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10 **Vouchering DNA-barcoded specimens: Test of a**
11 **non-destructive extraction protocol for arthropods**

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26 Running head: VOUCHERING DNA-BARCODED SPECIMENS

27 **Abstract**

28

29 The correct identification of species is essential to the performance of ecological and evolutionary
30 research. Morphology-based keys support accurate identification of many taxa. However, for taxa
31 that are not well studied, or for which distinguishing morphological characters have not been
32 discerned, identification can be difficult. Accurate identification is especially problematic for
33 very small organisms, for members of cryptic species complexes, for eggs, and for immature
34 stages. For such cases, DNA barcodes may provide diagnostic characters. Ecologists and
35 evolutionary biologists deposit museum vouchers to document the species studied in their
36 research. If DNA barcodes are to be used for identification, then both the DNA and the specimen
37 from which it was extracted should be vouchered. We describe a protocol for the non-destructive
38 extraction of DNA from terrestrial arthropods, using as examples members of the orders Acarina,
39 Araneae, Coleoptera, Diptera, and Hymenoptera, which were chosen to represent the ranges in
40 size, overall sclerotization, and delicacy of key morphological characters in terrestrial arthropods.
41 We successfully extracted sequenceable DNA from all species after 1 – 4 h of immersion in
42 extraction buffer. The extracted carcasses, processed and imaged using protocols standard for the
43 taxon, were distinguishable from closely related species, and adequate as morphological
44 vouchers.

45

46 **Introduction**

47

48 The correct identification of species is essential to the performance of ecological and evolutionary
49 research. Morphology-based keys support accurate identification of many taxa. However, for taxa
50 that are not well studied, or for which distinguishing morphological characters have not been
51 discerned, identification can be difficult. Accurate identification is especially problematic for
52 very small organisms, for members of cryptic species complexes, for eggs, and for immature
53 stages (Toft 1983; Cockburn 1990; Sperling & Hickey 1994; Brunner *et al.* 2002; Chen *et al.*
54 2002; Armstrong & Ball 2005; Ball *et al.* 2005; Greenstone *et al.* 2005; Barber & Boyce 2006;
55 Grosjean *et al.* 2006). For such situations, species-specific fragments of DNA, known as DNA
56 barcodes (Ball *et al.* 2005), may provide a new source of characters for species level
57 identification.

58

59 Ecologists and evolutionary biologists should deposit museum specimens, referred to as
60 vouchers, to document the species studied in their research (Thomas 1994). If DNA barcodes are
61 to be used for identification, then the DNA as well as the specimen from which it was extracted
62 should be vouchered (Hafner 1994). Many protocols for DNA extraction, especially for small
63 specimens, require maceration of the entire specimen, precluding deposition of the carcass as a
64 museum voucher (Whitfield & Cameron 1994). One suggested approach is to take multiple
65 images of the specimen before maceration (De Lay *et al.* 2005). Another approach, for
66 sufficiently large, bilaterally symmetric animals, is to remove a single appendage for DNA
67 extraction (Starks & Peters 2002). However, if there are appendage-specific characters essential
68 for species identification, subsequent loss of the remaining appendage of the pair, during
69 shipment or routine examination, would render the specimen useless as a voucher. Alternatively,

70 the removed appendage could be curated with the rest of the specimen, but this is tedious and
71 introduces opportunities for mix-ups.

72

73 An on-line resource, MorphBank (<http://morphbank.net>), links specimen images directly
74 to GeneBank sequences. However, GenBank contains numerous errors (Harris 2003; Vilgalys
75 2003). For this reason as well, it is important to be able to link a DNA sequence to the
76 morphologically identifiable specimen from which the DNA was extracted.

77

78 Besides providing new characters for hitherto poorly known groups, the study of DNA
79 sequence data has enabled new insights into the ecology and phylogenetic relationships of well
80 studied taxa, including the largest phylum of organisms, Arthropoda (e.g., Paskewitz & Collins
81 1990; Brower 1999; Gleeson *et al.* 2000; Anderson *et al.* 2000; Wells & Sperling 2001; Chen *et*
82 *al.* 2002; Brunner *et al.* 2002; Jarman *et al.* 2002; Besansky *et al.* 2003; Ball *et al.* 2005; Barrett
83 & Hebert 2005; Greenstone *et al.* 2005; Hogg & Hebert 2005; Mitchell *et al.* 2005; Monaghan *et*
84 *al.* 2005; Greenstone 2006; Ball & Armstrong 2006; Barber & Boyce 2006; Hajibabael *et al.*
85 2006; Kaila & Ståhls 2006). Here we present and evaluate a protocol for the non-destructive
86 extraction of DNA from terrestrial arthropods, using as our subjects a variety of animals chosen
87 to be representative of the ranges in size, overall sclerotization, and delicacy of key
88 morphological characters in this group.

89

90 **Materials and methods**

91

92 *Choice of taxa*

93

94 On the basis of our intimate knowledge of their systematics and taxonomy, we selected five
95 species from two arachnid and three insect orders of great ecological significance in terrestrial
96 ecosystems.

97

98 Tenuipalpidae is a cosmopolitan mite family comprising more than 800 phytophagous
99 species in 32 genera. Because they are small (200-300 μm), slow moving, and exhibit cryptic
100 coloration and stationary behavior, tenuipalps are very difficult to recognize, collect, and
101 identify in the field (Jeppson *et al.* 1975). Having another tool to help distinguish closely related
102 species is therefore of utmost importance. The red palm mite, *Raoiella indica* Hirst (ACARI:
103 Tenuipalpidae), is a new invasive pest in the Americas that infests coconut, bananas, and several
104 ornamental plants (Flechtmann & Etienne 2004). *Raoiella* contains several species that are not
105 well known or are poorly described; *R. indica* is distinguished from its congeners by the shape of
106 the dorsal setae.

107

108 The basilica spider, *Mecynogea lemniscata* (Walckenaer) (ARANEAE: Araneidae),
109 belongs to a New World genus comprising about a dozen species (Levi 1980; Platnick 2006); as
110 with spiders generally, congeners are distinguished primarily on the basis of subtle morphological
111 differences in the genitalia.

112

113 The pink ladybug, *Coleomegilla maculata* (De Geer) (COLEOPTERA: Coccinellidae), is
114 a common denizen of row crops in eastern North America; the genus is restricted to the New
115 World and is most diverse in the tropics and subtropics. Although numerous names have been
116 recognized, most species have been incorrectly treated as subspecies or varieties of *C. maculata*.
117 The limits between *Coleomegilla* and the related genera *Naemia*, *Paranaemia* and *Eumegilla* are
118 in need of clarification and the subject of a forthcoming revision (NJV, J. Obrycki, and W.
119 Steiner, in progress). Genitalia and color patterns in this group are conservative, and often appear

120 very similar among related taxa. *Naemia* can generally be recognized by the fact that the elytral
121 spots are connected longitudinally, but some specimens from the northern and southern limits of
122 the range have disconnected spots and may be mistaken for *Coleomegilla*. These look-alikes are
123 most easily separated by the form of the tarsal claw, simple and scythelike in *Naemia* but bearing
124 a large quadrate tooth in *Coleomegilla*. Other structural differences used to distinguish certain
125 species of *Coleomegilla* and allied New World taxa include the length of the legs, the shape and
126 size of the pronotum, and the exact shape of the basal lobe and aedeagus of the male genitalia.
127 Some *Coleomegilla* species can also be distinguished on the basis of small differences in the
128 shape of the black maculae on the elytra or pronotum.

129

130 *Delphinia picta* (Fabricius) (DIPTERA: Ulidiidae) is a ubiquitous saprophage in eastern
131 North America with larvae that feed primarily on decaying vegetation. Ulidiids are closely related
132 to fruit flies (Tephritidae), a group that includes numerous agricultural pests, and the key
133 characters for distinguishing species within both families are similar. These include wing
134 patterns, body color patterns, number and positions of setae (chaetotaxy), microtrichia patterns,
135 and genitalic morphology.

136

137 *Eurytoma rhois* Crosby (HYMENOPTERA: Eurytomidae) belongs to the most
138 commonly collected genus of the family Eurytomidae (Hymenoptera), a cosmopolitan family of
139 phytophagous and entomophagous parasitic wasps. The key diagnostic features for *E. rhois*
140 concern relative sizes of sclerites and the propodeal surface sculpture

141

142 *Collection of arthropods*

143

144 A variety of methods, some of them taxon-specific, are used to collect and preserve terrestrial
145 arthropods (U.S. Department of Agriculture 1986; Aguiar and Sharkov 1997; Noyes 1998;

146 Triplehorn & Johnson 2004). Because all specimens were to be extracted in an aqueous buffer, all
147 were collected into EtOH, regardless of customary methods of preservation for the taxon; we
148 chose an EtOH concentration of 80% as sufficiently high to preserve DNA but not so high as to
149 cause desiccation that would unduly distort the animal's external morphology.

150

151 The methods and localities of collection for all taxa are given in Table 1.

152

153 *DNA extraction protocol*

154

155 Each specimen was removed from the 80% EtOH, allowed to air dry, and placed in a 1.5 ml
156 microfuge tube with forceps that had been soaked in 0.5 % NaClO. A minimum 100 µl of a
157 GuSCN-based extraction buffer (Rohland *et al.* 2004) was added to the tube, which was then
158 placed in a 60 °C water bath for 1, 2, or 4 h. The extraction buffer was removed to a clean tube
159 and the DNA was precipitated by addition of an equal volume of isopropanol. The sample was
160 incubated over night at -20 °C and centrifuged for 20 min at 13,000 x g and 4 °C. After a single
161 rinse in 70% EtOH, the DNA was vacuum-dried, resuspended in an equal volume of 0.1X TE pH
162 8.0, and stored at -20 °C. Four individuals of each taxon were subjected to
163 each extraction interval, and two were used as controls that went through all procedures except
164 extraction. Two DNA samples of each species, extracted by conventional means from whole-
165 body homogenates (Greenstone *et al.* 2005), were provided for reference.

166

167 The extracted arthropod carcasses and unextracted controls were again immersed in 80%
168 EtOH and stored at 4 °C until prepared for imaging.

169

170 *PCR and sequencing*

171

172 PCR conditions and components were as described in Greenstone *et al.* (2005), with 5-6 µl of the
173 DNA extract used in the reaction. DNA of all species was amplified with primers C1-J-1751 and
174 C1-N-2191, and C1-J-2195-C1-N-2568 (Simon *et al.* 1994), with expected amplicon sizes of 488
175 and 421 bp, respectively. *Mecynogea* DNA was additionally amplified with cytochrome oxidase I
176 primer pairs C1-J-1751 "SPID" (Hedin & Maddison 2001) and C1-N-2776 (Simon *et al.* 1994),
177 with an expected amplicon size of 1070 bp, to ensure complete coverage of the sequence.

178

179 Amplified DNA was visualized by electrophoresis of 6 µl of the PCR/Stop reaction (12
180 µl for *Raioella* and *Eurytoma* because of their very small size) in 1.5 % agarose. The remainder of
181 the reaction mixture was loaded, electrophoresed in 1.5% NuSieve agarose (Cambrex Bio Science
182 Rockland Inc., Rockland, Maine, USA) in 1x TAE modified to have a final EDTA concentration
183 of 0.1 mM, and the fragments excised for sequencing by BigDye terminator v3.1 kits on an ABI
184 3100 sequencer (Applied Biosystems, Foster City, California, USA). Editing was performed with
185 Lasergene (DNASStar, Madison, Wisconsin, USA).

186

187 *Deposition of morphological vouchers, DNA, and DNA sequences*

188

189 Extracted arthropod carcasses were deposited as morphological vouchers, prepared according to
190 standard museum practices, in the Insect and Mite National Collection of the Smithsonian
191 Institution, National Museum of Natural History (NMNH) in Washington, D.C.; the companion
192 DNA samples were deposited in the NMNH Tissue Collection. DNA sequences were deposited
193 in GenBank (Accession Nos. EF185147-EF185157, and EF192134).

194

195 *Imaging of extracted carcasses*

196

197 Arthropod carcasses were processed and imaged after DNA extraction using protocols standard
198 for the taxon. Carcasses of *R. indica* were slide-mounted and viewed by Nomarski interference.
199 Specimens of *M. lemniscata* were photographed in EtOH under a dissecting microscope.
200 Carcasses of *C. maculata* were removed from the EtOH and point-mounted; scanning electron
201 microscope (SEM) images of the tarsi were made from coated specimens mounted on stubs.
202 *Delphinia picta* carcasses were removed from EtOH and dried for 48 h in ethyl acetate, then air-
203 dried or critical-point-dried, mounted on pins, and imaged by light microscopy. Wings of several
204 specimens were removed and slide mounted in Euparal. Carcasses of *E. rhois* were removed
205 from the EtOH and dehydrated using HMDS (Heraty & Hawks 1998); dried specimens were
206 carefully disarticulated prior to imaging via SEM.

207

208 For SEM imaging, specimens were affixed to 12.7 x 3.2 mm Leica/Cambridge aluminum
209 SEM stubs with carbon adhesive tabs (Electron Microscopy Sciences, Hatfield, Pennsylvania,
210 USA; #77825-12). Stub-mounted specimens were sputter-coated using a Cressington Scientific
211 108 Auto with a gold-palladium mixture from at least three different angles to ensure complete
212 coverage (~20-30nm coating). SEM images were taken with an Amray 1810 with LaB₆ source
213 (Amray, Inc., Bedford, Massachusetts, USA).

214

215 **Results and discussion**

216

217 The effects of our extraction protocol on the resultant morphological vouchers ranged from slight
218 discoloration to slight-to-significant distortion of surface features that did not prevent
219 identification to species.

220

221 The diagnostic shapes of the dorsal setae and other characteristics of *R. indica* were
222 readily observable in the extracted specimens (Fig. 1). Spider genitalia are in most cases highly
223 sclerotized and thus resistant to most chemical treatments: our DNA extraction protocol had no
224 visible effect on the morphology of the female genitalia of *M. lemniscata*, (Fig. 2), but did leave a
225 flocculent precipitate on most of the specimens (Fig. 2A). This precipitate could be removed
226 manually, but might pose a problem for some kinds of morphological research, such as
227 examination of spinneret spigots (which typically are not species-specific).

228

229 In *C. maculata*, the cuticle became more translucent, lost the saturated red or pink tones,
230 and tended to brown after extraction (Figs. 3A and 3B). However, the black pigment that forms
231 the dorsal maculae seems to be quite stable, so that the color pattern could be easily assessed even
232 in the specimens that underwent 4 h of extraction (not shown), and distinguished from those of *N.*
233 *seriata* (Figs. 3B and 3C). After DNA-extraction the claw of *C. maculata* was sometimes more
234 flaccid, but still clearly exhibited the diagnostic large quadrate tooth (Figs. 3D and 3E). Generally
235 the pronotal shape was not altered by extraction, with the exception of one of the 4-h specimens
236 where the disk buckled (not shown). The thick portions of the legs retained their shape well, but
237 the narrow last tarsal segment sometimes became droopy. Problems with structural integrity
238 could be minimized by placing the specimen on its back to prevent the abdomen from folding
239 down, and carefully positioning key structures and providing temporary support until dry.
240 Limiting extraction time to 1 h decreased the severity of this effect.

241

242 There was no visible effect of the extraction on color pattern or cuticular structures of *D.*
243 *picta* (Fig. 4); genitalic morphology was also not affected (not shown). Specimens that were dried
244 after extraction using critical point drying or after transfer from alcohol to ethyl acetate shriveled
245 to varying degrees (Figs. 4A and 4B), somewhat less in the critical-point-dried material. In some
246 cases this limited the study of chaetotaxy and color and microtrichial patterns of various parts of

247 the body, particularly the thorax. Extracted specimens often were unevenly covered with a
248 powdery whitish precipitate that sometimes partially obscured surface features. This sometimes
249 made it difficult to observe microtrichia patterns or other surface characters. The wings of the *D.*
250 *picta* specimens were virtually indistinguishable regardless of treatment (Figs. 4D – 4F).

251

252 *E. rhois* exhibited setae that were slightly lighter in color than the control after
253 dehydration but prior to SEM. The key diagnostic features for *E. rhois*, relative sizes of sclerites
254 and propodeal surface sculpture, were little affected by the DNA extraction process. The
255 extracted specimen pictured, a male, had matted antennal setation (Fig. 4B). Setation on extracted
256 material generally appeared to be abraded more easily (compare controls versus extracted
257 mesosoma and head, Figs. 4C and 4D, 4G and 4H). We do not know whether these setation
258 artifacts were a direct result of the extraction or might be due to the transferral of extraction
259 buffer into and out of the extraction tube.

260

261 Gels containing the amplified 421 and 488 bp PCR products from all specimens used in
262 the study are shown in Fig. 6 (the 1070 bp *M. lemniscata* amplicons, used for sequencing, are not
263 shown but gave similar results). We were able to amplify DNA from all species, with the success
264 of amplification roughly proportional to the size of the specimen and the length of time of
265 extraction. Thus almost all *D. picta* and *C. maculata* specimens produced PCR products
266 regardless of extraction time, *M. lemniscata* specimens were most effectively extracted after 2-4 h
267 extraction, and both *R. indica* and *E. rhois* tended to require the full 4 h for effective extraction.

268

269 Overall, our extraction protocol yielded DNA suitable for sequencing, with effects on the
270 extracted carcass ranging from slight discoloration to slight-to-significant distortion of surface
271 features that did not prevent identification to species and effective presentation as morphological
272 vouchers. The flocculent precipitate noted on the *Mecynogaea* and *Delphinia* specimens might

273 be removed by more assiduous rinsing of the specimens following extraction. Other so-called
274 non-destructive DNA extraction protocols have required breaches of the cuticle ranging from pin-
275 pricks (Phillips & Simon 1995; Favret 2005) to amputation (Stark & Peters 2002) and even
276 decapitation (Johnson *et al.* 2001) or more extensive disarticulation, slicing, and injection
277 (Knölke *et al.* 2005; Barr & McPheron 2006). Though these protocols may provide useable
278 vouchers, they are more tedious and labor-intensive than our procedure, which requires only
279 soaking the specimen in buffer. They also create opportunities for cross-contamination via the
280 piercing or cutting instrument and, if structures that have been separated for extraction are
281 rejoined in the voucher specimen, for creation of chimaeric morphological vouchers.

282

283 Ongoing research on different preservation methods (e.g., Paabo *et al.* 2004; Mulligan
284 2005) may lead to protocols that cause less distortion, leaving more photogenic morphological
285 vouchers following DNA extraction. In the mean time, use of our protocol to extract a series of
286 specimens from 1-4 h should provide a number of individuals for which sequenceable DNA can
287 be matched to a presentable morphological voucher. Optimized protocols would make joint
288 vouchering of morphological specimens and the DNA extracted from them a routine part of DNA
289 barcoding.

290

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292

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423

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425

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436 **Author identification box**

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443 **Figure captions**

444

445 **Fig. 1.** *Raioella indica* morphological vouchers. A, extracted for 4 h, dorsal view. B, same
446 specimen, ventral view. C, unextracted control.

447

448 **Fig. 2.** *Mecynogea lemniscata* morphological vouchers. A, epigynum extracted 4 h. B,
449 unextracted control epigynum.

450

451 **Fig. 3.** *Coleomegilla maculata* morphological vouchers and related taxa. Top, pinned and live
452 specimens; bottom, scanning electron micrographs of anterior tarsomere showing shape of claw.
453 A, pinned unextracted *C. maculata* control. B, pinned *C. maculata* extracted for 1 h. C, group of
454 three live beetles: *Naemia seriata* from Maryland (bottom); *C. maculata* from Maryland (middle
455 right); *Naemia* sp. from Nova Scotia (top). D, unextracted *C. maculata* control. E, *C. maculata*
456 extracted for 1 h; arrow = quadrate tooth. F, unextracted *N. seriata* from Maryland.

457

458 **Fig. 4.** *Delphinia picta* morphological vouchers. A, extracted for 2 h and critical-point-dried. B,
459 extracted for 2 h and ethyl acetate-dried. C, unextracted control. D, wing extracted for 1h. E, wing
460 extracted for 4 h. F, wing of unextracted control. E and F were air-dried after dehydration in ethyl
461 acetate.

462

463 **Fig. 5.** *Eurytoma rhois* morphological voucher. Unextracted control, left; extracted for 4 h, right.
464 A and B, antenna; C and D, mesosoma; E and F, forewing; G and H, head.

465

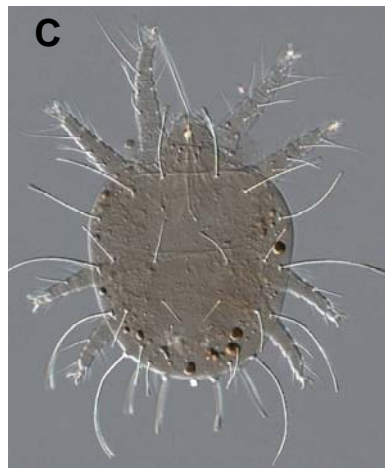
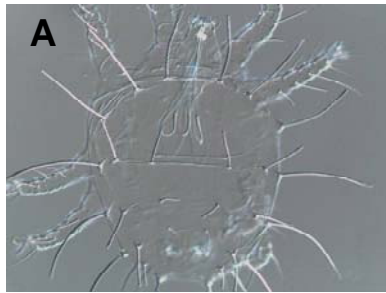
466 **Fig. 6.** 421 bp (A and B) and 488 bp (C and D) gels. Lanes 1, 16, 31, and 46, 100 bp ladder. Lane
467 46, no-DNA control. For A and C, lanes 2-15, *Raioella indica*; lanes 17-30, *Mecynogea*

468 *lemniscata*; lanes 32-45, *Coleomegilla maculata*. For B and D, lanes 2-15, *Delphinia picta*; lanes
469 17-30, *Eurytoma rhois*. For each species, the first two-lanes are conventionally-extracted DNA,
470 the next 4 wells are 1-h extractions, the following 4 wells are 2-h extractions, and the last 4 wells
471 are 4-h extractions.

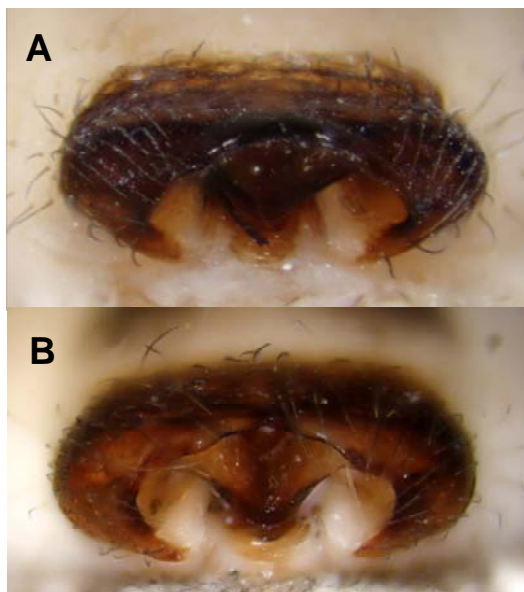
472 **Table 1.** Collecting localities for animals used in the study. *Delphinia picta* were collected in
 473 fruit fly traps and *Eurytoma rhois* by sweeping; all other species were collected by hand.
 474

Taxon	Locality and Habitat
<i>Raoiella indica</i> Hirst (ACARI: Tenuipalpidae)	Saint Lucia, West Indies On coconut palm (<i>Cocos nucifera</i>)
<i>Mecynogea lemniscata</i> (Walckenaer) ARANEAE: Araneidae	Maryland, Howard CO, Ellicott City Understory of deciduous forest remnant
<i>Delphinia picta</i> (Fabricius) DIPTERA: Ulidiidae	Georgia, Fulton CO, Atlanta
<i>Coleomegilla maculata</i> (De Geer) COLEOPTERA: Coccinellidae <i>Naemia seriata</i> (Melsheimer) COLEOPTERA: Coccinellidae	Maryland, Prince Georges CO, Beltsville Laboratory colony, originally from potato fields Granville Beach, Nova Scotia, Canada On <i>Spartina</i> sp. Maryland, Talbot Georges CO, Wittman On <i>Spartina</i> sp.
<i>Eurytoma rhois</i> Crosby HYMENOPTERA: Eurytomidae	Rhode Island, Kent CO, Warwick Powerline right-of-way at junction of Route 117 and Toll Gate Road On blooming <i>Rhus copallina</i>

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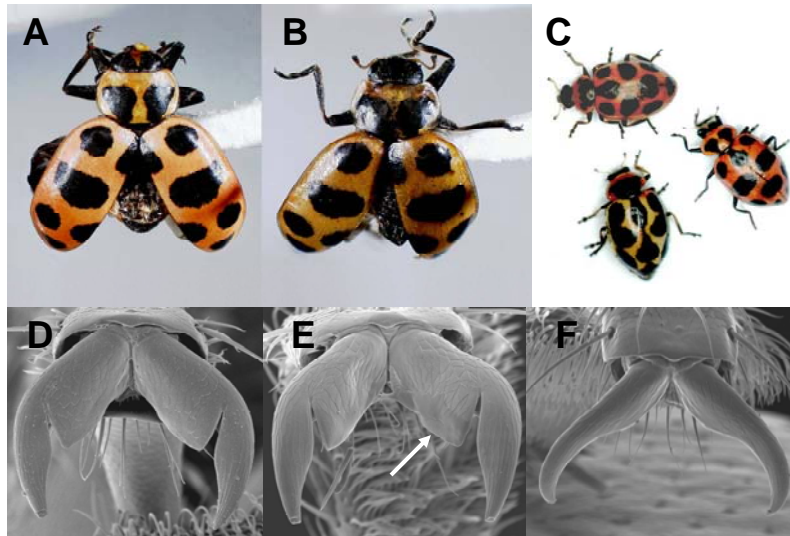
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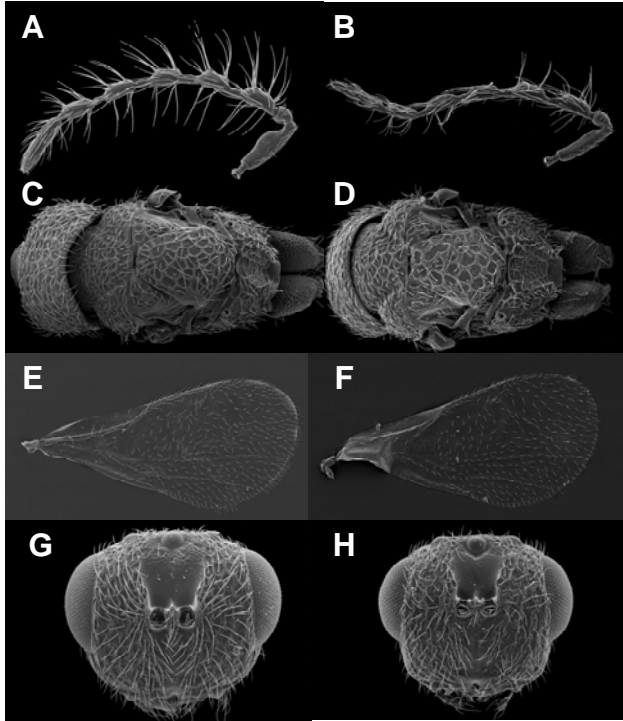


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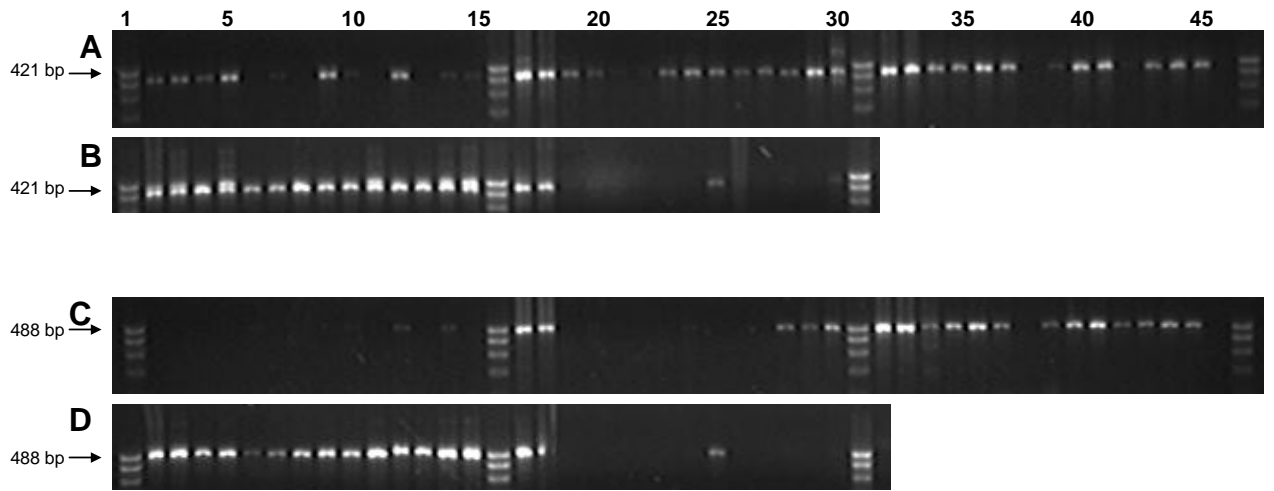
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