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Evaluation of short mitochondrial metabarcodes for the identification of Amazonian mammals

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Summary

1. DNA barcoding and metabarcoding are increasingly used as alternatives to traditional morphological identifications. For animals, the standard barcode is a c. 658-bp portion of the COI gene, for which reference libraries now cover a large proportion of described mammal species. Unfortunately, because its sequence is too long and does not contain highly conserved primer binding sites, this marker is not adapted for metabarcoding. Although alternative metabarcodes have been developed, their performances are generally seldom assessed.

2. We evaluate the reliability of a short metabarcode located in the mitochondrial 12S ribosomal RNA for the identifications of Amazonian mammals. We (i) constitute a nearly exhaustive reference library for species found in French Guiana, (ii) assess the taxonomic resolution of the marker and validate its use with dipteran blood meal analyses, (iii) assess the conservation of the primer binding sites, and (iv) compare its theoretical performances with that of a newly designed metabarcode located within the standard COI barcode.

3. About 576 specimens representing 164 species were gathered and sequenced. We show that the 12S marker allows remarkably accurate taxonomic assignations despite its very short size, and that primer binding sites are highly conserved, which is important to avoid PCR amplification bias potentially leading to detection failure. Additionally, our results stress that the identifications should only be considered at the generic level when they are based on incomplete reference libraries, even when a stringent similarity cut-off is used. A new short COI metabarcode was designed based on 569 reference sequences of mammals retrieved on BOLD. Our results clearly show that, while both markers provide similar taxonomic resolution, much higher rates of primer mismatches are found with COI.

4. Besides demonstrating the accuracy of the short 12S marker for the identification of Amazonian mammals and providing a reliable molecular reference database, this study emphasizes that the accuracy of taxonomic assignations highly depends on the comprehensiveness of the reference library and that great caution should be taken for interpreting metabarcoding results based on scarce reference libraries. The comparison with a short COI metabarcode also provides novel evidence in support for the use of ribosomal markers in metabarcoding studies.

Key-words: blood meals, COI, French Guiana, mitochondrial 12S rRNA gene, sand fly

Introduction

The accurate identification of species is an essential component in most of the empirical ecological studies. Traditional methods based on morphological features are time consuming and often rely on taxonomic expertise that is increasingly lacking. In addition, morphological identifications may require whole specimens, which can be particularly difficult to obtain for mammals because of the practical, ethical, or legal reasons. DNA-based identification methods have been increasingly used as an efficient alternative over the last decades. Today, one of the most used techniques is DNA barcoding (Hebert et al. 2003), which uses the sequence from a short standard fragment of the genome for the taxonomic assignment of a specimen. More recently, high-throughput sequencing has allowed the extension of DNA barcoding for the identification of multiple species in a single sample (Taberlet et al. 2012). This approach, referred to as metabarcoding, allows the simultaneous identifications of multiple specimens from a single bulk-DNA extraction (Yu et al. 2012; Kocher et al. 2016). In addition, it has the great advantage to be applicable on degraded DNA present in the environment such as soil.
bases, it was shown to gather good properties for

mitochondrial 12S ribosomal RNA gene (12S rRNA) (Riaz et al. 2011; Catzeflis 2015). This may not be a problem for barcoding single specimens, because a few primer-template mismatches will not impede PCR amplification. On the contrary, small variations in the number and position of primer-template mismatches can lead to significant amplification bias or even detection failure when mixtures of DNA are amplified for metabarcoding (Bru, Martin-Laurent & Philippot 2008; Taberlet et al. 2012). To find suitable metabarcodes and their associated primers, specific softwares have been developed [notably ‘ECOPRIMERS’, (Riaz et al. 2011)], that seek to minimize amplification bias while maximizing the divergence between taxa. Most animal metabarcoding markers developed using this approach are located within the mitochondrial ribosomal RNA genes (Riaz et al. 2011; Clarke et al. 2014; Deagle et al. 2014). Indeed, because of the secondary structure of their RNA products, these genes exhibit a mosaic pattern of variation with highly conserved regions (within stems) in which primers can be designed, adjacent to variable regions (within loops) that allow interspecific discrimination. The existence of a standard marker for DNA barcoding has allowed the constitution of a collaborative and taxonomically comprehensive reference library. On the contrary, there is no real consensus on the choice of metabarcoding markers (except for bacteria and fungi), leading to scarce reference libraries (Pompanon & Samadi 2015).

The prerequisites of these methods are the choice of appropriate DNA markers, the design of corresponding PCR primers and the constitution of reliable reference sequences libraries. For DNA barcoding, the Consortium for the Barcode of Life (CBOL, http://www.barcodeoflife.org/) handled these issues, by providing standardized laboratory protocols and curated reference libraries linked to voucher specimens. For animals, the current standard barcode is a c. 658-bp portion of the mitochondrial cytochrome oxidase 1 subunit (COI), and the Barcode of Life Database comprises reference sequences for more than 174 000 animal species to date (BOLD, http://www.boldsystems.org/, accessed in September 2016). Unfortunately, this marker is not the best choice when it comes to metabarcoding (Deagle et al. 2014). First, the fragment is too long concerning the limitations of the current sequencing platforms (typically an Illumina Miseq; Illumina, Inc., San Diego, CA, USA). This can be regarded as a rather technical issue that might be overcome in a near future with the rapid improvement of the sequencing technologies. However, the size of the targeted fragment is also critical when dealing with degraded DNA, as typically found in the environment or in biological samples such as faeces or gut content. Second, it is virtually impossible to find perfectly conserved primer binding sites within this coding gene because of high mutation rate at the third codon position (Deagle et al. 2014). This may not be a problem for barcoding single specimens, because a few primer-template mismatches will not impede PCR amplification. On the contrary, small variations in the number and position of primer-template mismatches can lead to significant amplification bias or even detection failure when mixtures of DNA are amplified for metabarcoding (Bru, Martin-Laurent & Philippot 2008; Taberlet et al. 2012). To find suitable metabarcodes and their associated primers, specific softwares have been developed [notably ‘ECOPRIMERS’, (Riaz et al. 2011)], that seek to minimize amplification bias while maximizing the divergence between taxa. Most animal metabarcoding markers developed using this approach are located within the mitochondrial ribosomal RNA genes (Riaz et al. 2011; Clarke et al. 2014; Deagle et al. 2014). Indeed, because of the secondary structure of their RNA products, these genes exhibit a mosaic pattern of variation with highly conserved regions (within stems) in which primers can be designed, adjacent to variable regions (within loops) that allow interspecific discrimination. The existence of a standard marker for DNA barcoding has allowed the constitution of a collaborative and taxonomically comprehensive reference library. On the contrary, there is no real consensus on the choice of metabarcoding markers (except for bacteria and fungi), leading to scarce reference libraries (Pompanon & Samadi 2015).

The 12S-V5 marker is a c. 100 base pairs (bp) portion of the mitochondrial 12S ribosomal RNA gene (12S rRNA) (Riaz et al. 2011). Based on the sequences available in public databases, it was shown to gather good properties for metabarcoding of vertebrates. However, a comprehensive taxonomic sampling is necessary to precisely assess the taxonomic resolution of a DNA marker (Meyer & Paulay 2005). In this study, we assess the reliability of the 12S-V5 markers for metabarcoding of Amazonian mammals. We (i) constitute a nearly exhaustive reference library for the species found in French Guiana, (ii) assess the variability at the 12S-V5 primer binding sites, (iii) evaluate the taxonomic resolution of the marker and further validate its use with dipteran blood meal analyses, and (iv) compare its theoretical performances with that of a newly designed metabarcode located within the classical COI barcode.

Materials and methods

SAMPLING

French Guiana and its >90% of well-preserved Amazonian rainforest cover has been the study site of intense ecological and taxonomic research (see for instance the research undertaken under the frame of the labex CEBa; http://www.labex-ceba.fr/en/). The mammalian fauna of French Guiana is well characterized, and is representative of a larger part of the northern Amazon region (Lim 2012; Catzeflis 2015). Our aim was to generate a first comprehensive DNA library for the mammals of French Guiana that can be used directly for metabarcoding studies in this region, and that may be further completed for studies in other Amazonian locations. Tissue samples of mammals from French Guiana were gathered from field sampling, museum collections, hunting or road-killed specimens, and biopsies of captured animals (see Supporting Information for details). The taxonomic identifications were based on external and/or craniodental morphology, and confirmed by COI barcoding for the vast majority of the specimens [following classical procedures (Borisenko et al. 2008) and the primers C_VF1di/C_VR1LRt1 or LCO1490/HCO2198 recommended by the Barcode of Life Project (www.boldsystems.org)].

REFERENCE LIBRARY

Our aim was to build a reference sequence library based on a marker that was previously developed for the identifications of vertebrates through metabarcoding (12S-V5, Riaz et al. 2011). The constitution of reference libraries with the previously designed PCR primers leads to the loss of all the information concerning the primer binding sites. This impedes the possibility to further improve the primers for specific purposes and to predict potential amplification bias (Bru, Martin-Laurent & Philippot 2008). To overcome this issue, we designed a set of primers to amplify a region that contains the complete 12S-V5 fragment including primer binding sites (see Fig. 1). We used blastn 2.2.29+ (Camacho et al. 2009) on Genbank (release 197) with the query being a c. 700 bp portion of Rattus rattus 12S rRNA (GenBank accession: NC_012374.1) containing the fragment amplified by the 12S-V5 primers and 300 bp flanking each end. We selected all the matching sequences of mammals presenting at least 95% query coverage and kept one sequence per species. The resulting database contained sequences for 1557 mammal species representing 26 orders and was used to design new primers with the ecoprimers program (Riaz et al. 2011). These primers (Mam12S-340-F, 5′-CCACCGCCTATATGATT-3′; Mam12S-340-R, 5′-GATGGCGGTATATAGACTG-3′) had a maximum of two mismatches with 98.4% of the species represented in the database. They amplify a fragment of 302–350 bp that contains the full
DNA AMPLIFICATION AND SEQUENCING

DNA was extracted using the DNeasy Blood and Tissue kit (Qiagen, Valencia, CA, USA). PCR amplification was performed in 25 μL mixtures containing 2 μL of DNA template, 0.2 μL of AmpliTaq Gold® (5 U μL⁻¹, Applied Biosystems, Foster City, CA, USA), 2.5 μL 10X PCR buffer (provided with AmpliTaq Gold®, Applied Biosystems), 0.5 μL dNTPs (2.5 mM each, Promega, Madison, WI, USA), 1 μL of each primer (10 μM), 0.25 bovine serum albumin (10 mg mL⁻¹, Promega), 2.5 μL MgCl₂ (25 mM, Applied Biosystems) and nuclease-free water (Promega). The PCR mixture was denatured at 95°C (10 min) and followed by 35 cycles of 30 s at 95°C, 30 s at 50°C and 30 s at 72°C, completed at 72°C (10 min). Tags of eight base pairs with at least five differences between them were added at the 5’ end of each primer to enable the sequencing of the multiple PCR products in a single sequencing run (Binladen et al. 2007).

PCR products were pooled and sent for library construction and sequencing to the GeT-PlaGe core facilities of Genotoul (Toulouse, France). Samples were diluted in ultrapure water. A volume of 130 μL containing 3 μg of DNA was purified using the HighPrep PCR system (Magbio Genomics, Gaithersburg, MD, USA) and used for library construction with the Illumina NEXTflex PCR-Free DNA sequencing kit following the instructions of the supplier (Bioo Scientific corp., Austin, TX, USA). Purified fragments were end-repaired, A-tailed and ligated to sequencing indexed adapters. The quality of the library was controlled using the Fragment Analyzer. The PCR mixture was denatured at 95°C (10 min) and followed by 35 cycles of 30 s at 95°C, 30 s at 50°C and 30 s at 72°C, completed at 72°C (10 min). Tags of eight base pairs with at least five differences between them were added at the 5’ end of each primer to enable the sequencing of the multiple PCR products in a single sequencing run (Binladen et al. 2007).

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BIOMETRICS

Sequence reads were analysed using the OBITOOLS package (Boyer et al. 2016). Pair-end reads were aligned and merged, taking into account the Phred quality scores for consensus construction and alignment score computation. The reads were then assigned to their corresponding sample based on the tagged primer sequences with two mismatches allowed. Low quality reads (alignment scores <50, containing Ns or shorter than 50 bp) were removed. Reads were then dereplicated while keeping the coverage information (number of reads merged). For each sample, the majority sequence was considered as the genuine most abundant sequence in the specimen and kept for the reference library. The script used for these bioinformatic steps are available in the Supporting Information. The library was further completed by 12S rRNA sequences extracted from complete mitogenomes of Xenarthra (Gibb et al. 2016) and Chiroptera (F. Botero-Castro, unpublished data).

METABARCODE EVALUATION

Primer-template mismatches were checked by mapping the 12S-V5 primers on the resulting sequences (see Fig. 1; 12S-V5-F: TAGAA CAGGCTCCTCTTAG; 12S-V5-R: TTAGATACCCCACCATAGGC), using Geneious 6.0.6 Pro (Biomatters, Auckland, New Zealand). The region corresponding to the 12S-V5 metabarcoding was then extracted from each sequence for the following analyses.

Most studies that validate the reliability of DNA barcoding for molecular identifications provide statistics based on K2P genetic distances (Kimura 1980) computed from a multiple sequence alignment of the reference sequences. Uncorrected distances have been judged more appropriate for studying the success of distance-based identification techniques (Srivathsan & Meier 2012). In this study, we used genetic distances as they are computed by the ecotag program (included in the obitools) for taxonomic assignments (uncorrected distances based on pairwise alignments of the sequences) to generate a neighbour-joining tree using the R package ‘ape’ (Saitou & Nei 1987; Paradis, Claude & Strimmer 2004; Team 2014) and to compute distance statistics using the R package ‘spider’ (Brown et al. 2012).

To assess the reliability of the metabarcode for species identification, we performed the taxonomic assignment of each specimen using the ecotag program with all other sequences as reference library. Resulting assignations were then compared with the genuine identities of the specimens. ecotag first searches for the reference sequence(s) showing the highest similarity with the query sequence (primary reference sequence(s); see Fig. 2). Then it looks for all other reference sequences whose similarity with the primary reference sequence(s) is equal or higher than the similarity between the primary reference sequence(s) and the query sequence (secondary reference sequence(s)). Finally, it assigns the query sequence to the most recent common ancestor of the primary and secondary reference sequences. This procedure is similar in essence to the lowest common ancestor algorithms.

![Fig. 1.](image-url)
implemented in the MG-RAST server (Meyer et al. 2008) and the MEGAN program (Huson et al. 2007) for the assignment of metagenomic reads. It allows to deal with ambiguous identifications, which can arise because several taxa are poorly distinguishable, or that the DNA library does not contain a close reference for the query. Taxonomic assignments were discarded if the closest match exhibited less than 97% similarity. To assess the effect of potential taxonomic gaps in the reference database, we then tested the taxonomic assignations of each sequence after removing all conspecifics. To further validate the applicability of the 12S-V5 marker for mammal species identification in field studies, we analysed blood meals of hematophagous dipteran collected in forest sites in French Guiana (sand flies and mosquitoes, see Supporting Information for details on sampling and laboratory protocols). Indeed, metabarcodes provide good properties (small size and wide taxonomic coverage) for such application, because arthropod blood meals may contain low quantities of degraded DNA from a diverse array of vertebrate species.

**Comparison with COI**

Currently, COI is rarely used for metabarcoding because of previously explained reasons (see Introduction). In particular, no satisfying COI metabarcode has been developed for mammals. Therefore, to allow relevant comparison, we designed new PCR primers to amplify a short fragment located within the classical COI barcode. All the sequences of mammal species found in French Guiana were retrieved from BOLD, and a maximum of five sequences per species were kept. PCR primers were designed using ECOPRIMERS in the same way it was done for the 12S-V5 primers (i.e. 18-bp long, to amplify a fragment of c. 100 bp, and to maximize taxonomic coverage and resolution). The selected primers were compared with their target sites on the reference sequences to compute mismatch statistics. The theoretical amplified fragment was then extracted from references sequences to evaluate its taxonomic resolution in the same way it has been done for the 12S-V5 marker.

**Results**

**Reference Library**

Sequences were obtained for 576 specimens representing 164 species, including *Uroderma* cf. *magnirostrum* (although *U. magnirostrum* has not been officially reported in French Guiana, and no voucher specimen is available, it is not unlikely that this taxon occurs and the samples used in this study have been identified as *U. magnirostrum* using classical COI barcoding). Hence, 82.7% [163/197; (Catzeflis 2015)] of the mammal species recorded in French Guiana were included in the database, whereas 116 over 126 genera and all the 32 families were represented. All the sequences were deposited on Genbank (accessions: KX381203–KX381784). On average, 3.5 specimens per species were sequenced with 118 species (72%) being represented by at least 3 specimens and 28 (17%) represented by only one. The sequence length of the Mam12S-340 fragment ranged from 334 to 345 bp whereas the length of the 12S-V5 fragment ranged from 96 to 103 bp.

**Metabarcode Evaluation**

The inspection of the 12S-V5 primer binding sites revealed that the forward primer could be slightly improved by degenerating the 5’ end (12S-V5-F’: YAGAACAGGCTCCTCTAG). 95.0, 2.8 and 2.2% of the sequences had respectively 0, 1, and 2 mismatches.

Fig. 2. Schematization of a taxonomic assignation as performed by ECOTAG: (i) search of the reference sequences (R1s) that have the highest similarity with the query sequence (Q), (ii) search for all other reference sequences (R2s) whose similarity with the primary reference sequences is equal or higher than the similarity between the primary reference sequences and the query sequences, (iii) assignment of the query sequence to the most recent clade containing all R1s and R2s.

Fig. 3. Distribution of genetic distance at various taxonomic resolutions. Only the distances between specimens belonging to (i) the same taxon at a given rank and to (ii) distinct taxa at the inferior rank are considered.
mismatches with the forward primer (mean number of mismatches = 0.072; degenerated version), whereas 97.6 and 2.4% had respectively 0 and 1 mismatch with the reverse primers (mean number of mismatches = 0.024). No sequence had mismatches with both primers. No sequence had mismatch towards the 3' end on the forward primer (within the first eight positions). One mismatch was found at the second position from the 3' end of the reverse primer in *Tonatia saurophila* and *Rhynophylla pumilio*, which may hamper amplification for these species.

In the 12S-V5 metabarcode, 34.3% of sites were identical in all sequences and the mean pairwise identity was of 80.2%. The distribution of genetic distances at the specific, generic, familial and ordinal levels shows significant overlap between each consecutive taxonomic rank (Fig. 3). In particular, intraspecific distances range from 0.0 to 5.1% for a mean of 0.5%, while interspecific distances within the same genus range from 0.0 to 19.6% for a mean of 3.5%. The neighbour-joining tree is shown in Fig. 4. Some closely related species were poorly or not distinguishable based on the marker, mostly in Chiroptera and in Felidae: *Pteronotus rubiginosus* and *Pteronotus* cf. sp. 3, *Molossus molossus* and *Molossus rufus*, *Carollia breviceps* and *Carollia perspicillata*, *Eptesicus furinalis* and *Eptesicus chiriquinus*, *Artibeus planirostris* and *Dermatonycteris yucatanica*, *Oecomys rex* and *Oecomys sp.* 1, *Puma concolor* and *Puma yagouaroundi* and *Leopardus wiedii* and *Leopardus pardalis*.

When considering the species represented by more than one specimen (548 sequences), 90.0 and 9.5% of the assinations were made at the species and genus level, respectively (Table 1). 99.6% of these assignments were correct. Only two errors were found: a sequence of *L. wiedii* was assigned to *L. pardalis* and a sequence of *D. gnomus* was assigned to the genus *Artibeus*. Most of the assignments made at the genus level were found in Chiroptera (genera *Carollia*, *Eptesicus*, *Molossus*, and *Pteronotus*). Three sequences (two *Glyphonycteris sylvestris* and one *Makalata didelphoides*) were not identified because of the absence of a close match in the reference database (>97% similarity). When all conspecifics were removed from the references before taxonomic assignment, 65.2% of the sequences.

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**Fig. 4.** Neighbour-joining tree based on raw distances computed from pairwise alignments of the 12S-V5 metabarcode. Numbers in brackets indicate the number of specimens sequenced per species. Species names are coloured by order.
were not identified because they did not find a close match, as it was expected. However, 23.6% of the sequences were falsely assigned at the specific level. 10.5% of the sequences were assigned at the generic rank with an error rate of 41%, corresponding to confusion between the genera *Artibeus* and *Dermatophagoides, Didelphimorphia*, *Pig* and *Panthera*. Finally, four sequences were assigned at the family level, all correctly. The overall proportion of the specimens that were wrongly identified was 10%. If identifications made at the specific level were only considered at the generic level, respectively, 7% of sequences would have been assigned at the specific and generic level, respectively while, 7.6% would have remained unidentified (i.e., 1%). With an incomplete reference database, 10% of the sequences would have been wrongly identified at the specific level, while the all others would have remained unidentified (i.e. an overall error rate of 10%).

### Discussion

By enabling the identification of species from degraded DNA contained in environmental samples, DNA metabarcoding has opened great avenues for the study of vertebrates’ communities. It has already been proved successful in various applications such as the characterization of the present or ancient terrestrial fauna from the soil (Andersen et al. 2012; Giguet-Covex et al. 2014), aquatic communities from water (Valentini et al. 2016) or feeding behaviours from faeces (De Barba et al. 2014). Because the standard COI barcode is not adapted for the development of other markers.

First, we show that the 12S-V5 primer binding sites are extremely conserved among the mammal species included in our database. Second, we show that the marker allows reliable and precise identifications of mammals, which was further highlighted by the successful analysis of dipteran blood meals. Using a similarity cut-off of 97%, almost all specimens could be correctly identified and more than 90% of these identifications were made at the specific level, while the others were made at the generic level. Only two sequences were assigned to a wrong taxon (false-positive errors), while three specimens were not identified because their closest match did not reach the similarity cut-off (false-negative errors). This level of accuracy is remarkable regarding that the marker is only 100 bp long and can be amplified with the same PCR primers virtually in all vertebrates (Riaz et al. 2011). Our results emphasize that the quality of taxonomic assignments is largely dependent on the comprehensiveness of the reference database. Indeed, when all conspecific sequences were removed prior to taxonomic assignments, almost 30% of the specimens were assigned to a wrong taxon. This error rate is largely dependent on the choice of the similarity cut-off. A more stringent (higher) cut-off would have resulted in a lower false-positive error rate, but also in a higher false-negative error rate. The wide overlap observed between intraspecific and interspecific genetic distances, and thus, the absence of a clear barcoding gap precludes the existence of a perfect similarity cut-off. The choice of an optimum was not in the scope of this work. However, we have shown that bringing the taxonomic assignments to the generic rank restores the reliability of the identifications when the species of the query is not represented in the reference library. Therefore, besides using a stringent similarity threshold, we recommend to consider taxonomic assignments only at the generic level when using the 12S-V5 metabarcode with an incomplete reference library. The importance of the comprehensiveness of reference libraries to avoid erroneous identifications and the difficulty to define similarity cut-off because of the overlapping intra and interspecific genetic distances has already been highlighted for classical COI barcoding (Meyer et al. 2008; Puillandre et al. 2009). This should be even more significant for shorter and less discriminant metabarcodes. Numerous studies provide thoroughly sampled COI reference libraries together with an evaluation of barcoding in specific animal groups. On the contrary, DNA metabarcoding studies usually rely on public databases, and the current literature mainly focuses on biomolecular and bioinformatic issues, such as the management of PCR and sequencing artefacts, rather than providing the evaluation of metabarcodes accuracy based on comprehensive reference libraries. This is understandable because metabarcodes frequently target very wide taxonomic ranges or taxa in which a large proportion of species are unknown. In addition, there exists no real standard for metabarcoding markers (at the exception of bacteria and fungi), which impedes the creation of a single collaborative and well-curated reference database as the BOLD for barcoding (Pompanon & Samadi 2015). Nevertheless, we argue that these limitations should be considered seriously when interpreting metabarcoding results.

Finally, we compared the theoretical performances of the 12S-V5 marker with that of a newly designed COI metabarcode. The COI reference database retrieved on BOLD contained similar number of sequences and taxonomic coverage than the 12S reference database constituted in this study, which allowed relevant comparisons. The COI_minimam was selected using the same procedure than for the 12S-V5 marker. However, it is noteworthy that 12S-V5 primers were designed to amplify DNA of all vertebrates, whereas the COI_minimam was specifically directed to Amazonian mammals, which represent a rather conservative approach for our comparison. We show that while both metabarcodes provide comparable taxonomic resolution, the COI_minimam primers present high rates of primer binding site mismatches (Fig. 5), constituting a serious disadvantage for metabarcoding studies.

Besides providing reliable and comprehensive molecular data for the identification of mammals in French Guiana and more largely for the northern Amazon region, our study emphasizes that great caution should be taken concerning metabarcoding results based on scarce reference libraries and that molecular identifications should be trusted only using a stringent similarity threshold and at appropriate taxonomic ranks. Our results also provide novel evidence in support for the use of ribosomal markers in metabarcoding studies.

Authors’ contributions

J.M., AL.B. and A.K. designed the study. B.d.T. and F.C. provided the samples. A.K., M.H., B.d.T. and S.V. performed the laboratory work. A.K. analysed the data. A.K. prepared the manuscript and all authors contributed in its improvement.

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Data accessibility

All sequences were deposited in GenBank (accessions: KX381203-KX381784).

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