



A new species of *Apecholinus* Bernhauer, 1933 (Coleoptera: Staphylinidae: Staphylininae) from Mangshan, China

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Abstract

A new species, *Apecholinus speciosus* Sun & Liu, **sp. nov.** collected from Mangshan, Hunan Province, China, is described. Illustrations of taxonomically important characters and photographs of the habitus are provided. The new species is compared to *Apecholinus imitator* Smetana & Hu, 2019. The complete mitochondrial genome of *A. speciosus* was sequenced, assembled, and annotated. Phylogenetic analysis based on mitochondrial genomes showed that two *Apecholinus* species form a clade sister to *Ocypus* and *Dinothenarus*, and they all belong to the *Ocypus* lineage.

Key words: Staphylininae, *Apecholinus*, new species, aedeagus, Hunan, Mangshan, mitochondrial genome

Introduction

The genus *Apecholinus* Bernhauer, a member of the subtribe Staphylinina, was erected by Bernhauer (1933) with *Apecholinus kaiseri* Bernhauer, 1933 as the type species fixed by monotypy. Smetana & Davies (2000) synonymized the monobasic genus *Apecholinus* with *Agelosus* Sharp, 1889, but subsequently Smetana (2003) reinstated *Apecholinus* as a separate genus. Smetana (2018) reviewed *Apecholinus*, and transferred *Ocypus fraternus* Fairmaire, 1891, *Agelosus ohkurai* Hayashi, 1973, *Ocypus aglaosemanticus* He & Zhou, 2017, *Ocypus liui* He & Zhou, 2017 and *Ocypus pterosemanticus* He & Zhou, 2017 to *Apecholinus*, and placed *Agelosus ohkurai* and *Agelosus pterosemanticus*, *Agelosus chinensis* in synonymy with *Apecholinus fraternus*. The revised generic concepts were particularly based on the entirely differently developed mandibles. Smetana & Hu (2019) reviewed the species of *Apecholinus* from Taiwan, China. Senda & Han (2023) provided a key to the species of *Apecholinus*. So far, seven *Apecholinus* species have been described and the genus only occurs in East Asia. Of these, six species are known to occur in the Chinese mainland and Taiwan, and only one species is from North Korea (Smetana 2018; Smetana & Hu 2019; Senda & Han 2023). They are *Apecholinus aglaosemanticus* (He & Zhou, 2017) (China: Fujian, Yunnan), *A. canifer* Smetana & Hu, 2019 (China: Taiwan), *A. fraternus* (Fairmaire, 1891) (China: Guangxi, Guizhou, Henan, Hubei, Hunan, Liaoning, Shaanxi, Sichuan, Yunnan, Taiwan), *A. imitator* Smetana & Hu, 2019 (China: Taiwan), *A. kaiseri* Bernhauer, 1933 (China: Chongqing, Sichuan), *A. liui* (He & Zhou, 2017) (China: Yunnan), and *A. septentrionalis* Senda & Han, 2023 (North Korea).

Apecholinus is recognized by mandibles each bearing one simple tooth at the medial edge, subdental mandibular indentation absent; last segment of maxillary palpi short, dilated anteriorly, broadly truncate apically, asetose; last segment of labial palpi dilated anteriorly, broadly truncate apically, setose (Smetana 2018). The characters of the genitalia are necessary for species level identification of *Apecholinus*. Recently, the first author examined specimens collected in Mangshan, Hunan Province, China. After close examination, one *Apecholinus* specimen turned out

to belong to a new species, which is described below. Mangshan, the north foot of Nanling Mountains, has a lush forest, vast territory, and rich resources to provide a superior place for animals to multiply, live, and flourish. It has the reputation of ‘the largest biological gene bank’ in Hunan Province. The discovery of the new species provides a glimpse into the rich biodiversity of Mangshan.

Material and methods

The type material is deposited in the Insect Collection of College of Plant Protection, Southwest University, Chongqing, China (SWU). For detailed examination, specimens were relaxed in water prior to dissection. Dissected body parts were cleared in aqueous 0.1 N solution of potassium hydroxide, dehydrated in xylene, and steeped in glycerin on acetate slides. Illustrations of the sternites, tergites, aedeagus, and habitus were taken using a digital microscope (Leica M205 A). All images were modified and grouped in Adobe PHOTOSHOP CC (64 Bit).

DNA was obtained from the specimen’s thorax muscle by TIANamp Micro DNA Kit, constructed DNA-library at Beijing Genomics institution, and did Genome Re-sequencing on the DNBSEQ sequencing platform. Finally, the genomic DNA of *A. speciosus* sp. nov. and *A. liui* were obtained. The complete mitochondrial genome was assembled with MITOFINDER v.1.4.1 (Allio *et al.* 2020) with *Ocypus olens* (KT876908) as the reference. The genes of tRNA were predicted with MITOS WEBSEVER (Bernt *et al.* 2013) and acquired a similar mitochondrial genome sequence by blasting in NCBI. The mitochondrial genome was annotated with GENEIOUS PRIME v.2022.0.1 (Kearse *et al.* 2012), according to protein-coding genes and rRNA genes of similar sequence and predictive tRNA genes. And the protein-coding genes were verified with EDITSEQ. The mitochondrial genomes for twelve taxa were downloaded from GenBank (eight other Staphylinina and four Philonthina as outgroup). Phylogenetic analysis was conducted using Maximum likelihood (ML). The following steps were performed in PHYLOSUITE v.1.2.3 (Zhang *et al.* 2020). All genes were extracted, aligned, and trimmed with MAFFT and Gblocks (Talavera *et al.* 2007; Katoh & Standley 2013). The protein-coding genes were optimized with MACSE (Ranwez *et al.* 2011), after MAFFT. The dataset was partitioned by gene and the protein-coding genes were partitioned by codon position. Models were selected using MODELFINDER (Kalyaanamoorthy *et al.* 2017). The processed dataset was analyzed using IQTREE 1.6.12 (Nguyen *et al.* 2015).

Abbreviations for morphological measurements used in this paper are as follows:

BL body length (from the apex of the labrum to the apex of the abdomen);

FL forebody length (combined length of head, pronotum, and elytra);

HL greatest length of head (measured from the frontal margin of head to the posterior angle of head, labrum, and mouthparts not included);

HW greatest width of head, including eyes;

PL greatest length of pronotum;

PW greatest width of pronotum;

EL greatest length of elytra (from the humeral angle to the most distal margin of elytra);

EW greatest width of both elytra.

Taxonomy

Apecholinus speciosus Sun & Liu, sp. nov.

Chinese common name: 炫丽背眼隐翅虫

(Fig. 1: A–J)

Type material. HOLOTYPE: CHINA: ♂, labeled ‘CHINA: Hunan Prov., Chenzhou City (郴州市), Yizhang County (宜章县), Mangshan (莽山), VI.3.2019, leg. Jianyue Qiu’, in SWU.

Description. *Male.* Habitus as in Fig. 1A, B. BL 19.05 mm; FL 10.75 mm; HL 3.70 mm; HW 3.90 mm; PL 3.57 mm; PW 3.85 mm; EL 4.00 mm; EW 4.33 mm.

Body black, slightly shining; body pubescence black to brown, each elytron with more or less triangular patch of luminous golden-yellow tomentose pubescence below humerus; and abdominal tergites 6 and 7 each with two almost separated patches comprised of golden-yellow tomentose pubescence; maxillary and labial palpi reddish brown;

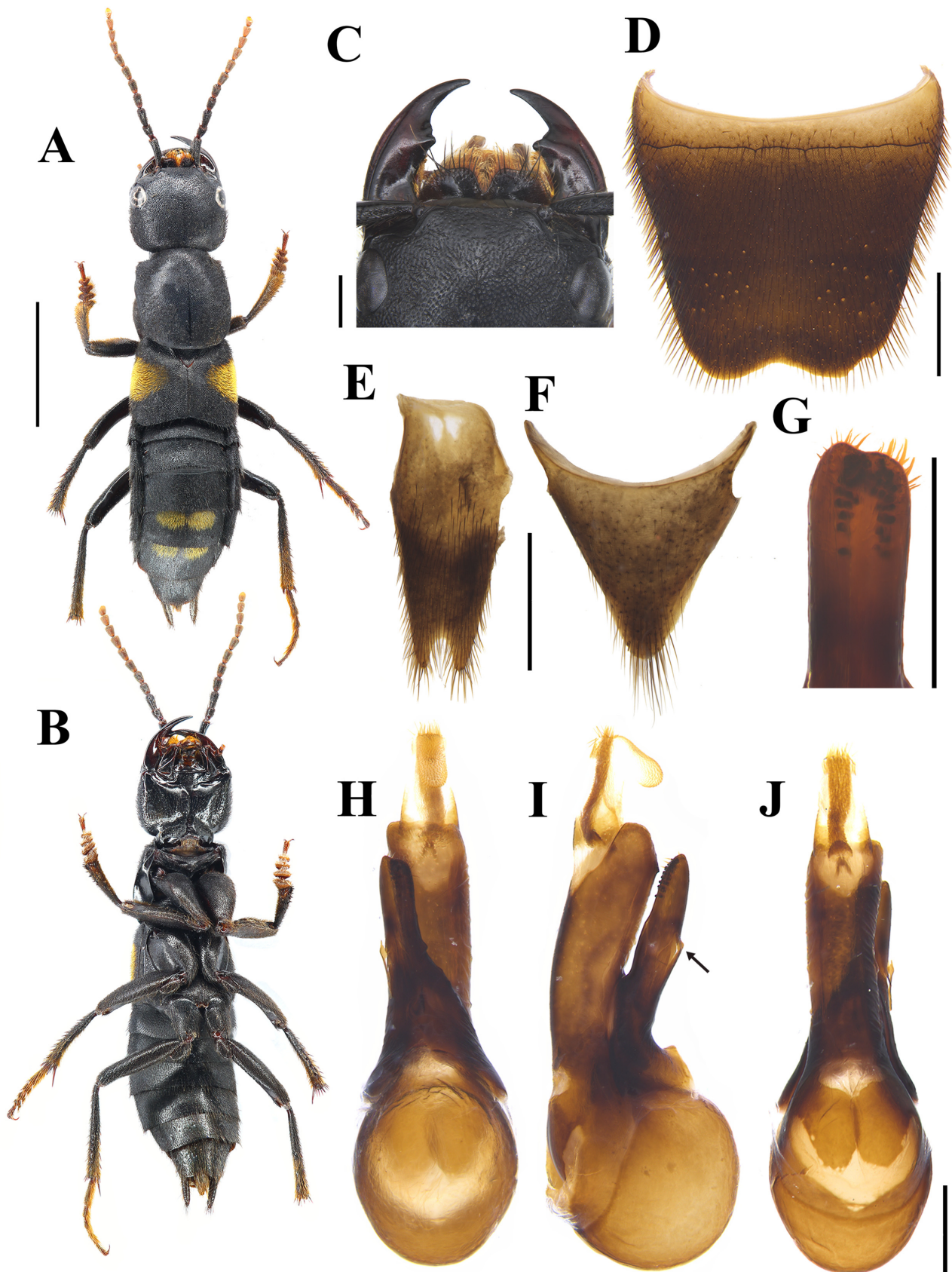


FIGURE 1. Habitus and diagnostic characters of male *Apecholinus speciosus* sp. nov. **A.** Dorsal habitus. **B.** Ventral habitus. **C.** Mandible. **D.** Sternite 8. **E.** Sternite 9. **F.** Tergite 10. **G.** Underside of the apical portion of paramere. **H.** Aedeagus in ventral view. **I.** Aedeagus in lateral view. **J.** Aedeagus in dorsal view. Scale bars: 5 mm in A–B; 1 mm in C–F; 0.5 mm in G–J. The black arrow indicates the partial damage in the middle of the paramere.

antennae with three basal segments reddish black, following segments gradually becoming paler, 8–11 segments yellowish brown; legs piceous to piceous black, with tarsi paler brown, tarsi and proximal tibiae covered with yellowish brown pubescence.

Head (Fig. 1 A–C) rounded quadrangular, with rounded posterior angles, slightly wider than long; eyes small, moderately convex, slightly shifted dorsad, tempora much longer than length of eyes seen from above (ratio 1.76); disc of head finely and densely punctate; linear impunctate midline apparent; interspaces between punctures without microsculpture. Antenna moderately long, hardly thickened toward the apex, segment 3 longer than segment 2, segments 4–10 longer than wide, gradually becoming shorter, segment 11 small, asymmetrically emarginated, along lateral margin longer than penultimate segment.

Pronotum (Fig. 1 A) sub-scutellate, slightly wider than long (ratio 1.07), moderately convex, moderately narrowed anteriorly; narrow marginal groove disappearing downwards at about anterior third of pronotal length; punctation on disc slightly finer than that on disc of the head, interspaces between punctures without microsculpture; impunctate midline distinct. Scutellum densely punctate-setose, with granulose microsculpture.

Elytra (Fig. 1 A) short, vaguely dilated posteriorly, at suture shorter than pronotum at midline (ratio 0.55), at sides shorter than pronotum at midline; punctation very fine and very dense, interspaces between punctures with fine microscopic irregularities.

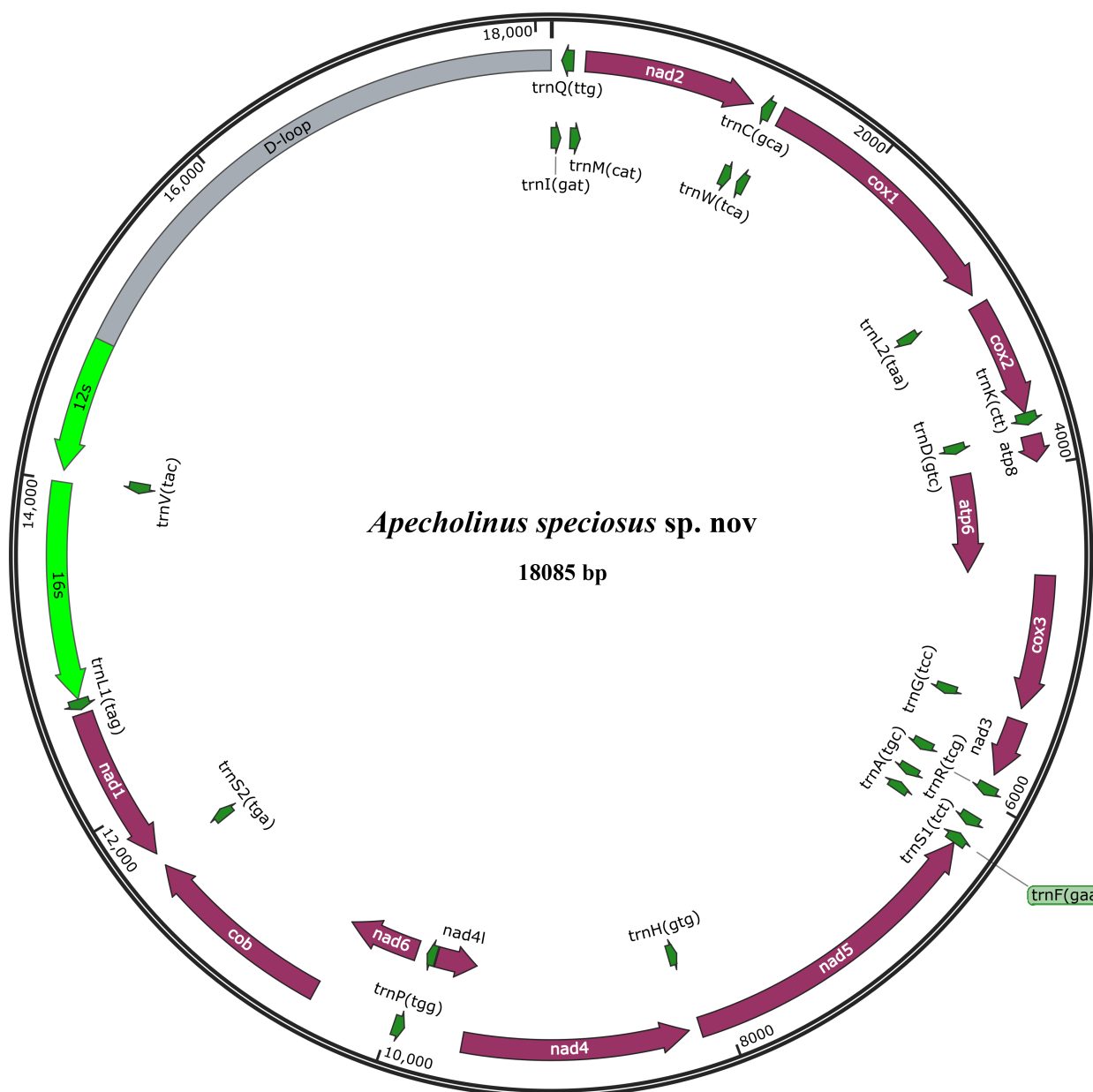


FIGURE. 2 The complete mitochondrial genome of *Apecholinus speciosus* sp. nov.

Abdomen (Fig. 1 A, B) with the fifth visible tergite without pale apical seam of palisade setae; tergite 2 (in front of first fully visible tergite) moderately densely punctate-setose, surface with extremely fine, superficial microsculpture of mostly oblique striae; punctuation of all tergites finer and denser than that on elytra, punctuation becoming gradually somewhat sparser toward apex of abdomen, interspaces with extremely fine, granulose microsculpture.

Sternite 8 (Fig. 1 D) with shallow, obtuse medioapical emargination. Sternite 9 (Fig. 1 E) with minute, narrow basal portion, apical portion with deep and wide medioapical U-shaped emargination. Tergite 10 (Fig. 1 F) narrow, markedly, and evenly narrowed toward narrowly arcuate apex, apical portion with moderately long setae at apex, rest of tergite moderately densely setose.

Aedeagus (Fig. 1 G–J) distinctly sclerotized; median lobe almost parallel-sided, apex subtruncate, slightly asymmetrical, left side extending a bit further distad than right side in ventral view; paramere (partially broken at the middle in holotype) situated on median lobe quite asymmetrically toward left margin of median lobe, with obliquely sinuate apex, the left apparently higher than the right from ventral view, markedly not reaching apex of median lobe; with several unequally short apical setae (>20); underside with numerous, closely set sensory peg setae (>30) arranged in two rows, merged apically.

Female. Unknown.

Comparison. The new species is very similar to *A. imitator* Smetana & Hu, 2019 in general appearance. They share a more or less triangular patch of golden-yellow tomentose pubescence behind the humerus on each elytron and basal patches of golden-yellow tomentose pubescence on abdominal tergites 6 and 7. However, the new species has two almost separated patches on tergites 6 and 7 respectively; the latter has one basal continuous big spot. They have obviously different aedeagus structures, with the peg setae in a different pattern and differently shaped apices of the paramere and median lobe.

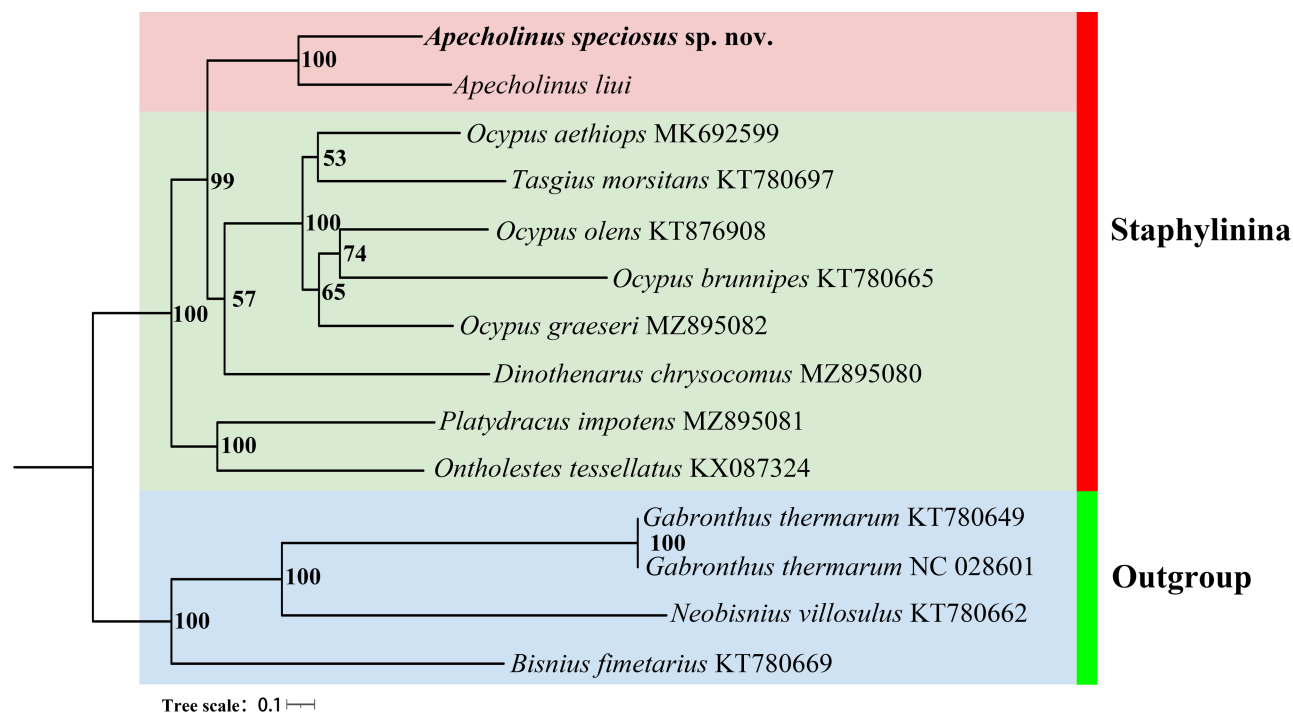


FIGURE. 3 Maximum likelihood (ML) tree derived from analysis of mitochondrial genome. Bootstrap values are shown above branches.

Until now, most members of *Apecholinus* have uniform, dark body pubescence, without any patches of tomentose pubescence of different colors. While the new species from Hunan and *A. imitator* from Taiwan have patches of golden-yellow tomentose pubescence, *A. canifer* from Taiwan has patches of grey tomentose pubescence on the body. The three species share tomentose pubescence with an almost similar pattern, markedly imitating numerous species of *Agelosus* with variably developed patches of tomentose pubescence (Smetana & Hu 2019). However, *A. canifer* and *A. imitator* have one basal continuous big spot on tergites 6 and 7 respectively, different from the new species. They can be separated by using the following key:

- 1 Body with patches of golden-yellow tomentose pubescence..... 2
 - Body with patches of grey tomentose pubescence..... *A. canifer* Smetana & Hu, 2019
 2 Abdominal tergites 6 and 7 with a single patch of golden-yellow tomentose pubescence; paramere with single apical patch of
 peg setae..... *A. imitator* Smetana & Hu, 2019
 - Abdominal tergites 6 and 7 with two patches of golden-yellow tomentose pubescence; paramere with two subparallel rows of
 peg setae, merged apically..... *A. speciosus* Sun & Liu, **sp. nov.**

Distribution and habitat. China (Hunan). Little is known about the collecting circumstances of the specimen.

Etymology. The specific name is derived from ‘*speciosus*’ (dazzling) in Latin.

Mitochondrial genome

The complete mitochondrial genome (Fig. 2) of *A. speciosus* is 18,085 bp in length, with 22 tRNA genes, 13 protein-coding genes (PCGs), two rRNA genes, and an AT-rich region. The genome is AT-rich (79.0%), the compositions of A, C, G, and T are 40.1%, 12.8%, 8.3%, and 38.9%, respectively. Gene overlaps are found in 21 locations, ranging from 1 to 9 bp in length, and the longest overlap occurs between *trnW* and *trnC*. Intergenic spacers are found in 7 locations, ranging from 3 to 68 bp in length, with the longest interval between *trnR* and *trnN*. For PCGs, they encode a total of 3749 amino acids, with ATN as start codons (ATG, ATA, ATT). Stop codons are TAA or TAG, except *cox1* and *cox2* with T as stop codons and *nad5* with TA as stop codons, respectively, which leaves out base A or AA. The lengths of 16S rRNA and 12S rRNA are 1,277 bp, and 784 bp, respectively.

The ML tree (Fig. 3) shows that the ten Staphylinina species form a clade. Two *Apecholinus* species form a clade. *Tasgius morsitans* (Rossi, 1790), *Dinothenarus chrysocomus* (Mannerheim, 1830), and *Ocypus* species form a clade, as the sister group of *Apecholinus*. *Platydracus impotens* (Eppelsheim, 1889) and *Ontholestes tessellatus* (Geoffroy, 1785) form a clade, as the sister group of the other Staphylinina species. *Tasgius morsitans* is embedded in the *Ocypus* clade, as in Hernando & Carmelo (2021), which form the sister group of *Dinothenarus chrysocomus*. In Brunke & Smetana (2019), the *Ocypus* lineage containing *Ocypus* and *Tasgius* was the sister group of the *Platydracus* lineage containing *Platydracus* and *Ontholestes*. Our results showed *Apecholinus* having a close relationship with *Ocypus* and *Dinothenarus* should belong to the *Ocypus* lineage. Our results support both the *Ocypus* and *Platydracus* lineages of Brunke & Smetana (2019) based on mitochondrial genome. Enrichment of mitochondrial genome data of the genus should be useful for future phylogenetic studies of Staphylinina.

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中国莽山背眼隐翅虫属*Apecholinus*一新种（鞘翅目：隐翅虫科：隐翅虫亚科）

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摘要: 记述中国湖南省莽山隐翅虫一新种, 炫丽背眼隐翅虫*Apecholinus speciosus* **sp. nov.**, 并提供整体和特征图。该新种与*Apecholinus imitator*拟凹颚背眼隐翅虫相区别。对新种的线粒体基因组进行了测序, 组装和注释。基于线粒体基因组的系统发育分析显示背眼隐翅虫属*Apecholinus*的两个种类形成一个分支, 与迅隐翅虫属*Ocybus*和叉叶隐翅虫属*Dinothenarus*形成姐妹群关系, 且共同属于迅隐翅虫属支系。

关键词: 隐翅虫亚科; 背眼隐翅虫属; 新种; 阳茎; 湖南; 莽山; 线粒体基因组