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1 **Description of a new species of *Hypaeus* (Araneae: Salticidae: Salticinae:**  
2 **Amycini) based on integrative taxonomy**

3

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15

16 **Abstract**

17 A new species of *Hypaeus* Simon 1900 is described from French Guiana based on both sexes,  
18 *Hypaeus olympeae* **sp. nov.** We employed morphological evidence, field observation, as well  
19 the mitochondrial COI rapidly evolving loci to confirm that both males and females belongs to  
20 the same species. Finally, nine species are newly recorded for the salticid fauna of French  
21 Guiana, *Cyllodania fasciata* (Caporicaco, 1954) **syn. nov.** is considered junior synonym of

22 *Gypogyna forceps* Simon, 1900 and 12 COI sequences corresponding to four previously  
23 unsequenced *Hypaeus* species are added to GenBank.

24

25 **Key words:** jumping spiders, barcoding, cytochrome c oxydase 1 subunit 1, taxonomy, French  
26 Guiana.

27

28

## 29 **Introduction**

30 Neotropical spider faunas are still largely understudied (e.g. Dupérré, 2022), owing to their high  
31 diversity (Cardoso et al. 2011; Privet & Pétilon 2018) and the high human and material costs  
32 to study them. Additionally, large proportions of rare species and juveniles make up tropical  
33 spider assemblages (Coddington et al. 2009), being difficult or impossible to identify and  
34 describe. Spiders are a model group for ecological studies (Birkhofer & Wolters 2012; Cardoso  
35 et al. 2011; Malumbres-Olarte et al. 2018; Moya-Laraño et al. 2013) and the only group to be  
36 exclusively predatory among the dominant terrestrial arthropods (Birkhofer & Wolters 2012;  
37 Pekár & Toft 2015). Improving knowledge on their taxonomy is thus crucial to understand  
38 neotropical diversity and ecology.

39 Within the forests of the Amazon, the most abundant and speciose spiders are the jumping-  
40 spiders (Salticidae Blackwall, 1841; Bodner & Maddison 2012) and the richest subfamily is  
41 Amycinae (Araújo & Ruiz 2015; Maddison 2015). Among them, *Hypaeus* Simon 1900 is one  
42 of the richest genera with 28 described species distributed from south to central America (World  
43 Spider Catalog 2021).

44 Species of *Hypaeus* are distinguished by: high carapaces, plumose setae over front eyes,  
45 pluridentate chelicerae with 4-5 teeth on promargin and 3-6 on retromargin, mastidia on male

46 chelicerae and third legs longer than fourth (Galiano, 1968; Ruiz & Madisson 2015). However,  
47 *Hypaeus* is still poorly described with inadequate sampling across the genus' range. Thus, the  
48 boundaries of *Hypaeus* are not completely understood (Araújo & Ruiz 2015).

49 Galiano (1963, 1968) redescribed and revised 18 *Hypaeus* species described by Crane (1943),  
50 Mello-Leitão (1948), Peckham & Peckham (1885), Simon (1900) and Taczanowski (1871,  
51 1878). She also transferred two species to this genus, *Amycus mystacalis* (Taczanowski, 1878)  
52 and *Triptolemus benignus* (Peckham & Peckham, 1885); and synonymized one, *Mago*  
53 *budoninus* (Caporiacco, 1954). Two others were described by Crane, *H. duodentatus* Crane,  
54 1943, and by Caporiacco, *H. barromachadoi* Caporiacco, 1947. Recently, the male and the  
55 female of the type species of the genus *Hypaeus*, *H. taczanowskyii* (Mello-Leitao, 1948), were  
56 redescribed by Araújo & Ruiz (2015). The same authors added four new species to the genus,  
57 *H. tridactylus*, *H. famoratus*, *H. poseidon* and *H. terramediae* Araújo & Ruiz 2015, and  
58 transferred *Hasarius pauciaculeis* (Caporiacco, 1947) to *Hypaeus*. The last issue from Martinez  
59 & Galvis (2017) added three new species, *H. arhuaco*, *H. proszynskii* and *H. varzea* Martinez  
60 & Galvis, 2017. Of the resulting 28 *Hypaeus* species, 17 have been described only from males  
61 (Araújo & Ruiz 2015; Martinez & Galvis 2017; World Spider Catalog 2021).

62 Combining multiple lines of evidence such as morphology and DNA barcoding in species  
63 delimitation, could help alleviate the limitations on tropical spider diversity knowledge linked  
64 to juveniles and rare species. Phylogenetic analyses are also needed to resolve the relationships  
65 within *Hypaeus* (Ruiz et al. 2019). However, only sequences for two *Hypaeus* species, *H.*  
66 *mystacalis* (Taczanowski, 1878) and *H. miles* (Simon, 1900), are available to date.

67 One hundred and two species of Salticidae are currently listed for French Guiana (Courtial et  
68 al. 2014; Vedel et al. 2013) and among them three *Hypaeus* species: *H. flavipes* (Simon, 1900),  
69 *H. porcatus* (Taczanowski, 1871) and *H. taczanowskyii* (Mello-Leitao, 1948). During our last

70 expeditions to French Guiana (see Privet et al. 2018; Privet & Petillon 2018), in the National  
71 Nature Reserves of La Trinité and Les Nouragues, numerous Salticidae were collected, among  
72 them several specimens of an undescribed *Hypaeus* species. In this study, we used a  
73 combination of morphology and DNA barcoding targeting COI to match and describe the male  
74 and female from the new species, *Hypaeus olympeae* **sp. nov.**, produce sequences for four other  
75 *Hypaeus* species never sequenced so far, and add nine species to the list of salticids from French  
76 Guiana.

77

78

## 79 **Material and Methods**

### 80 *Taxon sampling*

81 Taxa sequenced in this study are 12 individuals of salticids belonging to the genus *Hypaeus*.  
82 They were collected in La Trinité (4°35'20"N; 53°18'1"W) and Les Nouragues (4°04'18"N;  
83 52°43'57"W) Nature Reserves (French Guiana) during two surveys conducted in 2010 and 2013  
84 (see Privet et al. 2018; Privet & Pétillon 2018). In these reserves, seasonally flooded (Aya and  
85 Pararé) and summit inselberg (La Roche Bénitier and Nouragues) forests were sampled.  
86 Inselbergs are rocky outcrops rising abruptly from the surrounding landscape where little  
87 research has been devoted to invertebrates, especially spiders (Privet et al. 2018). These  
88 specimens were separated based on morphology and sequenced. Six specimens were identified  
89 as *H. taczanowskii* and four to *H. porcatus*. Two specimens, impossible to assign to any of the  
90 currently recognized *Hypaeus* species, correspond to the new species described here, *Hypaeus*  
91 *olympeae* **sp. nov.** Total DNA of the 12 *Hypaeus* specimens was then extracted using non-  
92 destructive method (see below).

93

94 ***Specimens***

95 The type material examined is deposited at the Museum national d'Histoire naturelle (MNHN,  
96 Paris). Preserved specimens were studied using an OlympusSZX9 stereomicroscope with a  
97 Moticom5 (5.0MP) camera. Live specimens (holotype male and paratype female) were  
98 photographed with a Canon EOS 450 D digital reflex camera with a 60 mm macro lens. The  
99 epigyne was macerated in 10% KOH. The specimens were preserved in 70% ethanol.  
100 Measurements were taken according to Edwards (2004) in millimeters (mm), for direct  
101 comparison with *Hypaeus* spp. described by Araújo & Ruiz (2015). The following  
102 abbreviations are used:

103 AERW: anterior eye row width; AMEW: anterior median eyes width; CH: carapace height; CL:  
104 carapace length; CLH: clypeus height; co: copulatory opening; CW: carapace wide; dg: digital  
105 gland; eb: embolus base; et: embolus tip; OQL: ocular quadrangle length; MNHN: Muséum  
106 national d'Histoire naturelle, Paris; PERW: posterior eye row width; po: pocket; RNN: Réserve  
107 Naturelle Nationale (National Nature Reserve); sp: spermathecae; ta: tibial apophysis, TL: total  
108 length.

109 The drawings of male individuals of Galiano (1963, 1968), Crane (1943), Ruiz & Brescovit  
110 (2008), Araujo & Ruiz (2015) and Martinez & Galvis (2017), as well as the reviewing of type  
111 specimens stored at the MNHN (Paris, France), allowed us to identify the new species *Hypaeus*  
112 *olympae* **sp. nov.** collected in French Guiana.

113

114 ***DNA extraction, amplification, sequencing and data assembly***

115 DNA was extracted using DNeasy 96 Blood and Tissue Kit (Qiagen) following manufacturer's  
116 recommendations. The entire specimens were directly placed in lysis buffer with proteinase K  
117 overnight to extract DNA without compromising morphological requirements for further  
118 examination (Paquin & Vink 2009). The standard animal DNA barcode fragment of the  
119 mitochondrial cytochrome-c-oxidase subunit 1 (COI) was targeted by PCR using the primers  
120 C1-J-1718 "SPID" (Simon *et al.* 1994) and C1-N-2776 (Hedin & Maddison 2001). PCR  
121 reactions were performed in 25  $\mu$ L and contained 0.5X PCR Buffer, 0.2 mM dNTPs, 1 mM  
122 MgCl<sub>2</sub>, 0.15  $\mu$ M of each primer, 0.02 U/ $\mu$ L of Taq polymerase (GoTaq, Promega) and 2 $\mu$ L of  
123 DNA. PCR amplification started with an initial 94°C denaturation step for 2 min, followed by  
124 35 cycles of (i) denaturation at 94°C for 45 s, (ii) annealing at 50°C for 45 s, and (iii) extension  
125 at 72°C for 60 s; a final 72°C extension step lasted 10 min. Sequencing of PCR products was  
126 performed by Genoscreen (Lille, France) using the same primers than for amplification.  
127 Sequence fragments were imported, assembled, and edited in Geneious 6.1.8 (Biomatters Ltd.,  
128 Auckland, New Zealand). All sequences, with voucher information, are archived in GenBank  
129 (Table 1).

130

### 131 ***Phylogenetic analysis***

132 The taxonomic sampling used for the phylogenetic analyses included the 12 sequences newly  
133 generated for the study as well as one GenBank accession of *Sarinda cutleri* (Richman, 1965)  
134 (JX145669), a closely related species (see Maddison *et al.* 2014) that served as the outgroup.  
135 All sequences were aligned in Geneious using MAFFT v.7.017 (Kato & Standley 2013).

136 The resulting COI matrix was subjected both to Bayesian inference (BI) and maximum  
137 likelihood (ML) analyses. We first searched for the best-fitting nucleotide substitution model  
138 using the Akaike information criterion (AIC) estimated by MrModeltest v.2.3 (Nylander 2004);

139 the GTR + G model was selected and assigned to all following phylogenetic analyses. The  
140 software MrBayes 3.2.6 (Huelsenbeck & Ronquist 2001) and RaxML-HPC v.8.1.24  
141 (Stamatakis 2014) implemented on the CIPRES Science Gateway (Miller *et al.* 2010) platform  
142 were used to perform BI and ML analyses, respectively. MrBayes analyses constituted two  
143 independent parallel runs of four Markov chains each, implemented for one million generations  
144 and sampled every 100 generations. Adequate mixing of the Markov chains and convergence  
145 of the two runs were confirmed with Tracer v1.6 (Rambaut et al. 2014). After removing a 10%  
146 burnin, the remaining trees were used to generate a 50% Bayesian majority-rule consensus tree.  
147 For the RaxML analyses, node support was assessed using a rapid bootstrapping algorithm with  
148 1000 bootstrap iterations.

149

150

## 151 **Results**

### 152 *Taxonomy*

153 Class Arachnida Cuvier, 1812

154 Order Araneae Clerck, 1757

155 Family Salticidae Blackwall, 1841

156 Subfamily Salticinae Blackwall, 1841

157 Tribe Amycini F.O Pickard-Cambridge, 1900

158 Genus *Hypaeus* Simon, 1900

159 *Hypaeus* Simon, 1900: type species *Acragas taczanowskii* Mello-Leitão, 1948.



160 *Hypaeus olympeae* Courtial & Picard sp. nov.

161 Figs 1-18

### 162 ***Diagnosis***

163 Males of *Hypaeus olympeae* **sp. nov.** are similar to those of *H. miles* Simon, *H. femoratus*  
164 Araújo & Ruiz and *H. terraemediae* Araújo & Ruiz for having dilated femora (Fig 4). However,  
165 *H. olympeae* **sp. nov.** has wider rounded TA, which is small and pointed in aforementioned  
166 species. Females of *H. olympeae* **sp. nov.** are similar to those of *H. femoratus* and *H.*  
167 *terraemediae* (the female of *H. miles* is unknown). Digitiform glands curve from the center of  
168 the epigyne to the antero-lateral portion. Females of *H. olympeae* **sp. nov.** are slightly similar  
169 in shape to those of *H. femoratus* and *H. terraemediae* but the COs openings are less curved  
170 and space further apart them is bigger.

### 171 ***Etymology***

172 The species is named “*olympeae*” to pay tribute to Olympe Delavalle, daughter of Marguerite  
173 Delavalle, the Curator of the NNR Nouragues during our survey.

### 174 ***Material examined***

#### 175 *Holotype*

176 1♂ from RNN des Nouragues (4°02'N, 52°41'W), Camp Pararé, French Guiana (AR 16169),  
177 11.XII.2013, Cyril Courtial coll.

#### 178 *Paratypes*

179 1♀ from RNN des Nouragues (4°02'N, 52°41'W), Camp Pararé, French Guiana (AR 16170),  
180 11.XII.2013, Cyril Courtial coll.; 1♂, 2♀ from RNN de la Trinité (04°36'N, 53°24'W), Camp  
181 Aya, French Guiana, 08.XII.2010, Alain Canard coll.

182 *Additional material examined*

183 French Guiana. RNN de la Trinité, Camp Aya (04°36'N, 53°24'W): 1♂, 01.XI.2008, Frédéric  
184 Ysnel coll.; RNN des Nouragues, Camp Inselberg (4°05'N, 52°41'W): 1♀, 09.XII.2013, Cyril  
185 Courtial coll.; RNN des Nouragues, Camp Pararé (4°02'N, 52°41'W): 1♀, 26.VI.2010, Vincent  
186 Vedel coll.; Montagne des Chevaux (4 43'N, 52 24'W): 1♀, 09.XI.2010, Vincent Vedel coll.;  
187 Roche Bénitier (04°36'N, 53°24'W) : 1♀, 06.IV.2010, Vincent Vedel coll.

188 *Description*

189 *Male (Holotype, AR 16169)*

190 TL:6.00. CL:3.10. CW: 2.30. CH:1.80. OQL: 2.00. AERW:2.20. PERW:2.00. AMEW:0.70.  
191 CLH: 0.45. Carapace dark brown with light spot behind the fovea bearing white setae (Fig 1).  
192 Chelicera dark brown (Fig 3) with short mastidions pointed forward; 3 posterior cheliceral teeth,  
193 2 anterior cheliceral teeth. Palp: femur curved with dorsal bump (Fig 4); tibia with quiet short  
194 rounded RTA (Figs 5, 7, 11-12); embolus emerging from proximal tegulum with median  
195 portion slightly narrowed (Figs 6, 13). Abdomen pale with median longitudinal light stripe (Figs  
196 1, 17) and ventrally with median longitudinal dark brown stripe. Spinnerets light brown. Legs  
197 1342 (10.00/6.90/7.80/7.50). Length of femur I 2.80, II 2.20, III 2.60, IV 2.40. Patella + tibia I  
198 4.30, II 2.70, III 2.70, IV 2.40. Metatarsus + tarsus I 2.90, II 2.00, III 2.50, IV 2.70.

199 *Variation Male (n=3)*

200 Total length: 6.00-7.10. Carapace length: 3.05-3.20. Length of leg I 9.05-10.00.

201 *Female (AR 16170)*

202 TL:9.00. CL:3.90. CW: 2.70. CH:2.00. OQL: 1.90. AERW:2.40. PERW:2.10. AMEW:0.80.  
203 CLH: 0.30. Carapace light brown with darker cephalic area, base of the cephalothorax bearing

204 dark spots (Fig 2). Chelicera dark brown with no mastidion; 3 posterior cheliceral teeth, 4  
205 anterior cheliceral teeth. Epigyne with a pair of oblique COs (Figs 8-9, 14), long digitiform  
206 gland ducts and long and thin COs (Figs 10, 15-16). Legs 1-432 (8.60/8.60/8.40/6.90). Length  
207 of femur I 2.60, II 2.30, III 2.90, IV 2.90. Patella + tibia I 3.70, II 2.80, III 3.00, IV 3.00.  
208 Metatarsus + tarsus I 2.30, II 1.80, III 2.50, IV 2.80.

209 Variation Female (n=6)

210 Total length: 6.20-9.00. Carapace length: 2.70-3.90. Length of leg I 7.30-8.60.

### 211 ***Distribution***

212 Only known from French Guiana.

### 213 ***Comments***

214 The holotype male and female were caught together during mating behaviour in a building at  
215 the Nouragues field station.

216

### 217 ***DNA sequences and phylogenetic analysis***

218 The COI alignment was 442 base pairs (bp) long and included 92 variable sites of which 72  
219 were informative in parsimony. The BI and ML topologies are congruent; there was no  
220 topological conflict detected between the 50% Bayesian majority-rule consensus tree (Fig. 19)  
221 and the ML bootstrap 50% majority-rule consensus tree (not shown). The topology we obtained  
222 showed (1) that the two individuals of *H. olympeae* **sp. nov.** included in the study form a  
223 strongly supported monophyletic grouping (PP = 1; BS = 100), highly divergent from the two  
224 other clades in the tree, (2) that the four accessions sampled for *H. porcatus* are part of a strongly  
225 supported clade (PP = 1; BS = 99) resolved as sister to *H. olympeae* **sp. nov.** but with poor

226 support (PP = 0.81; BS = 67) and (3) that the 6 accessions identified as *H. taczanowskii* (3 male  
227 and 3 female individuals) were all included in a monophyletic grouping strongly supported in  
228 BI (PP = 0.99; BS = 74). The analysis of COI sequences then confirms the current  
229 morphological circumscriptions for the three *Hypaeus* species sampled here. Also, the branch  
230 lengths observed between the three clades recognized here are relatively high when compared  
231 with the magnitude of the divergence between the ingroup (viz. genus *Hypaeus*) and the  
232 outgroup (viz. *Sarinda cutleri*); this further supports the recognition of *H. olympeae* **sp. nov.** as  
233 a distinct species.

#### 234 *New records of Salticidae from French Guiana*

235 According to Vedel et al. (2013), Courtial et al. (2014) and Logunov (2015) we add nine new  
236 species for French Guiana.

#### 237 *Eustiromastix moraballi* Mello-Leitao, 1940

238 RNN Nouragues, camp Pararé (4°02'N, 52°41'W), 1♂, 06.XII.2013, Canard Alain, Courtial  
239 Cyril, Leroy Boris, Pétilion Julien & Vedel Vincent, at sight in low vegetation.

#### 240 *Lyssomanes tenuis* Peckham & Wheeler, 1889

241 RNN Nouragues, camp Inselberg (4°05'N, 52°41'W), 1♂, 08.XII.2013, Courtial Cyril, by  
242 beating by beating the lower branches of trees.

#### 243 *Scopocira abaporu* Costa & Ruiz, 2014

244 Nouragues, Camp Pararé (4°02'N, 52°41'W), 1♂, 13.XII.2013, Courtial Cyril, by beating the  
245 lower branches of trees.

#### 246 *Scopocira histrio* Simon, 1900

247 Nouragues, camp Inselberg (4°05'N, 52°41'W), 1♀, 10.XII.2013, Courtial Cyril, by beating  
248 the lower branches of trees. Nouragues, camp Pararé (4°02'N, 52°41'W), 1♂, 06.XII.2013,  
249 Canard Alain, Courtial Cyril, Leroy Boris, Pétilion Julien & Vedel Vincent, by beating the  
250 lower branches of trees.

251 *Colonus germaini* Simon, 1900

252 Nouragues, camp Pararé (4°02'N, 52°41'W), 1♀, 12.XII.2013, Courtial Cyril, by beating the  
253 lower branches of trees.

254 *Corcovetella aemulatrix* Galiano, 1975

255 Kourou, degrad saramak (5°01'N, 52°41'W), 1♀, collection date unknown, Vedel Vincent, by  
256 beating vegetation in garden near primary forest.

257 *Pachomius nigrus* Caporiacco, 1947

258 RNN Trinité, camp Aya (04°36'N, 53°24'W), 1♂, X.2010, Canard Alain, Courtial Cyril, Leroy  
259 Boris & Ysnel Frédéric, by beating the lower branches of trees.

260 *Gypogyna forceps* Simon, 1900

261 *Cyllodania fasciata* (Caporicaco, 1954) syn. nov: 150, f.48, French Guiana, Saint-Jean  
262 du Maroni, 1914, Benoist leg, 1♀ examined.

263 After examination of species described by Caporiacco (1954) deposited in the MNHN, the type  
264 species of *Cyllodania fasciata* (Caporicaco, 1954), considered as a subadult by Caporiacco  
265 (1954) and Galiano (1977) is in fact an adult female of *Gypogyna forceps* Simon, 1900.  
266 *Cyllodania fasciata* (Caporicaco, 1954) is here presented as a new synonym of *Gypogyna*  
267 *forceps* Simon, 1900.

268 Kourou, degrad saramak (5°01'N, 52°41'W), 1♀, collection date unknown, Vedel Vincent, by  
269 beating vegetation in garden near primary forest.

270 *Marma nigritarsis* (Simon, 1900)

271 Saül (3°37'N, 53°12'W), 1♂, 08.X.2013, 1♂, 18.X.2013, Bellanger Yannick (Asper Society).

272

273

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#### 286 **Disclosure statement**

287 No potential conflict of interest was reported by the authors.

288

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410 Table 1

411 Summary of GenBank accession numbers, species name and voucher information (site  
412 coordinates are given in the Material and Methods) for the sequences newly generated for the  
413 study.

GenBank accessions	Name in topology	Voucher	Collection location	Sex
OK501209	<i>Hypaeus olympeae</i> 1	ACAV07 3	La Trinité, French Guyana	♂
OK501210	<i>Hypaeus olympeae</i> 2	ACAV07 2	La Trinité, French Guyana	♀
OK501211	<i>Hypaeus porcatus</i> 1	NPTN11	Les Nouragues, French Guyana	♀
OK501212	<i>Hypaeus porcatus</i> 2	AQJ5	La Trinité, French Guyana	♀
OK501213	<i>Hypaeus porcatus</i> 3	AQN1	La Trinité, French Guyana	♂
OK501214	<i>Hypaeus porcatus</i> 4	AQJ5	La Trinité, French Guyana	♂
OK501215	<i>Hypaeus taczanowskii</i> 1	NITJ3	Les Nouragues, French Guyana	♂
OK501216	<i>Hypaeus taczanowskii</i> 2	NIQN9	Les Nouragues, French Guyana	♂
OK501217	<i>Hypaeus taczanowskii</i> 3	IQN10	Les Nouragues, French Guyana	♂
OK501218	<i>Hypaeus taczanowskii</i> 4	NPQJ7	Les Nouragues, French Guyana	♀
OK501219	<i>Hypaeus taczanowskii</i> 5	PQJ4	Les Nouragues, French Guyana	♀
OK501220	<i>Hypaeus taczanowskii</i> 6	NPQJ5	Les Nouragues, French Guyana	♀

414

415 Figures 1 – 2

416 *Hypaeus olympeae* **sp. nov.** 1 male, dorsal view, scale 0,5mm; 2. Female, dorsal view, scale  
417 1mm.

418 Figures 3 – 4

419 *Hypaeus olympeae* **sp. nov.** male. 3. Chelicerae detail (ma: mastidion), scale 0.5mm; 4. Left  
420 male palp with bump on femur (arrow), scale 1mm.

421 Figures 5 – 7

422 *Hypaeus olympeae* **sp. nov.** left male palp; 5. retrolateral view; 6. Same ventral view; 7. Same  
423 dorsal view showing tibial apophysis, scale 0.5mm.

424 Figures 8 – 10

425 *Hypaeus olympeae* **sp. nov.** female; 8. epigyne, ventral view; 9. same, cleared; 9. ventral view,  
426 cleared, scale 0.5mm.

427 Figures 11 – 13

428 *Hypaeus olympeae* **sp. nov.** left male palp drawings; 11. retrolateral view; 12. same, dorsal  
429 view showing tibial apophysis; 13 same, ventral view, scale 0.5mm.

430 Figures 14 – 16

431 *Hypaeus olympeae* **sp. nov.** female; 13. Epigyne drawing; 14. same ventral view; 15. path  
432 within epigyne, scale 0.5mm.

433 Figures 17 - 18

434 *Hypaeus olympeae* **sp. nov.** pictures of living specimens; 16. male holotype; 17. female  
435 paratype.

436 Figure 19

437 50% majority-rule tree from the Bayesian analysis of the COI matrix. Numbers above each  
438 branch are bootstrap values > 50% followed by posterior probabilities from the Bayesian

439 analysis. Branch lengths are proportional to the number of substitutions per nucleotide position  
440 (scale bar=0.01 substitutions). See Table 1 for complete voucher information.

Figures 1 – 2

*Hypaeus olympeae* sp. nov. 1 male, dorsal view, scale 0,5mm; 2. Female, dorsale view, scale 1mm.



Figures 3 – 4

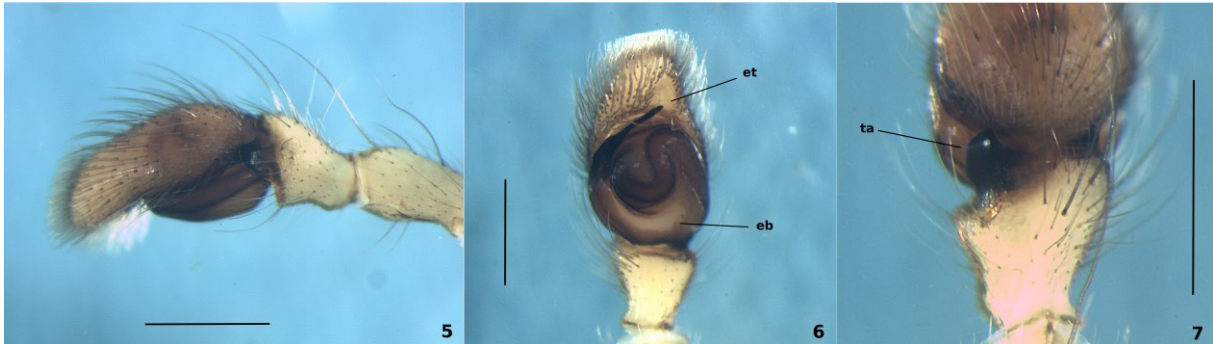
*Hypaeus olympeae* sp. nov. male. 3. Chelicerae detail (ma: mastidion), scale 0.5mm; 4. Left male palp with bump on femur (arrow), scale 1mm.





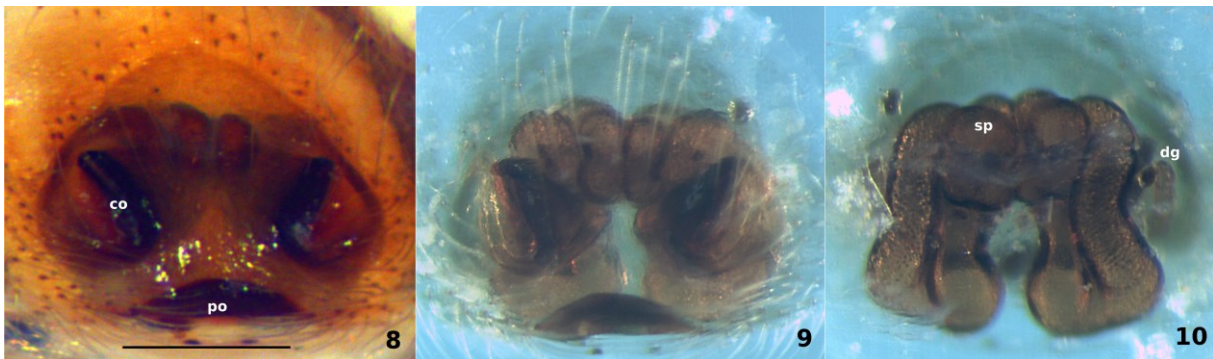
Figures 5 – 7

*Hypaeus olympeae* **sp. nov.** left male palp; 5. retrolateral view; 6. Same ventral view; 7. Same dorsal view showing tibial apophysis, scale 0.5mm.



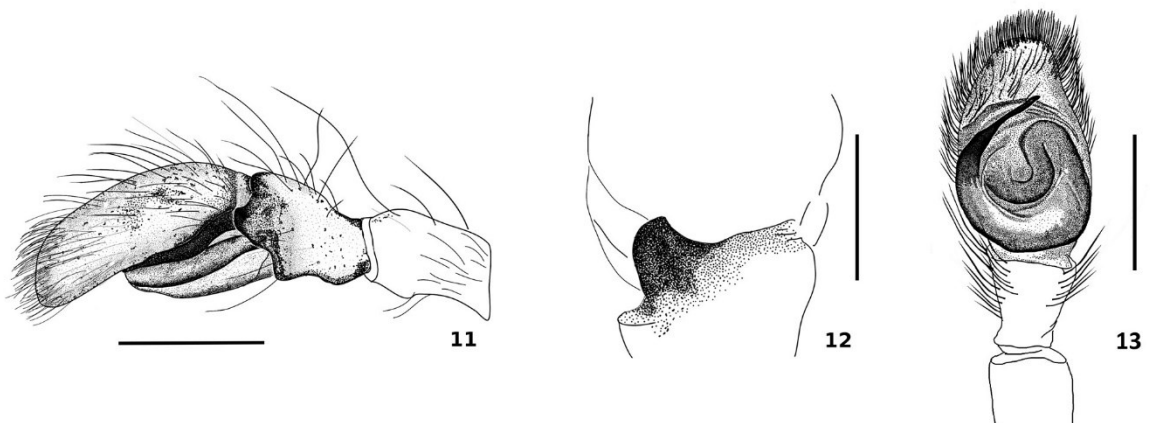
Figures 8 – 10

*Hypaeus olympeae* **sp. nov.** female; 8. epigyne, ventral view; 9. same, cleared; 9. ventral view, cleared, scale 0.5mm.



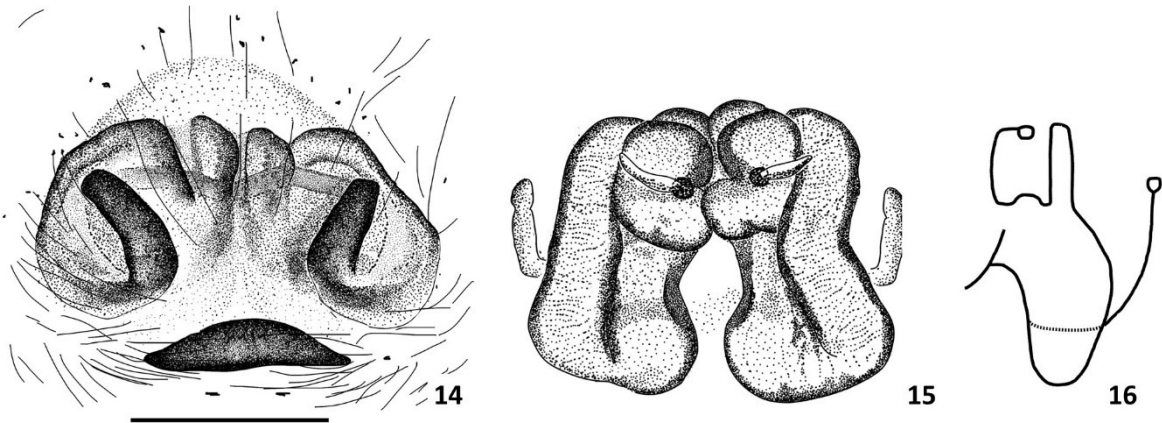
Figures 11 – 13

*Hypaeus olympeae* **sp. nov.** left male palp drawings; 11. retrolateral view; 12. same, dorsal view showing tibial apophysis; 13 same, ventral view, scale 0.5mm.



Figures 14 – 16

*Hypaeus olympeae* sp. nov. female; 14. Epigyne drawing; 15. same ventral view; 16. path within epigyne, scale 0.5mm.



Figures 17 - 18

*Hypaeus olympeae* sp. nov. pictures of living specimens; 17. male holotype; 18. female paratype.



Figure 19

50% majority-rule tree from the Bayesian analysis of the COI matrix. Numbers above each branch are bootstrap values > 50% followed by posterior probabilities from the Bayesian analysis. Branch lengths are proportional to the number of substitutions per nucleotide position (scale bar=0.01 substitutions). See Table 1 for complete voucher information.

