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A new species of *Paranthrene* Hübner  
(Lepidoptera: Sesiidae) from the northern  
midwest United States

William H. Smith III

Albert J. Cook Arthropod Research Collection, Department of Entomology, Michigan State University,  
East Lansing, MI

William H. Taft Jr.

Albert J. Cook Arthropod Research Collection, Department of Entomology, Michigan State University,  
East Lansing, MI

Anthony I. Cognato

Albert J. Cook Arthropod Research Collection, Department of Entomology, Michigan State University,  
East Lansing, MI

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# A new species of *Paranthrene* Hübner (Lepidoptera: Sesiidae) from the northern midwest United States

William H. Smith III

Albert J. Cook Arthropod Research Collection, Department of Entomology, Michigan State University,  
East Lansing, MI

William H. Taft Jr.

Albert J. Cook Arthropod Research Collection, Department of Entomology, Michigan State University,  
East Lansing, MI

Anthony I. Cognato

Albert J. Cook Arthropod Research Collection, Department of Entomology, Michigan State University,  
East Lansing, MI  
cognato@msu.edu

**Abstract.** A clearwing moth species, *Paranthrene sogaardi* Taft and Smith, 2024, **new species**, is described from Michigan and Minnesota. The recognition of this new species is based on a phylogeny estimated from mitochondrial cytochrome oxidase I and wingless DNA sequences of 25 specimens representing all *Paranthrene* Hübner species including individuals from various locations. *Paranthrene sogaardi* **new species** was monophyletic and differed from *Paranthrene tabaniformis* Rottenburg, 1775 by a mean of 7.6% COI pairwise “p” distance, coloration, and genitalic morphology.

**Key words.** Clearwing moths, Michigan, mitochondrial DNA, nuclear DNA, phylogeny, systematics.

**ZooBank registration.** urn:lsid:zoobank.org:pub:8B9ED6CE-4DEB-4CB2-9235-3CA593F4D9DB

## Introduction

The dusky clearwing, *Paranthrene tabaniformis* Rottenburg, 1775 (Sesiidae: Lepidoptera) (Fig. 1) is a Holarctic species (Solomon 1995). Like all other *Paranthrene* Hübner species found in North America, *P. tabaniformis* is a diurnal wasp mimic (Eichlin and Duckworth 1988). Its North American range includes the continental United States, Alaska, and Canada, with the exception of California (Taft et al. 1991). The larval host plants are poplars and willows and the species can also be a major pest of nursery plants (Solomon 1995). Adults emerge from their 2-year cycle in June and July (Taft et al. 1991).

Several *Paranthrene* are known to have various color variants (Eichlin and Duckworth 1988). *Paranthrene tabaniformis* is no exception with three recognized color forms in North America (Eichlin 1989). This species is typically characterized by a blue-black head with a grey-black frons and white lateral margins, the thorax is blue-black with yellow on the anterior margins and beneath the wings, and the abdomen is blue-black with yellow bands on segments two, four, six and seven (Eichlin 1989; Fig. 1). The color forms “denotata” and “oslari” are largely similar with a few chromatic differences. Most notable is the form “oslari”, which is differentiated by a yellow band on all abdominal segments except segment one, with the bands on segments two and six wider than the rest (Eichlin 1989).

In 2022, near Bath Township, Clinton County, Michigan, a specimen originally identified as *P. tabaniformis* was collected with a unique color morphology and large transparent areas in the forewings which suggested it was a distinct species. This specimen was similar to one photographed by Mr. James Sogaard, in Minnesota in 2007. We investigated this color variant’s phylogenetic placement among *Paranthrene* species and its morphological variation. We demonstrated that it is distinct from the typical *P. tabaniformis* color variant and we concluded that it is a new species.



**Figure 1.** *Paranthrene tabaniformis*, habitus, dorsal view.

## Materials and Methods

**Collection of specimens.** In July 2022 along Stoll and State Roads in Clinton County (Rose Lake State Game Area), Michigan the second author collected three male sesiid moths using Multi-Pher #1<sup>®</sup> pheromone canister traps (Distributions Solida Inc) baited with Western Poplar Borer pheromone lure, a blend of ZZ 3,13 OH and EZ 3,13 OH (50:50) (Scentry Biologicals, Inc). Specimens were deposited in the Albert J. Cook Arthropod Research Collection, Department of Entomology, Michigan State University, East Lansing, MI (MSUC) and James Sogaard's personal collection.

**Specimen preparation and imaging.** One specimen of *P. tabaniformis* and the new form was selected for genital comparison. Abdomens were removed at the 4th or 5th segment. The removed segments were placed in separate vials filled with water and two 116 mg tablets of potassium hydroxide and allowed to sit on a hot plate set just below boiling for 2 hours. Softened abdominal segments were removed from the vials and teased apart under a dissecting microscope with fine-tipped forceps until genitalia were revealed. Genitalia were preserved in glycerin and placed in 5mm glass micro vials and pinned under the associated specimen. The genitalia were not stained.

Specimens were photographed with a Visionary Digital Passport II system (Dun Inc., Palmyra, VA) using a Canon EOS 5D Mark II, 65.0-mm Canon Macro photo lens, two Dynalite (Union, NJ) MH2015 road flash heads, Dynalite RoadMax MP8 power pack and a Stack Shot (Cognisys, Inc, Traverse City, MI). Montage images were assembled using Zerene Stacker 1.04 and sized in Adobe Photoshop 2021 v. 22.5.1 (San Jose, CA).

**DNA sequence data and phylogenetic analyses.** DNA was extracted from a metathoracic leg from 25 frozen specimens representing *P. tabaniformis* and six other *Paranthrene* and outgroup species (Table 1) using a Qiagen

**Table 1.** Species, specimens, localities and Genbank numbers.

Species	DNA voucher #	Location	GenBank # COI	GenBank # Wg
<i>C. laurelae</i>	BT 178	Palmer Bridge, SC	PP333557	PP338690
<i>V. admiranda</i>	BT 204	Medicine Park, OK	PP333558	PP338691
<i>V. admiranda</i>	BT 205	Medicine Park, OK	PP333559	PP338692
<i>P. simulans</i>	BT 129	Jacksonville, NC	PP333560	PP338693
<i>P. simulans</i>	BT 142	Manistee County, MI	PP333561	PP338694
<i>P. fenestrata</i>	BT 179	Emory Pass, NM	PP333575	PP338706
<i>P. fenestrata</i>	BT 180	Emory Pass, NM	PP333576	PP338707
<i>P. fenestrata</i>	BT 181	Pinos Altos, NM	PP333577	PP338708
<i>P. fenestrata</i>	BT 183	Emory Pass, NM	PP333578	PP338709
<i>P. asilipennis</i>	BT 175	North Lima, OH	PP333574	PP338705
<i>P. asilipennis</i>	BT196	Swanton, OH	PP333579	PP338710
<i>P. tabaniformis</i>	BT 151	McClellanville, SC	PP333564	PP338697
<i>P. tabaniformis</i>	BT 152	Bath Township, MI	PP333565	PP338698
<i>P. tabaniformis</i>	BT 153	Bath Township, MI	PP333566	PP338699
<i>P. tabaniformis</i>	BT 210	Princeton, MN	PP333580	PP338711
<i>P. tabaniformis</i>	BT 168	Ravalli County, MT	PP333571	PP338702
<i>P. robiniae</i>	BT 148	Grant County, NM	PP333562	PP338695
<i>P. robiniae</i>	BT 149	Grant County, NM	PP333563	PP338696
<i>P. dolli</i>	BT 160	Clinton County, MI	PP333569	NA
<i>P. dolli</i>	BT 161	Clinton County, MI	PP333570	NA
<i>P. sogardi</i>	BT 154	Bath Township, MI	PP333567	PP338700
<i>P. sogardi</i>	BT 155	Bath Township, MI	PP333568	PP338701
<i>P. sogardi</i>	BT 211	Princeton, MN	PP333581	PP338712
<i>P. sogardi</i>	BT 169	Clinton County, MI	PP333572	PP338703
<i>P. sogardi</i>	BT 170	Clinton County, MI	PP333573	PP338704

DNeasy blood and tissue kit (Hilden, Germany) following the manufacturer's protocol. The remaining bodies were vouchered in the A. J. Cook Arthropod Research Collection. The purified DNA underwent PCR for mitochondrial cytochrome oxidase I and wingless (Table 2). EXO-SAP-IT (USB Corp., Cleveland, OH, USA) was used to ready the PCR products for sequencing at the Michigan State University Research Technology Support Facility using Big-Dye Terminator v. 1.1 (Applied Biosystems, Foster City, CA, USA) and an ABI 3730 Genetic Analyzer (Applied Biosystems). Sense and antisense strands were compiled using Sequencher (Ann Arbor, MI) to trim sequences of primer sequences, align the sequences and to create consensus sequences. Final sequences were deposited in Genbank (Table 1) and assembled in a Nexus file for a total of 1056 nucleotides (including 639 from COI and 417 from Wingless) which included 205 parsimony-informative characters.

Phylogenetic parsimony analysis of the aligned sequences consisted of a branch and bound search using default options in PAUP v4.0a (build 168; Swofford 2002). Gaps were treated as missing data. Bootstrap values were determined with 500 pseudo-replicates each conducted by heuristic search with simple stepwise addition. Percent pairwise DNA difference was calculated as p-distance in PAUP\*. In addition, Bayesian analysis under a likelihood optimality criterion was used to assess phylogenetic relationships. Using MrBayes 3.2.6 (Ronquist et al. 2012), two simultaneous analyses were conducted in which both genes were partitioned by codon position and a model of general time reversal + gamma + proportion of invariable sites was applied to each partition (unlinked

**Table 2.** PCR primers and cycling conditions.

PCR Primers						
Gene	Forward Primer	Primer Sequence	Reverse Primer	Primer Sequence	Annealing	Reference
COI	LCO1490	5' GGT CAA CAA ATC ATA AAG ATA TTG G 3'	HCO2198	5' TAA ACT TCA GGG TGA CCA AAA AAT CA 3'	95°C (15 min); 5 cycles of 94°C (30 s) / 45°C (90s) / 72°C (90 s); 30 cycles of 94°C (30 s) / 50°C (90s) / 72°C (90 s); 72°C (5min)	Folmer et al. (1994)
Wg	LepWg1	5' GAR TGY AAR TGY CAY GGY ATG TCT GG 3'	LepWg2	5' ACT ICG CAR CAC CAR TGG AAT GTR CA 3'	95°C (15 min); 36 cycles of 95°C (30 s) / 55°C (45s) / 72°C (60 s); 72°C (10 min)	Brower and DeSalle (1998)

parameters). Four Metropolis-coupled Markov chain Monte Carlo (MCMC) searches (one cold, three heated chains) were analyzed for 5 million generations. Each analysis was sampled every 100th iteration and all parameters reached stability indicated by 0.002 standard deviation of split deviation between analyses. The effective sample sizes (ESS) of parameters were >1000 indicating the parameters were well-sampled. Bayesian posterior probabilities of clades were based on 75,000 trees—the total of both runs after a 25% burn-in.

## Results

The PAUP\* analysis found six most parsimonious trees that were mostly resolved in the strict consensus (Fig. 2). Intraspecific relationships in two clades and one interclade relationship were unresolved (Fig. 2). All clades of species had 100 bootstrap values and whereas values for internal nodes varied most were >85 (Fig. 2). The topology of the Bayesian tree was generally similar to the parsimony tree but differed in placing the clade containing the new species described below as sister to *Vitacea* Engelhardt and the remaining *Paranthrene* species. Posterior probabilities were >0.9 for all species clades except “sogaardi” at 0.7. The average interspecific pairwise “p” distance among sister species within the genus ranged between 0.062–0.101 for COI and 0.008–0.034 for Wingless. The average “p” distance between “sogaardi” and *P. tabaniformis* was 0.076 and 0.031 for COI and wingless, respectively, both of which are within interspecific ranges for other species within the genus. In comparison, intraspecific “p” distance amongst “sogaardi” specimens was 0.005 and 0.003 while *P. tabaniformis* was 0.014 and 0.002. The genetic distance between “sogaardi” and *P. tabaniformis* is comparable to the interspecific distance between *P. tabaniformis* and *P. asilipennis* Guérin-Méneville (Table 3). This genetic divergence, in addition to monophyly and morphological diagnostic characters, supports the recognition of a new species.

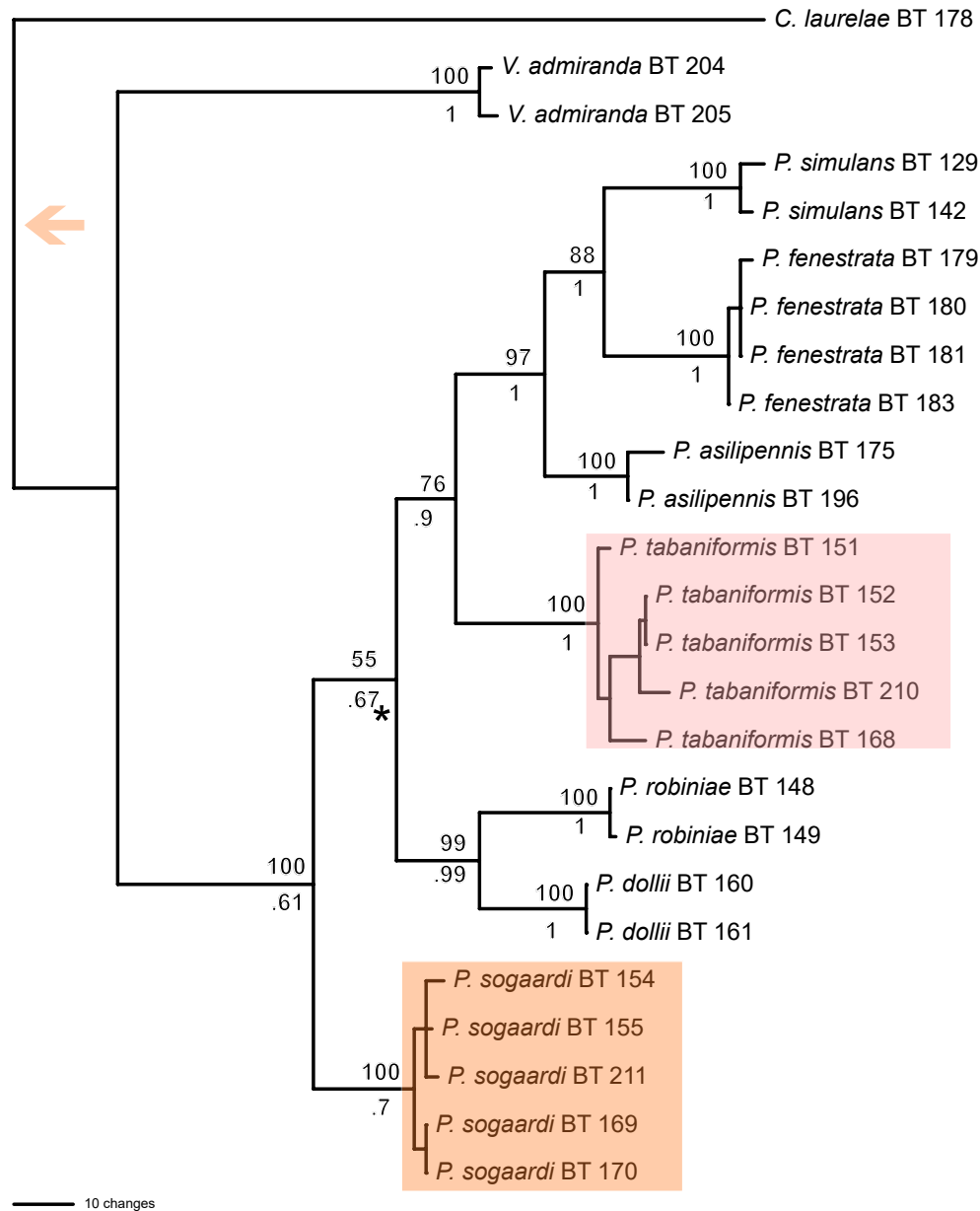
## Taxonomy

### *Paranthrene* Hübner

An apical spine on the aedeagus diagnoses *Paranthrene* from other Paranthrenini genera (Eichlin and Duckworth 1988).

### *Paranthrene sogardi* Taft and Smith, new species

**Diagnosis.** *Paranthrene sogardi* new species differs from *P. tabaniformis* by its lack of scales in the discal cell of the forewing, a dark orange discal spot on the forewings, and uniform yellow bands along abdominal segments 2–7. Whereas the discal cell in the forewing of *P. tabaniformis* is covered in dark scales, without a discal spot, and has yellow bands only on abdominal segments 2, 4, 6 and 7. Concerning the male genitalia, the apical point of the valves of *P. sogardi* n. sp. are more rounded than *P. tabaniformis* and the setae are denser at the base of the valves



**Figure 2.** One of six parsimonious trees; the asterisked clade and the intraspecific relationships of *P. fenestrata* and *P. sogardi* are unresolved in a strict consensus of the six trees. Numbers above branches are bootstrap values and numbers below the branches are posterior probabilities. The arrow indicates the placement of *P. sogardi* in Bayesian analysis.

where setal density is relatively uniform along the valve margins in *P. tabaniformis* (Fig. 3, 4). The distal end of the saccus in *P. sogardi* **new species** is flattened and squared off, while the saccus in *P. tabaniformis* ends in a point. Both aedeagi have a sclerotized, toothed ridge (Fig. 5, 6). In contrast, this ridge is covered by a semi-translucent shingle-like sclerite in *P. tabaniformis*, a feature absent in *P. sogardi*.

*Paranthrene sogardi* **new species** superficially resembles several other species of North American Sesiidae, most notably *Paranthrene pellucida* Greenfield and Karandinos and *Synanthedon rileyana* Hy. Edwards. The following characters distinguish *P. sogardi* **new species** from *P. pellucida*. The cell below the Cu vein to the anal margin in the forewing of *P. sogardi* **new species** is covered in orange-brown scales, whereas the same cell in *P. pellucida* is without scales and transparent. The yellow bands on the abdomen of *P. pellucida* are thicker distally from the thorax while all bands are roughly equal in thickness on *P. sogardi* **new species**.

**Table 3.** Genetic distances between *Paranthrene sogardi* **new species** and relatives. The intraspecific line is ordered as (Wg/COI). “P” distance values above the intraspecific line represent average interspecific Wg values and below the line are average interspecific COI values. Values in bold signify the comparison between *Paranthrene sogardi* **new species** and *P. tabaniformis*.

Wg and COI p-distance									
	<i>P. asilipennis</i>	<i>P. dolli</i>	<i>P. fenestrata</i>	<i>P. robiniae</i>	<i>P. simulans</i>	<i>P. sogardi</i>	<i>P. tabaniformis</i>	<i>C. laurelae</i>	<i>V. admiranda</i>
<i>P. asilipennis</i>	.002/.008	0	.008	.032	.013	.036	.022	.204	.075
<i>P. dolli</i>	.085	0/0	0	0	0	0	0	0	0
<i>P. fenestrata</i>	.072	.104	.001/.002	.028	.009	.031	.018	.205	.071
<i>P. robiniae</i>	.084	.062	.101	.002/0	.034	.023	.029	.202	.066
<i>P. simulans</i>	.07	.095	.071	.092	.005/.006	.037	.028	.206	.075
<i>P. sogardi</i>	.073	.077	.098	.087	.09	.003/.005	<b>.031</b>	.201	.065
<i>P. tabaniformis</i>	.076	.08	.101	.09	.081	<b>.076</b>	.002/.014	.206	.068
<i>C. laurelae</i>	.149	.164	.163	.164	.168	.153	.155	NA/NA	.213
<i>V. admiranda</i>	.136	.149	.139	.149	.134	.133	.141	.174	.005/.005

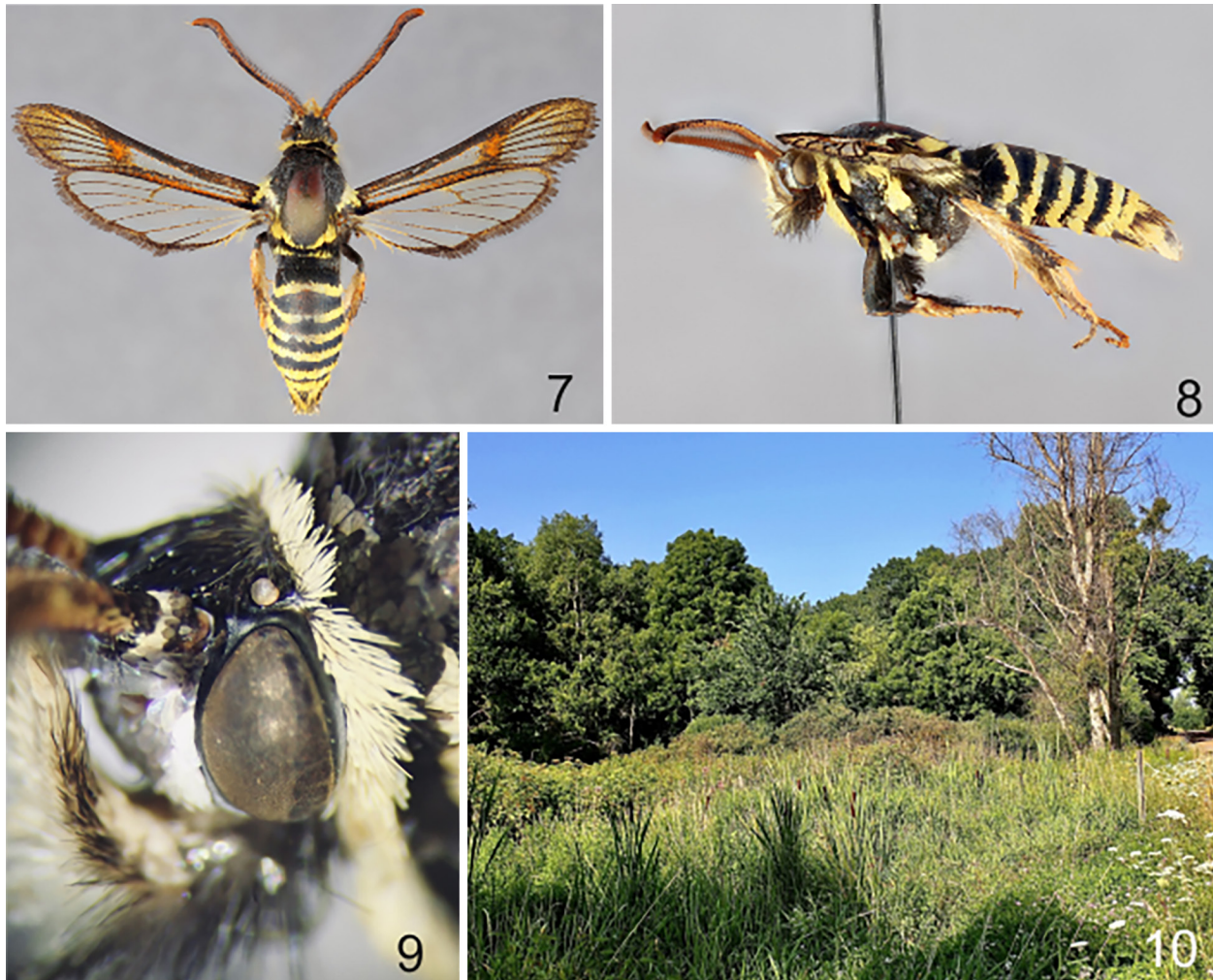


**Figures 3–6.** Adult male genitalia. 3) *Paranthrene sogardi*, **new species** 4) *Paranthrene tabaniformis*. 5) *Paranthrene sogardi* **new species** aedeagus. 6) *Paranthrene tabaniformis* aedeagus.



Scaling on the wings also differs between *P. sogardi* **new species** and *S. rileyana*. *Paranthrene sogardi* **new species** has brown-black scales on the tips of the forewings and brown-black scales along the M vein in the hind wings. *Synanthedon rileyana* lacks scales in both the aforementioned areas. In addition, *P. sogardi* **new species** has yellow tarsi while *S. rileyana* has black tarsi.

**Description.** Male (Fig. 7, 8). *Head:* Vertex primarily flat black with fine light gray hair mixed near the base; frons light translucent pearl with a blue sheen, white laterally (Fig. 9); occipital fringe straw yellow; labial palp strongly roughened, pale yellow with brown-black scales mixed laterally; haustellum coiled, antenna orange with a narrow line of brown-black dorsally. *Thorax:* Dorsum flat black with fine light gray hair-like setae mixed throughout, base of forewing surrounded by a yellow spot, mixed with pale white scales, a patch of yellow setae posterior to the cape (visible in lateral view, Fig. 8), yellow scales on the posterior and posterolateral margins of the metathorax. Legs with coxae flat black with bright yellow outer margins, femora dark brown-black; tibiae light orange-yellow with a small patch of brown-black setae medially covered by orange setae, tibial spurs, and tarsi light yellow-orange mixed with black setae. *Forewing* mostly hyaline with an outer brown-black margin, discal spot light orange with a light edging of brown scales around the margins; anal margin lined with orange and black scales; veins and fringe brown-black with pale yellow scales on outer margin between veins (often faded in older individuals). *Hindwing* hyaline with narrow margins; dark brown fringe transitions to pale yellow near the wing



Figures 7–10. *Paranthrene sogardi* **new species**. 7) Dorsal view. 8) Lateral view. 9) Frons. 10) Michigan collection site of *Paranthrene tabaniformis*.

base. *Abdomen*: Brown-black with yellow bands encircling segments two-seven (the band width appears variable across its range); anal tuft short with a mix of black and yellow scales. *Male genitalia*: (Fig. 3) Valves rounded apically, with setal density thickest toward the base. Socii with dense light-colored setae. Saccus ending in a flat squared-off tip.

**Female.** Unknown.

**Host.** Unknown, but all *Paranthrene* moth species bore into trees and large shrubs (i.e., oak, poplar, aspen, and willow species) as larvae.

**Distribution.** Known from Central Michigan and Minnesota. Additional images of specimens from western Quebec suggest that the range of *P. sogaardi* **new species** may extend into Quebec (iNaturalist.com). Because of the scattered locations of both collected specimens and images we suspect their range may include parts of Wisconsin and Ontario.

**Types.** Holotype: Male, Michigan: Clinton Co., Bath Township, Rose Lake State Game Area, Lat/Long (42.7988, -84.40185), July 2, 2022, Coll. William H. Taft, MSUC\_ARC\_320053, deposited in the Albert J. Cook Arthropod Research Collection, Michigan State University, East Lansing (MSUC). Michigan paratypes (2 males) and Minnesota paratypes (1 male) at MSUC and (3) in James Sogaard's personal collection.

**Etymology.** The species is named for Mr. James Sogaard of Princeton, Minnesota who first captured and photographed a male specimen from the same area.

**Remarks.** In Michigan, the moth was collected in a wetland swale depression (Fig. 10.) characterized by willow thickets and shrub wetlands surrounded by oak uplands. The common plant species of the type location were quaking aspen (*Populus tremuloides* Michx.), northern red oak (*Quercus rubra* L.), red maple (*Acer rubrum* L.), sand bar willow (*Salix interior* Rowlee), heart-leaved willow (*Salix eriocephala* Michx.), black willow (*Salix nigra* Marshall), elm (*Ulmus* sp. L.), gray dogwood (*Cornus racemose* Lam.), and a non-native plant—common buckthorn (*Rhamnus cathartica* L.). The herbaceous plants were Joe-Pye weed (*Eutrochium purpureum* L.), elderberry (*Sambucus canadensis* L.), raspberry (*Rubus* sp. L.), boneset (*Eupatorium perfoliatum* L.), and cattail (*Typha latifolia* L.).

The EPA ecoregion designation for the type location in Michigan is the southern Michigan /North Indiana Drift Till Plains/ Lansing Loamy Plain with the mid-elevation forests and the foothills woodlands and shrub lands designation. In Minnesota, EPA ecoregion designation for the Princeton area is the Anoka Sand Plain and Mississippi Valley Outwash (White 2020). It is characterized by substantial agriculture, but much of the region is too wet and poorly drained to be cultivated, so is left as natural wetlands (Albert 1995).

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