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DNA-barcoding of forensically important blow flies (Diptera: Calliphoridae) in the Caribbean Region

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Abstract

Correct identification of forensically important insects, such as flies in the family Calliphoridae, is a crucial step for them to be used as evidence in legal investigations. Traditional identification based on morphology has been effective, but has some limitations when it comes to identify immature stages of certain species. DNA-barcoding, using COI, has demonstrated potential for rapid and accurate identification of Calliphoridae, however, this gene does not reliably distinguish among some recently diverged species, raising questions about its use for delimitation of species of forensic importance. To facilitate DNA based identification of Calliphoridae in the Caribbean; we developed a vouchered reference collection from across the region, and a DNA sequence database, and further added the nuclear ITS2 as a second marker to increase accuracy of identification through barcoding. We morphologically identified freshly collected specimens, did phylogenetic analyses and employed several species delimitation methods for a total of 468 individuals representing 19 described species. Our results show that combination of COI + ITS2 genes yields more accurate identification and diagnoses, and better agreement with morphological data, than the mitochondrial barcodes alone. All of our results from independent and concatenated trees and most of the species delimitation methods yield considerably higher diversity estimates than the distance based approach and morphology. Molecular data support at least 24 distinct clades within Calliphoridae in this study recovering substantial geographic variation for *Lucilia eximia*, *Lucilia retroversa*, *Lucilia rica* and *Chloroprocta idioidea*, probably indicating several cryptic species. In sum, our study demonstrates the importance employing a second nuclear marker for barcoding analyses and species delimitation of calliphorids and the power of molecular data in combination with a complete reference database to enable identification of taxonomically and geographically diverse insects of forensic importance.

Introduction Forensic entomology is the application of the study of insects in legal investigations. Although several group of insects, mainly of the orders Diptera and Coleoptera, are associated with cadaveric decomposition, blow flies (Diptera: Calliphoridae) are among the most dominant and conspicuous insects in the decomposition process (Catts, 1992). They are useful to determine time of death and, in particular situations, cause of death (Goff 2000) or relocation of a body (Matuszewski, Szafalowicz & Jarmusz, 2013). During the last five decades of intensive studies in forensic entomology (Byrd & Castner, 2010; Catts & Haskell, 1990; Goff, 2000; Smith, 1986; Tomberlin & Benbow, 2015), the acceptance of insects as evidence in legal investigations has increased gradually and they are now included as standard operating procedures in crime scene investigations in many countries (Tomberlin & Benbow, 2015).

40 Determining the post mortem interval (PMI) is one of the most important tasks during an
41 investigation, and the use of immature stages of Calliphoridae is essential whenever time of
42 death is difficult to establish based on other means (Catts & Haskell, 1990). Although the
43 accurate determination of PMI and period of insect activity (PIA) depend of several factors that
44 are discuss in detail by Catts (1992), the first one, and most important to resolve, is the correct
45 identification of the specimens found at the crime scene. As each species has a specific
46 developmental rate and range of distribution, the accurate identification of insects, mainly the
47 larval stages, is critical because the incorrect determination will invalidate the estimated post
48 mortem interval and impact other interpretations of the evidence (Goff, 2000; Wells & LaMotte,
49 2001).

50 Morphology has been largely used to identify adult insects involve in cadaveric decomposition
51 and taxonomic keys are available for most of the Calliphoridae species. In general, these
52 taxonomic keys include the detailed description of the male and female genitalia, which is
53 examined when external characteristics are not sufficient to establish identity (Tantawi,
54 Whitworth & Sinclair, 2017; Whitworth, 2010; Whitworth, 2014; Whitworth & Rognes, 2012).
55 Identification of immature stages (eggs, larvae and pupae) is more challenging, but possible
56 when detailed taxonomic descriptions exist (Greenberg & Szyska, 1984; Sukontason et al., 2005;
57 Szpila et al., 2013a; Szpila et al., 2014; Szpila & Villet, 2011; Wells, Byrd & Tantawi, 1999).
58 However, in places like the Caribbean, where forensic entomology has not been yet developed,
59 this approach is limited due to the lack of detailed descriptions of immature stages. For instance,
60 from the 18 forensically important calliphorid species currently recognized in the Caribbean plus
61 the most important livestock pest parasite in the Americas, *C. hominivorax* (Whitworth, 2010),
62 only eight have been documented well enough to be identified based on larvae, mainly using
63 morphology of the third instar (Florez & Wolff, 2009; Wells, Byrd & Tantawi, 1999). For the
64 other species, the identification of immature specimens would need to be done by rearing them to
65 adulthood (Goff, 2000), which is time consuming, may delay legal investigations, and relies on
66 the survival of larvae in the laboratory. Given local endemism, the scarce studies on this group in
67 the Caribbean, and the lack of knowledge of immature stages for at least 11 species, developing
68 alternative tools for identification is important.

69 With the advances in molecular methods, DNA barcoding has become a widely used technique
70 for species delimitation and identification. This approach allows the identification of specimens
71 during any development stage, including incomplete or damaged specimens, does not require
72 taxonomic expertise, and it is also useful to recognize cryptic species that morphology
73 approaches may not detect (Hebert et al., 2003; Hebert et al., 2004a; Hebert et al., 2004b).
74 Worldwide many authors have used this method to identify species of the family Calliphoridae
75 and these studies showed the potential of the ‘standard barcoding gene’ cytochrome c oxidase
76 subunit I (COI) to distinguish between forensically significant species (Aly & Wen, 2013; Chen
77 et al., 2009; Harvey et al., 2003; Liu et al., 2011; Nelson, Wallman & Dowton, 2007; Wells &
78 Williams, 2007). However, COI does not reliably distinguish among certain closely related

79 calliphorid pairs, specifically *Chrysomya saffranea* and *Ch. megacephala* (Harvey et al., 2008;
80 Nelson, Wallman & Dowton, 2007), *Ch. semimetalica* and *Ch. latifrons* (Nelson, Wallman &
81 Dowton, 2007), *Calliphora stygia* and *C. albifrontalis*, *C. dubia* and *C. augur* (Harvey et al.,
82 2008; Wallman & Donnellan, 2001), *C. aldrichia* and *C. montana* (Tantawi, Whitworth &
83 Sinclair, 2017), *Cochliomyia macellaria* and *Co. aldrichi* (Yusseff-Vanegas and Agnarsson,
84 2016), *Lucilia mexicana* and *L. coeruleiviridis* (DeBry et al., 2013; Whitworth, 2014), *L. bazini*
85 and *L. hainanensis* (Chen et al., 2014), *L. illustris* and *L. caesar* (Reibe, Schmitz & Madea,
86 2009; Sonet et al., 2012), *L. cuprina* and *L. sericata* (Williams & Villet, 2013). Given the serious
87 implications of misidentification of forensic insects, an improved protocol for accurate
88 identification is necessary. We propose using the nuclear internal transcribed spacer ITS2 as a
89 second barcoding locus for taxonomic species determinations in calliphorids as suggested by
90 GilArriortua et al. (2014). Although evaluations of ITS2 as unique identification marker have
91 limitations for some taxa (Agnarsson, 2010), several studies have shown the potential application
92 of ITS2 for blowfly species identification (Jordaens et al., 2013a; Nelson, Wallman & Dowton,
93 2007; Nelson, Wallman & Dowton, 2008; Song, Wang & Liang, 2008; Yusseff-Vanegas &
94 Agnarsson, 2016). We expect a combination of barcodes from the nuclear and mitochondrial
95 genomes to offer a general, simple and reliable way of identifying forensically important insects,
96 even problematic sister species, as successfully done in certain other arthropod groups (Ansari &
97 Tedersoo, 2015; Cao et al., 2016).

98 The success of DNA barcoding directly links to the quality of the underlying database (Candek
99 & Kuntner, 2015; Coddington et al., 2016; DeBry et al., 2013; Harvey et al., 2003) not only in
100 terms of quality of identifications but also in terms of taxon sampling (species, geographic
101 localities, populations). Existing efforts in this respect are lacking for Calliphoridae in the
102 Caribbean, limiting the reliability of this technique for delimitation of species. Hitherto, three
103 studies have included molecular data of a few Calliphoridae from the Caribbean (McDonagh,
104 Garcia & Stevens, 2009; Whitworth, 2014; Yusseff-Vanegas & Agnarsson, 2016), they lack the
105 geographic variation necessary to estimate the ratio between intraspecific variation and
106 interspecific divergence from which barcoding accuracy depends (Meyer & Paulay, 2005). Our
107 study provides the first thorough molecular study of Caribbean Calliphoridae.

108 Our aims are: 1) to establish COI barcode libraries for all Caribbean species and to test if
109 barcodes offer reliable means of identification of all Calliphoridae species in the Caribbean, 2) to
110 assess the usefulness of ITS2 as a second barcoding locus in species delimitation and
111 identification, and, 3) to improve online databases with sequences from the Caribbean including
112 specimens from multiple localities in each island covering the geographic range for each species.
113 To achieve these goals, we sampled 468 specimens of Calliphoridae representing 19 species.

114 Methods

115 Specimens and DNA extraction

116 A total of 473 specimens were included in this study. Of these, 468 represented ingroup taxa and
117 five represented outgroup taxa from the family Sarcophagidae (*Sarcophaga Carnaria* Linnaeus,
118 1758; *Neobellieria bullata* Parker, 1916; *Ravinia stimulans* Walker, 1849; *Blaesoxipha*
119 *masculina* Aldrich, 1916 and *Blaesoxipha alcedo* Aldrich, 1916). We used a total of 600 DNA
120 sequences, we obtained 521 (COI=398, ITS2=123) while 79 (COI=44, ITS2=35) were
121 previously published (Table 1). The specimens were collected throughout the Caribbean (Fig 1)
122 from between 2011 and 2013 (see Table 1 for details). All specimens were collected under
123 appropriate permits: USA, Florida, Everglades, United States Department of the Interior National
124 Park Service EVER-2013-SCI-0028; Puerto Rico, DRNA: 2011-IC-035 (O-VS-PVS15-SJ-
125 00474-08042011); Jamaica, NEPA, reference number #18/27; USA, USDI National Park
126 Service, EVER-2013-SCI-0028; Costa Rica, SINAC, pasaporte científico no. 05933, resolución
127 no. 019-2013-SINAC; Cuba, Departamento de Recursos Naturales, PE 2012/05, 2012003 and
128 2012001; Dominican Republic, Ministerio de Medio Ambiente y Recursos Naturales, no 0577;
129 Colombia, Autoridad Nacional de Licencias Ambientales, 18.497.666 issued to Alexander
130 Gómez Mejía; Saba, The Executive Council of the Public Entity Saba, no 112/2013; Martinique,
131 Ministère de L'Écologie, du Développement Durable, et de L'Énergie; Nevis, Nevis Historical &
132 Conservation Society, no F001; Barbados, Ministry of Environment and Drainage, no 8434/56/1
133 Vol. II. Although *L. vulgata*, *L. mexicana* and *L. coeruleiviridis* are not present in the Caribbean
134 islands, they are included as outgroups to the Calliphoridae from the West Indies. James (1970)
135 reported *L. coeruleiviridis* from Cuba, however, this is likely an error as no specimens have been
136 seen in collections from the region (Whitworth, 2010) and no specimens were collected during
137 this study. All specimens, except the ones from Mexico, were collected using a novel trap
138 designed for this study. We modified a standard butterfly trap by adding a conic form on the top
139 with a vessel attached to the highest point like in the Malaise trap. Flies entered the trap attracted
140 by the bait (chicken) and funneled into the collecting vessel containing 95% ethanol. Traps were
141 hung 1m off the ground and were used to collect flies for 2-3 days at each locality. These traps
142 proved efficient in collecting specimens for our molecular purposes, given that caught specimens
143 were preserved in ethanol while the trap remained in the field. Collected specimens were
144 transferred to Whirl-paks with 95% ethanol and stored at -20 °C. Adults were identified using the
145 Whitworth (2010) taxonomic keys and the specimens with uncertain identity were sent to Dr.
146 Whitworth at Washington State University for detailed examination and species confirmation.
147 DNA was isolated from thoracic muscle or two legs of each individual with the QIAGEN
148 DNeasy Tissue Kit (Qiagen, Inc., Valencia, CA). The remainder of the specimen was retained as
149 a voucher currently held by the Agnarsson Lab; they will be placed in the Zadock Thompson
150 Zoological Collections at the UVM Natural History Museum following completion of other
151 studies currently being conducted using the material..

152 *PCR amplification and sequencing*

153 A region of the mitochondrial genome encoding COI was amplified in a single fragment using
154 the primers LCO1490 (Folmer et al., 1994), and C1-N-2776 (Hedin & Maddison, 2001). Those

155 primers amplified successfully in all Calliphoridae except *Lucilia* Robineau-Desvoidy. From the
156 eight Caribbean species of *Lucilia*, only *Lucilia retroversa* amplified successfully using these
157 primers. For the remaining *Lucilia* species two different primer-pairs were used. the Primer 1
158 (Gibson et al., 2011) with C1-N-2191 (Simon et al., 1994) and the C1-J-1751 (Gibson et al.,
159 2011) with C2-N-3014. For the second internal transcribed spacer ITS2 we used the primers
160 ITS4 and ITS5.8 (White et al. 1990). The primer sequences and protocols are listed in Table 2.
161 Amplified fragments were sequenced in both directions by University of Arizona Genetics Core.
162 Sequences were interpreted from chromatograms using Phred and Phrap (Green, 1999.; Green &
163 Ewing, 2002) using the Chromaseq module (Maddison & Maddison, 2010a) in Mesquite 3.03
164 (Maddison & Maddison, 2010b) with default parameters. The sequences were then proofread by
165 examining chromatograms by eye. Alignments were done using MAFFT (Katoh et al., 2002)
166 through the online portal EMBL-EBI with default settings. The matrices were exported to
167 Mesquite 3.03 (Maddison & Maddison, 2010b) and the translation of coding sequences to
168 proteins for COI were checked for potential errors.

169 *Phylogenetic analysis*

170 The COI gene was partitioned by codon positions, each partition and ITS2 gene were exported
171 from Mesquite for model choice. The appropriate models were chosen using jModeltest v2.1.4
172 (Posada & Crandall, 1998), and the AIC criterion (Posada & Buckley, 2004). The corresponding
173 model of evolution was used for the Bayesian analysis: GTR + Γ + I for COI1st, F81+ I for
174 COI2nd, GTR + Γ for COI3rd and HKY + Γ + I for ITS2. We ran the MC³ (Metropolis Coupled
175 Markov Chain Monte Carlo) chain in MrBayes v3.2.3 (Huelsenbeck & Ronquist, 2001) through
176 the online portal Cipres Science Gateway v3.3 (Miller, Pfeiffer & Schwartz, 2010). The analysis
177 was run for 20.000.000 generations, sampling every 1000 generations, and the sample points of
178 the first 5,000,000 generations were discarded as ‘burnin’, after which the chains had reached
179 stationarity as determined by analysis in Tracer (Rambaut & Drummond, 2009). Maximum
180 likelihood (ML) analysis of the concatenated matrix was done in Garli (Zwickl, 2006) using the
181 same partitioning scheme and models. Sequences were submitted to GenBank and BOLD.

182 *Species delimitation*

183 We used MEGA6 to calculated genetic distances within and among species level clades
184 suggested by the barcoding analysis of the COI data and by morphology. We used the species
185 delimitation plugin in Geneious 8.1.5 (Kearse et al., 2012; Masters, Fan & Ross, 2011) to
186 estimate species limits under Rosenberg’s reciprocal monophyly P(AB) (Rosenberg, 2007) and
187 Rodrigo’s P(RD) method (Rodrigo et al., 2008). For this analysis we used a 317 taxa subset of
188 our data, produced by reducing the most densely sampled species like *Co. minima*, *Co.*
189 *macellaria*, *Ch. rufifacies* and *L. retroversa* to 38 exemplars since P(RD) probability cannot be
190 computed when there are more than 40 exemplars per clade. We also estimated the probability of
191 population identification of a hypothetical sample based on the groups being tested P ID (Strict)
192 and P ID (Liberal)). The genealogical sorting index (gsi) statistic (Cummings, Neel & Shaw,

193 2008) was calculated using the gsi webserver (<http://genealogicalsorting.org>) on the estimated
194 tree. As genetic distances in MEGA6, gsi and species delimitation metrics from Geneious require
195 a priory species designation, 26 putative species were assigned to the data based on combined
196 analysis of phylogenetic topology from COI and morphological and geographic information.
197 Finally, we used a single locus Bayesian implementation (bPTP) of the Poisson tree processes
198 model (Zhang et al., 2013) to infer putative species boundaries on a given single locus
199 phylogenetic input tree available on the webserver: <http://species.h-its.org/ptp/>. The analysis was
200 run as a rooted tree from the MrBayes analysis, for 500,000 generations with 10% burnin
201 removed. For gsi and bPTP analysis we reduced the data to 103 taxa representing the 26 putative
202 species because of limitations of the server.

203 Results

204 We present by far the most extensive DNA barcoding dataset of Calliphoridae from the
205 Caribbean. It includes a ~1200 bp fragment of the mitochondrial COI gene from 437
206 Calliphoridae specimens and ~450 bp of the ITS2 gene from 158 specimens chosen to represent
207 unique COI haplotypes of all putative species and all localities (20 different islands in the
208 Caribbean plus Florida, Colombia and Mexico). Ninety nine of the sequences are from
209 specimens collected in the mainland and the other 496 are from the Caribbean Islands. In total,
210 we included 19 species of Calliphoridae identified morphologically (Whitworth, 2006, 2010) 16
211 of them reported from the Caribbean and three species, *L. coeruleiviridis*, *L. mexicana* and *L.*
212 *vulgata*, from the mainland. The sequences from the Caribbean represent 16 of the 18 species of
213 forensically important Calliphoridae that occur in the West Indies plus one of the most important
214 livestock pest parasite in the Americas, *C. hominivorax* (Whitworth, 2010). The two species not
215 included in this dataset are reported from Bahamas (*Phormia regina*) and Trinidad (*Hemilucilia*
216 *segmentaria*), where we were not able to sample. For most species we included numerous
217 exemplars, covering the geographic range of each species in the region.

218 Species delimitation using COI

219 Although based on traditional taxonomy we recognized 19 species of Calliphoridae in this study,
220 COI gene analyses suggest that the diversity of Calliphoridae in the Caribbean is greater than
221 morphology can detect. The phylogenetic analysis of COI recuperates 24 distinct clades (Fig 2,
222 S1), showing substantial geographic variation for *L. eximia* (four clades), *C. idioidea* (three
223 clades), *L. retroversa* (two clades) and *L. rica* (two clades). However, COI did not distinguish
224 between the pairs, *Co. macellaria* and *Co. aldrichi* from the Caribbean and *L. coeruleiviridis* and
225 *L. mexicana* from the mainland. These four species are clearly identifiable based on
226 morphological characteristics. Most putative species lineages showed genetic distances >2.7%
227 (Table 3) and most of them are separated by a barcoding gap (Table 4). All species delimitation
228 methods supported *Ca. maestrica*, *C. idioidea-DR*, *Co. minima*, *Co. hominivorax*, *Ch. albiceps*,
229 *Ch. rufifacies*, *Ch. megacephala*, *L. cluvia*, *L. cuprina*, *L. eximia-CO+ME*, *L. eximia-LA*, *Lucilia*
230 *eximia-GA*, *L. lucigerens*, *Lucilia retroversa-DR*, and *L. rica* 1 and 2 (Fig 2, Table 5); however,

231 the other eight putative species were poorly supported in our analyses. Lower divergences,
232 between 0.5 and 1.2% were found between clades, *L. coeruleiviridis*+*L. mexicana*, *L. vulgata*
233 and *L. eximia*-FL, *L. fayeae* and *L. retroversa* CU, and between *L. rica* 1 and 2 (Table 3). All but
234 bPTP methods of species determination supported *L. eximia*-FL clade, *L. vulgata*, *L. fayeae*, *L.*
235 *retroversa*-CU (Table 5). Regarding *C. idioidea*, the Cuban and Mexico species-clades are only
236 supported by bPTP and P ID (liberal). The bPTP analysis estimated between 21 and 29 species
237 including the initial 26 putative species. Other species delimitation methods showed similar
238 results, 22 putative species had P ID (liberal) higher of 89, 20 had significant Rosenberg values
239 and 21 had GSI values of 100. All species determination methods fail in distinguishing between
240 the pairs *Co. macellaria* and *Co. aldrichi*, and *L. coeruleiviridis* and *L. mexicana* as sequence
241 divergences between species pairs are extremely low <0.08%. Given that no one method can
242 distinguish between these species, the addition of ITS2 as a second barcoding locus was
243 necessary to clarify the monophyly and validity of these species and increase the confidence of
244 delimitation and identification of species with low genetic divergences.

245 Phylogenetic Inference

246 From the 26 putative species analyzed here, 25 were represented by multiple individuals and one
247 by a single individual in the COI analysis. All phylogenetic analyses (COI, ITS2, COI+ITS2)
248 yielded well resolved trees with strong posterior probability support for most of the branches and
249 broadly agreed on species limits but with some differences in topology (Figs 2 – 4, S1 – S3). The
250 Bayesian analysis of the ITS2 supported the monophyly of 21 of 26 putative species. It recovered
251 the monophyly of *Co. aldrichi*, *Co. macellaria*, *L. mexicana* and *L. coeruleiviridis*, which failed
252 with all other analysis. However it did not recover the geographic variation of *C. idioidea* from
253 Mexico and Dominican Republic, *L. retroversa* from Cuba and Dominican Republic or *L. rica* 1
254 and 2, and it only recovers three of the four *L. eximia* clades indicated by COI analyses (Fig 3,
255 S2). The concatenated tree supports 24 of the 26 putative species including two clades within *L.*
256 *retroversa*, *L. rica*, and *C. idioidea*, and three clades within *L. eximia*. The concatenated matrix
257 did not support the monophyly of *C. idioidea*-CU that is nested within *C. idioidea*-ME and *L.*
258 *eximia*-CO+ME nested within *L. eximia*-LA (Fig 4, S3).

259 Discussion

260 Accurate identification of insects is a crucial step to using them as reliable evidence in legal
261 investigations. Although morphology has been successfully used to identify immature specimens
262 involve in cadaveric decomposition (Cardoso et al., 2014; Florez & Wolff, 2009; Szpila et al.,
263 2013a; Szpila et al., 2013b; Szpila et al., 2014; Szpila & Villet, 2011; Wells, Byrd & Tantawi,
264 1999), this approach depend of the availability of taxonomic keys of the species present in the
265 region. In the Caribbean, the immature stages of 11 species are unknown and other approaches
266 are needed in order to identify them. Besides this, morphology may overlook potentially cryptic
267 species and cannot be used on incomplete or destroyed specimens found in a crime scene. Here,
268 we show DNA barcoding to be useful in overcoming these problems and provide tools to

269 accelerate the identification and discovery of species. This is particularly important in areas like
270 the Caribbean, where studies of insects involved in cadaveric decomposition are scarce
271 (Whitworth, 2010; Yusseff-Vanegas & Agnarsson, 2016; Yusseff-Vanegas, 2007; Yusseff-
272 Vanegas, 2014). One of the first steps required for this approach is creating a reliable DNA
273 barcode database that can be used with confidence in order to identify unknown specimens found
274 in death scenes investigation (DeBry et al., 2013; Harvey et al., 2003).

275 The success of DNA barcoding relies on the quality of the underlying database used to compare
276 DNA sequences of new samples. A good database should contain DNA barcodes of expertly
277 identified individuals, and preferably taxon sampling covering the distribution range of each
278 species. Our study complies with both requirements and is the first thorough molecular study of
279 Calliphoridae from the Caribbean. It includes a representative collection from all but two
280 forensically relevant Calliphoridae from the region, and covers the whole geographic range of
281 most of the investigated species (Table 1). All specimens in this study were carefully identified
282 using traditional morphological taxonomy (Whitworth, 2006; Whitworth, 2010; Whitworth,
283 2014) and each individual was successfully allocated in one of the species of Calliphoridae
284 currently recognized except for specimen CO027 that identification was only possible to genus
285 level. Although morphological identification of specimens collected in this study corresponded
286 to 19 species previously reported (Whitworth, 2010), our results based on molecular data
287 indicate higher diversity. In all, 26 putative species lineages were identified, and in particular our
288 results indicate that *Lucilia* and *Chloroprocta* are more diverse than suggested by current
289 taxonomy. COI recovered substantial geographic variation for *C. idioidea*, *L. eximia*, *L.*
290 *retroversa* and *L. rica* such that molecular data indicate up to eleven putative species lineages
291 that cannot be, or at least have not been, recognized by morphology.

292 *Lucilia eximia* is consider a widespread species being found from the southern United States
293 through Central America to southern South America (Whitworth, 2014). Nevertheless, our
294 molecular results show four distinct genetic clusters with an average inter-cluster divergence
295 from 2.5 to 7.4% (Table 3). The clusters are geographically structured and three of them widely
296 separated (Fig 2, S1); the first one is the Greater Antilles cluster (GA) that includes specimens
297 from Puerto Rico, Mona Island and Dominican Republic; the second is a small cluster that
298 includes specimens from Florida (FL), the third one contains specimens from Colombia and
299 Mexico (CO-MEX), and the fourth contains specimens from the Lesser Antilles of Dominica and
300 Saint Lucia (LA). Similar results were reported by Solano, Wolff & Castrol (2013) and
301 Whitworth (2014) where widely separate clades of *L. eximia* were found using DNA barcodes.
302 All species delimitation methods supported the uniqueness and genetic isolation of the four
303 clades, each showing low intra-clade divergence (<1%, Table 4), and thus likely representing
304 four distinct species. Although we found some morphological variation between *L. eximia* from
305 mainland and islands and among islands as previously reported (James, 1967; Whitworth, 2010;
306 Woodley & Hilburn, 1994), detailed revision of those specimens by Dr. Whitworth from
307 Washington State University, concluded that there is not enough evidence to separate them as

308 different morphological species, suggesting they may be morphologically cryptic species.
309 Further studies on these populations will be necessary to establish their taxonomic status.

310 *Lucilia rica* was collected throughout the Lesser Antilles and is very abundant in most of the
311 islands (personal observation). Although James (1970) listed this species from Puerto Rico, we
312 did not find any specimen after very extensive collections on the island. Thus, we believe that *L.*
313 *rica* is restricted to the Lesser Antilles and has not dispersed beyond Anguilla. Whitworth (2010)
314 reported this species from Antigua, Bermuda, Guadalupe and St. Lucia; however, we found it in
315 eight more islands (Table 1) and our data showed two geographic clusters (Figs 2, 4; S1, S3).
316 The first cluster (*L. rica-1*) contains specimens from St Martin, Saba, St Eustatius, St Kitts,
317 Nevis and Martinique and the second one (*L. rica 2*) from Barbuda, Antigua, Montserrat and
318 Guadeloupe). Although the genetic distance between clades is low (1%), it is much greater than
319 the intra-clade divergences (<0.3%). While all species delimitation methods support the
320 possibility of two different species (Tables 5, 6); we did not find morphological evidence to
321 support it. Nevertheless, given that this is the most abundant *Lucilia* species of the Lesser
322 Antilles, additional studies on these populations are important to determine if the genetic
323 difference is due to intraspecific variation or if they are cryptic species.

324 Our results of *Lucilia retroversa* show two geographic clusters, one from Cuba and one from the
325 Dominican Republic with an average mtDNA distance of 2.5% (Table 3) and with low intra-
326 clade divergence (<0.2%, Table 4). Whitworth (2010) reported some morphological differences
327 between specimens from Bahamas (which share morphology with Cuban specimens) and
328 Dominican Republic, but after examination of male and female genitalia he concluded that those
329 differences were intraspecific variation. However, he noticed that our *L. retroversa* specimens
330 have a brown basicosta instead of white or yellow basicosta which is an important character used
331 to separate *L. retroversa* from other species (see taxonomic key in Whitworth 2010). Given that
332 all our species delimitation results support two possible cryptic species, we recommend further
333 detailed molecular and morphological studies of these populations to determine if they merit the
334 description of a separate species.

335 *Chloroprocta idioidea*, the only species of *Chloroprocta*, is a widespread species being found
336 from southern North America to southern South America (Dear, 1985; Whitworth, 2010). Our
337 results show that *C. idioidea* also displays a geographic structure in three clades, one from
338 Dominican Republic, one from Cuba and one from Mexico (Fig 2, S1). Analysis of the genetic
339 divergence between clades show more than 2% divergence between Cuba and Dominican
340 Republic clades but less than 2% divergence between Mexico and Cuba clades (Table 3). Some
341 authors (Hall, 1948; Shannon, 1926) believed there were two species of the genus in the
342 Americas, however (Dear, 1985) concluded that was only one single widespread species that
343 exhibits some color variations which is dependent upon geographic distribution. Our molecular
344 results indicate at least two, and perhaps three, separate species of *Chloroprocta*. All species
345 delimitation methods (Table 5) and the concatenated matrix (Fig 4, S3) suggest that the
346 Dominican Republic versus the Cuba and Mexico clade are separate species, but were

347 ambiguous about the status of *C. idioidea-CU* that is nested within *C. idioidea-ME*. Our Cuban
348 and Mexican's specimens were morphologically similar, dark-bluish color and brownish to
349 orange legs, however the Cuban females have brownish calypters instead of yellow to white as
350 Dear (1985) reported. Our specimens from Dominican Republic are similar to the southern
351 U.S.A specimens described by Dear (1985) but have darker post spiracles and clear wings with
352 only the costa faintly tinted. Although we could see morphological differences between
353 populations, those differences were based on a limited number of specimens (e.g. five specimens
354 from Dominican Republic and three from Mexico). Further studies with larger number of
355 specimens of *C. idioidea*, including detailed morphological descriptions and expanded molecular
356 analysis, are necessary to further test species limits within this genus.

357 Our focus here is not to fully resolve calliphorid taxonomy. However, it is important to highlight
358 the consequences of our findings for forensic entomology studies. Currently *L. eximia* is one of
359 the most widespread and abundant *Lucilia* in the Neotropics (Whitworth, 2014). However, our
360 results suggest that, in fact, this is not one widely distributed species, but potentially several
361 species that differ in geographic range and possibly in biological traits (rates of development,
362 diapause, habitat preference, feeding habits etc.). The same is true for *L. retroversa* and *C.*
363 *idioidea* from the Caribbean; both species show two distinctive clades, one for Dominican
364 Republic and other from Cuba (Figs 2, 4). This finding will have direct consequences for the use
365 of these species in legal investigations, if that variation reflects differences in behavior and
366 biology, that can affect post mortem interval estimations (Tarone, Singh & Picard, 2015).
367 Previous studies of *Phormia regina* (Byrd & Allen, 2001), *C. macellaria* and *C. rufifacies*
368 (Yusseff-Vanegas, 2007) have shown that their developmental rate differ from different
369 populations. Picard & Wells (2009) suggested that that variation is in part due to differences in
370 population genetic structure, and for that reason, ecological data obtained from one population
371 should not be generalized or extrapolated to other populations (Byrne et al. 1995). This is
372 important at least for specimens collected in Cuba where both populations are present, probably
373 as the result of recent dispersal of *L. retroversa* and *C. idioidea* from the Dominican Republic to
374 Cuba. Our results (S1) show that two of the southeast Cuban specimens, CU007 (*L. retroversa*)
375 and CU008 (*C. idioidea*), collected in Turquino National Park in Cuba (Table 1), cluster tightly
376 with Dominican Republic specimens (S1). To confirm the genetic affinity of these specimens we
377 added three more nuclear genes for a limited number of individuals from both populations and
378 re-ran the analysis. The multi-gene analysis again strongly clustered CU007 and CU008 with the
379 Dominican Republic specimens for each species. Thus, both the Dominican Republic and Cuban
380 populations are clearly present in Cuba.

381 COI recuperated substantial geographic variation with high COI sequences divergence between
382 populations of *Lucilia eximia*, *L. retroversa*, *L. rica* and *C. idioidea* (Fig 2, S1), suggesting the
383 possibility of different species (Hebert et al., 2003; Hebert, Ratnasingham & deWaard, 2003).
384 However, not always genetic variation is indicative of species differentiation. For instance,
385 studies including *Phormia regina* have found that the genetic distance between N American and

386 W European populations is higher than 4% (Boehme, Amendt & Zehner, 2012; Desmyter &
387 Gosselin, 2009). But After detailed molecular and morphological analysis of both populations,
388 Jordaens et al. (2013a) concluded that the high differentiation at COI, COII and *cytb*, but low
389 (16S, nDNA) and lack of morphological differentiation, was indicative of substantial
390 intraspecific mtDNA sequence divergence, rather than a species level differentiation. In light of
391 those results, definite conclusion about the taxonomy of these species is not possible yet and
392 further studies between populations of the four species in question are strongly recommended. A
393 comprehensive molecular analysis including several mitochondrial and nuclear genes in
394 combination with morphological examination and detailed description of the genitalia, are
395 required to determine if they are in fact different species, or if the genetic difference between
396 populations is the product of intraspecific variation. Meanwhile the use of these species for
397 forensic purposes should be evaluated carefully and with reference to genetic and behavioral
398 differences among its populations.

399 Regarding the other Calliphoridae species, *Ca. maestrica*, *Co. minima*, *Co hominivorax*, *Ch.*
400 *albiceps*, *Ch. rufifacies*, *Ch. megacephala*, *L. cluvia*, *L. cuprina* and *L. lucigerens*, all showed
401 reciprocal monophyly with strong posterior probability support and all can be successfully
402 identified using the DNA barcoding approach. All species delimitation methods, phylogenetic
403 analysis of ITS2, and the concatenated tree support their monophyly and species status, and the
404 results are congruent with morphology. *Calliphora maestrica* is the only *Calliphora* species
405 reported for the Caribbean and is endemic from the region. This species was originally described
406 from Sierra Maestra region in Cuba (Peris et al., 1998) and later reported also from Jamaica and
407 Dominican Republic (Whitworth, 2010). Although we collected on all three islands, we only
408 found *C. maestrica* in Villa Pajon, Dominican Republic, a cold region at altitudes >2140 m. We
409 did not find it in Cuba or Jamaica, likely due to lack of sampling at altitudes above 1200 m on
410 both islands.

411 The three species of *Chrysomya* were recently introduced to the New World (Baumgartner &
412 Greenberg, 1984). Although Whitworth (2010) reported *Ch. megacephala* and *Ch. rufifacies*
413 from Dominica, Dominican Republic, Jamaica and Puerto Rico, they are abundantly present in
414 most of the islands being found from Cuba to Martinique (Table 1). In contrast, *Chrysomya*
415 *albiceps* has more restricted distribution being found in islands closer to South America (Table 1,
416 Whitworth, 2010). Although Dear 1985 reported this species from Puerto Rico, we did not find it
417 after extensive collections on the island. That report was based on a single larva found in a goat,
418 probably of *Ch. albiceps* but the species was not confirmed (Gagne, 1981). We believe that *Ch.*
419 *albiceps* has not dispersed beyond Dominica and that the species reported by Dear 1985 was in
420 fact *Ch. rufifacies*. Given the high dispersal abilities of the species of this genus (Baumgartner &
421 Greenberg, 1984) and their invasive behavior (Aguiar-Coelho & Milward-De-Azevedo, 1998;
422 De Andrade et al., 2002; Faria et al., 1999; Wells & Greenberg, 1992), it is not surprising to find
423 them widely distributed and very well established throughout the Caribbean. They do not show

424 any geographic structure, suggesting their recent colonization from the mainland and the
425 constant gene flow among populations.

426 *Lucilia cluvia* and *L. cuprina*, are widely distributed flies found in different parts of the world
427 (Byrd & Castner, 2010). *Lucilia cluvia* is considered rare (Whitworth, 2010). Although it has
428 been reported from several locations in Puerto Rico, Cuba, and Martinique, we have only found
429 two specimens in a suburban area in Toa Baja, Puerto Rico. *Lucilia cuprina* is reported from
430 several islands in the Caribbean, but we only found it in urban areas of Puerto Rico as our focus
431 on other islands was on non-urban areas. Finally *L. lucigerens* is an endemic species from
432 Jamaica and was collected abundantly throughout the Island.

433 DNA barcoding in animals typically employs a single mitochondrial marker for identification
434 and delimitation of species (Herbert et al 2003ab), and this approach has shown to be useful in
435 Calliphoridae species identification. However it does not reliably distinguish among some
436 recently diverged species (Harvey et al., 2003; Nelson, Wallman & Dowton, 2007), leading to
437 doubt that COI alone is sufficient for identification of species (Nelson, Wallman & Dowton,
438 2007; Wells, Wall & Stevens, 2007). Rather, the use of multiple markers has been suggested as a
439 means to increase the accuracy of species identification. Indeed, our results show that COI
440 barcoding successfully identified most species, but did not distinguish between the pairs *L.*
441 *mexicana* and *L. coeruleiviridis* as previously reported (DeBry et al., 2013; Whitworth, 2014;
442 Williams, Lamb & Villet, 2016) and between *Co. aldrichi* and *Co. macellaria* (Tables 3, 5, S1).
443 The latter species is considered one of the most important Calliphoridae for forensic studies in
444 the Americas (see discussion in Yusseff-Vanegas and Agnarsson, 2016). Additionally, COI
445 showed very low genetic divergences (<0.7%, Table 3) between the putative species *L. vulgata*
446 and *L. coeruleiviridis*, and *L. fayeae* and *L. retroversa-CU*; species that are clearly distinguished
447 based on morphological characteristics. This low genetic divergence may reflect short histories
448 of reproductive isolation (Hebert, Ratnasingham & deWaard (2003), or mitochondrial
449 introgression. In either case the addition of the nuclear gene ITS2 resolved the monophyly of the
450 four species that COI alone did not support, and added resolution for uncertain groups with
451 mtDNA genetic distances lower than 2%. This findings agreed with previous studies where the
452 analysis of ITS2 resolve complex species delimitation (GilArriortua et al., 2014; Song, Wang &
453 Liang, 2008), however, not always addition of more genes resolve the monophyly of the sister
454 species like is the case of *L. illustris* and *L. caesar* where after analysis including six genes the
455 monophyly remain unresolved (Sonet et al., 2012).

456 In sum, our study demonstrates the importance employing a second nuclear marker for barcoding
457 analyses and species delimitation of calliphorids and the power of molecular data in combination
458 with a complete reference database to enable identification of taxonomically and geographically
459 diverse insects of forensic importance. The combination of the two markers supported the higher
460 diversity of Calliphoridae in the Caribbean recovering the monophyly of nine of the eleven
461 possible cryptic species. However, definite conclusion about the taxonomy of these species will
462 depend on further studies combining molecular and morphological approaches.

463 Conclusion

464 From almost a decade many studies have applied DNA-based methods for the identification of
465 insects of forensic importance to enable identification of unknown insect specimens found in
466 death scene investigations. However, this technique is not being implemented and the traditional
467 time consuming methods of raising immature stages to adulthood is still in practice. The use of
468 this approach has been unsuccessful because of lack of confidence due to sequence gaps and
469 errors, unauthenticated reference DNA sequences in the database, and incomplete reference data
470 set with partial taxon sampling. Thus, the base science foundation for application of DNA
471 sequences analysis is unsolid for identification of evidentiary samples. Despite all studies of
472 DNA based identification for insects involved in forensics, only a few of them include a
473 complete reference data set. But even with a complete reference database, COI has failed in
474 demonstrating reciprocal monophyly for several recently diverged species creating uncertainty
475 about its use for identification. The addition of ITS2 as a second marker may be the key to
476 increase certainty in identification and make this technique useful for forensic purposes. A great
477 effort to build complete reference databases including extensive collections, accurate
478 identification, geographical genetic variation for each targeted insect group and the addition of
479 ITS2 as a second marker is needed. In general, COI barcodes are highly useful for species
480 identification of the Caribbean calliphorids. ITS2 appears to be a good second marker that allows
481 higher resolution and accurate identification of specimens that cannot be separated by COI alone.
482 Our study provides, for the first time, a reliable dataset to accurately identify species of the
483 family Calliphoridae from the Caribbean, and opens the door for future studies on biodiversity,
484 biogeography, distribution and ecology of these forensically important flies.

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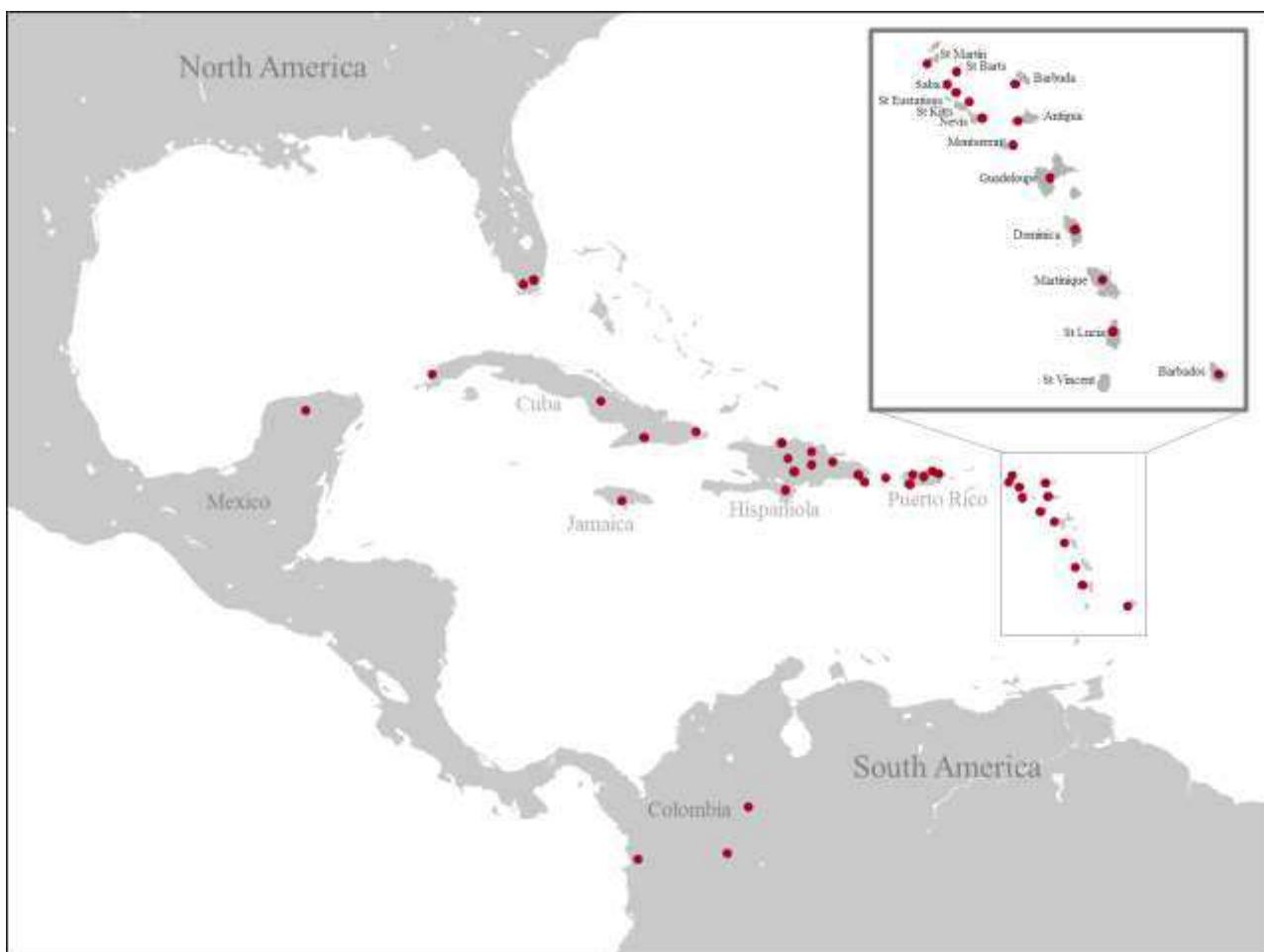
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Figure 1. Map of collecting localities of all specimens used for the molecular analysis. Source: map based on the <http://gmt.soest.hawaii.edu/> Generic Mapping Tools

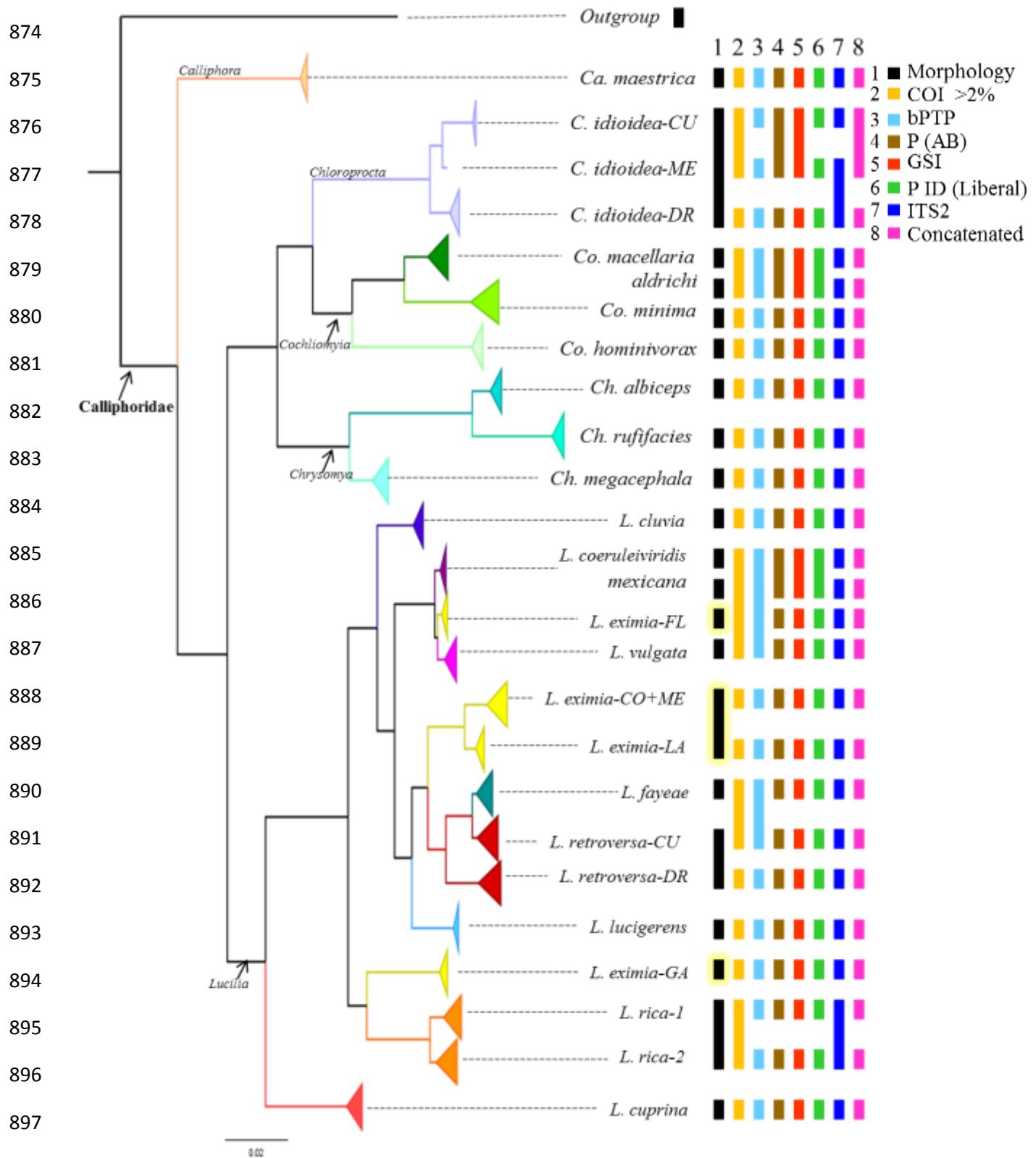
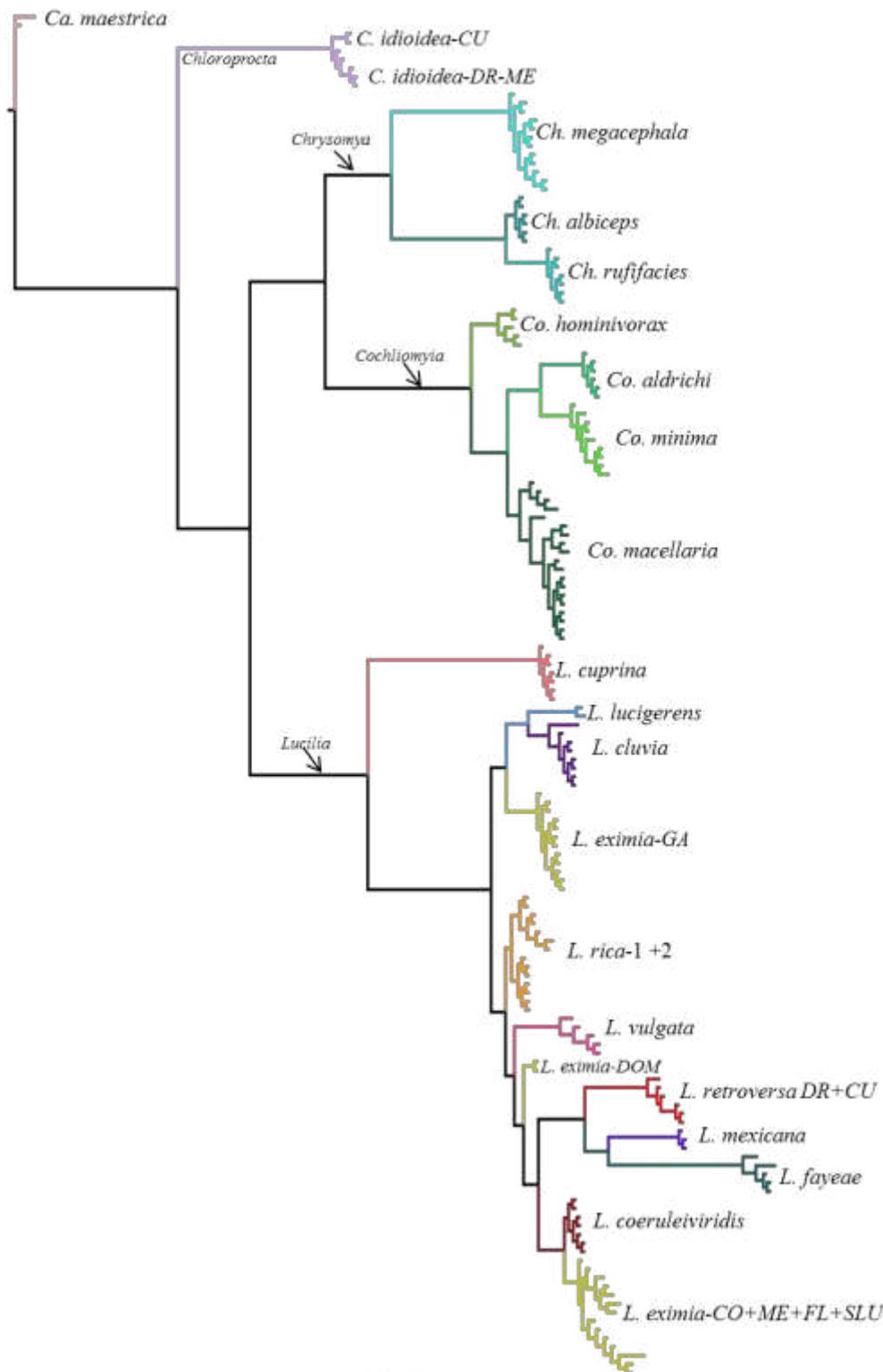
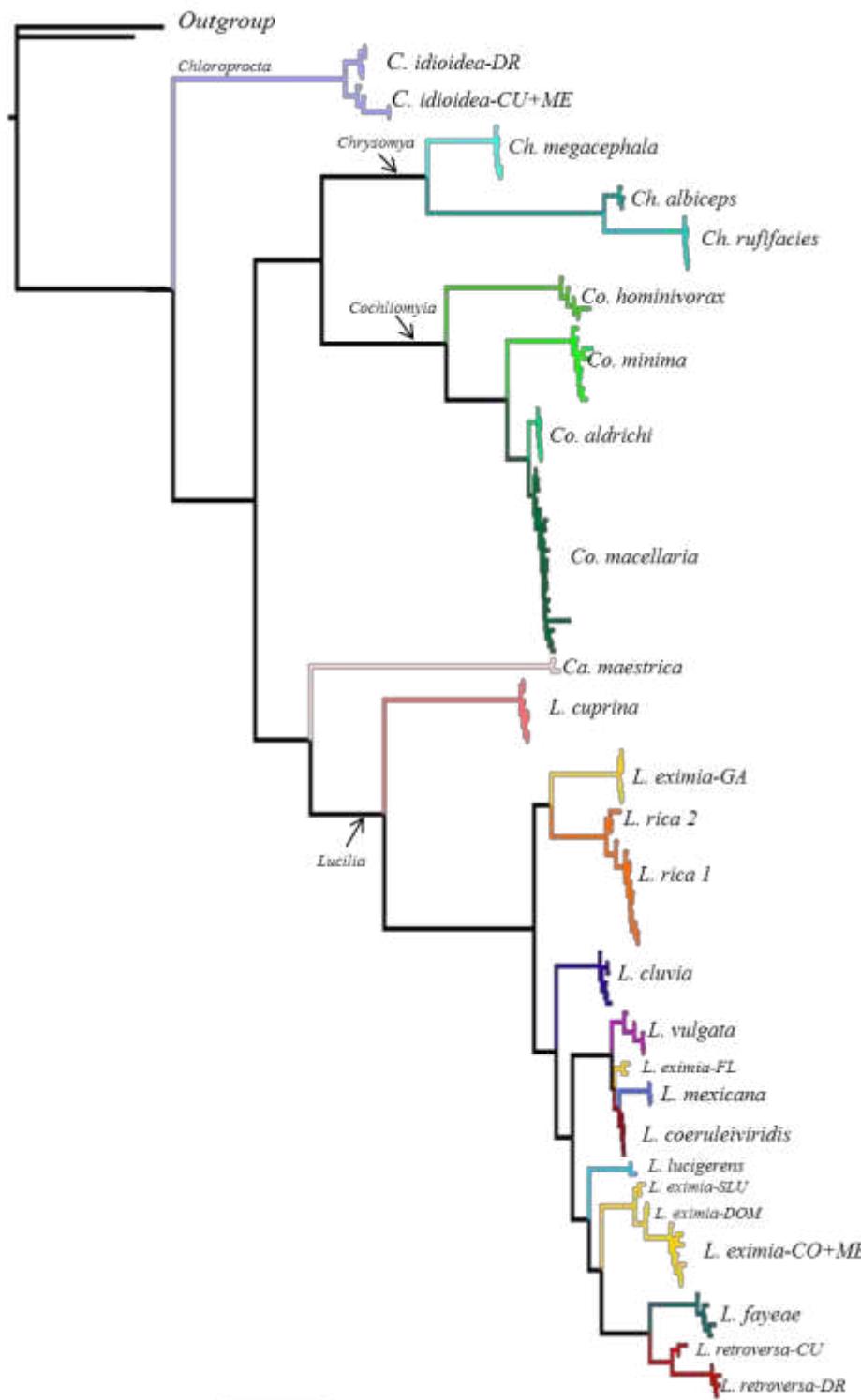


Figure 2. Summary of the Bayesian tree based on the COI dataset including 442 individuals, with the results of four different species delimitation approaches in addition to morphology, genetic distances of >2% mtDNA, ITS2 and the concatenated matrix. See figure S1 for bootstrap support values.



901

902 **Figure 3.** Bayesian tree based on ITS2 dataset including 158 specimens. Individual terminal taxa have
903 been replaced with species names, while full taxon clade structure is retained. Colors represent different
904 species based on morphology. See figure S2 for bootstrap support values.



905

906 **Figure 4.** Bayesian tree based on the concatenate dataset including 137 specimens. Individual terminal
907 taxa have been replaced with species names, while full taxon clade structure is retained. Colors represent
908 different species based on morphology. See figure S3 for bootstrap support values.

909
910**Table 1.** Specimen details, collection information and GenBank accession numbers. *Estimated coordinate points.

^Accession numbers from BOLD systems. - blank.

Genus	Species	Voucher ID	Country	Latitude	longitude	COI	ITS2
<i>Calliphora</i>	<i>maestrica</i>	DR084	Hispaniola	N 18.82138	W 70.67935	MF097182	MF097580
<i>Calliphora</i>	<i>maestrica</i>	DR085	Hispaniola	N 18.82138	W 70.67935	MF097183	-
<i>Calliphora</i>	<i>maestrica</i>	DR086	Hispaniola	N 18.82138	W 70.67935	MF097184	-
<i>Calliphora</i>	<i>maestrica</i>	DR087	Hispaniola	N 18.82138	W 70.67935	MF097185	-
<i>Calliphora</i>	<i>maestrica</i>	DR088	Hispaniola	N 18.82138	W 70.67935	MF097186	MF097581
<i>Chloroprocta</i>	<i>idioidea</i>	CU008	Cuba	N 20.054178	W 76.917603	MF097187	MF097582
<i>Chloroprocta</i>	<i>idioidea</i>	CU047	Cuba	N 21.582414	W 77.783464	MF097188	MF097583
<i>Chloroprocta</i>	<i>idioidea</i>	CU048	Cuba	N 21.582414	W 77.783464	MF097189	MF097584
<i>Chloroprocta</i>	<i>idioidea</i>	CU049	Cuba	N 21.582414	W 77.783464	MF097190	-
<i>Chloroprocta</i>	<i>idioidea</i>	DR031	Hispaniola	N 18.316572	W 71.576447*	MF097191	-
<i>Chloroprocta</i>	<i>idioidea</i>	DR044	Hispaniola	N 18.316572	W 71.576447*	MF097192	MF097585
<i>Chloroprocta</i>	<i>idioidea</i>	DR045	Hispaniola	N 18.316572	W 71.576447*	MF097193	-
<i>Chloroprocta</i>	<i>idioidea</i>	DR051	Hispaniola	N 19.06753	W 69.46445	MF097194	-
<i>Chloroprocta</i>	<i>idioidea</i>	DR052	Hispaniola	N 19.06753	W 69.46445	MF097195	MF097586
<i>Chloroprocta</i>	<i>idioidea</i>	ME001	Mexico	N 21.07645	W 89.501083	-	MF097587
<i>Chloroprocta</i>	<i>idioidea</i>	ME002	Mexico	N 21.07645	W 89.501083	MF097196	MF097588
<i>Chrysomya</i>	<i>albiceps</i>	CO003	Colombia	N 5.900544	W 74.852897*	-	MF097589
<i>Chrysomya</i>	<i>albiceps</i>	CO004	Colombia	N 5.900544	W 74.852897*	-	MF097590
<i>Chrysomya</i>	<i>albiceps</i>	CO005	Colombia	N 5.900544	W 74.852897*	-	MF097591
<i>Chrysomya</i>	<i>albiceps</i>	LA103	Martinique	N 14.47428	W 60.81463	MF097199	MF097592
<i>Chrysomya</i>	<i>albiceps</i>	LA104	Martinique	N 14.47428	W 60.81463	MF097200	MF097593
<i>Chrysomya</i>	<i>albiceps</i>	LA125	Saint Lucia	N 14.100031	W 60.92654	MF097201	MF097594
<i>Chrysomya</i>	<i>albiceps</i>	LA135	Barbados	N 13.2051667	W 59.5295556	MF097197	-
<i>Chrysomya</i>	<i>albiceps</i>	LA136	Barbados	N 13.2051667	W 59.5295556	MF097198	-
<i>Chrysomya</i>	<i>megacephala</i>	CO006	Colombia	N 5.900544	W 74.852897*	MF097202	MF097595
<i>Chrysomya</i>	<i>megacephala</i>	CO007	Colombia	N 5.900544	W 74.852897*	-	MF097596
<i>Chrysomya</i>	<i>megacephala</i>	CO008	Colombia	N 6.266242	W 77.374903*	MF097203	MF097597
<i>Chrysomya</i>	<i>megacephala</i>	CO009	Colombia	N 5.900544	W 74.852897*	-	MF097598
<i>Chrysomya</i>	<i>megacephala</i>	DR017	Hispaniola	N 19.89155	W 071.65806	MF097205	-
<i>Chrysomya</i>	<i>megacephala</i>	DR018	Hispaniola	N 19.89155	W 071.65806	MF097206	-
<i>Chrysomya</i>	<i>megacephala</i>	DR068	Hispaniola	N 19.06710	W 69.46004	MF097207	-
<i>Chrysomya</i>	<i>megacephala</i>	DR069	Hispaniola	N 19.06710	W 69.46004	MF097208	-
<i>Chrysomya</i>	<i>megacephala</i>	DR101	Hispaniola	N 18.35698	W 68.61609	MF097209	-
<i>Chrysomya</i>	<i>megacephala</i>	DR102	Hispaniola	N 18.35698	W 68.61609	MF097210	-
<i>Chrysomya</i>	<i>megacephala</i>	DR103	Hispaniola	N 18.35698	W 68.61609	MF097211	-
<i>Chrysomya</i>	<i>megacephala</i>	DR104	Hispaniola	N 18.35698	W 68.61609	MF097212	-
<i>Chrysomya</i>	<i>megacephala</i>	DR116	Hispaniola	N 18.32902	W 68.80995	MF097213	MF097599
<i>Chrysomya</i>	<i>megacephala</i>	DR117	Hispaniola	N 18.32902	W 68.80995	MF097214	MF097611
<i>Chrysomya</i>	<i>megacephala</i>	DR118	Hispaniola	N 18.32902	W 68.80995	MF097215	-
<i>Chrysomya</i>	<i>megacephala</i>	DR119	Hispaniola	N 18.32902	W 68.80995	MF097216	-
<i>Chrysomya</i>	<i>megacephala</i>	FL003	Florida, USA	N 25.614383	W 80.584467	KX529521	KX529561
<i>Chrysomya</i>	<i>megacephala</i>	FL004	Florida, USA	N 25.614383	W 80.584467	MF097218	-
<i>Chrysomya</i>	<i>megacephala</i>	FL011	Florida, USA	N 25.086633	W 80.452217	MF097219	-
<i>Chrysomya</i>	<i>megacephala</i>	JA004	Jamaica	N 18.0598056	W 77.5311944	-	MF097600
<i>Chrysomya</i>	<i>megacephala</i>	LA062	Dominica	N 15.34066	W 61.33351	MF097220	-
<i>Chrysomya</i>	<i>megacephala</i>	LA001	Saint Eustatius	N 17.47637	W 62.97470	MF097225	-
<i>Chrysomya</i>	<i>megacephala</i>	LA003	Saint Eustatius	N 17.47637	W 62.97470	MF097217	-
<i>Chrysomya</i>	<i>megacephala</i>	LA025	Saint-Martin	N 18.07779	W 63.05772	MF097235	-
<i>Chrysomya</i>	<i>megacephala</i>	LA055	Saint Barthélemy	N 17.91924	W 62.86366	MF097234	-
<i>Chrysomya</i>	<i>megacephala</i>	LA063	Dominica	N 15.34066	W 61.33351	MF097204	-
<i>Chrysomya</i>	<i>megacephala</i>	LA088	Guadeloupe	N 16.37752	W 61.47869	MF097221	-
<i>Chrysomya</i>	<i>megacephala</i>	LA089	Guadeloupe	N 16.37752	W 61.47869	MF097222	-
<i>Chrysomya</i>	<i>megacephala</i>	LA093	Nevis	N 17.14145	W 62.57784	MF097226	-
<i>Chrysomya</i>	<i>megacephala</i>	LA116	Saint Kitts	N 17.3404083	W 62.7410389	MF097223	-
<i>Chrysomya</i>	<i>megacephala</i>	LA117	Saint Kitts	N 17.3404083	W 62.7410389	MF097224	-
<i>Chrysomya</i>	<i>megacephala</i>	LA123	Saint Lucia	N 14.100031	W 60.92654	-	MF097604
<i>Chrysomya</i>	<i>megacephala</i>	ME013	Mexico	N 25.598592	W 103.441156	-	MF097601
<i>Chrysomya</i>	<i>megacephala</i>	ME014	Mexico	N 25.598592	W 103.441156	-	MF097602

<i>Chrysomya</i>	<i>megacephala</i>	PR038	Puerto Rico	N 18.412972	W 66.026619	MF097227	-
<i>Chrysomya</i>	<i>megacephala</i>	PR124	Puerto Rico	N 18.370953	W 66.026619	MF097228	-
<i>Chrysomya</i>	<i>megacephala</i>	PR125	Puerto Rico	N 18.370953	W 66.026619	MF097229	MF097603
<i>Chrysomya</i>	<i>megacephala</i>	PR1251	Puerto Rico	N 18.370953	W 66.026619	MF097230	-
<i>Chrysomya</i>	<i>megacephala</i>	PR126	Puerto Rico	N 18.370953	W 66.026619	MF097231	-
<i>Chrysomya</i>	<i>megacephala</i>	PR138	Puerto Rico	N 18.447911	W 65.948617	MF097232	-
<i>Chrysomya</i>	<i>megacephala</i>	PR139	Puerto Rico	N 18.447911	W 65.948617	MF097233	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA056	Saint Barthélemy	N 17.91924	W 62.86366	MF097236	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA057	Saint Barthélemy	N 17.91924	W 62.86366	MF097237	-
<i>Chrysomya</i>	<i>rufifacies</i>	CU001	Cuba	N 20.054178	W 76.917603	MF097238	-
<i>Chrysomya</i>	<i>rufifacies</i>	CU003	Cuba	N 20.054178	W 76.917603	MF097239	-
<i>Chrysomya</i>	<i>rufifacies</i>	CU004	Cuba	N 20.054178	W 76.917603	KX529555	KX529562
<i>Chrysomya</i>	<i>rufifacies</i>	CU005	Cuba	N 20.054178	W 76.917603	MF097240	-
<i>Chrysomya</i>	<i>rufifacies</i>	CU009	Cuba	N 20.054178	W 76.917603	MF097241	-
<i>Chrysomya</i>	<i>rufifacies</i>	CU034	Cuba	N 22.621386	W 83.725944	MF097242	-
<i>Chrysomya</i>	<i>rufifacies</i>	CU035	Cuba	N 22.621386	W 83.725944	MF097243	-
<i>Chrysomya</i>	<i>rufifacies</i>	CU036	Cuba	N 22.621386	W 83.725944	MF097244	-
<i>Chrysomya</i>	<i>rufifacies</i>	CU037	Cuba	N 22.621386	W 83.725944	MF097245	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR001	Hispaniola	N 19.89155	W 71.65806	MF097248	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR002	Hispaniola	N 19.89155	W 71.65806	MF097249	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR003	Hispaniola	N 19.89155	W 71.65806	MF097250	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR004	Hispaniola	N 19.89155	W 71.65806	MF097251	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR006	Hispaniola	N 19.89155	W 71.65806	MF097252	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR007	Hispaniola	N 19.89155	W 71.65806	MF097253	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR008	Hispaniola	N 19.89155	W 71.65806	MF097254	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR016	Hispaniola	N 19.89155	W 71.65806	MF097255	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR036	Hispaniola	N 18.316572	W 71.576447*	MF097256	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR037	Hispaniola	N 18.316572	W 71.576447*	MF097257	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR038	Hispaniola	N 18.316572	W 71.576447*	MF097258	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR039	Hispaniola	N 18.316572	W 71.576447*	MF097259	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR070	Hispaniola	N 19.06710	W 69.46004	MF097260	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR071	Hispaniola	N 19.06710	W 69.46004	MF097261	MF097605
<i>Chrysomya</i>	<i>rufifacies</i>	DR0711	Hispaniola	N 19.06710	W 69.46004	-	MF097606
<i>Chrysomya</i>	<i>rufifacies</i>	DR093	Hispaniola	N 18.35698	W 68.61609	MF097262	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR094	Hispaniola	N 18.35698	W 68.61609	MF097263	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR095	Hispaniola	N 18.35698	W 68.61609	MF097264	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR096	Hispaniola	N 18.35698	W 68.61609	MF097265	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR097	Hispaniola	N 18.35698	W 68.61609	MF097266	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR098	Hispaniola	N 18.35698	W 68.61609	MF097267	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR099	Hispaniola	N 18.35698	W 68.61609	MF097268	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR100	Hispaniola	N 18.35698	W 68.61609	MF097269	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR132	Hispaniola	N 18.32902	W 68.80995	MF097270	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR133	Hispaniola	N 18.32902	W 68.80995	MF097271	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR135	Hispaniola	N 19.741319	W 70.654975*	MF097272	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR150	Hispaniola	N 19.34405	W 70.14824	MF097273	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR151	Hispaniola	N 19.34405	W 70.14824	MF097274	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR152	Hispaniola	N 19.34405	W 70.14824	MF097275	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR155	Hispaniola	N 19.34405	W 70.14824	MF097276	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR157	Hispaniola	N 18.32902	W 68.80995	MF097277	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR158	Hispaniola	N 18.32902	W 68.80995	MF097278	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR159	Hispaniola	N 18.32902	W 68.80995	MF097279	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR160	Hispaniola	N 18.32902	W 68.80995	MF097280	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR161	Hispaniola	N 18.32902	W 68.80995	MF097281	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR162	Hispaniola	N 18.32902	W 68.80995	MF097282	-
<i>Chrysomya</i>	<i>rufifacies</i>	DR163	Hispaniola	N 18.32902	W 68.80995	MF097283	-
<i>Chrysomya</i>	<i>rufifacies</i>	FL001	Florida, USA	N 25.614383	W 80.584467	MF097288	-
<i>Chrysomya</i>	<i>rufifacies</i>	FL010	Florida, USA	N 25.086633	W 80.452217	MF097289	MF097607
<i>Chrysomya</i>	<i>rufifacies</i>	JA003	Jamaica	N 18.0598056	W 77.5311944	MF097293	MF097608
<i>Chrysomya</i>	<i>rufifacies</i>	LA002	Saint Eustatius	N 17.47637	W 62.97470	MF097284	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA004	Saint Eustatius	N 17.47637	W 62.97470	MF097285	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA005	Saint Eustatius	N 17.47637	W 62.97470	MF097286	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA006	Saint Eustatius	N 17.47637	W 62.97470	MF097287	-

<i>Chrysomya</i>	<i>rufifacies</i>	LA041	Saint-Martin	N 18.11677	W 63.03902	MF097316	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA042	Saint-Martin	N 18.11677	W 63.03902	MF097317	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA043	Saint-Martin	N 18.11677	W 63.03902	MF097318	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA044	Saint-Martin	N 18.11677	W 63.03902	MF097319	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA069	Dominica	N 15.34066	W 61.33351	MF097246	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA072	Dominica	N 15.34066	W 61.33351	MF097247	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA090	Guadeloupe	N 16.37752	W 61.47869	MF097290	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA091	Guadeloupe	N 16.37752	W 61.47869	MF097291	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA092	Guadeloupe	N 16.37752	W 61.47869	MF097292	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA101	Martinique	N 14.47428	W 60.81463	MF097310	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA108	Montserrat	N 16.77608	W 62.30904	MF097309	-
<i>Chrysomya</i>	<i>rufifacies</i>	LA110	Saint Kitts	N 17.3404083	W 62.7410389	MF097294	MF097609
<i>Chrysomya</i>	<i>rufifacies</i>	M074	Mona, Puerto Rico	N 18.086239	W 67.906339	MF097295	-
<i>Chrysomya</i>	<i>rufifacies</i>	M075	Mona, Puerto Rico	N 18.086239	W 67.906339	MF097296	-
<i>Chrysomya</i>	<i>rufifacies</i>	M082	Mona, Puerto Rico	N 18.11125	W 67.933447	MF097297	-
<i>Chrysomya</i>	<i>rufifacies</i>	M083	Mona, Puerto Rico	N 18.11125	W 67.933447	MF097298	-
<i>Chrysomya</i>	<i>rufifacies</i>	M089	Mona, Puerto Rico	N 18.06301	W 67.88728	MF097299	-
<i>Chrysomya</i>	<i>rufifacies</i>	M090	Mona, Puerto Rico	N 18.06301	W 67.88728	MF097300	-
<i>Chrysomya</i>	<i>rufifacies</i>	M091	Mona, Puerto Rico	N 18.06301	W 67.88728	MF097301	-
<i>Chrysomya</i>	<i>rufifacies</i>	M093	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097302	-
<i>Chrysomya</i>	<i>rufifacies</i>	M094	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097303	-
<i>Chrysomya</i>	<i>rufifacies</i>	M095	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097304	-
<i>Chrysomya</i>	<i>rufifacies</i>	M096	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097305	-
<i>Chrysomya</i>	<i>rufifacies</i>	M101	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097306	-
<i>Chrysomya</i>	<i>rufifacies</i>	M108	Mona, Puerto Rico	N 18.11125	W 67.933447	MF097307	-
<i>Chrysomya</i>	<i>rufifacies</i>	M109	Mona, Puerto Rico	N 18.11125	W 67.933447	MF097308	-
<i>Chrysomya</i>	<i>rufifacies</i>	PR117	Puerto Rico	N 18.370953	W 66.026619	MF097311	-
<i>Chrysomya</i>	<i>rufifacies</i>	PR118	Puerto Rico	N 18.370953	W 66.026619	MF097312	-
<i>Chrysomya</i>	<i>rufifacies</i>	PR119	Puerto Rico	N 18.370953	W 66.026619	MF097313	-
<i>Chrysomya</i>	<i>rufifacies</i>	PR120	Puerto Rico	N 18.370953	W 66.026619	MF097314	-
<i>Chrysomya</i>	<i>rufifacies</i>	PR130	Puerto Rico	N 18.093306	W 65.556083	MF097315	MF097610
<i>Cochliomyia</i>	<i>aldrichi</i>	M080	Mona, Puerto Rico	N 18.084222	W 65.939417	KX529529	KX529563
<i>Cochliomyia</i>	<i>aldrichi</i>	M084	Mona, Puerto Rico	N 18.11125	W 67.933447	MF097320	-
<i>Cochliomyia</i>	<i>aldrichi</i>	M085	Mona, Puerto Rico	N 18.11125	W 67.933447	KX529530	KX529564
<i>Cochliomyia</i>	<i>aldrichi</i>	M086	Mona, Puerto Rico	N 18.06301	W 67.88728	KX529531	KX529565
<i>Cochliomyia</i>	<i>aldrichi</i>	M087	Mona, Puerto Rico	N 18.06301	W 67.88728	MF097321	-
<i>Cochliomyia</i>	<i>aldrichi</i>	M088	Mona, Puerto Rico	N 18.06301	W 67.88728	MF097322	-
<i>Cochliomyia</i>	<i>aldrichi</i>	M102	Mona, Puerto Rico	N 18.11125	W 67.933447	MF097323	-
<i>Cochliomyia</i>	<i>aldrichi</i>	M103	Mona, Puerto Rico	N 18.11125	W 67.933447	KX529532	KX529566
<i>Cochliomyia</i>	<i>aldrichi</i>	M104	Mona, Puerto Rico	N 18.085972	W 67.933447	MF097324	-
<i>Cochliomyia</i>	<i>aldrichi</i>	M105	Mona, Puerto Rico	N 18.085972	W 67.933447	KX529533	KX529567
<i>Cochliomyia</i>	<i>aldrichi</i>	M106	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097325	-
<i>Cochliomyia</i>	<i>aldrichi</i>	M107	Mona, Puerto Rico	N 18.084222	W 67.939417	KX529534	KX529568
<i>Cochliomyia</i>	<i>hominivorax</i>	CO001	Colombia	N 5.900544	W 74.852897*	-	MF097612
<i>Cochliomyia</i>	<i>hominivorax</i>	CU020	Cuba	N 22.621386	W 83.725944	-	MF097613
<i>Cochliomyia</i>	<i>hominivorax</i>	CU033	Cuba	N 22.621386	W 83.725944	KX529556	KX529571
<i>Cochliomyia</i>	<i>hominivorax</i>	DR042	Hispaniola	N 18.316572	W 71.576447*	KX529557	KX529572
<i>Cochliomyia</i>	<i>hominivorax</i>	DR105	Hispaniola	N 18.35698	W 68.61609	KX529558	KX529573
<i>Cochliomyia</i>	<i>macellaria</i>	LA137	Saint Barthélemy	N 17.910299	W 62.847221	MF097326	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA139	Saint Barthélemy	N 17.910299	W 62.847221	MF097327	-
<i>Cochliomyia</i>	<i>macellaria</i>	CO002	Colombia	N 5.900544	W 74.852897*	KX529522	KX529574
<i>Cochliomyia</i>	<i>macellaria</i>	CO010	Colombia	N 6.266242	W 77.374903*	KX529545	KX529575
<i>Cochliomyia</i>	<i>macellaria</i>	CU012	Cuba	N 22.621386	W 83.725944	MF097330	-
<i>Cochliomyia</i>	<i>macellaria</i>	CU013	Cuba	N 22.621386	W 83.725944	MF097331	-
<i>Cochliomyia</i>	<i>macellaria</i>	CU014	Cuba	N 22.621386	W 83.725944	KX529541	KX529577
<i>Cochliomyia</i>	<i>macellaria</i>	CU015	Cuba	N 22.621386	W 83.725944	MF097332	-
<i>Cochliomyia</i>	<i>macellaria</i>	CU016	Cuba	N 22.621386	W 83.725944	MF097333	-
<i>Cochliomyia</i>	<i>macellaria</i>	CU017	Cuba	N 22.621386	W 83.725944	MF097334	-
<i>Cochliomyia</i>	<i>macellaria</i>	CU018	Cuba	N 22.621386	W 83.725944	KX529526	KX529578
<i>Cochliomyia</i>	<i>macellaria</i>	CU019	Cuba	N 22.621386	W 83.725944	MF097335	MF097614
<i>Cochliomyia</i>	<i>macellaria</i>	CU050	Cuba	N 21.582414	W 77.750131	MF097336	-
<i>Cochliomyia</i>	<i>macellaria</i>	CU051	Cuba	N 21.582414	W 77.750131	MF097337	-

<i>Cochliomyia</i>	<i>macellaria</i>	DR009	Hispaniola	N 19.89155	W 71.65806	MF097341	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR010	Hispaniola	N 19.89155	W 71.65806	KX529536	KX529579
<i>Cochliomyia</i>	<i>macellaria</i>	DR011	Hispaniola	N 19.89155	W 71.65806	MF097342	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR012	Hispaniola	N 19.89155	W 71.65806	MF097343	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR013	Hispaniola	N 19.89155	W 71.65806	MF097344	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR014	Hispaniola	N 19.89155	W 71.65806	MF097345	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR015	Hispaniola	N 19.89155	W 71.65806	MF097346	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR043	Hispaniola	N 18.316572	W 71.576447*	MF097347	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR062	Hispaniola	N 19.06710	W 69.46004	MF097348	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR063	Hispaniola	N 19.06710	W 69.46004	MF097349	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR064	Hispaniola	N 19.06710	W 69.46004	MF097350	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR065	Hispaniola	N 19.06710	W 69.46004	MF097351	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR066	Hispaniola	N 19.06710	W 69.46004	MF097352	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR106	Hispaniola	N 18.35698	W 68.61609	MF097353	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR107	Hispaniola	N 18.35698	W 68.61609	MF097354	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR108	Hispaniola	N 18.35698	W 68.61609	MF097355	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR109	Hispaniola	N 18.35698	W 68.61609	MF097356	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR1091	Hispaniola	N 18.35698	W 68.61609	MF097357	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR120	Hispaniola	N 18.32902	W 68.80995	MF097358	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR121	Hispaniola	N 18.32902	W 68.80995	MF097359	-
<i>Cochliomyia</i>	<i>macellaria</i>	DR134	Hispaniola	N 19.741319	W 70.654975*	KX529527	KX529580
<i>Cochliomyia</i>	<i>macellaria</i>	DR154	Hispaniola	N 19.34405	W 70.14824	MF097360	-
<i>Cochliomyia</i>	<i>macellaria</i>	FL006	Florida, USA	N 25.614383	W 80.584467	-	MF097615
<i>Cochliomyia</i>	<i>macellaria</i>	FL009	Florida, USA	N 25.457514	W 80.4863	MF097361	-
<i>Cochliomyia</i>	<i>macellaria</i>	JA002	Jamaica	N 18.0598056	W 77.5311944	-	MF097616
<i>Cochliomyia</i>	<i>macellaria</i>	LA022	Saint-Martin	N 18.07779	W 63.05772	MF097384	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA023	Saint-Martin	N 18.07779	W 63.05772	MF097385	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA024	Saint-Martin	N 18.07779	W 63.05772	MF097386	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA032	Saint-Martin	N 18.11677	W 63.03902	MF097387	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA033	Saint-Martin	N 18.11677	W 63.03902	MF097388	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA034	Saint-Martin	N 18.11677	W 63.03902	MF097389	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA035	Saint-Martin	N 18.11677	W 63.03902	MF097390	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA036	Saint-Martin	N 18.11677	W 63.03902	MF097391	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA049	Saint Barthélemy	N 17.91924	W 62.86366	MF097371	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA0491	Saint Barthélemy	N 17.91924	W 62.86366	MF097372	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA050	Saint Barthélemy	N 17.91924	W 62.86366	MF097373	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA053	Saint Barthélemy	N 17.91924	W 62.86366	MF097383	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA054	Saint Barthélemy	N 17.91924	W 62.86366	MF097374	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA066	Dominica	N 15.34066	W 61.33351	MF097338	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA067	Dominica	N 15.34066	W 61.33351	MF097339	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA068	Dominica	N 15.34066	W 61.33351	MF097340	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA071	Dominica	N 15.34066	W 61.33351	KX529525	KX529583
<i>Cochliomyia</i>	<i>macellaria</i>	LA079	Guadeloupe	N 16.37752	W 61.47869	MF097362	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA080	Guadeloupe	N 16.37752	W 61.47869	MF097363	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA081	Guadeloupe	N 16.37752	W 61.47869	MF097364	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA094	Nevis	N 17.14145	W 62.57784	MF097368	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA096	Martinique	N 14.47428	W 60.81463	KX529524	KX529584
<i>Cochliomyia</i>	<i>macellaria</i>	LA097	Martinique	N 14.47428	W 60.81463	MF097367	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA115	Saint Kitts	N 17.3404083	W 62.7410389	MF097365	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA118	Saint Kitts	N 17.3404083	W 62.7410389	MF097392	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA131	Barbuda	N 17.6054722	W 61.8005833	MF097328	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA132	Barbuda	N 17.6054722	W 61.8005833	MF097329	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA138	Saint Barthélemy	N 17.897522	W 62.849694	MF097375	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA140	Saint Barthélemy	N 17.897522	W 62.849694	MF097376	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA141	Saint Barthélemy	N 17.897522	W 62.849694	MF097377	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA142	Saint Barthélemy	N 17.897522	W 62.849694	KX529523	KX529592
<i>Cochliomyia</i>	<i>macellaria</i>	LA143	Saint Barthélemy	N 17.897522	W 62.849694	MF097378	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA144	Saint Barthélemy	N 17.897522	W 62.849694	MF097379	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA145	Saint Barthélemy	N 17.897522	W 62.849694	MF097380	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA146	Saint Barthélemy	N 17.897522	W 62.849694	MF097381	-
<i>Cochliomyia</i>	<i>macellaria</i>	LA147	Saint Barthélemy	N 17.897522	W 62.849694	MF097382	-
<i>Cochliomyia</i>	<i>macellaria</i>	ME015	Mexico	N 25.598592	W 103.441156	-	MF097617

<i>Cochliomyia</i>	<i>macellaria</i>	M077	Mona, Puerto Rico	N 18.086239	W 67.906339	KX529539	KX529585
<i>Cochliomyia</i>	<i>macellaria</i>	M081	Mona, Puerto Rico	N 18.11125	W 67.933447	KX529537	KX529586
<i>Cochliomyia</i>	<i>macellaria</i>	M112	Mona, Puerto Rico	N 18.11125	W 67.933447	KX529544	KX529589
<i>Cochliomyia</i>	<i>macellaria</i>	ME004	Mexico	N 21.07645	W 89.501083	MF097366	-
<i>Cochliomyia</i>	<i>macellaria</i>	PR029	Puerto Rico	N 17.961111	W 66.863806	MF097369	-
<i>Cochliomyia</i>	<i>macellaria</i>	PR047	Puerto Rico	N 18.178722	W 66.488111	MF097370	-
<i>Cochliomyia</i>	<i>macellaria</i>	PR121	Puerto Rico	N 18.370953	W 66.026619	KX529544	KX529589
<i>Cochliomyia</i>	<i>macellaria</i>	PR128	Puerto Rico	N 18.093306	W 65.552111	KX529540	KX529590
<i>Cochliomyia</i>	<i>macellaria</i>	PR129	Puerto Rico	N 18.093306	W 65.552111	KX529542	KX529591
<i>Cochliomyia</i>	<i>minima</i>	CU010	Cuba	N 20.054178	W 76.917603	MF097393	-
<i>Cochliomyia</i>	<i>minima</i>	CU021	Cuba	N 22.621386	W 83.725944	MF097394	-
<i>Cochliomyia</i>	<i>minima</i>	CU022	Cuba	N 22.621386	W 83.725944	KX529549	KX529593
<i>Cochliomyia</i>	<i>minima</i>	CU023	Cuba	N 22.621386	W 83.725944	KX529550	KX529594
<i>Cochliomyia</i>	<i>minima</i>	CU024	Cuba	N 22.621386	W 83.725944	MF097395	-
<i>Cochliomyia</i>	<i>minima</i>	CU025	Cuba	N 22.621386	W 83.725944	MF097396	-
<i>Cochliomyia</i>	<i>minima</i>	CU026	Cuba	N 22.621386	W 83.725944	MF097397	-
<i>Cochliomyia</i>	<i>minima</i>	CU027	Cuba	N 22.621386	W 83.725944	MF097398	-
<i>Cochliomyia</i>	<i>minima</i>	CU043	Cuba	N 20.517817	W 74.65865	MF097399	-
<i>Cochliomyia</i>	<i>minima</i>	CU044	Cuba	N 20.517817	W 74.65865	MF097400	-
<i>Cochliomyia</i>	<i>minima</i>	CU045	Cuba	N 20.517817	W 74.65865	MF097401	-
<i>Cochliomyia</i>	<i>minima</i>	CU046	Cuba	N 20.517817	W 74.65865	KX529547	KX529595
<i>Cochliomyia</i>	<i>minima</i>	DR026	Hispaniola	N 19.04995	W 70.89046	MF097402	-
<i>Cochliomyia</i>	<i>minima</i>	DR027	Hispaniola	N 19.04995	W 70.89046	MF097403	-
<i>Cochliomyia</i>	<i>minima</i>	DR028	Hispaniola	N 19.04995	W 70.89046	MF097404	-
<i>Cochliomyia</i>	<i>minima</i>	DR029	Hispaniola	N 19.04995	W 70.89046	MF097405	-
<i>Cochliomyia</i>	<i>minima</i>	PR013	Hispaniola	N 18.316572	W 71.576447*	MF097406	-
<i>Cochliomyia</i>	<i>minima</i>	DR032	Hispaniola	N 18.316572	W 71.576447*	MF097407	-
<i>Cochliomyia</i>	<i>minima</i>	DR033	Hispaniola	N 18.316572	W 71.576447*	MF097408	-
<i>Cochliomyia</i>	<i>minima</i>	DR034	Hispaniola	N 18.316572	W 71.576447*	MF097409	-
<i>Cochliomyia</i>	<i>minima</i>	DR035	Hispaniola	N 18.316572	W 71.576447*	MF097410	-
<i>Cochliomyia</i>	<i>minima</i>	DR053	Hispaniola	N 19.06753	W 69.46445	MF097411	-
<i>Cochliomyia</i>	<i>minima</i>	DR054	Hispaniola	N 19.06753	W 69.46445	MF097412	-
<i>Cochliomyia</i>	<i>minima</i>	DR055	Hispaniola	N 19.06753	W 69.46445	KX529552	KX529596
<i>Cochliomyia</i>	<i>minima</i>	DR056	Hispaniola	N 19.06753	W 69.46445	MF097413	-
<i>Cochliomyia</i>	<i>minima</i>	DR067	Hispaniola	N 19.06710	W 69.46004	MF097414	-
<i>Cochliomyia</i>	<i>minima</i>	DR072	Hispaniola	N 19.34864	W 70.14910	MF097415	-
<i>Cochliomyia</i>	<i>minima</i>	DR073	Hispaniola	N 19.34864	W 70.14910	MF097416	-
<i>Cochliomyia</i>	<i>minima</i>	DR074	Hispaniola	N 19.34864	W 70.14910	MF097417	-
<i>Cochliomyia</i>	<i>minima</i>	DR075	Hispaniola	N 19.34864	W 70.14910	MF097418	-
<i>Cochliomyia</i>	<i>minima</i>	DR076	Hispaniola	N 19.34864	W 70.14910	MF097419	-
<i>Cochliomyia</i>	<i>minima</i>	DR136	Hispaniola	N 19.741319	W 70.654975	KX529548	KX529597
<i>Cochliomyia</i>	<i>minima</i>	DR137	Hispaniola	N 19.741319	W 70.654975	MF097420	-
<i>Cochliomyia</i>	<i>minima</i>	DR138	Hispaniola	N 19.741319	W 70.654975	MF097421	-
<i>Cochliomyia</i>	<i>minima</i>	DR139	Hispaniola	N 19.741319	W 70.654975	MF097422	-
<i>Cochliomyia</i>	<i>minima</i>	DR153	Hispaniola	N 19.34405	W 70.14824	MF097423	-
<i>Cochliomyia</i>	<i>minima</i>	DR164	Hispaniola	N 18.32902	W 68.80995	MF097424	-
<i>Cochliomyia</i>	<i>minima</i>	PR006	Puerto Rico	N 18.412972	W 66.727222	MF097425	-
<i>Cochliomyia</i>	<i>minima</i>	PR007	Puerto Rico	N 18.412972	W 66.727222	MF097426	-
<i>Cochliomyia</i>	<i>minima</i>	PR016	Puerto Rico	N 18.321333	W 65.818722	MF097427	-
<i>Cochliomyia</i>	<i>minima</i>	PR018	Puerto Rico	N 18.321333	W 65.818722	MF097428	-
<i>Cochliomyia</i>	<i>minima</i>	PR019	Puerto Rico	N 18.321333	W 65.818722	MF097429	-
<i>Cochliomyia</i>	<i>minima</i>	PR041	Puerto Rico	N 18.174722	W 66.491861	MF097430	-
<i>Cochliomyia</i>	<i>minima</i>	PR131	Puerto Rico	N 18.093306	W 65.552111	MF097431	-
<i>Cochliomyia</i>	<i>minima</i>	PR132	Puerto Rico	N 18.093306	W 65.552111	KX529553	KX529598
<i>Cochliomyia</i>	<i>minima</i>	PR133	Puerto Rico	N 18.093306	W 65.552111	KX529554	KX529599
<i>Cochliomyia</i>	<i>minima</i>	PR140	Puerto Rico	N 18.447911	W 65.948617	MF097432	MF097618
<i>Cochliomyia</i>	<i>minima</i>	PR141	Puerto Rico	N 18.447911	W 65.948617	KX529551	KX529600
<i>Cochliomyia</i>	<i>minima</i>	PR145	Puerto Rico	N 18.449889	W 65.595333	MF097433	-
<i>Cochliomyia</i>	<i>minima</i>	PR146	Puerto Rico	N 18.449889	W 65.595333	MF097434	-
<i>Lucilia</i>	<i>cluvia</i>	FL005	Florida, USA	N 25.614383	W 80.584467	-	MF097619
<i>Lucilia</i>	<i>cluvia</i>	FL017	Florida, USA	N 25.136917	W 80.94855	MF097436	MF097620

<i>Lucilia</i>	<i>cluvia</i>	FL018	Florida, USA	N 25.136917	W 80.94855	-	MF097621
<i>Lucilia</i>	<i>cluvia</i>	FL019	Florida, USA	N 25.323331	W 80.833094	MF097437	-
<i>Lucilia</i>	<i>cluvia</i>	FL020	Florida, USA	N 25.323331	W 80.833094	MF097438	MF097622
<i>Lucilia</i>	<i>cluvia</i>	FL025	Florida, USA	N 25.423053	W 80.679114	MF097439	MF097623
<i>Lucilia</i>	<i>cluvia</i>	FL026	Florida, USA	N 25.423053	W 80.679114	MF097440	MF097624
<i>Lucilia</i>	<i>cluvia</i>	PR147	Puerto Rico	N 18.429222	W 66.178022	MF097441	MF097625
<i>Lucilia</i>	<i>cluvia</i>	PR148	Puerto Rico	N 18.429222	W 66.178022	MF097442	MF097626
<i>Lucilia</i>	<i>coeruleiviridis</i>	FL007	Florida, USA	N 25.457514	W 80.4863	-	MF097627
<i>Lucilia</i>	<i>coeruleiviridis</i>	FL013	Florida, USA	N 25.136917	W 80.94885	MF097443	MF097628
<i>Lucilia</i>	<i>coeruleiviridis</i>	FL014	Florida, USA	N 25.136917	W 80.94855	-	MF097629
<i>Lucilia</i>	<i>coeruleiviridis</i>	FL015	Florida, USA	N 25.136917	W 80.94885	MF097444	MF097630
<i>Lucilia</i>	<i>coeruleiviridis</i>	FL016	Florida, USA	N 25.136917	W 80.94885	MF097445	MF097631
<i>Lucilia</i>	<i>coeruleiviridis</i>	FL023	Florida, USA	N 25.457514	W 80.4863	MF097446	MF097632
<i>Lucilia</i>	<i>coeruleiviridis</i>	FL024	Florida, USA	N 25.457514	W 80.4863	MF097447	MF097633
<i>Lucilia</i>	<i>cuprina</i>	FL027	Florida, USA	N 25.457514	W 80.4863	MF097448	MF097634
<i>Lucilia</i>	<i>cuprina</i>	FL028	Florida, USA	N 25.457514	W 80.4863	MF097449	MF097635
<i>Lucilia</i>	<i>cuprina</i>	FL029	Florida, USA	N 25.457514	W 80.4863	MF097450	MF097636
<i>Lucilia</i>	<i>cuprina</i>	FL030	Florida, USA	N 25.457514	W 80.4863	MF097451	MF097637
<i>Lucilia</i>	<i>cuprina</i>	PR070	Puerto Rico	N 18.370953	W 66.026619	MF097452	-
<i>Lucilia</i>	<i>cuprina</i>	PR071	Puerto Rico	N 18.370953	W 66.026619	MF097453	-
<i>Lucilia</i>	<i>cuprina</i>	PR072	Puerto Rico	N 18.370953	W 66.026619	MF097454	-
<i>Lucilia</i>	<i>cuprina</i>	PR073	Puerto Rico	N 18.370953	W 66.026619	KX529559	KX529602
<i>Lucilia</i>	<i>cuprina</i>	PR122	Puerto Rico	N 18.370953	W 66.026619	MF097455	MF097638
<i>Lucilia</i>	<i>cuprina</i>	PR123	Puerto Rico	N 18.370953	W 66.026619	MF097456	-
<i>Lucilia</i>	<i>cuprina</i>	PR153	Puerto Rico	N 18.461053	W 66.729803	MF097457	-
<i>Lucilia</i>	<i>cuprina</i>	PR154	Puerto Rico	N 18.461053	W 66.729803	MF097458	MF097639
<i>Lucilia</i>	<i>eximia</i>	CO011	Colombia	N 5.900544	W 74.852897*	MF097459	-
<i>Lucilia</i>	<i>eximia</i>	CO012	Colombia	N 5.900544	W 74.852897*	MF097460	MF097640
<i>Lucilia</i>	<i>eximia</i>	CO013	Colombia	N 5.900544	W 74.852897*	MF097461	MF097641
<i>Lucilia</i>	<i>eximia</i>	CO015	Colombia	N 5.900544	W 74.852897*	MF097462	MF097642
<i>Lucilia</i>	<i>eximia</i>	CO016	Colombia	N 5.900544	W 74.852897*	-	MF097643
<i>Lucilia</i>	<i>eximia</i>	CO022	Colombia	N 6.067217	W 73.645411	MF097463	MF097644
<i>Lucilia</i>	<i>eximia</i>	CO023	Colombia	N 6.067217	W 73.645411	MF097464	MF097645
<i>Lucilia</i>	<i>eximia</i>	CU002	Cuba	N 20.054178	W 76.917603	-	MF097646
<i>Lucilia</i>	<i>eximia</i>	CU006	Cuba	N 20.054178	W 76.917603	-	MF097647
<i>Lucilia</i>	<i>eximia</i>	DR019	Hispaniola	N 19.89155	W 071.65806	MF097467	MF097650
<i>Lucilia</i>	<i>eximia</i>	DR049	Hispaniola	N 18.316572	W 71.576447*	MF097468	-
<i>Lucilia</i>	<i>eximia</i>	DR050	Hispaniola	N 18.316572	W 71.576447	-	MF097651
<i>Lucilia</i>	<i>eximia</i>	DR129	Hispaniola	N 18.32902	W 68.80995	MF097469	-
<i>Lucilia</i>	<i>eximia</i>	FL021	Florida, USA	N 25.086633	W 80.452217	MF097470	MF097652
<i>Lucilia</i>	<i>eximia</i>	FL022	Florida, USA	N 25.086633	W 80.452217	MF097471	MF097653
<i>Lucilia</i>	<i>eximia</i>	LA064	Dominica	N 15.34066	W 61.33351	MF097465	MF097648
<i>Lucilia</i>	<i>eximia</i>	LA065	Dominica	N 15.34066	W 61.33351	MF097466	MF097649
<i>Lucilia</i>	<i>eximia</i>	LA124	Saint Lucia	N 14.100031	W 60.92654	MF097483	MF097665
<i>Lucilia</i>	<i>eximia</i>	LA126	Saint Lucia	N 14.100031	W 60.92654	-	MF097666
<i>Lucilia</i>	<i>eximia</i>	LA127	Saint Lucia	N 14.100031	W 60.92654	MF097484	MF097667
<i>Lucilia</i>	<i>eximia</i>	M076	Mona, Puerto Rico	N 18.086239	W 67.906339	MF097472	MF097654
<i>Lucilia</i>	<i>eximia</i>	M099	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097473	-
<i>Lucilia</i>	<i>eximia</i>	M100	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097474	-
<i>Lucilia</i>	<i>eximia</i>	M110	Mona, Puerto Rico	N 18.11125	W 67.933447	MF097475	MF097655
<i>Lucilia</i>	<i>eximia</i>	M111	Mona, Puerto Rico	N 18.11125	W 67.933447	MF097476	MF097656
<i>Lucilia</i>	<i>eximia</i>	ME005	Mexico	N 21.07645	W 89.501083	MF097477	MF097657
<i>Lucilia</i>	<i>eximia</i>	ME006	Mexico	N 21.07645	W 89.501083	-	MF097658
<i>Lucilia</i>	<i>eximia</i>	ME007	Mexico	N 21.07645	W 89.501083	MF097478	MF097659
<i>Lucilia</i>	<i>eximia</i>	PR050	Puerto Rico	N 18.449889	W 66.595333	MF097479	MF097660
<i>Lucilia</i>	<i>eximia</i>	PR060	Puerto Rico	N 17.971611	W 66.865361	MF097480	MF097661
<i>Lucilia</i>	<i>eximia</i>	PR111	Mona, Puerto Rico	N 18.11125	W 67.933447	-	MF097662
<i>Lucilia</i>	<i>eximia</i>	PR114	Puerto Rico	N 18.370953	W 66.026619	MF097481	-
<i>Lucilia</i>	<i>eximia</i>	PR134	Puerto Rico	N 18.093306	W 65.552111	-	MF097663
<i>Lucilia</i>	<i>eximia</i>	PR135	Puerto Rico	N 18.093306	W 65.552111	-	MF097664
<i>Lucilia</i>	<i>eximia</i>	PR150	Puerto Rico	N 18.084222	W 67.939417	MF097482	-
<i>Lucilia</i>	<i>fayeae</i>	M079	Mona, Puerto Rico	N 18.084222	W 67.939417	MF097485	MF097668

<i>Lucilia</i>	<i>fayeae</i>	PR008	Puerto Rico	N 18.412972	W 67.727222	MF097486	MF097669
<i>Lucilia</i>	<i>fayeae</i>	PR012	Puerto Rico	N 18.412972	W 67.727222	MF097487	-
<i>Lucilia</i>	<i>fayeae</i>	PR020	Puerto Rico	N 18.321333	W 65.818722	MF097488	-
<i>Lucilia</i>	<i>fayeae</i>	PR022	Puerto Rico	N 18.321333	W 65.818722	MF097489	-
<i>Lucilia</i>	<i>fayeae</i>	PR023	Puerto Rico	N 18.293444	W 65.791917	MF097490	MF097670
<i>Lucilia</i>	<i>fayeae</i>	PR045	Puerto Rico	N 18.174722	W 66.491861	MF097491	MF097671
<i>Lucilia</i>	<i>fayeae</i>	PR053	Puerto Rico	N 18.449889	W 66.595333	MF097492	MF097672
<i>Lucilia</i>	<i>fayeae</i>	PR116	Puerto Rico	N 18.370953	W 66.032175	MF097493	-
<i>Lucilia</i>	<i>lucigerens</i>	JA005	Jamaica	N 18.0598056	W 77.5311944	MF097494	MF097673
<i>Lucilia</i>	<i>lucigerens</i>	JA006	Jamaica	N 18.0598056	W 77.5311944	MF097495	-
<i>Lucilia</i>	<i>lucigerens</i>	JA007	Jamaica	N 18.0598056	W 77.5311944	MF097496	MF097674
<i>Lucilia</i>	<i>mexicana</i>	ME016	Mexico	N 25.598592	W 103.441156	MF097497	MF097675
<i>Lucilia</i>	<i>mexicana</i>	ME020	Mexico	N 25.598592	W 103.441156	MF097498	MF097676
<i>Lucilia</i>	<i>mexicana</i>	ME021	Mexico	N 25.598592	W 103.441156	MF097499	MF097677
<i>Lucilia</i>	<i>retroversa</i>	CU007	Cuba	N 20.054178	W 76.917603	MF097500	MF097678
<i>Lucilia</i>	<i>retroversa</i>	CU028	Cuba	N 22.621386	W 83.725944	MF097501	-
<i>Lucilia</i>	<i>retroversa</i>	CU029	Cuba	N 22.621386	W 83.725944	MF097502	-
<i>Lucilia</i>	<i>retroversa</i>	CU030	Cuba	N 22.621386	W 83.725944	MF097503	MF097679
<i>Lucilia</i>	<i>retroversa</i>	CU031	Cuba	N 22.621386	W 83.725944	MF097504	-
<i>Lucilia</i>	<i>retroversa</i>	CU038	Cuba	N 20.517817	W 20.517817	MF097505	-
<i>Lucilia</i>	<i>retroversa</i>	CU039	Cuba	N 20.517817	W 20.517817	MF097506	-
<i>Lucilia</i>	<i>retroversa</i>	CU040	Cuba	N 20.517817	W 20.517817	MF097507	-
<i>Lucilia</i>	<i>retroversa</i>	CU041	Cuba	N 20.517817	W 20.517817	MF097508	MF097680
<i>Lucilia</i>	<i>retroversa</i>	CU042	Cuba	N 20.517817	W 20.517817	MF097509	-
<i>Lucilia</i>	<i>retroversa</i>	DR020	Hispaniola	N 19.04871	W 70.88084	MF097510	-
<i>Lucilia</i>	<i>retroversa</i>	DR021	Hispaniola	N 19.04871	W 70.88084	MF097511	-
<i>Lucilia</i>	<i>retroversa</i>	DR022	Hispaniola	N 19.04871	W 70.88084	MF097512	-
<i>Lucilia</i>	<i>retroversa</i>	DR023	Hispaniola	N 19.04871	W 70.88084	MF097513	-
<i>Lucilia</i>	<i>retroversa</i>	DR024	Hispaniola	N 19.04871	W 70.88084	MF097514	MF097681
<i>Lucilia</i>	<i>retroversa</i>	DR025	Hispaniola	N 19.04871	W 70.88084	MF097515	-
<i>Lucilia</i>	<i>retroversa</i>	DR030	Hispaniola	N 19.04871	W 70.88084	MF097516	-
<i>Lucilia</i>	<i>retroversa</i>	DR040	Hispaniola	N 18.316572	W 71.576447	MF097517	-
<i>Lucilia</i>	<i>retroversa</i>	DR046	Hispaniola	N 18.316572	W 71.576447	MF097518	-
<i>Lucilia</i>	<i>retroversa</i>	DR047	Hispaniola	N 18.316572	W 71.576447	MF097519	-
<i>Lucilia</i>	<i>retroversa</i>	DR048	Hispaniola	N 18.316572	W 71.576447	MF097520	-
<i>Lucilia</i>	<i>retroversa</i>	DR057	Hispaniola	N 19.06753	W 69.46445	MF097521	-
<i>Lucilia</i>	<i>retroversa</i>	DR058	Hispaniola	N 19.06753	W 69.46445	MF097522	-
<i>Lucilia</i>	<i>retroversa</i>	DR059	Hispaniola	N 19.06753	W 69.46445	MF097523	-
<i>Lucilia</i>	<i>retroversa</i>	DR060	Hispaniola	N 19.06753	W 69.46445	MF097524	-
<i>Lucilia</i>	<i>retroversa</i>	DR061	Hispaniola	N 19.06753	W 69.46445	MF097525	-
<i>Lucilia</i>	<i>retroversa</i>	DR079	Hispaniola	N 19.34864	W 70.14910	MF097526	-
<i>Lucilia</i>	<i>retroversa</i>	DR080	Hispaniola	N 19.34864	W 70.14910	MF097527	-
<i>Lucilia</i>	<i>retroversa</i>	DR081	Hispaniola	N 19.34864	W 70.14910	MF097528	-
<i>Lucilia</i>	<i>retroversa</i>	DR082	Hispaniola	N 19.34864	W 70.14910	MF097529	-
<i>Lucilia</i>	<i>retroversa</i>	DR083	Hispaniola	N 19.34864	W 70.14910	MF097530	-
<i>Lucilia</i>	<i>retroversa</i>	DR089	Hispaniola	N 19.34864	W 70.14910	MF097531	-
<i>Lucilia</i>	<i>retroversa</i>	DR090	Hispaniola	N 19.34864	W 70.14910	MF097532	-
<i>Lucilia</i>	<i>retroversa</i>	DR091	Hispaniola	N 19.34864	W 70.14910	MF097533	-
<i>Lucilia</i>	<i>retroversa</i>	DR092	Hispaniola	N 19.34864	W 70.14910	MF097534	-
<i>Lucilia</i>	<i>retroversa</i>	DR111	Hispaniola	N 18.35698	W 68.61609	MF097535	-
<i>Lucilia</i>	<i>retroversa</i>	DR110	Hispaniola	N 18.35698	W 68.61609	MF097536	-
<i>Lucilia</i>	<i>retroversa</i>	DR112	Hispaniola	N 18.35698	W 68.61609	MF097537	-
<i>Lucilia</i>	<i>retroversa</i>	DR122	Hispaniola	N 18.32902	W 68.80995	MF097538	-
<i>Lucilia</i>	<i>retroversa</i>	DR123	Hispaniola	N 18.32902	W 68.80995	MF097539	MF097682
<i>Lucilia</i>	<i>retroversa</i>	DR124	Hispaniola	N 18.32902	W 68.80995	MF097540	MF097683
<i>Lucilia</i>	<i>retroversa</i>	DR125	Hispaniola	N 18.32902	W 68.80995	MF097541	-
<i>Lucilia</i>	<i>retroversa</i>	DR126	Hispaniola	N 18.32902	W 68.80995	MF097542	-
<i>Lucilia</i>	<i>retroversa</i>	DR128	Hispaniola	N 18.32902	W 68.80995	MF097543	-
<i>Lucilia</i>	<i>retroversa</i>	DR140	Hispaniola	N 19.741319	W 70.654975*	MF097544	-
<i>Lucilia</i>	<i>retroversa</i>	DR141	Hispaniola	N 19.741319	W 70.654975*	MF097545	-
<i>Lucilia</i>	<i>retroversa</i>	DR142	Hispaniola	N 18.09786	W 71.18925	MF097546	-
<i>Lucilia</i>	<i>retroversa</i>	DR143	Hispaniola	N 18.09786	W 71.18925	MF097547	-

<i>Lucilia</i>	<i>retroversa</i>	DR144	Hispaniola	N 18.09786	W 71.18925	MF097548	-
<i>Lucilia</i>	<i>retroversa</i>	DR145	Hispaniola	N 18.09786	W 71.18925	MF097549	-
<i>Lucilia</i>	<i>retroversa</i>	DR146	Hispaniola	N 18.09786	W 71.18925	MF097550	-
<i>Lucilia</i>	<i>retroversa</i>	DR147	Hispaniola	N 18.09786	W 71.18925	MF097551	-
<i>Lucilia</i>	<i>retroversa</i>	DR148	Hispaniola	N 18.09786	W 71.18925	MF097552	-
<i>Lucilia</i>	<i>rica</i>	LA007	Saint Eustatius	N 17.47637	W 62.97470	MF097558	-
<i>Lucilia</i>	<i>rica</i>	LA008	Saint Eustatius	N 17.47637	W 62.97470	MF097559	-
<i>Lucilia</i>	<i>rica</i>	LA009	Saint Eustatius	N 17.47637	W 62.97470	-	MF097684
<i>Lucilia</i>	<i>rica</i>	LA010	Saint Eustatius	N 17.47637	W 62.97470	MF097560	-
<i>Lucilia</i>	<i>rica</i>	LA016	Saint-Martin	N 18.07779	W 63.05772	MF097572	-
<i>Lucilia</i>	<i>rica</i>	LA017	Saint-Martin	N 18.07779	W 63.05772	MF097573	MF097697
<i>Lucilia</i>	<i>rica</i>	LA026	Saba	N 17.63980	W 63.23373	MF097435	-
<i>Lucilia</i>	<i>rica</i>	LA027	Saba	N 17.63980	W 63.23373	-	MF097692
<i>Lucilia</i>	<i>rica</i>	LA028	Saba	N 18.07779	W 63.05772	MF097569	MF097693
<i>Lucilia</i>	<i>rica</i>	LA037	Saint-Martin	N 18.11677	W 63.03902	MF097574	-
<i>Lucilia</i>	<i>rica</i>	LA045	Saint Barthélemy	N 17.91924	W 62.86366	MF097570	MF097694
<i>Lucilia</i>	<i>rica</i>	LA061	Saint Barthélemy	N 17.91924	W 62.86366	MF097571	MF097696
<i>Lucilia</i>	<i>rica</i>	LA073	Nevis	N 17.14145	W 62.57784	MF097567	MF097690
<i>Lucilia</i>	<i>rica</i>	LA074	Nevis	N 17.14145	W 62.57784	MF097568	MF097691
<i>Lucilia</i>	<i>rica</i>	LA098	Martinique	N 14.47428	W 60.81463	MF097565	MF097688
<i>Lucilia</i>	<i>rica</i>	LA099	Martinique	N 14.47428	W 60.81463	MF097566	MF097689
<i>Lucilia</i>	<i>rica</i>	LA106	Montserrat	N 16.77608	W 62.30904	MF097564	MF097687
<i>Lucilia</i>	<i>rica</i>	LA114	Saint Kitts	N 17.3404083	W 62.7410389	MF097563	-
<i>Lucilia</i>	<i>rica</i>	LA128	Antigua	N 17.0358611	W 61.8246389	MF097553	-
<i>Lucilia</i>	<i>rica</i>	LA129	Antigua	N 17.0358611	W 61.8246389	MF097554	-
<i>Lucilia</i>	<i>rica</i>	LA130	Antigua	N 17.0358611	W 61.8246389	MF097555	-
<i>Lucilia</i>	<i>rica</i>	LA133	Barbuda	N 17.6054722	W 61.8005833	MF097556	-
<i>Lucilia</i>	<i>rica</i>	LA134	Barbuda	N 17.6054722	W 61.8005833	MF097557	-
<i>Lucilia</i>	<i>rica</i>	LA083	Guadeloupe	N 16.37752	W 61.47869	MF097561	MF097685
<i>Lucilia</i>	<i>rica</i>	LA087	Guadeloupe	N 16.37752	W 61.47869	MF097562	MF097686
<i>Lucilia</i>	<i>rica</i>	TLW042	Antigua and Barbuda	As published (a)	BNNR042^	-	
<i>Lucilia</i>	<i>rica</i>	TLW043	Antigua and Barbuda	As published (a)	BNNR043^	-	
<i>Lucilia</i>	<i>rica</i>	TLW044	Antigua and Barbuda	As published (a)	BNNR044^	-	
<i>Lucilia</i>	<i>rica</i>	TLW046	Antigua and Barbuda	As published (a)	BNNR046^	-	
<i>Lucilia</i>	<i>sp.</i>	C0027	Colombia	N 6.067217	W 73.645411	MF097575	MF097698
<i>Lucilia</i>	<i>vulgata</i>	C0019	Colombia	N 6.067217	W 73.645411	MF097576	MF097699
<i>Lucilia</i>	<i>vulgata</i>	C0025	Colombia	N 6.067217	W 73.645411	MF097577	MF097700
<i>Lucilia</i>	<i>vulgata</i>	C0026	Colombia	N 6.067217	W 73.645411	MF097578	MF097701
<i>Lucilia</i>	<i>vulgata</i>	C0028	Colombia	N 6.067217	W 73.645411	MF097579	MF097702
Outgroups							
<i>Neobellieria</i>	<i>bullata</i>	BG64		As published (b)	JQ807156.1	-	
<i>Ravinia</i>	<i>stimulans</i>	AZ60		As published (b)	JQ807112.1	-	
<i>Sarcophaga</i>	<i>carnaria</i>	NICC0410		As published (c)	JQ582094.1	-	
<i>Blaesoxipha</i>	<i>alcedo</i>	AY09		As published (b)	JQ806830.1	-	
<i>Blaesoxipha</i>	<i>masculina</i>	AW36		As published (b)	JQ806832.1	-	

(a) Whitworth (2014), (b) Stamper et al. (2012), (c) Jordaens et al. (2013).

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Table 2. COI amplification primers and protocols

Primer name		Sequence (5' to 3')	Protocol						Source protocol
			ID	CY	D	AN	E	FE	
LCO1490	F	GGTCAACAAATCATAAAGATATTGG	95°C 2 min	35	95°C 30 sec	44°C 45 sec	72°C 45 sec	72°C 10 min	Agnarsson et al. (2007)
CI-N-2776	R	GGATAATCAGAATATCGTCGAGG							
Primer 1	F	TACAATTATCGCCTAACCTCAGCC	95°C	35	94°C 15 sec	51°C 15 sec	72°C 30 sec	72°C 5 min	Debry et al. (2012)
C1-N-2191	R	CCCGGTAAAATTAAAATATAAACCTC	3 min						
C1-J-1751	F	GGAGCTCCTGACATAGCATTCCC	94°C 90 sec	36	94°C 22 sec	48°C 30 sec	72°C 80 sec	72°C 60 sec	Harvey et al (2003)
C2-N-3014	R	TCCATTGCACTAATCTGCCATATTA							
ITS4	F	TCCTCCGCTTATTGATATGC	94°C 2 min	38	94°C 30 sec	44°C 35 sec	72°C 30 sec	72°C 3 min	Agnarsson (2010)
ITS5.8	R	GGGACGATGAAGAACCGCAGC							

F, Forward; R, reverse; ID, Initial denaturation; CY, cycles; D, Denaturation; AN, annealing; E, Extension; FE, Final extension.

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Table 3. Genetic distances expressed in percentage among the 26 putative species groups as determined by an analysis in MEGA6.

Putative species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
1 <i>Ca. maestrica</i>																										
2 <i>C. idioidea-CU</i>	16.3																									
3 <i>C. idioidea-DR</i>	15.3	2.8																								
4 <i>C. idioidea-ME</i>	15.6	2.1	2.1																							
5 <i>Ch. albiceps</i>	15.5	13.8	13.1	13.1																						
6 <i>Ch. megacephala</i>	14.4	9.5	10.6	10.2	5.7																					
7 <i>Ch. rufifacies</i>	15.5	14.5	14.1	14.1	2.8	6.7																				
8 <i>Co. aldrichi</i>	14.4	10.6	9.5	9.9	10.2	9.2	12.0																			
9 <i>Co. hominivorax</i>	13.7	8.7	9.1	8.0	11.5	9.8	12.6	8.4																		
10 <i>Co. macellaria</i>	14.4	10.6	9.5	9.9	10.3	9.2	12.0	0.1	8.4																	
11 <i>Co. minima</i>	15.7	10.5	10.5	10.2	9.8	8.8	11.0	4.2	9.7	4.2																
12 <i>L.. cluvia</i>	11.1	11.4	12.1	12.1	14.9	11.4	14.5	12.4	11.6	12.4	13.7															
13 <i>L.. coeruleiviridis</i>	12.1	11.3	13.4	13.4	15.9	12.7	15.2	11.7	12.6	11.6	11.4	4.6														
14 <i>L. cuprina</i>	11.6	9.2	9.5	10.2	13.1	9.5	13.8	10.6	11.9	10.6	11.2	8.2	8.5													
15 <i>L. eximia-CO-ME</i>	12.4	12.3	11.7	12.4	14.0	11.8	14.0	12.8	13.0	12.8	13.4	5.4	7.1	7.6												
16 <i>L. vulgata</i>	11.4	11.3	12.7	12.7	15.9	12.7	15.9	11.7	12.6	11.7	12.0	3.9	0.7	8.5	6.4											
17 <i>L. eximia-FL</i>	11.6	11.0	12.4	12.4	15.5	12.4	14.8	12.0	12.4	11.9	11.1	4.8	1.2	8.7	6.9	1.2										
18 <i>L. eximia-GA</i>	13.5	12.0	13.4	14.1	14.5	12.7	15.2	12.7	13.7	12.7	13.0	7.1	4.9	9.5	7.4	4.9	5.5									
19 <i>L. eximia-LA</i>	12.1	11.3	9.9	11.3	13.1	11.3	13.8	11.7	11.5	11.6	12.3	4.3	6.0	6.7	2.6	5.3	5.8	6.4								
20 <i>L. fayeae</i>	13.2	11.2	12.6	12.6	13.5	11.7	13.9	12.6	10.9	12.6	13.3	4.7	4.9	8.4	5.7	4.9	5.4	5.6	4.5							
21 <i>L. lucigerens</i>	11.9	11.7	12.4	12.4	14.5	11.7	14.1	12.7	11.9	12.7	12.7	3.2	4.9	7.8	3.7	4.2	4.8	6.0	3.2	4.2						
22 <i>L. mexicana</i>	12.1	11.3	13.4	13.4	15.9	12.7	15.2	11.7	12.6	11.6	11.4	4.6	0.0	8.5	7.1	0.7	1.2	4.9	6.0	4.9	4.9					
23 <i>L. retroversa-CU</i>	13.7	11.2	12.6	12.6	14.0	12.2	14.4	12.6	11.4	12.6	13.3	5.2	4.8	8.4	5.6	4.8	5.4	5.3	4.5	0.5	4.1	4.8				
24 <i>L. retroversa-DR</i>	13.5	12.4	13.1	13.1	14.8	13.4	14.5	12.7	13.3	12.7	13.4	4.0	5.0	9.2	5.4	4.3	4.8	5.7	4.6	2.8	3.6	5.0	2.7			
25 <i>L. rica_1</i>	13.9	12.1	12.1	11.6	14.8	11.9	14.7	13.0	11.1	13.0	13.6	6.1	6.8	8.2	6.6	6.1	6.6	7.5	5.4	5.0	5.4	6.8	4.7	5.0		
26 <i>L. rica_2</i>	13.4	11.9	11.9	11.2	14.7	11.6	14.8	12.6	10.7	12.6	13.3	5.6	6.3	8.0	6.4	5.6	6.1	7.3	5.6	5.6	5.2	6.3	5.3	5.3	1.0	

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CO, Colombia; CU, Cuba; DR, Dominican Republic; FL, Florida; GA, Greater Antilles; LA, Lesser Antilles; ME, Mexico.

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919 **Table 4.** Genetic distances within the 26 putative species groups, as determined by an analysis in MEGA6. The values are expressed as a percentage.

Putative species	% variation within species
<i>Ca. maestrica</i>	0.14
<i>C. idioidea-CU</i>	0.00
<i>C. idioidea-DR</i>	0.00
<i>C. idioidea-ME</i>	n/a
<i>Ch. albiceps</i>	0.00
<i>Ch. megacephala</i>	0.00
<i>Ch. rufifacies</i>	0.01
<i>Co. aldrichi</i>	0.00
<i>Co. hominivorax</i>	0.24
<i>Co. macellaria</i>	0.15
<i>Co. minima</i>	0.29
<i>L.. cluvia</i>	0.10
<i>L.. coeruleiviridis</i>	0.00
<i>L. cuprina</i>	0.00
<i>L. eximia-CO-ME</i>	0.61
<i>L. vulgata</i>	0.00
<i>L. eximia-FL</i>	1.06
<i>L. eximia-GA</i>	0.00
<i>L. eximia-LA</i>	0.00
<i>L. fayeae</i>	0.14
<i>L. lucigerens</i>	0.00
<i>L. mexicana</i>	0.00
<i>L. retroversa-CU</i>	0.18
<i>L. retroversa-DR</i>	0.08
<i>L. rica_1</i>	0.40
<i>L. rica_2</i>	0.15

920 CO, Colombia; CU, Cuba; DR, Dominican Republic; FL, Florida; GA, Greater Antilles; LA, Lesser Antilles; ME, Mexico.

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923 **Table 5. Results of species delimitation analysis based on COI.** The various measures of distance and isolation and exclusivity metrics of these
 924 clades follow including: (D), the probability of population identification of a hypothetical sample based on the groups being tested (P ID (Strict) and
 925 P ID (Liberal)), Rosenberg's reciprocal monophyly (P(AB)), the genealogical sorting index (gsi), and a single locus Bayesian implementation of the
 926 Poisson tree processes model (bPTP). Sp congru. refers to species hypothesis that are congruent with all methods, and Sp cons. is our conservative
 927 estimate of actual species richness based on agreement among all methods and >2% mtDNA sequence divergence. Morph, refers to species richness
 928 based morphology and Concat. refers to species richness based on the concatenated tree.

Putative species	Mono	D Intra	D Inter	Dtra/ Dter	P ID(Strict)	P ID(Liberal)	P(AB)	GSI	bPTP	Sp congru	Sp cons	Morph	Concat
1. <i>C. maestrica</i>	yes	0.001	0.096	0.01	0.93 (0.80, 1.0)	0.98 (0.88, 1.0)	NAN	1	Y	1	1	1	1
2. <i>C. idioidea-CU</i>	yes	0.0009	0.012	0.07	0.74 (0.57, 0.92)	0.97 (0.82, 1.0)	0.17	1	Y	2	2	2	2
3. <i>C. idioidea-ME</i>	yes	n/a	0.012	n/a	n/a	0.96 (0.83, 1.0)	0.17	NA	Y				
4. <i>C. idioidea-DR</i>	yes	0.003	0.014	0.19	0.81 (0.68, 0.93)	0.95 (0.85, 1.0)	1.98E-03	1	Y	3	3		3
5. <i>Co. aldrichi</i>	no	0.0008	0.002	0.46	0.82 (0.75, 0.89)	0.95 (0.91, 0.99)	NA	0.39	N	4	4	3	4
6. <i>Co. macellaria</i>	no	0.003	0.002	1.47	0.00 (0.00, 0.00)	0.31 (0.28, 0.34)	NA	0.61	N			4	5
7. <i>Co. minima</i>	yes	0.002	0.030	0.07	0.97 (0.92, 1.0)	0.99 (0.96, 1.0)	6.30E-27	1	Y	5	5	5	6
8. <i>Co. hominivorax</i>	yes	0.004	0.066	0.07	0.75 (0.57, 0.92)	0.97 (0.83, 1.0)	1.90E-07	1	Y	6	6	6	7
9. <i>Ch. albiceps</i>	yes	0.002	0.033	0.05	0.90 (0.77, 1.0)	0.97 (0.87, 1.0)	4.90E-08	1	Y	7	7	7	8
10. <i>Ch. rufifacies</i>	yes	0.0009	0.033	0.03	0.99 (0.93, 1.0)	1.00 (0.97, 1.0)	4.90E-08	1	Y	8	8	8	9
11. <i>Ch. megacephala</i>	yes	0.001	0.054	0.02	0.99 (0.94, 1.0)	1.00 (0.97, 1.0)	1.40E-24	1	Y	9	9	9	10
12. <i>L. cluvia</i>	yes	0.002	0.033	0.07	0.91 (0.81, 1.0)	0.98 (0.92, 1.0)	7.10E-12	1	Y	10	10	10	11
13. <i>L. coeruleiviridis</i>	no	0.0008	0.0008	1.12	0.18 (0.05, 0.31)	0.49 (0.38, 0.59)	NA	0.59	N	11	11	11	12
14. <i>L. mexicana</i>	no	0.0007	0.0008	0.88	0.20 (0.02, 0.39)	0.51 (0.36, 0.66)	NA	0.49	N			12	13
15. <i>L. eximia-FL</i>	yes	0.002	0.005	0.40	0.39 (0.24, 0.54)	0.74 (0.58, 0.89)	0.03	1	N			13	14
16. <i>L. vulgata</i>	yes	0.002	0.007	0.32	0.65 (0.51, 0.79)	0.89 (0.78, 1.0)	0.03	1	N			14	15
17. <i>L. eximia-ME-CO</i>	yes	0.004	0.016	0.27	0.82 (0.71, 0.92)	0.93 (0.87, 0.99)	3.60E-04	1	Y	12	12		16
18. <i>L. eximia-LA</i>	yes	0.002	0.016	0.12	0.79 (0.64, 0.93)	0.95 (0.84, 1.0)	3.60E-04	1	Y	13	13		
19. <i>L. fayeae</i>	yes	0.002	0.008	0.31	0.82 (0.73, 0.91)	0.94 (0.89, 0.99)	2.40E-06	1	N	14	14	15	17
20. <i>L. retroversa-CU</i>	yes	0.004	0.008	0.46	0.75 (0.67, 0.84)	0.92 (0.87, 0.97)	2.40E-06	1	N			16	18
21. <i>L. retroversa-DR</i>	yes	0.002	0.024	0.09	0.96 (0.91, 1.0)	0.99 (0.96, 1.0)	2.60E-14	1	Y	15	15		19
22. <i>L. lucigerens</i>	yes	0.002	0.035	0.05	0.76 (0.58, 0.94)	0.98 (0.84, 1.0)	9.90E-07	1	Y	16	16	17	20
23. <i>L. eximia-GA</i>	yes	0.001	0.048	0.03	0.98 (0.91, 1.0)	1.00 (0.96, 1.0)	1.30E-11	1	Y	17	17		21
24. <i>L. rica_1</i>	yes	0.003	0.011	0.24	0.90 (0.83, 0.96)	0.97 (0.92, 1.0)	4.40E-09	1	Y	18	18	18	22
25. <i>L. rica_2</i>	yes	0.002	0.011	0.22	0.90 (0.83, 0.97)	0.97 (0.92, 1.0)	4.40E-09	1	Y	19			23
26. <i>L. cuprina</i>	yes	0.002	0.076	0.03	0.98 (0.91, 1.0)	1.00 (0.96, 1.0)	4.30E-19	1	Y	20	19	19	24

929 CO, Colombia; CU, Cuba; DR, Dominican Republic; FL, Florida; GA, Greater Antilles; LA, Lesser Antilles; ME, Mexico.

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932**Table 6.** Results of species delimitation analysis based on the concatenated tree. (D), the probability of population identification of a hypothetical sample based on the groups being tested (P ID (Strict) and P ID (Liberal)), Rosenberg's reciprocal monophyly (P(AB))

Putative species	Closest Species	Mono	D Intra	D Inter	Dtra/ Dter	P ID(Strict)	P ID(Liberal)	P(AB)
1. <i>Ca. maestrica</i>	<i>L. cuprina</i>	yes	0.005	0.19	0.03	0.58 (0.43, 0.73)	0.97 (0.82, 1.0)	1.00E-05
2. <i>L. cluvia</i>	<i>L. coeruleiviridis</i>	yes	0.005	0.05	0.10	0.87 (0.74, 0.99)	0.97 (0.87, 1.0)	5.50E-09
3 <i>L. coeruleiviridis</i>	<i>L. eximia-FL</i>	yes	0.001	0.01	0.14	0.84 (0.72, 0.97)	0.96 (0.86, 1.0)	0.01
4. <i>L. mexicana</i>	<i>L. coeruleiviridis</i>	yes	0.0009	0.02	0.06	0.75 (0.58, 0.93)	0.97 (0.83, 1.0)	0.01
5. <i>L. eximia-FL</i>	<i>L. coeruleiviridis</i>	yes	0.005	0.01	0.48	0.34 (0.19, 0.50)	0.69 (0.53, 0.84)	4.94E-03
6. <i>L. vulgata</i>	<i>L. coeruleiviridis</i>	yes	0.003	0.02	0.18	0.75 (0.60, 0.89)	0.94 (0.83, 1.0)	0.1
7. <i>L. eximiaCO-ME</i>	<i>L. eximia-LA</i>	yes	0.006	0.02	0.32	0.79 (0.69, 0.90)	0.92 (0.86, 0.99)	0.01
8. <i>L. fayeae</i>	<i>L. retroversa-CU</i>	yes	0.006	0.04	0.15	0.84 (0.71, 0.96)	0.96 (0.86, 1.0)	4.30E-04
9. <i>L. retroversa-CU</i>	<i>L. retroversa-DR</i>	yes	0.004	0.02	0.18	0.50 (0.35, 0.65)	0.87 (0.72, 1.0)	0.03
10. <i>L. lucigerens</i>	<i>L. eximia-LA</i>	yes	0.003	0.04	0.08	0.55 (0.40, 0.70)	0.93 (0.78, 1.0)	3.10E-04
11 <i>L. eximia-GA</i>	<i>L. rica 2</i>	yes	0.002	0.06	0.04	0.91 (0.78, 1.0)	0.98 (0.87, 1.0)	2.70E-06
12. <i>L. rica 1</i>	<i>L. rica 2</i>	yes	0.005	0.02	0.33	0.81 (0.72, 0.90)	0.94 (0.88, 0.99)	4.20E-04
13. <i>L. rica 2</i>	<i>L. rica 1</i>	yes	0.004	0.02	0.30	0.59 (0.42, 0.77)	0.84 (0.69, 0.98)	4.20E-04
14. <i>L. cuprina</i>	<i>L. cluvia</i>	yes	0.003	0.15	0.02	0.94 (0.83, 1.0)	1.00 (0.94, 1.0)	1.90E-11
15. <i>Ch. albiceps</i>	<i>Ch. rufifacies</i>	yes	0.003	0.04	0.06	0.75 (0.57, 0.93)	0.97 (0.83, 1.0)	2.98E-03
16. <i>Ch. rufifacies</i>	<i>Ch. albiceps</i>	yes	0.002	0.04	0.05	0.90 (0.78, 1.0)	0.97 (0.87, 1.0)	2.98E-03
17. <i>Ch. megacephala</i>	<i>Ch. albiceps</i>	yes	0.003	0.11	0.02	0.92 (0.79, 1.0)	0.98 (0.87, 1.0)	2.80E-05
18. <i>Co. aldrichi</i>	<i>Co. macellaria</i>	yes	0.002	0.01	0.13	0.85 (0.72, 0.97)	0.96 (0.86, 1.0)	4.70E-07
19. <i>Co. macellaria</i>	<i>Co. aldrichi</i>	yes	0.007	0.01	0.52	0.84 (0.78, 0.89)	0.96 (0.93, 0.99)	4.70E-07
20. <i>Co. minima</i>	<i>Co. aldrichi</i>	yes	0.007	0.05	0.14	0.88 (0.77, 0.99)	0.96 (0.90, 1.0)	4.50E-09
21. <i>Co. hominivorax</i>	<i>Co. aldrichi</i>	yes	0.007	0.09	0.08	0.88 (0.76, 1.0)	0.97 (0.87, 1.0)	1.00E-07
22. <i>C. idioidea-DR</i>	<i>C. idioidea-ME</i>	yes	0.003	0.02	0.19	0.74 (0.60, 0.88)	0.94 (0.83, 1.0)	4.08E-03
23 <i>C. idioidea-CU</i>	<i>C. idioidea-ME</i>	yes	0.001	0.01	0.06	0.56 (0.41, 0.71)	0.94 (0.79, 1.0)	0.33
24: <i>L. retroversa-DR</i>	<i>L. retroversa-CU</i>	yes	0.004	0.02	0.16	0.76 (0.62, 0.90)	0.94 (0.83, 1.0)	0.03
25: <i>C. idioidea-ME</i>	<i>C. idioidea-CU</i>	no	0.005	0.01	0.38	0.40 (0.24, 0.55)	0.75 (0.59, 0.90)	NA
26. <i>L. eximia-LA</i>	<i>L. eximiaCO-ME</i>	no	0.007	0.02	0.36	0.63 (0.48, 0.77)	0.88 (0.77, 0.99)	NA

933 CO, Colombia; CU, Cuba; DR, Dominican Republic; FL, Florida; GA, Greater Antilles; LA, Lesser Antilles; ME, Mexico.

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