

Supplementary information

Cryptic species within the rotifer *Lecane bulla* (Rotifera, Monogononta, Lecanidae) based on molecular species delimitation

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Table S1 Name and acronyms of each locality, as well as the biogeographic province where are located. Locations from 1 to 19 belong to Mexico, and locations from 20 to 25 belong to the United States of America. Localities 6 to 17 were obtained from García-Morales and Elías-Gutiérrez (2013) and localities 18 to 25 were obtained from Walsh et al. (2009)

Locality	Code	Biogeographic province
1. Manantial Huamio †	MH	Trans-Mexican Volcanic Belt (TMVB)
2. La Magdalena †	MAG	
3. Uranden †	URA	
4. La Joya †	JOY	
5. Calderon dam †	CAL	
6. Zempoala lagoon	ZEM	
7. Emiliano Zapata lagoon	EZ	
8. Capulteol lagoon	CAP	Gulf of Mexico (GM)
9. Majahual lagoon	MAJ	
10. Escondida lagoon	ESC	
11. Apompal lagoon	APO	
12. Catemaco lake	CAT	
13. Silvituc lagoon	SIL	Yucatan Peninsula (YP)
14. Rumbo al Tigre II	TIG	
15. Puente Milagros 1 lagoon	PM1	
16. Humedal Puente Milagros	HPM	
17. Encantada lagoon	ENC	
18. Tio Julio, Cuatro Ciénegas	TJ	Chihuahuan Desert (CHD)
19. Poza Tortugas, Cuatro Ciénegas	PT	
20. Cattail Spring Pool D, Big Bend National Park	CSD	
21. Cattail Spring Pool H, Big Bend National Park	CSH	
22. Rio Grande Village Pond, Big Bend National Park	RGV	
23. Croton Springs, Big Bend National Park	CRS	
24. San Solomon Spring wetland, Reeves Co.	SSS	
25. East Sandia Preserve, Reeves Co.	ES	

† Samples collected in this study.

Table S2 Shared haplotypes and their locations

Shared haplotypes	Sequences	Locations
H2	JX216652 JX216653 JX216654 JX216655 JX216656 JX216657	10. Escondida (ESC) 11. Apompal (APO)
H10	JX216660 JX216661 JX216663	16. Humedal Puente Milagros (HPM) 14. El Tigre II (TIG)
H13	JX216649 JX216650 JX216651 EU188928 EU188935	10. Escondida (ESC) 9. Majahual (MAJ) 20. Cattail Spring D (CSD) 22. Rio Grande Village (RGV)
H17	LbullaMH4 LbullaMH5 LbullaMH6 LbullaMH7 LbullaMH8 LbullaMH9 JX216666	1. Manantial Huamio (MH) 6. Zempoala (ZEM)

Table S3 Average percentages of uncorrected genetic distances of COI gene. On diagonal genetic distances within the 13 *Lecane bulla* putative species and under the diagonal genetic distances among the 13 putative species discriminated by the species delineation methods

Linaje	Lb1	Lb2	Lb3	Lb4	Lb5	Lb6	Lb7	Lb8	Lb9	Lb10	Lb11	Lb12	Lb13
Lb1	0												
Lb2	6.4	0											
Lb3	13.5	14.4	0										
Lb4	13.7	13.9	6.0	0									
Lb5	11.7	12.1	13.2	13.0	0								
Lb6	12.8	13.3	13.3	14.3	9.3	0							
Lb7	14.6	14.8	13.5	15.2	13.9	15.2	-						
Lb8	14.4	14.3	15.9	15.2	14.8	15.4	14.1	-					
Lb9	13.5	13.9	15.6	14.8	15.2	15.1	15.2	9.4	0.9				
Lb10	11.0	10.8	13.7	13.4	11.4	12.8	13.0	14.5	14.6	0.06			
Lb11	6.8	8.2	11.7	12.2	9.7	11.3	12.1	13.2	13.1	4.6	-		
Lb12	14.6	14.1	15.3	15.5	13.9	15.1	14.7	16.6	15.0	13.2	9.3	0.52	
Lb13	13.6	13.7	14.9	14.6	14.6	15.6	14.3	17.6	16.7	12.8	8.3	6.9	1.2

Table S4 Cryptic species and the number of individuals sequenced (N) and number of haplotypes (H) for the COI gene for *Lecane bulla*. *Hd* and π are the haplotype and nucleotide diversity respectively with the standard deviation in parentheses

Cryptic species	N	H	Hd	π
Lb1	3	1	0.000	0.000
Lb2	6	1	0.000	0.000
Lb3	3	1	0.000	0.000
Lb4	4	1	0.000	0.000
Lb5	2	1	0.000	0.000
Lb6	3	1	0.000	0.000
Lb7	1	1	0.000	0.000
Lb8	1	1	0.000	0.000
Lb9	6	4	0.800 (0.172)	0.00972 (0.00403)
Lb10	6	2	0.333 (0.215)	0.00056 (0.00036)
Lb11	1	1	0.000	0.000
Lb12	9	3	0.417 (0.191)	0.00556 (0.00386)
Lb13	8	5	0.786 (0.151)	0.01514 (0.00377)