

Nucleotide differences found in the complete 18S ribosomal DNA (rDNA) sequence
of the lymnaeid species compared and their location in the secondary structure

Variable areas	VVVVV V	VVVVVVVVVV	VVVVVVVVVV	VVVVVVVVVV V	VV	VV	VV
	11111 2	2222222222	2222222222	2222222222 2	45	79	99
Helix	666668E999	EEEEEEEEEE	EEEEEEEEEE	EEEEEEEEEE E11111511E	EEEE223344	44	
	8	1111111111	1111111111	1111111111 122222 882	2222782513	47	
		0000000000	0000000000	0000000000 1	1 11111		
		-----	-----	-----	- - - - -		
		1111111111	1111111111	1111111111	1 25777		
Position					111111 11		
	11112	2222222222	2222222222	2222222222 3333334557	7788123347		
	6777925550	3333333444	4444445555	5555556666 1999996882	4935530133	59	
	9234892786	3456789012	3456790123	4567890126 2145784025	7496643763	23	
<i>Lymnaea (Lymnaea) stagnalis</i>	GTG-T---C	CG-----TGC	CGGGGGACTC	GTGC---GC -CGTAC-CC-	AACGT-GCTG	TA	
<i>Lymnaea (Stagnicola) palustris</i>CA--	
<i>Omphiscola glabra</i>	TAAC-----	
<i>Galba truncatula</i>AA--	T-----	.CTTT.CGAG	-----T-TT-	CG.A...-C.	.G
<i>Lymnaea cubensis</i>AA--	T.TCGTGCCG	...T.A.GC.	...GTCGC.CTTG	CG...-T-C.	CG
<i>Lymnaea viatrix = Lymnaea neotropica</i>AA--	T.TGCCTCCG	...T.A.GC.	...GTCGC.CTT-	CG...CT-C.	CG
<i>Lymnaea humilis</i>AA--	T-----CG	...C.AGGC.	.A.G-----CTT-	CG...CT-CC	CG
<i>Pseudosuccinea columella</i>AA--	T-----C.G	TCCC...-G	.G...CG--TCTT-	CG...CT-C.	..
<i>Lymnaea diaphana</i>AA--	-----CCG	...CT.C---	.CCGTG--CTT-	TG...CT-C.	..
<i>Radix auricularia</i>CAA--	-----TG	.TCTT.CGGG	-----T	CGTACT-TAG	CG.AC-T-C.	..
<i>Radix balthica</i>CATT.	-----TG	.TCTT.CGGG	-----T	CGTACT-TT-	CG.AC...-C.	..
Total variable positions (n = 62)	1	1111111111	2222222222	3333333333 4444444444	5555555555	66	
	1234567890	1234567890	1234567890	1234567890 1234567890	1234567890	12	

numbers (to be read in vertical) refer to positions obtained in the alignment made with MEGA 5.0. Shaded area corresponds to variable area V2 and helix E10-1 where Lymnaeidae differences in the 18S rRNA gene are concentrated. .: identical; -: indel.

