A New Pest Species of *Copitarsia* (Lepidoptera: Noctuidae) from the Neotropical Region Feeding on *Asparagus* and Cut Flowers

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ABSTRACT The egg, first and last instars, and adult of *Copitarsia corruda*, n. sp. from Mexico, Colombia, Ecuador, and Peru are described and illustrated. Larval host plant genera include *Asparagus* (Liliaceae) (Mexico, Colombia, and Ecuador), *Iris* (Iridaceae) (Ecuador), *Ammi* (Apiaceae) (Ecuador), *Lysimachia* (Primulaceae) (Colombia), *Callistephus* (Asteraceae) (Colombia), and *Aster* (Asteraceae) (Colombia). The larva of *Copitarsia decolora* (Guenée) is described and illustrated. In addition to genitalic and larval characters, mitochondrial gene cytochrome oxidase I (COI) was analyzed to differentiate *C. corruda* from *Copitarsia decolora* (Guenée), and to examine geographic and host plant differences between the two species.

KEY WORDS cryptic species, mitochondrial DNA, morphology, agriculturally important species, phylogeny

The identification of species, particularly agriculturally important pests, can be hampered by many factors, including misidentification in the literature, misplacement at higher taxonomic levels, and morphologically cryptic species. All of these situations occur in the noctuid genus *Copitarsia* Hampson, 1906. Here, we address these three issues by describing a new pest species of *Copitarsia* that was revealed during a mitochondrial DNA study of a group of morphologically similar populations of the *Copitarsia decolora* (Guenée) complex (Simmons and Scheffer 2004).

Members of *Copitarsia* are agricultural pests of at least 39 crops from 19 plant families, and they are found throughout Mexico, and Central and South America (Venette and Gould 2006). Including the species described here, there are 22 recognized species of *Copitarsia* (Angulo and Olivares 2003). *Copitarsia* eggs and larvae are often detected at U.S. ports-of-entry on cut flowers and vegetable commodities. Thus, there is concern that undetected populations of *Copitarsia* could become established near these ports and beyond. A risk assessment study by Venette and Gould (2006) indicated that if *Copitarsia* species are able to form breeding populations, these species could become major agricultural pests of domestic commodities. The major pest species *C. decolora* is regularly found on imported commodities, including cut flowers, lettuce, peas, beets, carrots, beans, and potatoes (Castillo and Angulo 1991, Arce de Hamity and Neder de Roman 1992).

This article provides diagnostic morphological characters and molecular sequences for one of the cryptic species of the *C. decolora* complex (Simmons and Scheffer 2004). This species is described formally, and locality data are provided.

Materials and Methods

Genitalia Dissections. Standard genitalia dissections were performed following Winter (2000) and Pogue (2002). Vesicas were everted using 99% isopropyl alcohol in a syringe and then stained with orcein dissolved in 99% isopropyl alcohol. Digital photographs were made of selected specimens. Genital morphology follows Klots (1970), Forbes (1939, 1954), and Lafontaine (2004). Specimen deposition and genital preparation numbers are indicated under Specimens Examined.

Terminology for adult external morphology of wing pattern follows Lafontaine (2004). Exact label data are presented for holotype. Collections consulted include BMNH, The Natural History Museum, London (D. Carter and D. Goodger); MNHP, Muséum National d'Histoire Naturelle, Laboratorie d'Entomologie, Paris (J. Minet); MZUC, Museo Zoologia de Universidad de Concepción, Chile (A. O. Angulo); and USNM, National Museum of Natural History, Smithsonian Institution, Washington, DC.

Larval descriptions follow terminology from Godfrey (1987) and Beck (1999). Pupal terminology follows Patocka and Turcani (2005).

Gene Region and Analysis. Individuals were collected in the field by R.B.S., as well as border interceptions by USDA–APHIS personnel and donations

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Table 1. List of specimens used in COI studies

Species	Stage[a]	Country/yr	*n*	Host plant (family)	Haplotype no.	GenBank no.
C. corruda	L	Colombia/2001–2	2	*Aster* (Asteraceae)	2, 24	EU371409 EU371420 EU371421
	L	Colombia/2002	2	*Callostephus* (Asteraceae)	26, 32	EU371423 EU371423
	L	Colombia/2002	1	*Lysimachia* (Primaluceae)	33	EU371424
	L	Ecuador/2002	1	*Ammi* (Apiaceae)	18	EU372410
	L	Ecuador/2004	1	*Iris* (Iridaeae)	58	EU371426
	L	Mexico/2002	1	*Asparagus* (Liliaceae)	35	EU371425
	L, A	Peru/2001	10	*Asparagus* (Liliaceae)	2–3, 15, 18–20, 23	EU371408 EU371411-19 EU371422
C. decolora	L	Colombia/2004	1	*Allium* (Alliaceae)	56	EU371480
		Colombia/2001–5	22	*Alstroemeria* (Liliaceae)	12, 22, 25, 27, 30, 34, 40–43, 46–49, 52	EU371428 EU371431 EU371436-40 EU371442-6 EU371451 EU371457-60 EU371465-8 EU371472
	L	Colombia/2002	1	*Aster* (Asteraceae)	12	EU371447
	A	Colombia/2005	1	*Dianthus* (Caryophyllaceae)	16	EU371463
	A	Colombia/2005	1	*Eryngium* (Apiacaeae)	21	EU371456
	A	Colombia/2005	4	*Helianthis* (Asteraceae)	45, 50–52	EU371461 EU371469-71
	L	Colombia/2002	1	*Limonium* (Plumbaginaceae)	12	EU371453
	L	Colombia/2005	1	*Mentha* (Lamiaceae)	55	EU371479
	L	Colombia/2002	2	Mixed flowers	12	EU371448 EU371450
	L	Colombia/2002	1	*Molucella* (Lamiaceae)	12	EU371455
	L	Colombia/2004	1	*Origanum* (Lamiaceae)	38	EU371454
	A	Colombia/2005	1	*Rosa* (Rosaceae)	44	EU371462
	A	Colombia/2004	1	*Solidaster* (Asteraceae)	12	EU371464
	L	Ecuador/2002	1	*Campanula* (Campanulaceae)	31	EU371449
	L	Ecuador/2001	2	*Hypericum* (Clusiaceae)	13–14	EU371429-30
	L	Ecuador/2002	1	*Limonium* (Plumbaginaceae)	29	EU371441
	L	Mexico/2001–4	4	*Apium* (Apiaceae)	10–11, 60–61	EU371474 EU371483 EU371485 EU371494
	A	Mexico/1999	2	*Argemone* (Papaveraceae)	5, 17	EU371432-3
	L	Mexico/2001	1	*Brassica* (Brassicaceae)	7	EU371484
	L	Mexico/2001	1	*Chamaemelum* (Asteraceae)	5	EU371434
	L	Mexico/2001–5	16	*Chenopodium* (Chenopodiaceae)	1, 5–6, 11, 28, 36, 53–54, 59	EU371435 EU371452 EU371473 EU371475-7 EU371482 EU371486-91 EU371495
	L	Mexico/2001	1	*Coriandrum* (Apiaceae)	8	EU371492
	L	Mexico/2004	1	*Pisum* (Fabaceae)	4	EU371427
	L	Mexico/2001	1	*Sueadea* (Lamiaceae)	57	EU371481
Copitarsia sp.	L	Argentina/2004	2	*Fragaria* (Rosaceae)	37, 39	EU371496-7

[a] A, adult; L, larva.

by Rebecca Lee (Ascoloflores, Colombia) and Walter Diaz (SENASA, Peru) (Table 1). Larval abdominal segments or one to two adult legs were used to extract DNA from fresh material. Most representatives sequenced in this study were larvae. Adult museum specimens were used to obtain further DNA samples (25 individuals). DNA was extracted from two to three legs per museum specimen, which were <30 yr old. In total, 90 individuals of *C. decolora* and *Copitarsia corruda* Pogue & Simmons were sampled from five countries: Argentina, Colombia, Ecuador, Peru, and Mexico. Pogue identified larvae before they were included in the study; larval identifications were verified by comparing resulting DNA sequences through comparison with previously published sequences in GenBank (Simmons and Scheffer 2004). Representatives from a third species, likely *Copitarsia naenoides* (Butler), also were included, because previous work indicated that *C. corruda* and *C. decolora* may not be sister taxa (Simmons and Scheffer 2004; Table 1). Inclusion of the third species also allows determination of species limits for both *C. corruda* and *C. decolora.*

DNA extractions were performed using the DNeasy tissue kit (QIAGEN, Valencia, CA) and the Insect Extraction Protocol B (DNeasy tissue protocol 2007) with a 10-min incubation at 70°C and final elution into 70 μl of 70°C EB buffer from the QIAGEN polymerase chain reaction (PCR) purification kit (part number 28106). This protocol was followed with frozen material stored dry or in absolute ethanol, as well as museum material. Museum specimens were extracted

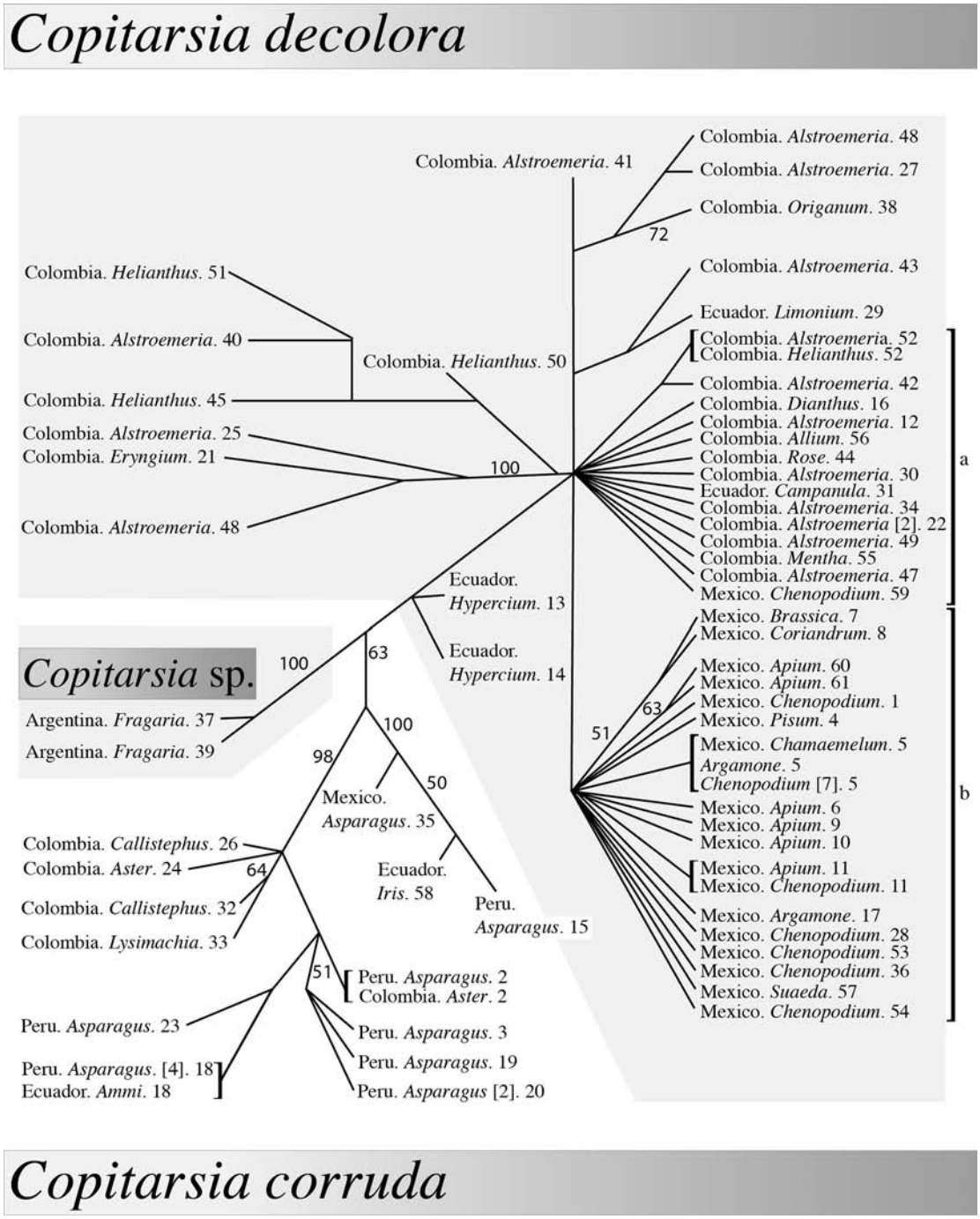


Fig. 1. The strict consensus of 605 unrooted MP trees (L, 384; CI, 0.64; RI, 0.82), showing the relationships of 65 haplotypes of three species of *Copitarsia* based on 1,168 bp of COI. Haplotype numbers are referenced to Table 1 and are given after each locality/plant host. Numbers in brackets represent the number of individual specimens from the same locality/host plant. Bootstrap values >50% are given next to appropriate branches.

on separate days from fresh material to minimize risk of contamination from fresh material. Extraction control blanks were run along with each extraction set. Verification of these blanks and quantification of DNA concentration in the extractions was performed via an ND-1000 spectrophotometer (NanoDrop, Wilmington, DE). Extraction blanks, when used as template for PCR, were also negative, indicating that no foreign

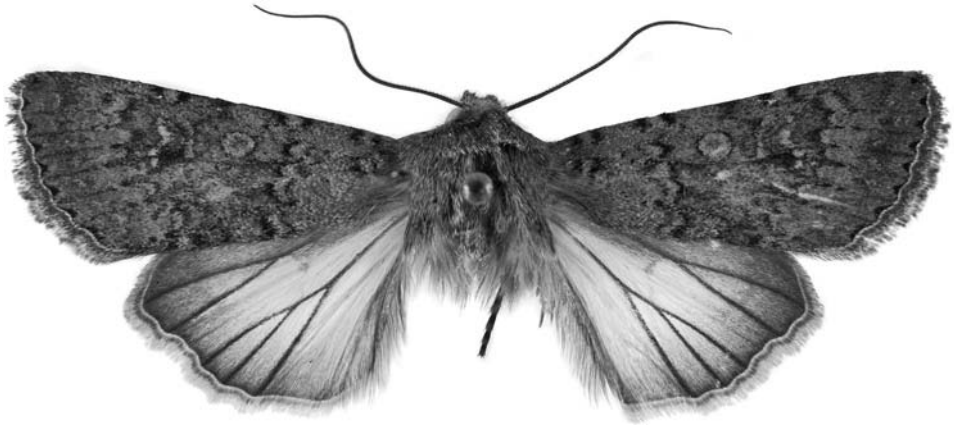
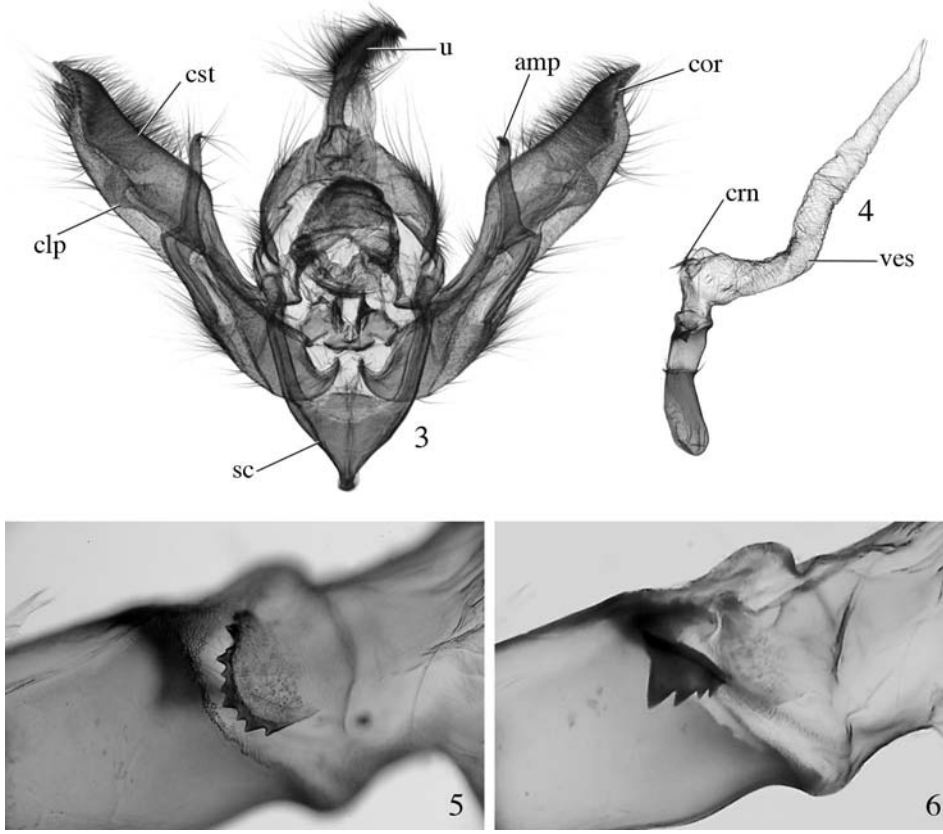


Fig. 2. *Copitarsia corruda*, holotype male.

DNA was present in the extractions. Genitalia were dissected from adult specimens to verify identifications.

Two portions of the mitochondrial gene cytochrome oxidase I (COI) were amplified using PCR in a PCR Mastercycler thermocycler (Eppendorf, Hamburg, Germany) (Saiki et al. 1988). Combinations of five primers, four from Simon et al. (1994) and one novel primer, were used to amplify and sequence a 1,168-bp portion that spanned COI, leaving an ≈200-bp gap in the middle (position on the *Drosophila yakuba* Burla genome given before sequence; Clary and Wolstenholme 1985): K698 (forward 1435; TACAATTTATCGCCTAAACTTCAGCC),



Figs. 3–6. Male genitalia, *Copitarsia corruda*. (3) Genital capsule. (4) Aedoeagus. (5) Round lateral sclerotized plate at apex of aedoeagus. (6) Triangular lateral sclerotized plate at apex of aedoeagus on opposite side of round plate (amp, ampulla; cor, corona; crn, cornuti; sc, saccus; u, uncus; ves, vesica).

Mace (forward 1612; GGAGATGATCAAATTTATAATACTATTG), Nancy (reverse 2191; CCCGGTAAAATTAAAATATAAACTTC), revNancy (forward 2191; GAAGTTTATATTTTAATTTTACCGGG), and Pat (reverse 3015; TCCATTACATATAATCTGCCATATTAG). The PCR protocol was 29 cycles of the following steps (94°C, 1 min; 45°C, 1 min; and 72°C, 2 min), followed by one cycle with these steps (94°C, 1 min; 45°C, 1 min; 72°C, 10 min), and ending with a 4°C dwell. All reactions were performed in a PCR hood, and equipment was treated with UV light after each session.

PCR products were cleaned for automated sequencing with the QiaQuik PCR purification kit (QIAGEN) according to the manufacturer's protocol except that the product was eluted with 40 μl of double distilled H_2O. Sequencing reactions were performed using the BigDye Terminator version 3.1 cycle sequencing ready reaction sequencing kit (Applied Biosystems, Foster City, CA) following the manufacturer's recommended protocol. An ABI 3100 system was used to visualize and record the sequence.

Data were imported into Sequencher 4.5 (Gene Codes, Ann Arbor, MI). Sequences for each individual were aligned manually to produce a consensus sequence. The sequence was translated and checked for stop codons. Consensus sequences for individuals were then aligned by conserved motifs and adjusted manually when necessary.

Phylogenetic Analysis. *Copitarsia* haplotypes were analyzed using maximum parsimony (MP) heuristic searches in PAUP* (Swofford 2000) on a Macintosh Dual 2.5-GHz Power PC Processor. Each haplotype (Table 1) was represented only once in the analysis. Five hundred random addition replicates were performed to avoid hidden tree topology islands. Intraspecific analyses were unrooted to avoid midpoint-rooting artifacts, because noctuine relationships are unclear, making outgroup choice difficult. To assess the branch strength of the resulting haplotype trees, we resampled all data sets using 531 pseudoreplications of bootstrapping (Felsenstein 1985). Because of the computational time required, bootstraps were performed on an Aspen Beowulf Cluster at the Shale High Performance Computing Cluster at University of North Dakota (Grand Forks, ND). Even on the Cluster, time and memory required for bootstrap replications became prohibitive, and the analysis had to be terminated after 2 mo of run time. Once analyses were completed, geographic locality and host plant were mapped onto the tree to examine geographic patterns. Patterns of host plant distribution were examined assuming both ACCTRAN and DELTRAN conditions in MacClade 4.06 (Maddison and Maddison 2003).

Results

COI in *Copitarsia*. We were able to amplify two fragments yielding 1,168 bp of COI from the specimens listed in Table 1. As documented previously (Simmons and Scheffer 2004), COI in *Copitarsia* displays an A/T bias (A, 37%; T, 34.8%). Of the 1,168 characters collected for these specimens, 908 of these were constant, 139 were uninformative, and 121 were parsimony informative.

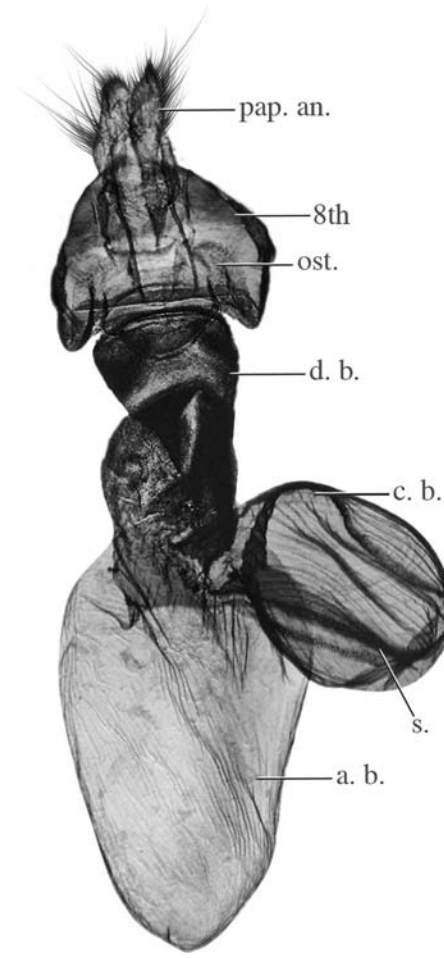
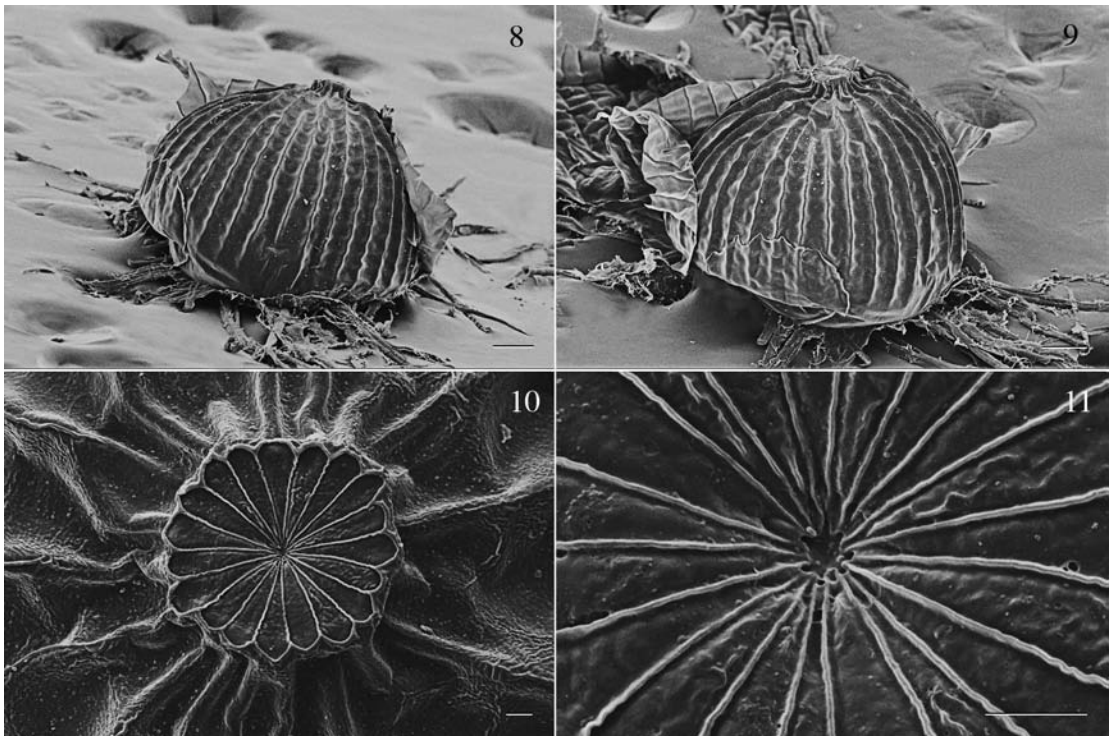


Fig. 7. Female genitalia, *Copitarsia corruda* (eighth, eighth segment; a.b., accessory bursae; c.b., corpus bursae; d.b., ductus bursae; ost, ostium bursae; pap. an., papillae anales; s, signa).

Of 90 individuals sampled (Table 1), we found 65 unique haplotypes. The maximum pairwise distance (uncorrected "p" distance) was 9.86%, found between haplotypes 15 (Peru, host: *Asparagus* sp.; Liliaceae) and 42 (Colombia: host: *Alstroemeria* sp.; Liliaceae). The most common haplotype (5) was found in nine samples from Mexico, feeding on species of *Chamaemelum* (Asteraceae), *Argamone* (Papaveraceae), and *Chenopodium* (Chenopodiaceae).

***Copitarsia* Haplotype Phylogenies.** Analysis of these data via MP resulted in a total of 605 most parsimonious topologies (length [L] = 384 steps; consistency index, corrected for noninformative characters [CI] = 0.64; and retention index [RI] = 0.82). The unrooted topology is shown in Fig. 1. Three lineages exist within the 65 haplotypes, which are representative of three species of *Copitarsia.* Each lineage is well



Figs. 8–11. Egg, *Copitarsia corruda.* (8) Lateral view (scale bar = 100 μm). (9) Dorsolateral view (scale bar = 100 μm). (10) Dorsal view of micropylar rosette (scale bar = 10 μm). (11) Center of micropylar rosette showing micropyles (scale bar = 10 μm).

supported, according to the high recovery of these nodes in the bootstrap replications of the data set.

One of these three species, represented by two individuals from Argentina that was intercepted on a species of *Fragaria* (Rosaceae), is labeled as *Copitarsia* sp. This species may be *Copitarsia naenoides* (Butler), based on previous literature (Klein Koch and Waterhouse 2000); however, because there are only larval samples, adult vouchers are needed to confirm this identification.

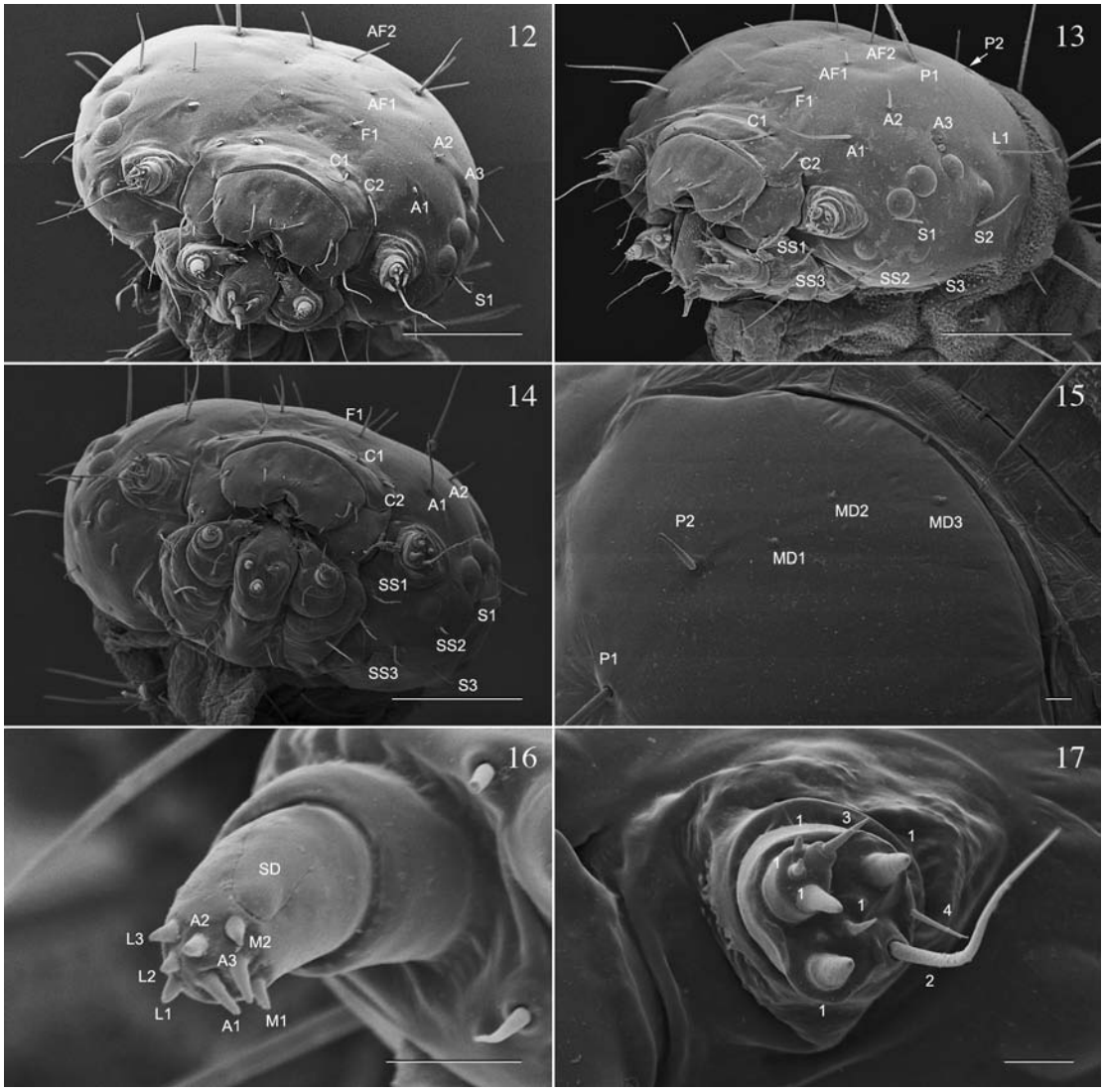
Copitarsia decolora is the best represented lineage in this study, with a total of 69 individuals within 50 unique haplotypes (Table 1; Fig. 1). This species is found in Colombia, Ecuador and Mexico. This species feeds on an array of hosts within Alliaceae, Apiaceae, Asteraceae, Brassicaceae, Campanulaceae, Caryophyllaceae, Chenopodiaceae, Clusiaceae, Fabaceae, Lamiaceae, Liliaceae, Papaveraceae, Plumbaginaceae, and Rosaceae. Optimization of locality data onto the cladogram in Fig. 1 indicates that *Copitarsia* originated in Ecuador and Colombia and later spread into Mexico. Based on the two star-like radiations of haplotypes within *C. decolora*, rapid incorporation of novel plant hosts has occurred independently in the Colombian radiation (Fig. 1, bracket a) and in the Mexican radiation (Fig. 1, bracket b). In the Colombian radiation, seven novel plant hosts have been incorporated into the diet; in the Mexican radiation, nine novel hosts have been acquired.

The third lineage, labeled *C. corruda*, is represented by 18 individuals with 13 haplotypes. Members of this clade were collected from Colombia, Ecuador, Mexico, and Peru. Host plants of *C. corruda* are found within the Apiaceae, Asteraceae, Iridaceae, Liliaceae, and Primulaceae. Notably feeding on *Asparagus* plants is exclusive to this clade. Based on optimization of geographic locality data onto the cladogram in Fig. 1, the center of origin is probably Peru, with later populations spreading into Colombia, Ecuador, and Mexico.

Discussion

Previous work has indicated that *C. decolora* was composed of at least two divergent lineages, one lineage that occurred mostly in Mexico and another lineage that occurred mostly in Peru (Simmons and Scheffer 2004). Our additional morphological and molecular investigations confirm this assertion; thus, this "cryptic" species is named and described below. Further studies indicate that the two lineages do indeed overlap, as on the same farm in Colombia (R.B.S., personal observation). Continued study is necessary to understand species isolation mechanisms temporally and spatially within *Copitarsia.*

Individuals of the cryptic species, *C. corruda*, have reliably been documented from Colombia, Ecuador, and Peru. One individual larva (haplotype 35); however, was

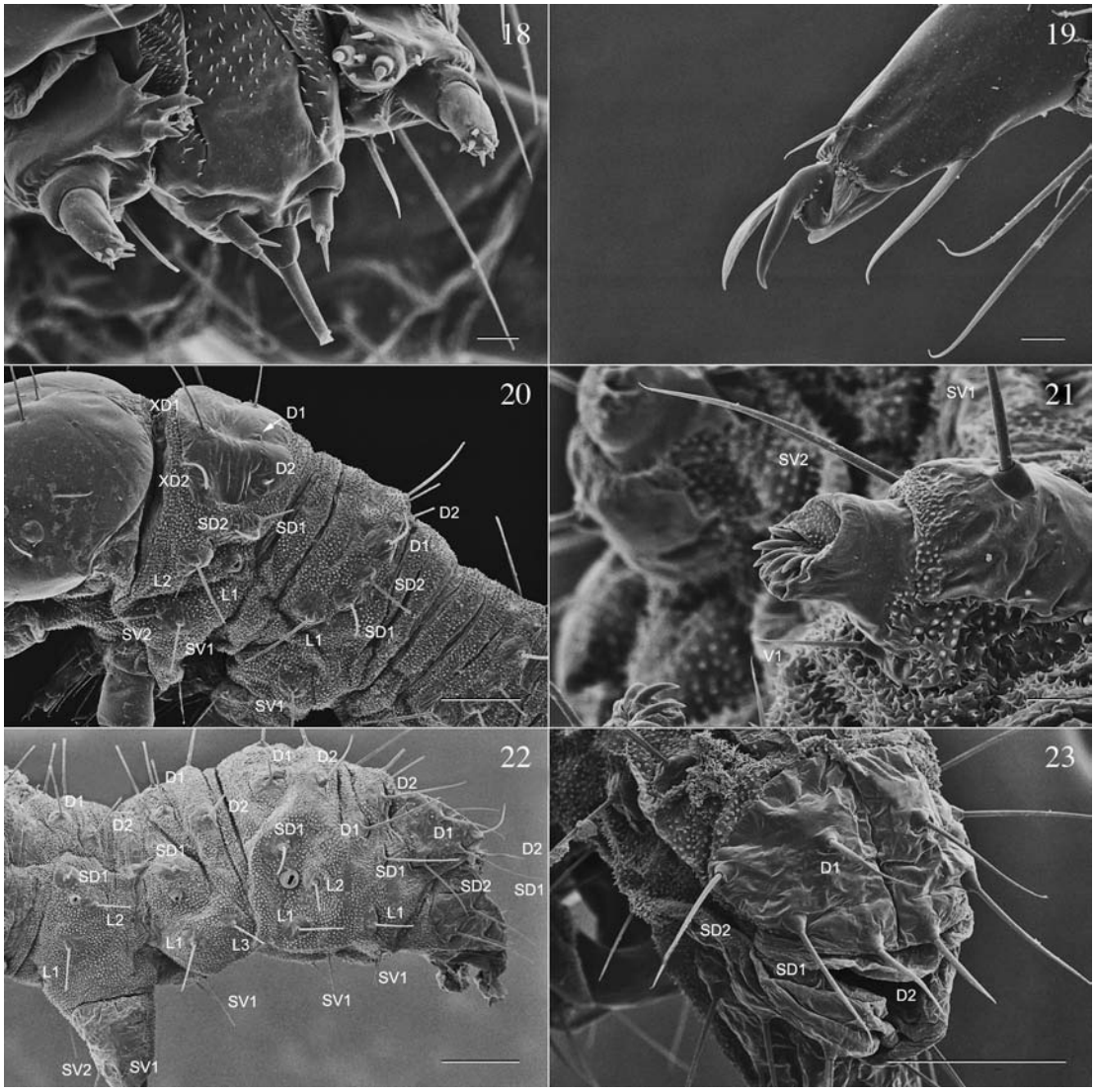


Figs. 12–17. First instar, head, and mouthparts, *Copitarsia corruda.* (12) Frontal view (scale bar = 100 μm). (13) Frontolateral view (scale bar = 100 μm). (14) Ventral view (scale bar = 100 μm). (15) Dorsoposterior view (scale bar = 100 μm). (16) Maxillary palpus, right (scale bar = 10 μm). (17) Antenna, left (scale bar = 10 μm); (1, sensilla basiconica; 2, sensillum chaetica; 3, sensillum styloconicum; 4, sensillum trichodeum).

intercepted on a Mexican shipment of *Asparagus* plants in San Diego (California) by USDA–APHIS. This record is problematic because it is extremely disjunct from the South American populations. We offer two possible explanations for this record. First, this larva may have originated from a South American shipment of produce and during transport, contaminated the Mexican shipment. Mature noctuid larvae can be highly mobile, and this scenario is not unlikely. The second explanation is that a small population of *C. corruda* has become established in Mexico (most likely facilitated by human commerce activity), but this population has not yet been detected. No other larvae or adults, however, have been intercepted from Mexico to date. We prefer the first explanation, but we cannot rule out the second.

Some separation in host plant preference occurs between the two species. *C. corruda* seems to prefer a narrower spectrum of host plant families than that of *C. decolora*, although this observation could be a sampling artifact. The only overlap between the two species in host plant choice is the diverse genus *Aster.* Host plant preference may provide a causal mechanism of speciation within *Copitarsia*, but further behavioral and population studies are needed to confirm this assertion.

Optimization of geographic location data onto the cladogram in Fig. 1 indicates that *Copitarsia* originated in South America and spread north into Mexico. Two recent expansions occur: one in Colombia/Mexico and another in Mexico. These star like haplotype clusters are indicative of recent expansions into localities



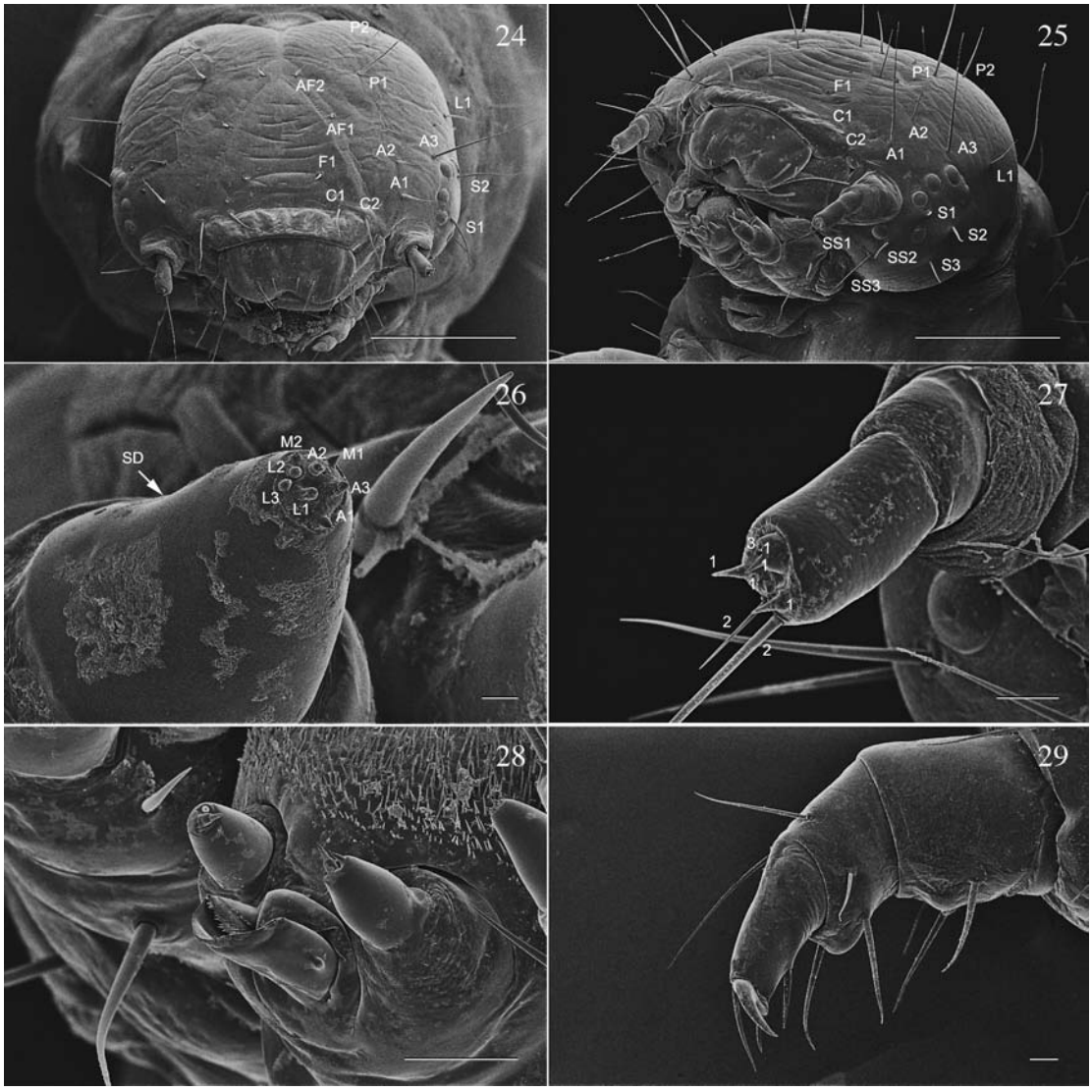
Figs. 18–23. First instar, mouthparts, thorax, and abdomen, *Copitarsia corruda.* (18) Spinneret (scale bar = 10 μm). (19) Right leg of T1 (scale bar = 10 μm). (20) Lateral view of thorax (scale bar = 100 μm). (21) Left proleg of A4 (scale bar = 10 μm). (22) Lateral view of A6–10 (scale bar = 100 μm). (23) Dorsoposterior view of A10 anal plate (scale bar = 100 μm).

(Scheffer 2000, Scheffer and Grissell 2003). Unfortunately, samples are not present from Central America to confirm and examine the number of invasions from South America into Mexico.

Copitarsia corruda Pogue & Simmons, new species
(Figs. 2–45)

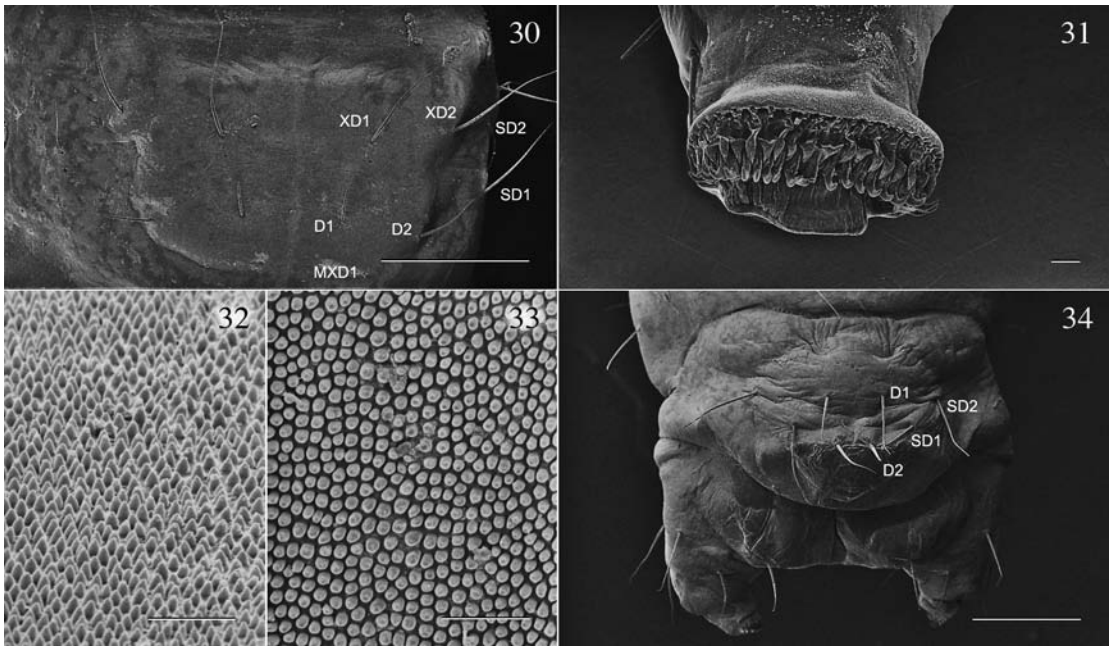
Diagnosis. There is no reliable way to differentiate adult *C. decolora*, *Copitarsia incommoda* (Walker), and *C. corruda* based on morphology other than characters in the genitalia. In the male genitalia, the apex of the uncus is broad in *C. decolora* (Simmons and Pogue 2004) and pointed in *C. corruda.* The clasper has a concave, truncate apex in *C. decolora* and has a straight to slightly convex apex in *C. corruda.* The lateral serrate plate at the base of the vesica on the noncornuti side is rounded and well developed in *C. corruda;* in *C. decolora* it is reduced and about half the width of the plate in *C. corruda.* The cornuti in *C. corruda* are slighter and not as robust as they are in *C. decolora.* In the female genitalia, the lateral lobes of the ostium bursae are much larger in *C. decolora* than in *C. corruda.* The valve lacks a corona in *C. incommoda,* which is present in both *C. decolora* and *C. corruda.* Diagnostic differences among larvae are provided in the following description of *C. decolora.*

Description. *Adult Male (Fig. 2). Head:* Frons with long gray scales, tipped white, giving tufted appearance; labial palpus mixed with black and tan scales, ventral fringe long, apical segment at angle from middle segment, porrect; scape with long dorsal tufts,



Figs. 24–29. Last instar, *Copitarsia corruda.* (24) Frontal view (scale bar = 1 mm). (25) Ventrolateral view (scale bar = 1 mm). (26) Right maxillary palpus (scale bar = 10 μm) (A2, sensillum styloconicum; A1, A3, M1, M2, L1–3, sensilla basiconica; SD, sensillum digitiform). (27) Right antenna (scale bar = 100 μm) (1, sensilla basiconica; 2, sensillum chaetica; 3, sensillum styloconicum). (28) Spinneret (scale bar = 100 μm). (29) Right leg of T3 (scale bar = 10 μm).

concolorous with vertex; antenna filiform with dark gray basal scales and tan distal scales on dorsal surface of each segment, ventral surface with dense white microtrichiae, scales absent; eyes large and round. *Thorax:* Prothorax gray with dirty white tipped scales along distal border; meso- and metathorax gray with more scales tipped with dirty white giving slightly paler overall coloration; foretibia with mixture of gray and dirty white scales; basitarsus dirty white with dark gray median band and row of large, curved spines ventrolaterally, remaining tarsal segments dark gray with dirty white apical bands; middle tibia mixed with dirty white and gray, tarsal segments dark gray with dirty white apical bands; hind tibia mixed with dirty white and dark gray but with more white than middle tibia, basitarsus mixed with dirty white and dark gray with distinct dirty white apical band, rest of tarsal segments dark gray with dirty white apical bands; underside with long, gray mixed with dirty white hair-like scales that become completely dirty white caudally. *Forewing:* Length 15–18 mm (n = 5). Ground color gray; costa with pairs of black spots at basal, antemedial, and postmedial lines, single spot present at median line; basal line with white spot bordered by sparse black scales between R and M veins; claviform spot absent; antemedial line crenulate with curved edge toward outer margin, white bordered by black from costa to posterior margin; orbicular spot round, white, bordered by sparse black scales; median line crenulate, obscure from costa between orbicular and



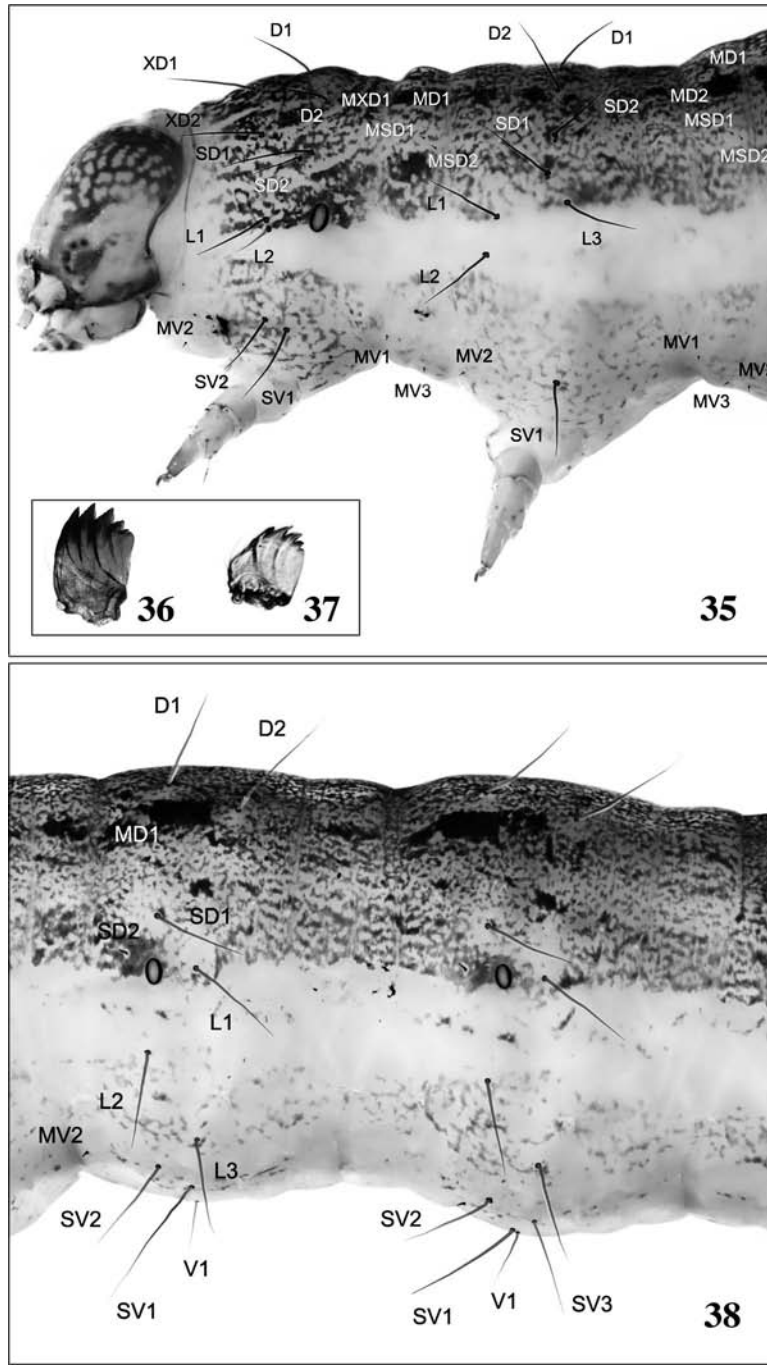
Figs. 30–34. Last instar, *Copitarsia corruda.* (30) T1 shield (scale bar = 1 mm). (31) Right A4 proleg (scale bar = 100 μm). (32) Lateral view of integument on A6 in area in line with SD2 below spiracle (scale bar = 10 μm). (33) Dorsal view of integument on A6 in area dorsad of D2 (scale bar = 10 μm). (34) A10, anal plate (scale bar = 1 mm).

reniform spots to Cu2 vein, pale gray bordered by black from Cu2 vein to posterior margin line; reniform spot white with gray center bordered by sparse black scales; postmedial line crenulate with curved edge toward body, black with scallops filled with white; subterminal area indistinct with mixture of gray and white scales; subterminal line with series of obscure black spots bordered by indistinct areas of white scales; terminal area gray mixed with white scales; terminal line with series of triangular black spots between wing veins; fringe gray with scales tipped white. *Hindwing:* Ground color white; veins dark gray with dark gray shading distally; fringe with pale brown base, gray median band, and rest white. *Abdomen:* First four dorsal segments with long, pale gray, hairlike scales, slightly tipped with white, remainder of segments mixed with hairlike, pale gray scales and black and white short scales; black ventrolateral spots on segments 4–7; ventral surface light brown mixed with sparse black scales. *Male genitalia* (Figs. 3-6): Uncus elongate, apex pointed; valve with sinuate costa; apex produced into a point; corona present; ampulla elongate, apex twisted and pointed; clasper spatulate with a round distal margin; base of sacculus with a curved apex extending into annellus; juxta a transverse band with a wedge-shaped ventral cutout and ventrally produced arms with a dorsal notch near apex; saccus V-shaped with a slightly produced, round, apex; aedoeagus slightly bent medially; a lateral, heavily sclerotized, serrate, triangular plate at apex of aedoeagus; a lateral round, serrate, sclerotized plate at apex of aedoeagus on opposite side of triangular plate; vesica elongate, base slightly bulbous and divided into two rounded projections each with a cluster of apical cornuti, a row of slender cornuti from the apical cluster on the triangular plate side of the vesica.

Adult Female. Description as in male except forewing length 16–18 mm (n = 5). *Genitalia* (Fig. 7): Papillae anales fleshy, rectangulate with round apices; eighth segment with lateral margins produced ventrally; small pockets of setae on either side of eighth segment; ostium bursae consists of two moderately produced lobes; ductus bursae heavily sclerotized, approximately three-fourths length of appendix bursae, numerous internal spicules present; appendix bursae elongate oval, larger than corpus bursae; corpus bursae round with prominent pleats; two signa present, one signum an elongate sclerotized ribbon extending completely around corpus bursae from opening with appendix bursae and second signum a shorter sclerotized ribbon approximately one-half length of former.

Egg (Figs. 8–11). Upright, hemispherical, somewhat narrowed apically, with narrowly raised, cylindrical micropylar neck (Figs. 8 and 9); aeropyle with rounded, longitudinally branched or unbranched ridges, (if branched, union occurs on top portion of egg); ridges connected by short, slightly raised crossbranches, forming faint lattice like framework; micropylar area with rosette of many oblong cells, each cell narrowly raised marginally (Fig. 10); central part of rosette with small rosette of several short cells marginally demarcating smaller, sunken, rosette-shaped hub with several short arms, each arm leading to single micropyle; hub with eight micropyles (Fig. 11).

First Instar (Figs. 12–23). Length, 2.5–2.8 mm (n = 5): Body white; head capsule, prothoracic shield, legs,



Figs. 35–38. *Copitarsia corruda*, larva. (35) Lateral view of head and T1–2 of last instar. (36) Inner surface of mandible of last instar. (37) Inner surface of mandible of first instar. (38) Lateral view of A1–2 of last instar.

spiracular rims, and pinacula shinny, dark brown; prolegs on A3–4 reduced. *Head* (Figs. 12–18): Hypognathous; epicranial suture short; epicranial notch deeply emarginated medially; AF2 slightly above or even with apex of frons, nearly twice the length of AF1 and F1; C1 and C2 about equal in length; P1 in line with AF2, about twice length of and ventromedial to P2; MD1-3 posterolateral to P2; L1 dorsolateral to A3; A3 closest to stemma 2, A1 and A2 in line slightly lateral to C2; S3 near lower margin of gena; S2 ventroposterior to stemma 1; S1 slightly ventrolateral to stemma 4; SS-group setae in triangular pattern; SS1 ventral to antenna; SS2 lateral to stemma 5; and SS1 on genal margin near labial complex; stemmata arranged in

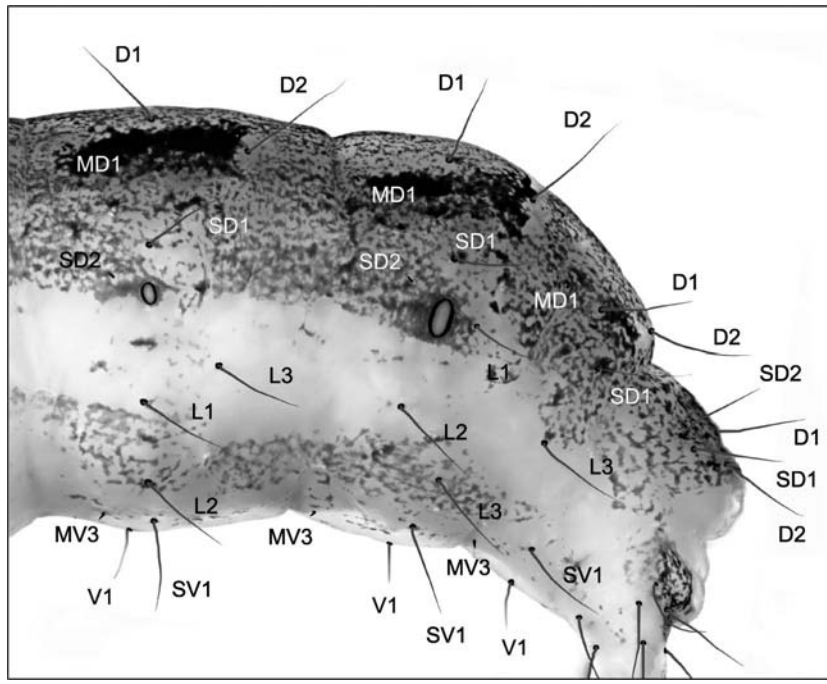
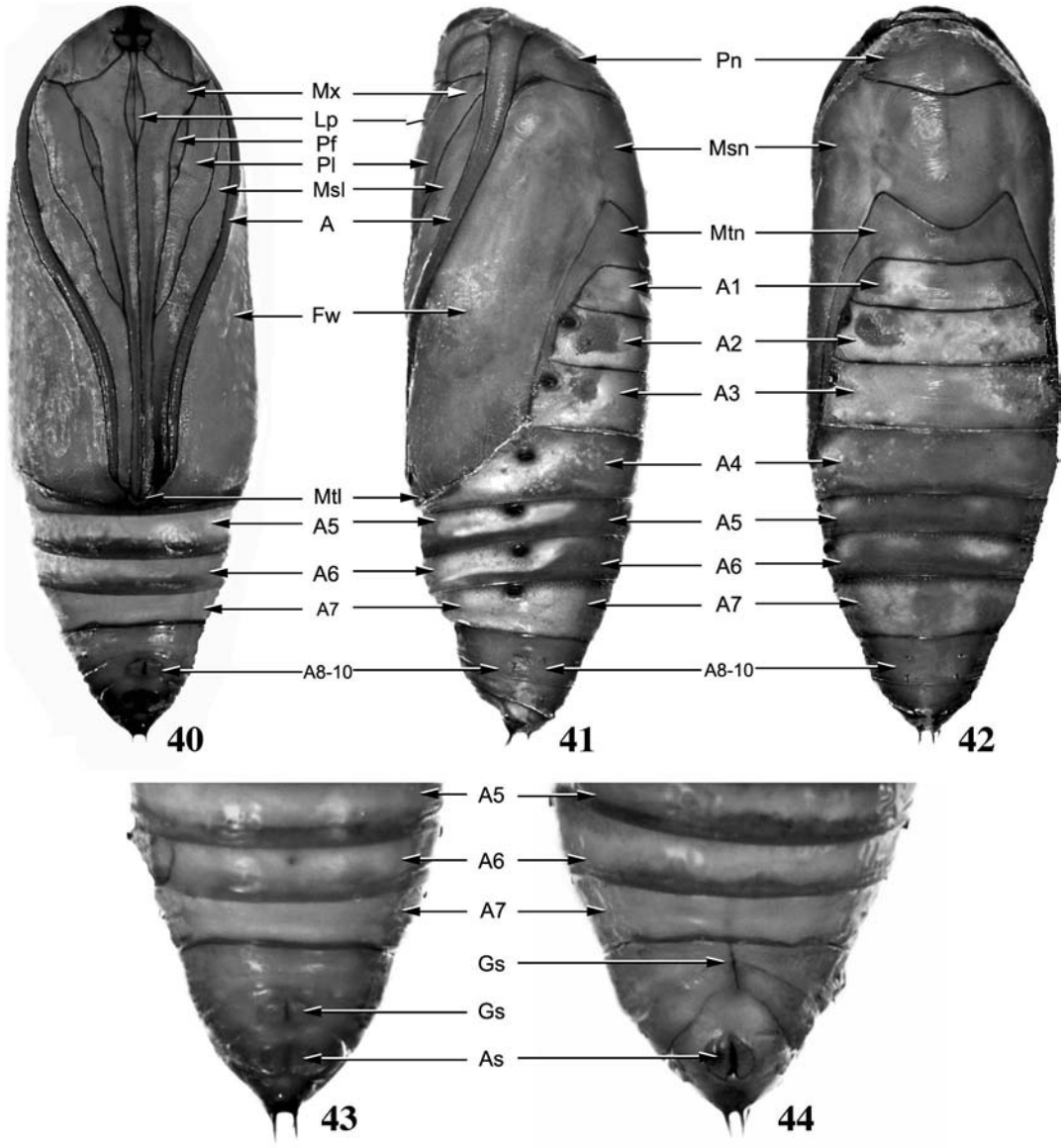


Fig. 39. Last instar, *Copitarsia corruda*; lateral view of A7–10.

C-shaped pattern with stemma 1–2 paired but separate, stemmata 3–4 nearly touching, and stemmata 5–6 paired but separate; maxillary palpus cylindrical, elongate, with sensilla arranged as in Fig. 16; antenna cylindrical and short, with sensilla arranged as in Fig. 17; spinneret, narrow, cylindrical, porrect, extending beyond labial palpus (Fig. 18); mandible with four large, acutely angled, narrowly rounded dentitions in series, with one shorter, rounded dentition on dorsal end; one small, pointed dentition on inner surface of first dentition nearest condyle; mandibular setae subequal; clypeus with six pairs of setae, two pairs on lateral margin, two pairs on ventral margin, and two pairs along midline; lateral and medial pairs subequal. *Thorax* (Figs. 19 and 20): shield on T1 with XD1 and XD2 equal in length, in virtually straight line along anterior margin; D1 closer to longitudinal body axis than XD1; D2 closer to longitudinal body axis than XD2; SD2 longer than SD1, both approximate and separate from shield; SD1 at least twice length of D-group setae; L1 3–4 times longer than L2; L2 hairlike; spiracular rim conical; SV-group bisetose, equal in length; procoxae slightly closer than coxae on T2–3; V1s approximate, near anterior margin of coxae (not shown); claw simple, flattened seta with pointed apex extending from laterodistal surface of tarsus to beyond claw and flattened seta with rounded apex extending from ventrodistal surface of tarsus (Fig. 19). T2–3 with D1, D2, SD1, SD2 equally spaced and in straight line, L1 slightly anterior; D1 on larger pinaculum than D2; SV1 slightly posterior to SD1; V1s farther apart than V1s on T1, slightly anterior or even with posterior margins of coxae; claw as in Fig. 19. *Abdomen:* A1–A2 (Figs. 21–23): D1 dorsoanterior to D2; SD1 dorsoanterior to spiracle; spiracle conical, largest on T1 and A8; L1 in straight line with spiracle and SD1 on A1; L1 and SD1 anterior to spiracle on A2; L2 dorsoposterior to spiracle on A1, medioposterior or ventroposterior to spiracle on A2; SV-group unisetose on A1, bisetose on A2; SV1s in straight line with V1s on A1, slightly anterior to V1s on A2; SV2 ventroanterior to SV1, and on smaller pinaculum. A3–A6 as above except: SV-group bisetose; prolegs on A3–4 about equal in length, both smaller than prolegs on A5–6; prolegs on A3–4 with 5–6 crochets in mesoseries, prolegs on A5–6 with 7–8 crochets. A7 as above except: L2 closer to L1 than to spiracle, SV1 in straight line with L2, both posterior to V1s; V1s as in A1–2. A8 as above except: L2 closer to spiracle than to L1 and spiracle larger than on T1; spiracular opening elliptical. A9 with D1 anteroventral to D2; D2, SD1, and L1 almost in straight line; SV1 along posterior margin. Anal plate of A10 with D1, SD1, and SD2 about equal in length and equidistant; D2 slightly shorter, closer to median axis than D1; SV-group with six setae; prolegs with eight crochets in mesoseries.

Last Instar. Coloration and pattern (Figs. 35, 38, and 39). Length, 37.2–41.9 mm (n = 16). *Head:* Epicranium brown; tonofibrillary platelets, genal area, frontoclypeus, and area between A1–2 and A3 from base of antenna to point in line with L1 pale brownish yellow. *Thorax:* Prothoracic shield yellowish brown mottled with brown; legs pale brownish yellow; pinacula pale yellowish brown, small. *Abdomen:* Integument covered with short, conical projections, each with rounded apices (Figs. 32 and 33); dorsal



Figs. 40–44. Pupa, *Copitarsia corruda.* (40) Ventral view. (41) Lateral view. (42) Dorsal view. (43) Ventral view of male segments A5–10. (44) Ventral view of female segments A5–10. (A, antenna; As, anal suture; Fw, forewing; Gs, genital suture; Lp, labial palp; Msl, mesothoracic leg; Msn, mesonotum; Mtl, metathoracic leg; Mtn, metanotum; Mx, maxillae; Pf, prothoracic femora; Pl, prothoracic leg; Pn, pronotum).

stripe mottled gray intermixed with grayish brown and pale gray with dark-pigmented, irregular, V-shaped or triangular-shaped marking on medioanterior part of segments on A1–9; subdorsal stripe dark brown on anterior one third to one half, extending slightly beyond spiracle; spiracular stripe as dorsal stripe except ventral margin darkly pigmented; subspiracular stripe pale gray or pale brown with few markings; ventrolateral area with mottled gray marking intermixed with pale gray or pale brown; pinacula pale yellowish brown, small; A10 with anal plate and large SV pinaculum mottled dark brown intermixed with brownish yellow. Morphology. *Head* (Figs. 24–28): Hypognathous; epicranial suture short; epicranial notch deeply emarginated dorsally; AF2, AF1, and F1 subequal in length, AF2 at apex of frons or slightly above; C1 and C2 slightly longer than above setae, both ventrolateral to F1; P1 ≈2.5 times length of P2; P2 dorsolateral to P1; 3 MD setae dorsal to P2 (not shown); L1 as far above stemma one as distance between stemma one and stemma 6; stemmata 3–4 approximate, stemma five ventral to antenna, and stemma six lateral to antenna; A1 and A3 about equal in length, both ≈2.5 times longer than A2; A2 in horizontal line with and slightly farther from A3 than to A1; S-group setae about equal in length; S3 ventral to S2; S2 slightly ventrolateral to

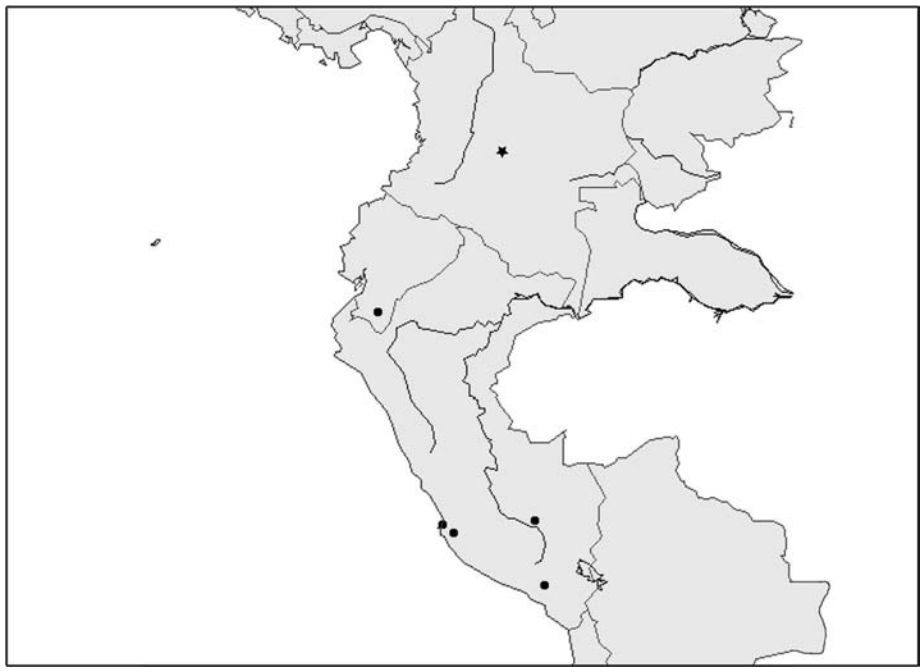
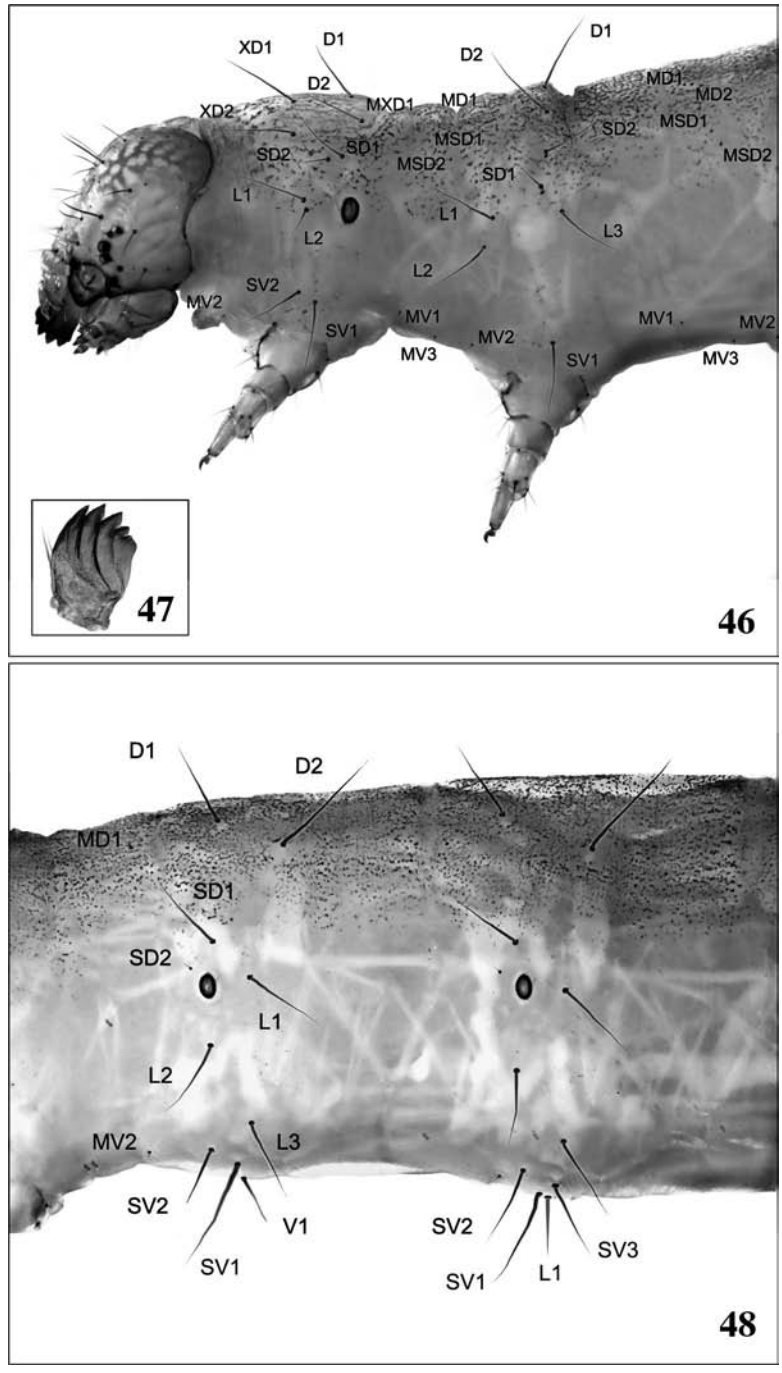


Fig. 45. Collecting localities of *C. corruda.* (★, no specific locality).

stemma 1; S1 approximate and lateral to stemma 4; SS-group setae nearly equal in length, in compact triangular pattern ventral to antenna; maxillary palpus subconical, sensilla arranged as in Fig. 26; antenna cylindrical and elongate, sensilla arranged as in Fig. 27; spinneret slightly longer than labial palpus, broadly arched, concave dorsally; lower lip smooth, margin entire, extending beyond upper lip, upper lip wrinkled medially from base to margin, margin with irregularly spaced, elongate serrations, medial area flanked by two broad lateral lobes; mandible longer than wide, with four large dentitions in series, each with minute serrations; dorsal dentition lobe like with small serrations; ventral dentition with sharp tooth on inner surface; mandibular setae subequal; clypeus with six pairs of setae, two pairs on lateral margin, two pairs on ventral margin, and two pairs along midline; lateral and medial pairs subequal. *Thorax* (Figs. 29 and 30): T1: XD-group slightly longer than D-group; XD2 slightly posterior to XD1; D2 near posterior margin, closer to XD1 than to XD2; D1 near median longitudinal axis; MXD1 on posterior margin between D1 and D2, posterior to D1; SD1 and SD2 approximate, separate from shield; SD1 slightly longer than SD2, SD2 hair-like; spiracle on T1 larger than spiracles on A1–7; L-group subequal, approximate; L1 dorsoanterior to L2, in line with XD2; L2 hairlike, slightly above or in line with ventral rim of spiracle; SV-group subequal; procoxae juxtaposed medially, V-group approximate, slightly anterior to posterior margins of coxal bases; MV2 posterolateral to median cervical gland; lobe-bearing gland transversely elliptical; MDs approximate, slightly closer than distance between V1s and slightly anterior to anterior margin of coxal bases; claw as figured (Fig. 29). T2–T3 with MD1 on anterior part of segment between D1 and D2; T3 with MD-group bisetose between D1 and D2; D1, D2, SD1, and SD2 subequal in length and nearly in straight line; SD1 and SD2 with small, darkly pigmented tonofibrillary platelet ventral to base; SD2 hairlike (in some specimens may be shorter than SD1); MSD1 and MSD2 approximate, ventral to MD-group and in line with or slightly ventral to SD2; L2 anteroventral to L1; L3 dorsoposterior to L2 and in straight line or slightly anterior to SV1; V1s slightly posterior to coxal bases, ≈5 times distance apart as distance between V1s on T1; MV-group trisetose, anterior to coxal base; MV1 near anterior margin, slightly above MV2; MV2 anterior to L2 and beneath SV1; MV3 ventral to and between MV1 and MV2, in line with middle of coxa. *Abdomen* (Figs. 31–34): A1 and A2: MD1 in line with D2; D2 slightly longer than D1; D1 dorsoanterior to D2 and closer to median longitudinal axis; SD1 dorsal to and slightly posterior to spiracle on A1 and dorsal and slightly anterior to spiracle on A2; SD2 min, dorsoanterior to spiracle on A1 and medioanterior to spiracle on A2; L1 medioposterior to spiracle; L2 ventroanterior to spiracle and in line with SV2; L3 ventroposterior to L1 and in line with SV1; SV-group bisetose on A1, trisetose on A2; SV1 slightly longer than SV2 and SV3 and ≈2.5 times longer than V1; SV1 slightly closer to V1 than to L3; V1 in line with L3; MV2 in line and closest to SV1 on A1, between SV3 and SV1 on A2. A3–6 as above except: L3 posterior to D2; SV-group trisetose on proleg; V1 on proleg above planta; MV3 anterior to midline of base of proleg; proleg with 18–25 crochets in mesoseries, with slightly more crochets on anterior prolegs than on posterior prolegs. A7 as above except:



Figs. 46–48. Last instar, *Copitarsia decolora*. (46). Lateral view of head and T1–2. (47) Inner surface of mandible. (48) Lateral view of A1–2.

SD1 dorsoposterior to spiracle; SD1, L1, L2 in vertical line; L3 slightly anterior to D2; L2 in line with V1 with SV1 and slightly posterior to both; MV3 anterior to V1 and SV1 forming an equilateral triangle. A8 as above except: spiracle larger than spiracle on T1; L2, SV1, and V1 nearly in straight line; MV3 between and ≈2 times farther from V1 and SV1 than on A7, forming acute triangle. A9 with D1 anteroventral to D2; D2 SD1, and L3 in straight line; SD1 hairlike; SV1 and V1 in straight line; MV3 as in A7. Anal plate (A10) with distance between SD1 and SD2 slightly greater than distance between D2 and SD1; D1 closer to SD1 than to D2; D1 and SD1 nearly in straight line; proleg with five lateral setae, two ventral setae, and 22–26 crochets.

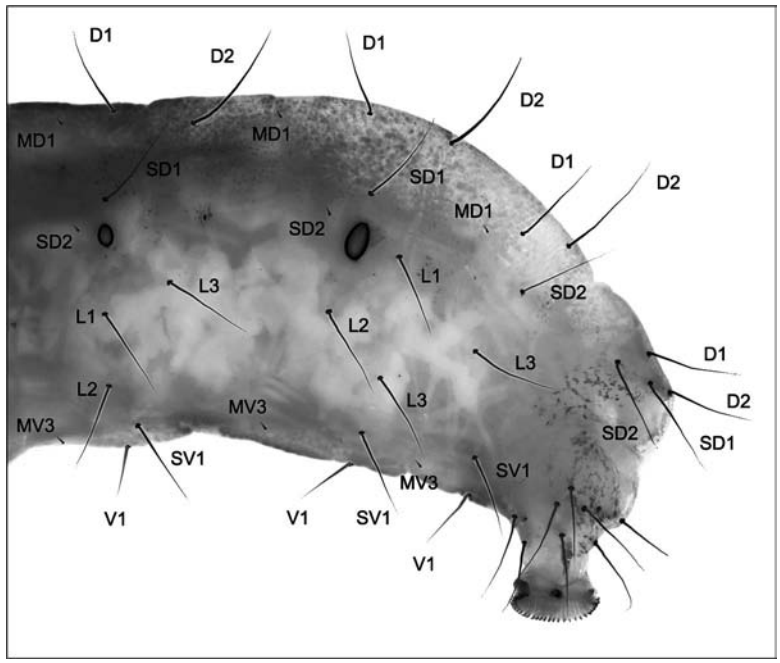


Fig. 49. Last instar, *Copitarsia decolora*; lateral view of A7–10.

Pupa (Figs. 40–44). Length, 18.0–8.5 mm in male ($n = 5$), 17.0–17.9 mm in female ($n = 5$). Obtect; adecticous; smooth, brownish yellow to dark brown; labial palpus (Lp) extends from clypeus to middle or beyond middle of foreleg (Pf); foreleg short, between anterior part of maxilla (Mx) and prothoracic leg; maxillae long, extending to posterior margin of A4, exposing distal apex of metathoracic leg (Mtl); mesothoracic leg (Ml) slightly shorter than metathoracic leg; antenna (A) widely arched anteriorly, converging posteriorly, slightly shorter than midlegs; abdominal rotation between A4 and A5; A8–10 fused; genital suture on A9 in male (Fig. 43), A8 in female (Fig. 44); cremaster with 3–7 elongate spines (Figs. 43 and 44).

Type Material (Fig. 2). HOLOTYPE: male, Peru, Arequipa, Lima-Tacna Rd. ≈2 km NW intersect. Ave. Parra, 27-III-1979, G. Buckingham, on cabbage GRB-79-29.1. USNMENT 00142164, USNM genitalia slide 49785. Deposited in USNM.

PARATYPES: COLOMBIA: [no locality data], Fassel, 3 males, USNMENT 00142076-, 00142077, 0042078, USNM genitalia slides 46487, 49791, 49792. ECUADOR: LOJA PROVINCE: Environs de Loja, 1890, Dognin Coll., 2 males, USNMENT 00142090, USNM genitalia slide 46481, USNMENT 00142092, 1 female, USNMENT 00142095, USNM genitalia slide 46483; Environs de Loja, 87, Dognin Coll., 1 male, USNMENT 00142091; Loja, 1 male, USNMENT 00142093, USNM genitalia slide 46482; Loja, février 86, 1 female, USNMENT 00142094. PERU: AREQUIPA PROVINCE: Arequipa, Dognin Coll., 1 female, USNMENT 00142255, USNM genitalia slide 46495; Arequipa, Lima–Tacna Rd., 1 km NW intersect. Ave. Parra, 27-III-1979, G. Buckingham, on cabbage GRB-79–29.3, 1 male, USNMENT 00142163, USNM genitalia slide 46985. CUZCO PROVINCE: Cuzco, 15-VII-1973, 1 male, USNMENT 00147941, USNM genitalia slide 46982, USNM metathorax slide 49432. ICA DEPARTMENT: Ica, 20-XII-1970, C. Garcia, 1 female, USNMENT 00147940, USNM genitalia slide 49794; PISCO PROVINCE: Pisco, Agroparacas, 24/I/97, 1 male, USNMENT 00142244, USNM genitalia slide 46960.

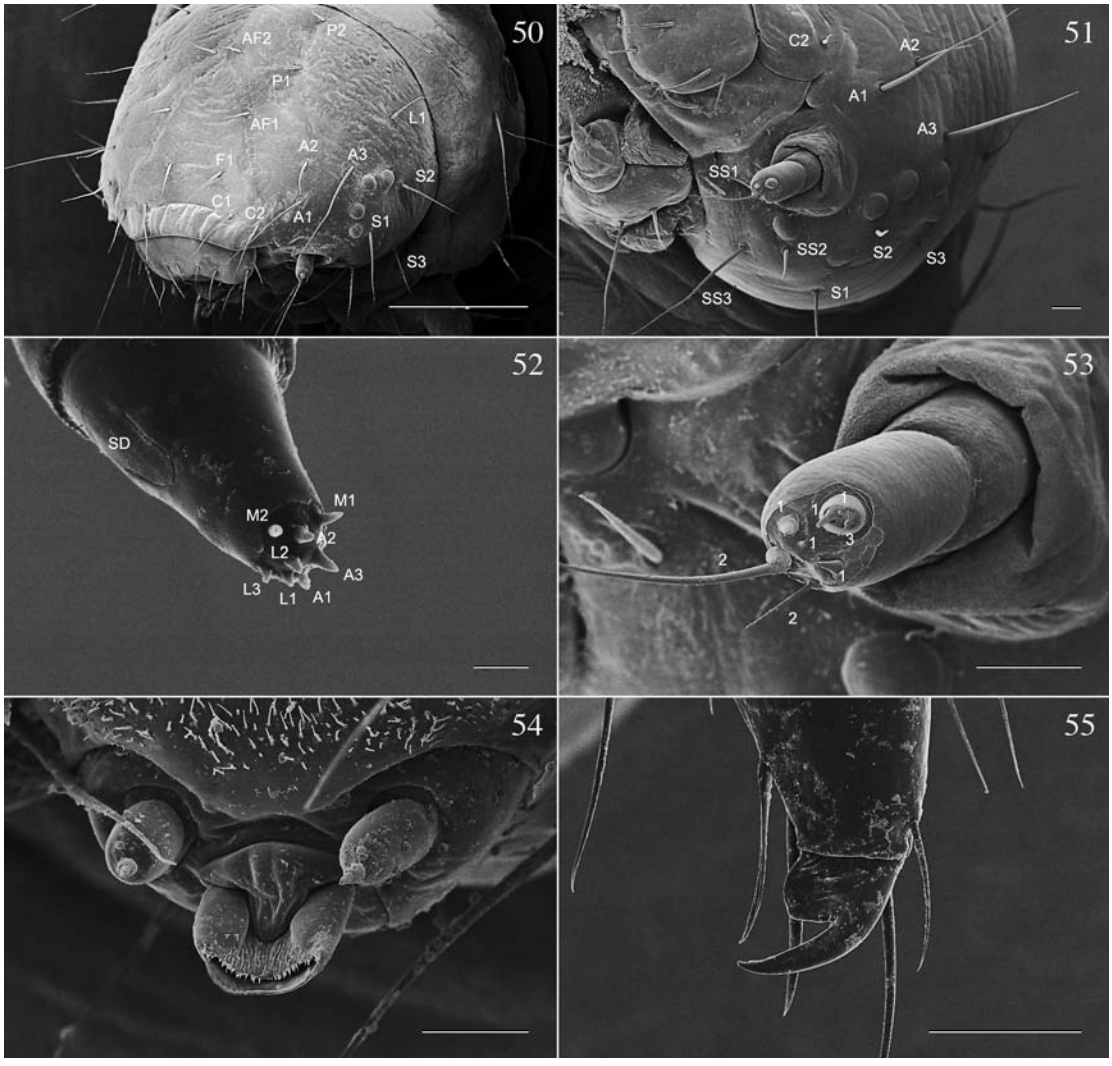
Etymology. The name *corruda* is Latin for wild asparagus and its gender is feminine. Larvae are pests of many species, including asparagus from coastal Peru.

Flight Period. From the collection dates on specimen labels this species is active from December through March and in July. Given the paucity of correctly identified specimens, we predict that future study will reveal a continuously brooded species.

Distribution (Fig. 45). Along the Andes from southern Ecuador to southern Peru and from the southern desert coast (Pisco and Ica, Peru). One individual larva intercepted on an *Asparagus* shipment from Mexico is probably not a valid record as discussed above.

Discussion. Due to the confusion of the *Copitarsia* species similar to *C. decolora*, the economic literature cannot be reliably used to obtain information on distribution, phenology, and larval hosts. Simmons and Pogue (2004) sorted out the taxonomy and described the differences between *C. decolora* and *C. incommoda.*

Larval hosts for *C. decolora* include species from 12 genera in nine families, and in *C. corruda* larval hosts include species from nine genera and seven families (Simmons and Scheffer 2004). Hosts from only the two genera *Limonium* (Plumbaginaceae) and *Alstroemeria* (Liliaceae) are shared by both species. These



Figs. 50–55. Last instar, *Copitarsia decolora.* (50) Frontolateral view of head (scale bar = 1 mm). (51) Ventrolateral view of head (scale bar = 100 μm). (52) Left maxillary palpus (scale bar = 10 μm) (A2, sensillum styloconicum; A1, A3, M1, M2, L1–3, sensilla basiconica; SD, sensillum digitiform). (53) Left antenna (scale bar = 100 μm) (1, sensilla basiconica, 2, sensillum chaetica, 3, sensillum styloconicum). (54) Spinneret (scale bar = 100 μm). (55) Left leg on T2 (scale bar = 100 μm).

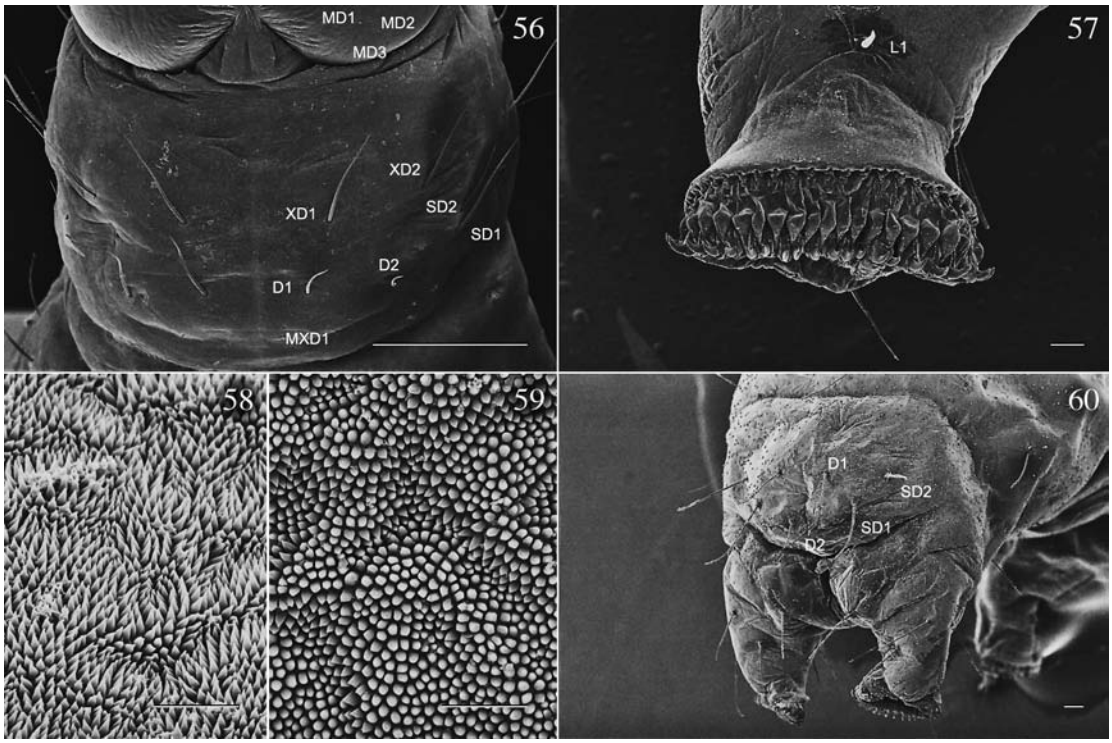
shared hosts are from specimens originating in Colombia and Ecuador. Larvae may show some host plant partitioning in areas where both species occur.

Copitarsia decolora (Guenée)
(Figs. 46–60)

The last instar of *C. decolora* is described to provide comparison with that of *C. corruda.*

Diagnosis. There are considerable differences in the overall color pattern between *C. decolora* and *C. corruda.* The overall coloration of the integument is less pigmented and the reticulate pattern is finer in *C. decolora* than the much heavier reticulations and darker coloration in *C. corruda. C. corruda* also has irregular black patches dorsolaterally which are lacking in *C. decolora.* The ventral surface of *C. decolora* lacks reticulations, but these are present in *C. corruda.*

Last Instar. Coloration and pattern (Figs. 46, 48, and 49). Length, 39.8 mm ($n = 1$). *Head:* Epicranium pale brown; tonofibrillary platelets, genal area, frontoclypeus, and area between A1–2 and A3 from base of antenna to point in line with L1 pale yellow to near white. *Thorax:* Prothoracic shield pale yellowish brown with several narrow, irregularly shaped, grayish longitudinal stripes; legs pale yellowish brown; pinacula pale yellowish brown. *Abdomen:* Integument covered with short, conical projections with pointed apices (Figs. 48 and 49); dorsal and subdorsal stripes with several narrow, irregularly shaped, grayish longitudinal stripes; other areas unpigmented or with few markings; A10 with anal plate and large SV pinaculum



Figs. 56–60. Last instar, *Copitarsia decolora*. (56) T1 shield (scale bar = 1 mm). (57) Left proleg on A3 (scale bar = 100 μm). (58) Lateral view of integument on A6 in area above SD1 (scale bar = 10μ). (59) Dorasl view of integument on A6 dorsad of D2 (scale bar = 10 μm). (60) A10 anal plate (scale bar = 100 μm).

pale brownish yellow with several narrow, irregularly shaped, grayish longitudinal stripes. Morphology. *Head* (Figs. 50–54): Hypognathous; epicranial suture short; epicranial notch deeply emarginate dorsally; AF2, AF1, and F1 about equal in length, AF2 at apex of frons or slightly above (including observations from previous instars); C1 and C2 slightly longer than above setae, both ventrolateral to F1; P1 ≈2.5 times length of P2; P2 dorsal or slightly dorsolateral to P1; 3 MD setae dorsal to P2; L1 as far above stemma 1 as distance between stemma 1 and stemma 6; stemmata 3–4 approximate, stemma 5 ventral to antenna, and stemma 6 lateral to antenna; both A1 and A3 ≈2.5 times longer than A2; A2 in horizontal line with and slightly further from A3 than to A1; S-group setae about equal in length; S3 ventral to S2; S2 slightly ventrolateral to stemma 1; S1 approximate and lateral to stemma 4; SS-group nearly equal in length, in a triangular pattern ventral to antenna; maxillary palpus conical, sensilla arranged as in Fig. 52; antenna cylindrical and elongate, sensilla arranged as in Fig. 53; spinneret slightly longer than labial palpus, broadly arched and concave dorsally; lower lip smooth, margin entire, extending beyond upper lip, upper lip wrinkled medially from base to margin; margin with irregularly spaced, elongate serrations, medial area flanked by two broad lateral lobes; mandible longer than wide, with four large dentitions in series, each with minute serrations; dorsal dentition lobe-like with small serrations; ventral dentition with a sharp tooth on inner surface; mandibular setae subequal; clypeus with six pairs of setae, two pairs on lateral margin, two pairs on ventral margin, and two pairs along midline, lateral and medial pairs subequal. *Thorax* (Figs. 55 and 56): XD-group setae slightly longer than D-group setae; XD2 slightly posterior or in line with XD1; D2 near posterior margin, about equidistant from XD1 and XD2; D1 anterior to D2 and close to median longitudinal axis; MXD1 on posterior margin between D1 and D2, posterior to D1; SD1 and SD2 approximate, separate from shield; SD2 hairlike, anteroventrad of SD1; spiracle larger on T1 than spiracles on A1–7; L-group subequal, approximate; L1 dorsoanterior to L2, in line with or slightly posterior to XD2; L2 hairlike, slightly above or in line with ventral rim of spiracle; SV-group subequal; procoxae juxtaposed medially, V-group approximate, slightly anterior to posterior margins of coxal bases; MV2 posterolateral to median cervical gland; lobe-bearing gland transversely elliptical; MV3s approximate, slightly closer than distance between V1s and slightly anterior to anterior margin of coxal bases; claw as figured (Fig. 55). T2–T3 with MD1 on anterior part of segment between D1 and D2; T3 with MD-group bisetose between D1 and D2; D1, D2, SD1, and SD2 about equal in length, and in a straight line; SD1 and SD2 with a small, darkly pigmented tonofibrillary platelet ventral to base; SD2 hairlike; MSD1 and MSD2 approximate, ventral to MD-group and in line with or

slightly ventral to SD2; L2 anteroventral to L1; L3 dorsoposterior to L2 and in a straight line with or slightly anterior to SV1; V1s slightly posterior to coxal bases, ≈5 times the distance apart as distance between V1s on T1; MV-group trisetose, anterior to coxal base; MV1 near anterior margin, slightly above MV2; MV2 anterior to L2 and beneath SV1; MV3 ventral to and between MV1 and MV2, in line with middle of coxa. *Abdomen* (Figs. 57–60): A1 and A2: MD1 in line with D2; D2 slightly longer than D1; D1 dorsoposterior to D2 and closer to median longitudinal axis; SD1 dorsal to and slightly posterior to spiracle on A1 and dorsal and slightly anterior to spiracle on A2; SD2 min, dorsoanterior to spiracle; L1 dorsoposterior to spiracle on A1 and medioposterior to spiracle on A2–6; L3 in near vertical line with L1 and slightly posterior to SV1; SV-group bisetose on A1, trisetose on A2; SV1 slightly longer than SV2 and SV3 and ≈2.5 times longer than V1; SV1 in line with V1; MV2 on anterior part of segment between SV2 and SV1. A3–6 as above except: L3 posterior to D2; SV-group trisetose on proleg, V1 above planta; MV3 anterior to medial base of proleg; proleg with 24–27 crochets in mesoseries, with more crochets on posterior prolegs. A7 as above except: SD1 dorsomedial to spiracle; L-group ventral to spiracle, with L3 dorsal to L1 and L2; SV1 in line with V1. A8 as above except: spiracle larger than spiracle on T1; L1 in vertical line with or slightly posterior to L3; SV1 and V1 in straight line anterior to L3. A9 with MD1 on anterior part of segment, between D1 and SD2; D1 anteroventral to D2; D2, SD1, and L3 in nearly a straight line; SD1 hairlike; SV1 and V1 in a straight line; MV3 between SV1 and V1. Anal plate (A10) with distance between SD1 and SD2 slightly greater than distance between D2 and SD1; D1 closer to SD1 than to D2; D1 and SD1 nearly in a transverse straight line; proleg with 30 crochets.

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