

Supplementary Material

Molecular phylogeny and systematic revision of the Brazilian species of *Mastigoproctus* Pocock, 1894 (Arachnida: Uropygi: Mastigoproctinae)

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Table S1. PCR cycles implemented for each molecular marker.

Marker	PCR cycle
<i>COI</i> and <i>12S</i>	98°C for 3 min; 35× (98°C for 10 s, 45°C for 30 s, 72°C for 20 s), 72°C for 3 min
<i>18S</i>	98°C for 3 min; 35× (98°C for 10 s, 55°C for 30 s, 72°C for 25 s), 72°C for 3 min
<i>ITS2</i>	98°C for 3 min; 35× (98°C for 10 s, 55°C for 30 s, 72°C for 20 s), 72°C for 3 min

Table S2. Primers implemented for each molecular marker.

Marker	Primer/5'–3' sequence	Reference
<i>COI</i>	LCO1490 GGTCAACAAATCATAAAGATATTGG	Folmer <i>et al.</i> (1994)
	HCO2198 TAAACTTCAGGGTGACCAAAAAATCA	Folmer <i>et al.</i> (1994)
<i>12S</i>	12SAIN AAAAACWAGGATTAGATACCCT	Pinto-da-Rocha <i>et al.</i> (2014)
	12SOP2RN CCCTTAAAYTACTTTGTTACGACC	Pinto-da-Rocha <i>et al.</i> (2014)
<i>18S</i>	18SC CGGTAATTCAGCTCCAATAG	Medlin <i>et al.</i> (1988)
	WORMB CTTGTTACGACTTTTACTTCC	Littewood and Olson (2001)
	930F GCATGGAATAATGGAATAGG	Littewood and Olson (2001)
	1200F CAGGTCTGTGATGCCC	Littewood and Olson (2001)
<i>ITS2</i>	5.8SF CACGGGTCGATGAAGAACGC	Ji <i>et al.</i> (2003)
	CAS28SB1D TTCTTTTCCTCCSCTTAYTRATATGCTTAA	Ji <i>et al.</i> (2003)

Table S3. Morphological matrix and list of characters plotted in the ML phylogeny.

Taxa	Characters																
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
<i>Thelyphonellus amazonicus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Mayacentrum</i>	1	1	0	0	2	1	0	1	0	0	0	0	0	0	0	0	0
<i>Mastigoproctus</i>	1	1	1	1	1	0	0	1	0	1	1	1	0	1	1	0	0
<i>Amauromastigon maximum</i>	1	1	1	0	1	0	0	1	0	1	0	1	0	0	1	0	1
<i>Heptatarsus brasiliensis</i>	1	0	0	0	0	0	1	2	0	1	0	1	1	0	0	1	0
<i>Heptatarsus custodii</i>	1	0	1	0	0	0	1	2	1	1	0	1	1	0	1	1	0

Morphological characters: **1.** Carapace, anterolateral carina: 0, absent; 1, present. **2.** Carapace, epistome: 0, reduced; 1, conspicuous. **3.** Carapace, projection between main lateral median and posterior ocelli: 0, absent; 1, present. **4.** Carapace, median ocular tubercle, supraciliary carina: 0, absent; 1, present. **5.** Opisthosoma, segments V to VII, longitudinal median suture: 0, incomplete; 1, absent; 2, complete. **6.** Opisthosoma, segments VIII and IX, longitudinal median suture: 0, absent; 1, present. **7.** Opisthosoma, segments X and XI, dorsal row of granules: 0, absent; 1, present. **8.** Opisthosoma, segment XII, ommatoids: 0, absent; 1, present, oval; 2, present, circular. **9.** Opisthosoma, segment XII, ommatoids, size: 0, smaller than half the height of pygidium; 1, higher than half the height of pygidium. **10.** Flagellum, flagellar organs: 0, absent; 1, present. **11.** Stridulatory organ: 0, absent; 1, present. **12.** Pedipalp, granulosity: 0, lustrous; 1, granular. **13.** Leg I, number of tarsomeres: 0, eight; 1, seven. **14.** Leg II, tibial spurs: 0, absent; 1, present. **15.** Leg III, tibial spurs: 0, absent; 1, present. **16.** Coxa I, retrolateral row of tubercles: 0, tubercles of same size; 1, tubercles crescent in size distally. **17.** Female genitalia, spermathecal neck: 0, short and large; 1, long and narrow.

Appendix S1. Implemented scripts for maximum parsimony phylogenetic inference.

Direct optimization (DO) script:

```
read("FILE_NAME.fasta")
set(log:"FILE_NAME.log",root:"ROOT")
report(timer:"search_start")
build(250)
swap(threshold:5.0)
select()
fuse(iterations:200,swap())
select()
report("FILE_DO.tre",trees:(total),"FILE_DO.pdf",graphconsensus,"FILE_DO.txt",diagnosis)
report(timer:"search_end")
set(nolog)
exit()
```

Iterative pass (IP) script:

```
read("FILE_NAME.fasta")
read("FILE_DO.tre")
set(log:"FILE_NAME.log",root:"ROOT")
set(iterative:exact)
fuse()
select()
report("FILE_IP.ia",ia,"FILE_IP.tre",trees:(total),"FILE_IP.pdf",graphconsensus,"FILE_IP.txt",diagnosis)
exit()
```

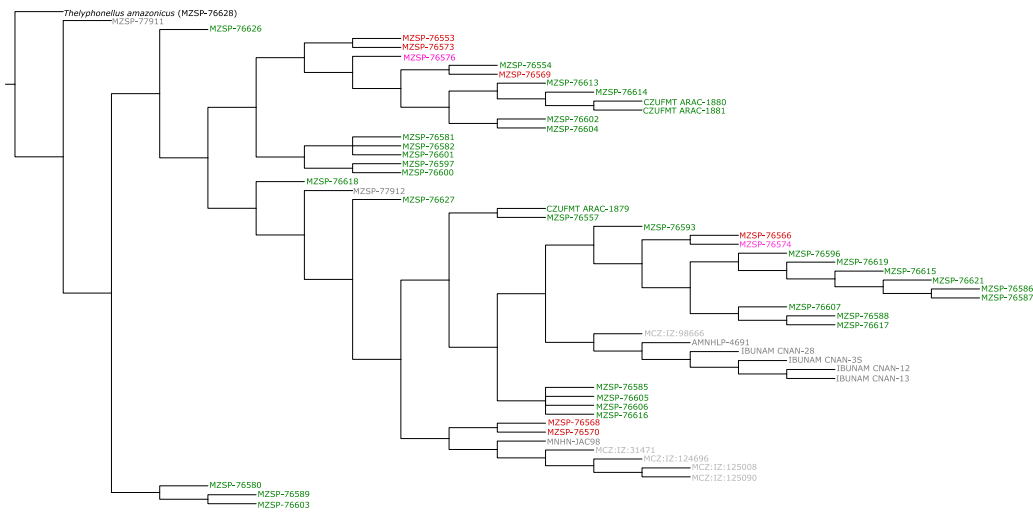


Fig. S1. Topology recovered under maximum parsimony inference. Terminal names' colours match clade colours in Figure 3.

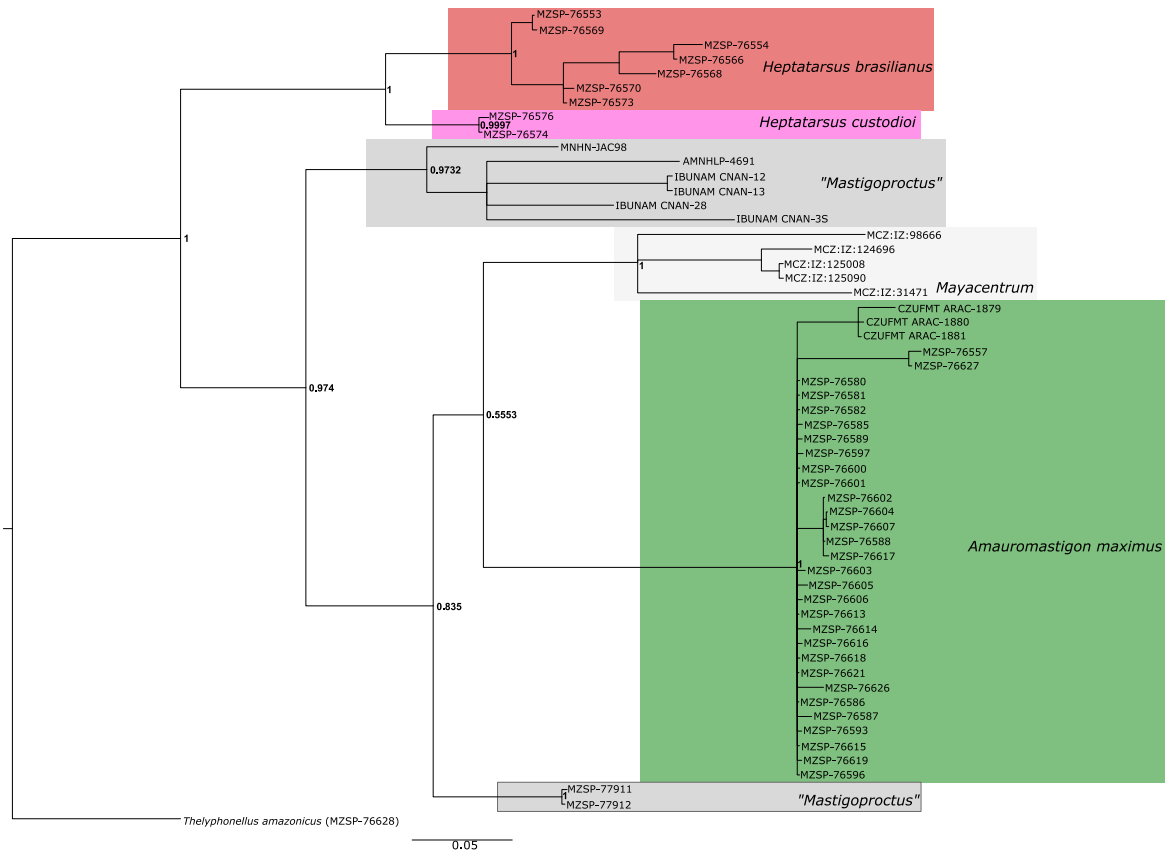


Fig. S2. Topology recovered under Bayesian inference, with posterior probability values on nodes. Colours match clade colours in Figure 3.

A



B



Fig. S3. Holotype of *Mastigoproctus annectens* Werner, 1916 (MWNH-1115). A, dorsal view. B, ventral view. Scale bar: 5 mm. Photographs by F. Geller-Grimm.

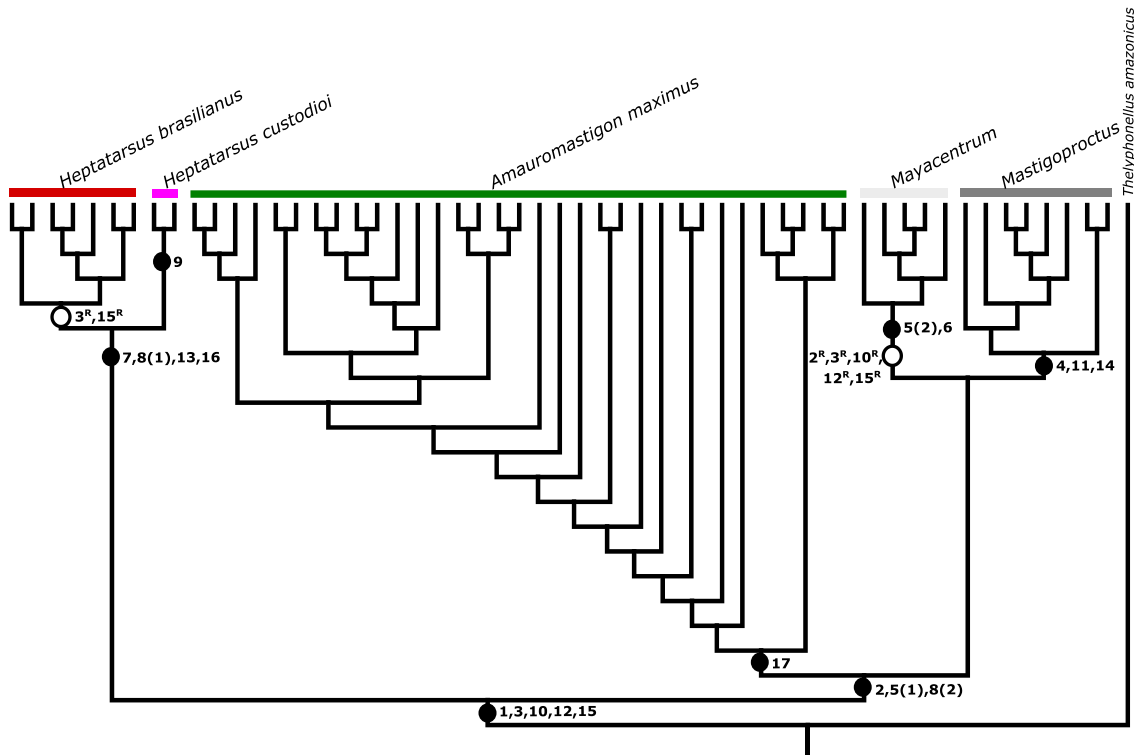


Fig. S4. Topology recovered under maximum likelihood inference, with a summary of the 17 morphological characters plotted within it.

References

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