

Supplementary material 1. List of MOTUs recovered by the 2% sequence divergence approach and corrected pairwise COI distances (%) among the chalcidoid specimens examined in this study.

1. *H. depressus* CNIN 3675, 3729, 3758, 3757, 3847
2. *H. depressus* CNIN 3829, 3831
3. *H. depressus* CNIN3782
4. *H. depressus* CNIN 3830
5. *H. depressus* CNIN 3795
6. *H. depressus* CNIN 3832
7. *H. depressus* CNIN 3834
8. *Horismenus* sp. 1 CNIN 3673, 3679, 3770
9. *Horismenus* sp. 1 CNIN 3702
10. *Horismenus* sp. 2 CNIN 3678, 3750
11. *Horismenus* sp. 2 CNIN 3677
12. *Horismenus* sp. 3 CNIN 3772, 3774
13. *Horismenus* sp. 4 CNIN 3674, 3701, 3767
14. *Horismenus* sp. 4 CNIN 3751
15. *H. bruchophagus* CNIN 3716, 3718, 3688, 3694, 3711
16. *H. bruchophagus* CNIN 3692, 3714
17. *H. bruchophagus* CNIN 3695
18. *H. missourensis* CNIN 3712
19. *H. missourensis* CNIN 3713, 3715, 3693, 3773
20. *H. missourensis* CNIN 3775, 3690, 3689
21. *E. sp. aff. pulchriceps* CNIN 3776, 3778, 3699
22. *E. sp. aff. pulchriceps* CNIN 3731, 3746, 3747
23. *E. sp. aff. pulchriceps* CNIN 3724, 3870
24. *E. sp. aff. pulchriceps* CNIN 3826
25. *E. sp. aff. pulchriceps* CNIN 3871
26. *E. annulatus* CNIN3671, 3700
27. *B. bruchivora* CNIN 3748, 3698
28. *B. neococcidis* CNIN 3835, 3836
29. *M. dorsiplana* CNIN 3696, 3717, 3730, 3691
30. *L. texanus* CNIN3707
31. *Eurydinoteloides* sp. 1 CNIN3818, 3820
32. *E. incerta* CNIN 3793

Specimens	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43					
1 Elachertus_spCNIN3755QUE																																																
2 H_missourensisCNIN3712QUE	26.3																																															
3 H_missourensisCNIN3713QUE	27.1	0.4																																														
4 H_missourensisCNIN3715QUE	26.3	0.4	0.4																																													
5 H_missourensisCNIN3693QUE	26.7	0.6	0.6	0.2																																												
6 H_missourensisCNIN3773JAL	27.5	0.6	0.6	0.6	0.8																																											
7 H_missourensisCNIN3775JAL	26.3	0.4	0.4	0.4	0.6	0.6																																										
8 H_missourensisCNIN3690QUE	26.3	1.0	1.0	1.0	1.2	1.2	1.0																																									
9 H_missourensisCNIN3689QUE	25.6	1.4	1.4	1.4	1.6	1.6	1.0	0.8																																								
10 H_bruchophagusCNIN3716QUE	25.7	19.3	20.0	20.0	20.3	20.3	19.3	18.3	17.7																																							
11 H_bruchophagusCNIN3718QUE	25.3	19.0	19.7	19.7	20.0	20.0	19.0	18.0	17.4	0.2																																						
12 H_bruchophagusCNIN3688QUE	24.6	18.4	19.0	19.0	19.3	19.3	18.4	17.4	16.8	0.6	0.4																																					
13 H_bruchophagusCNIN3694QUE	25.0	19.6	20.3	20.3	20.7	20.7	19.6	18.6	18.0	0.6	0.4	0.8																																				
14 H_bruchophagusCNIN3692QUE	26.0	19.3	19.3	20.0	20.3	20.3	19.3	18.4	17.7	1.8	1.6	2.0	1.6																																			
15 H_bruchophagusCNIN3695QUE	23.9	18.1	18.7	18.7	19.0	19.0	18.1	17.1	16.5	1.6	1.4	1.4	1.4	2.2																																		
16 H_bruchophagusCNIN3711QUE	24.9	19.0	19.6	19.6	20.0	20.0	19.0	18.0	17.4	1.2	1.0	0.6	1.2	2.4	2.0																																	
17 H_bruchophagusCNIN3714QUE	28.2	20.9	20.9	21.6	21.9	21.9	20.9	19.9	19.2	2.4	2.6	3.0	3.0	1.4	3.3	3.3																																
18 Horismenus_sp3CNIN3774JAL	24.9	18.5	18.5	18.5	18.8	18.8	17.9	17.3	16.4	8.4	8.1	7.6	8.2	7.9	7.9	7.4	7.7																															
19 Horismenus_sp3CNIN3772JAL	23.2	17.9	17.9	17.9	18.2	18.2	17.3	16.7	15.8	7.4	7.2	6.7	7.2	7.0	7.0	6.9	8.6	1.2																														
20 Horismenus_sp1CNIN3673QUE	21.5	21.2	21.2	21.9	22.3	22.3	21.2	20.2	19.6	17.1	16.9	16.5	16.8	16.9	15.4	17.1	18.3	16.2	14.7																													
21 Horismenus_sp1CNIN3769QUE	21.5	21.2	21.2	21.9	22.3	22.3	21.2	20.2	19.6	17.1	16.9	16.5	16.8	16.9	15.4	17.1	18.3	16.2	14.7	0.0																												
22 Horismenus_sp1CNIN3770QUE	21.2	20.5	20.5	21.2	21.6	21.6	20.5	19.5	18.9	16.8	16.5	16.2	16.5	16.5	15.1	16.8	18.0	15.9	14.5	0.4	0.4																											
23 Horismenus_sp1CNIN3702QUE	22.2	18.0	17.3	18.0	17.6	18.3	17.3	16.4	15.8	14.5	14.2	13.9	14.2	14.2	12.8	14.2	15.3	14.1	13.1	4.4	4.4	4.0																										
24 Horismenus_sp4CNIN3674QUE	24.6	15.9	15.9	15.6	15.9	16.2	15.3	14.4	13.9	16.9	16.6	16.0	16.5	16.6	15.1	16.5	18.0	15.8	14.7	14.2	14.2	13.9	11.4																									
25 Horismenus_sp4CNIN3701QUE	24.6	15.9	15.9	15.6	15.9	16.2	15.3	14.4	13.9	16.9	16.6	16.0	16.5	16.6	15.1	16.5	18.0	15.8	14.7	14.4	14.4	14.2	11.7	0.2																								
26 Horismenus_sp4CNIN3767QUE	24.6	15.9	15.9	15.6	15.9	16.2	15.3	14.4	13.9	16.9	16.6	16.0	16.5	16.6	15.1	16.5	18.0	15.8	14.7	14.2	14.2	13.9	11.4	0.0	0.2																							
27 Horismenus_sp4CNIN3751QUE	23.2	15.4	16.0	15.7	16.0	16.3	15.4	14.5	13.9	16.3	16.0	15.4	15.7	15.7	14.5	15.6	17.4	15.2	14.1	14.4	14.4	14.4	12.5	2.9	3.1	2.9																						
28 Horismenus_sp2CNIN3677QUE	22.2	16.5	16.8	16.5	16.8	17.5	16.5	15.6	15.0	15.6	15.3	14.7	14.8	15.4	14.5	15.1	17.4	16.4	15.3	12.6	12.6	12.0	11.5	13.1	13.4	13.1	11.8																					
29 Horismenus_sp2CNIN3678ROO	20.9	15.4	15.7	15.4	15.7	16.3	15.4	14.5	13.9	15.3	15.1	14.5	15.1	14.5	14.2	14.8	16.5	14.7	13.6	12.0	12.0	11.5	11.0	11.3	11.5	11.3	9.7	2.9																				
30 Horismenus_sp2CNIN3750CHP	20.9	15.7	16.0	15.7	16.0	16.6	15.7	14.8	14.2	15.6	15.4	14.8	15.4	14.8	13.9	15.1	16.8	15.0	13.9	12.3	12.3	11.7	11.2	11.5	11.8	11.5	10.0	3.1	0.2																			
31 H_depressusCNIN3675QUE	23.9	20.3	20.3	20.3	20.6	20.6	19.6	19.3	18.6	20.2	19.9	19.2	19.8	20.2	18.6	19.8	21.8	19.6	18.4	14.6	14.6	14.6	13.2	14.3	14.6	14.3	13.9	14.0	14.6	14.9																		
32 H_depressusCNIN3729QUE	22.9	20.6	21.3	21.3	21.7	21.7	20.6	20.3	19.6	19.5	19.2	18.5	19.2	20.2	18.6	19.2	21.8	20.3	19.0	14.0	14.0	14.0	13.2	14.3	14.6	14.3	13.6	14.3	14.3	14.6	1.2																	
33 H_depressusCNIN3758QUE	22.9	20.6	21.3	21.3	21.7	21.7	20.6	20.3	19.6	19.5	19.2	18.5	19.2	20.2	18.6	19.2	21.8	20.3	19.0	14.0	14.0	14.0	13.2	14.3	14.6	14.3	13.6	14.3	14.3	14.6	1.2	0.0																
34 H_depressusCNIN3757QUE	23.6	20.3	21.0	21.0	21.3	21.3	20.3	19.3	18.6	19.5	19.2	18.5	19.2	19.5	17.9	19.2	21.1	19.6	18.4	14.6	14.6	14.6	13.2	14.0	14.3	14.0	13.1	13.4	14.0	14.3	1.0	1.4	1.4															
35 H_depressusCNIN3782MEX	22.9	19.9	20.6	20.6	21.0	21.0	19.9	18.9	18.3	20.2	19.9	19.2	19.8	19.5	18.2	19.8	21.1	19.6	18.4	14.9	14.9	14.9	12.9	13.4	13.7	13.4	13.1	14.0	13.7	13.7	2.6	3.1	3.1	2.0														
36 H_depressusCNIN3830MOR	22.9	20.6	21.3	21.3	21.7	21.7	20.6	20.3	19.6	19.5	19.2	18.5	19.2	20.2	17.6	19.2	21.8	19.9	18.7	14.3	14.3	14.3	13.5	14.3	14.6	14.3	13.9	13.4	14.3	14.3	2.0	2.9	2.9	2.2	2.2													
37 H_depressusCNIN3847MEX	23.6	19.6	19.6	19.6	20.0	20.0	19.0	18.0	17.4	19.5	19.2	18.5	19.1	19.8	17.9	19.1	21.4	19.9	18.7	14.6	14.6	14.6	12.3	13.4	13.7	13.4	13.3	13.7	14.3	14.6	1.2	2.0	2.0	1.8	3.3	3.3												
38 H_depressusCNIN3795MOR	21.6	20.2	20.9	20.9	21.3	21.3	20.2	19.2	18.6	20.5	20.2	19.5	20.1	19.8	18.2	20.1	21.4	20.6	19.3	13.4	13.4	13.4	13.1	14.0	14.3	14.0	13.1	14.6	14.2	14.0	2.9	2.9	2.9	2.7	2.0	3.3	3.1											
39 H_depressusCNIN3832GUE	22.6	20.6	21.3	21.3	21.6	21.6	20.6	19.6	18.9	18.5	18.2	17.5	18.1	18.5	16.9	18.1	20.0	19.2	18.0	13.4	13.4	13.4	12.6	13.4	13.7	13.4	12.5	14.6	14.5	14.8	2.4	2.4	2.4	2.2	3.1	3.5	3.3	2.4										
40 H_depressusCNIN3834GUE	23.2	21.2	21.9	21.9	22.2	22.2	21.2	20.2	19.5	20.0	19.7	19.1	19.7	20.1	18.5	19.7	21.7	19.8	18.6	14.5	14.5	14.5	13.7	13.4	13.7	13.4																						

41 H_depressusCNIN3829MOR 22.9 21.2 21.9 21.9 22.3 22.3 21.2 20.2 19.6 20.8 20.5 19.8 20.4 20.1 19.2 20.4 21.7 20.2 19.0 14.2 14.2 14.2 13.4 14.0 13.7 14.0 13.6 15.4 15.1 15.4 2.9 2.9 2.9 2.6 3.1 3.5 3.5 2.9 2.4 3.5

42 H_depressusCNIN3831MOR 22.9 20.9 21.6 21.6 22.0 22.0 20.9 19.9 19.3 20.5 20.2 19.5 20.1 19.8 18.9 20.1 21.4 19.9 18.7 14.0 14.0 14.0 13.1 13.7 13.4 13.7 13.4 15.2 14.8 15.1 2.7 2.7 2.7 2.4 2.9 3.3 3.3 2.7 2.2 3.3 0.2

43 H_butcheriCNIN3796MOR 20.9 17.9 18.2 18.2 18.6 18.9 17.9 17.0 17.0 18.9 18.6 18.3 18.6 19.2 17.3 18.8 20.8 18.5 17.6 12.9 12.9 12.6 12.3 14.6 14.9 14.6 13.7 16.7 15.2 15.5 15.1 14.5 14.5 14.8 15.0 15.6 14.5 14.2 12.8 14.2 13.9

44 P_pluteusCNIN3676QUE 20.9 21.5 21.5 21.8 22.2 22.2 21.5 21.5 20.5 22.9 22.5 22.2 21.9 21.9 21.5 22.5 24.2 21.2 19.6 17.9 17.9 18.2 17.5 19.7 20.0 19.7 18.5 18.8 17.5 17.8 20.9 20.6 20.6 20.9 21.3 20.6 20.3 20.9 20.3 21.5 21.2 20.9 19.7

Uncorrected COI distances among examined specimens of *Elachertus*, *Horismenus* and *Paracrias* (Eulophidae). Forty-four sequences, 514 bp.

Specimens	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1 E_pulchricepsCNIN3776VER																
2 E_pulchricepsCNIN3778VER	0.7															
3 E_pulchricepsCNIN3699QUE	0.4	0.7														
4 E_pulchricepsCNIN3731MOR	8.9	8.9	9.4													
5 E_pulchricepsCNIN3746QUE	8.9	8.9	9.4	0.0												
6 E_pulchricepsCNIN3747QUE	8.9	8.9	9.4	0.2	0.2											
7 E_pulchricepsCNIN3724JAL	10.5	10.0	10.5	10.8	10.8	11.0										
8 E_pulchricepsCNIN3826GUE	11.5	11.0	11.5	11.7	11.7	11.8	1.1									
9 E_pulchricepsCNIN3870GUE	10.7	10.7	11.2	10.3	10.3	10.5	1.7	2.1								
10 E_pulchricepsCNIN3871GUE	10.7	10.7	11.2	10.3	10.3	10.5	1.7	2.1	0.0							
11 E_pulchricepsCNIN3823OAX ♂	11.7	11.2	11.2	12.0	12.0	12.2	2.1	2.1	2.7	2.7						
12 E_annulatusCNIN3671QUE	10.5	10.5	11.0	12.2	12.2	12.2	11.8	12.5	11.7	11.7	12.0					
13 E_annulatusCNIN3700QUE	10.7	10.7	11.2	12.5	12.5	12.5	12.0	12.8	12.0	12.0	12.2	0.2				
14 B_bruchivoraCNIN3748QUE	16.9	16.9	16.9	16.9	16.9	17.2	15.0	15.8	15.3	15.3	15.9	16.9	17.2			
15 B_bruchivoraCNIN3698QUE	17.5	16.4	17.5	16.1	16.1	16.4	15.8	17.2	16.7	16.7	16.7	17.5	17.8	6.8		
16 B_neococcidisCNIN3835MEX	14.8	14.8	15.0	14.8	14.8	14.8	15.3	16.1	16.1	16.1	16.7	15.8	15.8	10.3	10.7	
17 B_neococcidisCNIN3836MEX	14.8	14.8	15.0	14.8	14.8	14.8	15.3	16.1	16.1	16.1	16.7	15.8	15.8	10.3	10.7	0.0

Uncorrected COI distances among examined specimens of *Eupelmus* and *Brasema* (Eupelmidae). Seventeen sequences, 544 bp.

	Specimens	1	2	3	4	5	6	7
1	L_texanusCNIN3707ROO							
2	Eurydinoteloides_sp1CNIN3818MEX	14.2						
3	Eurydinoteloides_sp1CNIN3820MEX	14.7	1.1					
4	E_incertaCNIN3793MEX	13.5	16.7	17.0				
5	M_dorsiplanaCNIN3696QUE	14.0	19.1	19.1	17.5			
6	M_dorsiplanaCNIN3717QUE	14.0	19.1	19.1	17.5	0.0		
7	M_dorsiplanaCNIN3730QUE	14.0	19.1	19.1	17.5	0.0	0.0	
8	M_dorsiplanaCNIN3691QUE	13.7	18.9	18.9	17.8	0.2	0.2	0.2

Uncorrected COI distances among examined specimens of *Eurydinoteloides*, *Lariophagus* and *Monoksa* (Pteromalidae). Eight sequences, 577 bp.