

Figure S1: Bayesian majority rule consensus tree based on combined nuclear markers (ITS2+28S-D2). Posterior probabilities ≥ 0.9 are shown above branches. The tree was rooted using the midpoint-rooted tree option.

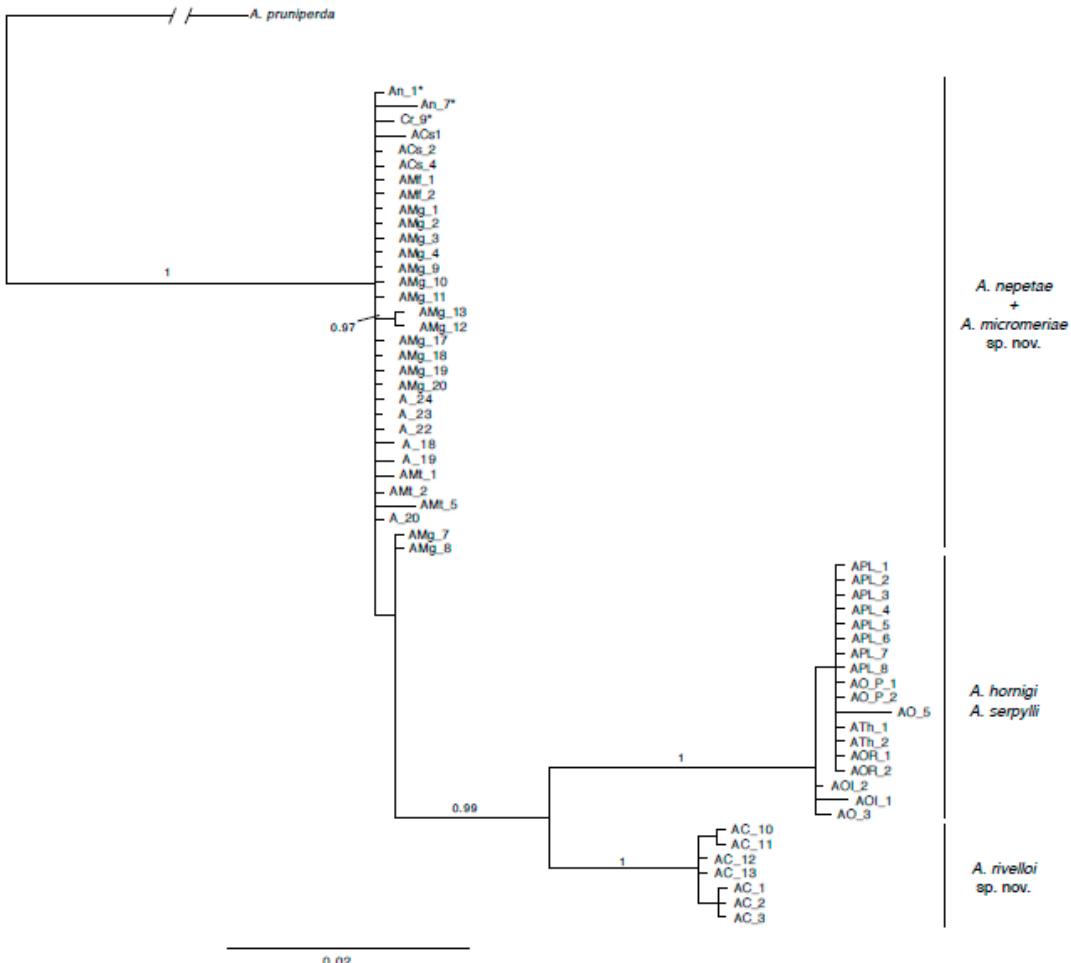


Figure S2: Bayesian majority rule consensus tree based on COI alignments of *Asphondylia* specimens of the present work and sequences (*) from [4]. Posterior probabilities ≥ 0.9 are shown above branches.

Table S1. Differences in nuclear genes ITS2+28S-D2 among the studied *Asphondylia* species.

Species	Sites/bp							
	7	12	18	307-336	37	41	415	88
0	2	3			4	0		8
<i>A. nepetae</i>	A	T	T	-	G	C/T	G	A
<i>A. rivelloi</i> sp. nov.	G	T	T	ATACATTAAATAAACCAAGAAATATTA T	-	C/T	A/ G	A
<i>A. micromeria</i> e sp. nov.	A	T	T	ATACATTAAATAAACCAAGAAATATTA T	G	T	G	G
<i>A. hornigi</i> <i>A. serpylli</i>	A	A	G	ATACATTAAATAAACCAAGAAATATTA T	-	T	G	A

Table S2. Length/maximum width ratios of *A. nepetae* and *A. micromeriae* flagellomeres.

Antennal flagellomere	Species	
	<i>A. nepetae</i>	<i>A. micromeriae</i>
F1	6.14	4.51
F2	4.12	3.6
F3	4.00	3.18
F4	3.75	3.14
F5	3.75	3.19
F6	3.50	3.10
F7	4.00	2.88
F8	2.62	2.07
F9	2.25	1.64
F10	1.30	1.00
F11	1.00	0.94
F12	1.00	0.83