New taxonomic insights for Brazilian *Syrbatus* Reitter (Coleoptera: Staphylinidae: Pselaphinae), including three new species and their mitochondrial genomes (#91286)

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New taxonomic insights for Brazilian *Syrbatus* Reitter (Coleoptera: Staphylinidae: Pselaphinae), including three new species and their mitochondrial genomes

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Here we present a taxonomic treatment for the Brazilian species of *Syrbatus* (Reitter, 1882), including the description of three new species (*Syrbatus moustache* Asenjo & Valois **sp. nov.**, *Syrbatus obsidian* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.**) from the Quadrilátero Ferrífero (Minas Gerais, Brazil). In addition, we designated new lectotypes for the Brazilian species of species-group 2, *Syrbatus centralis* (Raffray, 1898), *Syrbatus hetschkoi* (Reitter, 1888), *Syrbatus hiatusus* (Reitter, 1888), *Syrbatus transversalis* (Raffray, 1898), and *Syrbatus trinodulus* (L.W.Schaufuss, 1887), besides recognizing the holotype for *Syrbatus brevispinus* (Reitter, 1882), *Syrbatus bubalus* (Raffray, 1898), and *Syrbatus grouvellei* (Raffray, 1898). The mitochondrial genomes (mitogenomes) of the three new species are presented, for which we present the phylogenetic placement among Staphylinidae species with previously published data.

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Abstract

Here we present a taxonomic treatment for the Brazilian species of *Syrbatus* (Reitter, 1882), including the description of three new species (*Syrbatus moustache* Asenjo & Valois **sp. nov.**, *Syrbatus obsidian* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.**) from the Quadrilátero Ferrífero (Minas Gerais, Brazil). In addition, we designated new lectotypes for the Brazilian species of species-group 2, *Syrbatus centralis* (Raffray, 1898), *Syrbatus hetschkoi* (Reitter, 1888), *Syrbatus hiatusus* (Reitter, 1888), *Syrbatus transversalis* (Raffray, 1898), and *Syrbatus trinodulus* (L.W.Schaufuss, 1887), besides recognizing the holotype for *Syrbatus brevispinus* (Reitter, 1882), *Syrbatus bubalus* (Raffray, 1898), and *Syrbatus grouvellei* (Raffray, 1898). The mitochondrial genomes (mitogenomes) of the three new species are presented, for which we present the phylogenetic placement among Staphylinidae species with previously published data.

Keywords: Quadrilátero Ferrífero, mtDNA, Pselaphinae, rove beetle, taxonomy

INTRODUCTION

The species of *Syrbatus* (Reitter, 1882) are distributed in Africa (89 spp.) and South America (30 spp.) (Newton & Chandler, 1989; Asenjo et al., 2019), where, to date, 25 species were recorded for Brazil, three for Paraguay and two for Argentina (Asenjo et al., 2019; Newton, 2022). In Brazil, the genus is known to occur in the states of Santa Catarina (13 spp.), São Paulo (8 spp.), Bahia (3 spp.), Rio de Janeiro (2 spp.) and Minas Gerais (1 sp.) (Asenjo et al., 2013). Since the description of *Syrbatus* as a subgenus of *Batrisus* (Aubé, 1833) by Reitter (1882), based on the characters of the pronotum, Raffray (1897) raised it to the rank of genus, discussing

mainly the characters of head and pronotum among the species of these two taxa and *Arthmius* (LeConte, 1849). Afterwards, Raffray (1904) used characters of the antenna and head to organize the South American species of the genus into six species-group, with posterior reorganization of these subdivisions made by Park (1942) and designation of *Batrisus clypeatus* (Reitter, 1882) as the type species of *Syrbatus* by Jeannel (1949).

The biology of the genus is poorly known, with its species, in general, being part of the soil fauna, as *Syrbatus demoniacus* (Raffray, 1898) and *Syrbatus leleupi* (Jeannel, 1950), for instance, that were originally found in tobacco plantations in Brazil (Raffray, 1898) and in the entrance a of cave in the Democratic Republic of the Congo (Jeannel, 1950), respectively. Interestingly, several authors have related cave specimens of undescribed species of *Syrbatus* from Brazil in the last three decades (Gnaspini & Trajano, 1994; Pinto da Rocha, 1995; Trajano & Bichuette, 2010; Gallão & Bichuette, 2018). Therefore, the aim of this study was to describe three new species of the group from Brazil, *Syrbatus moustache* Asenjo & Valois **sp. nov.**, *Syrbatus obsidian* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.**, all of which collected in caves of the Quadrilátero Ferrífero, in the state of Minas Gerais. In addition, we sequenced the mitochondrial genomes (mitogenomes) of the three, exploring the phylogenetic relationships within Staphylinidae and Pselaphinae.

MATERIAL & METHODS

Field collection

The three species described in this work are associated with siliciclastic caves in the Quadrilátero Ferrífero, one of the most important regions for the conservation of subterranean biodiversity in Minas Gerais. This region comprises a large mosaic of phytophysiognomies

65 shaped by the conjunction of topography, lithology, climate, and altitude (Jacobi & Carmo,
66 2008), being inserted in a transition zone between two Brazilian biodiversity hotspots, the
67 Atlantic Forest and the Cerrado biomes (Mittermeier et al., 2004). In general, the climate is
68 characterized as Cwb (subtropical highland climate), with mild and humid summers, and cool
69 and dry winters (Köppen, 1948), although it can be strongly influenced by the relief since the
70 average altitude exceeds 1,000 m, with the tallest regions reaching 2× this height. The annual
71 precipitation ranges between 1,250-1,550 mm, with an average annual temperature between 18-
72 19 °C.

73 The Quadrilátero Ferrífero has an area of approximately 7,200 km^2, being considered one
74 of the most important mineral provinces in Brazil, mainly due to its gold and iron deposits. At
75 the same time, the region presents one of the most diverse floras in South America with high
76 rates of endemism (Giulietti, Pirani & Harley, 1997). The area is of special biological relevance
77 due to the presence of ferruginous fields, the occurrence of several endemic plant species,
78 besides constituting a unique environment in the country. Formed by ancient and geologically
79 complex terrains of the Minas Super Group, with varied lithologies (Alkmim & Marshak, 1998;
80 Klein & Ladeira, 2000), with more than two thousand caves currently known in the region
81 (CECAV, 2021), and dozens of cave species have been discovered and described in recent years.
82 This large set of caves are distributed in different mountain ranges (geomorphological units),
83 with the species described in this work found in caves in the Serra da Moeda and the Escarpa
84 Oriental do Caraça (Figure 1). All studied specimens were collected in accordance with the
85 sampling permits 065/2013 NUFAS/MG and 424.033/2018, granted by IBAMA/MMA and
86 SEMAD/MG, respectively.
87

Morphological analyses

Specimens. The apical segments were cleared in a double boiler using 10% KOH for 3 min. Dissections were made under a Zeiss Discovery V12 (4×-125×) stereomicroscope. Pictures were obtained using an AxioCam 506 (ZEISS, Oberkochen, Germany) connected to an Axio Zoom V16 (ZEISS) stereomicroscope, and Photoshop CC 2021 was used for image processing. Morphological character terminology, including foveation and its abbreviation followed Chandler (2001). All measurements were based using a ZEISS Discovery V12 (4×-125×) stereomicroscope, and the width/length ratios were acquired using the widest and longest parts of the respective structures, being presented in millimeters, based on the holotype. We also performed additional measurements using the paratypes, comparing with the data obtained for the holotypes (Data S1).

Measurements symbols:

BL: body length (from margin of clypeus to posterior margin of tergite VIII)

BW: body width (maximum width of elytra)

EL: elytral length (maximum)

EW: elytral width (maximum)

HL: head length (from anterior margin of clypeus to posterior margin of head disc)

HW: head width (maximum, including eyes)

NW: neck width (minimum)

PL: pronotum length (maximum)

PW: pronotum width (maximum)

In the type label data, quotation marks (“ ”) separate different labels, and a slash (/) separates different lines within a label. Text within square brackets [ ] is explanatory and is not included on the original labels.

Depositories

The specimens examined in this revision are deposited in the following collections (curators in parenthesis):

CEMT – Setor de Entomologia da Coleção Zoológica da Universidade Federal de Mato Grosso, Departamento de Biologia e Zoologia, Cuiabá, Mato Grosso, Brazil (Fernando Vaz-de-Mello).

ISLA – Coleção de Invertebrados Subterrâneos de Lavras, Setor de Zoologia, Departamento de Biologia, Universidade Federal de Lavras, Lavras, Minas Gerais State, Brazil (Rodrigo Lopes Ferreira).

ITV – Coleção de DNA do Instituto Tecnológico Vale, Belém, Pará, Brazil (Santelmo Vasconcelos).

MPEG – Museu Paraense Emilio Goeldi, Terra Firme, Belém, Brazil (Orlando Silveira).

MNHN – Muséum National d’Histoire Naturelle, Paris, France (Antoine Mantilleri).

SDEI – Senckenberg Deutschen Entomologischen Institut, Eberswalder, Germany (Mariana Simões).

Nomenclatural acts

The electronic version of this article in Portable Document Format (PDF) will represent a published work according to the International Commission on Zoological Nomenclature (ICZN), and hence the new names contained in the electronic version are effectively published under that Code from the electronic edition alone. This published work and the nomenclatural acts it contains have been registered in ZooBank, the online registration system for the ICZN. The ZooBank LSIDs (Life Science Identifiers) can be resolved, and the associated information viewed through any standard web browser. The LSID for this publication is:

http://zoobank.org/urn:lsid:zoobank.org:pub:2084B581-B904-486A-B237-0A9D9C839434.

The online version of this work is archived and available from the following digital repositories: PeerJ, PubMed Central and CLOCKSS.

DNA sequencing, mitogenome assemblies and phylogenetic analysis

A total of seven specimens of the three new species described here were separated and processed to obtain total genomic DNA, being one individual of *Syrbatus moustache* Asenjo & Valois **sp. nov.** (MPEG-01052552/ITV22155), three of *Syrbatus obsidian* Asenjo & Valois **sp. nov.** (ISLA-110327/ITV22166, ISLA-110326/ITV22168, and MPEG-01052558/ITV22169), and three of *Syrbatus superciliata* Asenjo & Valois **sp. nov.** (ITV10831, ITV10835 and MPEG-01052550/ITV39056). The DNA samples were obtained using the DNeasy Blood & Tissue kit (Qiagen), following the manufacturer's protocol for insect samples, subsequently being deposited at the DNA bank of the Instituto Tecnológico Vale (ITV).

Paired-end libraries were constructed from ~5 ng of the obtained genomic DNA using the Illumina DNA Prep kit (Illumina, Inc., San Diego, CA, USA), following the manufacturer's

157 instructions for low-input samples. After the final purification step, the resultant libraries were
158 quantified with a Qubit 3.0 (Invitrogen, Waltham, MA, USA) fluorimeter, using the Qubit
159 dsDNA High Sensitivity kit (Invitrogen), and analyzed for fragment sizes in a 4200 TapeStation
160 (Agilent Technologies, Santa Clara, CA, USA). Then, the libraries were sequenced in an
161 Illumina NextSeq 2000 platform, with a P1 kit (240 cycles, 2× 120 bp). Resulting raw
162 sequencing reads with base quality < Phred 20 and length <50 bp were trimmed with
163 AdapterRemoval v.2 (Schubert, Lindgreen & Orlando, 2016), and the resulting high-quality
164 reads were used to assemble the mitochondrial genomes using NovoPlasty v.4.2 (Dierckxsens,
165 Mardulyn & Smits, 2017). Finally, the mitogenomes were annotated with MITOS2 (Bernt et al.,
166 2013), with subsequent minor manual corrections using Geneious Prime v.2023 (Biomatters), by
167 comparing the annotated mitogenomes with previously available data for Pselaphinae species.
168 To position the three new described species in the context of the phylogenetic tree of the
169 family, we obtained all previously published mitogenomes of Staphylinidae species available in
170 the GenBank database (https://www.ncbi.nlm.nih.gov/genbank/) which presented, at least, the
171 complete sequences of the 13 protein coding genes (PCGs), totaling 84 species from 14
172 subfamilies, plus one species of Hydrophilidae (*Cercyon borealis*) and one of Histeridae
173 (*Euspilotus scissus*) to be used as outgroups. Amino acid sequences of the 13 PCGs were aligned
174 with MAFFT v7.45 (Katoh et al., 2002; Data S2) and maximum likelihood (ML) and Bayesian
175 inference (BI) phylogenetic trees were obtained using RAxML v8 (Stamatakis, 2014) and
176 MrBayes v3.2.7 (Ronquist et al., 2012), as implemented in the CIPRES portal
177 (http://www.phylo.org/). The ML analysis was performed using the model PROTGAMMA and
178 1,000 replicates of rapid bootstrapping, and the BI trees were obtained using four simultaneous
179 runs, each with four Markov chains (T = 0.2) extended through 20,000,000 generations,

sampling every 2,000, and using a burn-in fraction of 25% of the trees. Additionally, to further investigate the differentiation among the mitogenomes of the three new species, we employed two different lineage delimitation approaches, using the sequences of three specimens of the recently described *Metopiellus crypticus* (Asenjo et al., 2023), which was identified as the closest Pselaphinae species among the sampled mitogenomes in the phylogenetic reconstruction. In the first, Assemble Species by Automatic Partitioning (ASAP; Puillandre, Brouillet & Achaz, 2021), which uses a genetic distance matrix to identify putative species using a genetic distance matrix, we employed a concatenated matrix of nucleotide sequences of all 13 PCGs as a single locus with the mitogenomes as a single locus, choosing the K80 model (ts/tv = 2.0). The second approach, Bayesian Phylogenetics and Phylogeography (BPP; Yang, 2015), is based on the multispecies coalescent model under a Bayesian Markov chain Monte Carlo (MCMC) algorithm, for which we provided the nucleotide alignments of the 13 PCGs as independent loci and a guide tree as obtained in the ML phylogenetic reconstruction, using the default parameters.

RESULTS

Description

Family Staphylinidae (Latreille, 1802)

Subfamily Pselaphinae (Latreille, 1802)

Tribe Batrisini (Reitter, 1882)

Subtribe Batrisina (Reitter, 1882)

Genus *Syrbatus* (Reitter, 1882)

Syrbatus moustache Asenjo & Valois, new species

(Figs. 1, 2 and 5)

http://zoobank.org/urn:lsid:zoobank.org:act:469E3B88-F2C7-4724-9F4C-7A51D1F5FABC

Type material (one male, two females). *Holotype:* BRAZIL: male, labeled "BRAZIL: Minas Gerais, / Nova Lima, SM_0046 / cave, 29.vii[July]-02.viii[August].2019, / -20.188606, -43.838583 [20°11'18.98"S, 43°50'18.89"W], / Spelayon et al.", "[image data matrix] / Instituto / Tecnológico / Vale / ITV22154", "HOLOTYPE ♂ [red label] / *Syrbatus* / *moustache* sp. nov. / Desig. Asenjo et al., 2023" (one male, ISLA-110319). *Paratype:* (two females), labeled: "BRAZIL: Minas Gerais, / Nova Lima, SM_0046 / cave, 29.vii[July]- / 02.viii[August].2019, / -20.188606, -43.838583 [20°11'18.98"S, 43°50'18.89"W], / Spelayon et al.", "[image data matrix] / Instituto / Tecnológico / Vale / ITV22156" (one female, ISLA-110320). "BRAZIL: Minas Gerais, / Nova Lima, SM_0042 / cave, 29.vii[July]-02.viii[August].2019, / -20.192874, -43.836350 [20°11'34.34"S, 43°50'10.86"W], / Spelayon et al.", "[image data matrix] / Instituto / Tecnológico / Vale / ITV22158" (one female, MPEG-01052551). All paratypes with label "PARATYPE [yellow label] / *Syrbatus* / *moustache* sp. nov. / Desig. Asenjo et al., 2023".

Molecular voucher. "BRAZIL: Minas Gerais, / Nova Lima, SM_0042 / cave, -20.192874, / -43.836350 [20°11'34.34"S, 43°50'10.86"W], 26-31.iii[March].2019, / Spelayon et al.", "[image data matrix] / Instituto / Tecnológico / Vale / ITV22155" (one female, MPEG-01052552).

Diagnosis. *Syrbatus mustache* Asenjo & Valois **sp. nov.** belong to species-group 2 (see the Discussion section below), being similar to *Syrbatus superciliata* Asenjo & Valois **sp. nov.**, considering both the habitus and head shape. The main differences between the two are the

darker color of the body of *Syrbatus mustache* **sp. nov.**, which is reddish brown, while *Syrbatus superciliata* Asenjo & Valois **sp. nov.** is a yellowish brown; head with oval transversal area in the anterior region (sling transversal area in *Syrbatus superciliata* Asenjo & Valois **sp. nov.**); posterior margin of sternum VIII with a stout conical projection and its apex rounded in *Syrbatus mustache* **sp. nov.**, posterior margin of sternum VIII with thin pointed projection at middle (thin pointed projection at the middle in with its apex rounded in *Syrbatus superciliata* Asenjo & Valois **sp. nov.**); and aedeagus with thin paramere in *Syrbatus mustache* **sp. nov.** Asenjo & Valois (paramere thick in *Syrbatus superciliata* Asenjo & Valois **sp. nov.**).

Holotype male (Fig. 2A). BL: 2.11. Head, pronotum, elytra and abdomen reddish brown; antennae, mouth parts, tibial apex brown.

Head. Subrectangular (Figs. 2A and 2C-D), longer (HL: 0.58) than wide (HW: 0.42). Antennal insertions on head not visible in dorsal view. Anterior margin rounded, genal edge rounded and not carinated. Eye composed of 13 ommatidia and situated more posteriorly at head length in lateral view. Neck almost one-half width of head (NW: 0.20), with margins rounded. Anterior region with wide oval transversal area, 2.0 wider than long; and its surface covered with long setae (Fig. 2C). Eyes connected by long curved transversal slim carina covered of long setae. Both regions cited anteriorly connected by short medial longitudinal keel covered by long setae. The vertex area between eyes with one deep sulcus in format of W-shaped (Fig. 2D) and with vertexal foveae [vf]. Ventral surface of head with one gular fovea, without visible gular sulcus. Antennae (Fig. 2A) 2/3 body length. Scape rectangular, deeply impressed medially with margins rounded. Pedicel subclaviform, only slightly shorter than scape. Antennomeres 3-7 cylindrical, gradually broadening to apex, about 2× longer than wide. Antennomere 8 oval, only

slightly longer than wide; smaller than the other antennomeres. Antennomeres 9-10 rounded, approximately 2× longer than wide. Antennomere 11 sub-fusiform, 2.5× longer than wide. All antennomeres covered with short and long microsetae.

Thorax: Pronotum hexagonal (Figs. 2A and 2E), slightly longer than wide (PL: 0.45; PW: 0.44) broader at two-third anterior portion and narrower at posterior one-third (Fig. 2F). Surface of pronotum shinning, with long setae direct to center. Pronotal disc distinctly convex in lateral view. Antebasal sulcus [as] present and complete, curved and slender, reaching the posterior ending of the longitudinal sulcus; and one strong lateral longitudinal sulcus on each side of pronotum. Pronotum with anterior margin almost right and posterior margin convex; with a lateral antebasal fovea [laf], an outer basolateral fovea [oblf], and an inner basolateral fovea [iblf]. Posterior angles of pronotum slightly obtuse (Fig. 2E). Prosternum with one lateral procoxal fovea [lpcf]. Mesoventrite with one lateral mesosternal foveae [lmsf], one lateral mesocoxal fovea [lmcf], and two median metasternal fovea [mmtf].

Elytra: Trapezoidal (EL: 0.70; EW: 0.80), posterior margin 2× larger than anterior margin (Figs. 2A and 2F). Surface of elytra shining, with long setae sparse and direct posteriorly. Posterior margin curved, with sutural stria [ss] present. Elytron with three basal elytral fovea [bef] at anterior margin. Flight wings extremely reduced (brachypterous species).

Legs: Elongated and slender (Fig. 2A). Femora thickened medially; tibiae slightly widened toward apex, similar in length to femora. Protibiae with microsetae and one apical spur on its internal face. Tarsi 3-segmented, with basal tarsomere minute and the two other segments longer. Second segment longer than third. All tarsi with two apical claws; one thicker and other setiform and slender. Pro- and mesocoxae conical, prominent and contiguous. Metacoxae transversely and weakly separated. Procoxae with small prosternal processed, rounded at apex.

Abdomen: With five visible tergites (morphological tergites IV-VIII) bordered by fine carina. Tergite IV with a short discal carina [dc] and one basolateral fovea [blf]. Sternite IV with two basolateral fovea [blf] and a mediobasal fovea [mbf]. Tergite VIII with apex convex. Tergum IX small, subtriangular approximately 8× wider than long (Fig. 2M). Sternum VIII deeply impressed medially, posterior margin sinuous having a conical projection at middle, apex of projection rounded (Figs. 2J-K). Tergum VIII subrectangular with anterior and posterior margins rounded (Fig. 2L).

Aedeagus: Asymmetric (Figs. 2G-I) strongly asymmetric, length 0.53 mm; median lobe with large basal capsule and triangular basal foramen; the median lobe strongly bifurcated, with both branches twist. Paramere fused to median lobe to with apex divided into two long curved prolongation. The genital plate divided in two small elongated plates, both attached to aedeagus by a membrane almost transparent.

Female. It differs from males by frons of head with not distinctly expanded over antennal insertions and the absence of excavation, oblique impressions, or cephalic keel (Fig. 5A). The sternum VIII lacking modification such as projections or impressions. Genital complex (Fig. 5D) transversal with lateral corns elongated; anterior border with two central prolongations and one small prolongation on each side.

Etymology. The specific epithet name "*moustache*" refers to long setae on the anterior region of front. This is a noun in apposition.

Distribution. Known only from Nova Lima, Minas Gerais, Brazil (Fig. 1).

***Syrbatus obsidian* Asenjo & Valois, new species**

(Figs. 1, 3 and 5)

295 http://zoobank.org/urn:lsid:zoobank.org:act:C42D432B-4893-4324-A859-
296 1BD40E47E6D7
297
298 *Type material* (seven males, four females). *Holotype:* BRAZIL: male, labeled: "BRAZIL:
299 Minas Gerais, / Catas Altas, FZ_0054 / cave, 04.ix[September].2019, / -20.116420, -43.417677
300 [20°6'59.11"S, 43°25'3.63"W], / Spelayon et al.", "[image data matrix] / Instituto / Tecnológico
301 / Vale / ITV22170", "HOLOTYPE ♂ [red label] / *Syrbatus* / *obsidian* sp. nov. / Desig. Asenjo et
302 al., 2023" (MPEG-01052553). *Paratype:* (six males, four females), the first label as the holotype;
303 "[image data matrix] / Instituto / Tecnológico / Vale / ITV22172" (one male, ISLA-110321);
304 "[image data matrix] / Instituto / Tecnológico / Vale / ITV22171" (one female, MPEG-
305 01052554); "[image data matrix] / Instituto / Tecnológico / Vale / ITV22173" (one female,
306 ISLA-110322). "BRAZIL: Minas Gerais, / Catas Altas, FZ_0050 / cave, 04.ix[September].2019,
307 / -20.117065, -43.416092 [20°7'1.43"S, 43°24'57.93"W], / Spelayon et al.", "[image data
308 matrix] / Instituto / Tecnológico / Vale / ITV22161" (one male, CEMT-00138995). "BRAZIL:
309 Minas Gerais, / Catas Altas, FZ_0050 / cave, 04.ix[September].2019, / -20.117065, -43.416092
310 [20°7'1.43"S, 43°24'57.93"W], / Spelayon et al.", "[image data matrix] / Instituto / Tecnológico
311 / Vale / ITV22162" (one male, MPEG-01052555). "BRAZIL: Minas Gerais, / Catas Altas,
312 FZ_0050 / cave, 04.ix[September].2019, / -20.117065, -43.416092 [20°7'1.43"S,
313 43°24'57.93"W], / Spelayon et al.", "[image data matrix] / Instituto / Tecnológico / Vale /
314 ITV22163" (one male, ISLA-110323). "BRAZIL: Minas Gerais, / Catas Altas, FZ_0050 / cave,
315 04.ix[September].2019, / -20.117065, -43.416092 [20°7'1.43"S, 43°24'57.93"W], / Spelayon et
316 al.", "[image data matrix] / Instituto / Tecnológico / Vale / ITV22164" (one male, ISLA-
317 110324). "BRAZIL: Minas Gerais, / Catas Altas, FZ_0050 / cave, 04.ix[September].2019, / -

20.117065, -43.416092 [20°7’1.43”S, 43°24’57.93”W], / Spelayon et al.”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV22165” (one male, ISLA-110325). “BRAZIL: Minas Gerais, / Catas Altas, FZ_0053 / cave, 04.ix[September].2019, / -20.116519, -43.417599 [20°6’59.46”S, 43°25’3.35”W], / Spelayon et al.”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV22167” (one female, MPEG-01052556). “BRAZIL: Minas Gerais, / Catas Altas, FZ_0049 / cave, 04.ix[September].2019, / -20.117099, -43.415814 [20°7’1.55”S, 43°24’56.93”W], / Spelayon et al.”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV22159” (one female, CEMT-00138996). All paratypes with label “PARATYPE [yellow label] / *Syrbatus* / *obsidian* sp. nov. / Desig. Asenjo et al., 2023”.

Molecular voucher. “BRAZIL: Minas Gerais, / Catas Altas, FZ_0053 / cave, 24.ix[September].2019, / -20.116519, -43.417599 [20°6’59.46”S, 43°25”3.35”W], / Spelayon et al.”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV22166” (one female, ISLA-110327). “BRAZIL: Minas Gerais, / Catas Altas, FZ_0054 / cave, 04.ix[September].2019, / -20.116420, -43.417677 [20°6’59.11”S, 43°25’3.63”W], / Spelayon et al.”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV22168” (one male. ISLA-110326). “BRAZIL: Minas Gerais, / Catas Altas, FZ_0054 / cave, 04.ix[September].2019, / -20.116420, -43.417677 [20°6’59.11”S, 43°25’3.63”W], / Spelayon et al.”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV22169” (one female, MPEG-01052558).

Diagnosis. *Syrbatus obsidian* Asenjo & Valois **sp. nov.** belong to species-group 5 (see the Discussion section). Among the species of species-group 5, *Syrbatus obsidian* Asenjo & Valois **sp. nov.** is similar to *Syrbatus nasutus* (Reitter, 1888) in the shape of head and pronotum; *Syrbatus obsidian* Asenjo & Valois **sp. nov.** presents scape moderately dilated (*Syrbatus nasutus*

with scape strongly dilated), anterior margin of head rounded (right in *Syrbatus nasutus*), and genal edge rounded (right angulated in *Syrbatus nasutus*).

Holotype male (Fig. 3A). BL: 1.98 mm. Head, pronotum and abdomen dark brown; antennae, mouth parts legs and elytra reddish brown.

Head: Subtriangular (Figs. 3A and 3C-D), slightly wider (HW: 0.59) than long (HL: 0.44). Antennal insertions on head not visible in dorsal view. Anterior margin rounded and emarginated, genal edge rounded and carinated. Eyes composed of right side 19 and left 20 ommatidia situated at posterior third of head length. Neck almost one-half width of head (NW: 0.23), with margins rounded. Dorsal region with longitudinal oval deep excavation (Fig. 3A). The basal margin of excavation with U-shaped carinated and connected to neck by deep longitudinal sulcus. Head with two vertexal foveae [vf]. Ventral surface of head with one gular fovea [gf], with indistinct gular sulcus. Antennae (Fig. 3A) 2/3 body length. Scape thick and claviform, apex one-third wider than base, deeply impressed medially and lateral margins strongly margined (Fig. 3B). Pedicel subrectangular, only slightly shorter than scape. Antennomeres 3-7 cylindrical, gradually broadening to apex, about 2× longer than wide. Antennomere 8 oval, only slightly longer than wide; smaller than the other antennomeres. Antennomeres 9-10 rounded, approximately 2× longer than wide. Antennomere 11 sub-fusiform, 2.5× longer than wide. All antennomeres covered by long and short microsetae.

Thorax: Pronotum hexagonal (Figs. 3A and 3E), as long as wide (PL: 0.48; PW: 0.48) broader at two-third anterior portion and narrower at posterior one-third (Fig. 3F). Surface of pronotum shinning, with sparse long setae direct to center. Pronotal disc distinctly convex in lateral view. Antebasal sulcus [as] sinuous and widened medially, reaching the posterior ending

of the longitudinal sulcus; and one strong lateral longitudinal sulcus on each side of pronotum. Pronotum with anterior margin convex and posterior margin straight; with a lateral antebasal fovea [laf], an outer basolateral fovea [oblf], and an inner basolateral fovea [iblf]. Posterior angles of pronotum straight (Fig. 3E). Prosternum with lateral procoxal fovea [lpcf]. Mesoventrite with lateral mesosternal foveae [lmsf], lateral mesocoxal fovea [lmcf], and two median metasternal fovea [mmtf].

Elytra: (Figs. 3A and 3F). Subrectangular (EL: 0.79; EW: 0.87), apex 2× larger than base. Surface of elytra shinning, with long setae and direct posteriorly; setae spars and lacking on the center of elytral disc. Posterior margins curved, with sutural stria [ss] present. Elytron with three basal elytral fovea [bef] at anterior margin. Flight wings extremely reduced (brachypterous species).

Legs: Elongated and slender (Fig. 3A). Femora thickened medially; tibiae slightly widened toward apex, similar in length to femora. Protibiae with microsetae and one apical spur on its internal face. Tarsi 3-segmented, with basal tarsomere minute and the two other segments longer. Second segment longer than third. All tarsi with two apical claws; one thicker and other setiform and slender. Pro- and mesocoxae conical, prominent and contiguous. Metacoxae transversely and weakly separated. Procoxae with small prosternal processed, rounded at apex.

Abdomen: With five visible tergites (morphological tergites IV-VIII) bordered by fine carina. Tergite IV with a short discal carina [dc] and one basolateral fovea [blf]. Sternite IV with one basolateral fovea [blf] and a mediobasal fovea [mbf]. Tergite VIII with apex convex. Tergum IX triangular approximately 5× wider than long (Fig. 3M). Sternum VIII with a small conical projection at posterior margin and a round impression medially (Figs. 3J-K). Tergum VIII subrectangular with anterior and posterior margins rounded (Fig. 3L).

Aedeagus (Figs. 3G-I): strongly asymmetric, length 0.35 mm; median lobe with stout large basoventral projection in the basal capsule and roundly basal foramen; the median lobe strongly bifurcated, in one large and one small branches. Paramere fused to median lobe and broaden to apex. The genital plate large and curved not divided attached to aedeagus by a membrane almost transparent.

Female. It differs from male by frons on head not distinctly expanded over antennal insertions and the absence of excavation, oblique impressions, or cephalic keel (Fig. 5B). The sternum VIII without modifications. Genital complex (Fig. 5E) with semicircular shape; and anterior border with one wide emargination.

Etymology. The specific epithet name "*obsidian*" refers to black light color of body. This is a noun in apposition.

Distribution. Known only from Catas Altas, Minas Gerais, Brazil (Fig. 1).

***Syrbatus superciliata* Asenjo & Valois, new species**

(Figs. 1, 4 and 5)

http://zoobank.org/urn:lsid:zoobank.org:act:489AB8BC-FF86-4214-AC28-850C99EA37B1

Type material (one male, two females). *Holotype:* BRAZIL: male, labeled "BRAZIL: Minas Gerais, / Nova Lima, ABOB_0028 / cave, -20.163733, / -43.863682 [20°9'49.44"S, 43°51'49.25"W], 29.iv[April].2019, / R.Zampaulo & M.Simões", "[image data matrix] / Instituto / Tecnológico / Vale / ITV39053", "HOLOTYPE ♂ [red label]/ *Syrbatus* / *superciliata* sp. nov. / Desig. Asenjo et al., 2023" (one male, ISLA-110317). *Paratype:* (two females), labeled: "BRAZIL: Minas Gerais, / Nova Lima, ABOB_0028 / cave, -20.163733, -43.863682

[20°9’49.44”S, 43°51’49.25”W], / 29.iv[April].2019, R.Zampaulo & / M.Simões”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV39054” (one female, ISLA-110318). “BRAZIL: Minas Gerais, / Nova Lima, ABOB_0015 / cave, 29.iv[April].2019, / -20.165292, -43.861671 [20°9’55.05”S, 43°51’42.01”W], / R.Zampaulo & M.Simões”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV39055” (one female, MPEG-01052549). All paratypes with label “PARATYPE [yellow label] / *Syrbatus* / *superciliata* sp. nov. / Desig. Asenjo et al., 2023”.

Molecular vouchers. “BRAZIL: Minas Gerais, Nova Lima, ABOB_0015 / cave, 01.viii[August].2013, / -20.165292, -43.861671 [20°9’55.05”S, 43°51’42.01”W], / M.Simões”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV10831” (one female, ITV10831). “BRAZIL: Minas Gerais, Nova Lima, ABOB_0015 / cave, 01.viii[August].2013, / -20.165292, -43.861671 [20°9’55.05”S, 43°51’42.01”W], / M.Simões, “[image data matrix] / Instituto / Tecnológico / Vale / ITV10835” (one female, ITV10835). “BRAZIL: Minas Gerais, / Nova Lima, ABOB_0015 / cave, 29.iv[April].2019, / -20.165292, -43.861671 [20°9’55.05”S, 43°51’42.01”W], / R.Zampaulo & M.Simões”, “[image data matrix] / Instituto / Tecnológico / Vale / ITV39056” (one female, ITV39056).

Diagnosis. As mentioned above, *Syrbatus superciliata* Asenjo & Valois **sp. nov.** is, in general, similar to *Syrbatus mustache* Asenjo & Valois **sp. nov.** within the species-group 2. For diagnostical characters, see the diagnosis of *Syrbatus mustache* Asenjo & Valois **sp. nov.** above.

Holotype male (Fig. 4A). BL: 1.52 mm. Head, pronotum and abdomen brown; antennae, mouth parts legs and elytra light brown.

Head: slightly oval (Figs. 4A and 4C-D), longer (HL: 0.47) than wide (HW: 0.37). Antennal insertions on head not visible in dorsal view. Anterior margin rounded, genal edge rounded and not carinated. Eyes composed of 10 (right side) and 9 (left side) ommatidia situated at posterior third of head length. Neck almost one-half width of head (NW: 0.21), with margins rounded. Anterior region with slim rounded transversal area, 3.5× wider than long; surface with very long setae concentrated near margin (Fig. 4C). Eyes connected by long curved transversal slim carina covered of long setae. Both regions cited anteriorly connected by short medial longitudinal keel covered by small setae. The vertex area between eyes with one deep sulcus in format of W-shaped (Fig. 4D) and with vertexal foveae [vf]. Ventral surface of head with one gular fovea [gf], without visible gular sulcus. Antennae (Fig. 4B) 2/3 body length. Scape rectangular and slightly stout, deeply impressed medially with margins rounded. Pedicel subclaviform, only slightly shorter than scape. Antennomeres 3-7 cylindrical, gradually broadening to apex, about 2× longer than wide. Antennomere 8 oval, only slightly longer than wide; smaller than the other antennomeres. Antennomeres 9-10 rounded, approximately 2× longer than wide. Antennomere 11 sub-fusiform, 2.5× longer than wide. All antennomeres covered by long microsetae.

Thorax: Pronotum hexagonal (Figs. 4A and 4E), slightly longer than wide (PL: 0.46; PW: 0.42) broader at medio-anterior portion and narrower at posterior one-third (Fig. 4F). Surface of pronotum shinning, with long setae direct to center. Pronotal disc distinctly convex in lateral view. Antebasal sulcus [as] present and complete, regularly curved and slender, reaching the posterior ending of the longitudinal sulcus on the lateral portions of the pronotal disc. Pronotum with basal and anterior margins weakly convex; with a lateral antebasal fovea [laf], an outer basolateral fovea [oblf], and an inner basolateral fovea [iblf]. Posterior angles of pronotum

obtuse (Fig. 4F). Prosternum with lateral procoxal fovea [lpcf]. Mesoventrite with one lateral mesosternal foveae [lmsf], one lateral mesocoxal fovea [lmcf], and two median metasternal fovea [mmtf].

Elytra: (Figs. 4A and 4F). Subrectangular (EL: 0.75; EW: 0.77), apex 2× larger than base. Surface of elytra shinning, with long setae directed posteriorly, setae sparsely distributed. Posterior margins curved, sutural stria [ss] present. Elytron with three basal elytral fovea [bef] at anterior margin. Flight wings extremely reduced (brachypterous species).

Legs: Elongated and slender (Fig. 4A). Femora thickened medially; tibiae slightly widened toward apex, similar in length to femora. Protibiae with microsetae and one apical spur on its internal face. Tarsi 3-segmented, with basal tarsomere minute and the other two tarsomeres longer. Second tarsomere longer than third. All tarsi with two apical claws; one thicker and other setiform and slender. Pro- and mesocoxae conical, prominent and contiguous. Metacoxae transversely and weakly separated. Procoxae with small prosternal process, rounded at apex.

Abdomen: With five visible tergites (morphological tergites IV-VIII) bordered by fine carina. Tergite IV with a short discal carina [dc] and one basolateral fovea [blf]. Sternite IV with two basolateral fovea [blf] and a mediobasal fovea [mbf]. Tergite VIII with apex convex. Tergum IX triangular approximately 5× wider than long (Fig. 4M). Sternum VIII deeply impressed medially, posterior margin sinuous having a pointed projection at middle (Figs. 4J-K). Tergite VIII subrectangular with anterior and posterior margins rounded (Fig. 4L).

Aedeagus (Figs. 4G-I): strongly asymmetric, length 0.47 mm; median lobe with large basal capsule and roundly basal foramen; the median lobe strongly bifurcated, with both branches twist. Paramere fused to median lobe with apex divided into two long and slim

prolongation curved. The genital plate divided in two small elongated plates, both attached to aedeagus by a membrane almost transparent.

Female. It differs from males by frons not distinctly expanded over antennal insertions and the absence of excavation, oblique impressions, or cephalic keel (Fig. 5C). The sternum VIII lacks modifications such as projections or impressions. Genital complex (Fig. 5F) oblong with anterior border with broad two central prolongations and one broad prolongation on each side.

Etymology. The specific epithet name "*superciliata*" refers to similar eyebrow above compound eyes. This is a noun in apposition.

Distribution. Known only from Nova Lima, Minas Gerais, Brazil (Fig. 1).

***Syrbatus brevispinus* (Reitter, 1882)**

(Fig. S1)

Batrisus (*Syrbatus*) *brevispinus*: Reitter, 1882: 137 (original description, drawings pl. 5, fig. 8. Type locality: "Brasilia: Sao Paolo, 3000 Fufs über dem Meere"), Reitter, 1888: 245 (revision).

Batrisus brevispinus: C.Schaufuss, 1888: 11 (distribution).

Arthmius (*Syrbatus*) *brevispina*: Raffray, 1898: 446, 454 (revision), Raffray, 1904: 70 (catalogue, species-group 2, and distribution), Raffray, 1908: 150 (checklist, distribution), Raffray, 1911: 55 (catalogue, distribution).

Arthmius brevispina: Blackwelder, 1944: 91 (checklist Latin American species, distribution).

Syrbatus brevispinus: Park, 1942: 234, 237 (revision, species-group 2, and distribution), Asenjo et al., 2013: 14 (checklist Brazilian species, distribution).

Type material (Fig. S1). “Brésil / Sao. Paulo”, “80 Juli / Brasilien / Sao Paolo / 3000 FB / leg. [unreadable]”, “*Syrbatus* / *brevispina* / Type Reitter / Bresil”, “HOLOTYPE / *Syrbatus* / *brevispina* (Reitter, 1882)”, “MUSÉUM PARIS / 1917 / COLL. A. RAFFRAY”, “S. Brevispina / A. Raffray det.”, “HOLOTYPE”, “TYPE”, “MNHN, Paris / EC21615 / [image data matrix]”.

Comments. Reitter (1882), in the original description, specified that he studied one incomplete female. We studied, by photography, one specimen of the Raffray collection with the abdomen absent, probably female, deposited in the MNHN Entomological Collection labeled as “Type”, and we recognize it as the Holotype.

Distribution. Full record and distribution are described in Asenjo et al. (2013).

***Syrbatus bubalus* (Raffray, 1898)**

(Fig. S2)

Arthmius (*Syrbatus*) *bubalus*: Raffray, 1898: 444, 454 (original description, drawings pl. 17, fig. 1. Type locality: “Brésil: Bahia”), Raffray, 1904: 70 (catalogue, species-group 2, and distribution), Raffray, 1908: 150 (checklist, distribution), Raffray, 1911: 55 (catalogue, distribution).

Arthmius bubalus: Blackwelder, 1944: 91 (checklist Latin American species, distribution).

Syrbatus bubalus: Park, 1942: 234, 237 (revision, species-group 2, and distribution), Asenjo et al., 2013: 14 (checklist Brazilian species, distribution).

Type material (Fig. S2). “Bahia”, “S. Bubalus / A. Raffray det.”, “MUSÉUM PARIS / 1917 / COLL. A. RAFFRAY”, “*Syrbatus* Reitt. / *bubalus* Raffr. / male symbol type / Bahia”,

522 "HOLOTYPE / *Syrbatus* / *bubalus* (Raffray, 1898)", "HOLOTYPE", "TYPE", "MNHN, Paris /
523 EC21624 / [image data matrix]".

524 *Comments.* Raffray (1898), in the original description, specified that he studied one male
525 collected by A. Grouvelle [Antoine Henri Grouvelle] from Brazil (Bahia). We studied, by
526 photography, one specimen of Raffray collection deposited in the MNHN Entomological
527 Collection labeled as "Type", and we recognize it as the Holotype.

528 *Distribution.* Full record and distribution are described in Asenjo et al. (2013).

529

530 ***Syrbatus centralis* (Raffray, 1898)**

531 (Fig. S3)

532 *Arthmius* (*Syrbatus*) *centralis*: Raffray, 1898: 445, 454 (original description. Type
533 locality: "Brésil: Blumenau"), Raffray, 1904: 70 (catalogue, species-group 2, and distribution),
534 Raffray 1908: 150 (checklist, distribution), Raffray, 1911: 55 (catalogue, distribution).

535 *Arthmius centralis*: Blackwelder, 1944: 91 (checklist Latin American species,
536 distribution).

537 *Syrbatus centralis*: Park, 1942: 234, 237 (revision, species-group 2, and distribution),
538 Asenjo et al., 2013: 14 (checklist Brazilian species, distribution).

539 *Arthmius centralis* Reitter: Raffray, 1898: 454 (*in litteris* name).

540 *Type material* (Fig. S3). "Brésil / Blumenau", "S. centralis / A. Raffray det.", "B.
541 centralis / m. Blūmenaū", "MUSÉUM PARIS / 1917 / COLL. A. RAFFRAY", "Syrbatus /
542 centralis ♂ / Type Reitter / Brésil", "HOLOTYPE / *Syrbatus* / *centralis* (Raffray, 1898)",
543 "HOLOTYPE", "TYPE", "MNHN, Paris / EC21623 / [image data matrix]".

544 *Comments.* Raffray (1898), in the original description, does not specify the number of
545 specimens that he studied, but he, at least, studied one male specimen collected from Brazil
546 (Blumenau). We studied, by photography, one specimen of the Raffray collection deposited in
547 the MNHN Entomological Collection labeled as "Type", and we are designating it as Lectotype.
548 *Distribution.* Full record and distribution are described in Asenjo et al. (2013).
549
550 ***Syrbatus grouvellei* (Raffray, 1898)**
551 (Fig. S4)
552 *Arthmius* (*Syrbatus*) *grouvellei*: Raffray, 1898: 445, 454 (original description, drawings
553 pl. 17, fig. 3. Type locality: "Brésil: Bahia"), Raffray, 1904: 70 (catalogue, species-group 2, and
554 distribution), Raffray 1908: 150 (checklist, distribution), Raffray, 1911: 55 (catalogue,
555 distribution).
556 *Arthmius grouvellei*: Blackwelder, 1944: 91 (checklist Latin American species,
557 distribution).
558 *Syrbatus grouvellei*: Park, 1942: 234, 237 (revision, species-group 2, and distribution),
559 Asenjo et al. 2013: 15 (checklist Brazilian species, distribution).
560 *Type material* (Fig. S4). "Bahia", "S. Grouvellei / A. Raffray det.", "MUSÉUM PARIS /
561 1917 / COLL. A. RAFFRAY", "'Syrbatus Reitt. / grouvellei / Type. Raffr. / Bahia.',
562 HOLOTYPE / *Syrbatus* / *grouvellei* (Raffray, 1898)", "TYPE", "HOLOTYPE", "MNHN, Paris /
563 EC21622 / [image data matrix]"
564 *Comments.* Raffray (1898), in the original description, specified that he studied one male
565 collected by A. Grouvelle [Antoine Henri Grouvelle] from Brazil (Bahia). We studied, by

photography, one specimen of the Raffray collection deposited in the MNHN Entomological Collection labeled as "Type", and we recognize it as the Holotype.

Distribution. Full record and distribution are described in Asenjo et al. (2013).

***Syrbatus hetschkoi* (Reitter, 1888)**

(Figs. S5 and S6)

Batrisus (*Syrbatus*) *hetschkoi*: Reitter, 1888: 245, 250 (original description. Type locality: "Brésil: Bahia").

Arthmius (*Syrbatus*) *hetschkoi*: Raffray, 1898: 446, 455 (revision, drawings pl. 17, fig. 8), Raffray, 1904: 70 (catalogue, species-group 2, and distribution), Raffray, 1908: 150 (checklist, distribution), Raffray, 1911: 55 (catalogue, distribution).

Arthmius hetschkoi: Blackwelder, 1944: 91 (checklist Latin American species, distribution).

Syrbatus hetschkoi: Park, 1942: 234, 237 (revision, species-group 2, and distribution), Asenjo et al., 2013: 15 (checklist Brazilian species, distribution).

Type material. First specimen (Fig. S5): "Brésil / Blumenau", "S. Hetschkoi / A. Raffray det.", "MUSÉUM PARIS / 1917 / COLL. A. RAFFRAY", "Syrbatus Reitt. / Hetschkoi Reitt. / ♂ Type / Brésil", "SYNTYPE / *Syrbatus* / *hetschkoi* (Reitter, 1888)", "SYNTYPE", "TYPE", "MNHN, Paris / EC21619 / [image data matrix]"; second specimen (Fig. S6): "Brésil / Blumenau", "S. Hetschkoi / A. Raffray det.", "MUSÉUM PARIS / 1917 / COLL. A. RAFFRAY", "SYNTYPE / *Syrbatus* / *hetschkoi* (Reitter, 1888)", "SYNTYPE", "MNHN, Paris / EC21620 / [image data matrix]".

588 *Comments.* Reitter (1888), in the original description, does not specify the number of
589 specimens that he studied; the specimen(s) was(were) collected by Lothar Hetschko from Brazil
590 (Blumenau). We studied by photography two specimens of Raffray collection deposited in the
591 MNHN Entomological Collection labeled as "Type" [first specimen] and "syntype" [second
592 specimen], and we are designating Lectotype and Paralectotype respectively.
593 *Distribution.* Full record and distribution are described in Asenjo et al. (2013).
594
595 ***Syrbatus hiatusus* (Reitter, 1888)**
596 (Figs. S7 and S8)
597 *Batrisus* (*Arthmius*) *hiatusus*: Reitter, 1888: 247, 257 (original description. Type locality:
598 "Brésil: Blumenau").
599 *Arthmius* (*Syrbatus*) *hiatusus*: Raffray, 1898: 445, 454 (revision), Raffray, 1904: 70
600 (catalogue, species-group 2, and distribution), Raffray, 1908: 150 (checklist, distribution),
601 Raffray, 1911: 55 (catalogue, distribution), Bruch, 1914: 304 (catalog Argentinean species).
602 *Arthmius hiatusus*: Blackwelder, 1944: 91 (checklist Latin American species,
603 distribution).
604 *Syrbatus hiatusus*: Jeannel, 1949: 128 (drawings fig. 57), Park, 1942: 234, 237 (revision,
605 species-group 2, and distribution), Asenjo et al., 2013: 15 (checklist Brazilian species,
606 distribution).
607 *Type material.* First specimen (Fig. S7): "Brésil / Blumenau", "B. hiatusus / m.
608 Blūmenaū", "[red square label]", "MUSÉUM PARIS / 1917 / COLL. A. RAFFRAY", "S.
609 Hiatúsus / A. Raffray det.", "Syrbatus Reitt. / hiatusus Reitt. / ♂ Type / Brésil", "HOLOTYEPE /
610 *Syrbatus* / *hiatusus* (Reitter, 1888)", "HOLOTYPE", "MNHN, Paris / EC21616 / [image data

matrix]"; second specimen (Fig. S8): "Brésil / Blumenau", "S. Hiatusus / A. Raffray det.", "MUSÉUM PARIS / 1917 / COLL. A. RAFFRAY", "MNHN, Paris / EC21617 / [image data matrix]".

Comments. Reitter (1888), in the original description, mentioned that he studied some specimens, but without specifying the number, collected by Lothar Hetschko from Brazil (Blumenau). We studied, by photography, two specimens of the Raffray collection deposited in the MNHN Entomological Collection first specimen and second specimen, and we are designating the specimen labeled as Lectotype and Paralectotype, respectively.

Distribution. Full record and distribution are described in Asenjo et al. (2013), and for Argentina (Buenos Aires) in Bruch (1914).

***Syrbatus transversalis* (Raffray, 1898)**

(Fig. S9)

Arthmius (*Syrbatus*) *transversalis*: Raffray, 1898: 447, 455 (original description. Type locality: "Brésil: S. Antonio"), Raffray, 1904: 70 (catalogue, species-group 2, and distribution), Raffray 1908: 150 (checklist, distribution), Raffray, 1911: 55 (catalogue, distribution).

Arthmius transversalis: Blackwelder, 1944: 92 (checklist Latin American species, distribution).

Syrbatus transversalis: Park, 1942: 234, 237 (revision, species-group 2, and distribution), Asenjo et al., 2013: 17 (checklist Brazilian species, distribution).

Type material (Fig. S9). "Brésil / St.Antonio", "S.Transversalis / A. Raffray det.", "MUSÉUM PARIS / 1917 / COLL. A. RAFFRAY", "Syrbatus Reitt. / transversalis / Type.

Raffr. / Brésil", "HOLOTYEPE / *Syrbatus* / *transversalis* (Raffray, 1898)", "TYPE", "HOLOTYPE", "MNHN, Paris / EC21621 / [image data matrix]".

Comments. Raffray (1898), in the original description, does not specify the number of specimens that he studied, but he, at least, studied one male specimen collected by S. Antonio from Brazil. We studied, by photography, one specimen of the Raffray collection deposited in the MNHN Entomological Collection labeled as "Type", and we are designating it as Lectotype.

Distribution. Full record and distribution are described in Asenjo et al. (2013).

***Syrbatus trinodulus* (L.W.Schaufuss, 1887)**

(Fig. S10)

Batrisus (*Syrbatus*) *trinodulus*: L.W.Schaufuss, 1887: 145 (original description. Type locality: "Minas Geraes, Brasilia").

Batrisus trinodulus: Gaedike, 1984: 456 (catalogue of type specimens).

Arthmius trinodulus: C.Schaufuss, 1888: 17 (distribution).

Arthmius (*Syrbatus*) *trinodulus*: Raffray, 1904: 71 (catalogue, distribution and unplaced any group), Raffray, 1908: 151 (checklist, distribution), Raffray, 1911: 55 (catalogue, distribution), Park, 1942: 237 (revision, unplaced any group, and distribution), Blackwelder, 1944: 92 (checklist Latin American species, distribution).

Syrbatus trinodulus: Asenjo et al., 2013: 17 (checklist Brazilian species, distribution).

Type material (Fig. S10). "min geraes [Minas Gerais state in Brazil]", "Minas / geraes", "Syntypus", "Batrisus / (Syrbatus) / 3-nodulus.", "SDEI Coleoptera / # 302700".

Comments. L.W.Schaufuss (1887), in the original description, does not specify the number or sex of the specimens studied. We studied, by photography, one specimen deposited in

the SDEI Entomological Collection labeled as "syntypus", and we are designating it as Lectotype. The species is considered unplaced in any species-group, as proposed by Raffray (1904).

Distribution. Full record and distribution are described in Asenjo et al. (2013).

Mitogenomes and phylogenetic placement

All seven assembled mitochondrial genomes [*Syrbatus moustache* Asenjo & Valois **sp. nov.**: OR625193 (ITV22155); *Syrbatus obsidian* Asenjo & Valois **sp. nov.**: OR625194 (ITV22166), OR625195 (ITV22168) and OR625196 (ITV22169); and *Syrbatus superciliata* Asenjo & Valois **sp. nov.**: OR625197 (ITV10831), OR625198 (ITV10835) and OR625199 (ITV39056)] presented the standard structure and gene content of Metazoans, although the genes were arranged in an unusual order, considering the pattern described for all other Staphylinidae species with available mitogenomes (Fig. 6A; Table 1). Most genes were encoded in the light (L) strand in the mitogenomes of the three new species, except for four PCGs (ND1, ND4, ND4L and ND5), the two rRNA genes (rrnL and rrnS), and eight tRNA genes (trnC, trnF, trnH, trnL1, trnP, trnP, trnQ, trnV and trnY), which were observed in the heavy (H) strand (Table 1). Thus, using the L strand as the standard, we observed the following gene order for the three new species: trnM, COX1, trnK, ND3, trnR, trnC, COX3, ND4, trnT, trnP, ND6, CYTB, trnI, trnQ, ND2, trnW, trnY, trnL2, COX2, trnD, ATP8, ATP6, trnG, trnA, trnN, trnS1, trnE, trnF, ND5, trnH, ND4L, trnS2, ND1, trnL1, rrnL, rrnS and trnV. Moreover, since some of the mitogenome assemblies presented different levels of completeness, we could not recover genes in the extremities for some specimens, as in the case of all three accessions of *Syrbatus obsidian* Asenjo & Valois **sp. nov.** (OR625194, OR625195 and OR625196), missing part of the rrnL,

besides the whole rrnS and trnV genes, and one accession of *Syrbatus superciliata* Asenjo & Valois **sp. nov.** (OR625199), missing part of the rrnL, and the complete sequences of rrnS, trnM and trnV (Table 1).

The mitogenomes of the three new species were largely syntenic, presenting intergenic regions and gene superpositions with similar lengths along the fully aligned extension (from COX1 to mid rrnL, due to the missing parts of some accessions), except for a non-coding intergenic region with 473 bp between trnS2 and NAD1, which was only present in the mitogenomes of *Syrbatus obsidian* Asenjo & Valois **sp. nov.** (Figure 6B). We also observed similar nucleotide contents between *Syrbatus moustache* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.**, with %GC = 17.3 and 17.0, respectively, and *Syrbatus obsidian* Asenjo & Valois **sp. nov.** as the most diverging species, with %GC = 18.9. Overall, the three species shared most of the start codons, which presented the usual ATN configuration, except in the case of COX1 of *Syrbatus obsidian* Asenjo & Valois **sp. nov.**, which presented TTA, which is an alternative start codon (encoding the amino acid leucine) for invertebrate mitogenomes (Table 1). In addition, only two genes were recorded with diverging stop codons among the three species: COX3, for which *Syrbatus obsidian* Asenjo & Valois **sp. nov.** presented TAG instead of TAA; and CYTB, with an incomplete stop codon T in *Syrbatus superciliata* Asenjo & Valois **sp. nov.**, also TAA in the other two species (Table 1).

The phylogenetic reconstruction within Staphylinidae based on ML and BI analyses using a concatenated matrix with amino acid sequences of all 13 PCGs resulted in mostly well-resolved trees, with most of the 14 sampled subfamilies being recovered as well-supported clades (Figure 7). However, the only two species of Tachiporinae included in the phylogenetic analyses appeared within two distinct lineages, in which *Sepedophilus bipunctatus* (Gravenhorst, 1802)

appeared as sister to the clade composed of Steninae and Euaesthetinae species, and *Tachinus subterraneus* (Linnaeus, 1758) was more closely related to Apateticinae and Omaliinae. Also, Paederinae was recovered as paraphyletic, with *Habrocerus capillaricornis* (Gravenhorst, 1806), from Habrocerinae, appearing deeply nested within the former subfamily. On the other hand, while Staphylininae was poorly supported in the ML analysis (BS = 68), the group presented the maximum value of posterior probability in the BI trees (PP = 1).

Regarding Pselaphinae, the subfamily was recovered as monophyletic with strong support (BS = 100; PP = 1), forming, with Neophoninae, the sister clade to the remaining Staphylinidae subfamilies (Figure 7). The three new species of *Syrbatus* formed a fully supported monophyletic group (BS = 100; PP = 1) with well-resolved interspecific relationships, forming, alongside *Metopiellus crypticus*, another clade with maximum statistical support (BS = 100; PP = 1). As also indicated by the morphological similarity, *Syrbatus moustache* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.** were more closely related to each other, with a considerably lower interspecific divergence in comparison to the phylogenetic distance of both to *Syrbatus obsidian* Asenjo & Valois **sp. nov.** (Figure 7).

In addition, we also recovered the three new species as clearly separated clusters in both lineage delimitation approaches. In the ASAP analysis, the best score was obtained for four subsets and a threshold distance of 0.0467 (asap-score = 1.00; P-val = 0.0019; W = 0.0387; Table S1), considering the three species of *Syrbatus* and *Metopiellus crypticus*, grouping in the same pattern as observed in the phylogenetic reconstruction. Similarly, the four species were recovered as independent lineages with strong support (PP = 0.9828), all of which presenting individual high posterior probabilities in the BPP analysis, being 0.9829 for *Syrbatus moustache*

Asenjo & Valois **sp. nov.**, 0.9901 for *Syrbatus obsidian* Asenjo & Valois **sp. nov.**, 0.9997 for *Syrbatus superciliata* Asenjo & Valois **sp. nov.**, and 0.9930 for *Metopiellus crypticus*.

DISCUSSION

The three new species described here of the Brazilian state of Minas Gerais state belong to *Syrbatus*, based on a sub-basal transverse sulcus on the base of pronotum (Figs. 2E, 3E and 4E), and lateral longitudinal sulcus on each side of the pronotum (Figs. 2E, 3E and 4E) (Reitter, 1882; Park, 1942). Raffray (1904) grouped the South American species of the genus in six species-group based on morphological characters of head and antenna. Posteriorly, the concept groups were updated by Park (1942), which were used here for the analysis and description of the three new Brazilian species of *Syrbatus* in the present work. In addition, to describe the new species with greater confidence, we found it necessary to study the other species of the species-group 2 (*Syrbatus brevispinus*, *Syrbatus bubalus*, *Syrbatus centralis*, *Syrbatus grouvellei*, *Syrbatus hetschkoi*, *Syrbatus hiatusus* and *Syrbatus transversalis*), besides *Syrbatus trinodulus*, which is also known from Minas Gerais.

As mentioned above, *Syrbatus moustache* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.** were included in the species-group 2, characterized by the dorsally excavated head of the male (Figs. 2C and 4C), antennae simple (similar in both sexes; Figs. 2C and 4C), and genal region of the head not carinated (Figs. 2C and 4C). On the other hand, *Syrbatus obsidian* Asenjo & Valois **sp. nov.** was included in the species-group 5, considering the genal area of the head longitudinally carinated (Fig. 3C), and antennae abnormal (Fig. 3B). Furthermore, the genital complex for female specimens of *Syrbatus* was studied,

illustrated, and described for the first time (Fig. 5), showing its usefulness for the identification of the species with female sexual characters.

The three species described in the present study were found in caves inserted in siliciclastic rocks. These caves have between 10-500 m of horizontal projection, being inserted in all compartments of the landscape (low, medium, and high slopes) at altitudes that vary between 900-1100 m. In general, such caves are formed by talus deposits, with perennial underground drainage, and the presence of aphotic zones in the larger ones. However, the occurrence of *Syrbatus moustache* Asenjo & Valois **sp. nov.**, *Syrbatus obsidian* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.** in caves of small dimensions, and therefore without aphotic zones, besides the absence of evident troglomorphisms (Christiansen, 2012), suggests that the distribution of these new species may also be related to surface environments, characterizing the three of them as troglophiles.

The gene content and order tend to be highly conserved among the subdivisions of Insecta, with the structure of the ancestral insect mitogenomes being almost ubiquitous (Cameron, 2014). Nevertheless, some deviations from the standard configuration have been observed in the class, as in the case of some species of seed beetles (Chrysomelidae; Bruchinae), with long intergenic repeats and a minor reshuffling related to the gene trnQ (Sayadi et al., 2017). On the other hand, the three new species described here presented the mitochondrial genes in quite different positions, while all other currently known Staphylinidae mitogenomes share the standard insect gene order, as represented in the Figure 6B. Additionally, a somewhat long intergenic region between trnS2 and ND1 was observed only for *Syrbatus obsidian* Asenjo & Valois **sp. nov.**, as another feature that differentiates this species from *Syrbatus moustache* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.**, besides the

morphologic characters discussed above. Yet, the phylogenetic reconstruction with ML and BI, plus the high statistical support obtained in the ASAP and BPP analyses evidenced a robust delimitation among the three new species of *Syrbatus* described here.

Most of the sampled Staphylinidae subfamilies were recovered here as monophyletic and well supported in our phylogenetic reconstruction, at least in one of the two employed approaches, as, for instance, Staphylininae (BS = 68; PP = 1), which have been recovered only weakly supported in other analyses based on whole mitogenome data (Song, Zhai & Zhang, 2021; Ji et al., 2023). Considering the huge diversity of one of the largest Metazoan families (Grebennikov & Newton, 2009; Newton, 2022), one should expect the retelling of phylogenetic history of Staphylinidae to be, at least, very challenging. With its approximately 67,000 species (Newton, 2022), there are numerous difficulties in achieving relevant coverage and proportionality to reconstruct a robust molecular phylogeny of such an immense group. Depending on which taxa is included or left out, the resulting topology may vary considerably regarding recovered clades and support values, with genomic coverage and differences in evolutionary rates among used markers/genome portions also being an immense influence on the outcome (e.g., McKenna et al., 2015; Kim et al., 2020; Motyka et al., 2021; Song, Zhai & Zhang, 2021; Ji et al., 2023). Therefore, the divergences among topologies presented by different studies on the phylogenetic relationships within and among Staphylinidae subdivisions, even those employing the same set of markers/regions, such as whole mitogenomes, are not surprising. Yet, as the availability of genetic data for beetle taxa are continuously increasing, the causes of such conflicting phylogenetic signals may be clarified, allowing us to better address the many standing systematic issues of the infrafamilial relationships.

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Competing Interests

The authors declare that they have no competing interests.

Author Contributions

- Angélico Asenjo conceived and designed the experiments, analyzed the data, performed species identification and description, prepared figures, authored and reviewed preliminary drafts of the text, and approved the final draft of the manuscript.
- Marcely Valois analyzed the data, performed species identification and description, prepared figures, authored and reviewed preliminary drafts of the text, and approved the final draft of the manuscript.
- Robson de A. Zampaulo collected part of the evaluated material, analyzed the biological data, prepared figures, authored and reviewed preliminary drafts of the text, approved the final draft of the manuscript.
- Renato R. M. Oliveira analyzed and curated the data, reviewed preliminary drafts of the text, and approved the final draft of manuscript.

- Michele Molina performed the experiments, analyzed the data, reviewed preliminary drafts of the text, and approved the final manuscript.
- Guilherme Oliveira conceived and designed the experiments, reviewed preliminary drafts of the text, and approved the final manuscript.
- Santelmo Vasconcelos conceived and designed the experiments, analyzed the data, prepared figures and tables, authored and reviewed drafts of the paper, approved the final draft.

Data Availability

The assembled mitogenomes were deposited in GenBank under the accession numbers OR625193, OR625194, OR625195, OR625196, OR625197, OR625198 and OR625199, and raw data were deposited in the BioProject PRJNA862473.

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FIGURE CAPTIONS

Figure 1: Geographic distribution of *Syrbatus moustache* Asenjo & Valois sp. nov., *Syrbatus obsidian* Asenjo & Valois sp. nov. and *Syrbatus superciliata* Asenjo & Valois sp. nov.

Geographic delimitation of geomorphological units in the Quadrilátero Ferrífero, Minas Gerais, Brazil (Map data: Google, ©2023 CNES/Airbus, Maxar Technologies), showing the occurrence sites of *Syrbatus moustache* Asenjo & Valois **sp. nov.** (yellow triangles) and *Syrbatus superciliata* Asenjo & Valois **sp. nov.** (red crosses) in the mountain range of Serra da Moeda (A

993 and D), and *Syrbatus obsidian* Asenjo & Valois **sp. nov.** (pink stars) in the mountain range of the
994 Escarpa Oriental do Caraça (B and E). Habitus of *Syrbatus superciliata* Asenjo & Valois **sp.**
995 **nov.** (C) and general appearance of the interior of the cave ABOB_0015 (F).
996
997 **Figure 2: Habitus and diagnostic characters of holotype male *Syrbatus moustache* Asenjo &**
998 **Valois sp. nov. (ISLA-110319).**
999 Habitus, dorsal view (A); antenna (B); head, dorsal view (C); head, frontal-dorsal view (D);
1000 pronotum (E); elytra (F); aedeagus (G-I); sternum VIII (J-K); tergum VIII (L); sternite IX (M). f:
1001 foramen, p: paramere.
1002
1003 **Figure 3: Habitus and diagnostic characters of holotype male *Syrbatus obsidian* Asenjo &**
1004 **Valois sp. nov. (MPEG-01052553).**
1005 Habitus, dorsal view (A); antenna (B); head, dorsal view (C); head, frontal-dorsal view (D);
1006 pronotum (E); elytra (F); aedeagus (G-I); sternum VIII (J-K); tergum VIII (L); sternite IX (M). f:
1007 foramen, p: paramere.
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1009 **Figure 4: Habitus and diagnostic characters of holotype male *Syrbatus superciliata* Asenjo**
1010 **& Valois sp. nov. (ISLA-110317).**
1011 Habitus, dorsal view (A); antenna (B); head dorsal view (C); head frontal-dorsal view (D);
1012 pronotum (E); elytra (F); aedeagus (G-I); sternum VIII (J); sternum VIII (K-L); sternite IX (M).
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1014
1015 **Figure 5: Morphology of the female of the three new species of *Syrbatus*.**

Frontal-dorsal view of the head (A; ISLA-110320) and genital complex (MPEG-01052551) (D) of *Syrbatus moustache* Asenjo & Valois **sp. nov.**; frontal-dorsal view of the head (B; MPEG-01052554) and genital complex (E; MPEG-01052554) (F) of *Syrbatus obsidian* Asenjo & Valois **sp. nov.**; and frontal-dorsal view of the head (C; MPEG-01052549) and genital complex (F; ISLA-110318) of *Syrbatus superciliata* Asenjo & Valois **sp. nov.**

Figure 6: Mitochondrial genome representation of the three new species of *Syrbatus*, comparing the gene order with *Metopiellus crypticus*.

Comparison of the order of all 37 mitochondrial genes between *Syrbatus moustache* Asenjo & Valois **sp. nov.** and *Metopiellus crypticus* (A); colored arrows pointing to the left and right represent the transcription regions of protein coding genes (blue), rRNA genes (red) and tRNA genes (purple) on the L and H strands, respectively; green, orange, and pink and connections between genes indicate the reorganization of the mitogenome of *Syrbatus moustache* Asenjo & Valois **sp. nov.** in relation to the gene disposition of *Metopiellus crypticus*, a species presenting the ancestral pattern of insect species. Detail of the region between the genes trnS2 and ND1 in the mitogenomes of *Syrbatus moustache* Asenjo & Valois **sp. nov.**, SM, *Syrbatus obsidian* Asenjo & Valois **sp. nov.**, SO, and *Syrbatus superciliata* Asenjo & Valois **sp. nov.**, SS, evidencing the extended intergenic region in the three accessions of the former; the green and brownish bars above the arrows indicate monomorphic and polymorphic nucleotide sites, respectively.

Figure 7: Phylogenetic placement of the three new species of *Syrbatus* within Staphylinidae, based on whole mitogenome data.

1039 Majority-rule consensus phylogram of the Bayesian inference analysis evidencing the
1040 phylogenetic relationships among Staphylinidae species with available mitogenomes in the
1041 GenBank database and the three specimens of *Syrbatus moustache* Asenjo & Valois **sp. nov.**,
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Figure 1

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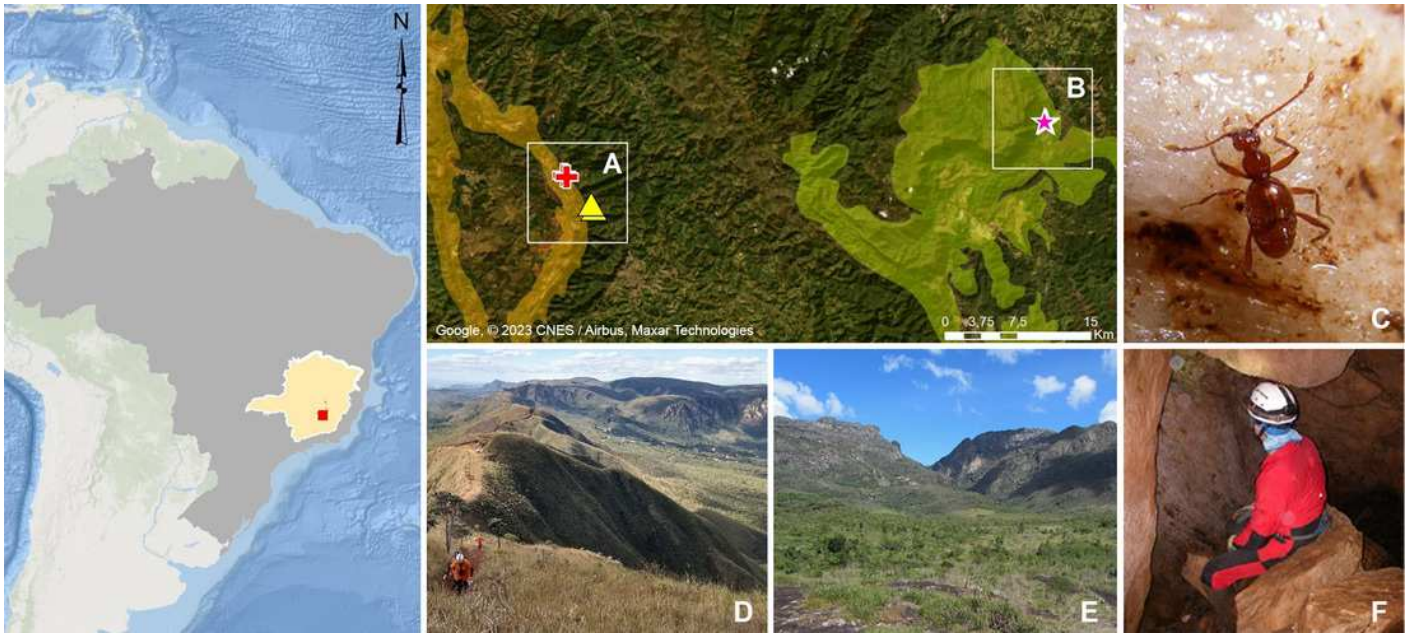
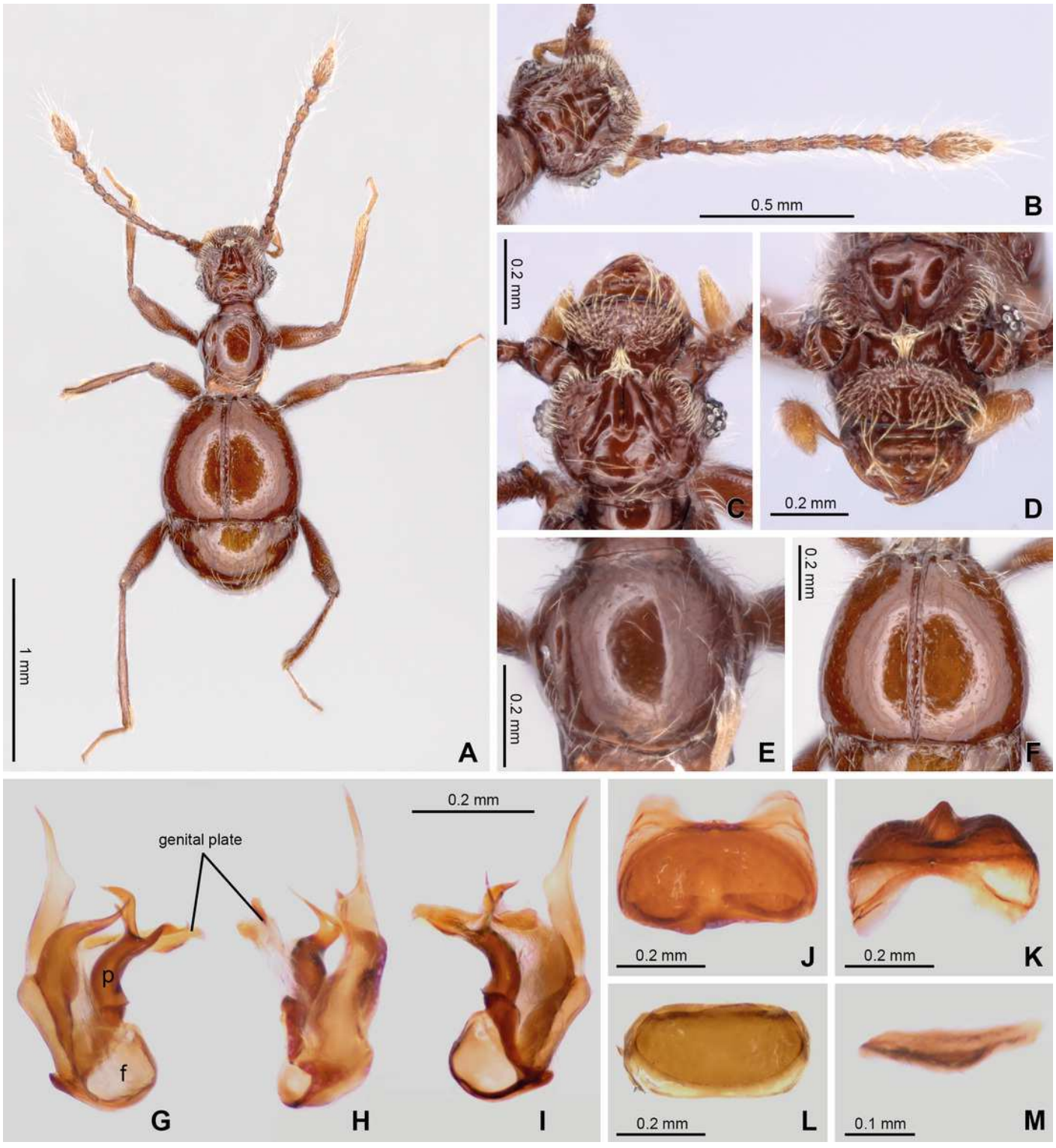


Figure 2

Habitus and diagnostic characters of holotype male *Syrbatus moustache* Asenjo & Valois sp. nov. (ISLA-110319).

Habitus, dorsal view (A); antenna (B); head, dorsal view (C); head, frontal-dorsal view (D); pronotum (E); elytra (F); aedeagus (G-I); sternum VIII (J-K); tergum VIII (L); sternite IX (M). f: foramen, p: paramere.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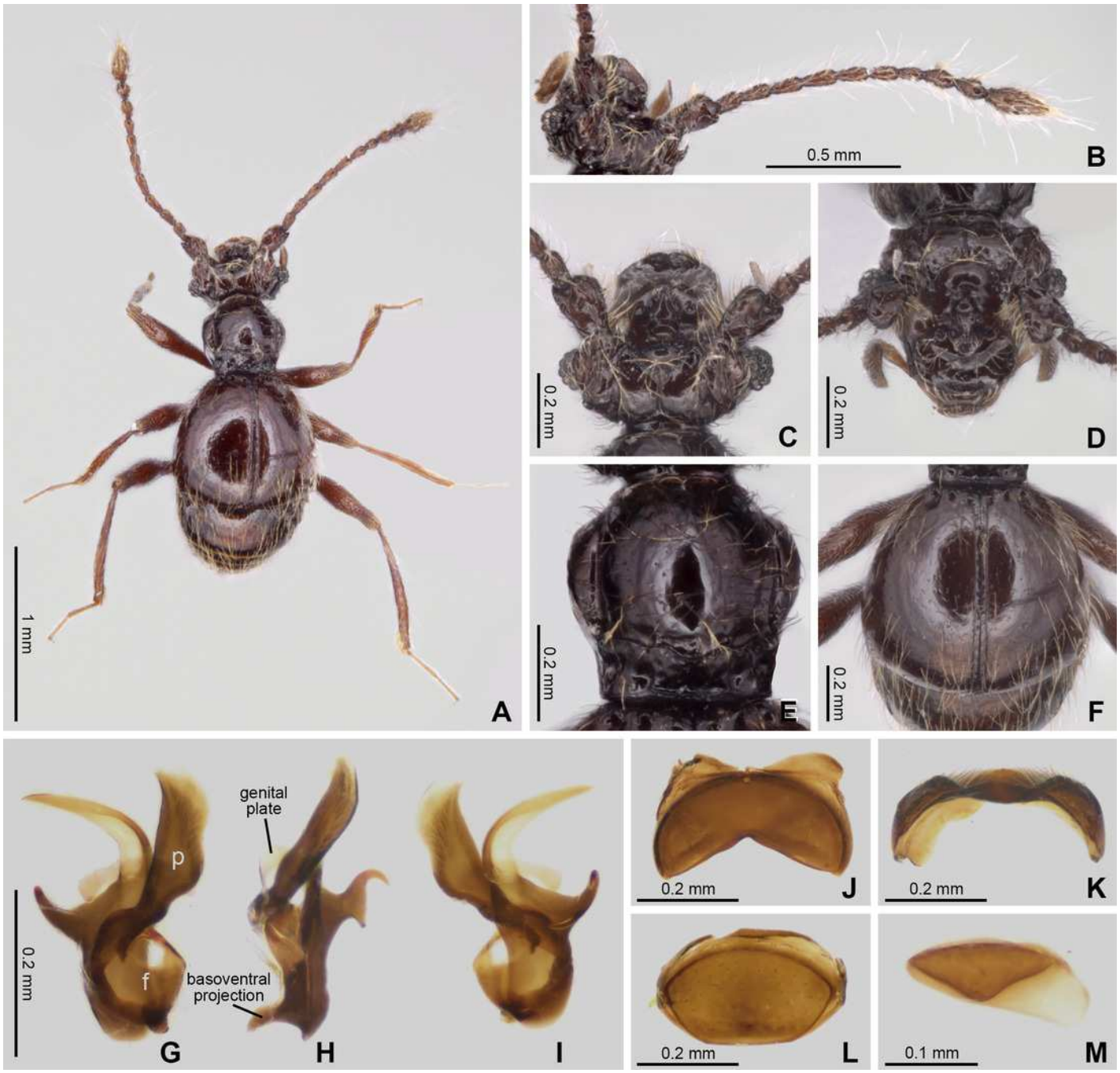
A
0.5 mm
B
0.2 mm
C
0.2 mm
D
0.2 mm
E
0.2 mm
F
0.2 mm
genital plate
p
f
G
H
I
0.2 mm
J
0.2 mm
K
0.2 mm
L
0.1 mm
M

Figure 3

Habitus and diagnostic characters of holotype male *Syrbatus obsidian* Asenjo & Valois sp. nov. (MPEG-01052553).

Habitus, dorsal view (A); antenna (B); head, dorsal view (C); head, frontal-dorsal view (D); pronotum (E); elytra (F); aedeagus (G-I); sternum VIII (J-K); tergum VIII (L); sternite IX (M). f: foramen, p: paramere.


1 mm
A
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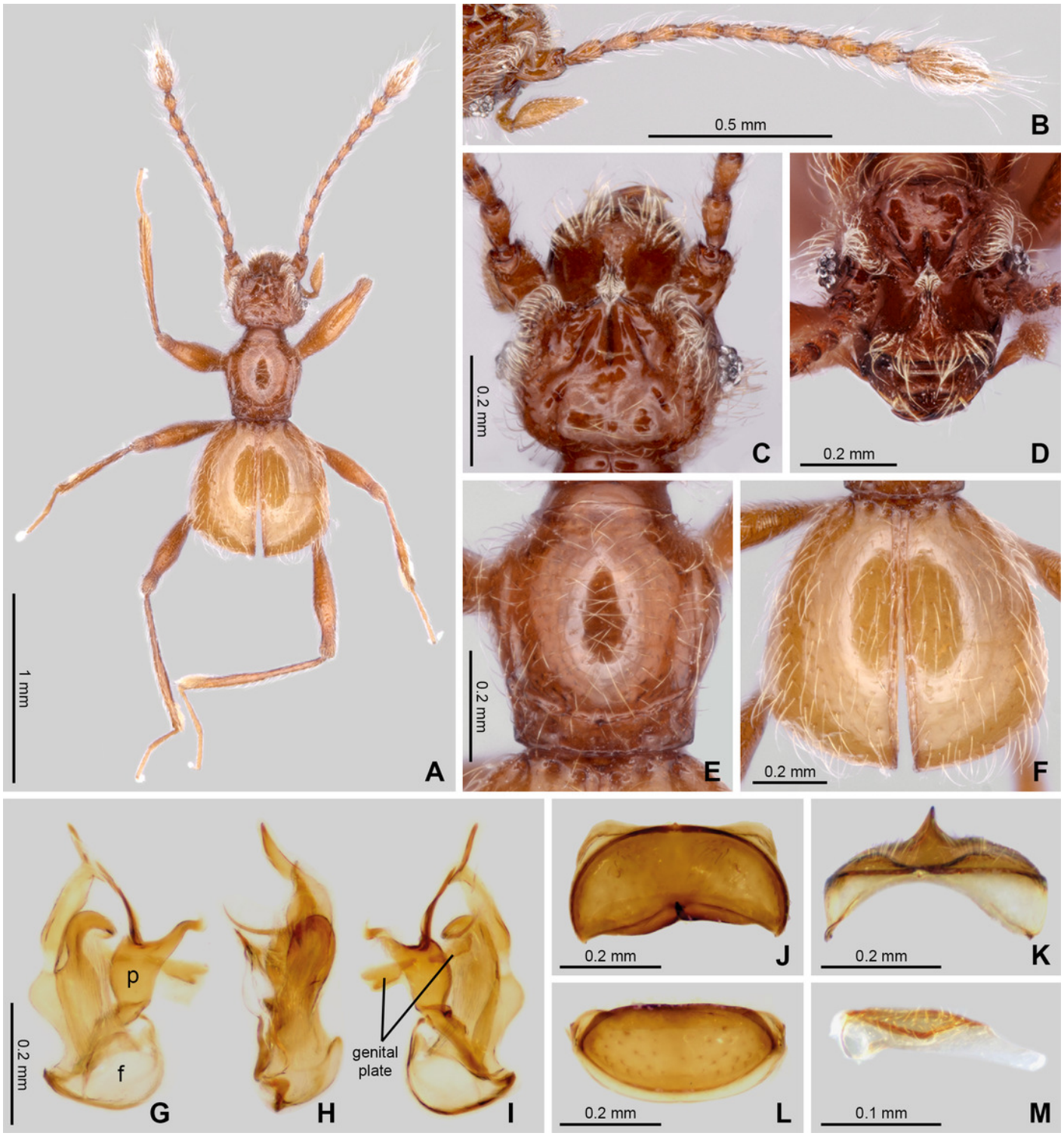
B
0.2 mm
C
0.2 mm
D
0.2 mm
E
0.2 mm
F
genital plate
p
f
basoventral projection
0.2 mm
G
H
I
0.2 mm
J
0.2 mm
K
0.2 mm
L
0.1 mm
M

Figure 4

Habitus and diagnostic characters of holotype male *Syrbatus superciliata* Asenjo & Valois sp. nov. (ISLA-110317).

Habitus, dorsal view (A); antenna (B); head dorsal view (C); head frontal-dorsal view (D); pronotum (E); elytra (F); aedeagus (G-I); sternum VIII (J); sternum VIII (K-L); sternite IX (M). f: foramen, p: paramere.


1 mm
A
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D
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E
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F
p
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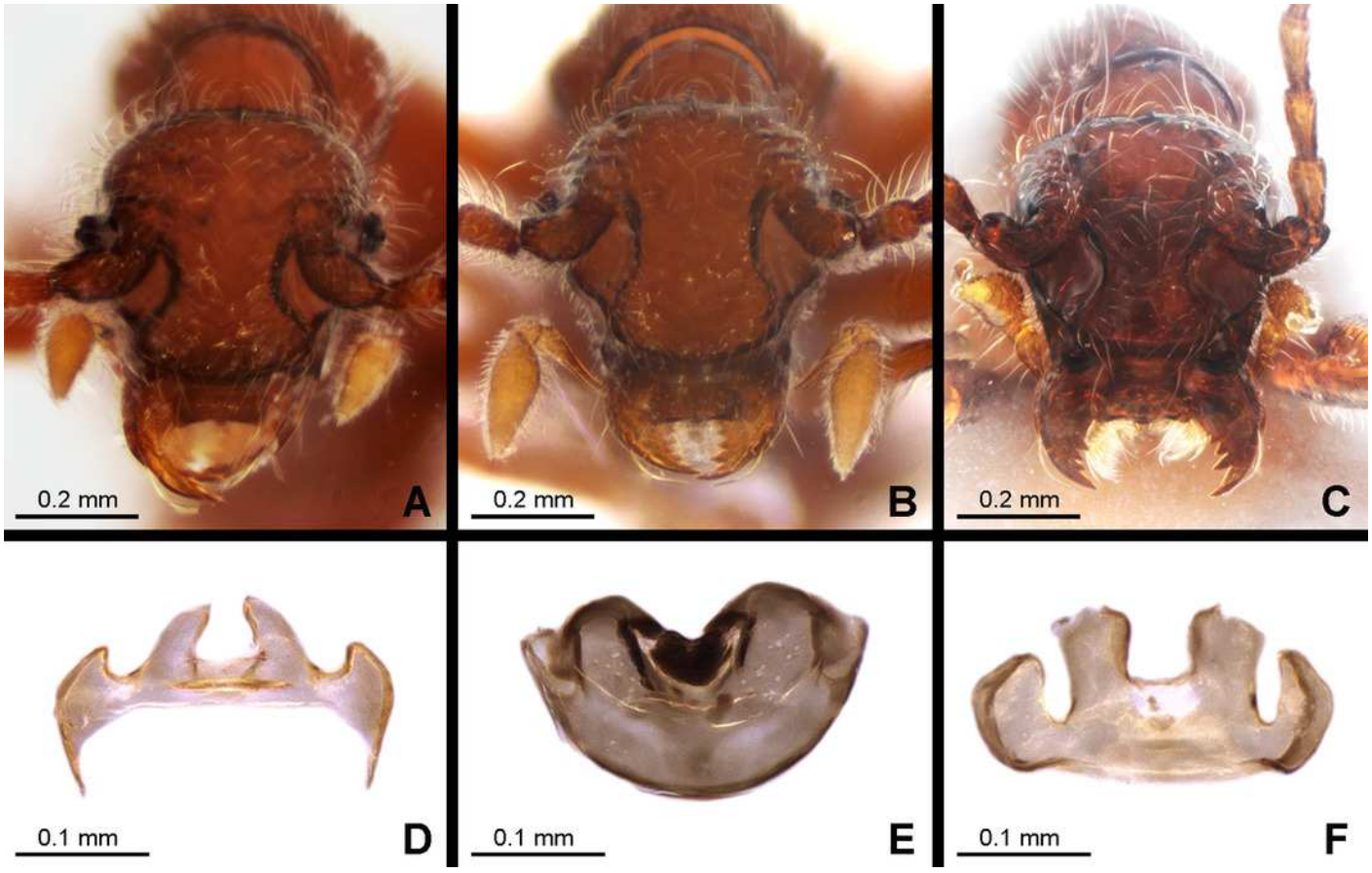
0.2 mm
G
H
genital plate
I
0.2 mm
J
0.2 mm
K
0.2 mm
L
0.1 mm
M

Figure 5

Morphology of the female of the three new species of *Syrbatus*.

Frontal-dorsal view of the head (A; ISLA-110320) and genital complex (MPEG-01052551) (D) of *Syrbatus moustache* Asenjo & Valois **sp. nov.**; frontal-dorsal view of the head (B; MPEG-01052554) and genital complex (E; MPEG-01052554) (F) of *Syrbatus obsidian* Asenjo & Valois **sp. nov.**; and frontal-dorsal view of the head (C; MPEG-01052549) and genital complex (F; ISLA-110318) of *Syrbatus superciliata* Asenjo & Valois **sp. nov.**



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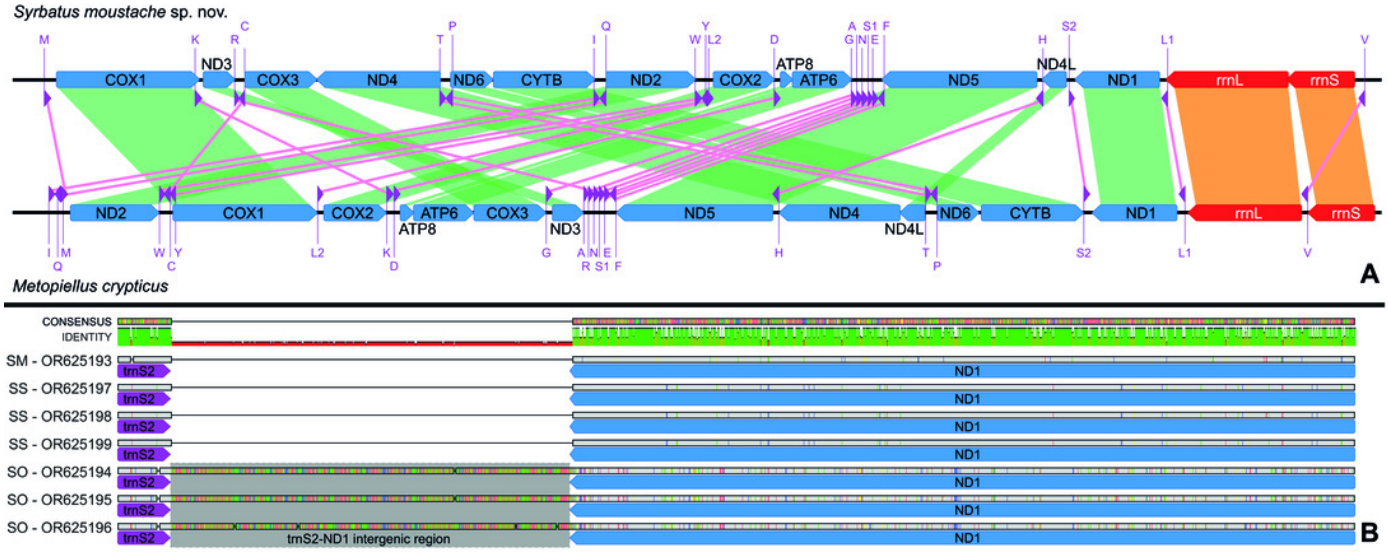
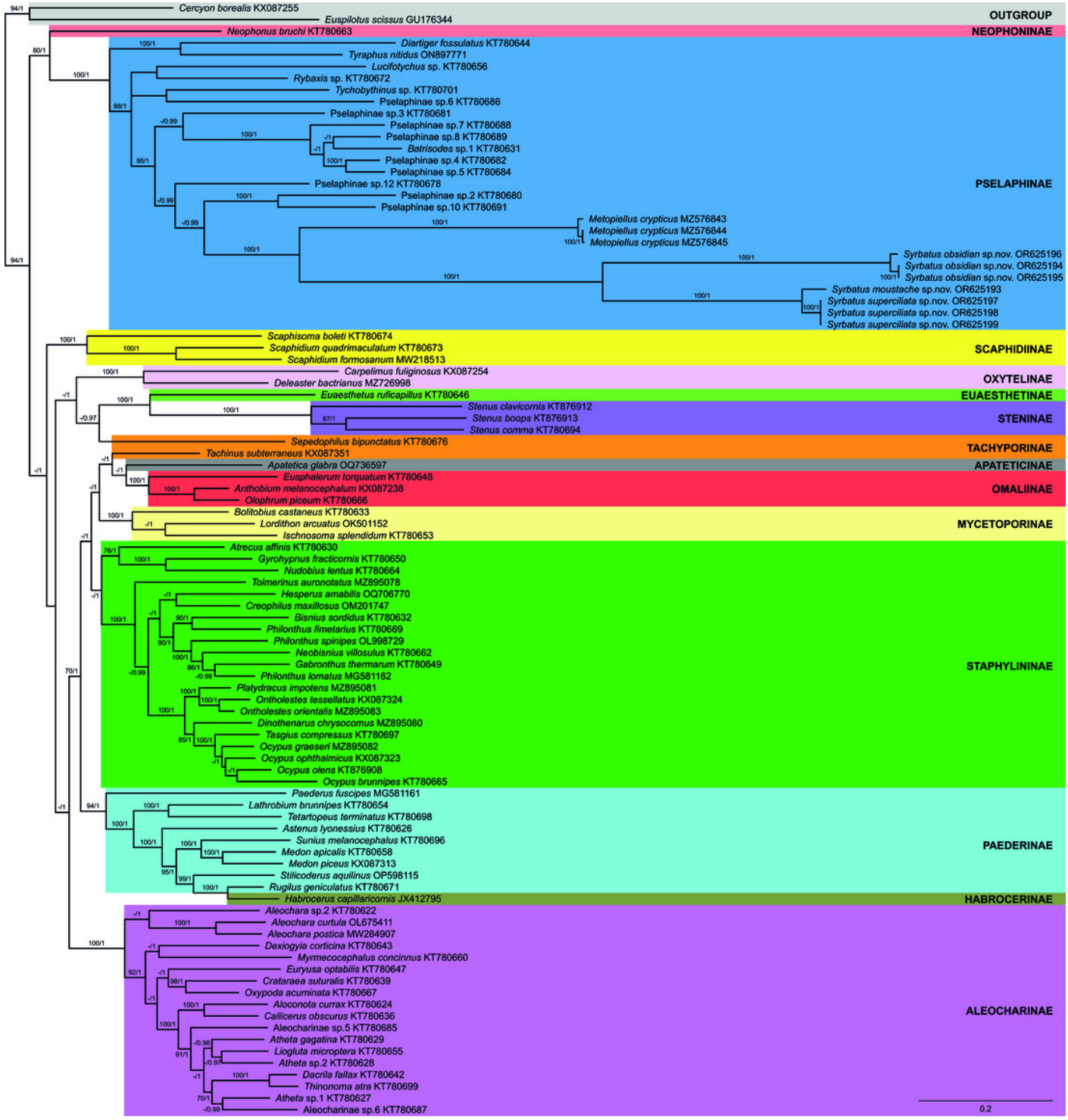


Figure 7

Phylogenetic placement of the three new species of *Syrbatus* within Staphylinidae, based on whole mitogenome data.

Majority-rule consensus phylogram of the Bayesian inference analysis evidencing the phylogenetic relationships among Staphylinidae species with available mitogenomes in the GenBank database and the three specimens of *Syrbatus moustache* Asenjo & Valois **sp. nov.**, *Syrbatus obsidian* Asenjo & Valois **sp. nov.** and *Syrbatus superciliata* Asenjo & Valois **sp. nov.**, indicating their respective GenBank accessions and subfamily affiliations. Statistical support values (BS ≥ 70 and PP ≥ 0.90) are indicated near the branches.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Euspilotus scissus GU176344
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NEOPHONINAE
Diartiger fossulatus KT780644
Tyraphus nitidus ON897771
Lucifotychus sp. KT780656
Rybaxis sp. KT780672
Tychobythinus sp. KT780701
Pselaphinae sp.6 KT780686
Pselaphinae sp.3 KT780681
Pselaphinae sp.7 KT780688
Pselaphinae sp.8 KT780689
Batrisodes sp.1 KT780631
Pselaphinae sp.4 KT780682
Pselaphinae sp.5 KT780684
Pselaphinae sp.12 KT780678
Pselaphinae sp.2 KT780680
Pselaphinae sp.10 KT780691
Metopiellus crypticus MZ576843
Metopiellus crypticus MZ576844
Metopiellus crypticus MZ576845
Syrbatus obsidian sp.nov. OR625196
Syrbatus obsidian sp.nov. OR625194
Syrbatus obsidian sp.nov. OR625195
Syrbatus moustache sp.nov. OR625193
Syrbatus superciliata sp.nov. OR625197
Syrbatus superciliata sp.nov. OR625198
Syrbatus superciliata sp.nov. OR625199
PSELAPHINAE
Scaphisoma boleti KT780674
Scaphidium quadrimaculatum KT780673
Scaphidium formosanum MW218513
SCAPHIDIINAE
Carpelimus fuliginosus KX087254
Deleaster bactrianus MZ726998
OXYTELINAE
Euaesthetus ruficapillus KT780646
EUAESTHETINAE
Stenus clavicornis KT876912
Stenus boops KT876913
Stenus comma KT780694
STENINAE
Sepedophilus bipunctatus KT780676
Tachinus subterraneus KX087351
TACHYPORINAE
Apatetica glabra OQ736597
APATETICINAE
Eusphalerum torquatum KT780648
Anthobium melanocephalum KX087238
Olophrum piceum KT780666
OMALIINAE
Bolitobius castaneus KT780633
Lordithon arcuatus OK501152
Ischnosoma splendidum KT780653
MYCETOPORINAE
Atrecus affinis KT780630
Gyrohypnus fracticornis KT780650
Nudobius lentus KT780664
Tolmerinus auronotatus MZ895078
Hesperus amabilis OQ706770
Creophilus maxillosus OM201747
Bisnius sordidus KT780632
Philonthus fimetarius KT780669
Philonthus spinipes OL998729
Neobisnius villosulus KT780662
Gabronthus thermarum KT780649
Philonthus lomatus MG581162
Platydracus impotens MZ895081
Ontholestes tessellatus KX087324
Ontholestes orientalis MZ895083
Dinothenarus chrysocomus MZ895080
Tasgius compressus KT780697
Ocypus graeseri MZ895082
Ocypus ophthalmicus KX087323
Ocypus olens KT876908
Ocypus brunnipes KT780665
STAPHYLININAE
Paederus fuscipes MG581161
Lathrobium brunnipes KT780654
Tetartopeus terminatus KT780698
Astenus lyonessius KT780626
Sunius melanocephalus KT780696
Medon apicalis KT780658
Medon piceus KX087313
Stilicoderus aquilinus OP598115
Rugilus geniculatus KT780671
PAEDERINAE
Habrocerus capillaricornis JX412795
HABROCERINAE
Aleochara sp.2 KT780622
Aleochara curtula OL675411
Aleochara postica MW284907
Dexiogyia corticina KT780643
Myrmecocephalus concinnus KT780660
Euryusa optabilis KT780647
Crataraea suturalis KT780639
Oxypoda acuminata KT780667
Aloconota currax KT780624
Callicerus obscurus KT780636
Aleocharinae sp.5 KT780685
Atheta gagatina KT780629
Liogluta microptera KT780655
Atheta sp.2 KT780628
Dacrila fallax KT780642
Thinonoma atra KT780699
Atheta sp.1 KT780627
Aleocharinae sp.6 KT780687
ALEOCHARINAE
0.2

Table 1(on next page)

General features of the mitochondrial genes of *Syrbatus moustache* Asenjo & Valois sp. nov., *Syrbatus obsidian* Asenjo & Valois sp. nov. and *Syrbatus superciliata* Asenjo & Valois sp. nov.

Sequenced mitogenomes of *Syrbatus moustache* Asenjo & Valois **sp. nov.** (Sm – OR625193), *Syrbatus obsidian* Asenjo & Valois **sp. nov.** (So – OR625194, OR625195 and OR625196) and *Syrbatus superciliata* Asenjo & Valois **sp. nov.** (Ss– OR625197, OR625198 and OR625199), indicating the size of the transcription regions, presence of indel events, number of intraspecific mismatches after the alignment of the mitogenomes, coding strand, and sequences of both start and stop codons. [a]Whenever any of the accessions presented incomplete or missing genes in the mitogenome assembly, we showed the data for those with a complete sequence; also, in the cases with intraspecific variation in the gene sizes, we presented the data of the largest one; [b]the rrnL, rrnS and trnV genes were either incomplete or missing in the three mitogenomes assembled for *Syrbatus obsidian* Asenjo & Valois **sp. nov.**

Table 1: General features of the mitochondrial genes of *Syrbatus moustache* Asenjo & Valois sp. nov., *Syrbatus obsidian* Asenjo & Valois sp. nov. and *Syrbatus superciliata* Asenjo & Valois sp. nov.

Gene	Size (bp)[a] (Sm/So/Ss)	Indels (Sm/So/Ss)	Mismatches (Sm/So/Ss)	% Mismatches (Sm/So/Ss)	Coding strand	Start codon	Stop codon
ATP6	653/638/653	NA/0/0	NA/15/1	NA/2.35/0.15	L	ATA	TA
ATP8	138/150/135[b]	NA/0/6	NA/3/0	NA/2.00/0.00	L	ATC	TAA
COX1	1566/1533/1566	NA/0/0	NA/26/0	NA/1.70/0.00	L	ATT/TTA/ATT	TAA
COX2	672/687/672	NA/0/0	NA/9/0	NA/1.31/0.00	L	ATA	TAA
COX3	792/783/792	NA/0/0	NA/24/3	NA/3.07/0.38	L	ATA/ATT/ATA	TAA/TAG/TAA
CYTB	1116/1077/1126	NA/0/0	NA/29/1	NA/2.69/0.09	L	ATG	TAA/TAA/T
ND1	927/927/927	NA/0/NA	NA/22/1	NA/2.37/0.11	H	ATT/ATA/ATT	TAA
ND2	975/978/975	NA/0/0	NA/20/0	NA/2.04/0.00	L	ATT	TAA
ND3	351/351/348	NA/0/0	NA/4/0	NA/1.14/0.00	L	ATT/ATT/ATA	TAA
ND4	1353/1314/1347	NA/0/0	NA/25/0	NA/1.90/0.00	H	ATG	TAA
ND4L	256/262/256	NA/0/0	NA/4/0	NA/1.45/0.00	H	ATA	T
ND5	1695/1710/1695	NA/0/0	NA/36/2	NA/2.11/0.12	H	ATT	TAA
ND6	465/468/465	NA/0/0	NA/9/0	NA/1.92/0.00	L	ATT	TAA
rrnL	1340/NA[b]/1336	NA/NA/2	NA/NA/1	NA/NA/0.00	H	NA	NA
rrnS	747/NA[b]/764	NA/NA/0	NA/NA/0	NA/NA/0.00	H	NA	NA
trnA (tgc)	63/70/63	NA/0/0	NA/3/0	NA/4.29/0.00	L	NA	NA
trnC (gca)	61/62/61	NA/0/0	NA/1/0	NA/1.61/0.00	H	NA	NA
trnD (gtc)	64/63/62	NA/0/0	NA/0/0	NA/0.00/0.00	L	NA	NA
trnE (ttc)	63/63/61	NA/0/0	NA/0/0	NA/0.00/0.00	L	NA	NA
trnF (gaa)	61/60/61	NA/0/0	NA/0/0	NA/0.00/0.00	H	NA	NA
trnG (tcc)	60/60/60	NA/0/0	NA/0/0	NA/0.00/0.00	L	NA	NA
trnH (gtg)	70/63/72	NA/0/0	NA/1/0	NA/1.59/0.00	H	NA	NA
trnI (gat)	61/62/63	NA/0/0	NA/1/0	NA/1.61/0.00	L	NA	NA
trnK (ctt)	71/70/71	NA/0/0	NA/0/0	NA/0.00/0.00	L	NA	NA
trnL1 (tag)	62/67/62	NA/4/0	NA/1/0	NA/1.49/0.00	H	NA	NA

trnL2 (taa)	64/63/64	NA/0/0	NA/0/0	NA/0.00/0.00	L	NA	NA
trnM (cat)	68/69/NA	NA/0/NA	NA/1/NA	NA/1.45/NA	L	NA	NA
trnN (gtt)	64/66/63	NA/0/0	NA/0/0	NA/0.00/0.00	L	NA	NA
trnP (tgg)	70/67/70	NA/0/0	NA/3/0	NA/4.48/0.00	H	NA	NA
trnQ (ttg)	66/68/66	NA/0/0	NA/1/0	NA/1.47/0.00	H	NA	NA
trnR (tcg)	53/57/54	NA/1/0	NA/2/0	NA/3.51/0.00	L	NA	NA
trnS1 (tct)	52/54/52	NA/0/0	NA/0/0	NA/0.00/0.00	L	NA	NA
trnS2 (tga)	61/61/62	NA/0/0	NA/0/0	NA/0.00/0.00	L	NA	NA
trnT (tgt)	63/61/63	NA/0/0	NA/1/0	NA/1.64/0.00	L	NA	NA
trnV (tac)	62/NA[b]/63	NA/NA/NA	NA/NA/NA	NA/NA/NA	H	NA	NA
trnW (tca)	68/67/72	NA/0/2	NA/1/0	NA/1.49/0.00	L	NA	NA
trnY (gta)	61/64/61	NA/0/0	NA/1/0	NA/1.56/0.00	H	NA	NA

Sequenced mitogenomes of *Syrbatus moustache* Asenjo & Valois **sp. nov.** (Sm – OR625193), *Syrbatus obsidian* Asenjo & Valois **sp. nov.** (So – OR625194, OR625195 and OR625196) and *Syrbatus superciliata* Asenjo & Valois **sp. nov.** (Ss– OR625197, OR625198 and OR625199), indicating the size of the transcription regions, presence of indel events, number of intraspecific mismatches after the alignment of the mitogenomes, coding strand, and sequences of both start and stop codons. [a]Whenever any of the accessions presented incomplete or missing genes in the mitogenome assembly, we showed the data for those with a complete sequence; also, in the cases with intraspecific variation in the gene sizes, we presented the data of the largest one; [b]the rrnL, rrnS and trnV genes were either incomplete or missing in the three mitogenomes assembled for *Syrbatus obsidian* Asenjo & Valois **sp. nov.**