

## Additional File 1

### The list of primers used in the PCR and sequencing for all species of the genus *Asymmetron*

L primers	Sequence (5' → 3')	Ref.	H primers	Sequence (5' → 3')	Ref.
<i>Long PCR primers (A. inferum-specific primer)</i>					
Asin-LA-cox1-L	GCGGGCAAGCATCGAATGAAATCGTGTTC		Asif-LA-rrnLH	GGACAAGTGATTATGCTACCTTTGCACAGTC	
<i>Long PCR primers (A. lucayanum-specific primer)</i>					
			AlH6890-COI (981)	GGCGTTTCTCATTTAATCTGCTTAGATCCT	a
<i>Long PCR primers (lancelet-versatile primers)</i>					
AmphLAL1076-cox1	CTGTAGGTGGGTTAACAGGAATTGTATTAGC	a	AmphLAH916-cox1	CCTGTTGGTACAGCAATTACTATAAGTAGCAGC	a
AmphLAL11947-rrnL	GACTGTGCAAAGGTAGCATAATCACTTGCCC	a	AmphLAH12317-rrnL	CTAGGAATCTTGATCCAACATCGAGGTCCG	a
<i>Long PCR primers (fish-versatile primers)</i>					
S-LA-16SL (12411)	CGATTAAAGTCCTACGTGATCTGAGTTCAG	b			
<i>PCR and sequencing primers (A. inferum-specific primer)</i>					
Asin-cox1-L1	TTCTTTGGTCACCCAGAGGT		Asin-cox2-H	TCGGTATATTCATAGCTTCAG	
Asin-atp6-L	ACGCAATGCTTCTCTCTTAG		Asin-nad4L-H1	GAGTGCTAAACCTGAACTGG	
Asin-nad4-L1	ACCTTTGAGGCCCTATAAAC		Asin-nad4-H	GTCTACTTGTAAGTCAAGCGG	
Asin-nad4-L2	ATTCTACACTTAACACCAGC		Asin-trnH-H	TGCCATTGGGATTAATAAA	
Asin-nad5-L1	AGACAAATAGTAACACGTCAC		Asin-nad6-H	CGGGTAGAGCTGTTTTGTAA	
Asin-nad5-L2	TTTAGGGGTCATAAAAGCAA		Asin-cob-H	AATGTACAATAGCTAGTCCTG	
			Asin-nad2-H	TGCTCCGATTGATTGATTGAG	
<i>PCR and sequencing primers (A. lucayanum-specific primer)</i>					
Aslu(spA)-nad5-L	TGTTCAATTTTGCAAGCCATG		AlH6012-COI (109)	GGCTGGGATAGTTCTGCWCGAAT	a
El-L6744-nad6	TTCGATCTCTATGAGCGCGG	a	El-H7103-nad6	GATTCTGCCTCTAATGTGGC	a
El-L6994-nad6	TAAAGACGTTTGCGCTTGAG	a	Aslu(spA)-nad5-H	AGAGATGCAAATACTGCGGC	
			El-H8317-nad5	ATACTAATTCTAGTCAGCGC	a
<i>PCR and sequencing primers (lancelet-versatile primers)</i>					
AmphL1325-cox1	GGNATACCWCGNCGRTATTCNGA	a	AmphH131-cox1	GGCTGNGANARTTCNGCNCGAAT	
AmphL1573-trnS	GTCTATTGGTTTCAAGCC	a	AmphH1580-trnS	TATGCGATTGGCTTGAAACC	a
AmphL2429-trnK	GCGTTAACCTTTTAAGTTAATGATGAG	a	AmphH2005-cox2	TCTGTRTAYTCRTARCTTCA	a
AmphL3328-cox3	CAYCCRTGRCAYT TAGTDGARCC	a	AmphH2403-trnK	CTCATCATTAACCTAAAAGGTTAACGC	a
AmphL4471-trnR	ATTTGGTTTCGGCCANAAG	a	AmphH4049-cox3	CCTCACCAGTAAATACAWACG	a
AmphL5013-nad4	CCTTTGATATTAATTGCTAGHCAAC	a	AmphH4452-trnR	CTTNTGGGCCGAAACCAAAT	a
AmphLAL5212-nad4	GGAGCACAAAAAGAGCGTTATCAAGCAGGAACATA	a	AmphH4989-nad4	GTTGGCTAGCAATTAATATYAAAGG	a
AmphL5429-nad4	GGCTGCCTAAGGCTCAYGTDGAG	a	AmphH5407-nad4	CTCCACGTGTGCCTTWGGMARCC	a
AmphL6166-trnH	CTAGTTTAATWAGAATWCTAAGTTGTGGTC	a	AmphH6137-trnH	GACCACAACCTTAGWATTCTWATTAACCTAG	a

AmphL6244- <i>trnS</i>	ATGTTGCTACCRTRRYYNATTARAGTTC	a	AmphH6217- <i>trnS</i>	GAACTTTAATNARTTATGGTAGCAACAT	a
AmphL7442- <i>nad5</i>	TGTTTCTTTATTGGKAGTGC	a	AmphH8842- <i>trnE</i>	ATAACRYAAGCTTTTCATGC	a
AmphL8307- <i>trnG</i>	AGAYTTCCAMTCTRARGRTCC	a	AmphH9081- <i>cob</i>	ACATCWCGRCARATATGNGC	a
AmphL8842- <i>trnE</i>	GCATGAAAARCTTRYGTTAT		AmphLAH9480- <i>cob</i>	CCTGTTGGATTATTKGCCCTGTTTGRGTAA	a
AmphLAL9412- <i>cob</i>	GGGYTTCTCYGTTGATAATGCMACACTAACTCG	a	AmphH10129- <i>trnP</i>	TAARCTTTGGGAGTTTAAARYG	
AmphL10108- <i>trnP</i>	CRTYTTAAACTCCCAAAGYTTA		AmphH11475- <i>rrnL</i>	CATTTCTTAARYAACAGCTA	
AmphL10383- <i>rrnS</i>	GTGCCAGCCGCCGCGGTTA		AmphH12522- <i>trnL</i>	GCTTAGGCCTTWYGCAATAC	a
AmphL11103- <i>trnV</i>	TAAGCGTYTCTTTTACACGG		AmphH13633- <i>trnM</i>	CTCATGGTAGAGGATGGATT	a
AmphLAL11918- <i>rrnL</i>	GACTGTGCAAAGGTAGCATAATCACTTGCCC				
AmphL13396- <i>nad1</i>	TGRTTTCGKGCWTCNTACCC	a			
AmphL14219- <i>nad2</i>	GGAGGNYTNGGNCARACRCAANTRCG				
AmphL14488- <i>trnN</i>	CATCKTTGGATTAACAGTC	a			
AmphL14842- <i>trnW</i>	AGACCTTTAGCCTTCAAAGCTG				
<i>PCR and sequencing primers (fish-versatile primers)</i>					
L6631-COI (726)	TGRTTTTTTGGTCACCCTGAAGT	a	H7227-COI (1324)	CATGTAGTGTATGCATCAGGGTARTC	g
L6730-COI (805)	TATATAGGAATRGTMGTGAGC	b	H7892-COII (1996)	TCGTAGCTTCAGTATCATTG	a
L7255-COI (1352)	GATGCCTACACMCTGTGAAA	b	H8168-COII (2272)	CCGCAGATTTTCWGAGCATTG	b
L7905-COII (2009)	GGCCAYCARTGGTAYTGAAG	a	H8589-ATP6 (2767)	AAGCTTAKTGTCATGGTCAGT	b
L8343-Lys (2402)	AGCGTTGGCCTTTTAAAGCTAAWGATWGGTG	a	H9076-ATP6 (3144)	GGGCGGATAAAKAGGCTAAT	b
L8894-ATP6 (2879)	TTGGACTACTWCCSTATAAC	b	H10244-ND3 (4275)	AGGAGSGCGATTTTCWAGRTC	a
L9514-COIII (3599)	TTCTGAGCCTTCTAYCA	b	H10433-Arg (4458)	AACCATGGWTTTTTGAGCCGAAAT	b
L11895-ND4 (5899)	CCTAACCTWATGGGRRGAAGT	b	H11618-ND4 (5622)	TGGCTGACKGAKGAGTAGGC	c
L13280-ND5 (6749)	CAACTWGGKCTAATAATAGT	a	H12145-His (6138)	CTAGTGTTTTKGTTAAACTA	b
L15927-Thr (10062)	AGAGCGTCGGTCTTGTAACKCCG	c	H12632-ND5 (6586)	GATCAGGTTACGTAKAGKGC	b
L1085-12S (10530)	TAAACCAGGATTAGATACCC	d	H14086-ND5 (7764)	AGGSTKAGGTAKGTTTTRAT	c
L1496i-12S (10909)	GTACATATCGCCCGTCGCTT	e	H1358-12S (10691)	CGACGGCGGTATATAGGC	b
L2188-16S (11601)	AGTGGGCCTAAAAGCAGCCA	a	H1478-12S (10842)	GAGAGTGACGGGCGATGTGT	d
L2510i-16S (11855)	CGCCTGTTTAAACAAAACAT	f	H1903-16S (11341)	GTAGCTCGTYTAGTTTCGGG	b
S-LA-16SL (12411)	GATTAAAGTCCTACGTGATCTGAGTTCAG	b	H2491c-16S (11836)	ATGTCTTTGTTAAACAGGCG	a
L3686-ND1 (12964)	TGAGCMTCWAATTCMAAATA	a	H2716i-16S (12051)	AAGTTTTATAGGGTCTTATCGTC	e
L4180-ND1 (13437)	CAACTCATGCATTTTRGTWTGRAAAA	c	H3466-ND1 (12744)	ATKGGTCTTTTGATGAAKAGTTT	c
L4438-Met (13618)	AAGCTTTTGGCCCCATRCCC	a	H3976-ND1 (13254)	ATGTTGGCGTATTCKGCKAGGAA	a
			H5622-Ala (14916)	TTAATTAAGTGTCTGKKTGCA	a
			H4557-ND2 (14752)	GTATTAATTTCTAGKCCTATTCA	a

a, Nohara et al. (2005); b, Miya and Nishida (1999); c, Miya and Nishida (2000); d, Miya and Nishida (1998); e, Kitaura, Wada and Nishida (1998); f, Palumbi et al. (1991); g, Nishida, Ohkawa and Iwata (1998)

## References

- Kitaura J, Wada K, Nishida M: **Molecular phylogeny and evolution of unique mud-using territorial behavior in ocypodid crabs (Crustacea: Brachyura: Ocypodidae).** *Mol Biol Evol* 1998, **15**(6):626-637.
- Miya M, Nishida M: **Molecular phylogeny and evolution of the deep-sea fish genus *Sternoptyx*.** *Mol Phylogenet Evol* 1998, **10**(1):11-22.
- Miya M, Nishida M: **Organization of the mitochondrial genome of a deep-sea fish, *Gonostoma gracile* (Teleostei: Stomiiformes): First example of transfer RNA gene rearrangements in bony fishes.** *Mar Biotechnol* 1999, **1**(5):416-426.
- Miya M, Nishida M: **Use of mitogenomic information in teleostean molecular phylogenetics: A tree-based exploration under the maximum-parsimony optimality criterion.** *Mol Phylogenet Evol* 2000, **17**(3):437-455.
- Nishida M, Ohkawa T, Iwata Y: **Methods of analysis of genetic population structure with mitochondrial DNA markers.** *Fish Genet Breed Sci* 1998, **26**:81–100. (in Japanese)
- Nohara M, Nishida M, Miya M, Nishikawa T: **Evolution of the mitochondrial genome in Cephalochordata as inferred from complete nucleotide sequences from two *Epigonichthys* species.** *J Mol Evol* 2005, **60**:526–537.
- Palumbi SR, Martin A, Romano S, McMillan WO, Stice L, Grabowski G: **The simple fool's guide to PCR. ver. 2.** Honolulu: University of Hawaii Press; 1991.