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RESEARCH PAPER

Stenocephus janseni sp. nov., a new species of stem-sawfly from Germany (Hymenoptera: Cephidae)

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Abstract. *Stenocephus janseni* sp. nov. (Hymenoptera: Cephidae) is described from Brandenburg, eastern Germany, known only from the female holotype. It possesses an unusual combination of "generic" morphological characters, which makes its placement in *Stenocephus* Shinohara, 1999 provisional. Compared to other *Stenocephus* species, differences in the morphology of the lancet are particularly striking. Genetic data for *S. janseni* sp. nov. place it unequivocally in the Hartigiini, but rather distantly from other genera of this tribe which have so far been sequenced. The three previously described *Stenocephus* species are recorded from the East Palaearctic. No genetic data are currently available for these. *Pachycephus nigratus* Dovnar-Zapolskij, 1931, comb. restit., is no longer treated as belonging to *Phylloecus* Newman, 1838, but as a member of the genus in which it was originally described.

Key words. Hymenoptera, Cephidae, Hartigiini, *Stenocephus*, *Pachycephus nigratus*, new species, DNA barcoding, Germany, Palaearctic Region

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Introduction

The larvae of Cephidae tunnel in the stems or twigs of their hosts. A few species are of major significance as pests of grain crops (Shanower & Hoelmer 2004). Smith & Schmidt (2009) provided a key to the three extant subfamilies of Cephidae: the Cephinae (Holarctic and Oriental), Athetocephinae (Afrotropical and Australasian), and Australcephinae (Australasian). The latter two subfamilies contain only three and one species respectively, whereas the Cephinae contains about 160 described species, mostly Palaearctic (Taeger et al. 2010). Suprageneric classification of the Cephinae currently remains as proposed by Benson (1946), i.e. divided into the three tribes Cephini, Hartigiini, and Pachycephini. The tribes, as far as the hosts of species are known, have different groups of larval host plants: Cephini feed on Poaceae (Taeger et al. 1998), Hartigiini on Rosaceae and various other families of woody dicots (Lacourt 2020, Macek et al. 2020), and Pachycephini on poppy (*Papaver*, Papaveraceae) (Scheibelreiter 1978), and perhaps also on Lamiaceae (Gussakovskij 1935: see under *Janus nigratus*) and Asteraceae (Zhelochovtsev 1968: see under *Characopygus* Konow, 1899).

Our main purpose here is to describe a new species of cephid, belonging to the Hartigiini, recently collected in eastern Germany. The specimen is morphologically highly distinctive, with an unusual combination of characters which does not fit current circumscriptions of the genera. Accordingly, before describing the new species, provisionally placed in the genus *Stenocephus* Shinohara, 1999, we discuss these characters, as far as they are relevant to its placement.

Material and methods

Morphology and systematics. The extensive adult material in the Senckenberg Deutsches Entomologisches Institut (DEI), Müncheberg, Germany, was used in comparative morphological studies. Most observations, and images, were made with an Olympus SZX12 microscope

and Leica DFC295 camera. The images presented here, except that of the antenna (a single image), are composites, derived from stacks of images taken sequentially (from top to bottom) at different focal planes. Helicon Focus was used to collate the stacks. The lancets of *Stenocephus janseni* sp. nov., now gummed with all other detached parts to cards pinned with the specimen, were photographed with a Leica DFC450 through an Olympus BX51.

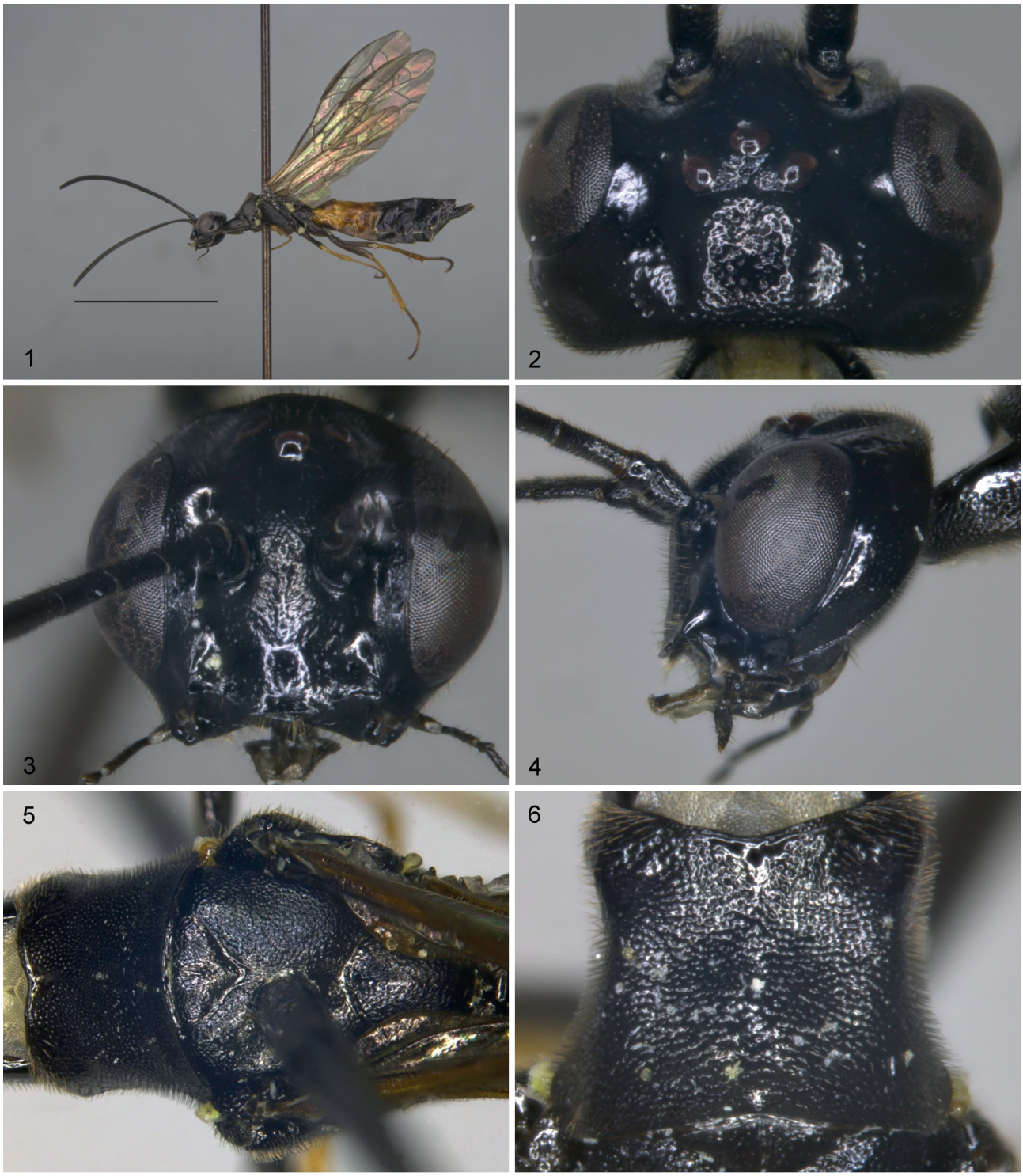
We have not included in the references the works in which taxa which we mention were first described, unless these publications are cited for other reasons. Such information can be found in Taeger et al. (2010).

Phylogenetic analyses. To assess the phylogenetic placement of *Stenocephus janseni* sp. nov. within the Cephidae, published as well as newly obtained mitochondrial and nuclear DNA sequences were used. DNA extraction, primers used, PCR protocols, and Sanger sequencing are described in Prous et al. (2019). Additionally, some of the amplicons were pooled and sequenced with the MinION R10.3 flow cell using a Ligation Sequencing Kit (SQK -LSK109) (Oxford Nanopore). Each amplicon sequenced with MinION was amplified using different combinations of tailed forward and reverse primers (variable 4–12 bp added to the 5'-end) to confirm the identity of the final consensus sequences. The raw sequencing signal from MinION was basecalled (translated into a DNA sequence) with Guppy v4.0.11 or 4.2.3 in high accuracy mode. Using available cephid sequences as query, corresponding single molecule Nanopore reads were identified with BLAST 2.9.0+ (https://www.ncbi.nlm.nih.gov/books/NBK279690/). A maximum of 3000 single reads were aligned with MAFFT v7.427 (Katoh & Standley 2013) and the trees were built with FastTree 2.1.11 (Price et al. 2010). Based on the resulting trees, separate clusters of reads were identified and subsequently used to create consensus sequences. All sequences, except nuclear sequences of two specimens (DEI-GISHym89964, DEI-GISHym86341), separated clearly at single read level. Based on 200 reads of each amplicon, MAFFT v7.427 + EMBOSS cons v6.6.0.0 and abPOA 1.0.4 (https://github.com/yangao07/abPOA) were used to create initial consensus sequences that were further polished with Medaka 1.0.1 (https://github.com/nanoporetech/medaka). Medaka variant calling was used to separate the very similar nuclear sequences of DEI-GISHym89964 and DEI-GISHym86341. A more detailed protocol and data analysis workflow will be published separately. For most specimens, one mitochondrial and two nuclear genes were sequenced. The mitochondrial gene used is partial (1078–1087 bp) cytochrome c oxidase subunit I (COI), amplified with forward primer SymF1 or SymF4 and reverse primer A2590 (see Prous et al. 2019). The amplified COI fragment covers the entire barcode region (658 bp). The two nuclear markers are fragments of sodium/potassium-transporting ATPase subunit alpha (NaK, 1654 bp; primers NaK_263F and NaK_1918R) and DNA dependent RNA polymerase II subunit RPB1 (POL2, 1771 or 2573–2577 bp; forward primer POL2_797F or POL2_104Fv2 and reverse primer POL2_2569R). The NaK fragment does not include any introns, but POL2 has one short intron (109–113 bp) that was excluded from phylogenetic analyses. When excluding the intron in POL2, algorithm-based alignment was not necessary due to the lack of insertions or deletions in the studied specimens (length differences were only due to the extent the gene regions were amplified and sequenced, and the alignment was manually adjusted accordingly). Some of the analyzed sequences were published previously by Malm & Nyman (2015) and Schmidt et al. (2017). COI sequences of some cephids were extracted from published mitochondrial genomes (see references and GenBank accessions in Aydemir & Korkmaz 2020). Nuclear sequences of *Cephus cinctus* Norton, 1872 were extracted from whole genome shotgun contigs in GenBank (accessions AMWH01001469 and AMWH01002735). Additionally, a few of the COI sequences were obtained from BOLD (http://www.boldsystems.org/). The newly obtained DNA sequences have been submitted to NCBI GenBank (accessions MW353980–MW353997). To concatenate separate gene alignments, we used R (R Core Team 2019) package *apex* (Jombart et al. 2017). Phylogenetic analyses using maximum likelihood (ML) were done with IQ-TREE 1.6.1 (http://www.iqtree.org/) (Nguyen et al. 2015). By default, IQ-TREE runs ModelFinder (Kalyaanamoorthy et al. 2017) to find the best-fit substitution model and then reconstructs the tree using the model selected according to Bayesian information criterion (BIC). The alignments were treated as a single partition to avoid over-parametrization of the small alignments and the rather similar sequences analyzed here. We complemented the default option of IQ-TREE with a SH-like approximate likelihood ratio (SH-aLRT) test (Guindon et al. 2010) and ultrafast bootstrap (Hoang et al. 2018) with 1000 replicates to estimate robustness of reconstructed splits. Ultrafast bootstrap support values above 95% are generally considered reliable (Hoang et al. 2018).

Results

Identity of *Pachycephus nigratus* Dovnar-Zapolskij, 1931, comb. restit.

Benson (1946) proposed that *Pachycephus nigratus* Dovnar-Zapolskij, 1931 belongs to *Hartigia* Schiødte, 1839 (= *Phylloecus* Newman, 1838: Liston & Prous 2014). Previously, the species had been transferred to *Janus* Stephens, 1829 by Gussakovskij (1935). Benson's opinion was followed by Taeger et al. (2010). However, the latter authors did not give due regard to Zhelochovtsev (1976), who had refuted Benson's placement and treated the species once more as a *Pachycephus*. We now accept Zhelochovtsev's decision, because his association of the previously unknown male is convincing, and its prolonged and in lateral view pre-apically constricted subgenital plate unequivocally places it in the Pachycephini. The placement of this species, which has two pre-apical metatibial spurs, is relevant to our generic placement of *Stenocephus janseni* sp. nov., because all known *Phylloecus* species have only one.



Figs 1–6. *Stenocephus janseni* sp. nov., holotype, female. 1 – lateral, scale bar 5 mm; 2 – head, dorsal; 3 – head, frontal; 4 – head, lateral; 5 – thorax, dorsal; 6 – pronotum, dorsal.

Morphological character states in Hartigiini

Shape of claw. Much use has been made of the form of the claw as a character for the separation of cephid genera, and even of the tribes Cephiini and Hartigiini (e.g. Benson 1946, Goulet 1992). In the West Palaearctic Hartigiini the strongly-developed, acutely-apexed basal lobe of *Janus* distinguishes it from *Phylloecus*, *Syrista* Konow, 1896 and *Caenocephus* Konow, 1896, in which the claw lacks a basal lobe, although it may be gently expanded towards the base. In the East Palaearctic and Oriental Regions, five other described genera have an acute basal lobe resembling that of *Janus*: *Jungicephus* Maa, 1949, *Magnitarsijanus* Wei, 2007, *Megajanus* Wei, 1999, *Stigmatijanus* Wei, 2007, and *Tibetajanus* Wei, 1996. Additional East Palaearctic and Oriental genera lacking a basal lobe are *Miscocephus* Wei, 1999, *Sinicephus* Maa, 1949, *Stenocephus* Shinohara, 1999 and *Urosyrista* Maa, 1944. *Stenocephus janseni* sp. nov. lacks a basal lobe, and the two teeth are not very close to-

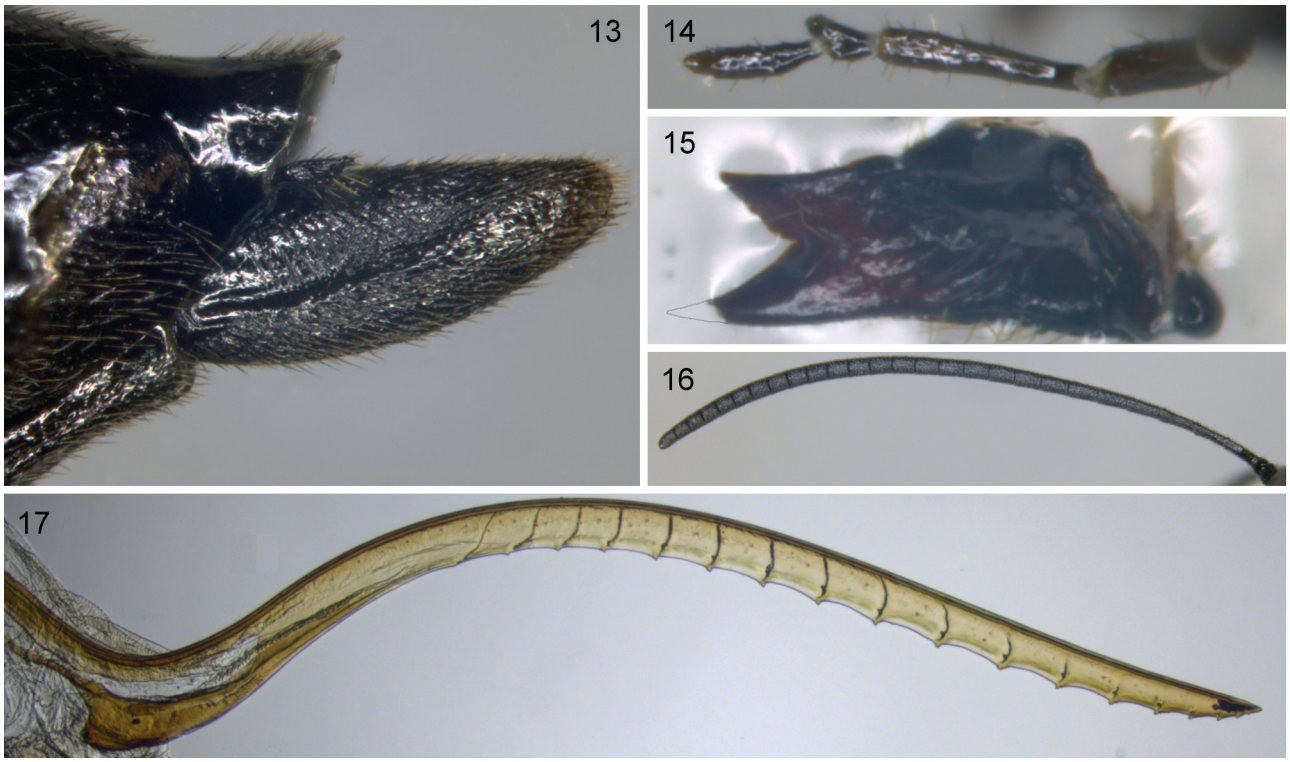
Figs 7–12. *Stenocephus janseni* sp. nov., holotype, female. 7 – anterior thorax, lateral; 8 – mesoscutellum, dorsal; 9 – metatibial claw; 10 – metatibial spurs; 11 – abdomen base, lateral; 12 – abdomen apex, dorsal.

gether, with the inner tooth markedly longer and wider than the outer one (Fig. 9). As regards the teeth, this is similar to *Phylloecus*, *Sinicephus*, and *Syrista*, whereas *Urosyrista* has approximately equally sized teeth (Smith 1999), and in previously known *Stenocephus* the inner tooth is shorter than the outer (Wei et al. 2015). The taxonomic review of *Syrista*, by Wei & Smith (2010), in which the claws of both sexes of two species are illustrated, reveals, however, that sexual dimorphism in claw shape, particularly the orientation, proportions and size of the outer tooth relative to the inner, can be greater than differences sometimes stated to be diagnostic of genera.

Shape of the left mandible. Nearly all authors since Benson (1946) have made use of this character. Benson (1946) and Shinohara (1999) provided illustrations of its form in various genera, and a figure for *Urosyrista* was given by Smith (1999). In *Stenocephus janseni* sp. nov. the outer (anterior) tooth is longer than the inner, and the inner tooth, of about the same basal width as the outer, has a simple outline (not conspicuously "shouldered" on anterior edge) (Fig. 15). In these characters, *S. janseni* sp. nov. resembles previously known species of *Stenocephus* more closely than species in other genera of Hartigiini.

Maxillary palps. According to Benson (1946), and our own observations, *Phylloecus* differs from other cephids in typically with palpomere 4 about as long as 6, as opposed to palpomere 4 about 1.5× length of 6. *Stenocephus janseni* sp. nov. has palpomere 4 about 1.5× length of 6 (Fig. 14).

Lancet. The lancet of *Stenocephus janseni* most closely resembles those of *Phylloecus* species (Smith 1986 [Nearctic species]; Palaearctic species examined by us), in having rather small, simple serrulae, and distinct annuli (Fig. 17). However, whereas *Phylloecus* have two ctenidial teeth per annulus, *S. janseni* sp. nov. has only one. The lancet of *Caenocephus lunulatus* (Strobl, 1895) is also similar, but the serrulae are much more prominent, and ctenidial



Figs 13–17. *Stenocephus janseni* sp. nov., holotype, female. 13 – valvula 3 and cerci, lateral; 14 – maxillary palp; 15 – left mandible [broken tip of external tooth outlined]; 16 – antenna; 17 – lancet.

teeth are absent (based on examination of the single known German specimen: Liston 2006). Other *Stenocephus* have numerous ctenidial teeth on the basal annuli, and some of the serrulae with a more complex outline (almost bifid) (Wei et al. 2015). *Syrista* have no ctenidial teeth, indistinct annuli, and at least the apical serrulae with a more complex outline (Wei & Smith 2010). *Miscocephus* has apparently no (or indistinct) ctenidial teeth, distinct annuli, and simple serrulae (Wei 1999). *Janus* have no ctenidial teeth, indistinct annuli, and serrulae sub-rectangular, almost bifid (Smith & Solomon 1989, Liu et al. 2017).

Number of pre-apical metatibial spurs. This has been used by several taxonomists as the prime distinction between some genera of Cephidae. Ries (1937) first pointed out that it is not always a stable character, although his findings relate mainly to the Cephiini. In the Hartigiini, Shinohara (1999) remarked on variability (1–2 spurs) in *Stenocephus*. On the other hand, the absence of a pre-apical spine in *Caenocephus*, and presence of only one in *Phylloecus*, has so far been observed to be constant. Benson (1946) stated that *Phylloecus* (as *Hartigia*) sometimes could have two, but this was based on his wrong placement of *Pachycephus nigratus* (see above). The holotype of *Stenocephus janseni* sp. nov. has two pre-apical spurs (Fig. 10), as in all other hartigiine genera, perhaps excepting only *Magnitarsijanus* (1) (but character state not known to us for *Tibetajanus*).

Body shape. *Phylloecus*, *Caenocephus* and *Janus* species are stockier than most other Hartigiini, this being most apparent in the shape of the abdomen, which is nearly cylindrical distal to tergum 2 in the former. In the others, including *Stenocephus janseni* sp. nov., the abdomen gradually widens distally from tergum 2 to about two thirds of the abdomen length (Fig. 1).

Cenchri and tegulae. Wei (1999) stated that the presence of cenchri and absence of [fore wing] tegulae distinguish *Miscocephus* from all other cephids. The presence of cenchri would be remarkable in the Cephidae, in which their absence is generally regarded as an autapomorphy of the family (e.g. Vilhelmsen 2000). Examinations of the type specimen of *M. cyaneus* Wei, 1999 by S. M. Blank (personal communication) and an unidentified species (one male specimen) in the DEI from Nepal, which based on other characters seems to belong to this lineage, reveal that the "cenchri" are actually small pale areas, contrasting with the surrounding black integument, but are not raised structures (i.e. they are not cenchri), and that tegulae are present, albeit inconspicuous (small and strongly downwardly deflected towards the anterior).

Genetic data. Three gene fragments were obtained for *Stenocephus janseni* sp. nov. to examine its phylogenetic position within Cephidae. Most of the new sequences were obtained either with the Sanger or Nanopore method, except COI of *S. janseni* sp. nov. holotype that was sequenced with both methods. The Sanger and Nanopore consensus sequences of COI of *S. janseni* sp. nov. holotype were identical, indicating reliability of the relatively new Nanopore sequencing technology. Nevertheless, a Nanopore consensus sequence of COI of one specimen (DEI-GISHym89964) probably contained a deletion error in a homopolymer region (6 G instead of probable 7) causing a frame shift mutation that is not expected in

the protein coding regions. This one-nucleotide gap was replaced with an undetermined nucleotide ("N") to preserve the protein translation frame. For both alignments, COI only and combined COI and nuclear (Figs 18–19), the best-fit model chosen according to Bayesian information criterion (ModelFinder implemented in IQ-TREE) was GTR+F+I+G4. The maximum likelihood analyses of the data (Figs 18–19) clearly place *S. janseni* sp. nov. within the Hartigiini (excluding *Syrista*), but its exact phylogenetic position remains uncertain. Unfortunately, genetic data are lacking for any other *Stenocephus* and many other, possibly relevant, East-Asian genera. Based on the current taxon sampling, *S. janseni* sp. nov. is weakly supported as sister group of *Phylloecus* based on mitochondrial COI (Fig. 18) or as sister of *Janus* based on combined COI and nuclear data (Fig. 19).

Stenocephus janseni sp. nov.

Type material examined. HOLOTYPE: ♀ (DEI-GISHym84482), 'Germany: Brandenburg, Müncheberg 4 km NW, 52.521°N 14.064°E [58 m a.s.l. in woodland beside railway track "Ostbahn"; Berlin to Kostryn], 20.V.2020, leg. A. Liston, M. Prous' [white label, printed], 'Holotype ♀ Stenocephus janseni n. sp. det. A. Liston' [red label, handwritten], 'DEI-GISHym84482' [white label, printed]. Deposited in the Senckenberg Deutsches Entomologisches Institut, Müncheberg.

Description. ***Female*** (Figs 1–17). Length: 10 mm, without ovipositor.

Colour (Fig. 1). Black. Parapterum whitish. Yellow-brown are: extreme dorsal apex of profemur, all tibiae, more or less all tarsi except for distally progressively somewhat darker tarsomeres (from apex of basitarsomere), abdominal terga 3 and 4 and corresponding sterna, and tergum 2 with corresponding sternum except for their more or less fuscous dorsal / ventral parts. Wing membrane subhyaline. Venation basally yellowish, apically (including pterostigma) becoming brown.

Head in dorsal view (Fig. 2) slightly contracted behind eyes; lateral length (from anterior of eye to most posterior point) approximately 0.5× width. Temple much shorter than length of eye (Fig. 4). Genal carina developed from malar space to about 0.33 height of eye. Ratio of distance between inner edges of toruli : distance between lower edge of torulus and centre of anterior tentorial pit approx. 1.2 : 1.0 (Fig. 3). Postocellar area rather densely punctured, with shiny interspaces (Fig. 2). Frontal area more densely and finely punctured; dull (Fig. 3). Vertex, temple and supraclypeal area shiny, with weak, scattered punctures. Left mandible (Fig. 15) outer (anterior) tooth longer than the inner; inner and outer teeth of about equal basal width; inner tooth anterior edge slightly convex; posterior edge concave. Labial palp with four palpomeres, much shorter than maxillary palp. Apical labial palpomere much wider than apical maxillary palpomeres. Maxillary palp (Fig. 14): palpomere 6 arising at approximately 0.6 of length of 5 (from base); palpomeres 5 and 6 combined length slightly less than 4 (or palpomere 4 about 1.5× as long as 6). Antenna (Fig. 16) long and slender; about as long as combined length of fore wing costa and stigma; 28 antennomeres. Flagellum widest at about 0.75 from base, gently expanding from apex of flagellomere 3. Flagellomere 1 slightly longer than 2 (1.2 : 1.0). All flagellomeres longer than broad. Pubescence on upper head about 0.25× as long as diameter of anterior ocellus, and sparser than on thorax.

Most of thorax (Figs 5–8) deeply punctured, with narrow interspaces, and dull. Dorsal part of propleuron glabrous and without punctures (Fig. 7). Longest setae on thorax about 0.5× as long as diameter of anterior ocellus. Pronotum in dorsal view (Fig. 6) slightly wider than long (ca. 1.1 : 1.0); anteriorly and posteriorly strongly carinate on dorsal margins; a longitudinal furrow present, deeper and wider posteriorly, ending posteriorly in a shallow marginal notch and anteriorly in a small triangular area without punctures or sculpture. Mesoscutellum almost circular in outline in dorsal view (Fig. 8). Protibia without preapical spurs; mesotibia with one preapical spur; metatibia with two preapical spurs (Fig. 10). Metatibial preapical spurs longer than apical ones (Fig. 10). Metatarsomere 1 slightly longer than combined lengths of 2–4 (1.03 : 1.00). Claw with inner tooth close to outer tooth and clearly larger; no basal lobe (Fig. 9). Fore wing stigma 8.6× as long as broad. Fore wing anal cell with cross-vein. Cross-vein 3r-m present in hind wing; 7 hamuli on hind wing.

Abdominal terga shallowly and indistinctly punctate; shiny between the punctures. Tergum 1 with a complete longitudinal median incision extending anteriorly. Tergum 2 in lateral view (Fig. 11) strongly widened towards posterior (distal height approx. 1.25× length). Terga 3–7 progressively widened distally (Fig. 1). Cerci short (Figs 12, 13): appearing about 0.15× as long as valvula 3 in dorsal view (Fig. 12). Valvifer 2 about as long as valvula 3. In lateral view upper edge of valvula 3 with straight profile; longitudinally with a ridge running approximately parallel to lower edge (Fig. 13). In dorsal view (Fig. 12) slightly expanded from base to middle, then gently narrowing towards apex. Lancet (Fig. 17): 19 annulets; a single, robust, ventrally-placed ctenidial tooth on each annulus; serrulae narrow, and small in comparison to length of annulet, not clearly developed on annulus 1 [numbered from base, excluding the radix]. Lance of similar proportions to lancet, with about 12 proximal dorsal serrulae; annular sutures not visible.

Male. Unknown.

Differential diagnosis. As already indicated in our brief comparative review of morphological character states in Hartigiini, *Stenocephus janseni* sp. nov. is readily distinguished from other known taxa by an unusual combination of characters: claw without angled basal lobe and inner tooth longer and wider than the outer; mandible outer tooth longer than inner and teeth of about same basal width, inner tooth with simple outline (not conspicuously "shouldered"); maxillary palpomere 4 about 1.5× length of 6; lancet with distinct annuli, simple serrulae, and one ctenidial tooth per annulus.

Body colour pattern alone, if stable, might distinguish female *Stenocephus janseni* sp. nov. from most other West Palaearctic cephid species. Whereas *S. janseni* sp. nov. has some of the basal terga and sterna entirely pale, most others have only parts of the terga or sterna banded or flecked

Fig. 18. Maximum likelihood tree of Cephidae based only on mitochondrial COI gene. Numbers at branches show SH-aLRT support (%) / ultrafast bootstrap support (%) values. Support values for weakly supported branches (<90) are not shown. Letters "f" and "m" stand for "female" and "male" if known. Numbers at the end of the tip labels refer to the length of the sequence. The tree was rooted according to the results of Malm & Nyman (2015) and Aydemir & Korkmaz (2020). The scale bar shows the number of estimated substitutions per nucleotide position.

with pale. In the Hartigiini, *Syrista parreyssii* (Spinola, 1843) has a similarly coloured body and legs, but differs in its greater body length (female 15–18 mm), temple much longer than length of eye, and a strongly downcurved valvula 3. *Janus compressus* (Fabricius, 1793) also has some entirely pale terga, but in the female at least terga 3–7 are entirely pale, and the metatibia is largely black, with the base clear-white.

Characters which separate *Stenocephus janseni* sp. nov. from the four European *Phylloecus* species (*Ph. etorofensis* (Takeuchi, 1955), *Ph. faunus* Newman, 1838, *Ph. niger* (M. Harris, 1779), and *Ph. xanthostoma* (Eversmann, 1847))

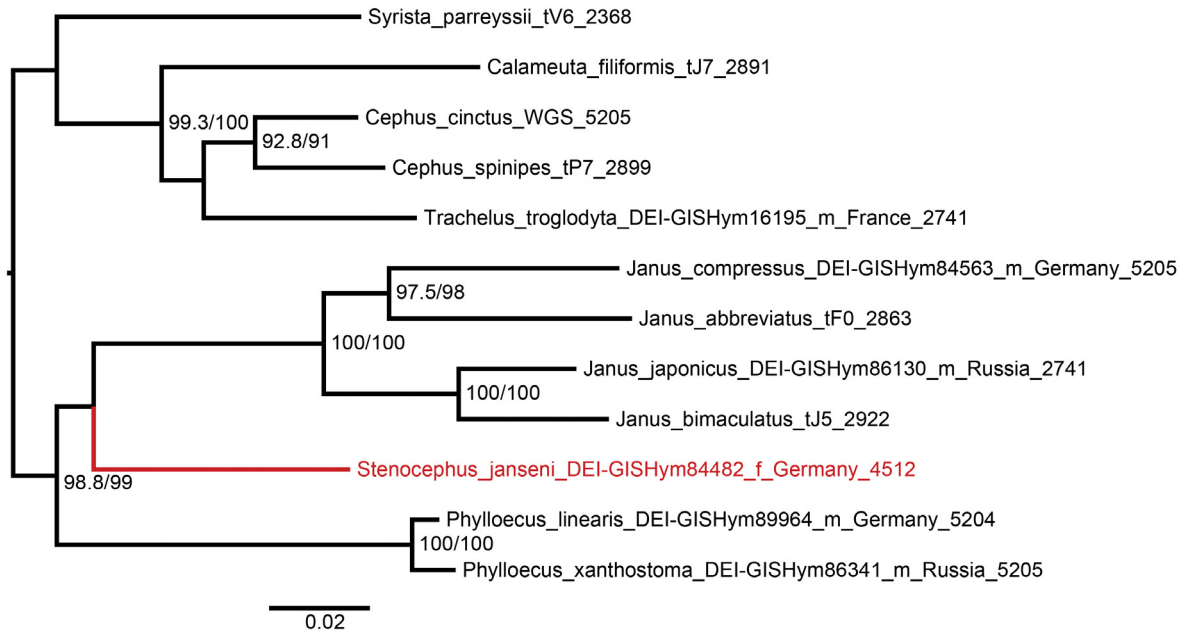


Fig. 19. Maximum likelihood tree of Cephidae based on combined COI and nuclear (POL2 + NaK) genes. Numbers at branches show SH-aLRT support (%) / ultrafast bootstrap support (%) values. Support values for weakly supported branches (<90) are not shown. Letters "f" and "m" stand for "female" and "male" if known. Numbers at the end of the tip labels refer to the length of the sequence. The tree was rooted according to the results of Malm & Nyman (2015) and Aydemir & Korkmaz (2020). The scale bar shows the number of estimated substitutions per nucleotide position.

are the absence of any pale markings on the head capsule (in the others, there is at least a small pale spot near the eye on the upper inner orbit), maxillary palpomere 4 about 1.5× as long as 6 (others: about equal in length), and its long and thin antennae. Its two metatibial preapical spurs separate *S. janseni* sp. nov. from *Phylloecus* species, which have one, and from *Caenocephus*, which have none.

Etymology. Named after Dipl.-Biol. Ewald Jansen, for his contributions to the study of European Hymenoptera, particularly the sawfly fauna of Germany.

Host plant. Unknown.

Habitat. Woodland dominated by *Pinus sylvestris*, with much *Betula pendula*, and some *Robinia pseudoacacia* and *Quercus robur*. Diverse woody plants in understorey, such as *Populus tremula*, *Crataegus* sp., *Prunus spinosa*, and *P. serotina*. Field layer dominated by grasses, with patches of *Rubus fruticosus* agg.

Distribution. Germany: Brandenburg.

Discussion and conclusions

Genetic data for many cephid taxa, both genera and species, are still unavailable, particularly for most of the monotypic or species-poor genera of Hartigiini proposed in the last two decades by taxonomists in China and Japan. Partly because no robust phylogenetic analysis of the Hartigiini is currently available, we refrain from describing a new genus for *Stenocephus janseni* sp. nov. Its placement in *Stenocephus* is necessarily provisional, and was decided upon after consideration of the extent to which existing characterisations of individual genera would have to be modified to accommodate it. Some grounds could have been found for placing it in *Phylloecus*, but, as outlined above (see: Morphological character states), most characters seem to fit *Stenocephus* better. The differences in the lancet of *S. janseni* sp. nov. to those of the other three described *Stenocephus* species are the most disturbing. On the other hand, in the absence of convincing phylogenetic hypotheses, one can question whether some of the nominal genera of Hartigiini currently treated as valid are really worth maintaining as separate.

We do not wish to speculate on the status of *Stenocephus janseni* sp. nov. in the central European fauna. Whether it is "native", but has previously escaped detection, or has recently extended its range, or has been introduced from elsewhere, may only become clearer when further specimens are collected.

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