The land flatworm *Amaga expatria* (Geoplanidae) in Guadeloupe and Martinique: new reports and molecular characterization including complete mitogenome

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**Background.** The land flatworm *Amaga expatria* Jones & Sterrer, 2005 (Geoplanidae) was described from two specimens collected in Bermuda in 1963 and 1988 and not recorded since. **Methods.** On the basis of a citizen science project, we received observations in the field, photographs and specimens from non-professionals and local scientists in Martinique and Guadeloupe. We barcoded (COI) specimens from both islands and studied the histology of the reproductive organs of one specimen. Based on Next Generation Sequencing, we obtained the complete mitogenome of *A. expatria* and some information on its prey from contaminating DNA. **Results.** We add records from 2006 to 2019 in two French islands of the Caribbean arc, Guadeloupe (six records) and Martinique (14 records), based on photographs obtained from citizen science and specimens examined. A specimen from Martinique was studied for histology of the copulatory organs and barcoded for the COI gene; its anatomy was similar to the holotype, therefore confirming species identification. The COI gene was identical for several specimens from Martinique and Guadeloupe and differed from the closest species by more than 10%; molecular characterisation of the species is thus possible by standard molecular barcoding techniques. The mitogenome is 14962 bp in length and contains 12 protein coding genes, two rRNA genes and 22 tRNA genes; for two protein genes it was not possible to determine the start codon. The mitogenome was compared with the few available mitogenomes from geoplanids and the most similar was *Obama nungara*, a species from South America. An analysis of contaminating DNA in the digestive system suggests that *A. expatria* preys on terrestrial molluscs, and citizen science observations in the field suggest that prey include molluscs and earthworms; the species thus could be a threat to biodiversity of soil animals.
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Abstract

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Methods. On the basis of a citizen science project, we received observations in the field, photographs and specimens from non-professionals and local scientists in Martinique and Guadeloupe. We barcoded (COI) specimens from both islands and studied the histology of the reproductive organs of one specimen. Based on Next Generation Sequencing, we obtained the complete mitogenome of *A. expatria* and some information on its prey from contaminating DNA.

Results. We add records from 2006 to 2019 in two French islands of the Caribbean arc, Guadeloupe (six records) and Martinique (14 records), based on photographs obtained from citizen science and specimens examined. A specimen from Martinique was studied for histology of the copulatory organs and barcoded for the COI gene; its anatomy was similar to the holotype, therefore confirming species identification. The COI gene was identical for several specimens from Martinique and Guadeloupe and differed from the closest species by more than 10%; molecular characterisation of the species is thus possible by standard molecular barcoding techniques. The mitogenome is 14962 bp in length and contains 12 protein coding genes, two rRNA genes and 22 tRNA genes; for two protein genes it was not possible to determine the start codon. The mitogenome was compared with the few available mitogenomes from geoplanids and the most similar was *Obama nungara*, a species from South America. An analysis of contaminating DNA in the digestive system suggests that *A. expatria* preys on terrestrial molluscs, and citizen science observations in the field suggest that prey include molluscs and earthworms; the species thus could be a threat to biodiversity of soil animals in the Caribbean.
Introduction

The land flatworm *Amaga expatria* Jones & Sterrer, 2005 (Platyhelminthes, Geoplanidae) was described from two specimens collected in Bermuda in 1963 and 1988 (Jones & Sterrer 2005). It has not been recorded since. Jones & Sterrer (2005) concluded that the species was an alien species in Bermuda, probably introduced from South America since other members of the genus have been collected in this region, including Colombia, Peru, Chile, Brazil, Paraguay and Argentina (Ogren & Kawakatsu 1990); the genus *Amaga* Ogren & Kawakatsu, 1990 currently includes 10 species (Grau et al. 2012).

In 2003, one of us (JLJ) undertook a citizen science program in France about alien land flatworms. Records were unexpectedly received from other locations including French overseas territories (Justine et al. 2014, 2015, 2018a, 2018b, 2019; Justine & Winsor 2020). Among these were several records of large land flatworms from the two Caribbean islands of Martinique and Guadeloupe with similar dimensions and pigmentation to *A. expatria* and tentatively identified as such. To confirm this identification, one specimen from Martinique has been partially sectioned for anatomical comparison with the type material. The same specimen was also subjected to molecular sequencing (COI barcoding). Another specimen from Martinique was included in a comparative study of the mitogenome of several land flatworms (Gastineau & Justine 2020; Gastineau et al. 2019, 2020).

We present here new records of *A. expatria* in two islands of the Caribbean, and provide additional morphological information, the first barcoding characterisation of the species and its complete mitogenome.

Material and Methods

Citizen science and collection of information

Records were collected from 2013 to 2019, a period of 7 years (single records from 2006 and 2012 are also included). We used the same methods as for our previous research on land flatworms (Justine et al. 2014, 2015, 2018a, 2018b, 2019). A blog (Justine 2019) and a twitter account (@Plathelminthe4) were the main tools for collecting and transmitting information. The collaboration of local natural history associations and of the FREDON (Regional federations for
the control of pests) in the departments of Martinique and Guadeloupe was also instrumental. Reports of sightings were received from the general public and from professionals, generally by email. We solicited and obtained specimens. Specimens were obtained alive, fixed in near boiling water and preserved in 95% ethanol, or sometimes fixed directly in cold ethanol. They were sent to the Muséum National d'Histoire Naturelle (MNHN) in Paris, registered, and processed for molecular studies.

**Histology**
A specimen from Martinique, MNHN JL146, was used for histology. It was killed alive in boiling water, then kept in 80% ethanol. A portion about 1.7 cm long containing the copulatory apparatus was removed for sectioning. Horizontal longitudinal sections (HLS) were cut at 12 µm thickness, mounted on 41 slides, stained in haematoxylin and eosin and mounted in Canada balsam (slides 1-5 and 38-41 remain unstained in wax). Slides are deposited in the MNHN, Paris, registration number MNHN JL146.

**Molecular barcoding**
For molecular analysis, a small piece of the body (1–3 mm³) was taken from the lateral edge of ethanol-fixed individuals. Extraction of DNA and PCR were performed as in previous similar works (Justine et al. 2019). Briefly, a fragment of 424 bp was amplified with the primers JB3 (=COI-ASmit1) and JB4.5 (=COI-ASmit2) (Bowles et al. 1995; Littlewood et al. 1997), and a fragment of 825 bp was amplified with the primers BarS (Álvarez-Presas et al. 2011) and COIR (Lázaro et al. 2009; Mateos et al. 2013). PCR products were purified and sequenced in both directions on a 96-capillary 3730xl DNA Analyzer sequencer (Applied Biosystems). Results of both analyses were concatenated to obtain a COI sequence of 903 bp in length. Sequences were edited using CodonCode Aligner software (CodonCode Corporation, Dedham, MA, USA), compared to the GenBank database content using BLAST, and deposited in GenBank under accession number MT602619-MT602626.

**Next Generation Sequencing, phylogeny and identification of contaminant DNA**
A slice of flesh from specimen MNHN JL305 was sent to the Beijing Genomics Institute (BGI) in Shenzhen, which provided DNA extraction and sequencing. Sequencing was performed on a DNBSEQ platform. A total of ca. 60 million clean paired-end reads were obtained. Reads were
assembled using SPAdes 3.14.0 (Bankevich et al. 2012) with a k-mer of 85. Contigs corresponding to the mitogenome and the nuclear ribosomal RNA genes were retrieved by customized blastn command line analyses, using already available sequences downloaded from GenBank as a custom database; ribosomal RNA genes (not used in this paper), were deposited into GenBank as MT860713 (18S) and MT860719 (partial 28S). In addition to the sequences related to *A. expatria*, other positive matches belonging to contaminant DNA were obtained as explained in the results. tRNA were identified using tRNA-scan (Lowe & Chan 2016). The mitogenome was verified using the Consed package (Gordon et al. 1998), and gene identification was performed using MITOS (Bernt et al. 2013). The genomic map was drawn using OGDRAW (Lohse et al. 2013). Amino acid sequences of the protein coding genes were concatenated following a protocol already described (Gastineau & Justine 2020; Gastineau et al. 2019; Gastineau et al. 2020), and aligned with corresponding sequences from other species using MAFFT (Katoh & Standley 2013); we used the command-line version of MAFFT, with the option “G-INS-I”. A maximum likelihood phylogeny was inferred from this alignment using RaxML version 8.0 (Stamatakis 2014) using the MtArt substitution model (Abascal et al. 2007). The best tree out of 100 was computed for 100 bootstrap replicates.

**COI trees and distances**

MEGA7 (Kumar et al. 2016) was used to evaluate distances, and construct trees. For the outgroup, we chose a sequence in GenBank from the South American species *O. nungara* Carbayo, Álvarez-Presas, Jones & Riutort, 2016 (Carbayo et al. 2016) (MN529572) which had a 100% query cover with our sequences.

**Results**

**Information obtained from citizen science and other scientists**

We obtained 14 verified records from Martinique (map in Figure 1), from 2006 to 2018, and six verified records from Guadeloupe, from 2012 to 2018 (map in Figure 2). Records were generally obtained as photographs, but we also received five specimens from Martinique and three specimens from Guadeloupe (Table 1). In addition, François Meurgey (email, 29.01.2016) added information about Guadeloupe: “*Amaga expatria* is quite common in the high series of the mesophilic forest and between 400 and 700 m altitude in the moist forest. I met it in the
131 municipalities of Baillif (St Louis river), Matouba, Trois-Rivières, and Gourbeyre. It seems more
132 frequent in the South of Basse-Terre. I have observed it attacking snails of the genera *Helicina*,
133 *Pleurodonte* and earthworms.” Laurent Charles (email, 15.05.2020) sent a photograph showing
134 predation on a snail identified as *Helicina platychila* (Megerle von Mühlfeld, 1824).

135 **Morphology and histology**

136 Live specimens mentioned in this study, measured on photographs (Figures 3-5), were 128-132
137 mm in length and 5.5-9 mm in width in extended state, and 35 × 12 mm in contracted state.

138 Description of Specimen MNHN JL146.

139 Living dimensions (Figure 3): length 128 mm, width 5.5 mm. Preserved dimensions: length 108
140 mm, width 9 mm, height 2 mm; mouth 53%; genital pore 75%.

141 The copulatory apparatus (Figure 6) is about 8 mm long from the anterior of the male system to
142 the posterior of the female system. The male system is about 5 mm long and the female system
143 about 3 mm long.

144 Two sperm ducts, about 1.2 mm apart, each with copious stored sperm (cyanophylic) approach
145 the copulatory apparatus, briefly turn anteriorly before opening separately into the ventral end of
146 a single duct (Figure 6d). This duct has a thick muscular wall and runs vertically from ventral to
dorsal for about 1080 µm (runs through 90 sections x 12 µm). At its dorsal end this duct
147 continues posteriorly as a narrow sinuous duct before broadening into the ejaculatory duct. The
148 ejaculatory duct terminates in a short penis about 800 µm long and 600 µm wide (Figure 6a,b).
149 There are atrial folds outside the penis in the common antrum.

150 The two ovovitelline ducts (Figure 6a,b) are about 2 mm apart anterior to the penis, they run
151 posteriorly and at about the level of the penis they turn dorsally to join and open into the
152 combined female duct. Copious shell glands (eosinophilic) are present and open into both
153 ovovitelline ducts before they join (Figure 6c) to form the combined female duct. The combined
154 female duct broadens, and has one or two longitudinal folds, before opening into the common
155 antrum.

156 The gonopore opens from the common antrum via a short, narrow duct.
Molecular characterization – COI

For 4 specimens, the amplified COI sequences obtained were identical along their whole length (903 bp). These specimens were JL289, JL305 (obtained both from Sanger sequencing and from the mitogenome) and JL310 from Martinique, and JL319 from Guadeloupe. This demonstrates that the same species was found in both islands. Specimen JL146 from Martinique, which was processed for histology, and three other specimens, JL216 and JL217 from Guadeloupe and JL262 from Martinique, provided shorter sequences but these were also identical between them and with the 4 sequences above for their portion in common. This demonstrates that the specimen studied for histology is from the same species, therefore confirming that the species in both islands is A. expatria. Differences with O. nungara, calculated on the 903 bp in common, were 12%.

Mitogenome

The mitogenome (Figure 7) is 14962 bp long (GenBank accession number: MT527191). It contains 12 protein coding genes, 2 ribosomal RNA genes and 22 transfer RNA genes. The mitogenome is completely colinear with that of O. nungara (KP208777) (Solà et al. 2015) and similar in size (14909 bp for O. nungara). A megablast query using the whole sequence of the mitogenome shows a global 83.77 % identity between these two species. The mitogenome is also colinear with those of Bipalium kewense, but not with those of Platydemus manokwari and Parakontikia ventrolineata. For 3 genes, atp6, cox2 and ND3, it was not possible to determine the start codon. The first methionine of the predicted proteins occurs at position 72/224 for atp6, 112/260 for cox2 and 44/112 for ND3. It is worth mentioning that the impossibility to evidence a start codon for these genes was observed with O. nungara, but not for example with B. kewense, Pl. manokwari or Pa. ventrolineata. Unlike O. nungara, however, no overlap between the ND4L and ND4 genes was evidenced.

In the tree representing a maximum likelihood phylogeny of amino acid sequences of protein coding genes, A. expatria is the sister-group of O. nungara (Figure 8).

Detection of an alien DNA

After assembly, sequences linked with contaminating DNA were identified. Three contigs of 3080 bp, 7274 bp and 15202 bp were retrieved. Megablast analyses were performed on the NCBI
The best results are listed thereafter. The 3080 bp fragment displayed a 99.66% of identity with the 18S ribosomal genes of sequences identified as the molluscs *Subulina striatella* (Rang, 1831) (MN022690), *Lissachatina fulica* (MN022692) and *Achatina fulica* (Férussac, 1821) (KU365375). The 7274 bp fragment showed a 99.97% of identity with the internal transcribed spacer 2 of a sequence identified as *Subulina octona* (Bruguière, 1789) (MF444887). The longest fragment appeared to be a nearly complete mitochondrial genome. The *cox1* gene was extracted from it, and it showed a 97.86% of identity with *S. octona* (JX988065).

**Discussion**

**New records**

*Amaga expatria* was described on the basis of two specimens from Bermuda, the holotype, collected in 1988, and a paratype, collected in 1963 (Jones & Sterrer 2005). The species has not been recorded since, but was mentioned in a book on molluscs of Martinique (Delannoye et al. 2015). These were originally identified by one of us (JLJ) and are also included in the present study. Our study has ten times more records than the original description, with 6 records from Guadeloupe and 14 records from Martinique (Table 1). This exemplifies again the power of citizen science for recording land flatworms (Justine et al. 2018b, 2019).

Maps (Figures 1-2) show that the species is widely spread in both Martinique and Guadeloupe. In Guadeloupe, most records were from Basse Terre and a single record (Sainte-Anne) was from Grande Terre, and in Martinique, most records were from the North of the island, with only one in the South, in Sainte-Luce. This suggests that the species is more abundant in, but not exclusive to, the parts of the islands with higher rainfalls (Basse Terre in Guadeloupe and the North in Martinique).

**Anatomy and morphology**

The copulatory apparatus of the Martinique specimen (Figure 6) is essentially the same as the type specimen of *A. expatria* from Bermuda (NHMUK.2002.10.16.1). The afferent male ducts have a similar structure, with two sperm ducts discharging into a ventro-dorsal duct which in turn opens into the ejaculatory duct and blunt penis via a sinuous duct. The duct wall is thickened in the same position about half way between the vertical duct and penis. We are confident of the identification of the Martinique specimen (MNHN JL146) as *A. expatria*. Given this and the
similarity of the external characteristics of the specimens from Martinique, Guadeloupe and Bermuda, we are confident that all specimens are *A. expatria*.

**Diet**

Analysis of prey DNA is an efficient method to determine the diet of land planarians (Cuevas-Caballé et al. 2019). All BLAST analyses of the contaminant DNA in a specimen of *A. expatria* identified it as belonging to the Gastropoda, and it is likely that the prey was a specimen of *Subulina octona*, or a closely related species. *Subulina octona* is a tropical terrestrial snail, with a cosmopolitan distribution; this mollusc is indeed present in Martinique where it is considered recently introduced (Anonymous 2020).

The original description of *A. expatria* included no direct observation about the diet, but Jones & Sterrer (2005), on the basis of the presence of a plicate pharynx, wrote “it is likely that earthworms are the sole or principal prey of *A. expatria*”. The observations by François Meurgey (predation on snails of the genera *Helicina, Pleurodonte* and earthworms) and Laurent Charles (predation on *Helicina platychila*) reported here, and the finding of the sequence of a terrestrial mollusc in the gut, indicate a generalist diet, including both molluscs and earthworms. This diet might be one of the reasons of the success of the species to invade various islands in the Caribbean.

**Molecular barcoding**

One specimen from Martinique was characterised for morphology, histology, and barcoding and thus represents the first attempt at a molecular characterization of the species. Specimens from Martinique and Guadeloupe provided identical sequences, therefore unequivocally demonstrating that the same species is present on both islands, and, from morphology and anatomy, is *A. expatria*. The absence of genetic divergence between our sequenced specimens suggests that the species was recently introduced into the two islands from a single population. The COI sequence closest to *A. expatria* found by BLAST was *O. nungara*, with a significant difference of 12%. This suggests that the COI sequences can be used for barcoding *A. expatria*, but this should be validated in the future by a comparative study with sequences of other species of *Amaga*, which are currently not available.
Mitochondrial genome and multigene phylogeny

In the maximum likelihood multigene phylogeny, the clade including *A. expatria* and *O. nungara* has a strong node support of 100, which is congruent with their position in the same Geoplaninae sub-family (Figure 8). It clearly discriminates them from the Bipaliinae *B. kewense*, the Caenoplaninae *Pa. ventroleata* and the Rhynchodeminae *Pl. manokwari*.

Among the features conserved between the mitogenomes of *A. expatria* and *O. nungara*, we would like to emphasize the conserved absence of canonical start codons for the three genes *atp6*, *cox2* and *ND3*. Instead, the first amino-acids evidenced from the putative proteins are always a leucine. This leucine is always coded by a TTG codon, except for *A. expatria* where it is replaced by TTA. While no such thing has been evidenced among the recently sequenced mitogenomes of *B. kewense*, *Pl. manokwari* and *Pa. ventroleata* (Gastineau & Justine 2020; Gastineau et al. 2019, 2020), similar features have also been observed among several Dugesiidae such as *Dugesia japonica* AB618487, *Dugesia ryukyuensis* AB618488 (both in Sakai & Sakaizumi 2012), *Girardia* sp. KP090061 and *Schmidtea mediterranea* NC_022448 and KM821047 (both in Ross et al. 2016). The possibility that TTG could act as an alternative start codon was already suggested by Ross et al. (2016). Based on our data, we may suggest that TTA could also be considered. Addressing properly this question might require N-terminal sequencing of these proteins.

We note that *Amaga* and *Obama* belong to the subfamily Geoplaninae, whereas *Platydemus* and *Parakontikia* are members of the Rhynchodeminae and *Bipalium* is a member of the Bipaliinae. This possible variation of the genetic code could thus be limited to a single subfamily within the Geoplanidae, the Geoplaninae.

Conclusion

Our study shows that a relatively large land flatworm species is common in two islands of the Caribbean, and, with 20 new records, adds ten times the previous number of records of the species, which were from a single location, Bermuda, an island located in the Northeast Atlantic Ocean. Jones & Sterrer (2005) hypothesized that the species originated from continental South America and was recently introduced in the Bermuda. Our genetic results show that COI sequences from Martinique and Guadeloupe were identical and thus suggest that the introduction
is recent in these islands. It remains that the locality of origin of the species in South America is still unknown. The species preys on molluscs and earthworms and might be a threat to the biodiversity of soil animals, especially molluscs which include endemic and rare species in the Caribbean islands (Delannoye et al. 2015). However, no proliferation was recorded and the threat may be minor, but it might also be that *A. expatria* is only in the first stages of invasion and that it will become an invading species in the future; similarly, recent observations have shown that the highly invasive species *Platydemus manokwari* is now invading Guadeloupe (Justine & Winsor 2020). The presence of *A. expatria* in two islands of the Caribbean suggests that it might be present in other islands, and perhaps in continental North America.

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Figure 1

*Amaga expatria*, map of records in Martinique.

The background colours indicate annual raindrop falls. Most records are from the Northern part of the island where raindrops are high, but the record in Sainte-Luce in the South is from a relatively drier part. Map by Jessica Thévenot, background provided by Météo-France and used with authorisation.
Figure 2

*Amaga expatria*, map of records in Guadeloupe.

The background colours indicate annual raindrop falls. Most records are from Basse Terre, where raindrops are high, but the record in Ste-Anne in Grande Terre is from a relatively drier part. Map by Jessica Thévenot, background provided by Météo-France and used with authorisation.
Figure 3

*Amaga expatria*, specimen MNHN JL146 from Martinique

A, living specimen, photograph by Clément Dromer; scale: the diameter of the coin is 24 mm; anterior tip is left. B, preserved specimen, photograph by Jean-Lou Justine. This specimen was used for anatomy.
Figure 4

*Amaga expatria* from Martinique, living specimens.

A, photograph by Cedric Rareg; B,C photograph by Régis Delannoye; C, scale in mm; D, photograph by Mathieu Coulis, specimen MNHN JL305. Anterior tip is left for all specimens.
Figure 5

*Amaga expatria* from Guadeloupe, living specimens in the field.

A, photograph by Pierre and Claude Guezenec (anterior tip is left); B, C, photographs by Laurent Charles, B, specimen MNHN JL216, C, MNHN JL217; the prey snail is *Helicina platychila*; D, photograph by Mathieu Coulis, specimen MNHN JL310; E-G, photographs by Guy van Laere, E,F, specimen MNHN JL319, E, dorsal side, F, showing ventral side, G, specimen with damaged posterior part.
Figure 6

*Amaga expatria*, specimen MNHN JL146 from Martinique, anatomy.

Anatomy of the copulatory apparatus, anterior to the right: A, B, respectively an HLS section and a diagrammatic reconstruction through the copulatory apparatus to the same scale; C, posterior of the female ducts showing the junction of the ovovitelline ducts; D, anterior of the male ducts showing the junction of the sperm ducts, both with copious stored sperm (cyanophylic) with the ventral end of the vertical sperm duct. Abbreviations: ed, ejaculatory duct; jod, junction of the ovovitelline ducts; jsd, junction of the sperm ducts and the vertical sperm duct; od, ovovitelline duct; p, penis; sd, sperm duct; shg, shell gland; vsd, vertical sperm duct. Scales: A, B, 2 mm; C, D, 500 µm.
Figure 7

*Amaga expatria*, map of the mitochondrial genome.

The mitogenome is 14,962 bp long and contains 12 protein coding genes, 2 ribosomal RNA genes and 22 transfer RNA genes. For 3 genes, *atp6*, *cox2* and *ND3*, it was not possible to determine the start codon.
Amaga expatria
mitochondrial genome
14,962 bp
Figure 8

Maximum likelihood tree of mitogenome proteins.

Mitogenome proteins were obtained from concatenated amino-acid sequences of all mitochondrial protein coding genes of *Amaga expatria* and other Platyhelminthes obtained using the MtArt model of evolution after 100 bootstrap replications. The tree with the best likelihood is shown (-62178.796969).
Records of *Amaga expatria* from Guadeloupe and Martinique.

The Table includes only observations based on photographs and specimens. François Meurgey provided additional findings in Guadeloupe: 10.10.2019, Goyave; 16.10.2019, Vieux-Fort; 22.06.2019, Petit Canal. * For MNHN JL305, we obtained both a COI sequence (GenBank MT602624) and the complete mitogenome (GenBank MT527191).
| Date       | Record (specimen number and/or photo) | Number of specimens | Commune          | Department | COI Sequences | Collector/Observer            |
|------------|---------------------------------------|---------------------|------------------|------------|---------------|-------------------------------|
| 28/02/2006 | photo                                 | 0                   | Case-Pilote      | Martinique | no            | Régis Delannoye               |
| 17/08/2013 | photo                                 | 0                   | Case-Pilote      | Martinique | no            | Régis Delannoye               |
| 25/11/2013 | movie                                 | 0                   | Fort de France   | Martinique | no            | Anonymous                     |
| 20/12/2013 | photo                                 | 0                   | Le Lamentin      | Martinique | no            | Pierre Damien Lucas           |
| 06/05/2014 | MNHN JL146 + photo                    | 1                   | Le Gros Morne    | Martinique | MT602619      | Clément Dromer                |
| 21/03/2015 | photo                                 | 0                   | La Trinité       | Martinique | no            | Régis Delannoye               |
| 05/08/2015 | MNHN JL262                            | 1                   | La Trinité       | Martinique | MT602622      | Olivier Palcy                 |
| 17/10/2015 | photo                                 | 0                   | Le Gros Morne    | Martinique | no            | Pierre Damien Lucas           |
| 12/11/2015 | MNHN JL305                            | 1                   | Le Morne Vert    | Martinique | MT602624 *    | Mathieu Coulis                |
| 13/11/2015 | photo                                 | 0                   | Ducs             | Martinique | no            | Cédric Rareg                  |
| 04/02/2016 | MNHN JL289                            | 1                   | Le Marigot       | Martinique | MT602623      | Régis Delannoye               |
| 18/06/2017 | MNHN JL310 + photo                    | 1                   | Le Lamentin      | Martinique | MT602625      | Mathieu Coulis                |
| 22/06/2017 | photo                                 | 0                   | Fort de France   | Martinique | no            | Marcel Bourgade               |
| 27/01/2018 | photo                                 | 0                   | Sainte-Luce      | Martinique | no            | Stéphane Bras                 |
| 12/02/2019 | photo                                 | 0                   | La Trinité       | Martinique | no            | Régis Delannoye               |
| 20/12/2012 | photo                                 | 0                   | Trois Rivières   | Guadeloupe | no            | Guy van Laere                 |
| 06/12/2014 | MNHN JL216 + photo                    | 1                   | Gourbeyre        | Guadeloupe | MT602620      | Laurent Charles               |
| 12/12/2014 | MNHN JL217 + photo                    | 1                   | Bouillante       | Guadeloupe | MT602621      | Laurent Charles               |
| 21/01/2016 | photo                                 | 0                   | Baillif          | Guadeloupe | no            | Pierre et Claudine Guezennecc |
| 20/12/2017 | MNHN JL319 + photo                    | 1                   | Trois Rivières   | Guadeloupe | MT602626      | Guy van Laere                 |
| 06/08/2018 | photo                                 | 0                   | Sainte-Anne      | Guadeloupe | no            | Jean-Christian Rotger         |