larval and adult sequences and GenBank. The number of base substitutions per site by estimating the net average between groups of sequences is shown. Standard error estimates are shown above the diagonal. Analyses were conducted using the maximum composite likelihood model. The rate variation among sites was modeled using gamma distribution (shape parameter=5). The analysis involved 110 nucleotide sequences. The codon positions that were included were 1st+2nd+3rd+Non-coding. All ambiguous positions were removed for each sequence pair and 570 positions were included in the final dataset. Abbreviated names: AH, *Argyropelecus hemigymnus*; BG, *Benthosema glaciale*; CM, *Ceratoscopelus maderensis*; DH, *Diaphus holsti*; ER, *Electrona rissso*; HB, *Hymaphum benetti*; HH, *Hymaphum hygromi*; LA, *Lampanyctus alatus*; LC, *Lampanyctus crocodilus*; LD, *Lobianchia dofleini*; LP, *Lampanyctus pusillus*; Lph, *Lampanyctus photonotus*; LT, *Lampanyctus tenuiformis*; MM, *Maurolicus muelleri*; MP, *Mycophthrum punctatum*; NB, *Notoscopelus elongatus*; SV, *Symbophorus veranyi*; VA, *Vinciguerria attenuata*; VP, *Vinciguerria poweriae*.

	AH	BG	CM	DH	ER	VA	HB	HH	LA	LC	LD	LP	Lph	LT	MM	MP	NB	NE	SV	VP
AH	0.022	0.024	0.022	0.025	0.024	0.025	0.026	0.023	0.026	0.025	0.024	0.023	0.022	0.025	0.026	0.024	0.024	0.019		
BG	0.216	0.021	0.020	0.018	0.027	0.021	0.021	0.024	0.023	0.024	0.023	0.023	0.024	0.021	0.020	0.020	0.020	0.020	0.020	
CM	0.249	0.197	0.021	0.022	0.025	0.023	0.022	0.019	0.018	0.022	0.022	0.021	0.019	0.020	0.024	0.024	0.021	0.022	0.017	
DH	0.209	0.195	0.197	0.207	0.194	0.200	0.027	0.020	0.022	0.023	0.022	0.020	0.022	0.021	0.023	0.024	0.022	0.020	0.021	0.017
ER	0.248	0.153	0.207	0.194	0.026	0.020	0.021	0.024	0.022	0.024	0.024	0.022	0.023	0.022	0.024	0.024	0.021	0.020	0.019	0.018
VA	0.257	0.269	0.254	0.281	0.266	0.028	0.027	0.029	0.029	0.026	0.026	0.029	0.028	0.028	0.025	0.027	0.025	0.025	0.026	0.015
HB	0.233	0.195	0.228	0.187	0.182	0.284	0.017	0.023	0.024	0.025	0.025	0.023	0.023	0.023	0.023	0.022	0.020	0.020	0.020	0.019
HH	0.257	0.205	0.218	0.215	0.193	0.280	0.137	0.025	0.024	0.021	0.022	0.025	0.024	0.024	0.024	0.024	0.021	0.022	0.021	0.018
LA	0.248	0.230	0.176	0.216	0.242	0.289	0.228	0.242	0.016	0.024	0.015	0.016	0.014	0.014	0.025	0.025	0.022	0.023	0.025	0.021
LC	0.227	0.218	0.170	0.201	0.203	0.285	0.232	0.235	0.127	0.024	0.016	0.014	0.014	0.026	0.024	0.024	0.022	0.022	0.023	0.019
LD	0.266	0.228	0.193	0.186	0.231	0.255	0.242	0.194	0.246	0.235	0.235	0.023	0.026	0.023	0.025	0.023	0.025	0.024	0.022	0.018
LP	0.240	0.221	0.189	0.206	0.208	0.297	0.222	0.213	0.111	0.135	0.232	0.018	0.016	0.016	0.026	0.023	0.022	0.023	0.023	0.019
Lph	0.247	0.222	0.174	0.195	0.218	0.281	0.220	0.249	0.127	0.108	0.251	0.148	0.015	0.027	0.024	0.021	0.021	0.023	0.019	
LT	0.231	0.214	0.187	0.218	0.211	0.283	0.223	0.232	0.100	0.107	0.230	0.125	0.118	0.023	0.024	0.024	0.020	0.020	0.023	0.018
MM	0.204	0.244	0.236	0.233	0.234	0.255	0.221	0.235	0.234	0.253	0.232	0.253	0.253	0.268	0.219	0.025	0.025	0.025	0.024	0.018
MP	0.270	0.201	0.228	0.214	0.195	0.269	0.204	0.187	0.250	0.229	0.215	0.218	0.234	0.239	0.240	0.022	0.022	0.019	0.018	
NB	0.251	0.173	0.196	0.206	0.187	0.246	0.182	0.219	0.189	0.206	0.231	0.209	0.184	0.177	0.247	0.211	0.010	0.023	0.018	
NE	0.237	0.179	0.207	0.193	0.185	0.258	0.181	0.211	0.200	0.206	0.228	0.218	0.187	0.176	0.249	0.205	0.062	0.023	0.019	
SV	0.234	0.184	0.207	0.201	0.173	0.267	0.188	0.196	0.241	0.222	0.208	0.220	0.213	0.219	0.233	0.170	0.213	0.220	0.017	
VP	0.152	0.143	0.103	0.113	0.137	0.093	0.146	0.135	0.161	0.143	0.124	0.150	0.145	0.135	0.127	0.135	0.133	0.132	0.122	