

S2 Table Primers used for amplification of mitochondrial *COI-tRNA(Leu)-COII* and *16S-tRNA(Leu)-ND1* gene regions in *Hyalesthes obsoletus* and archival paratype specimen of *H. thracicus*.

Gene region	Primer name	Primer sequence (5'→3')	Short amplicon length (with primers)	Main amplicon length (with primers)
<i>COI-tRNA(Leu)-COII</i>	S2792	ATACCTCGACGTTATTCAGA	291 bp	S2792/A3661
	Hy-TL-R1*	GRTTTWCTTTMTAGAYGAATTTTAAG		898 bp
	Hy-TL-F1*	TGGCAGAAAAGTGCTRTGAA	383 bp	
	Hy-COII-R1*	TCATATCTTCARTATCATTGATG		
	Hy-COII-F1*	CCATCAATTTCDATYAAAACHATAGG	320 bp	
	A3661	CCACAAATTTCTGAACATTGACCA		
<i>16S-tRNA(Leu)-ND1</i>	LR-N-12945	CGACCTCGATGTTGAATTAA	347 bp	LR-N-12945/
	Hy-ND1-R1*	TTWCGAAAYTGAATATAWCC		N1-J-12261
	Hy-ND1-F1*	GTTGCTTAYTTTATTCTTCTTGA	380 bp	671 bp
	N1-J-12261	TCGTAAGAAATTATTTGAGC		

*Degenerate primers designed in this study for amplification of short fragments in the archival specimen of *H. thracicus*. Design based on sequence alignment comparison among *Hyalesthes philesakis*, *H. luteipes*, *H. ponticorum*, *H. aylanus*, *Reptalus panzeri*, *R. melanochaetus*, *R. cuspidatus* and *Setapius apiculatus*.